

PF59082SeqList_PF59082.txt
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<141> 2008 05 19
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<170> PatentIn version 3.3 and Biomax PatentTool
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PF59082SeqList_PF59082.txt

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 Seite 22

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PF59082SeqList_PF59082.txt

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Ser Asp Tyr Lys Gly Arg Pro Ala Glu Arg Ser Lys Thr Gly Gly Trp
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Thr Ala Ser Ala Met Ile Leu Gly Gly Glu Val Met Glu Arg Leu Thr
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gac	ggg	cgc	gac	ccg	cgg	gag	gag	cgc	gcc	atg	gtg	ttc	ttc	ttc	aac	752
Asp	Gly	Arg	Asp	Pro	Arg	Glu	Glu	Arg	Ala	Met	Val	Phe	Phe	Phe	Asn	
			185					190					195			
cgc	ttc	tac	ttc	tgc	gtc	agc	ctg	ggg	tcg	ctg	ttc	gcg	gtc	acc	gtg	800
Arg	Phe	Tyr	Phe	Cys	Val	Ser	Leu	Gly	Ser	Leu	Phe	Ala	Val	Thr	Val	
		200					205					210				
ctg	gtg	tac	gtg	cag	gac	aac	gtg	ggg	cgg	ggc	tgg	ggc	tac	ggc	gtg	848
Leu	Val	Tyr	Val	Gln	Asp	Asn	Val	Gly	Arg	Gly	Trp	Gly	Tyr	Gly	Val	
	215				220						225					
tcc	gca	gtc	ggc	atg	gcg	ctc	gcc	gtc	gcc	gtg	ctc	gtg	ggc	ggc	acg	896
Ser	Ala	Val	Ala	Met	Ala	Leu	Ala	Val	Ala	Val	Leu	Val	Ala	Gly	Thr	
	230				235				240						245	
ccc	cgg	tac	agg	tac	cgc	ccg	cag	ggc	agc	ccg	ctg	acg	gcg	gtc	Val	944
Pro	Arg	Tyr	Arg	Tyr	Arg	Arg	Pro	Gln	Gly	Ser	Pro	Leu	Thr	Ala	Val	
				250				255						260		
ggc	cgg	gtg	ctc	ggc	gcg	gcg	tgg	agg	aag	cgc	cgg	ctg	ccg	ctg	ccc	992
Gly	Arg	Val	Leu	Ala	Ala	Ala	Trp	Arg	Lys	Arg	Arg	Leu	Pro	Leu	Pro	
			265					270					275			
gcc	gac	ggc	ggc	gag	ctc	cac	ggg	ttc	gcc	gcg	gcc	aag	gtc	ggc	cac	1040
Ala	Asp	Ala	Ala	Glu	Leu	His	Gly	Phe	Ala	Ala	Ala	Lys	Val	Ala	His	
		280					285					290				
act	gac	agg	ctc	agg	tgg	ctt	gac	aag	gcc	gcg	atc	gtg	gag	ggc	gag	1088
Thr	Asp	Arg	Leu	Arg	Trp	Leu	Asp	Lys	Ala	Ala	Ile	Val	Glu	Ala	Glu	
	295					300					305					
ctg	gcg	ggg	aag	cag	cgg	gcg	agc	gcg	gcg	gca	gcg	tcg	acg	gtg	acg	1136
Leu	Ala	Gly	Lys	Gln	Arg	Ala	Ser	Ala	Ala	Ala	Ala	Ser	Thr	Val	Thr	
	310				315					320					325	
gag	gtc	gag	gag	gtg	aag	atg	gtg	gcg	aag	ctg	ctg	ccc	atc	tgg	ttc	1184
Glu	Val	Glu	Glu	Val	Lys	Met	Val	Ala	Lys	Leu	Leu	Pro	Ile	Trp	Phe	
				330					335					340		
acg	tgc	atc	ctc	ttc	tgg	acg	gtc	tac	tcc	cag	atg	acc	acc	ttc	tcg	1232
Thr	Cys	Ile	Leu	Phe	Trp	Thr	Val	Tyr	Ser	Gln	Met	Thr	Thr	Phe	Ser	
			345					350					355			
gtg	gag	cag	ggc	acg	cgc	atg	gac	cgc	cac	ctc	cgc	ccg	ggc	tcc	ggc	1280
Val	Glu	Gln	Ala	Thr	Arg	Met	Asp	Arg	His	Leu	Arg	Pro	Gly	Ser	Gly	
		360					365					370				
gcc	ggc	ggc	ggc	ggc	ttc	ggc	gtc	ccg	gcc	ggc	ttc	ttc	ttc	gtc	ttc	1328
Ala	Gly	Ala	Gly	Gly	Phe	Ala	Val	Pro	Ala	Gly	Ser	Phe	Ser	Val	Phe	
	375					380					385					
cta	ttc	ctc	tcc	atc	ctg	ctc	ttc	acc	tcg	ctc	aac	gag	cgc	ctc	ctc	1376
Leu	Phe	Leu	Ser	Ile	Leu	Leu	Phe	Thr	Ser	Leu	Asn	Glu	Arg	Leu	Leu	
	390				395					400					405	

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Val	Pro	Leu	Ala	Ala	Arg	Leu	Thr	Gly	Arg	Pro	Gln	Gly	Leu	Thr	Ser	
			410					415						420		
ctg	cag	cg	gtc	ggg	gcc	ggg	ctc	gcg	ctc	tcc	gtc	gcc	gcc	atg	gcc	1472
Leu	Gln	Arg	Val	Gly	Ala	Gly	Leu	Ala	Leu	Ser	Val	Ala	Ala	Met	Ala	
			425					430						435		
gtc	tcc	gcg	ctc	gta	gag	agg	aag	cgg	cg	gac	gcg	gcc	aac	ggg	ccg	1520
Val	Ser	Ala	Leu	Val	Glu	Arg	Lys	Arg	Arg	Asp	Ala	Ala	Asn	Gly	Pro	
			440					445						450		
gac	cac	gtc	gcc	gtc	agc	gcc	ttc	tgg	ctc	gtc	ccg	cag	tac	ttc	ctc	1568
Asp	His	Val	Ala	Val	Ser	Ala	Phe	Trp	Leu	Val	Pro	Gln	Tyr	Phe	Leu	
			455					460						465		
gtc	ggc	gcc	ggc	gag	gcc	ttc	gcc	tac	gtg	ggc	cag	ctg	gag	ttc	ttc	1616
Val	Gly	Ala	Gly	Glu	Ala	Phe	Ala	Tyr	Val	Gly	Gln	Leu	Glu	Phe	Phe	
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atc	cg	gag	gcg	ccc	gag	cg	atg	aag	tcc	atg	agc	acc	ggc	ctc	ttc	1664
Ile	Arg	Glu	Ala	Pro	Glu	Arg	Met	Lys	Ser	Met	Ser	Thr	Gly	Leu	Phe	
			490					495						500		
ctc	gtc	acg	ctc	tcc	atg	ggc	ttc	ttc	ctc	agc	agc	ttc	ctc	gtc	ttc	1712
Leu	Val	Thr	Leu	Ser	Met	Gly	Phe	Phe	Leu	Ser	Ser	Phe	Leu	Val	Phe	
			505					510						515		
gcc	gtc	gac	gcc	gcc	acc	gcg	ggc	gcg	tgg	atc	cgg	aac	aac	ctc	gac	1760
Ala	Val	Asp	Ala	Ala	Thr	Ala	Gly	Ala	Trp	Ile	Arg	Asn	Asn	Leu	Asp	
			520					525						530		
cg	ggc	agg	ctc	gac	ctc	ttc	tac	tgg	atg	ctg	gcc	ctg	ctc	ggc	gtc	1808
Arg	Gly	Arg	Leu	Asp	Leu	Phe	Tyr	Trp	Met	Leu	Ala	Leu	Leu	Gly	Val	
			535					540						545		
gcc	aac	ttc	gcc	gtc	ttc	gtc	gtc	ttc	gcc	agg	cgg	cac	cag	tac	aag	1856
Ala	Asn	Phe	Ala	Val	Phe	Val	Val	Phe	Ala	Arg	Arg	His	Gln	Tyr	Lys	
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gcc	acc	agc	ttg	ccg	gcg	tcg	gtg	gcg	ccc	gac	ggc	acc	ggg	cac	aag	1904
Ala	Thr	Ser	Leu	Pro	Ala	Ser	Val	Ala	Pro	Asp	Gly	Thr	Gly	His	Lys	
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gag	atg	gac	gac	ttc	gtc	gca	gtc	acg	gag	gcc	gtg	gaa	gga	gtg	gac	1952
Glu	Met	Asp	Asp	Phe	Val	Ala	Val	Thr	Glu	Ala	Val	Glu	Gly	Val	Asp	
			585					590						595		
gtg	tagggcgcgc	atgtcaggct	cacacttcat	cggtgggtgg	cctctgctgt											2005
Val																
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tccagtttgc	tgctacttcg	gcctgctctc	ctgtaaataa	cataggagac	atgctaattg											2125
aggccaagtc	tttatccagt	tagatcaaca	agatattgaa	ttgggcatga	aggctgaaca											2185
ccatgtgtgt	gcattacagt	acccaaccca	aactctaaca	tagcatcggt	ataatggctg											2245
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 Val Cys Val Met Gly Ile Ser Met Asn Leu Val Thr Tyr Leu Val Gly
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Met	Gly	Thr	Leu	Asn 85	Leu	Leu	Ala	Leu	Val 90	Gly	Gly	Phe	Leu	Ala 95	Asp
Ala	Lys	Leu	Gly 100	Arg	Tyr	Leu	Thr	Ile 105	Ala	Ile	Ser	Ala	Thr 110	Ile	Ala
Ala	Thr	Gly 115	Val	Ser	Leu	Leu	Thr 120	Val	Asp	Thr	Thr	Val 125	Pro	Ser	Met
Arg	Pro 130	Pro	Ala	Cys	Leu	Asp 135	Ala	Arg	Gly	Pro	Arg 140	Ala	His	Glu	Cys
Val 145	Pro	Ala	Arg	Gly	Gly 150	Gln	Leu	Ala	Leu	Leu 155	Tyr	Ala	Ala	Leu	Tyr 160
Thr	Val	Ala	Ala	Gly 165	Ala	Gly	Gly	Leu	Lys 170	Ala	Asn	Val	Ser	Gly 175	Phe
Gly	Ser	Asp 180	Gln	Phe	Asp	Gly	Arg	Asp 185	Pro	Arg	Glu	Glu	Arg 190	Ala	Met
Val	Phe	Phe 195	Phe	Asn	Arg	Phe	Tyr 200	Phe	Cys	Val	Ser	Leu	Gly 205	Ser	Leu
Phe	Ala 210	Val	Thr	Val	Leu	Val 215	Tyr	Val	Gln	Asp	Asn 220	Val	Gly	Arg	Gly
Trp 225	Gly	Tyr	Gly	Val	Ser 230	Ala	Val	Ala	Met	Ala 235	Leu	Ala	Val	Ala	Val 240
Leu	Val	Ala	Gly	Thr 245	Pro	Arg	Tyr	Arg	Tyr 250	Arg	Arg	Pro	Gln	Gly 255	Ser
Pro	Leu	Thr	Ala 260	Val	Gly	Arg	Val	Leu 265	Ala	Ala	Ala	Trp	Arg 270	Lys	Arg
Arg	Leu	Pro 275	Leu	Pro	Ala	Asp	Ala 280	Ala	Glu	Leu	His	Gly 285	Phe	Ala	Ala
Ala	Lys 290	Val	Ala	His	Thr	Asp 295	Arg	Leu	Arg	Trp	Leu	Asp	Lys	Ala	Ala
Ile 305	Val	Glu	Ala	Glu	Leu 310	Ala	Gly	Lys	Gln	Arg 315	Ala	Ser	Ala	Ala	Ala 320
Ala	Ser	Thr	Val	Thr 325	Glu	Val	Glu	Glu	Val 330	Lys	Met	Val	Ala	Lys 335	Leu
Leu	Pro	Ile 340	Trp	Phe	Thr	Cys	Ile	Leu 345	Phe	Trp	Thr	Val	Tyr 350	Ser	Gln
Met	Thr	Thr 355	Phe	Ser	Val	Glu	Gln 360	Ala	Thr	Arg	Met	Asp 365	Arg	His	Leu
Arg	Pro 370	Gly	Ser	Gly	Ala	Gly 375	Ala	Gly	Gly	Phe	Ala 380	Val	Pro	Ala	Gly
Ser 385	Phe	Ser	Val	Phe	Leu 390	Phe	Leu	Ser	Ile	Leu 395	Leu	Phe	Thr	Ser	Leu 400
Asn	Glu	Arg	Leu	Leu 405	Val	Pro	Leu	Ala	Ala 410	Arg	Leu	Thr	Gly	Arg 415	Pro
Gln	Gly	Leu	Thr 420	Ser	Leu	Gln	Arg	Val 425	Gly	Ala	Gly	Leu	Ala 430	Leu	Ser
Val	Ala	Ala 435	Met	Ala	Val	Ser	Ala 440	Leu	Val	Glu	Arg	Lys 445	Arg	Arg	Asp
Ala	Ala 450	Asn	Gly	Pro	Asp	His 455	Val	Ala	Val	Ser	Ala 460	Phe	Trp	Leu	Val
Pro 465	Gln	Tyr	Phe	Leu	Val 470	Gly	Ala	Gly	Glu	Ala 475	Phe	Ala	Tyr	Val	Gly 480
Gln	Leu	Glu	Phe	Phe 485	Ile	Arg	Glu	Ala	Pro 490	Glu	Arg	Met	Lys	Ser 495	Met
Ser	Thr	Gly	Leu 500	Phe	Leu	Val	Thr	Leu 505	Ser	Met	Gly	Phe	Phe 510	Leu	Ser
Ser	Phe	Leu 515	Val	Phe	Ala	Val	Asp 520	Ala	Ala	Thr	Ala	Gly 525	Ala	Trp	Ile
Arg	Asn 530	Asn	Leu	Asp	Arg	Gly 535	Arg	Leu	Asp	Leu	Phe 540	Tyr	Trp	Met	Leu
Ala 545	Leu	Leu	Gly	Val	Ala 550	Asn	Phe	Ala	Val	Phe 555	Val	Val	Phe	Ala	Arg 560
Arg	His	Gln	Tyr	Lys 565	Ala	Thr	Ser	Leu	Pro 570	Ala	Ser	Val	Ala	Pro 575	Asp
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 acg gac gtc ctc ctc gac gcc tgg gac ttc aag ggc cgg ccg gcc ccg 577
 Thr Asp Val Leu Leu Asp Ala Trp Asp Phe Lys Gly Arg Pro Ala Pro
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 cgc gcc acc acc ggc cgc tgg ggc gcc gcc gcc atg atc cta gtg gcg 625
 Arg Ala Thr Thr Gly Arg Trp Gly Ala Ala Ala Met Ile Leu Val Ala
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 gag ctg aac gag cgg ctg acg acg ctg ggc atc gcc gtg aac ctg gtg 673
 Glu Leu Asn Glu Arg Leu Thr Thr Leu Gly Ile Ala Val Asn Leu Val
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 acg tac ctg acg ggc acc atg cac ctg ggc aac gcc gag tcc gcc aac 721
 Thr Tyr Leu Thr Gly Thr Met His Leu Gly Asn Ala Glu Ser Ala Asn
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 gtc gtc acc aac ttc atg ggc acc tcc ttc atg ctc tgc ctc ctc ggc 769
 Val Val Thr Asn Phe Met Gly Thr Ser Phe Met Leu Cys Leu Leu Gly
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 Gly Phe Val Ala Asp Ser ttc Leu Gly Arg Tyr Leu Thr Ile Ala Ile
 95 100 105
 ttc acc gcc gtc cag gcc tcg ggc gtg acg atc ctg acg atc tcg acg 865
 Phe Thr Ala Val Gln Ala Ser Gly Val Thr Ile Leu Thr Ile Ser Thr
 110 115 120 125
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 Ala Ala Pro Gly Leu Arg Pro Ala Ser Cys Ser Ala Thr Gly Asp Gly
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 gga ggc gtc gtc ggg gag tgc gcg cgg gcg tcg ggg gcg cag ctg ggg 961
 Gly Gly Val Val Gly Glu Cys Ala Arg Ala Ser Gly Ala Gln Leu Gly
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ggc Gly 190	ggg Gly	gag Glu	aag Lys	cgg Arg	cag Gln 195	atg Met	atg Met	cgc Arg	ttc Phe	ttc Phe 200	aac Asn	tgg Trp	ttc Phe	ttc Phe	ttc Phe 205	1105
ttc Phe	atc Ile	tcg Ser	ctg Leu	ggg Gly 210	tcg Ser	ctg Leu	ctg Leu	gcc Ala	gtc Val 215	acc Thr	gtg Val	ctg Leu	gtg Val	tac Tyr 220	gtc Val	1153
cag Gln	gac Asp	aac Asn	ctg Leu 225	ggc Gly	agg Arg	cgc Arg	tgg Trp	ggc Gly 230	tac Tyr	ggc Gly	gcc Ala	tgc Cys	gcc Ala 235	tgc Cys	gcc Ala	1201
atc Ile	gcc Ala 240	gcg Ala	ctc Gly	ctc Leu	gtc Val	ttc Phe 245	ctg Leu	gcc Ala	ggc Gly	aca Thr	cgc Arg 250	agg Arg	tac Tyr	cgc Arg		1249
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tcc Ser	tcc Ser	agc Ser 305	aag Lys	aag Lys	agc Ser	aag Lys	cgc Arg	aag Lys 310	gag Glu	cgc Arg	ctc Leu	ccc Pro	cac His 315	acc Thr	gac Asp	1441
cag Gln	ttc Phe 320	cgc Arg	ttc Phe	ctg Leu	gac Asp	cac His 325	gcg Ala	gcg Ala	atc Ile	aac Asn	gag Glu	gac Asp 330	ccg Pro	gcg Ala	gcg Ala	1489
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cag Gln	gcc Ala	acc Thr 385	acc Thr	atg Met	gac Asp	cgc Arg	cgc Arg	gtc Val 390	ggg Gly	ggc Gly	tcg Ser	ttc Phe	cag Gln 395	atc Ile	ccc Pro	1681
gcg Ala	ggc Gly 400	tcc Ser	ctc Leu	acc Thr	gtc Val	ttc Phe 405	ttc Phe	gtc Val	ggc Gly	tcc Ser	atc Ile 410	ctg Leu	ctc Leu	acc Thr	gtg Val	1729
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ccc Pro	atg Met	tcc Ser 480	gtg Val	ttc Phe	tgg Trp	ctc Leu	atc Ile 485	ccg Pro	cag Gln	ttc Phe	ttc Phe	ctc Leu 490	gtg Val	ggg Gly	gcg Ala	1969
ggc Gly	gag Glu 495	gcg Ala	ttc Phe	acg Thr	tac Tyr	atc Ile 500	ggc Gly	cag Gln	ctc Leu	gac Asp	ttc Phe 505	ttc Phe	ctg Leu	cgc Arg	gag Glu	2017
tgc Cys 510	ccc Pro	aag Lys	ggg Gly	atg Met	aag Lys 515	acc Thr	atg Met	agc Ser	acg Thr	ggg Gly 520	ctg Leu	ttc Phe	ctc Leu	agc Ser	acc Thr 525	2065

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Arg Val Thr Gly Asp Arg His Pro Trp Ile Ala Asn Asp Leu Asn Lys	
	545
ggc cgc ctc gac aac ttc tac tgg ctg ctc gcc gcc gtc tgc ctc gcc	2209
Gly Arg Leu Asp Asn Phe Tyr Trp Leu Leu Ala Ala Val Cys Leu Ala	
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aac cta cta gtc tac ctc gtc gcc gcc cgc tgg tac aag tac aag gcg	2257
Asn Leu Leu Val Tyr Leu Val Ala Ala Arg Trp Tyr Lys Tyr Lys Ala	
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Gly Arg Pro Gly Ala Asp Gly Ser Val Asn Gly Val Glu Met Ala Asp	
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Glu Pro Thr Leu His	
	610
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 35 40 45
 Glu Arg Leu Thr Thr Leu Gly Ile Ala Val Asn Leu Val Thr Tyr Leu
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 Thr Gly Thr Met His Leu Gly Asn Ala Glu Ser Ala Asn Val Val Thr
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 Asn Phe Met Gly Thr Ser Phe Met Leu Cys Leu Leu Gly Gly Phe Val
 85 90 95
 Ala Asp Ser Phe Leu Gly Arg Tyr Leu Thr Ile Ala Ile Phe Thr Ala
 100 105 110
 Val Gln Ala Ser Gly Val Thr Ile Leu Thr Ile Ser Thr Ala Ala Pro
 115 120 125
 Gly Leu Arg Pro Ala Ser Cys Ser Ala Thr Gly Asp Gly Gly Val
 130 135 140
 Val Gly Glu Cys Ala Arg Ala Ser Gly Ala Gln Leu Gly Val Leu Tyr
 145 150 155 160
 Leu Ala Leu Tyr Leu Thr Ala Leu Gly Thr Gly Gly Leu Lys Ser Ser
 165 170 175
 Val Ser Gly Phe Gly Ser Asp Gln Phe Asp Glu Ser Asp Gly Gly Glu
 180 185 190
 Lys Arg Gln Met Met Arg Phe Phe Asn Trp Phe Phe Phe Ile Ser
 195 200 205

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 Phe Leu Asp His Ala Ile Asn Glu Asp Pro Ala Ala Gly Ala Ser
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 Lys Thr Val Ala Arg Met Leu Pro Ile Trp Ala Thr Thr Ile Met Phe
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 Asp Arg Leu Val Val Pro Val Ala Arg Arg Val Ser Gly Asn Pro His
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 Gly Leu Thr Pro Leu Gln Arg Ile Ala Val Gly Leu Ala Leu Ser Val
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 Val Phe Trp Leu Ile Pro Gln Phe Phe Leu Val Gly Ala Gly Glu Ala
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 Ala Tyr Asp Tyr Arg Gly Asn Pro Pro Asp Lys Ser Lys Thr Gly Gly
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PF59082SeqList_PF59082.txt

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Gly	Thr	Leu	Asn	Leu	Leu	Gly	Leu	Leu	Gly	Gly	Phe	Leu	Ala	Asp	Ala	
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Lys	Leu	Gly	Arg	Tyr	Lys	Met	Val	Ala	Ile	Ser	Ala	Ser	Val	Thr	Ala	
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Pro	Pro	Ile	Cys	Asp	Asp	Phe	Arg	Arg	Leu	His	His	Gln	Cys	Ile	Glu	
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Phe	Phe	Asn	Arg	Phe	Tyr	Phe	Ser	Ile	Ser	Val	Gly	Ser	Leu	Phe	Ala	
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Thr	Thr	Ile	Trp	Arg	Val	Gly	Phe	Leu	Ala	Trp	Lys	Lys	Arg	Lys	Glu	
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Val	Ile	Thr	Val	Val	Val	Thr	Asp	Asp	Asp	Ser	Val	Glu	Lys	Glu	Val	
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 Lys Lys Ile Ser Ala Phe Trp Leu Val Pro Gln Tyr Phe Leu Val Gly
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<400> 37

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Gly	Arg	Pro	Ala	Asp	Lys	Ser	Lys	Thr	Gly	Gly	Trp	Ile	Thr	Ala	Ala	
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PF59082SeqList_PF59082.txt

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Glu	Lys	Ala	His	Met	Ala	Phe	Phe	Phe	Asn	Arg	Phe	Phe	Phe	Phe	Ile	
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His	Leu	Leu	Asp	Lys	Ala	Ala	Ile	Val	Ala	Glu	Gly	Asp	Phe	Glu	Gln	
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Thr	Lys	Val	Glu	Glu	Val	Lys	Met	Met	Val	Arg	Leu	Leu	Pro	Ile	Trp	
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Ala	Thr	Thr	Ile	Ile	Phe	Trp	Thr	Thr	Tyr	Ala	Gln	Met	Ile	Thr	Phe	
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Ser	Val	Glu	Gln	Ala	Ser	Thr	Met	Arg	Arg	Asn	Ile	Gly	Ser	Phe	Lys	
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atc	cca	gct	ggg	tcc	ctc	acc	gtg	ttt	ttc	gtt	gcg	gct	att	ctc	ata	1152
Ile	Pro	Ala	Gly	Ser	Leu	Thr	Val	Phe	Phe	Val	Ala	Ala	Ile	Leu	Ile	
	370				375						380					
act	cta	gct	gtc	tac	gac	cgt	gcc	ata	atg	cct	ttt	tgg	aag	aaa	tgg	1200
Thr	Leu	Ala	Val	Tyr	Asp	Arg	Ala	Ile	Met	Pro	Phe	Trp	Lys	Lys	Trp	
	385				390					395					400	
aaa	gga	aaa	cca	ggg	ttc	tct	agc	cta	caa	aga	ata	gct	att	gga	ttg	1248
Lys	Gly	Lys	Pro	Gly	Phe	Ser	Ser	Leu	Gln	Arg	Ile	Ala	Ile	Gly	Leu	
		405						410						415		
gtc	tta	tca	acc	gct	gga	atg	gca	gct	gca	gct	cta	gta	gag	caa	aag	1296

PF59082SeqList_PF59082.txt

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			420				425						430			
cgt	tta	tcc	ggt	gcg	aaa	tct	agt	tca	caa	aaa	aca	ttg	cct	ata	agt	1344
Arg	Leu	Ser	Val	Ala	Lys	Ser	Ser	Ser	Gln	Lys	Thr	Leu	Pro	Ile	Ser	
		435				440						445				
gtg	ttt	tta	ctt	ggt	cca	caa	ttc	tta	gta	gga	gct	ggg	gaa	gcc		1392
Val	Phe	Leu	Leu	Val	Pro	Gln	Phe	Phe	Leu	Val	Gly	Ala	Gly	Glu	Ala	
	450					455					460					
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Phe	Ile	Tyr	Thr	Gly	Gln	Leu	Asp	Phe	Phe	Ile	Thr	Gln	Ser	Pro	Lys	
	465				470					475					480	
gga	atg	aaa	act	atg	agc	act	gga	ctc	ttc	ttg	acc	act	tta	tca	cta	1488
Gly	Met	Lys	Thr	Met	Ser	Thr	Gly	Leu	Phe	Leu	Thr	Thr	Leu	Ser	Leu	
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ggg	ttc	ttt	gtc	agc	agt	ttc	ttg	gtc	tca	atc	gtc	aag	agg	gtc	act	1536
Gly	Phe	Phe	Val	Ser	Ser	Phe	Leu	Val	Ser	Ile	Val	Lys	Arg	Val	Thr	
			500					505					510			
tca	act	tct	act	gat	gta	gga	tgg	ctg	gct	gat	aac	att	aac	cac	ggc	1584
Ser	Thr	Ser	Thr	Asp	Val	Gly	Trp	Leu	Ala	Asp	Asn	Ile	Asn	His	Gly	
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cga	ctc	gat	tac	ttt	tat	tgg	ctt	tta	gtc	att	ctc	agt	gga	att	aac	1632
Arg	Leu	Asp	Tyr	Phe	Tyr	Trp	Leu	Leu	Val	Ile	Leu	Ser	Gly	Ile	Asn	
	530					535					540					
ttc	ggt	gtc	tat	atc	ata	tgt	gcc	ttg	tgg	ttt	aag	cca	acg	aag	ggt	1680
Phe	Val	Val	Tyr	Ile	Ile	Cys	Ala	Leu	Trp	Phe	Lys	Pro	Thr	Lys	Gly	
	545				550					555					560	
aaa	gac	tca	gta	gag	aag	gaa	aat	ggc	aag	gga	ttt	tca	gtt	gaa	gac	1728
Lys	Asp	Ser	Val	Glu	Lys	Glu	Asn	Gly	Lys	Gly	Phe	Ser	Val	Glu	Asp	
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tgc	tga															1734
Cys																

<210> 38

<211> 577

<212> PRT

<213> Arabidopsis thaliana

<400> 38

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Leu	Ile	Leu	Gly	Ile	Glu	Val	Val	Glu	Arg	Leu	Ser	Thr	Met	Gly	Ile	
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Ala	Val	Asn	Leu	Val	Thr	Tyr	Leu	Met	Glu	Thr	Met	His	Leu	Pro	Ser	
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Ser	Thr	Ser	Ala	Asn	Ile	Val	Thr	Asp	Phe	Met	Gly	Thr	Ser	Phe	Leu	
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Leu	Cys	Leu	Leu	Gly	Phe	Leu	Ala	Asp	Ser	Phe	Leu	Gly	Arg	Phe		
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Lys	Thr	Ile	Gly	Ile	Phe	Ser	Thr	Ile	Gln	Ala	Leu	Gly	Thr	Gly	Ala	
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		115					120					125				
His	Gly	Glu	Ala	Cys	Ile	Pro	Ala	Thr	Ala	Phe	Gln	Met	Thr	Ile	Leu	
	130					135					140					
Tyr	Val	Ser	Leu	Tyr	Leu	Ile	Ala	Leu	Gly	Thr	Gly	Gly	Leu	Lys	Ser	
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Ser	Ile	Ser	Gly	Phe	Gly	Ser	Asp	Gln	Phe	Asp	Asp	Lys	Asp	Pro	Lys	
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Glu	Lys	Ala	His	Met	Ala	Phe	Phe	Phe	Asn	Arg	Phe	Phe	Phe	Phe	Ile	
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Ser	Met	Gly	Thr	Leu	Leu	Ala	Val	Thr	Val	Leu	Val	Tyr	Met	Gln	Asp	
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Glu	Val	Gly	Arg	Ser	Trp	Ala	Tyr	Gly	Ile	Cys	Thr	Val	Ser	Met	Ala	
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Ile	Ala	Ile	Val	Ile	Phe	Leu	Cys	Gly	Thr	Lys	Arg	Tyr	Arg	Tyr	Lys	
225					230					235					240	

PF59082SeqList_PF59082.txt

Lys Ser Gln Gly Ser Pro Val Val Gln Ile Phe Gln Val Ile Ala Ala
 245 250 255
 Ala Phe Arg Lys Arg Lys Met Glu Leu Pro Gln Ser Ile Val Tyr Leu
 260 265 270
 Tyr Glu Asp Asn Pro Glu Gly Ile Arg Ile Glu His Thr Asp Gln Phe
 275 280 285
 His Leu Leu Asp Lys Ala Ala Ile Val Ala Glu Gly Asp Phe Glu Gln
 290 295 300
 Thr Leu Asp Gly Val Ala Ile Pro Asn Pro Trp Lys Leu Ser Ser Val
 305 310 315 320
 Thr Lys Val Glu Glu Val Lys Met Met Val Arg Leu Leu Pro Ile Trp
 325 330 335
 Ala Thr Thr Ile Ile Phe Trp Thr Thr Tyr Ala Gln Met Ile Thr Phe
 340 345 350
 Ser Val Glu Gln Ala Ser Thr Met Arg Arg Asn Ile Gly Ser Phe Lys
 355 360 365
 Ile Pro Ala Gly Ser Leu Thr Val Phe Phe Val Ala Ala Ile Leu Ile
 370 375 380
 Thr Leu Ala Val Tyr Asp Arg Ala Ile Met Pro Phe Trp Lys Lys Trp
 385 390 395 400
 Lys Gly Lys Pro Gly Phe Ser Ser Leu Gln Arg Ile Ala Ile Gly Leu
 405 410 415
 Val Leu Ser Thr Ala Gly Met Ala Ala Ala Ala Leu Val Glu Gln Lys
 420 425 430
 Arg Leu Ser Val Ala Lys Ser Ser Ser Gln Lys Thr Leu Pro Ile Ser
 435 440 445
 Val Phe Leu Leu Val Pro Gln Phe Phe Leu Val Gly Ala Gly Glu Ala
 450 455 460
 Phe Ile Tyr Thr Gly Gln Leu Asp Phe Phe Ile Thr Gln Ser Pro Lys
 465 470 475 480
 Gly Met Lys Thr Met Ser Thr Gly Leu Phe Leu Thr Thr Leu Ser Leu
 485 490 495
 Gly Phe Phe Val Ser Ser Phe Leu Val Ser Ile Val Lys Arg Val Thr
 500 505 510
 Ser Thr Ser Thr Asp Val Gly Trp Leu Ala Asp Asn Ile Asn His Gly
 515 520 525
 Arg Leu Asp Tyr Phe Tyr Trp Leu Leu Val Ile Leu Ser Gly Ile Asn
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 565 570 575
 Cys

<210> 39
 <211> 1701
 <212> DNA
 <213> Oryza sativa (japonica cultivar-group)

<220>
 <221> CDS
 <222> (1)..(1701)

<400> 39
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 Ala Thr Gly Gly Trp Val Ala Ala Ala Leu Val Leu Gly Ile Glu Leu
 20 25 30
 tgc gag cgg ctg tgc acg atg ggg atc gcg gtg aac ctg gtg acg tac 144
 Cys Glu Arg Leu Ser Thr Met Gly Ile Ala Val Asn Leu Val Thr Tyr
 35 40 45
 ctg acg ggc acc atg cac ctc ccc agc gcc gcc gcc aac gtc gtc 192
 Leu Thr Gly Thr Met His Leu Pro Ser Ala Ala Ala Ala Asn Val Val
 50 55 60
 acc gac ttc atg ggc acc tcc ttc ctc ctc tgc ctc ctc ggc ggc ttc 240
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 Seite 41

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Leu	Ala	Asp	Ser	Phe	Leu	Gly	Arg	Tyr	Leu	Thr	Ile	Ala	Val	Phe	Ala																			
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Leu	Val	Gln	Ser	Ile	Gly	Thr	Ala	Leu	Leu	Ala	Ala	Ser	Thr	Leu	Val																			
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Thr	His	Leu	Arg	Pro	Pro	Pro	Gly	Glu	Gln	Pro	Thr	Pro	Val	Gln	Met																			
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gcc	gtg	ctc	tac	gcc	tgc	ctc	tac	ctc	atc	gcc	ctc	ggc	acc	ggc	ggc	432																		
Ala	Val	Leu	Tyr	Ala	Cys	Leu	Tyr	Leu	Ile	Ala	Leu	Gly	Thr	Gly	Gly																			
	130					135					140																							
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Leu	Lys	Ser	Ser	Val	Ser	Gly	Phe	Gly	Thr	Asp	Gln	Phe	Asp	Asp	Arg																			
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gac	ggc	cgg	gag	cgc	gcc	gcc	atg	ggc	ctc	ttc	ttc	aac	cgc	ttc	ttc	528																		
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Phe	Phe	Ile	Ser	Leu	Gly	Thr	Leu	Leu	Ala	Val	Thr	Val	Leu	Val	Tyr																			
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Ala	Met	Leu	Ala	Ala	Ile	Ala	Val	Phe	Leu	Ser	Gly	Thr	Arg	Arg	Tyr																			
	210					215					220																							
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Ala	Ala	Glu	Leu	Tyr	Glu	Asp	Asp	Arg	Pro	Glu	His	Ala	Arg	Ile	Ala																			
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cac	acc	gcg	cag	ttc	ccg	tgc	ctg	gac	atg	gcg	gcg	gtg	gtg	gcc	ggc	864																		
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Glu	Glu	Asp	Asn	Glu	Val	Ala	Gly	Pro	Gly	Gly	Pro	Ala	Ala	Pro	Asn																			
	290					295				300																								
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Pro	Trp	Lys	Leu	Cys	Ser	Val	Ser	Arg	Val	Glu	Glu	Val	Lys	Met	Val																			
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Arg	Arg	Val	Gly	Ala	Gly	Phe	Glu	Ile	Pro	Ala	Ala	Ser	Leu	Thr	Val																			
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ttc	atc	ccg	ctc	tgc	cgc	gta	ctc	acc	ggc	aag	caa	ggc	ttc	acc	aac	1200																		
Phe	Ile	Pro	Leu	Cys	Arg	Val	Leu	Thr	Gly	Lys	Gln	Gly	Phe	Thr	Asn																			
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ctg	gag	aag	atc	ggc	atc	ggc	ctc	gcc	ctc	tcc	atc	ctc	ggc	atg	gcc	1248																		
Leu	Glu	Lys	Ile	Gly	Ile	Gly	Leu	Ala	Leu	Ser	Ile	Leu	Gly	Met	Ala																			
			405					410						415																				
gcc	gcc	gcg	ctc	tgc	gag	aag	aag	cgc	ctc	gcc	gtc	gcc	gtc	gcc	gcc	1296																		
Ala	Ala	Ala	Leu	Cys	Glu	Lys	Lys	Arg	Leu	Ala	Val	Ala	Val	Ala	Ala																			
			420					425				430																						
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PF59082SeqList_PF59082.txt

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gac ttc ttc atc acg agg tcg ccc aag ggg atg aag acg atg agc acg			1440
Asp Phe Phe Ile Thr Arg Ser Pro Lys Gly Met Lys Thr Met Ser Thr			
465	470	475	
ggg ctc ttc ctg acg acg ctc tcg ctc ggc ttc ttc ttc agc agc gtg			1488
Gly Leu Phe Leu Thr Thr Leu Ser Leu Gly Phe Phe Phe Ser Ser Val			
485	490	495	
ctc gtg tcg ctc gtc aag ggc gcc acc acc tgg ctc ggc gac acc atc			1536
Leu Val Ser Leu Val Lys Gly Ala Thr Thr Trp Leu Gly Asp Thr Ile			
500	505	510	
gac cgc agc cgc ctc gac tac ttc tac tgg ctc ctc gcc gtc ctc agc			1584
Asp Arg Ser Arg Leu Asp Tyr Phe Tyr Trp Leu Leu Val Leu Ser			
515	520	525	
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Val Leu Asn Leu Ala Ala Tyr Leu Val Cys Ala Lys Trp Ala Ala Thr			
530	535	540	
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<210> 40

<211> 566

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<400> 40

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35 40 45	
Leu Thr Gly Thr Met His Leu Pro Ser Ala Ala Ala Asn Val Val	
50 55 60	
Thr Asp Phe Met Gly Thr Ser Phe Leu Leu Cys Leu Leu Gly Gly Phe	
65 70 75 80	
Leu Ala Asp Ser Phe Leu Gly Arg Tyr Leu Thr Ile Ala Val Phe Ala	
85 90 95	
Leu Val Gln Ser Ile Gly Thr Ala Leu Ala Ala Ser Thr Leu Val	
100 105 110	
Thr His Leu Arg Pro Pro Pro Gly Glu Gln Pro Thr Pro Val Gln Met	
115 120 125	
Ala Val Leu Tyr Ala Cys Leu Tyr Leu Ile Ala Leu Gly Thr Gly Gly	
130 135 140	
Leu Lys Ser Ser Val Ser Gly Phe Gly Thr Asp Gln Phe Asp Asp Arg	
145 150 155 160	
Asp Gly Arg Glu Arg Ala Ala Met Gly Leu Phe Phe Asn Arg Phe Phe	
165 170 175	
Phe Phe Ile Ser Leu Gly Thr Leu Leu Ala Val Thr Val Leu Val Tyr	
180 185 190	
Val Gln Asp His Val Gly Arg Ser Trp Ala Tyr Gly Ile Cys Ser Ala	
195 200 205	
Ala Met Leu Ala Ala Ile Ala Val Phe Leu Ser Gly Thr Arg Arg Tyr	
210 215 220	
Arg Tyr Lys Arg Ser Ser Gly Ser Pro Ile Val His Ile Leu Gln Val	
225 230 235 240	
Leu Val Ala Ala Ala Arg Lys Arg Gly Val Val Lys Arg Pro Pro Thr	
245 250 255	
Ala Ala Glu Leu Tyr Glu Asp Asp Arg Pro Glu His Ala Arg Ile Ala	
260 265 270	
His Thr Ala Gln Phe Pro Cys Leu Asp Met Ala Ala Val Val Ala Gly	
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Glu Glu Asp Asn Glu Val Ala Gly Pro Gly Gly Pro Ala Ala Pro Asn	

PF59082SeqList_PF59082.txt

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290          295          300
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Tyr Ala Gln Met Pro Thr Phe Ser Val Thr Glu Gln Ala Thr Thr Met Asp
325 340 345 350
Arg Arg Val Gly Ala Gly Phe Glu Ile Pro Ala Ala Ser Leu Thr Val
355 360 365
Phe Phe Val Gly Ala Ile Met Leu Thr Leu Ala Val Tyr Asp Arg Val
370 375 380
Phe Ile Pro Leu Cys Arg Val Leu Thr Gly Lys Gln Gly Phe Thr Asn
385 390 395 400
Leu Glu Lys Ile Gly Ile Gly Leu Ala Leu Ser Ile Leu Gly Met Ala
405 410 415
Ala Ala Ala Leu Cys Glu Lys Lys Arg Leu Ala Val Ala Val Ala Ala
420 425 430
Thr Thr Gly Asn Ser Thr Pro Ile Ser Val Phe Leu Leu Thr Pro Gln
435 440 445
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450 455 460
Asp Phe Phe Ile Thr Arg Ser Pro Lys Gly Met Lys Thr Met Ser Thr
465 470 475 480
Gly Leu Phe Leu Thr Leu Ser Leu Gly Phe Phe Phe Ser Ser Val
485 490 495
Leu Val Ser Leu Val Lys Gly Ala Thr Thr Trp Leu Gly Asp Thr Ile
500 505 510
Asp Arg Ser Arg Leu Asp Tyr Phe Tyr Trp Leu Leu Ala Val Leu Ser
515 520 525
Val Leu Asn Leu Ala Ala Tyr Leu Val Cys Ala Lys Trp Ala Ala Thr
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Asp Ala Asp Glu Lys Cys
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<210> 41
 <211> 1785
 <212> DNA
 <213> Oryza sativa (japonica cultivar-group)

<220>
 <221> CDS
 <222> (1)..(1785)

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Gly Cys Ala Ala Met Ile Leu Gly Ala Glu Leu Phe Glu Arg Met Thr
35      40      45
acg ctg ggc atc gcc gtc aac ctg gtg ccg tac atg acc ggg acg atg      192
Thr Leu Gly Ile Ala Val Asn Leu Val Pro Tyr Met Thr Gly Thr Met
50      55      60
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His Leu Gly Asn Ala Ala Ala Asn Thr Val Thr Asn Phe Ile Gly
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85      90      95
ctc ggc cgc tac ctc acc atc gcc atc ttc gag gcc gtc cag gcc acc      336
Leu Gly Arg Tyr Leu Thr Ile Ala Ile Phe Glu Ala Val Gln Ala Thr
100      105      110
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PF59082SeqList_PF59082.txt

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ctg	ggc	acg	ggg	ggg	ctc	aag	tcc	agc	gtc	tcc	ggc	ttc	ggc	tcc	528
Leu	Gly	Thr	Gly	Gly	Leu	Lys	Ser	Ser	Val	Ser	Gly	Phe	Gly	Ser	
			165						170					175	
cag	ttc	gac	gag	tcc	gac	gtc	gac	ggc	gag	agg	aag	aag	atg	atg	576
Gln	Phe	Asp	Glu	Ser	Asp	Val	Asp	Gly	Glu	Arg	Lys	Lys	Met	Met	
			180					185					190		
ttc	ttc	aac	tgg	ttc	tac	ttc	ttc	gtc	agc	ctc	ggc	gag	ctg	ctc	624
Phe	Phe	Asn	Trp	Phe	Tyr	Phe	Phe	Val	Ser	Leu	Gly	Ala	Leu	Leu	
		195					200					205			
gtc	acc	gtg	ctg	gtg	tac	gtg	cag	gac	aac	gtc	gga	cgc	cgg	tgg	672
Val	Thr	Val	Leu	Val	Tyr	Val	Gln	Asp	Asn	Val	Gly	Arg	Arg	Trp	
	210					215					220				
tac	ggc	atc	tgc	gcc	gcc	ggc	atc	ctc	gcc	ggc	ctc	gcc	gtg	ttc	720
Tyr	Gly	Ile	Cys	Ala	Ala	Gly	Ile	Leu	Ala	Gly	Leu	Ala	Val	Phe	
225				230						235					
tcc	ggg	acc	agg	agg	tac	agg	ttc	aag	aag	ctg	gtg	ggg	agc	ccc	768
Ser	Gly	Thr	Arg	Arg	Tyr	Arg	Phe	Lys	Lys	Leu	Val	Gly	Ser	Pro	
			245						250					255	
acc	cag	gtc	gcc	gcc	gtc	acc	gcc	gcc	gcc	tgg	agc	aag	agg	tcg	816
Thr	Gln	Val	Ala	Ala	Val	Thr	Ala	Ala	Ala	Trp	Ser	Lys	Arg	Ser	
		260					265					270			
ccg	ctg	ccg	tcc	gac	cca	gac	atg	ctc	tac	gac	gtc	gac	gac	gcc	864
Pro	Leu	Pro	Ser	Asp	Pro	Asp	Met	Leu	Tyr	Asp	Val	Asp	Asp	Ala	
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gcc	gcc	ggc	cat	gac	gtc	aag	ggc	aag	cag	agg	atg	cca	cac	agc	912
Ala	Ala	Gly	His	Asp	Val	Lys	Gly	Lys	Gln	Arg	Met	Pro	His	Ser	
	290					295					300				
gag	tgc	cgg	ttc	ctg	gac	cat	gag	gag	atc	atc	gac	agg	tcg	gag	960
Glu	Cys	Arg	Phe	Leu	Asp	His	Ala	Ala	Ile	Ile	Asp	Arg	Ser	Ala	
305					310					315					
gag	tcg	ccg	gag	acg	gag	agc	aag	tgg	agg	ctg	tgc	acg	agg	acg	1008
Glu	Ser	Pro	Ala	Thr	Ala	Ser	Lys	Trp	Arg	Leu	Cys	Thr	Arg	Thr	
			325						330					335	
gtg	gag	gag	gtg	aag	cag	gtg	gtg	cgg	atg	ctc	ccc	atc	tgg	gag	1056
Val	Glu	Glu	Val	Lys	Gln	Val	Val	Arg	Met	Leu	Pro	Ile	Trp	Ala	
		340					345					350			
acc	atc	atg	ttc	tgg	acc	atc	cac	gcc	cag	atg	acc	acc	ttc	gcc	1104
Thr	Ile	Met	Phe	Trp	Thr	Ile	His	Ala	Gln	Met	Thr	Thr	Phe	Ala	
		355					360					365			
gag	cag	ggc	gag	ctc	atg	gac	cgc	cgc	ctc	gcc	ggc	ggc	ttc	ctc	1152
Ala	Gln	Ala	Glu	Leu	Met	Asp	Arg	Arg	Leu	Ala	Gly	Gly	Phe	Leu	
	370					375					380				
ccg	gag	ggc	tcc	ctc	acc	gtc	ttc	ctc	atc	gcc	tcc	atc	ctc	ctc	1200
Pro	Ala	Gly	Ser	Leu	Thr	Val	Phe	Leu	Ile	Ala	Ser	Ile	Leu	Leu	
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gtc	ccc	ttc	tac	gac	cgc	ctc	gtc	gtc	ccc	gtc	gag	cgc	cgc	gcc	1248
Val	Pro	Phe	Tyr	Asp	Arg	Leu	Val	Val	Pro	Val	Ala	Arg	Arg	Ala	
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gcc	aac	ccg	cac	ggc	ctc	acc	ccg	ctc	cag	cgc	gtc	ttc	gtg	ggc	1296
Ala	Asn	Pro	His	Gly	Leu	Thr	Pro	Leu	Gln	Arg	Val	Phe	Val	Gly	
			420				425					430			
tcc	ctc	tcc	atc	gcc	ggc	atg	gcc	gtc	gcc	gag	gcc	gtc	gag	cgc	1344
Ser	Leu	Ser	Ile	Ala	Gly	Met	Ala	Val	Ala	Ala	Ala	Val	Glu	Arg	
		435				440						445			
cgc	gcc	acc	gcc	tcc	gcc	tcc	gcc	gcc	gcc	gcc	gag	ccc	acg	gtg	1392
Arg	Ala	Thr	Ala	Ser	Ala	Ser	Ala	Ala	Ala	Ala	Ala	Pro	Thr	Val	
	450					455					460				
ctc	ctc	atg	ccg	cag	ttc	ctc	ctc	gtc	ggc	gcc	gag	gag	gag	ttc	1440
Leu	Leu	Met	Pro	Gln	Phe	Leu	Leu	Val	Gly	Ala	Gly	Glu	Ala	Phe	
				470					475						
tac	atg	ggc	cag	ctc	gac	ttc	ttc	ctc	cgc	gag	tgc	ccc	aag	ggg	1488
Tyr	Met	Gly	Gln	Leu	Asp	Phe	Phe	Leu	Arg	Glu	Cys	Pro	Lys	Gly	

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			500				505					510				
ttc	ttc	agc	acg	ctg	ctc	gtc	acc	atc	gtc	cac	aag	gtc	acc	ggc	cat	1584
Phe	Phe	Ser	Thr	Leu	Leu	Val	Thr	Ile	Val	His	Lys	Val	Thr	Gly	His	
		515					520					525				
ggc	gcc	cgc	ggc	ggc	ggc	tgg	ctc	gcc	gac	aac	ctc	gac	gac	ggc	agg	1632
Gly	Ala	Arg	Gly	Gly	Gly	Trp	Leu	Ala	Asp	Asn	Leu	Asp	Asp	Gly	Arg	
	530					535					540					
ctc	gac	tac	ttc	tac	tgg	ctg	ctc	gcc	gtc	atc	agc	gcc	atc	aac	ctc	1680
Leu	Asp	Tyr	Phe	Tyr	Trp	Leu	Leu	Ala	Val	Ile	Ser	Ala	Ile	Asn	Leu	
545					550					555					560	
gtc	ctc	ttc	acc	gtc	gcc	gcc	agg	ggg	tac	gtc	tac	aag	gag	aag	cgc	1728
Val	Leu	Phe	Thr	Val	Ala	Ala	Arg	Gly	Tyr	Val	Tyr	Lys	Glu	Lys	Arg	
			565					570						575		
ctc	gcc	gac	ggc	ggc	atc	gag	ctc	gcc	gac	gag	gag	acc	atc	gcc	gtc	1776
Leu	Ala	Asp	Ala	Gly	Ile	Glu	Leu	Ala	Asp	Glu	Glu	Thr	Ile	Ala	Val	
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ggc	cac	taa														1785
Gly	His															

<210> 42

<211> 594

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<400> 42

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			20					25					30			
Gly	Cys	Ala	Ala	Met	Ile	Leu	Gly	Ala	Glu	Leu	Phe	Glu	Arg	Met	Thr	
		35					40					45				
Thr	Leu	Gly	Ile	Ala	Val	Asn	Leu	Val	Pro	Tyr	Met	Thr	Gly	Thr	Met	
	50					55					60					
His	Leu	Gly	Asn	Ala	Ala	Ala	Ala	Asn	Thr	Val	Thr	Asn	Phe	Ile	Gly	
65				70					75					80		
Thr	Ser	Phe	Met	Leu	Cys	Leu	Leu	Gly	Gly	Phe	Val	Ala	Asp	Thr	Tyr	
			85					90						95		
Leu	Gly	Arg	Tyr	Leu	Thr	Ile	Ala	Ile	Phe	Glu	Ala	Val	Gln	Ala	Thr	
			100				105						110			
Gly	Val	Met	Ile	Leu	Thr	Ile	Ser	Thr	Ala	Ala	Pro	Gly	Leu	Arg	Pro	
		115					120					125				
Pro	Ala	Cys	Gly	Asp	Pro	Lys	Gly	Ala	Ser	Ala	Glu	Cys	Val	Ala	Ala	
	130					135					140					
Asp	Gly	Thr	Gln	Leu	Gly	Val	Leu	Tyr	Leu	Gly	Leu	Tyr	Leu	Thr	Ala	
145				150					155						160	
Leu	Gly	Thr	Gly	Gly	Leu	Lys	Ser	Ser	Val	Ser	Gly	Phe	Gly	Ser	Asp	
			165					170						175		
Gln	Phe	Asp	Glu	Ser	Asp	Val	Asp	Gly	Glu	Arg	Lys	Lys	Met	Met	Arg	
		180					185						190			
Phe	Phe	Asn	Trp	Phe	Tyr	Phe	Phe	Val	Ser	Leu	Gly	Ala	Leu	Leu	Ala	
		195					200					205				
Val	Thr	Val	Leu	Val	Tyr	Val	Gln	Asp	Asn	Val	Gly	Arg	Arg	Trp	Gly	
	210					215					220					
Tyr	Gly	Ile	Cys	Ala	Ala	Gly	Ile	Leu	Ala	Gly	Leu	Ala	Val	Phe	Leu	
225				230					235						240	
Ser	Gly	Thr	Arg	Arg	Tyr	Arg	Phe	Lys	Lys	Leu	Val	Gly	Ser	Pro	Leu	
			245					250						255		
Thr	Gln	Val	Ala	Ala	Val	Thr	Ala	Ala	Ala	Trp	Ser	Lys	Arg	Ser	Leu	
		260					265						270			
Pro	Leu	Pro	Ser	Asp	Pro	Asp	Met	Leu	Tyr	Asp	Val	Asp	Asp	Ala	Ala	
		275					280					285				
Ala	Ala	Gly	His	Asp	Val	Lys	Gly	Lys	Gln	Arg	Met	Pro	His	Ser	Lys	
	290					295					300					
Glu	Cys	Arg	Phe	Leu	Asp	His	Ala	Ala	Ile	Ile	Asp	Arg	Ser	Ala	Ala	
305				310					315						320	

PF59082SeqList_PF59082.txt

Glu Ser Pro Ala Thr 325 Ala Ser Lys Trp Arg 330 Leu Cys Thr Arg 335 Thr Asp
Val Glu Glu Val Lys Gln Val Val Arg Met Leu Pro Ile Trp Ala Thr
340 345 350
Thr Ile Met Phe Trp Thr Ile His 360 Ala Gln Met Thr Thr Phe Ala Val
355 365
Ala Gln Ala Glu Leu Met Asp Arg Arg Leu Ala Gly Gly Phe Leu Ile
370 375 380
Pro Ala Gly Ser Leu Thr Val Phe Leu Ile Ala Ser Ile Leu Leu Thr
385 390 400
Val Pro Phe Tyr Asp Arg Leu Val Val Pro Val Ala Arg Arg Ala Thr
405 410 415
Ala Asn Pro His Gly Leu Thr Pro Leu Gln Arg Val Phe Val Gly Leu
420 425 430
Ser Leu Ser Ile Ala Gly Met Ala Val Ala Ala Val Glu Arg His
435 440 445
Arg Ala Thr Ala Ser Ala Ser Ala Ala Ala Ala Pro Thr Val Phe
450 455 460
Leu Leu Met Pro Gln Phe Leu Leu Val Gly Ala Gly Glu Ala Phe Thr
465 470 475 480
Tyr Met Gly Gln Leu Asp Phe Phe Leu Arg Glu Cys Pro Lys Gly Met
485 490 495
Lys Thr Met Ser Thr Gly Leu Phe Leu Ser Thr Cys Ala Ile Gly Phe
500 505 510
Phe Phe Ser Thr Leu Leu Val Thr Ile Val His Lys Val Thr Gly His
515 520 525
Gly Ala Arg Gly Gly Gly Trp Leu Ala Asp Asn Leu Asp Asp Gly Arg
530 535 540
Leu Asp Tyr Phe Tyr Trp Leu Leu Ala Val Ile Ser Ala Ile Asn Leu
545 550 555 560
Val Leu Phe Thr Val Ala Ala Arg Gly Tyr Val Tyr Lys Glu Lys Arg
565 570 575
Leu Ala Asp Ala Gly Ile Glu Leu Ala Asp Glu Glu Thr Ile Ala Val
580 585 590
Gly His

<210> 43

<211> 1779

<212> DNA

<213> oryza sativa (japonica cultivar-group)

<220>

<221> CDS

<222> (1)..(1779)

<400> 43

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ttc agg gga aac ccg gtg gac aag gac cgg acc gga gga tgg ctc gga	96
Phe Arg Gly Asn Pro Val Asp Lys Asp Arg Thr Gly Gly Trp Leu Gly	
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gcc ggt ctc atc cta ggg acg gaa ttg gcg gag cgc gtg tgc gtg gtg	144
Ala Gly Leu Ile Leu Gly Thr Glu Leu Ala Glu Arg Val Cys Val Val	
35 40 45	
ggc atc tcg atg aac ctg gtg acg tac ctc gtc ggc gac ctg cac ctc	192
Gly Ile Ser Met Asn Leu Val Thr Tyr Leu Val Gly Asp Leu His Leu	
50 55 60	
tcc aac gcc agg tcg gcc aac atc gtc acc aac ttc ctg ggc acg ctc	240
Ser Asn Ala Arg Ser Ala Asn Ile Val Thr Asn Phe Leu Gly Thr Leu	
65 70 75 80	
aac ctc ctc gcc ctc ctc ggc ggc ttc ctc gcc gac gcc gtg ctc ggc	288
Asn Leu Leu Ala Leu Leu Gly Gly Phe Leu Ala Asp Ala Val Leu Gly	
85 90 95	
cgc tac ctc acc gtc gcc gtc tcc gcc acc atc gcc gcc atc ggt gtg	336
Arg Tyr Leu Thr Val Ala Val Ser Ala Thr Ile Ala Ala Ile Gly Val	
100 105 110	
agc ctg ctg gca gcg agc acg gta gtg ccg gga atg cgg ccg ccg ccg	384

PF59082SeqList_PF59082.txt

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tgc	ggc	gac	gcg	gtg	gcg	gag	gag	gag	gag	gag	gag	gag	gag	gag	gag	gag
Cys	Gly	Asp	Ala	Val	Ala	Ala	Ala	Ala	Ala	Ala	Glu	Ser	Gly	Gly	Cys	
432																
gtg	gag	gag	gag	gag	gag	gag	gag	gag	gag	gag	gag	gag	gag	gag	gag	gag
Val	Ala	Ala	Ser	Gly	Gly	Gln	Met	Ala	Met	Leu	Tyr	Ala	Ala	Leu	Tyr	
145	150	155	160	165	170	175	180	185	190	195	200	205	210	215	220	225
acg	gag	gag	gag	gag	gag	gag	gag	gag	gag	gag	gag	gag	gag	gag	gag	gag
Thr	Ala	Ala	Ala	Ala	Ala	Gly	Gly	Leu	Lys	Ala	Asn	Val	Ser	Gly	Phe	
528																
ggg	tcg	gac	cag	ttc	gac	ggg	cgc	gac	cgc	cgg	gag	ggg	aag	gcc	atg	
Gly	Ser	Asp	Gln	Phe	Asp	Gly	Arg	Asp	Arg	Arg	Glu	Gly	Lys	Ala	Met	
576																
ctc	ttc	ttc	ttc	aac	cgc	ttc	tac	ttc	tgc	atc	agc	ctc	ggc	tcg	gtg	
Leu	Phe	Phe	Phe	Asn	Arg	Phe	Tyr	Phe	Cys	Ile	Ser	Leu	Gly	Ser	Val	
624																
ctc	gag	gtc	acc	gag	ctg	gtg	tac	gtg	cag	gag	gac	gtc	ggc	cgc	ggc	
Leu	Ala	Val	Thr	Ala	Leu	Val	Tyr	Val	Gln	Glu	Asp	Val	Gly	Arg	Gly	
672																
tgg	ggc	tac	ggc	gag	tcg	gcc	gcc	atg	gtc	gcc	gag	gtg	gag	gtg	gtg	
Trp	Gly	Tyr	Gly	Ala	Ser	Ala	Ala	Met	Val	Ala	Ala	Val	Ala	Val	Val	
225	230	235	240	245	250	255	260	265	270	275	280	285	290	295	300	305
ttc	gcc	gcc	ggc	acg	ccg	agg	tac	cgg	tac	cgg	agg	ccc	cag	ggg	agc	
Phe	Ala	Ala	Gly	Thr	Pro	Arg	Tyr	Arg	Tyr	Arg	Arg	Pro	Gln	Gly	Ser	
768																
ccc	ctc	acg	gag	atc	ggc	cgc	gtg	ctg	tgg	gag	gag	tgg	cgc	aaa	cgg	
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816																
agg	atg	ccg	ttc	ccg	gag	gac	gcc	ggc	gag	ctc	cac	ggc	ttc	cac	aag	
Arg	Met	Pro	Phe	Pro	Ala	Asp	Ala	Gly	Glu	Leu	His	Gly	Phe	His	Lys	
864																
gct	aag	gtg	cca	cac	act	aac	agg	ctc	agg	tgt	ctg	gac	aaa	gcc	gca	
Ala	Lys	Val	Pro	His	Thr	Asn	Arg	Leu	Arg	Cys	Leu	Asp	Lys	Ala	Ala	
912																
atc	gtg	gag	gcc	gac	ctg	gag	gag	acg	cca	ccg	gag	cag	cca	gtg	gtg	
Ile	Val	Glu	Ala	Asp	Leu	Ala	Ala	Thr	Pro	Pro	Glu	Gln	Pro	Val	Val	
305	310	315	320	325	330	335	340	345	350	355	360	365	370	375	380	385
gag	gag	ctg	acg	gtg	acg	gag	gtg	gag	gag	gag	aag	atg	gtg	gtg	aag	
Ala	Ala	Leu	Thr	Val	Thr	Glu	Val	Glu	Ala	Lys	Met	Val	Val	Lys	Lys	
1008																
ctg	ctc	ccc	atc	tgg	tcc	acg	agc	atc	ctc	ttc	tgg	acg	gtc	tac	tcc	
Leu	Leu	Pro	Ile	Trp	Ser	Thr	Ser	Ile	Leu	Phe	Trp	Thr	Val	Tyr	Ser	
1056																
cag	atg	acc	acc	ttc	tcc	gtc	gag	cag	gag	tcg	cac	atg	gac	cgc	cgc	
Gln	Met	Thr	Thr	Phe	Ser	Val	Glu	Gln	Ala	Ser	His	Met	Asp	Arg	Arg	
1104																
gcc	ggc	ggc	ttc	gcc	gtg	ccg	gag	ggc	tcc	ttc	tcc	gtc	ttc	ctc	ttc	
Ala	Gly	Gly	Phe	Ala	Val	Pro	Ala	Gly	Ser	Phe	Ser	Val	Phe	Leu	Phe	
1152																
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Leu	Ser	Ile	Leu	Leu	Phe	Thr	Ser	Ala	Ser	Glu	Arg	Leu	Leu	Val	Pro	
1200																
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Leu	Ala	Arg	Arg	Leu	Met	Ile	Thr	Arg	Arg	Pro	Gln	Gly	Leu	Thr	Ser	
1248																
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Leu	Gln	Arg	Val	Gly	Ala	Gly	Leu	Val	Leu	Ala	Thr	Leu	Ala	Met	Ala	
1296																
gtc	tcg	gag	ctc	gtc	gag	aag	aag	cgc	gac	gag	tcg	ggc	gga	gcc	gcc	
Val	Ser	Ala	Leu	Val	Glu	Lys	Lys	Arg	Arg	Asp	Ala	Ser	Gly	Gly	Ala	
1344																
ggc	gga	gga	ggc	gtc	gag	atg	atc	agc	gag	ttc	tgg	ctg	gtg	ccg	cag	
Gly	Gly	Gly	Gly	Val	Ala	Met	Ile	Ser	Ala	Phe	Trp	Leu	Val	Pro	Gln	
1392																
ttc	ttc	ctg	gtg	ggc	gcc	ggc	gag	gag	ttc	gag	tac	gtg	ggg	cag	ctg	
Phe	Phe	Leu	Val	Gly	Ala	Gly	Glu	Ala	Phe	Ala	Tyr	Val	Gly	Gln	Leu	
1440																
gag	ttc	ttc	atc	agg	gag	gcc	ccc	gag	cgg	atg	aag	tcc	atg	agc	acg	
1488																

PF59082SeqList_PF59082.txt

Glu	Phe	Phe	Ile	Arg	Glu	Ala	Pro	Glu	Arg	Met	Lys	Ser	Met	Ser	Thr	
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Gly	Leu	Phe	Leu	Ala	Thr	Leu	Ala	Met	Gly	Phe	Phe	Leu	Ser	Ser	Leu	
			500					505					510			
ctc	gtg	tcc	gcc	gtc	gac	gcc	gcc	acg	cgg	ggc	gcg	tgg	atc	cgg	gac	1584
Leu	Val	Ser	Ala	Val	Asp	Ala	Ala	Thr	Arg	Gly	Ala	Trp	Ile	Arg	Asp	
		515				520						525				
ggc	ctg	gac	gac	ggg	agg	ctg	gac	ctg	ttc	tac	tgg	atg	ctc	gcc	gcg	1632
Gly	Leu	Asp	Asp	Gly	Arg	Leu	Asp	Leu	Phe	Tyr	Trp	Met	Leu	Ala	Ala	
	530					535					540					
ctc	ggg	gtg	gcc	aac	ttc	gcg	gcg	ttc	ctg	gtg	ttc	gcg	agc	cgg	cac	1680
Leu	Gly	Val	Ala	Asn	Phe	Ala	Ala	Phe	Leu	Val	Phe	Ala	Ser	Arg	His	
	545			550				555							560	
cag	tac	agg	ccg	gcg	ata	ctg	ccc	gcg	gcg	gac	tcg	ccg	ccg	gac	gac	1728
Gln	Tyr	Arg	Pro	Ala	Ile	Leu	Pro	Ala	Ala	Asp	Ser	Pro	Pro	Asp	Asp	
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gag	ggc	gcg	gtc	agg	gag	gcc	gcg	acg	aca	gtg	aaa	ggg	atg	gac	ttc	1776
Glu	Gly	Ala	Val	Arg	Glu	Ala	Ala	Thr	Thr	Val	Lys	Gly	Met	Asp	Phe	
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tag																1779

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 <212> PRT
 <213> Oryza sativa (japonica cultivar-group)

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 35 40 45
 Gly Ile Ser Met Asn Leu Val Thr Tyr Leu Val Gly Asp Leu His Leu
 50 55 60
 Ser Asn Ala Arg Ser Ala Asn Ile Val Thr Asn Phe Leu Gly Thr Leu
 65 70 75 80
 Asn Leu Leu Ala Leu Leu Gly Gly Phe Leu Ala Asp Ala Val Leu Gly
 85 90 95
 Arg Tyr Leu Thr Val Ala Val Ser Ala Thr Ile Ala Ala Ile Gly Val
 100 105 110
 Ser Leu Leu Ala Ala Ser Thr Val Pro Gly Met Arg Pro Pro Pro
 115 120 125
 Cys Gly Asp Ala Val Ala Ala Ala Ala Ala Glu Ser Gly Gly Cys
 130 135 140
 Val Ala Ala Ser Gly Gly Gln Met Ala Met Leu Tyr Ala Ala Leu Tyr
 145 150 155 160
 Thr Ala Ala Ala Gly Ala Gly Gly Leu Lys Ala Asn Val Ser Gly Phe
 165 170 175
 Gly Ser Asp Gln Phe Asp Gly Arg Asp Arg Arg Glu Gly Lys Ala Met
 180 185 190
 Leu Phe Phe Asn Arg Phe Tyr Phe Cys Ile Ser Leu Gly Ser Val
 195 200 205
 Leu Ala Val Thr Ala Leu Val Tyr Val Gln Glu Asp Val Gly Arg Gly
 210 215 220
 Trp Gly Tyr Gly Ala Ser Ala Ala Ala Met Val Ala Ala Val Ala Val
 225 230 235 240
 Phe Ala Ala Gly Thr Pro Arg Tyr Arg Tyr Arg Arg Pro Gln Gly Ser
 245 250 255
 Pro Leu Thr Ala Ile Gly Arg Val Leu Trp Ala Ala Trp Arg Lys Arg
 260 265 270
 Arg Met Pro Phe Pro Ala Asp Ala Gly Glu Leu His Gly Phe His Lys
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 Ala Lys Val Pro His Thr Asn Arg Leu Arg Cys Leu Asp Lys Ala Ala
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PF59082SeqList_PF59082.txt

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Gln Met Thr 340 Phe Ser Val Glu 345 Gln Ala Ser His Met 350 Asp Arg Arg
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Leu Ser Ile Leu Leu Phe Thr Ser Ala Ser Glu Arg Leu Leu Val Pro
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Leu Ala Arg Arg Leu Met Ile Thr Arg Arg Pro Gln Gly Leu Thr Ser
Leu Gln Arg Val Gly Ala Gly Leu Val Leu Ala Thr Leu Ala Met Ala
Val Ser Ala 420 Val Glu Lys Lys Arg Arg Asp Ala Ser Gly Gly Ala
Gly Gly Gly Gly Val Ala Met Ile Ser Ala Phe Trp Leu Val Pro Gln
Phe 450 Phe Leu Val Gly Ala Gly Glu Ala Phe Ala Tyr Val Gly Gln Leu
465 470 475 480
Glu Phe Phe Ile Arg Glu Ala Pro Glu Arg Met Lys Ser Met Ser Thr
Gly Leu Phe Leu Ala Thr Leu Ala Met Gly Phe Phe Leu Ser Ser Leu
Leu Val Ser 500 Ala Val Asp Ala Ala Thr Arg Gly Ala Trp Ile Arg Asp
Gly Leu Asp Asp Gly Arg Leu Asp Leu Phe Tyr Trp Met Leu Ala Ala
Leu Gly Val Ala Asn Phe 535 Ala Phe Leu Val Phe Ala Ser Arg His
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 <212> DNA
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 <221> CDS
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Val Leu Gly Asp Ala Trp Asp Tyr Arg Gly Arg Pro Ala Ala Arg Ser
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cgg acg ggg agg tgg ggc gcg gcg gcg atg ata ctg gtg gcg gag ctg      144
Arg Thr Gly Arg Trp Gly Ala Ala Met Ile Leu Val Ala Glu Leu
35 40 45
aac gag cgg ctg acg acg ctg ggg atc gcc gtg aac ctg gtc acc tac      192
Asn Glu Arg Leu Thr Thr Leu Gly Ile Ala Val Asn Leu Val Thr Tyr
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ctg acg gcg acg atg cac gcc ggc aac gcc gag gcc gcc aac gtc gtc      240
Leu Thr Ala Thr Met His Ala Gly Asn Ala Glu Ala Ala Asn Val Val
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acc aac ttc atg ggc acc tcc ttc atg ctc tgc ctc ctc ggc ggc ttc      288
Thr Asn Phe Met Gly Thr Ser Phe Met Leu Cys Leu Leu Gly Gly Phe
85 90 95
gtc gcc gac tcc ttc ctc ggc cgc tac ctc acc atc gcc atc ttc acc      336
Val Ala Asp Ser Phe Leu Gly Arg Tyr Leu Thr Ile Ala Ile Phe Thr
100 105 110
gcc gtc caa gcc tcg ggg gtg acg atc ctg acg atc tcg acg gcg gcg      384
Ala Val Gln Ala Ser Gly Val Thr Ile Leu Thr Ile Ser Thr Ala Ala

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PF59082SeqList_PF59082.txt

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Ser	Asp	Gln	Phe	Asp	Glu	Ser	Asp	Ser	Gly	Glu	Lys	Ser	Gln	Met	Met	
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Arg	Phe	Phe	Asn	Trp	Phe	Phe	Phe	Phe	Ile	Ser	Leu	Gly	Ser	Leu	Leu	
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Gly	Tyr	Gly	Ala	Cys	Ala	Ala	Ala	Ile	Ala	Ala	Gly	Leu	Val	Val	Phe	
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Leu	Ala	Gly	Thr	Arg	Arg	Tyr	Arg	Phe	Lys	Lys	Leu	Val	Gly	Ser	Pro	
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Lys	Leu	Ala	Ala	Ala	Glu	Val	Glu	Leu	Ala	Ala	Ser	Ser	Lys	Lys	Ser	
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Arg	Ile	Gly	Val	Gly	Leu	Val	Leu	Ser	Ile	Val	Ala	Met	Val	Cys	Ala	
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Ala	Gly	Val	Cys	Leu	Ala	Asn	Leu	Leu	Val	Tyr	Leu	Val	Ala	Ala	Arg		
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Trp	Tyr	Lys	Tyr	Lys	Ala	Gly	Arg	Ala	Ala	Ala	Ala	Gly	Asp	Gly	Gly		
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Leu	Glu	Leu	Pro	Ser	Asp	Pro	Ala	Met	Leu	Tyr	Asp	Ile	Asp	Val	Gly
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PF59082SeqList_PF59082.txt

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 Met Thr Thr Phe Ser Val Ser Gln Ala Thr Thr Met Asp Arg His Ile
 370 375 380
 Gly Ala Ser Phe Gln Ile Pro Ala Gly Ser Leu Thr Val Phe Phe Val
 385 390 400
 Gly Ser Ile Leu Leu Thr Val Pro Ile Tyr Asp Arg Leu Val Val Pro
 405 410 415
 Val Ala Arg Arg Ala Thr Gly Asn Pro His Gly Leu Thr Pro Leu Gln
 420 425 430
 Arg Ile Gly Val Gly Leu Val Leu Ser Ile Val Ala Met Val Cys Ala
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 Gly Gly Gly Glu Ala Val Pro Met Thr Val Phe Thr Leu Ile Pro Gln
 465 470 475 480
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 485 490 495
 Asp Phe Phe Leu Arg Glu Cys Pro Lys Gly Met Lys Thr Met Ser Thr
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 530 535 540
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 545 550 555 560
 Ala Gly Val Cys Leu Ala Asn Leu Leu Val Tyr Leu Val Ala Ala Arg
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 Thr Val Ala Asp Ala Val Asp Tyr Lys Gly Arg Pro Ala Asp Lys Ser
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 Lys Thr Gly Gly Trp Ile Thr Ala Leu Ile Leu Gly Ile Glu Val
 35 40 45
 gtg gag agg cta tca aca atg gga ata gca gtg aat ttg gta aca tat 192
 Val Glu Arg Leu Ser Thr Met Gly Ile Ala Val Asn Leu Val Thr Tyr
 50 55 60
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 Leu Met Glu Thr Met His Leu Pro Ser Ser Thr Ser Ala Asn Ile Val
 65 70 75 80
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 Thr Asp Phe Met Gly Thr Ser Phe Leu Leu Cys Leu Leu Gly Gly Phe
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 Leu Ala Asp Ser Phe Leu Gly Arg Phe Lys Thr Ile Gly Ile Phe Ser
 100 105 110
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PF59082SeqList_PF59082.txt

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Ala	Thr	Ala	Phe	Gln	Met	Thr	Ile	Leu	Tyr	Val	Ser	Leu	Tyr	Leu	Ile	
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Asp	Gln	Phe	Asp	Asp	Lys	Asp	Pro	Lys	Glu	Lys	Ala	His	Met	Ala	Phe	
			180					185					190			
ttc	ttc	aac	agg	ttc	ttc	ttc	ttt	att	agt	atg	ggg	aca	tta	ttg	gct	624
Phe	Phe	Asn	Arg	Phe	Phe	Phe	Phe	Ile	Ser	Met	Gly	Thr	Leu	Leu	Ala	
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Tyr	Gly	Ile	Cys	Thr	Val	Ser	Met	Ala	Ile	Ala	Ile	Val	Ile	Phe	Leu	
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Cys	Gly	Thr	Lys	Arg	Tyr	Arg	Tyr	Lys	Lys	Ser	Gln	Gly	Ser	Pro	Val	
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Ile	Val	Ala	Glu	Gly	Asp	Phe	Glu	Gln	Thr	Leu	Asp	Gly	Val	Ala	Ile	
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Thr	Thr	Tyr	Ala	Gln	Met	Ile	Thr	Phe	Ser	Val	Glu	Gln	Ala	Ser	Thr	
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Ala	Ala	Ala	Ala	Leu	Val	Glu	Gln	Lys	Arg	Leu	Ser	Val	Ala	Lys	Ser	
			435				440					445				
agt	tca	caa	aaa	aca	ttg	cct	ata	agt	gtg	ttt	tta	ctt	gtt	cca	caa	1392
Ser	Ser	Gln	Lys	Thr	Leu	Pro	Ile	Ser	Val	Phe	Leu	Leu	Val	Pro	Gln	
					455						460					
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Phe	Phe	Leu	Val	Gly	Ala	Gly	Glu	Ala	Phe	Ile	Tyr	Thr	Gly	Gln	Leu	
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Gly	Leu	Phe	Leu	Thr	Thr	Leu	Ser	Leu	Gly	Phe	Phe	Val	Ser	Ser	Phe		
			500					505					510				
ttg	gtc	tca	atc	gtc	aag	agg	gtc	act	tca	act	tct	act	gat	gta	gga	1584	
Leu	Val	Ser	Ile	Val	Lys	Arg	Val	Thr	Ser	Thr	Ser	Thr	Asp	Val	Gly		
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tgg	ctg	gct	gat	aac	att	aac	cac	ggc	cga	ctc	gat	tac	ttt	tat	tgg	1632	
Trp	Leu	Ala	Asp	Asn	Ile	Asn	His	Gly	Arg	Leu	Asp	Tyr	Phe	Tyr	Trp		
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ctt	tta	gtc	att	ctc	agt	gga	att	aac	ttc	gtt	gtc	tat	atc	ata	tgt	1680	
Leu	Leu	Val	Ile	Leu	Ser	Gly	Ile	Asn	Phe	Val	Val	Tyr	Ile	Ile	Cys		
		545			550				555					560			
gcc	ttg	tgg	ttt	aag	cca	acg	aag	ggg	aaa	gac	tca	gta	gag	aag	gaa	1728	
Ala	Leu	Trp	Phe	Lys	Pro	Thr	Lys	Gly	Lys	Asp	Ser	Val	Glu	Lys	Glu		
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aat	ggc	aag	gga	ttt	tca	gtt	gaa	gac	tgc	tga						1761	
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<211> 586

<212> PRT

<213> Arabidopsis thaliana

<400> 48

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Lys	Thr	Gly	Gly	Trp	Ile	Thr	Ala	Ala	Leu	Ile	Leu	Gly	Ile	Glu	Val		
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Thr	Asp	Phe	Met	Gly	Thr	Ser	Phe	Leu	Leu	Cys	Leu	Leu	Gly	Gly	Phe		
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Leu	Ala	Asp	Ser	Phe	Leu	Gly	Arg	Phe	Lys	Thr	Ile	Gly	Ile	Phe	Ser		
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Thr	Ile	Gln	Ala	Leu	Gly	Thr	Gly	Ala	Leu	Ala	Val	Ala	Thr	Lys	Leu		
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Pro	Glu	Leu	Arg	Pro	Pro	Thr	Cys	His	His	Gly	Glu	Ala	Cys	Ile	Pro		
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Asp	Gln	Phe	Asp	Lys	Asp	Pro	Lys	Glu	Lys	Ala	His	Met	Ala	Phe			
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Phe	Phe	Asn	Arg	Phe	Phe	Phe	Phe	Ile	Ser	Met	Gly	Thr	Leu	Leu	Ala		
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Cys	Gly	Thr	Lys	Arg	Tyr	Arg	Tyr	Lys	Lys	Ser	Gln	Gly	Ser	Pro	Val		
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 405 410 415
 Ser Leu Gln Arg Ile Ala Ile Gly Leu Val Leu Ser Thr Ala Gly Met
 420 425 430
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 435 440 445
 Ser Ser Gln Lys Thr Leu Pro Ile Ser Val Phe Leu Leu Val Pro Gln
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 Phe Phe Leu Val Gly Ala Gly Glu Ala Phe Ile Tyr Thr Gly Gln Leu
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 Asp Phe Phe Ile Thr Gln Ser Pro Lys Gly Met Lys Thr Met Ser Thr
 485 490 495
 Gly Leu Phe Leu Thr Thr Leu Ser Leu Gly Phe Phe Val Ser Ser Phe
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 Leu Val Ser Ile Val Lys Arg Val Thr Ser Thr Ser Thr Asp Val Gly
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 Trp Leu Ala Asp Asn Ile Asn His Gly Arg Leu Asp Tyr Phe Tyr Trp
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 Leu Leu Val Ile Leu Ser Gly Ile Asn Phe Val Val Tyr Ile Ile Cys
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<213> Oryza sativa

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114

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 1 5

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 Thr Ala Ala Glu Gly Lys Ala Leu Thr Asp Ala Trp Asp Tyr Lys Gly
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162

agg ccg gcg ggg agg gcg gcc acc ggc ggg tgg ggc tgc gcg gcg atg
 Arg Pro Ala Gly Arg Ala Ala Thr Gly Gly Trp Gly Cys Ala Ala Met
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210

atc ctc ggg gcg gag ctg ttc gag cgg atg acg acg ctg ggc atc gcc
 Ile Leu Gly Ala Glu Leu Phe Glu Arg Met Thr Thr Leu Gly Ile Ala
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258

gtc aac ctg gtg ccg tac atg acc ggg acg atg cac ctc ggc aat gcc
 Val Asn Leu Val Pro Tyr Met Thr Gly Thr Met His Leu Gly Asn Ala
 60 65 70

306

gcc gcc gcc aac acg gtc acc aac ttc atc ggc acc tcc ttc atg ctc
 Ala Ala Ala Asn Thr Val Thr Asn Phe Ile Gly Thr Ser Phe Met Leu
 75 80 85

354

tgc ctc ctc ggc ggc ttc gtc gcc acc tac ctc ggc cgc tac ctc
 Cys Leu Leu Gly Gly Phe Val Ala Asp Thr Tyr Leu Gly Arg Tyr Leu
 90 95 100

402

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 Thr Ile Ala Ile Phe Glu Ala Val Gln Ala Thr Gly Val Met Ile Leu
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450

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	Gly	Val	Leu	Tyr	Leu	Gly	Leu	Tyr	Leu	Thr	Ala	Leu	Gly	Thr	Gly	Gly	
	ctc	aag	tcc	agc	gtc	tcc	ggc	ttc	ggc	tcc	gac	cag	ttc	gac	gag	tcc	642
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	Asp	Val	Asp	Gly	Glu	Arg	Lys	Lys	Met	Met	Arg	Phe	Phe	Asn	Trp	Phe	
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	Tyr	Phe	Phe	Val	Ser	Leu	Gly	Ala	Leu	Leu	Ala	Val	Thr	Val	Leu	Val	
200	tac	gtg	cag	gac	aac	gtc	gga	cgc	cgg	tgg	ggg	tac	ggc	atc	tgc	gcc	786
	Tyr	Val	Gln	Asp	Asn	Val	Gly	Arg	Arg	Trp	Gly	Tyr	Gly	Ile	Cys	Ala	
	gcc	ggc	atc	ctc	gcc	ggc	ctc	gcc	gtg	ttc	ctc	tcc	ggg	acc	agg	agg	834
	Ala	Gly	Ile	Leu	Ala	Gly	Leu	Ala	Val	Phe	Leu	Ser	Gly	Thr	Arg	Arg	
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	Tyr	Arg	Phe	Lys	Lys	Leu	Val	Gly	Ser	Pro	Leu	Thr	Gln	Val	Ala	Ala	
	gtc	acc	gcc	gcc	gcc	tgg	agc	aag	agg	tcg	ctg	ccg	ctg	ccg	tcc	gac	930
	Val	Thr	Ala	Ala	Ala	Trp	Ser	Lys	Arg	Ser	Leu	Pro	Leu	Pro	Ser	Asp	
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	Pro	Asp	Met	Leu	Tyr	Asp	Val	Asp	Asp	Ala	Ala	Ala	Ala	Gly	His	Asp	
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	Val	Lys	Gly	Lys	Gln	Arg	Met	Pro	His	Ser	Lys	Glu	Cys	Arg	Phe	Leu	
	gac	cat	gcg	gcg	atc	atc	gac	agg	tcg	gcg	gcg	gag	tcg	ccg	gcg	acg	1074
	Asp	His	Ala	Ala	Ile	Ile	Asp	Arg	Ser	Ala	Ala	Glu	Ser	Pro	Ala	Thr	
	gcg	agc	aag	tgg	agg	ctg	tgc	acg	agg	acg	gac	gtg	gag	gag	gtg	aag	1122
	Ala	Ser	Lys	Trp	Arg	Leu	Cys	Thr	Arg	Thr	Asp	Val	Glu	Glu	Val	Lys	
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	Gln	Val	Val	Arg	Met	Leu	Pro	Ile	Trp	Ala	Thr	Thr	Ile	Met	Phe	Trp	
	acc	atc	cac	gcc	cag	atg	acc	acc	ttc	gcc	gtc	gcg	cag	gcc	gag	ctc	1218
	Thr	Ile	His	Ala	Gln	Met	Thr	Thr	Phe	Ala	Val	Ala	Gln	Ala	Glu	Leu	
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	acc	gtc	ttc	ctc	atc	gcc	tcc	atc	ctc	ctc	acc	gtc	ccc	ttc	tac	gac	1314
	Thr	Val	Phe	Leu	Ile	Ala	Ser	Ile	Leu	Leu	Thr	Val	Pro	Phe	Tyr	Asp	
	cgc	ctc	gtc	gtc	ccc	gtc	gcg	cgc	cgc	gcc	acg	gcc	aac	ccg	cac	ggc	1362
	Arg	Leu	Val	Val	Pro	Val	Ala	Arg	Arg	Ala	Thr	Ala	Asn	Pro	His	Gly	
	ctc	acc	ccg	ctc	cag	cgc	gtc	ttc	gtg	ggc	ctc	tcc	ctc	tcc	atc	gcc	1410
	Leu	Thr	Pro	Leu	Gln	Arg	Val	Phe	Val	Gly	Leu	Ser	Leu	Ser	Ile	Ala	
	ggc	atg	gcc	gtc	gcc	gcg	gcc	gtc	gag	cgc	cac	cgc	gcc	acc	gcc	tcc	1458
	Gly	Met	Ala	Val	Ala	Ala	Ala	Val	Glu	Arg	His	Arg	Ala	Thr	Ala	Ser	
440	gcc	tcc	gcc	gcc	gcc	gcg	ccc	acg	gtg	ttc	ctc	ctc	atg	ccg	cag	1506	
	Ala	Ser	Ala	Ala	Ala	Ala	Ala	Pro	Thr	Val	Phe	Leu	Leu	Met	Pro	Gln	
	ttc	ctc	ctc	gtc	ggc	gcc	ggc	gag	gcg	ttc	acc	tac	atg	ggc	cag	ctc	1554
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PF59082SeqList_PF59082.txt

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Gly Leu Phe Leu Ser Thr Cys Ala Ile Gly Phe Phe Phe Ser Thr Leu
      505      510      515
ctc gtc acc atc gtc cac aag gtc acc ggc cat ggc gcc cgc ggc ggc      1698
Leu Val Thr Ile Val His Lys Val Thr Gly His Gly Ala Arg Gly Gly
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ggc tgg ctc gcc gac aac ctc gac gac ggc agg ctc gac tac ttc tac      1746
Gly Trp Leu Ala Asp Asn Leu Asp Asp Gly Arg Leu Asp Tyr Phe Tyr
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tgg ctg ctc gcc gtc atc agc gcc atc aac ctc gtc ctc ttc acc gtc      1794
Trp Leu Leu Ala Val Ile Ser Ala Ile Asn Leu Val Leu Phe Thr Val
      555      560      565
gcc gcc agg ggg tac gtc tac aag gag aag cgc ctc gcc gac gcc ggc      1842
Ala Ala Arg Gly Tyr Val Tyr Lys Glu Lys Arg Leu Ala Asp Ala Gly
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atc gag ctc gcc gac gag gag acc atc gcc gtc ggc cac taatagtgc      1891
Ile Glu Leu Ala Asp Glu Glu Thr Ile Ala Val Gly His
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Thr Met His Leu Gly Asn Ala Ala Ala Ala Asn Thr Val Thr Asn Phe
65      70      75      80
Ile Gly Thr Ser Phe Met Leu Cys Leu Leu Gly Gly Phe Val Ala Asp
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Thr Tyr Leu Gly Arg Tyr Leu Thr Ile Ala Ile Phe Glu Ala Val Gln
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Ala Thr Gly Val Met Ile Leu Thr Ile Ser Thr Ala Ala Pro Gly Leu
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Arg Pro Pro Ala Cys Gly Asp Pro Lys Gly Ala Ser Ala Glu Cys Val
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Ala Ala Asp Gly Thr Gln Leu Gly Val Leu Tyr Leu Gly Leu Tyr Leu
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Thr Ala Leu Gly Thr Gly Gly Leu Lys Ser Val Ser Gly Phe Gly
      165      170      175
Ser Asp Gln Phe Asp Glu Ser Asp Val Asp Gly Glu Arg Lys Lys Met
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Met Arg Phe Phe Asn Trp Phe Tyr Phe Phe Val Ser Leu Gly Ala Leu
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Pro	Leu	Thr	Gln	Val	Ala	Ala	Val	Thr	Ala	Ala	Ala	Trp	Ser	Lys	Arg
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Ser	Lys	Glu	Cys	Arg	Phe	Leu	Asp	His	Ala	Ala	Ile	Ile	Asp	Arg	Ser
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Ala	Ala	Glu	Ser	Pro	Ala	Thr	Ala	Ser	Lys	Trp	Arg	Leu	Cys	Thr	Arg
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Thr	Asp	Val	Glu	Glu	Val	Lys	Gln	Val	Val	Arg	Met	Leu	Pro	Ile	Trp
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Phe	Gln	Gly	Arg	Pro	Ala	Asp	Arg	Ser	Lys	Thr	Gly	Gly	Trp	Ala	Ser		
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Gly	Asn	Ala	Thr	Ala	Ala	Asn	Thr	Val	Thr	Asn	Phe	Leu	Gly	Thr	Ser	
65					70				75						80	
ttc	atg	ctc	tgt	ctc	ctc	ggt	ggc	ttc	ata	gcg	gac	act	ttt	ctt	gga	288
Phe	Met	Leu	Cys	Leu	Leu	Gly	Gly	Phe	Ile	Ala	Asp	Thr	Phe	Leu	Gly	
				85					90					95		
agg	tac	cta	acc	att	gct	ata	ttc	gcc	gct	atc	caa	gcc	aca	ggt	ggt	336
Arg	Tyr	Leu	Thr	Ile	Ala	Ile	Phe	Ala	Ala	Ile	Gln	Ala	Thr	Gly	Val	
			100				105					110				
tcg	atc	tta	acc	ctc	tca	act	atc	ata	ccg	gga	ctg	aga	cca	cca	aga	384
Ser	Ile	Leu	Thr	Leu	Ser	Thr	Ile	Ile	Pro	Gly	Leu	Arg	Pro	Pro	Arg	
		115					120					125				
tgc	gat	cca	acg	acc	tcg	tct	cat	tgc	gta	caa	gcg	aat	gga	ata	caa	432
Cys	Asp	Pro	Thr	Thr	Ser	Ser	His	Cys	Val	Gln	Ala	Asn	Gly	Ile	Gln	
	130					135					140					
ctt	acg	gtc	cta	tac	tta	gcc	tta	tac	ctt	acg	gcc	cta	gga	act	gga	480
Leu	Thr	Val	Leu	Tyr	Leu	Ala	Leu	Tyr	Leu	Thr	Ala	Leu	Gly	Thr	Gly	
145					150				155						160	
gga	gtg	aag	gca	agc	gtc	tcc	ggt	ttt	ggg	tca	gac	caa	ttc	gat	gac	528
Gly	Val	Lys	Ala	Ser	Val	Ser	Gly	Phe	Gly	Ser	Asp	Gln	Phe	Asp	Asp	
				165				170						175		
act	gaa	ccg	aaa	gaa	cgg	tca	caa	atg	aca	tat	ttc	ttc	aac	cgt	ttc	576
Thr	Glu	Pro	Lys	Glu	Arg	Ser	Gln	Met	Thr	Tyr	Phe	Phe	Asn	Arg	Phe	
			180				185					190				
ttc	ttt	tgt	atc	aac	gtc	ggt	tct	ctt	atg	gcc	gtg	acg	gtc	ctt	gtc	624
Phe	Phe	Cys	Ile	Asn	Val	Gly	Ser	Leu	Met	Ala	Val	Thr	Val	Leu	Val	
		195					200					205				
tac	ata	caa	gat	gat	gtt	gga	cgt	aaa	tgg	ggc	tat	ggc	att	tgc	gcg	672
Tyr	Ile	Gln	Asp	Asp	Val	Gly	Arg	Lys	Trp	Gly	Tyr	Gly	Ile	Cys	Ala	
	210					215					220					
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Leu	Ala	Ile	Val	Leu	Ser	Leu	Ser	Ile	Phe	Leu	Ala	Gly	Thr	Asn	Arg	
225					230				235						240	
tac	cgg	ttc	aag	aag	ttg	att	ggt	agc	ccg	atg	acg	caa	gtt	ggc	acg	768
Tyr	Arg	Phe	Lys	Lys	Leu	Ile	Gly	Ser	Pro	Met	Thr	Gln	Val	Gly	Thr	
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gtt	ctt	gtg	gcg	gcg	tgg	agg	aat	agg	cgg	ctc	gag	ttg	cca	tcg	gac	816
Val	Leu	Val	Ala	Ala	Trp	Arg	Asn	Arg	Arg	Leu	Glu	Leu	Pro	Ser	Asp	
		260					265					270				
ccg	tcg	ttt	cta	tat	gac	ttg	gac	gat	ggt	att	gcg	gct	gaa	ggt	tcg	864
Pro	Ser	Phe	Leu	Tyr	Asp	Leu	Asp	Asp	Val	Ile	Ala	Ala	Glu	Gly	Ser	
		275					280				285					
atg	aag	agt	aaa	caa	aag	ttg	ccg	cat	acc	aat	cag	ttc	cgg	tca	ttg	912
Met	Lys	Ser	Lys	Gln	Lys	Leu	Pro	His	Thr	Asn	Gln	Phe	Arg	Ser	Leu	
	290					295					300					
gac	aaa	gca	gcg	ata	aag	gac	caa	gaa	atg	gca	atg	acc	caa	aac	gta	960
Asp	Lys	Ala	Ala	Ile	Lys	Asp	Gln	Glu	Met	Ala	Met	Thr	Gln	Asn	Val	
305					310				315						320	
tac	aac	aaa	tgg	aca	cta	tca	aca	gta	act	gat	att	gag	gaa	gtg	aaa	1008
Tyr	Asn	Lys	Trp	Thr	Leu	Ser	Thr	Val	Thr	Asp	Ile	Glu	Glu	Val	Lys	
				325				330						335		
caa	att	gta	cgg	atg	tta	cca	att	tgg	gca	aca	tgc	atc	ctc	ttt	tgg	1056
Gln	Ile	Val	Arg	Met	Leu	Pro	Ile	Trp	Ala	Thr	Cys	Ile	Leu	Phe	Trp	
		340					345					350				
act	gtc	cat	gct	caa	cta	acg	aca	tta	tcg	gtc	gcg	cag	tcc	gag	acc	1104
Thr	Val	His	Ala	Gln	Leu	Thr	Thr	Leu	Ser	Val	Ala	Gln	Ser	Glu	Thr	
		355				360					365					
atg	gac	cgt	cac	att	ggg	agc	ttt	gag	atc	cct	cca	gcc	gca	atg	gcc	1152
Met	Asp	Arg	His	Ile	Gly	Ser	Phe	Glu	Ile	Pro	Pro	Ala	Ala	Met	Ala	
	370					375					380					
gta	ttc	tat	atc	ggt	ggc	ctc	ctc	cta	acc	acc	gcc	gtc	tac	gac	cgt	1200
Val	Phe	Tyr	Ile	Gly	Gly	Leu	Leu	Leu	Thr	Thr	Ala	Val	Tyr	Asp	Arg	
385					390				395						400	
ctc	gcg	att	ccc	tta	tgc	aaa	aag	cta	ttc	aac	tac	ccc	cac	ggt	ctg	1248

PF59082SeqList_PF59082.txt

Leu	Ala	Ile	Pro	Leu	Cys	Lys	Lys	Leu	Phe	Asn	Tyr	Pro	His	Gly	Leu	
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Arg	Pro	Leu	Gln	Arg	Ile	Gly	Leu	Gly	Leu	Leu	Leu	Ala	Ala	Met	Gly	
			420					425					430			
atg	gcc	gta	gct	gct	ttg	gtc	gag	atc	aaa	cgt	ctt	aga	aca	gca	cat	1344
Met	Ala	Val	Ala	Ala	Leu	Val	Glu	Ile	Lys	Arg	Leu	Arg	Thr	Ala	His	
		435				440						445				
gcc	cac	ggt	cca	aca	gtc	aaa	acc	ctt	cct	cta	ggg	ttt	tct	cta	ctc	1392
Ala	His	Gly	Pro	Thr	Val	Lys	Thr	Leu	Pro	Leu	Gly	Phe	Ser	Leu	Leu	
	450					455					460					
atc	cca	caa	tac	ctt	att	gtg	ggt	atc	ggc	gag	gcg	ttg	atc	tac	aca	1440
Ile	Pro	Gln	Tyr	Leu	Ile	Val	Gly	Ile	Gly	Glu	Ala	Leu	Ile	Tyr	Thr	
465				470				475							480	
gga	cag	cta	gat	ttt	ttc	ttg	aga	gag	tgt	cct	aaa	ggt	atg	aaa	aca	1488
Gly	Gln	Leu	Asp	Phe	Phe	Leu	Arg	Glu	Cys	Pro	Lys	Gly	Met	Lys	Thr	
			485					490						495		
atg	agc	acg	ggt	tta	ttg	ttg	agc	aca	ttg	gct	tta	ggg	ttt	ttc	ttc	1536
Met	Ser	Thr	Gly	Leu	Leu	Leu	Ser	Thr	Leu	Ala	Leu	Gly	Phe	Phe	Phe	
			500					505					510			
agc	tcg	gtt	ctc	gta	acc	atc	gtt	gag	aaa	gtc	act	gat	aaa	gct	cat	1584
Ser	Ser	Val	Leu	Val	Thr	Ile	Val	Glu	Lys	Val	Thr	Asp	Lys	Ala	His	
		515					520					525				
ccg	tgg	ata	gct	gat	gat	ctc	aac	aag	ggc	cgt	cta	tac	aat	ttc	tat	1632
Pro	Trp	Ile	Ala	Asp	Asp	Leu	Asn	Lys	Gly	Arg	Leu	Tyr	Asn	Phe	Tyr	
	530					535					540					
tgg	ctt	gtg	gca	gta	att	gtt	gct	ttg	aac	ttc	ctc	ggt	ttc	ctt	gtt	1680
Trp	Leu	Val	Ala	Val	Ile	Val	Ala	Leu	Asn	Phe	Leu	Val	Phe	Leu	Val	
545				550					555						560	
ttc	tcc	aag	tgg	tac	gtc	tac	aag	gag	aag	aga	cta	gct	gac	ctt	ggg	1728
Phe	Ser	Lys	Trp	Tyr	Val	Tyr	Lys	Glu	Lys	Arg	Leu	Ala	Asp	Leu	Gly	
			565					570						575		
att	gag	ttg	gaa	gac	gag	cca	gac	att	ccc	atg	ggt	cat	tga			1770
Ile	Glu	Leu	Glu	Asp	Glu	Pro	Asp	Ile	Pro	Met	Gly	His				
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 <212> PRT
 <213> Brassica napus

<400> 52

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			20					25					30			
Ala	Ala	Met	Ile	Leu	Cys	Ile	Glu	Ala	Val	Glu	Arg	Leu	Thr	Thr	Leu	
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Gly	Ile	Gly	Val	Asn	Leu	Val	Thr	Tyr	Leu	Thr	Gly	Thr	Met	His	Leu	
	50					55					60					
Gly	Asn	Ala	Thr	Ala	Ala	Asn	Thr	Val	Thr	Asn	Phe	Leu	Gly	Thr	Ser	
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Phe	Met	Leu	Cys	Leu	Leu	Gly	Gly	Phe	Ile	Ala	Asp	Thr	Phe	Leu	Gly	
			85					90						95		
Arg	Tyr	Leu	Thr	Ile	Ala	Ile	Phe	Ala	Ala	Ile	Gln	Ala	Thr	Gly	Val	
			100					105					110			
Ser	Ile	Leu	Thr	Leu	Ser	Thr	Ile	Ile	Pro	Gly	Leu	Arg	Pro	Pro	Arg	
		115					120					125				
Cys	Asp	Pro	Thr	Thr	Ser	Ser	His	Cys	Val	Gln	Ala	Asn	Gly	Ile	Gln	
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Leu	Thr	Val	Leu	Tyr	Leu	Ala	Leu	Tyr	Leu	Thr	Ala	Leu	Gly	Thr	Gly	
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Gly	Val	Lys	Ala	Ser	Val	Ser	Gly	Phe	Gly	Ser	Asp	Gln	Phe	Asp	Asp	
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Thr	Glu	Pro	Lys	Glu	Arg	Ser	Gln	Met	Thr	Tyr	Phe	Phe	Asn	Arg	Phe	
			180					185					190			
Phe	Phe	Cys	Ile	Asn	Val	Gly	Ser	Leu	Met	Ala	Val	Thr	Val	Leu	Val	
		195					200					205				
Tyr	Ile	Gln	Asp	Asp	Val	Gly	Arg	Lys	Trp	Gly	Tyr	Gly	Ile	Cys	Ala	

PF59082SeqList_PF59082.txt

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Leu Ala Ile Val Leu Ser Leu Ser Ile Phe Leu Ala Gly Thr Asn Arg
225          230          235
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245
Val Leu Val Ala Trp Arg Asn Arg Arg Leu Glu Leu Pro Ser Asp
260
Pro Ser Phe Leu Tyr Asp Leu Asp Asp Val Ile Ala Ala Glu Gly Ser
275
Met Lys Ser Lys Gln Lys Leu Pro His Thr Asn Gln Phe Arg Ser Leu
290
Asp Lys Ala Ala Ile Lys Asp Gln Glu Met Ala Met Thr Gln Asn Val
305          310          315
Tyr Asn Lys Trp Thr Leu Ser Thr Val Thr Asp Ile Glu Glu Val Lys
325
Gln Ile Val Arg Met Leu Pro Ile Trp Ala Thr Cys Ile Leu Phe Trp
340
Thr Val His Ala Gln Leu Thr Thr Leu Ser Val Ala Gln Ser Glu Thr
355
Met Asp Arg His Ile Gly Ser Phe Glu Ile Pro Pro Ala Ala Met Ala
370
Val Phe Tyr Ile Gly Gly Leu Leu Leu Thr Thr Ala Val Tyr Asp Arg
385          390          395
Leu Ala Ile Pro Leu Cys Lys Lys Leu Phe Asn Tyr Pro His Gly Leu
405
Arg Pro Leu Gln Arg Ile Gly Leu Gly Leu Leu Ala Ala Met Gly
420
Met Ala Val Ala Ala Leu Val Glu Ile Lys Arg Leu Arg Thr Ala His
435
Ala His Gly Pro Thr Val Lys Thr Leu Pro Leu Gly Phe Ser Leu Leu
450
Ile Pro Gln Tyr Leu Ile Val Gly Ile Gly Glu Ala Leu Ile Tyr Thr
465          470          475
Gly Gln Leu Asp Phe Leu Arg Glu Cys Pro Lys Gly Met Lys Thr
485
Met Ser Thr Gly Leu Leu Leu Ser Thr Leu Ala Leu Gly Phe Phe Phe
500
Ser Ser Val Leu Val Thr Ile Val Glu Lys Val Thr Asp Lys Ala His
515
Pro Trp Ile Ala Asp Asp Leu Asn Lys Gly Arg Leu Tyr Asn Phe Tyr
530
Trp Leu Val Ala Val Ile Val Ala Leu Asn Phe Leu Val Phe Leu Val
545          550          555
Phe Ser Lys Trp Tyr Val Tyr Lys Glu Lys Arg Leu Ala Asp Leu Gly
565
Ile Glu Leu Glu Asp Glu Pro Asp Ile Pro Met Gly His
580          585

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 <212> DNA
 <213> Oryza sativa

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ggc ggc ggc ggc aac atg gtg cgg gac gcg gtg gac tac cgg gga tgc	96
Gly Gly Gly Gly Asn Met Val Arg Asp Ala Val Asp Tyr Arg Gly Cys	
20 25 30	
ccg gcg gac agg tcg gcg acg ggg tgg gtg gcg gcg ctg gtg	144
Pro Ala Asp Arg Ser Ala Thr Gly Gly Trp Val Ala Ala Ala Leu Val	
35 40 45	
ctg ggg atc gag ctg tgc gag cgg ctg tcg acg atg ggg atc gcg gtg	192
Leu Gly Ile Glu Leu Cys Glu Arg Leu Ser Thr Met Gly Ile Ala Val	

PF59082SeqList_PF59082.txt

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Asn Leu Val Thr Tyr Leu Thr Gly Thr Met His Leu Pro Ser Ala Ala			
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gcc gcc aac gtc gtc acc gac ttc atg ggc acc tcc ttc ctc ctc tgc			288
Ala Ala Asn Val Val Thr Asp Phe Met Gly Thr Ser Phe Leu Leu Cys			
85	90	95	
ctc ctc ggc ggc ttc ctc gcc gac tcc ttc ctc ggc cgc tac ctc acc			336
Leu Leu Gly Gly Phe Leu Ala Asp Ser Phe Leu Gly Arg Tyr Leu Thr			
100	105	110	
atc gcc gtc gtc gtc ctc gtc cag tcc atc ggc acc gcc ctc gcc			384
Ile Ala Val Phe Ala Leu Val Gln Ser Ile Gly Thr Ala Leu Leu Ala			
115	120	125	
gcc tcc acc ctc gtc acc cac ctc cgc ccg ccg ccc ggg gag cag ccg			432
Ala Ser Thr Leu Val Thr His Leu Arg Pro Pro Gly Glu Gln Pro			
130	135	140	
acg ccg gtg cag atg gcc gtg ctc tac gcc tgc ctc tac ctc atc gcc			480
Thr Pro Val Gln Met Ala Val Leu Tyr Ala Cys Leu Tyr Leu Ile Ala			
145	150	155	160
ctc ggc acc ggc ggc ctc aag tcc agc gtc tcc ggc ttc ggc acc gac			528
Leu Gly Thr Gly Gly Leu Lys Ser Ser Val Ser Gly Phe Gly Thr Asp			
165	170	175	
cag ttc gac gac cgc gac ggc cgg gag cgc gcc gcc atg ggc ctc ttc			576
Gln Phe Asp Asp Arg Asp Gly Arg Glu Arg Ala Ala Met Gly Leu Phe			
180	185	190	
ttc aac cgc ttc ttc ttc ttc atc agc ctc ggc acg ctg ctc gcc gtc			624
Phe Asn Arg Phe Phe Phe Phe Ile Ser Leu Gly Thr Leu Leu Ala Val			
195	200	205	
acc gtg ctc gtc tac gtc cag gac cac gtc ggc cgg agc tgg gcc tac			672
Thr Val Leu Val Tyr Val Gln Asp His Val Gly Arg Ser Trp Ala Tyr			
210	215	220	
ggc atc tgc tcc gcc gcc atg ctc gcc gcc atc gcc gtc ttc ctc tcc			720
Gly Ile Cys Ser Ala Ala Met Leu Ala Ala Ile Ala Val Phe Leu Ser			
225	230	235	240
ggg acc agg agg tac cgc tac aag cgg agc tcc ggg agc ccc atc gtc			768
Gly Thr Arg Arg Tyr Arg Tyr Lys Arg Ser Ser Gly Ser Pro Ile Val			
245	250	255	
cac atc ctc cag gtg ctc gtc gcc gcg gcg cgg aag cgc ggg gtc gtc			816
His Ile Leu Gln Val Leu Val Ala Ala Ala Arg Lys Arg Gly Val Val			
260	265	270	
aag cgc ccg ccc acc gcg gcg gag ctc tac gag gac gac cgc ccc gag			864
Lys Arg Pro Pro Thr Ala Ala Glu Leu Tyr Glu Asp Asp Arg Pro Glu			
275	280	285	
cac gcc cgg atc gcg cac acc gcg cag ttc ccg tgc ctg gac atg gcg			912
His Ala Arg Ile Ala His Thr Ala Gln Phe Pro Cys Leu Asp Met Ala			
290	295	300	
gcg gtg gtg gcc ggc gaa gag gac aac gag gtg gcc ggg ccg ggc ggc			960
Ala Val Val Ala Gly Glu Glu Asp Asn Glu Val Ala Gly Pro Gly Gly			
305	310	315	320
ccg gcg gcg ccc aac ccg tgg aag ctc tgc gtg tcg cgc gtg gag			1008
Pro Ala Ala Pro Asn Pro Trp Lys Leu Cys Ser Val Ser Arg Val Glu			
325	330	335	
gag gtg aag atg gtg gcg agg ctg atg ccg gtg tgg gcg acg acg atc			1056
Glu Val Lys Met Val Ala Arg Leu Met Pro Val Trp Ala Thr Ile			
340	345	350	
ctc ttc tgg acc atc tac gcg cag atg atc acc ttc tcc gtg gag cag			1104
Leu Phe Trp Thr Ile Tyr Ala Gln Met Ile Thr Phe Ser Val Glu Gln			
355	360	365	
gcc acc acc atg gac cgc cgc gtc ggc gcc gcc ttc gag atc ccg gcc			1152
Ala Thr Thr Met Asp Arg Val Gly Ala Gly Phe Glu Ile Pro Ala			
370	375	380	
gcc tcg ctc acc gtc ttc ttc gtc ggc gcc atc atg ctc acc ctc gcc			1200
Ala Ser Leu Thr Val Phe Phe Val Gly Ala Ile Met Leu Thr Leu Ala			
385	390	395	400
gtc tac gac cgc gtc ttc atc ccg ctc tgc cgc gta ctc acc ggc aag			1248
Val Tyr Asp Arg Val Phe Ile Pro Leu Cys Arg Val Leu Thr Gly Lys			
405	410	415	
caa ggc ttc acc aac ctg gag aag atc ggc atc ggc ctc gcc ctc tcc			1296
Gln Gly Phe Thr Asn Leu Glu Lys Ile Gly Ile Gly Leu Ala Leu Ser			

PF59082SeqList_PF59082.txt

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435																
440																
gtc	gcc	gtc	gcc	gcc	acc	acc	ggg	aac	tcc	acg	ccg	atc	agc	gtg	ttc	
Val	Ala	Val	Ala	Ala	Thr	Thr	Gly	Asn	Ser	Thr	Pro	Ile	Ser	Val	Phe	
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455																
ctg	ctg	acg	ccg	cag	ttc	ctg	ctg	gtg	ggc	gcc	ggc	gag	gcg	ttc	atc	
Leu	Leu	Thr	Pro	Gln	Phe	Leu	Leu	Val	Gly	Ala	Gly	Glu	Ala	Phe	Ile	
465																
470																
tac	acg	ggg	cag	ctg	gac	ttc	ttc	atc	acg	agg	tgc	ccc	aag	ggg	atg	
Tyr	Thr	Gly	Gln	Leu	Asp	Phe	Phe	Ile	Thr	Arg	Ser	Pro	Lys	Gly	Met	
485																
490																
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Lys	Thr	Met	Ser	Thr	Gly	Leu	Phe	Leu	Thr	Thr	Leu	Ser	Leu	Gly	Phe	
500																
505																
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Phe	Phe	Ser	Ser	Val	Leu	Val	Ser	Leu	Val	Lys	Gly	Ala	Thr	Thr		
515																
520																
ctc	ggc	gac	acc	atc	gac	cg	agc	cg	ctc	gac	tac	ttc	tac	tg	ctc	
Leu	Gly	Asp	Thr	Ile	Asp	Arg	Ser	Arg	Leu	Asp	Tyr	Phe	Tyr	Trp	Leu	
530																
535																
ctc	gcc	gtc	ctc	agc	gtc	ctc	aac	ctc	gcc	gcc	tac	ctc	gtc	tgc	gcc	
Leu	Ala	Val	Leu	Ser	Val	Leu	Asn	Leu	Ala	Ala	Tyr	Leu	Val	Cys	Ala	
545																
550																
aag	tg	ggc	ggc	acc	ggc	ggc	ggc	acc	tcg	cg	gag	cag	cag	cag	g	
Lys	Trp	Ala	Ala	Thr	Ala	Ala	Ala	Thr	Ser	Arg	Glu	Gln	Gln	Gln	Gln	
565																
570																
cac	acc	ggc	gtc	ggc	gac	ggc	gac	gag	aaa	tgc	tag					
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585																

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<212> PRT
<213> Oryza sativa
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Pro	Ala	Asp	Arg	Ser	Ala	Thr	Gly	Gly	Trp	Val	Ala	Ala	Ala	Leu	Val		
		35					40					45					
Leu	Gly	Ile	Glu	Leu	Cys	Glu	Arg	Leu	Ser	Thr	Met	Gly	Ile	Ala	Val		
	50					55					60						
Asn	Leu	Val	Thr	Tyr	Leu	Thr	Gly	Thr	Met	His	Leu	Pro	Ser	Ala	Ala		
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Thr	Pro	Val	Gln	Met	Ala	Val	Leu	Tyr	Ala	Cys	Leu	Tyr	Leu	Ile	Ala		
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			165					170					175				
Gln	Phe	Asp	Asp	Arg	Asp	Gly	Arg	Glu	Arg	Ala	Ala	Met	Gly	Leu	Phe		
			180					185					190				
Phe	Asn	Arg	Phe	Phe	Phe	Phe	Ile	Ser	Leu	Gly	Thr	Leu	Leu	Ala	Val		
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Gly	Ile	Cys	Ser	Ala	Ala	Met	Leu	Ala	Ala	Ile	Ala	Val	Phe	Leu	Ser		
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Gly	Thr	Arg	Arg	Tyr	Arg	Tyr	Lys	Arg	Ser	Ser	Gly	Ser	Pro	Ile	Val		

PF59082SeqList_PF59082.txt

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 His Ile Leu Gln Val Leu Val Ala Ala Ala Arg Lys Arg Gly Val Val
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 Lys Arg Pro Pro Thr Ala Ala Glu Leu Tyr Glu Asp Asp Arg Pro Glu
 275 280 285
 His Ala Arg Ile Ala His Thr Ala Gln Phe Pro Cys Leu Asp Met Ala
 290 295 300
 Ala Val Val Ala Gly Glu Glu Asp Asn Glu Val Ala Gly Pro Gly Gly
 305 310 315 320
 Pro Ala Ala Pro Asn Pro Trp Lys Leu Cys Ser Val Ser Arg Val Glu
 325 330 335
 Glu Val Lys Met Val Ala Arg Leu Met Pro Val Trp Ala Thr Thr Ile
 340 345 350
 Leu Phe Trp Thr Ile Tyr Ala Gln Met Ile Thr Phe Ser Val Glu Gln
 355 360 365
 Ala Thr Thr Met Asp Arg Arg Val Gly Ala Gly Phe Glu Ile Pro Ala
 370 375 380
 Ala Ser Leu Thr Val Phe Phe Val Gly Ala Ile Met Leu Thr Leu Ala
 385 390 395 400
 Val Tyr Asp Arg Val Phe Ile Pro Leu Cys Arg Val Leu Thr Gly Lys
 405 410 415
 Gln Gly Phe Thr Asn Leu Glu Lys Ile Gly Ile Gly Leu Ala Leu Ser
 420 425 430
 Ile Leu Gly Met Ala Ala Ala Ala Leu Cys Glu Lys Lys Arg Leu Ala
 435 440 445
 Val Ala Val Ala Ala Thr Thr Gly Asn Ser Thr Pro Ile Ser Val Phe
 450 455 460
 Leu Leu Thr Pro Gln Phe Leu Leu Val Gly Ala Gly Glu Ala Phe Ile
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 Tyr Thr Gly Gln Leu Asp Phe Phe Ile Thr Arg Ser Pro Lys Gly Met
 485 490 495
 Lys Thr Met Ser Thr Gly Leu Phe Leu Thr Thr Leu Ser Leu Gly Phe
 500 505 510
 Phe Phe Ser Ser Val Leu Val Ser Leu Val Lys Gly Ala Thr Thr Trp
 515 520 525
 Leu Gly Asp Thr Ile Asp Arg Ser Arg Leu Asp Tyr Phe Tyr Trp Leu
 530 535 540
 Leu Ala Val Leu Ser Val Leu Asn Leu Ala Ala Tyr Leu Val Cys Ala
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 <213> Oryza sativa

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 Val Val Asp Tyr Arg Gly Asn Pro Val Asp Lys Ser Lys Thr Gly Gly
 20 25 30
 tgg ctc ggc gcc ggg ctt atc cta ggg acg gag ctg gcg gag cgg gtg 144
 Trp Leu Gly Ala Gly Leu Ile Leu Gly Thr Glu Leu Ala Glu Arg Val
 35 40 45
 tgc gtg atg ggc atc tcg atg aac ctg gtg acg tac ctg gtc ggc gac 192
 Cys Val Met Gly Ile Ser Met Asn Leu Val Thr Tyr Leu Val Gly Asp
 50 55 60
 ctg cac ctc tcc aac gcc aag tcc gcc aac atc gtc acc aac ttc atg 240
 Leu His Leu Ser Asn Ala Lys Ser Ala Asn Ile Val Thr Asn Phe Met
 65 70 75 80

PF59082SeqList_PF59082.txt

ggc	acc	ctc	aac	ctc	ctc	gcc	ctc	gtc	ggc	ggc	ttc	ctc	gcc	gac	gcc	288
Gly	Thr	Leu	Asn	Leu	Leu	Ala	Leu	Val	Gly	Gly	Phe	Leu	Ala	Asp	Ala	
				85					90					95		
aag	ctc	ggc	cgc	tac	ctc	acc	atc	gcc	atc	tcc	gcc	acc	atc	gcc	gcc	336
Lys	Leu	Gly	Arg	Tyr	Leu	Thr	Ile	Ala	Ile	Ser	Ala	Thr	Ile	Ala	Ala	
			100					105					110			
acc	ggg	gtg	agc	ttg	ctg	acg	gtg	gac	acg	atg	gtg	ccg	ggg	atg	cgg	384
Thr	Gly	Val	Ser	Leu	Leu	Thr	Val	Asp	Thr	Met	Val	Pro	Gly	Met	Arg	
		115					120					125				
ccg	ccg	ccg	tgc	gcg	gac	gcg	cgc	ggc	gcc	ggg	gcg	cac	ctg	cgg	tgc	432
Pro	Pro	Pro	Cys	Ala	Asp	Ala	Arg	Gly	Ala	Gly	Ala	His	Leu	Arg	Cys	
	130					135					140					
gag	ccg	gcg	cgc	ggg	ggg	cag	ctg	gcg	atg	ctg	tac	gcg	gcg	ctg	tac	480
Glu	Pro	Ala	Arg	Gly	Gly	Gln	Leu	Ala	Met	Leu	Tyr	Ala	Ala	Leu	Tyr	
145				150						155					160	
acg	gtc	gcg	gcg	ggc	gcg	ggg	ggg	ctc	aag	gcg	aac	gtg	tcc	ggg	ttc	528
Thr	Val	Ala	Ala	Gly	Ala	Gly	Gly	Leu	Lys	Ala	Asn	Val	Ser	Gly	Phe	
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ggc	tcc	gac	cag	ttc	gac	ggc	ggc	gac	ccg	cgg	gag	gag	cgc	gcc	atg	576
Gly	Ser	Asp	Gln	Phe	Asp	Gly	Gly	Asp	Pro	Arg	Glu	Glu	Arg	Ala	Met	
			180					185					190			
gtg	ttc	ttc	ttc	aac	cgc	ttc	tac	ttc	tgc	atc	agc	ctc	ggc	tcc	ctc	624
Val	Phe	Phe	Phe	Asn	Arg	Phe	Tyr	Phe	Cys	Ile	Ser	Leu	Gly	Ser	Leu	
			195				200					205				
ttc	gcg	gtc	acc	gtg	ctg	gtg	tac	gtc	cag	gac	aac	gtc	ggc	cgg	ggc	672
Phe	Ala	Val	Thr	Val	Leu	Val	Tyr	Val	Gln	Asp	Asn	Val	Gly	Arg	Gly	
	210					215					220					
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Trp	Gly	Tyr	Gly	Val	Ser	Ala	Val	Ala	Met	Val	Leu	Ala	Val	Ala	Val	
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ctc	gtc	gcc	ggc	acg	ccc	aag	tac	cgg	tac	cgc	cgc	ccc	gag	ggg	agc	768
Leu	Val	Ala	Gly	Thr	Pro	Lys	Tyr	Arg	Tyr	Arg	Arg	Pro	Glu	Gly	Ser	
				245				250						255		
ccg	ctc	acc	gtg	atc	ggg	cgg	gtg	ctg	gca	acg	gcg	tgg	agg	aag	cgc	816
Pro	Leu	Thr	Val	Ile	Gly	Arg	Val	Leu	Ala	Thr	Ala	Trp	Arg	Lys	Arg	
			260				265						270			
cgc	ctg	ccg	ctc	ccc	gcc	gac	gcc	ggc	gag	ctc	cac	ggc	tac	cac	aca	864
Arg	Leu	Pro	Leu	Pro	Ala	Asp	Ala	Gly	Glu	Leu	His	Gly	Tyr	His	Thr	
		275				280						285				
tcc	aag	gtt	gcc	tac	acc	gac	cgc	ctc	agg	tgc	ctg	gac	agg	gcg	gcc	912
Ser	Lys	Val	Ala	Tyr	Thr	Asp	Arg	Leu	Arg	Cys	Leu	Asp	Arg	Ala	Ala	
	290					295					300					
atc	atg	gag	gcg	gac	ctg	gca	gcg	tcg	ccg	gcg	aag	acg	aac	cag	aca	960
Ile	Met	Glu	Ala	Asp	Leu	Ala	Ala	Ser	Pro	Ala	Lys	Thr	Asn	Gln	Thr	
305					310					315					320	
tcg	gcg	gcg	ccg	gcg	gcg	acg	gtg	acg	gag	gtg	gag	gag	gtg	aag	atg	1008
Ser	Ala	Ala	Pro	Ala	Ala	Thr	Val	Thr	Glu	Val	Glu	Glu	Val	Lys	Met	
			325					330						335		
gtg	gtg	aag	ctg	ctg	ccc	atc	tgg	tcg	acc	tgc	atc	ctc	ttc	tgg	acg	1056
Val	Val	Lys	Leu	Leu	Pro	Ile	Trp	Ser	Thr	Cys	Ile	Leu	Phe	Trp	Thr	
			340				345						350			
gtg	tac	tcc	cag	atg	acc	acc	ttc	tcc	gtc	gag	cag	gcc	acc	cgc	atg	1104
Val	Tyr	Ser	Gln	Met	Thr	Thr	Phe	Ser	Val	Glu	Gln	Ala	Thr	Arg	Met	
		355				360						365				
gac	cgc	cac	ctc	cgc	ccg	ggc	gcc	gcc	ccc	ggc	ggg	ttc	gcc	atc	ccg	1152
Asp	Arg	His	Leu	Arg	Pro	Gly	Ala	Ala	Pro	Gly	Gly	Phe	Ala	Ile	Pro	
	370					375					380					
gcg	ggc	tcc	ctc	tcc	gtc	ttc	ctc	ttc	ctc	tcc	atc	ctc	ctc	ttc	acc	1200
Ala	Gly	Ser	Leu	Ser	Val	Phe	Leu	Phe	Leu	Ser	Ile	Leu	Leu	Phe	Thr	
					390					395					400	
tcc	ctc	aac	gag	cgc	gtc	ctc	gtg	ccg	gcg	gcc	cgc	cgc	ctc	acc	cgc	1248
Ser	Leu	Asn	Glu	Arg	Val	Leu	Val	Pro	Ala	Ala	Arg	Arg	Leu	Thr	Arg	
			405					410						415		
cgc	ccc	cag	ggc	ctc	acc	tcg	ctc	cag	cgc	gtc	ggc	gcg	ggc	ctc	gtc	1296
Arg	Pro	Gln	Gly	Leu	Thr	Ser	Leu	Gln	Arg	Val	Gly	Ala	Gly	Leu	Val	
			420				425						430			
ctc	gcc	acc	gtc	gcc	atg	gcc	acc	tcc	gcg	ctc	gtc	gag	aag	aag	cgg	1344
Leu	Ala	Thr	Val	Ala	Met	Ala	Thr	Ser	Ala	Leu	Val	Glu	Lys	Lys	Arg	
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Trp	Leu	Val	Pro	Gln	Phe	Phe	Leu	Val	Gly	Ala	Gly	Glu	Ala	Phe	Ala	
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tac	gtc	ggg	cag	ctg	gag	ttc	ttc	atc	cg	gag	gcg	ccg	gag	cgg	atg	1488
Tyr	Val	Gly	Gln	Leu	Glu	Phe	Phe	Ile	Arg	Glu	Ala	Pro	Glu	Arg	Met	
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aag	tcg	atg	agc	acg	ggg	ctc	ttc	ctg	gtg	acg	ctg	tcc	atg	gga	ttc	1536
Lys	Ser	Met	Ser	Thr	Gly	Leu	Phe	Leu	Val	Thr	Leu	Ser	Met	Gly	Phe	
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Phe	Leu	Ser	Ser	Phe	Leu	Val	Phe	Ala	Val	Asp	Ala	Ala	Thr	Arg	Gly	
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gcg	tgg	ata	cgg	aac	gac	ctc	gac	gcc	ggc	agg	ctg	gac	ctc	ttc	tac	1632
Ala	Trp	Ile	Arg	Asn	Asp	Leu	Asp	Ala	Gly	Arg	Leu	Asp	Leu	Phe	Tyr	
	530					535					540					
tgg	atg	ctg	gcc	gtg	ctc	ggg	gtg	gcc	aac	ttc	gcc	gtg	ttc	ctc	gtg	1680
Trp	Met	Leu	Ala	Val	Leu	Gly	Val	Ala	Asn	Phe	Ala	Val	Phe	Leu	Val	
	545				550				555						560	
ttc	gcg	agg	cgc	cac	gag	tac	aag	cag	ccc	gcc	ggc	acg	gcc	gcc	gtg	1728
Phe	Ala	Arg	Arg	His	Glu	Tyr	Lys	Gln	Pro	Ala	Gly	Thr	Ala	Ala	Val	
				565				570						575		
gtg	gtg	gcg	ccc	gcc	gct	gcc	aag	gac	ggc	gcc	ggc	gag	gag	aag		1776
Val	Val	Ala	Pro	Ala	Ala	Lys	Lys	Asp	Gly	Gly	Ala	Gly	Glu	Glu	Lys	
			580					585					590			
gag	atg	gac	gac	ttc	gtc	gtg	gtc	aag	gag	gcc	gta	gaa	ggg	atg	gat	1824
Glu	Met	Asp	Asp	Phe	Val	Val	Val	Lys	Glu	Ala	Val	Glu	Gly	Met	Asp	
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Val																

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<211> 609

<212> PRT

<213> Oryza sativa

<400> 56

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Trp	Leu	Gly	Ala	Gly	Leu	Ile	Leu	Gly	Thr	Glu	Leu	Ala	Glu	Arg	Val	
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Cys	Val	Met	Gly	Ile	Ser	Met	Asn	Leu	Val	Thr	Tyr	Leu	Val	Gly	Asp	
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Leu	His	Leu	Ser	Asn	Ala	Lys	Ser	Ala	Asn	Ile	Val	Thr	Asn	Phe	Met	
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Gly	Thr	Leu	Asn	Leu	Leu	Ala	Leu	Val	Gly	Gly	Phe	Leu	Ala	Asp	Ala	
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Lys	Leu	Gly	Arg	Tyr	Leu	Thr	Ile	Ala	Ile	Ser	Ala	Thr	Ile	Ala	Ala	
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Pro	Pro	Pro	Cys	Ala	Asp	Ala	Arg	Gly	Ala	Gly	Ala	His	Leu	Arg	Cys	
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Glu	Pro	Ala	Arg	Gly	Gly	Gln	Leu	Ala	Met	Leu	Tyr	Ala	Ala	Leu	Tyr	
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Thr	Val	Ala	Ala	Gly	Ala	Gly	Gly	Leu	Lys	Ala	Asn	Val	Ser	Gly	Phe	
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Gly	Ser	Asp	Gln	Phe	Asp	Gly	Gly	Asp	Pro	Arg	Glu	Glu	Arg	Ala	Met	
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Val	Phe	Phe	Phe	Asn	Arg	Phe	Tyr	Phe	Cys	Ile	Ser	Leu	Gly	Ser	Leu	
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PF59082SeqList_PF59082.txt

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 260 265 270
 Arg Leu Pro Leu Pro Ala Asp Ala Gly Glu Leu His Gly Tyr His Thr
 275 280 285
 Ser Lys Val Ala Tyr Thr Asp Arg Leu Arg Cys Leu Asp Arg Ala Ala
 290 295 300
 Ile Met Glu Ala Asp Leu Ala Ala Ser Pro Ala Lys Thr Asn Gln Thr
 305 310 315 320
 Ser Ala Ala Pro Ala Ala Thr Val Thr Glu Val Glu Glu Val Lys Met
 325 330 335
 Val Val Lys Leu Leu Pro Ile Trp Ser Thr Cys Ile Leu Phe Trp Thr
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 Asp Arg His Leu Arg Pro Gly Ala Ala Pro Gly Gly Phe Ala Ile Pro
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 Ala Gly Ser Leu Ser Val Phe Leu Phe Leu Ser Ile Leu Leu Phe Thr
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 Arg Pro Gln Gly Leu Thr Ser Leu Gln Arg Val Gly Ala Gly Leu Val
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 Leu Ala Thr Val Ala Met Ala Thr Ser Ala Leu Val Glu Lys Lys Arg
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 Arg Asp Ala Ala Asn Asp Gly Gly Gly Gly Gly Met Ile Ser Ala Phe
 450 455 460
 Trp Leu Val Pro Gln Phe Phe Leu Val Gly Ala Gly Glu Ala Phe Ala
 465 470 475 480
 Tyr Val Gly Gln Leu Glu Phe Phe Ile Arg Glu Ala Pro Glu Arg Met
 485 490 495
 Lys Ser Met Ser Thr Gly Leu Phe Leu Val Thr Leu Ser Met Gly Phe
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 Phe Leu Ser Ser Phe Leu Val Phe Ala Val Asp Ala Ala Thr Arg Gly
 515 520 525
 Ala Trp Ile Arg Asn Asp Leu Asp Ala Gly Arg Leu Asp Leu Phe Tyr
 530 535 540
 Trp Met Leu Ala Val Leu Gly Val Ala Asn Phe Ala Val Phe Leu Val
 545 550 555 560
 Phe Ala Arg Arg His Glu Tyr Lys Gln Pro Ala Gly Thr Ala Ala Val
 565 570 575
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 580 585 590
 Glu Met Asp Asp Phe Val Val Val Lys Glu Ala Val Glu Gly Met Asp
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 Val

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<220>
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 tgg gat tac aaa ggc aga cca gcc ctt aga tcc tcc tct ggt ggt tgg 96
 Trp Asp Tyr Lys Gly Arg Pro Ala Leu Arg Ser Ser Ser Gly Gly Trp
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 gct agt ggt gca atg att tta ggt gtt gaa gct gtg gag agg cta aca 144
 Ala Ser Gly Ala Met Ile Leu Gly Val Glu Ala Val Glu Arg Leu Thr
 35 40 45

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His	Leu	Gly	Asn	Ala	Ser	Ser	Ala	Asn	Asn	Val	Thr	Asn	Phe	Leu	Gly	
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act	tct	ttc	atg	ctc	act	tta	ctt	ggg	ggg	ttt	gtc	gcc	gac	act	ttc	288
Thr	Ser	Phe	Met	Leu	Thr	Leu	Leu	Gly	Gly	Phe	Val	Ala	Asp	Thr	Phe	
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ctc	gga	agg	tat	ctt	aca	att	ggg	atc	ttt	gcc	act	gtt	caa	gca	atg	336
Leu	Gly	Arg	Tyr	Leu	Thr	Ile	Gly	Ile	Phe	Ala	Thr	Val	Gln	Ala	Met	
			100				105						110			
ggg	gtt	aca	atc	ttg	acc	atc	tca	act	ata	atc	cca	agc	cta	cga	cca	384
Gly	Val	Thr	Ile	Leu	Thr	Ile	Ser	Thr	Ile	Ile	Pro	Ser	Leu	Arg	Pro	
	115						120					125				
cca	aaa	tgt	gaa	caa	gtt	ggg	agc	tca	tca	tgc	atc	ccc	gca	aat	agc	432
Pro	Lys	Cys	Glu	Gln	Val	Gly	Ser	Ser	Ser	Cys	Ile	Pro	Ala	Asn	Ser	
	130					135					140					
aaa	caa	ctc	atg	gtc	cta	tat	att	gcc	cta	tac	atg	acg	gcc	ctc	ggc	480
Lys	Gln	Leu	Met	Val	Leu	Tyr	Ile	Ala	Leu	Tyr	Met	Thr	Ala	Leu	Gly	
	145				150					155					160	
acc	ggc	ggc	cta	aaa	tcg	agc	gtc	tcc	ggc	ttt	ggc	acc	gac	caa	ttc	528
Thr	Gly	Gly	Leu	Lys	Ser	Ser	Val	Ser	Gly	Phe	Gly	Thr	Asp	Gln	Phe	
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gac	gat	tct	gac	aag	aaa	gaa	aag	ggg	caa	atg	ata	aaa	ttc	ttc	gat	576
Asp	Asp	Ser	Asp	Lys	Lys	Glu	Lys	Gly	Gln	Met	Ile	Lys	Phe	Phe	Asp	
			180					185					190			
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Trp	Phe	Phe	Phe	Phe	Ile	Asn	Val	Gly	Ser	Leu	Gly	Ala	Val	Thr	Val	
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Leu	Val	Tyr	Ile	Gln	Asp	Asn	Leu	Gly	Arg	Glu	Trp	Gly	Tyr	Gly	Ile	
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Cys	Ala	Cys	Ala	Ile	Val	Ile	Ala	Leu	Val	Val	Phe	Leu	Phe	Gly	Thr	
	225				230					235					240	
agg	aaa	tat	agg	ttc	aag	aaa	ctt	ggg	ggg	agt	cca	ttg	aca	caa	att	768
Arg	Lys	Tyr	Arg	Phe	Lys	Lys	Leu	Gly	Gly	Ser	Pro	Leu	Thr	Gln	Ile	
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Ala	Ser	Val	Ile	Val	Ala	Ala	Trp	Lys	Lys	Arg	His	Leu	Glu	Leu	Pro	
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tca	gat	tct	tca	ctt	ctc	ttt	gaa	att	gat	gat	att	ttt	ggg	gaa	gga	864
Ser	Asp	Ser	Ser	Leu	Leu	Phe	Glu	Ile	Asp	Asp	Ile	Phe	Gly	Glu	Gly	
			275				280					285				
aat	aaa	aaa	agc	aaa	caa	aag	ttg	ccc	cat	agc	aag	gag	tac	cga	ttc	912
Asn	Lys	Lys	Ser	Lys	Gln	Lys	Leu	Pro	His	Ser	Lys	Glu	Tyr	Arg	Phe	
	290					295					300					
ttg	gac	aag	gca	gcc	att	aag	gaa	gat	gat	gac	ctt	gaa	tct	aat	ggc	960
Leu	Asp	Lys	Ala	Ala	Ile	Lys	Glu	Asp	Asp	Asp	Leu	Glu	Ser	Asn	Gly	
	305				310					315					320	
act	aac	gtt	gta	atc	aac	aag	tgg	aaa	tta	gca	acc	tta	acc	gat	gtt	1008
Thr	Asn	Val	Val	Ile	Asn	Lys	Trp	Lys	Leu	Ala	Thr	Leu	Thr	Asp	Val	
				325				330						335		
gaa	gaa	gta	aaa	ata	tta	atc	aga	atg	ttg	cca	act	tgg	gcc	aca	act	1056
Glu	Glu	Val	Lys	Ile	Leu	Ile	Arg	Met	Leu	Pro	Thr	Trp	Ala	Thr	Thr	
			340				345						350			
att	atg	ttc	tgg	act	gtc	tat	gca	caa	atg	acc	aca	ttt	tct	gtg	tca	1104
Ile	Met	Phe	Trp	Thr	Val	Tyr	Ala	Gln	Met	Thr	Thr	Phe	Ser	Val	Ser	
			355				360					365				
caa	gct	aca	aca	atg	gat	cgt	cac	att	gga	acc	ttt	gaa	att	cca	cct	1152
Gln	Ala	Thr	Thr	Met	Asp	Arg	His	Ile	Gly	Thr	Phe	Glu	Ile	Pro	Pro	
	370				375						380					
gct	aca	ctc	acc	gta	ttt	ttc	gtc	gga	agt	ata	ctc	ttg	acc	gta	att	1200
Ala	Thr	Leu	Thr	Val	Phe	Phe	Val	Gly	Ser	Ile	Leu	Leu	Thr	Val	Ile	
				385	390					395					400	
ttc	tac	gat	agg	att	atc	gtt	ccg	att	tgt	cgt	cgt	ttc	atg	aat	aaa	1248
Phe	Tyr	Asp	Arg	Ile	Ile	Val	Pro	Ile	Cys	Arg	Arg	Phe	Met	Asn	Lys	
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PF59082SeqList_PF59082.txt

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Pro	His	Gly	Leu	Thr	Pro	Leu	Gln	Arg	Ile	Phe	Thr	Gly	Leu	Val	Leu	
			420					425					430			
tca	att	ttg	gcc	atg	att	gct	gct	gcc	cta	aca	gag	gtt	aag	agg	cta	1344
Ser	Ile	Leu	Ala	Met	Ile	Ala	Ala	Ala	Leu	Thr	Glu	Val	Lys	Arg	Leu	
			435					440					445			
aaa	gtt	gca	cat	ttg	cat	gga	ttg	acc	aat	gat	gca	aat	gcc	acg	att	1392
Lys	Val	Ala	His	Leu	His	Gly	Leu	Thr	Asn	Asp	Ala	Asn	Ala	Thr	Ile	
			450					455					460			
cca	ttg	act	gta	ttt	ttg	tta	gtt	ccg	caa	ttc	ttg	cta	gtg	ggc	gca	1440
Pro	Leu	Thr	Val	Phe	Trp	Leu	Val	Pro	Gln	Phe	Leu	Leu	Val	Gly	Ala	
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ggg	gaa	gca	ttt	aca	tat	att	ggc	caa	ctt	gat	ttt	ttc	tta	agg	gaa	1488
Gly	Glu	Ala	Phe	Thr	Tyr	Ile	Gly	Gln	Leu	Asp	Phe	Phe	Leu	Arg	Glu	
				485					490					495		
tgt	cca	aaa	ggg	atg	aag	aca	atg	agt	aca	ggg	cta	ttt	ttg	agt	aca	1536
Cys	Pro	Lys	Gly	Met	Lys	Thr	Met	Ser	Thr	Gly	Leu	Phe	Leu	Ser	Thr	
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ctt	gca	ctt	gga	ttt	ttc	ttt	agt	tca	att	ttg	gtt	aca	att	gtg	cat	1584
Leu	Ala	Leu	Gly	Phe	Phe	Phe	Ser	Ser	Ile	Leu	Val	Thr	Ile	Val	His	
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gtt	gtg	act	ggg	aca	aca	aat	cca	tgg	cta	gct	gat	aat	ttg	aac	caa	1632
Val	Val	Thr	Gly	Thr	Thr	Asn	Pro	Trp	Leu	Ala	Asp	Asn	Leu	Asn	Gln	
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Gly	Arg	Leu	Tyr	Asp	Phe	Tyr	Trp	Leu	Leu	Ala	Ile	Leu	Ser	Val	Phe	
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Asn	Leu	Met	Phe	Phe	Leu	Tyr	Ser	Ser	Arg	Lys	Tyr	Val	Tyr	Lys	Glu	
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aag	aga	ctt	gct	gaa	atg	ggg	att	gaa	ttg	gaa	gat	gat	gga	ccg	gtt	1776
Lys	Arg	Leu	Ala	Glu	Met	Gly	Ile	Glu	Leu	Glu	Asp	Asp	Gly	Pro	Val	
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Cys	His															

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<211> 594

<212> PRT

<213> Nicotiana tabacum

<400> 58

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Ala	Ser	Gly	Ala	Met	Ile	Leu	Gly	Val	Glu	Ala	Val	Glu	Arg	Leu	Thr	
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Thr	Leu	Gly	Ile	Ala	Val	Asn	Leu	Val	Thr	Tyr	Leu	Thr	Gly	Thr	Met	
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His	Leu	Gly	Asn	Ala	Ser	Ser	Ala	Asn	Asn	Val	Thr	Asn	Phe	Leu	Gly	
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Thr	Ser	Phe	Met	Leu	Thr	Leu	Leu	Gly	Gly	Phe	Val	Ala	Asp	Thr	Phe	
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Leu	Gly	Arg	Tyr	Leu	Thr	Ile	Gly	Ile	Phe	Ala	Thr	Val	Gln	Ala	Met	
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Gly	Val	Thr	Ile	Leu	Thr	Ile	Ser	Thr	Ile	Ile	Pro	Ser	Leu	Arg	Pro	
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Pro	Lys	Cys	Glu	Gln	Val	Gly	Ser	Ser	Ser	Cys	Ile	Pro	Ala	Asn	Ser	
	130					135					140					
Lys	Gln	Leu	Met	Val	Leu	Tyr	Ile	Ala	Leu	Tyr	Met	Thr	Ala	Leu	Gly	
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Thr	Gly	Gly	Leu	Lys	Ser	Ser	Val	Ser	Gly	Phe	Gly	Thr	Asp	Gln	Phe	
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Asp	Asp	Ser	Asp	Lys	Lys	Glu	Lys	Gly	Gln	Met	Ile	Lys	Phe	Phe	Asp	
			180					185					190			
Trp	Phe	Phe	Phe	Phe	Ile	Asn	Val	Gly	Ser	Leu	Gly	Ala	Val	Thr	Val	
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PF59082SeqList_PF59082.txt

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 Cys Ala Cys Ala Ile Val Ile Ala Leu Val Val Phe Leu Phe Gly Thr
 225 230 235 240
 Arg Lys Tyr Arg Phe Lys Lys Leu Gly Gly Ser Pro Leu Thr Gln Ile
 245 250 255
 Ala Ser Val Ile Val Ala Ala Trp Lys Lys Arg His Leu Glu Leu Pro
 260 265 270
 Ser Asp Ser Ser Leu Leu Phe Glu Ile Asp Asp Ile Phe Gly Glu Gly
 275 280 285
 Asn Lys Lys Ser Lys Gln Lys Lys Pro His Ser Lys Glu Tyr Arg Phe
 290 295 300
 Leu Asp Lys Ala Ala Ile Lys Glu Asp Asp Asp Leu Glu Ser Asn Gly
 305 310 315 320
 Thr Asn Val Val Ile Asn Lys Trp Lys Leu Ala Thr Leu Thr Asp Val
 325 330 335
 Glu Glu Val Lys Ile Leu Ile Arg Met Leu Pro Thr Trp Ala Thr Thr
 340 345 350
 Ile Met Phe Trp Thr Val Tyr Ala Gln Met Thr Thr Phe Ser Val Ser
 355 360 365
 Gln Ala Thr Thr Met Asp Arg His Ile Gly Thr Phe Glu Ile Pro Pro
 370 375 380
 Ala Thr Leu Thr Val Phe Phe Val Gly Ser Ile Leu Leu Thr Val Ile
 385 390 395 400
 Phe Tyr Asp Arg Ile Ile Val Pro Ile Cys Arg Arg Phe Met Asn Lys
 405 410 415
 Pro His Gly Leu Thr Pro Leu Gln Arg Ile Phe Thr Gly Leu Val Leu
 420 425 430
 Ser Ile Leu Ala Met Ile Ala Ala Ala Leu Thr Glu Val Lys Arg Leu
 435 440 445
 Lys Val Ala His Leu His Gly Leu Thr Asn Asp Ala Asn Ala Thr Ile
 450 455 460
 Pro Leu Thr Val Phe Trp Leu Val Pro Gln Phe Leu Leu Val Gly Ala
 465 470 475 480
 Gly Glu Ala Phe Thr Tyr Ile Gly Gln Leu Asp Phe Phe Leu Arg Glu
 485 490 495
 Cys Pro Lys Gly Met Lys Thr Met Ser Thr Gly Leu Phe Leu Ser Thr
 500 505 510
 Leu Ala Leu Gly Phe Phe Phe Ser Ile Leu Val Thr Ile Val His
 515 520 525
 Val Val Thr Gly Thr Thr Asn Pro Trp Leu Ala Asp Asn Leu Asn Gln
 530 535 540
 Gly Arg Leu Tyr Asp Phe Tyr Trp Leu Leu Ala Ile Leu Ser Val Phe
 545 550 555 560
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 tgg gat tac aaa gga aga cca gct ctt aga tcc tcc tct ggt ggt tgg 96
 Trp Asp Tyr Lys Gly Arg Pro Ala Leu Arg Ser Ser Ser Gly Gly Trp
 20 25 30
 gct agt ggt gca atg att tta ggt gtt gaa gct gtg gag agg cta aca 144
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Thr	Leu	Gly	Ile	Ala	Val	Asn	Leu	Val	Thr	Tyr	Leu	Thr	Gly	Thr	Met		
	50					55					60						
cat	tta	ggg	aat	gct	act	gca	gcc	aac	aat	gtt	acc	aat	ttt	ctt	gga		240
His	Leu	Gly	Asn	Ala	Thr	Ala	Ala	Asn	Asn	Val	Thr	Asn	Phe	Leu	Gly		
	65				70					75					80		
act	tct	ttc	atg	ctc	act	tta	ttt	ggg	ggg	ttt	ggt	gct	gac	act	ttt		288
Thr	Ser	Phe	Met	Leu	Thr	Leu	Phe	Gly	Gly	Phe	Val	Ala	Asp	Thr	Phe		
				85						90				95			
ctc	gga	agg	tat	ctt	aca	att	ggg	atc	ttt	gcc	act	ggt	caa	gca	atg		336
Leu	Gly	Arg	Tyr	Leu	Thr	Ile	Gly	Ile	Phe	Ala	Thr	Val	Gln	Ala	Met		
			100				105						110				
ggg	gtt	aca	atc	ttg	acc	att	tcc	acc	ata	atc	cca	agc	cta	cgg	cca		384
Gly	Val	Thr	Ile	Leu	Thr	Ile	Ser	Thr	Ile	Ile	Pro	Ser	Leu	Arg	Pro		
		115					120					125					
cca	aaa	tgc	gaa	caa	gtt	ggg	agc	tca	tca	tgc	atc	ccc	gca	aat	agc		432
Pro	Lys	Cys	Glu	Gln	Val	Gly	Ser	Ser	Ser	Cys	Ile	Pro	Ala	Asn	Ser		
	130					135					140						
aaa	caa	ctt	atg	gtc	cta	tac	att	gcc	cta	tac	atg	acg	gcg	ctc	ggc		480
Lys	Gln	Leu	Met	Val	Leu	Tyr	Ile	Ala	Leu	Tyr	Met	Thr	Ala	Leu	Gly		
	145				150					155					160		
acc	ggc	ggc	cta	aaa	tcg	agc	gtc	tcc	ggc	ttt	ggc	acc	gac	caa	ttc		528
Thr	Gly	Gly	Leu	Lys	Ser	Ser	Val	Ser	Gly	Phe	Gly	Thr	Asp	Gln	Phe		
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gac	gat	gct	gac	aaa	aaa	gaa	aaa	ggg	caa	atg	ata	aaa	ttc	ttc	gat		576
Asp	Asp	Ala	Asp	Lys	Lys	Glu	Lys	Gly	Gln	Met	Ile	Lys	Phe	Phe	Asp		
			180					185					190				
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Trp	Phe	Phe	Phe	Phe	Ile	Asn	Val	Gly	Ser	Leu	Gly	Ala	Val	Thr	Val		
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Leu	Val	Tyr	Ile	Gln	Asp	Asn	Leu	Gly	Arg	Glu	Trp	Gly	Tyr	Gly	Ile		
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tgt	gca	tgt	gct	att	gta	att	gga	ctt	gtt	gtg	ttc	tta	tct	ggg	aca		720
Cys	Ala	Cys	Ala	Ile	Val	Ile	Gly	Leu	Val	Val	Phe	Leu	Ser	Gly	Thr		
	225				230					235					240		
aga	aaa	tat	agg	ttc	aag	aaa	ctt	gtg	ggg	agt	cca	ttg	aca	caa	att		768
Arg	Lys	Tyr	Arg	Phe	Lys	Lys	Leu	Val	Gly	Ser	Pro	Leu	Thr	Gln	Ile		
				245					250					255			
gct	tca	gtt	att	gtg	gct	gct	tgg	aaa	aaa	aga	cat	ttg	gaa	tta	ctt		816
Ala	Ser	Val	Ile	Val	Ala	Ala	Trp	Lys	Lys	Arg	His	Leu	Glu	Leu	Leu		
			260				265					270					
tca	gat	tct	tca	ctt	ctc	ttt	gaa	att	gat	gat	att	ttt	ggg	gaa	gga		864
Ser	Asp	Ser	Ser	Leu	Leu	Phe	Glu	Ile	Asp	Asp	Ile	Phe	Gly	Glu	Gly		
			275				280					285					
aat	aaa	aaa	aac	aag	caa	aag	ttg	cct	cat	agc	aag	gaa	tac	cga	ttc		912
Asn	Lys	Lys	Asn	Lys	Gln	Lys	Leu	Pro	His	Ser	Lys	Glu	Tyr	Arg	Phe		
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Leu	Asp	Lys	Ala	Ala	Ile	Lys	Glu	Asp	His	Asp	Leu	Glu	Ser	Asn	Gly		
					310					315					320		
act	aac	gtt	gta	atc	aac	aag	tgg	aaa	tta	gca	acc	tta	acc	gat	gtt		1008
Thr	Asn	Val	Val	Ile	Asn	Lys	Trp	Lys	Leu	Ala	Thr	Leu	Thr	Asp	Val		
				325						330				335			
gaa	gaa	gta	aaa	tta	tta	atc	aga	atg	tta	cca	act	tgg	gcc	aca	act		1056
Glu	Glu	Val	Lys	Leu	Leu	Ile	Arg	Met	Leu	Pro	Thr	Trp	Ala	Thr	Thr		
				340				345					350				
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Ile	Met	Phe	Trp	Thr	Val	Tyr	Ala	Gln	Met	Thr	Thr	Phe	Ser	Val	Ser		
			355				360					365					
caa	gct	aca	aca	atg	gat	cgt	cac	att	gga	acc	ttt	gaa	att	cca	ccg		1152
Gln	Ala	Thr	Thr	Met	Asp	Arg	His	Ile	Gly	Thr	Phe	Glu	Ile	Pro	Pro		
	370				375						380						
gct	tca	ctc	aca	gta	ttt	gtc	gga	agt	ata	ctc	ttg	acc	gta	att			1200
Ala	Ser	Leu	Thr	Val	Phe	Phe	Val	Gly	Ser	Ile	Leu	Leu	Thr	Val	Ile		
				390					395						400		
ttc	tac	gat	agg	gtt	atc	gtt	ccc	att	tgt	cgt	cgt	ttc	atg	aat	aaa		1248
Phe	Tyr	Asp	Arg	Val	Ile	Val	Pro	Ile	Cys	Arg	Arg	Phe	Met	Asn	Lys		

PF59082SeqList_PF59082.txt

[illegible]

$\langle 210 \rangle$ 60

<211> 594

<212> PRT

<213> *Nicotiana tabacum*

<400> 60

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Ala	Ser	Gly ³⁵	Ala	Met	Ile	Leu	Gly ⁴⁰	Val	Glu	Ala	Val	Glu ⁴⁵	Arg	Leu	Thr
Thr	Leu ⁵⁰	Gly	Ile	Ala	Val	Asn ⁵⁵	Leu	Val	Thr	Tyr	Leu ⁶⁰	Thr	Gly	Thr	Met
His ⁶⁵	Leu	Gly	Asn	Ala	Thr ⁷⁰	Ala	Ala	Asn	Asn	Val ⁷⁵	Thr	Asn	Phe	Leu	Gly ⁸⁰
Thr	Ser	Phe	Met ⁸⁵	Leu	Thr	Leu	Phe	Gly	Gly ⁹⁰	Phe	Val	Ala	Asp	Thr ⁹⁵	Phe
Leu	Gly	Arg	Tyr ¹⁰⁰	Leu	Thr	Ile	Gly	Ile ¹⁰⁵	Phe	Ala	Thr	Val	Gln ¹¹⁰	Ala	Met
Gly	Val	Thr ¹¹⁵	Ile	Leu	Thr	Ile	Ser ¹²⁰	Thr	Ile	Ile	Pro	Ser ¹²⁵	Leu	Arg	Pro
Pro	Lys ¹³⁰	Cys	Glu	Gln	Val	Gly ¹³⁵	Ser	Ser	Ser	Cys	Ile ¹⁴⁰	Pro	Ala	Asn	Ser
Lys ¹⁴⁵	Gln	Leu	Met	Val	Leu ¹⁵⁰	Tyr	Ile	Ala	Leu	Tyr ¹⁵⁵	Met	Thr	Ala	Leu	Gly ¹⁶⁰
Thr	Gly	Gly	Leu	Lys ¹⁶⁵	Ser	Ser	Val	Ser	Gly ¹⁷⁰	Phe	Gly	Thr	Asp	Gln ¹⁷⁵	Phe
Asp	Asp	Ala	Asp ¹⁸⁰	Lys	Lys	Glu	Lys	Gly ¹⁸⁵	Gln	Met	Ile	Lys	Phe ¹⁹⁰	Phe	Asp
Trp	Phe	Phe	Phe	Phe	Ile	Asn	Val	Gly	Ser	Leu	Gly	Ala	Val	Thr	Val

Seite 73

PF59082SeqList_PF59082.txt

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				245					250					255	
Ala	Ser	Val	Ile	Val	Ala	Ala	Trp	Lys	Lys	Arg	His	Leu	Glu	Leu	Leu
			260					265					270		
Ser	Asp	Ser	Ser	Leu	Leu	Phe	Glu	Ile	Asp	Asp	Ile	Phe	Gly	Glu	Gly
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Leu	Asp	Lys	Ala	Ala	Ile	Lys	Glu	Asp	His	Asp	Leu	Glu	Ser	Asn	Gly
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Thr	Asn	Val	Val	Ile	Asn	Lys	Trp	Lys	Leu	Ala	Thr	Leu	Thr	Asp	Val
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Glu	Glu	Val	Lys	Leu	Leu	Ile	Arg	Met	Leu	Pro	Thr	Trp	Ala	Thr	Thr
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Gln	Ala	Thr	Thr	Met	Asp	Arg	His	Ile	Gly	Thr	Phe	Glu	Ile	Pro	Pro
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Ala	Ser	Leu	Thr	Val	Phe	Phe	Val	Gly	Ser	Ile	Leu	Leu	Thr	Val	Ile
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Phe	Tyr	Asp	Arg	Val	Ile	Val	Pro	Ile	Cys	Arg	Arg	Phe	Met	Asn	Lys
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Pro	His	Gly	Leu	Thr	Pro	Leu	Gln	Arg	Ile	Phe	Thr	Gly	Leu	Val	Leu
			420					425					430		
Ser	Ile	Leu	Ala	Met	Ile	Ala	Ala	Ala	Leu	Thr	Glu	Val	Lys	Arg	Leu
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Lys	Val	Ala	His	Leu	His	Gly	Leu	Thr	Asn	Asp	Ala	Asn	Ala	Thr	Ile
	450				455					460					
Pro	Leu	Ser	Val	Phe	Trp	Leu	Val	Pro	Gln	Phe	Leu	Leu	Val	Gly	Ala
465					470					475					480
Gly	Glu	Ala	Phe	Thr	Tyr	Ile	Gly	Gln	Leu	Asp	Phe	Phe	Leu	Arg	Glu
			485					490						495	
Cys	Pro	Lys	Gly	Met	Lys	Thr	Met	Ser	Thr	Gly	Leu	Phe	Leu	Ser	Thr
			500					505					510		
Leu	Ala	Leu	Gly	Phe	Phe	Phe	Ser	Ser	Ile	Leu	Val	Thr	Ile	Val	His
		515					520					525			
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Asn	Leu	Met	Phe	Phe	Leu	Tyr	Phe	Ser	Arg	Lys	Tyr	Val	Tyr	Lys	Glu
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Cys	His														

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tgg	gat	tac	aaa	ggt	cga	cca	gct	gtt	cga	tcc	tcg	tcc	ggc	ggt	tgg		96
Trp	Asp	Tyr	Lys	Gly	Arg	Pro	Ala	Val	Arg	Ser	Ser	Ser	Gly	Gly	Trp		
			20				25						30				
tcc	agc	gcc	gcc	atg	att	tta	ggg	att	gag	gca	gtg	gag	agg	cta	acg		144

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Ser	Ser	Ala	Ala	Met	Ile	Leu	Gly	Ile	Glu	Ala	Val	Glu	Arg	Leu	Thr	
acg	tta	ggt	att	gct	gta	aat	ctg	gtg	aca	tac	ttg	act	gga	acc	atg	192
Thr	Leu	Gly	Ile	Ala	Val	Asn	Leu	Val	Thr	Tyr	Leu	Thr	Gly	Thr	Met	
cat	tta	gga	aat	gct	agt	tcg	gcc	aac	aac	ggt	aca	aat	ttt	ctt	gga	240
His	Leu	Gly	Asn	Ala	Ser	Ser	Ala	Asn	Asn	Val	Thr	Asn	Phe	Leu	Gly	
act	tca	ttt	atg	ctc	act	ttg	ctt	ggt	ggt	ttc	gta	gcc	gac	act	ttt	288
Thr	Ser	Phe	Met	Leu	Thr	Leu	Leu	Gly	Gly	Phe	Val	Ala	Asp	Thr	Phe	
ctt	gga	cga	tat	ctt	aca	att	ggc	atc	ttt	acc	act	att	caa	gcc	atg	336
Leu	Gly	Arg	Tyr	Leu	Thr	Ile	Gly	Ile	Phe	Thr	Thr	Ile	Gln	Ala	Met	
ggt	gtt	acc	ata	ttg	acc	atc	tcc	aca	ata	atc	cca	agc	cta	cga	cca	384
Gly	Val	Thr	Ile	Leu	Thr	Ile	Ser	Thr	Ile	Ile	Pro	Ser	Leu	Arg	Pro	
cca	aag	tgt	tcc	cca	ggg	agc	tca	aca	tgc	att	cca	gca	agt	tcc	aaa	432
Pro	Lys	Cys	Ser	Pro	Gly	Ser	Ser	Thr	Cys	Ile	Pro	Ala	Ser	Ser	Lys	
caa	ctc	atg	gtt	cta	tac	ata	gca	cta	tac	atg	acg	gcg	ctc	ggc	acc	480
Gln	Leu	Met	Val	Leu	Tyr	Ile	Ala	Leu	Tyr	Met	Thr	Ala	Leu	Gly	Thr	
ggc	ggc	ctg	aaa	tcc	agc	gtc	tcc	ggc	ttc	ggg	tca	gac	cag	ttc	gac	528
Gly	Gly	Leu	Lys	Ser	Ser	Val	Ser	Gly	Phe	Gly	Ser	Asp	Gln	Phe	Asp	
gaa	acc	gac	aag	aaa	gaa	aga	gga	cag	atg	ata	aaa	ttc	ttc	aac	tgg	576
Glu	Thr	Asp	Lys	Lys	Glu	Arg	Gly	Gln	Met	Ile	Lys	Phe	Phe	Asn	Trp	
ttc	ttt	ttc	ttc	att	aat	gtg	gga	tca	ctt	ggt	gca	gtg	aca	gta	cta	624
Phe	Phe	Phe	Phe	Ile	Asn	Val	Gly	Ser	Leu	Gly	Ala	Val	Thr	Val	Leu	
gtg	tat	att	caa	gat	aat	ttg	gga	aga	gaa	tat	ggt	tat	gga	ata	tgt	672
Val	Tyr	Ile	Gln	Asp	Asn	Leu	Gly	Arg	Glu	Tyr	Gly	Tyr	Gly	Ile	Cys	
gct	tgt	gct	att	gtt	att	ggt	ttg	gtc	ata	ttc	tta	tcg	ggc	aca	aga	720
Ala	Cys	Ala	Ile	Val	Ile	Gly	Leu	Val	Ile	Phe	Leu	Ser	Gly	Thr	Arg	
aaa	tat	cgt	ttc	aag	aaa	ctt	gtg	gga	agt	cca	ttg	aca	caa	att	gct	768
Lys	Tyr	Arg	Phe	Lys	Lys	Leu	Val	Gly	Ser	Pro	Leu	Thr	Gln	Ile	Ala	
tca	gtt	ttt	gtg	gct	gct	tgg	aac	aaa	agg	cat	atg	gaa	ttg	cct	tct	816
Ser	Val	Phe	Val	Ala	Ala	Trp	Asn	Lys	Arg	His	Met	Glu	Leu	Pro	Ser	
gat	tct	tct	ctt	tta	tac	aat	att	gat	gat	att	cct	ggg	gat	gga	aac	864
Asp	Ser	Ser	Leu	Leu	Tyr	Asn	Ile	Asp	Asp	Ile	Pro	Gly	Asp	Gly	Asn	
aaa	aaa	gct	aag	cag	agg	ttg	cct	cac	agc	aag	gaa	ttc	cgt	ttc	ttg	912
Lys	Lys	Ala	Lys	Gln	Arg	Leu	Pro	His	Ser	Lys	Glu	Phe	Arg	Phe	Leu	
gac	aag	gca	gcc	att	aaa	gta	cag	gac	cct	gaa	tcc	gct	gga	att	acc	960
Asp	Lys	Ala	Ala	Ile	Lys	Val	Gln	Asp	Pro	Glu	Ser	Ala	Gly	Ile	Thr	
gtg	gta	aat	aaa	tgg	aac	tta	tca	act	tta	acc	gac	gtt	gaa	gaa	gta	1008
Val	Val	Asn	Lys	Trp	Asn	Leu	Ser	Thr	Leu	Thr	Asp	Val	Glu	Glu	Val	
aaa	ttg	gta	gtc	cga	atg	tta	cca	aca	tgg	gcc	acg	acc	att	atg	ttt	1056
Lys	Leu	Val	Val	Arg	Met	Leu	Pro	Thr	Trp	Ala	Thr	Thr	Ile	Met	Phe	
tgg	act	gtc	tat	gct	caa	atg	aca	aca	ttt	tcc	gtg	tca	caa	gct	aca	1104
Trp	Thr	Val	Tyr	Ala	Gln	Met	Thr	Thr	Phe	Ser	Val	Ser	Gln	Ala	Thr	
acc	atg	gac	cgt	cac	atc	gga	aat	ttc	gaa	att	cct	ccg	gct	tca	ttg	1152
Thr	Met	Asp	Arg	His	Ile	Gly	Asn	Phe	Glu	Ile	Pro	Pro	Ala	Ser	Leu	
aca	ctc	ttc	ttc	gtc	gga	agt	atc	ctc	cta	acg	tgc	ata	ttc	tac	gac	1200
Thr	Leu	Phe	Phe	Val	Gly	Ser	Ile	Leu	Leu	Thr	Cys	Ile	Phe	Tyr	Asp	
cgc	gct	gtc	gtt	ccg	gtt	tgc	cga	cgt	gtc	ctc	aac	aac	cct	cac	ggt	1248

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Arg	Ala	Val	Val	Pro	Val	Cys	Arg	Arg	Val	Leu	Asn	Asn	Pro	His	Gly	
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aca	agc	ccg	ttg	caa	cgt	att	gca	gtt	ggc	tta	atc	ctt	tca	att	ata	1296
Thr	Ser	Pro	Leu	Gln	Arg	Ile	Ala	Val	Gly	Leu	Ile	Leu	Ser	Ile	Ile	
			420					425					430			
gcc	atg	att	gct	gct	gct	tta	act	gaa	gtg	aaa	aga	ttg	aat	gtt	gca	1344
Ala	Met	Ile	Ala	Ala	Ala	Leu	Thr	Glu	Val	Lys	Arg	Leu	Asn	Val	Ala	
			435				440					445				
cat	ttg	cat	gga	ttg	acc	aat	gat	gct	aat	gca	aag	gtt	cct	ttg	agt	1392
His	Leu	His	Gly	Leu	Thr	Asn	Asp	Ala	Asn	Ala	Lys	Val	Pro	Leu	Ser	
	450					455					460					
gtt	ttt	tgg	tta	gtc	cca	caa	ttc	ttg	cta	gta	ggg	gca	ggg	gag	gca	1440
Val	Phe	Trp	Leu	Val	Pro	Gln	Phe	Leu	Leu	Val	Gly	Ala	Gly	Glu	Ala	
465					470				475					480		
ttt	act	tac	att	gga	caa	ctt	gat	ttc	ttt	cta	agg	gaa	tgt	cct	aaa	1488
Phe	Thr	Tyr	Ile	Gly	Gln	Leu	Asp	Phe	Phe	Leu	Arg	Glu	Cys	Pro	Lys	
				485					490					495		
ggg	atg	aag	aca	atg	agc	aca	ggg	tta	ttc	ttg	agt	aca	ctt	tca	cta	1536
Gly	Met	Lys	Thr	Met	Ser	Thr	Gly	Leu	Phe	Leu	Ser	Thr	Leu	Ser	Leu	
			500				505						510			
ggg	ttt	ttc	ttt	agt	tct	att	ttg	gtg	act	ata	gtg	cac	aag	gtg	aca	1584
Gly	Phe	Phe	Phe	Ser	Ser	Ile	Leu	Val	Thr	Ile	Val	His	Lys	Val	Thr	
			515				520					525				
ggg	aaa	aac	cca	tgg	tta	gct	gat	aat	tta	aac	caa	ggg	agg	ctc	tat	1632
Gly	Lys	Asn	Pro	Trp	Leu	Ala	Asp	Asn	Leu	Asn	Gln	Gly	Arg	Leu	Tyr	
	530					535					540					
gat	ttc	tat	tgg	cta	ttg	gca	acg	ttg	agt	gtg	ttg	aat	ttg	atg	att	1680
Asp	Phe	Tyr	Trp	Leu	Leu	Ala	Thr	Leu	Ser	Val	Leu	Asn	Leu	Met	Ile	
545					550				555					560		
ttc	ttg	ttt	att	tcg	aga	cgg	tat	gtg	tac	aag	gag	aag	agg	ctt	gct	1728
Phe	Leu	Phe	Ile	Ser	Arg	Arg	Tyr	Val	Tyr	Lys	Glu	Lys	Arg	Leu	Ala	
				565					570					575		
gag	tgt	ggg	att	gaa	atg	gag	gat	tca	gaa	cca	gct	tgc	cac	taa		1773
Glu	Cys	Gly	Ile	Glu	Met	Glu	Asp	Ser	Glu	Pro	Ala	Cys	His			
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<210> 62

<211> 590

<212> PRT

<213> Nicotiana tabacum

<400> 62

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			20					25					30			
Ser	Ser	Ala	Ala	Met	Ile	Leu	Gly	Ile	Glu	Ala	Val	Glu	Arg	Leu	Thr	
		35					40					45				
Thr	Leu	Gly	Ile	Ala	Val	Asn	Leu	Val	Thr	Tyr	Leu	Thr	Gly	Thr	Met	
	50					55					60					
His	Leu	Gly	Asn	Ala	Ser	Ser	Ala	Asn	Asn	Val	Thr	Asn	Phe	Leu	Gly	
65					70					75				80		
Thr	Ser	Phe	Met	Leu	Thr	Leu	Leu	Gly	Gly	Phe	Val	Ala	Asp	Thr	Phe	
			85						90					95		
Leu	Gly	Arg	Tyr	Leu	Thr	Ile	Gly	Ile	Phe	Thr	Thr	Ile	Gln	Ala	Met	
			100				105						110			
Gly	Val	Thr	Ile	Leu	Thr	Ile	Ser	Thr	Ile	Ile	Pro	Ser	Leu	Arg	Pro	
		115					120					125				
Pro	Lys	Cys	Ser	Pro	Gly	Ser	Ser	Thr	Cys	Ile	Pro	Ala	Ser	Ser	Lys	
	130					135					140					
Gln	Leu	Met	Val	Leu	Tyr	Ile	Ala	Leu	Tyr	Met	Thr	Ala	Leu	Gly	Thr	
145					150					155					160	
Gly	Gly	Leu	Lys	Ser	Val	Ser	Gly	Phe	Gly	Ser	Asp	Gln	Phe	Asp		
			165					170					175			
Glu	Thr	Asp	Lys	Lys	Glu	Arg	Gly	Gln	Met	Ile	Lys	Phe	Phe	Asn	Trp	
			180				185						190			
Phe	Phe	Phe	Phe	Ile	Asn	Val	Gly	Ser	Leu	Gly	Ala	Val	Thr	Val	Leu	
		195					200					205				
Val	Tyr	Ile	Gln	Asp	Asn	Leu	Gly	Arg	Glu	Tyr	Gly	Tyr	Gly	Ile	Cys	

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210 215 220
 Ala Cys Ala Ile Val Ile Gly Leu Val Ile Phe Leu Ser Gly Thr Arg
 225 230 235 240
 Lys Tyr Arg Phe Lys Lys Leu Val Gly Ser Pro Leu Thr Gln Ile Ala
 245 250 255
 Ser Val Phe Val Ala Ala Trp Asn Lys Arg His Met Glu Leu Pro Ser
 260 265 270
 Asp Ser Ser Leu Leu Tyr Asn Ile Asp Asp Ile Pro Gly Asp Gly Asn
 275 280 285
 Lys Lys Ala Lys Gln Arg Leu Pro His Ser Lys Glu Phe Arg Phe Leu
 290 295 300
 Asp Lys Ala Ala Ile Lys Val Gln Asp Pro Glu Ser Ala Gly Ile Thr
 305 310 315 320
 Val Val Asn Lys Trp Asn Leu Ser Thr Leu Thr Asp Val Glu Glu Val
 325 330 335
 Lys Leu Val Val Arg Met Leu Pro Thr Trp Ala Thr Thr Ile Met Phe
 340 345 350
 Trp Thr Val Tyr Ala Gln Met Thr Thr Phe Ser Val Ser Gln Ala Thr
 355 360 365
 Thr Met Asp Arg His Ile Gly Asn Phe Glu Ile Pro Pro Ala Ser Leu
 370 375 380
 Thr Leu Phe Phe Val Gly Ser Ile Leu Leu Thr Cys Ile Phe Tyr Asp
 385 390 395 400
 Arg Ala Val Val Pro Val Cys Arg Arg Val Leu Asn Asn Pro His Gly
 405 410 415
 Thr Ser Pro Leu Gln Arg Ile Ala Val Gly Leu Ile Leu Ser Ile Ile
 420 425 430
 Ala Met Ile Ala Ala Ala Leu Thr Glu Val Lys Arg Leu Asn Val Ala
 435 440 445
 His Leu His Gly Leu Thr Asn Asp Ala Asn Ala Lys Val Pro Leu Ser
 450 455 460
 Val Phe Trp Leu Val Pro Gln Phe Leu Leu Val Gly Ala Gly Glu Ala
 465 470 475 480
 Phe Thr Tyr Ile Gly Gln Leu Asp Phe Phe Leu Arg Glu Cys Pro Lys
 485 490 495
 Gly Met Lys Thr Met Ser Thr Gly Leu Phe Leu Ser Thr Leu Ser Leu
 500 505 510
 Gly Phe Phe Phe Ser Ser Ile Leu Val Thr Ile Val His Lys Val Thr
 515 520 525
 Gly Lys Asn Pro Trp Leu Ala Asp Asn Leu Asn Gln Gly Arg Leu Tyr
 530 535 540
 Asp Phe Tyr Trp Leu Leu Ala Thr Leu Ser Val Leu Asn Leu Met Ile
 545 550 555 560
 Phe Leu Phe Ile Ser Arg Arg Tyr Val Tyr Lys Glu Lys Arg Leu Ala
 565 570 575
 Glu Cys Gly Ile Glu Met Glu Asp Ser Glu Pro Ala Cys His
 580 585 590

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 <211> 1773
 <212> DNA
 <213> Nicotiana tabacum

<220>
 <221> CDS
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tgg gat tac aaa ggt cga cca gct gtt cgt tcc tcg tcc ggc ggt tgg	96
Trp Asp Tyr Lys Gly Arg Pro Ala Val Arg Ser Ser Ser Gly Gly Trp	
20 25 30	
tcc agc gcc gcc atg att tta ggg att gag gca gtg gag agg ctg acg	144
Ser Ser Ala Ala Met Ile Leu Gly Ile Glu Ala Val Glu Arg Leu Thr	
35 40 45	
acg tta ggt att gct gta aat ctg gtg aca tat ttg act gga acc atg	192
Thr Leu Gly Ile Ala Val Asn Leu Val Thr Tyr Leu Thr Gly Thr Met	

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65	act	tca	ttt	atg	ctc	act	ttg	ctt	ggt	ggt	ttc	gta	gcc	gac	act	ttt	288
Thr	Ser	Phe	Met	Leu	Thr	Leu	Leu	Gly	Gly	Phe	Val	Ala	Asp	Thr	Phe		
	ctt	gga	cgg	tat	ctt	aca	att	ggt	atc	ttt	acc	act	att	caa	gcc	atg	336
Leu	Gly	Arg	Tyr	Leu	Thr	Ile	Gly	Ile	Phe	Thr	Thr	Ile	Gln	Ala	Met		
	ggt	gtt	acc	ata	ttg	acc	atc	tcc	acc	ata	atc	cca	agc	cta	cga	cca	384
Gly	Val	Thr	Ile	Leu	Thr	Ile	Ser	Thr	Ile	Ile	Pro	Ser	Leu	Arg	Pro		
	cca	aag	tgt	tcc	cca	ggg	agc	tca	aca	tgc	att	cca	gca	agt	tcc	aaa	432
Pro	Lys	Cys	Ser	Pro	Gly	Ser	Ser	Thr	Cys	Ile	Pro	Ala	Ser	Ser	Lys		
	caa	ctc	atg	gtt	cta	tac	ata	gca	cta	tac	atg	acg	gcg	ctc	ggc	acc	480
Gln	Leu	Met	Val	Leu	Tyr	Ile	Ala	Leu	Tyr	Met	Thr	Ala	Leu	Gly	Thr		
145	ggc	ggc	ctg	aaa	tcc	agc	gtc	tcc	ggc	ttc	ggc	tcc	gat	caa	ttc	gac	528
Gly	Gly	Leu	Lys	Ser	Ser	Val	Ser	Gly	Phe	Gly	Ser	Asp	Gln	Phe	Asp		
	gaa	acc	gac	aag	aaa	gaa	aga	gga	cag	atg	ata	aaa	ttc	ttc	aac	tgg	576
Glu	Thr	Asp	Lys	Lys	Glu	Arg	Gly	Gln	Met	Ile	Lys	Phe	Phe	Asn	Trp		
	ttc	ttt	ttc	ttc	att	aac	gtg	gga	tcc	ctt	ggt	gca	gtg	aca	gta	cta	624
Phe	Phe	Phe	Phe	Ile	Asn	Val	Gly	Ser	Leu	Gly	Ala	Val	Thr	Val	Leu		
	gtg	tat	att	caa	gat	aat	ttg	gga	aga	gaa	tat	ggt	tat	gga	ata	tgt	672
Val	Tyr	Ile	Gln	Asp	Asn	Leu	Gly	Arg	Glu	Tyr	Gly	Tyr	Gly	Ile	Cys		
	gct	tgt	gct	att	gtt	att	ggt	ttg	gtc	ata	ttc	tta	tcg	ggc	aca	aga	720
Ala	Cys	Ala	Ile	Val	Ile	Gly	Leu	Val	Ile	Phe	Leu	Ser	Gly	Thr	Arg		
225	aaa	tat	cgt	ttc	aag	aaa	ctt	gtg	gga	agt	cca	ttg	aca	caa	att	gct	768
Lys	Tyr	Arg	Phe	Lys	Lys	Leu	Val	Gly	Ser	Pro	Leu	Thr	Gln	Ile	Ala		
	tca	gtt	ttt	gtg	gct	gct	tgg	aac	aaa	aga	cat	atg	gat	ttg	cct	tct	816
Ser	Val	Phe	Val	Ala	Ala	Trp	Asn	Lys	Arg	His	Met	Asp	Leu	Pro	Ser		
	gat	tct	tat	ctt	cta	tat	aat	att	gat	gat	att	cct	ggg	gat	gga	aat	864
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	aaa	aaa	gct	aag	cag	aga	ttg	cct	cac	agc	aag	gaa	ttc	cgt	ttc	ttg	912
Lys	Lys	Ala	Lys	Gln	Arg	Leu	Pro	His	Ser	Lys	Glu	Phe	Arg	Phe	Leu		
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Asp	Lys	Ala	Ala	Ile	Lys	Val	Gln	Asp	Pro	Glu	Ser	Ala	Gly	Ile	Thr		
305	gtg	gta	aat	aaa	tgg	aac	tta	tca	act	tta	acc	gac	gtt	gaa	gaa	gta	1008
Val	Val	Asn	Lys	Trp	Asn	Leu	Ser	Thr	Leu	Thr	Asp	Val	Glu	Glu	Val		
	aaa	ttg	gta	gtc	cga	atg	tta	cca	aca	tgg	gcc	acg	acc	att	atg	ttt	1056
Lys	Leu	Val	Val	Arg	Met	Leu	Pro	Thr	Thr	Phe	Ser	Val	Ser	Gln	Ala	Thr	
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Trp	Thr	Val	Tyr	Ala	Gln	Met	Thr	Thr	Thr	Phe	Ser	Val	Ser	Gln	Ala	Thr	
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Thr	Met	Asp	Arg	His	Ile	Gly	Asn	Phe	Glu	Ile	Pro	Pro	Ala	Ser	Leu		
	aca	ctt	ttc	ttc	gtc	gga	agt	atc	ctc	tta	acg	tgc	ata	ttc	tac	gac	1200
Thr	Leu	Phe	Phe	Val	Gly	Ser	Ile	Leu	Leu	Leu	Thr	Cys	Ile	Phe	Tyr	Asp	
385	cgt	gcc	gtc	gta	ccg	gtt	tgt	cga	cgt	gtc	cta	aac	aat	cct	cac	ggt	1248
Arg	Ala	Val	Val	Pro	Val	Cys	Arg	Arg	Arg	Val	Leu	Asn	Asn	Pro	His	Gly	
	aca	acc	ccg	ttg	caa	cgt	att	gca	gtt	gga	tta	ata	ctt	tca	att	ata	1296
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Ala	Met	Val	Ala	Ala	Ala	Leu	Thr	Glu	Val	Lys	Arg	Leu	Asn	Val	Ala		
		435						440				445					
cat	ttg	cat	gga	ttg	acc	aat	gat	gca	aat	gcc	aag	gtt	cct	ttg	agt		1392
His	Leu	His	Gly	Leu	Thr	Asn	Asp	Ala	Asn	Ala	Lys	Val	Pro	Leu	Ser		
	450					455					460						
gtt	ttt	tgg	tta	gtt	ccg	caa	ttc	ttg	cta	gta	ggg	gca	ggt	gag	gca		1440
Val	Phe	Trp	Leu	Val	Pro	Gln	Phe	Leu	Leu	Val	Gly	Ala	Gly	Glu	Ala		
465					470				475						480		
ttt	act	tat	atc	gga	caa	ctt	gat	ttc	ttc	cta	agg	gag	tgt	cct	aaa		1488
Phe	Thr	Tyr	Ile	Gly	Gln	Leu	Asp	Phe	Phe	Leu	Arg	Glu	Cys	Pro	Lys		
				485				490						495			
gga	atg	aag	aca	atg	agc	acg	ggg	tta	ttc	ttg	agt	aca	ctt	tca	tta		1536
Gly	Met	Lys	Thr	Met	Ser	Thr	Gly	Leu	Phe	Leu	Ser	Thr	Leu	Ser	Leu		
			500					505					510				
ggg	ttt	ttc	ttt	agt	tct	att	ttg	gtg	act	ata	gtg	cat	aag	gtg	aca		1584
Gly	Phe	Phe	Phe	Ser	Ser	Ile	Leu	Val	Thr	Ile	Val	His	Lys	Val	Thr		
	515					520					525						
gtg	aaa	aac	cca	tgg	tta	gct	gat	aat	tta	aac	caa	gga	aga	ctc	tat		1632
Val	Lys	Asn	Pro	Trp	Leu	Ala	Asp	Asn	Leu	Asn	Gln	Gly	Arg	Leu	Tyr		
	530					535					540						
gat	ttc	tat	tgg	cta	ttg	gca	acg	ttg	agt	gtg	ttg	aat	ttg	atg	att		1680
Asp	Phe	Tyr	Trp	Leu	Leu	Ala	Thr	Leu	Ser	Val	Leu	Asn	Leu	Met	Ile		
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ttc	ttg	ttt	att	tca	aga	cgg	tat	gtg	tac	aag	gag	aag	aga	ctt	gct		1728
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PF59082SeqList_PF59082.txt

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Cys Val Met Gly Ile Ser Met Asn Leu Val Thr Tyr Leu Val Gly Asp	
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Glu	Val	Gly	Arg	Ser	Trp	Ala	Tyr	Gly	Ile	Cys	Thr	Val	Ser	Met	Ala	
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Ala	Thr	Thr	Ile	Ile	Phe	Trp	Thr	Thr	Tyr	Ala	Gln	Met	Ile	Thr	Phe	
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Ser	Val	Glu	Gln	Ala	Ser	Thr	Met	Arg	Arg	Asn	Ile	Gly	Ser	Phe	Lys	
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Lys	Gly	Lys	Pro	Gly	Phe	Ser	Ser	Leu	Gln	Arg	Ile	Ala	Ile	Gly	Leu	
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Arg	Leu	Cys	Val	Ala	Lys	Ser	Ser	Ser	Gln	Lys	Thr	Pro	Ile	Ser		
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PF59082SeqList_PF59082.txt

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Gly	Phe	Phe	Val 500	Ser	Ser	Phe	Leu	Val 505	Ser	Ile	Val	Lys	Arg 510	Val	Thr	
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Arg	Leu	Asp	Tyr	Phe	Tyr	Trp 535	Leu	Leu	Val	Ile	Leu	Ser	Gly	Ile	Asn	
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Cys																

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His	Gly 130	Glu	Ala	Cys	Ile	Pro 135	Ala	Thr	Ala	Phe	Gln 140	Met	Thr	Ile	Leu
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Ser	Ile	Ser	Gly	Phe 165	Gly	Ser	Asp	Gln	Phe 170	Asp	Asp	Lys	Asp	Pro 175	Lys
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Glu	Val	Gly 210	Arg	Ser	Trp	Ala 215	Tyr	Gly	Ile	Cys	Thr	Val	Ser	Met	Ala
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His	Leu 290	Leu	Asp	Lys	Ala	Ala 295	Ile	Val	Ala	Glu	Gly	Asp	Phe	Glu	Gln
Thr	Leu	Asp	Gly	Val	Ala	Ile	Pro	Asn	Pro	Trp	Lys	Leu	Ser	Ser	Val

PF59082SeqList_PF59082.txt

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Ser Val Glu Gln Ala Ser Thr Met Arg Arg Asn Ile Gly Ser Phe Lys
Ile Pro Ala Gly Ser Leu Thr Val Phe Phe Val Ala Ala Ile Leu Ile
Thr Leu Ala Val Tyr Asp Arg Ala Ile Met Pro Phe Trp Lys Lys Trp
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Lys Gly Lys Pro Gly Phe Ser Ser Leu Gln Arg Ile Ala Ile Gly Leu
Val Leu Ser Thr Ala Gly Met Ala Ala Ala Ala Leu Val Glu Gln Lys
Arg Leu Cys Val Ala Lys Ser Ser Gln Lys Thr Leu Pro Ile Ser
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Phe Ile Tyr Thr Gly Gln Leu Asp Phe Phe Ile Thr Gln Ser Pro Lys
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Ser Thr Ser Thr Asp Val Gly Trp Leu Ala Asp Asn Ile Asn His Gly
Arg Leu Asp Tyr Phe Tyr Trp Leu Leu Val Ile Leu Ser Gly Ile Asn
Phe Val Val Tyr Ile Ile Cys Ala Leu Trp Phe Lys Pro Thr Lys Gly
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Phe Gln Gly Arg Pro Ala Asp Arg Ser Lys Thr Gly Gly Trp Ala Ser
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Gly Ile Gly Val Asn Leu Val Thr Tyr Leu Thr Gly Thr Met His Leu
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Gly Asn Ala Thr Ala Ala Asn Thr Val Thr Asn Phe Leu Gly Thr Ser
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ttc atg ctc tgt ctc ctc ggt ggc ttc ata gct cac acc ttt ctt gga      288
Phe Met Leu Cys Leu Leu Gly Gly Phe Ile Ala His Thr Phe Leu Gly
85      90      95
agg tac tta acg att gct ata ttc gcc gca atc caa gcc acg ggt gtt      336
Arg Tyr Leu Thr Ile Ala Ile Phe Ala Ala Ile Gln Ala Thr Gly Val
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PF59082SeqList_PF59082.txt

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Ser	Lys	Trp	Tyr	Val	Tyr	Lys	Glu	Lys	Arg	Leu	Ala	Asp	Leu	Gly	Ile		
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gag	ttg	gaa	gac	gag	cca	gac	att	ccc	atg	ggt	cat	tga				1767	
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Leu	Lys	Ser	Ser	Val	Ser	Gly	Phe	Gly	Ser	Asp	Gln	Phe	Asp	Glu	Lys	
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Ser	Met	Ile	Ile	Ala	Ile	Ile	Val	Phe	Leu	Ser	Gly	Thr	Lys	Arg	Tyr	
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Arg	Tyr	Lys	Arg	Ser	Leu	Gly	Ser	Pro	Ile	Val	His	Ile	Phe	Gln	Val	
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Ile	Ala	Ala	Ser	Ile	Lys	Lys	Arg	Lys	Met	Gln	Leu	Pro	Tyr	Asn	Val	
	255				260					265					270	
ggt	tct	ttg	tat	gag	gac	act	ccc	gag	gct	tca	aga	ata	gag	cac	acc	925
Gly	Ser	Leu	Tyr	Glu	Asp	Thr	Pro	Glu	Ala	Ser	Arg	Ile	Glu	His	Thr	
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gaa	cag	ttc	cgt	ttc	ttg	gag	aaa	gca	gcc	att	gtg	gca	gaa	gat	gat	973
Glu	Gln	Phe	Arg	Phe	Leu	Glu	Lys	Ala	Ala	Ile	Val	Ala	Glu	Asp	Asp	
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Ser	Leu	Thr	Arg	Val	Glu	Glu	Val	Lys	Met	Met	Val	Arg	Leu	Leu	Pro	
	320					325					330					
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Val	Trp	Ala	Thr	Thr	Ile	Ile	Phe	Trp	Thr	Ile	Tyr	Ala	Gln	Leu	Ile	
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Thr	Phe	Ser	Val	Glu	Gln	Ala	Ser	Thr	Met	Glu	Arg	Asn	Ile	Gly	Ser	
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Phe	Gln	Ile	Pro	Ala	Gly	Ser	Val	Thr	Val	Phe	Phe	Val	Ala	Ala	Ile	
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Gly	Leu	Val	Phe	Ser	Ile	Phe	Gly	Met	Ala	Ala	Ala	Ser	Val	Cys	Glu	
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Arg	Lys	Arg	Leu	Ser	Val	Ala	Lys	Ser	Val	Ser	Gly	Gly	Asn	Gln	Ala	
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Ser Val Val Lys Lys Val Thr Gly Thr Arg Asp Gly Gln Gly Trp Leu	
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gca gac agc ata aac aag ggc agg ctc gat ttg ttc tat gca ctg ctt	1693
Ala Asp Ser Ile Asn Lys Gly Arg Leu Asp Leu Phe Tyr Ala Leu Leu	
530 535 540	
acc ata ctt agt ttc gtt aac ttt gca gca ttt gcg gta tgt gca gtt	1741
Thr Ile Leu Ser Phe Val Asn Phe Ala Ala Phe Ala Val Cys Ala Val	
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tgg ttc aaa cct aag aaa cct aaa caa cca gct gct atg caa atg ggg	1789
Trp Phe Lys Pro Lys Lys Pro Lys Gln Pro Ala Ala Met Gln Met Gly	
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Pro Val Asn Gly Ser Thr Ala Glu Glu Lys Cys	
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 Lys Thr Ile Gly Ile Phe Ala Ser Ile Gln Thr Leu Gly Thr Ala Thr
 100 105 110
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 130 135 140
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 Lys Arg Ser Leu Gly Ser Pro Ile Val His Ile Phe Gln Val Ile Ala
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 Ala Ser Ile Lys Lys Arg Lys Met Gln Leu Pro Tyr Asn Val Gly Ser
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 Leu Tyr Glu Asp Thr Pro Glu Ala Ser Arg Ile Glu His Thr Glu Gln
 Seite 91

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 Val Phe Ser Ile Phe Gly Met Ala Ala Ala Ser Val Cys Glu Arg Lys
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 Arg Leu Ser Val Ala Lys Ser Val Ser Gly Gly Asn Gln Ala Thr Thr
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 Phe Gln Gly Arg Pro Ala Asp Arg Ser Lys Thr Gly Gly Trp Ala Ser
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 gcc gcc atg att ctc tgt att gag gcg gtg gag cgg ttg acg acg tta 144
 Ala Ala Met Ile Leu Cys Ile Glu Ala Val Glu Arg Leu Thr Thr Leu
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 ggt atc ggc gtt aat cta gtg acg tat ttg aca gga act atg cat cta 192
 Gly Ile Gly Val Asn Leu Val Thr Tyr Leu Thr Gly Thr Met His Leu
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 ggc aat gca acg gca gct aac acc gtc acc aac ttc ctc gga act tcg 240
 Gly Asn Ala Thr Ala Ala Asn Thr Val Thr Asn Phe Leu Gly Thr Ser
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 Phe Met Leu Cys Leu Leu Gly Gly Phe Ile Ala Asp Thr Phe Leu Gly
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Thr	Glu	Pro	Lys	Glu	Gln	Ser	Gln	Met	Thr	Tyr	Phe	Phe	Asn	Arg	Phe	
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Pro	Ser	Phe	Leu	Tyr	Asp	Leu	Asp	Asp	Val	Ile	Ala	Ala	Glu	Gly	Ala	
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Arg	Pro	Leu	Gln	Arg	Ile	Gly	Leu	Gly	Leu	Leu	Leu	Ala	Ala	Met	Gly	
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Phe	Phe	Cys 195	Ile	Asn	Val	Gly	Ser 200	Leu	Leu	Ala	Val	Thr 205	Val	Leu	Val
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Ala Ser Ala Met Ile Leu Gly Gly Glu Val Met Glu Arg Leu Thr Thr
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Leu Gly Ile Ala Val Asn Leu Val Thr Tyr Leu Thr Gly Thr Met His
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Ser Phe Met Leu Cys Leu Leu Gly Gly Phe Leu Ala Asp Thr Phe Leu
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Gly Arg Tyr Arg Thr Ile Ala Ile Phe Ala Ala Val Gln Ala Thr Gly
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PF59082SeqList_PF59082.txt

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Thr Leu Pro Ile Ser Val Phe Leu Leu Ile Pro Gln Phe Phe Leu Val
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Gly Ser Gly Glu Ala Phe Ile Tyr Thr Gly Gln Leu Asp Phe Phe Ile
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Asp Tyr Lys Gly Arg Pro Ala Glu Arg Ser Lys Thr Gly Gly Trp Thr
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gct tcc gcc atg ata tta gga gga gaa gtg atg gag agg ttg aca aca      144
Ala Ser Ala Met Ile Leu Gly Gly Glu Val Met Glu Arg Leu Thr Thr
35          40          45
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Leu Gly Ile Ala Val Asn Leu Val Thr Tyr Leu Thr Gly Thr Met His
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65          70          75          80
tcc ttc atg ctc tgt ctg ctc ggt ggc ttc ctc gcc gat act ttt ctc      288
Ser Phe Met Leu Cys Leu Leu Gly Gly Phe Leu Ala Asp Thr Phe Leu
85          90          95
gga aga tac cgc acc atc gcc atc ttc gct gcc gtt caa gca act ggt      336
Gly Arg Tyr Arg Thr Ile Ala Ile Phe Ala Ala Val Gln Ala Thr Gly
100          105          110
gtg aca atc ttg aca ata tca acc ata att ccg agc ctt cac cct cca      384
Val Thr Ile Leu Thr Ile Ser Thr Ile Ile Pro Ser Leu His Pro Pro
115          120          125
aag tgc aac gga gac acc gtg cca cct tgc gtg aga gca aat gag aaa      432
Lys Cys Asn Gly Asp Thr Val Pro Pro Cys Val Arg Ala Asn Glu Lys
130          135          140
caa tta acg gtg ctt tat ttg gcg ctt tat gta acg gcg ctc ggc acc      480
Gln Leu Thr Val Leu Tyr Leu Ala Leu Tyr Val Thr Ala Leu Gly Thr
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PF59082SeqList_PF59082.txt

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Lys	Tyr	Arg	Phe	Lys	Lys	Leu	Val	Gly	Ser	Pro	Leu	Thr	Gln	Phe	Ala	
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Glu	Val	Phe	Val	Ala	Ala	Leu	Arg	Lys	Arg	Asn	Met	Glu	Leu	Pro	Ser	
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Asp	Ser	Ser	Leu	Leu	Phe	Asn	Asp	Tyr	Asp	Pro	Lys	Lys	Gln	Thr	Leu	
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Pro	His	Ser	Lys	Gln	Phe	Arg	Phe	Leu	Asp	Lys	Ala	Ala	Ile	Met	Asp	
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Trp	Ala	Thr	Thr	Ile	Met	Phe	Trp	Thr	Ile	His	Ala	Gln	Met	Thr	Thr	
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Leu	Phe	Leu	Ser	Thr	Leu	Ser	Leu	Gly	Phe	Phe	Phe	Ser	Thr	Leu	Leu	
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PF59082SeqList_PF59082.txt

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gaa	gca	gat	gct	gct	gct	ttc	cat	ggc	cat	tga						1761
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 485 490 495
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 35 40 45
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 Ala Val Asn Leu Val Thr Tyr Met Ile Ser Ile Met His Leu Pro Ser
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 Ser Thr Ala Ala Asn Thr Val Thr Asp Phe Met Gly Thr Ser Phe Leu
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Ser	Val	Glu	Gln	Ala	Ser	Thr	Met	Glu	Arg	Asn	Ile	Gly	Ser	Phe	Gln		
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Ile	Pro	Ala	Gly	Ser	Val	Thr	Val	Phe	Phe	Val	Ala	Ala	Ile	Leu	Ile		
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act	ctg	gct	gtc	tat	gac	cga	ctc	atc	atg	ccc	ctt	tgg	aaa	aag	tgg		1200
Thr	Leu	Ala	Val	Tyr	Asp	Arg	Leu	Ile	Met	Pro	Leu	Trp	Lys	Lys	Trp		
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aac	ggc	aaa	cca	ggt	ttc	act	gac	cta	caa	agg	ata	gca	att	ggg	ctt		1248
Asn	Gly	Lys	Pro	Gly	Phe	Thr	Asp	Leu	Gln	Arg	Ile	Ala	Ile	Gly	Leu		
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Val	Phe	Ser	Ile	Phe	Gly	Met	Ala	Ala	Ala	Ser	Val	Cys	Glu	Arg	Lys		
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Arg	Leu	Ser	Val	Ala	Lys	Ser	Val	Ser	Gly	Gly	Asn	Gln	Ala	Thr	Thr		
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Thr	Leu	Pro	Ile	Ser	Val	Phe	Leu	Leu	Ile	Pro	Gln	Phe	Phe	Leu	Val		
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Gly	Ser	Gly	Glu	Ala	Phe	Ile	Tyr	Thr	Gly	Gln	Leu	Asp	Phe	Phe	Ile		
	465				470					475					480		
aca	cgg	tca	cca	aaa	gga	atg	aaa	acc	atg	agc	act	ggt	ctc	ttt	ctc		1488
Thr	Arg	Ser	Pro	Lys	Gly	Met	Lys	Thr	Met	Ser	Thr	Gly	Leu	Phe	Leu		
			485					490						495			
aca	act	ttg	tct	ctc	ggt	ttc	ttc	ttc	agc	agt	ttc	ctt	gtc	tcg	gtt		1536
Thr	Thr	Leu	Ser	Leu	Gly	Phe	Phe	Phe	Ser	Ser	Phe	Leu	Val	Ser	Val		
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ggt	aag	aaa	ggt	act	ggg	aca	aga	gat	ggg	caa	ggg	tgg	cta	gca	gac		1584
Val	Lys	Lys	Val	Thr	Gly	Thr	Arg	Asp	Gly	Gln	Gly	Trp	Leu	Ala	Asp		
		515				520					525						
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Ser	Ile	Asn	Lys	Gly	Arg	Leu	Asp	Leu	Phe	Tyr	Ala	Leu	Leu	Thr	Ile		
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ctt	agt	ttc	ggt	aac	ttt	gca	gca	ttt	gcg	gta	tgt	gca	ggt	tgg	ttc		1680
Leu	Ser	Phe	Val	Asn	Phe	Ala	Ala	Phe	Ala	Val	Cys	Ala	Val	Trp	Phe		

PF59082SeqList_PF59082.txt

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 35 40 45
 Ala Val Asn Leu Val Thr Tyr Met Ile Ser Ile Met His Leu Pro Ser
 50 55 60
 Ser Thr Ala Ala Asn Thr Val Thr Asp Phe Met Gly Thr Ser Phe Leu
 65 70 75 80
 Leu Cys Leu Leu Gly Phe Leu Ala Asp Ser Phe Leu Gly Arg Tyr
 85 90 95
 Lys Thr Ile Gly Ile Phe Ala Ser Ile Gln Thr Leu Gly Thr Ala Thr
 100 105 110
 Leu Ala Ile Ser Thr Lys Leu Pro Gly Leu Arg Pro Pro Cys His
 115 120 125
 Ala Asn Ser Asp Ser Cys Lys Gln Ala Asn Gly Phe Gln Met Gly Ile
 130 135 140
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 145 150 155 160
 Ser Ser Val Ser Gly Phe Gly Ser Asp Gln Phe Asp Glu Lys Asp Glu
 165 170 175
 Lys Glu Lys Ser Gln Met Ala Tyr Phe Phe Asn Arg Phe Phe Phe
 180 185 190
 Ile Ser Phe Gly Thr Leu Ala Ala Val Thr Val Leu Val Tyr Leu Gln
 195 200 205
 Asp Glu Val Ser Arg Ser Leu Ala Tyr Gly Ile Cys Ser Val Ser Met
 210 215 220
 Ile Ile Ala Ile Ile Val Phe Leu Ser Gly Thr Lys Arg Tyr Arg Tyr
 225 230 235 240
 Lys Arg Ser Leu Gly Ser Pro Ile Val His Ile Phe Gln Val Ile Ala
 245 250 255
 Ala Ser Ile Lys Lys Arg Lys Met Gln Leu Pro Tyr Asn Val Gly Ser
 260 265 270
 Leu Tyr Glu Asp Thr Pro Glu Ala Ser Arg Ile Glu His Thr Glu Gln
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 Phe Arg Phe Leu Glu Lys Ala Ala Ile Val Ala Glu Asp Asp Phe Glu
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 Thr Asn Leu Cys Gly Ser Gly Pro Asn Pro Trp Lys Leu Cys Ser Leu
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 Thr Arg Val Glu Glu Val Lys Met Met Val Arg Leu Leu Pro Val Trp
 325 330 335
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 340 345 350
 Ser Val Glu Gln Ala Ser Thr Met Glu Arg Asn Ile Gly Ser Phe Gln
 355 360 365
 Ile Pro Ala Gly Ser Val Thr Val Phe Phe Val Ala Ala Ile Leu Ile
 370 375 380
 Thr Leu Ala Val Tyr Asp Arg Leu Ile Met Pro Leu Trp Lys Lys Trp
 385 390 395 400
 Asn Gly Lys Pro Gly Phe Thr Asp Leu Gln Arg Ile Ala Ile Gly Leu
 405 410 415
 Val Phe Ser Ile Phe Gly Met Ala Ala Ala Ser Val Cys Glu Arg Lys
 420 425 430
 Arg Leu Ser Val Ala Lys Ser Val Ser Gly Gly Asn Gln Ala Thr Thr

PF59082SeqList_PF59082.txt

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 Gly Ser Gly Glu Ala Phe 455 Ile Tyr Thr Gly Gln 460 Leu Asp Phe Phe Ile
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 Thr Arg Ser Pro Lys 470 Gly Met Lys Thr Met 475 Thr Gly Leu Phe 480
 485
 Thr Thr Leu Ser Leu Gly Phe Phe Phe Ser Ser Phe Leu Val Ser Val
 500
 Val Lys Lys Val Thr Gly Thr Arg Asp Gly Gln Gly Trp Leu Ala Asp
 515
 Ser Ile Asn Lys Gly Arg Leu Asp Leu Phe Tyr Ala Leu Leu Thr Ile
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 Leu Ser Phe Val Asn Phe 535 Ala Ala Phe Ala Val Cys Ala Val Trp Phe
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 Leu Leu Asp Ala Trp Asp Phe Lys Gly Arg Pro Ala Pro Arg Ala Thr 20
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 acc ggc cgc tgg ggc gcc gcc gcc atg atc cta gtg gcg gag ctg aac 144
 Thr Gly Arg Trp Gly Ala Ala Ala Met Ile Leu Val Ala Glu Leu Asn 35
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 gag cgg ctg acg acg ctg ggc atc gcc gtg aac ctg gtg acg tac ctg 192
 Glu Arg Leu Thr Thr Leu Gly Ile Ala Val Asn Leu Val Thr Tyr Leu 50
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 acg ggc acc atg cac ctg ggc aac gcc gag tcc gcc aac gtc gtc acc 240
 Thr Gly Thr Met His Leu Gly Asn Ala Glu Ser Ala Asn Val Val Thr 65
 70
 aac ttc atg ggc acc tcc ttc atg ctc tgc ctc ctc ggc ggc ttc gtc 288
 Asn Phe Met Gly Thr Ser Phe Met Leu Cys Leu Leu Gly Gly Phe Val 85
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 gcc gac tcc ttc ctc ggc cgc tac ctc acc atc gcc atc ttc acc gcc 336
 Ala Asp Ser Phe Leu Gly Arg Tyr Leu Thr Ile Ala Ile Phe Thr Ala 100
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 gtc cag gcc tcg ggc gtg acg atc ctg acg atc tcg acg gcg gcg ccg 384
 Val Gln Ala Ser Gly Val Thr Ile Leu Thr Ile Ser Thr Ala Ala Pro 115
 120
 ggg cta cgg ccg gcg tcc tgc tcc gcg acc ggc gac gga ggc gtc 432
 Gly Leu Arg Pro Ala Ser Cys Ser Ala Thr Gly Asp Gly Gly Gly Val 130
 135
 gtc ggg gag tgc gcg ccg gcg tcg ggg gcg cag ctg ggg gtg ctg tac 480
 Val Gly Glu Cys Ala Arg Ala Ser Gly Ala Gln Leu Gly Val Leu Tyr 145
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 ctg gcg ctg tac ctg acg gcg ctg ggc acg ggt ggg cta aag tcg agc 528
 Leu Ala Leu Tyr Leu Thr Ala Leu Gly Thr Gly Gly Leu Lys Ser Ser 165
 170
 gtg tcg ggg ttc ggg tcg gac cag ttc gac gag tcg gac ggc ggc gag 576
 Val Ser Gly Phe Gly Ser Asp Gln Phe Asp Glu Ser Asp Gly Gly Glu 180
 185
 aag cgg cag atg atg cgc ttc ttc aac tgg ttc ttc ttc ttc atc tcg 624
 Lys Arg Gln Met Met Arg Phe Phe Asn Trp Phe Phe Phe Phe Ile Ser 195
 200
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PF59082SeqList_PF59082.txt																
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Leu	Gly	Arg	Arg	Trp	Gly	Tyr	Gly	Ala	Cys	Ala	Cys	Ala	Ile	Ala	Ala	
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ggc	ctc	ctc	gtc	ttc	ctg	gcc	ggc	aca	cgc	agg	tac	cgc	ttc	aag	aag	768
Gly	Leu	Leu	Val	Phe	Leu	Ala	Gly	Thr	Arg	Arg	Tyr	Arg	Phe	Lys	Lys	
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Leu	Ala	Gly	Ser	Pro	Leu	Thr	Gln	Ile	Ala	Ala	Val	Val	Val	Ala	Ala	
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tgg	cgc	aag	cgc	cgc	ctc	cct	ctc	ccc	gcc	gac	ccc	gcc	atg	ctc	tac	864
Trp	Arg	Lys	Arg	Arg	Leu	Pro	Leu	Pro	Ala	Asp	Pro	Ala	Met	Leu	Tyr	
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Asp	Val	Asp	Val	Gly	Lys	Ala	Ala	Ala	Val	Glu	Asp	Gly	Ser	Ser	Ser	
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Lys	Lys	Ser	Lys	Arg	Lys	Glu	Arg	Leu	Pro	His	Thr	Asp	Gln	Phe	Arg	
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ttc	ctg	gac	cac	gcg	gcg	atc	aac	gag	gac	ccg	gcg	gcg	ggg	gcg	agc	1008
Phe	Leu	Asp	His	Ala	Ala	Ile	Asn	Glu	Asp	Pro	Ala	Ala	Gly	Ala	Ser	
				325				330						335		
agc	agc	agc	aag	tgg	cgg	ctg	gcg	acg	ctg	acg	gac	gtg	gag	gag	gtg	1056
Ser	Ser	Ser	Lys	Trp	Arg	Leu	Ala	Thr	Leu	Thr	Asp	Val	Glu	Glu	Val	
			340					345					350			
aag	acg	gtg	gcg	cgg	atg	ctg	ccg	atc	tgg	gcg	acc	acg	atc	atg	ttc	1104
Lys	Thr	Val	Ala	Arg	Met	Leu	Pro	Ile	Trp	Ala	Thr	Thr	Ile	Met	Phe	
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tgg	acg	gtg	tac	gcg	cag	atg	acc	acc	ttc	tcg	gtg	tcg	cag	gcc	acc	1152
Trp	Thr	Val	Tyr	Ala	Gln	Met	Thr	Thr	Phe	Ser	Val	Ser	Gln	Ala	Thr	
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Thr	Met	Asp	Arg	Arg	Val	Gly	Gly	Ser	Phe	Gln	Ile	Pro	Ala	Gly	Ser	
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ctc	acc	gtc	ttc	ttc	gtc	ggc	tcc	atc	ctg	ctc	acc	gtg	ccc	gtc	tac	1248
Leu	Thr	Val	Phe	Phe	Val	Gly	Ser	Ile	Leu	Leu	Thr	Val	Pro	Val	Tyr	
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gac	cgc	ctc	gtg	gtg	ccc	gtc	gcg	cgc	arg	gtc	agc	ggc	aac	ccg	cac	1296
Asp	Arg	Leu	Val	Val	Pro	Val	Ala	Arg	Arg	Val	Ser	Gly	Asn	Pro	His	
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Gly	Leu	Thr	Pro	Leu	Gln	Arg	Ile	Ala	Val	Gly	Leu	Ala	Leu	Ser	Val	
		435					440					445				
gtc	gcc	atg	gcg	ggc	gcc	gcg	ctc	acg	gag	gtc	cgc	cgc	ctc	cgc	gtc	1392
Val	Ala	Met	Ala	Gly	Ala	Ala	Leu	Thr	Glu	Val	Arg	Arg	Leu	Arg	Val	
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gcg	cgc	gag	tcc	tcc	gag	tcc	gcc	tcc	gga	ggc	gtc	gtg	ccc	atg	tcg	1440
Ala	Arg	Glu	Ser	Ser	Glu	Ser	Ala	Ser	Gly	Gly	Val	Val	Pro	Met	Ser	
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gtg	ttc	tgg	ctc	atc	ccg	cag	ttc	ttc	ctc	gtg	ggg	gcg	ggc	gag	gcg	1488
Val	Phe	Trp	Leu	Ile	Pro	Gln	Phe	Phe	Leu	Val	Gly	Ala	Gly	Glu	Ala	
				485				490						495		
ttc	acg	tac	atc	ggc	cag	ctc	gac	ttc	ttc	ctg	cgc	gag	tgc	ccc	aag	1536
Phe	Thr	Tyr	Ile	Gly	Gln	Leu	Asp	Phe	Phe	Leu	Arg	Glu	Cys	Pro	Lys	
			500					505					510			
ggg	atg	aag	acc	atg	agc	acg	ggg	ctg	ttc	ctc	agc	acc	ctg	tcg	ctg	1584
Gly	Met	Lys	Thr	Met	Ser	Thr	Gly	Leu	Phe	Leu	Ser	Thr	Leu	Ser	Leu	
		515					520					525				
gga	ttc	ttc	gtc	agc	tcc	gcg	ctc	gtc	gcc	gcc	gtg	cac	agg	gtc	acg	1632
Gly	Phe	Phe	Val	Ser	Ser	Ala	Leu	Val	Ala	Ala	Val	His	Arg	Val	Thr	
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ggc	gac	cgc	cac	ccc	tgg	atc	gcc	aac	gac	ctc	aac	aag	ggc	cgc	ctc	1680
Gly	Asp	Arg	His	Pro	Trp	Ile	Ala	Asn	Asp	Leu	Asn	Lys	Gly	Arg	Leu	
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Asp	Asn	Phe	Tyr	Trp	Leu	Leu	Ala	Ala	Val	Cys	Leu	Ala	Asn	Leu	Leu	
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ggc	gcc	gac	ggc	agc	gtc	aac	ggc	gtc	gag	atg	gcc	gac	gag	ccc	acg	1824
Gly	Ala	Asp	Gly	Ser	Val	Asn	Gly	Val	Glu	Met	Ala	Asp	Glu	Pro	Thr	
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Leu	His															
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 35 40 45
 Glu Arg Leu Thr Thr Leu Gly Ile Ala Val Asn Leu Val Thr Tyr Leu
 50 55 60
 Thr Gly Thr Met His Leu Gly Asn Ala Glu Ser Ala Asn Val Val Thr
 65 70 75 80
 Asn Phe Met Gly Thr Ser Phe Met Leu Cys Leu Leu Gly Gly Phe Val
 85 90 95
 Ala Asp Ser Phe Leu Gly Arg Tyr Leu Thr Ile Ala Ile Phe Thr Ala
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 Val Gln Ala Ser Gly Val Thr Ile Leu Thr Ile Ser Thr Ala Ala Pro
 115 120 125
 Gly Leu Arg Pro Ala Ser Cys Ser Ala Thr Gly Asp Gly Gly Gly Val
 130 135 140
 Val Gly Glu Cys Ala Arg Ala Ser Gly Ala Gln Leu Gly Val Leu Tyr
 145 150 155 160
 Leu Ala Leu Tyr Leu Thr Ala Leu Gly Thr Gly Gly Leu Lys Ser Ser
 165 170 175
 Val Ser Gly Phe Gly Ser Asp Gln Phe Asp Glu Ser Asp Gly Gly Glu
 180 185 190
 Lys Arg Gln Met Met Arg Phe Phe Asn Trp Phe Phe Phe Phe Ile Ser
 195 200 205
 Leu Gly Ser Leu Leu Ala Val Thr Val Leu Val Tyr Val Gln Asp Asn
 210 215 220
 Leu Gly Arg Arg Trp Gly Tyr Gly Ala Cys Ala Cys Ala Ile Ala Ala
 225 230 235 240
 Gly Leu Leu Val Phe Leu Ala Gly Thr Arg Arg Tyr Arg Phe Lys Lys
 245 250 255
 Leu Ala Gly Ser Pro Leu Thr Gln Ile Ala Ala Val Val Val Ala Ala
 260 265 270
 Trp Arg Lys Arg Arg Leu Pro Leu Pro Ala Asp Pro Ala Met Leu Tyr
 275 280 285
 Asp Val Asp Val Gly Lys Ala Ala Ala Val Glu Asp Gly Ser Ser Ser
 290 295 300
 Lys Lys Ser Lys Arg Lys Glu Arg Leu Pro His Thr Asp Gln Phe Arg
 305 310 315 320
 Phe Leu Asp His Ala Ala Ile Asn Glu Asp Pro Ala Ala Gly Ala Ser
 325 330 335
 Ser Ser Ser Lys Trp Arg Leu Ala Thr Leu Thr Asp Val Glu Glu Val
 340 345 350
 Lys Thr Val Ala Arg Met Leu Pro Ile Trp Ala Thr Thr Ile Met Phe
 355 360 365
 Trp Thr Val Tyr Ala Gln Met Thr Thr Phe Ser Val Ser Gln Ala Thr
 370 375 380
 Thr Met Asp Arg Arg Val Gly Gly Ser Phe Gln Ile Pro Ala Gly Ser
 385 390 395 400
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PF59082SeqList_PF59082.txt

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 Phe Thr Tyr Ile Gly Gln Leu Asp Phe Phe Leu Arg Glu Cys Pro Lys
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 Gly Met Lys Thr Met Ser Thr Gly Leu Phe Leu Ser Thr Leu Ser Leu
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 Gly Phe Phe Val Ser Ser Ala Leu Val Ala Ala Val His Arg Val Thr
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 Asp Asn Phe Tyr Trp Leu Leu Ala Ala Val Cys Leu Ala Asn Leu Leu
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PF59082SeqList_PF59082.txt

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 <222> (39)..(39)
 <223> Xaa in position 39 is any amino acid

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35      40      45
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85      90      95
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Seite 120

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Glu Arg Xaa Xaa Thr Xaa Gly Ile Xaa Val Asn Leu Val Xaa Tyr Xaa
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Xaa Xaa Xaa Met His Xaa Xaa Xaa Xaa Xaa Ala Asn Xaa Val Xaa
          20          25          30
Thr Xaa Phe Xaa Gly Thr Ser Phe Xaa Leu Xaa Leu Xaa Gly Gly Phe
          35          40          45
Xaa Ala Xaa Xaa Xaa Leu Gly Arg Xaa Xaa Thr Ile Xaa
          50          55          60

<210> 96
<211> 47
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<220>
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<220>
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<220>
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<222> (4)..(4)
<223> Xaa in position 4 is Ala, Cys or Ser

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<220>
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<223> Xaa in position 5 is Ser or Thr

<220>
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<223> Xaa in position 6 is any amino acid

<220>
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<223> Xaa in position 7 is Ser or Thr

<220>
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<223> Xaa in position 8 is Asp, Lys or Arg

<220>
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<223> Xaa in position 9 is Ile or Val

<220>
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<222> (14)..(14)
<223> Xaa in position 14 is any amino acid

<220>
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<223> Xaa in position 15 is Ile, Leu, Met or Val

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<223> Xaa in position 16 is Ala, Ile, Leu or Val

<220>
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<223> Xaa in position 18 is any or no amino acid

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<223> Xaa in position 20 is any or no amino acid

<220>
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<223> Xaa in position 22 is any amino acid

<220>
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<223> Xaa in position 26 is Cys or Thr

<220>
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<223> Xaa in position 28 is Ile, Leu or Met

<220>
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<223> Xaa in position 32 is any amino acid

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PF59082SeqList_PF59082.txt

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<220>
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<223> Xaa in position 36 is Leu or Met

<220>
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<223> Xaa in position 37 is any amino acid

<220>
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<223> Xaa in position 39 is Phe or Leu

<220>
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<222> (40)..(40)
<223> Xaa in position 40 is Ala or Ser

<220>
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<223> Xaa in position 42 is Ala, Glu or Ser

<220>
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<223> Xaa in position 44 is Ala or Ser

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<223> Xaa in position 45 is Glu, Ser or Thr

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<222> (46)..(46)
<223> Xaa in position 46 is any amino acid

<220>
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<222> (47)..(47)
<223> Xaa in position 47 is Leu or Met

<400> 96
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Arg Xaa Leu Xaa Pro Xaa Trp Ala Thr Xaa Ile Xaa Phe Trp Thr Xaa
      20      25      30
Xaa Ala Gln Xaa Xaa Thr Xaa Xaa Val Xaa Gln Xaa Xaa Xaa Xaa
      35      40      45

<210> 97
<211> 42
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<220>
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<220>

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<223> Xaa in position 4 is Ala or Pro

<220>
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<223> Xaa in position 5 is Asp, Asn, Ser or Thr

<220>
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<222> (6)..(6)
<223> Xaa in position 6 is Ala, Glu, Gly or Ser

<220>
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<222> (7)..(7)
<223> Xaa in position 7 is any amino acid

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<223> Xaa in position 9 is Leu or Met

<220>
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<223> Xaa in position 10 is any amino acid

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<223> Xaa in position 11 is Ile, Leu or Val

<220>
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<222> (14)..(15)
<223> Xaa in position 14 to 15 is any or no amino acid

<220>
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<223> Xaa in position 17 to 18 is any or no amino acid

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<223> Xaa in position 20 to 21 is any amino acid

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<220>
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<222> (28)..(28)
<223> Xaa in position 28 is Ile, Leu or Val

<220>
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<223> Xaa in position 30 is Ala or Ser

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PF59082SeqList_PF59082.txt

<220>
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 <223> Xaa in position 31 is Asn or Ser

 <220>
 <221> Variant
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 <223> Xaa in position 32 is Ile or Val

 <220>
 <221> Variant
 <222> (37)..(37)
 <223> Xaa in position 37 is Ser or Thr

 <220>
 <221> Variant
 <222> (42)..(42)
 <223> Xaa in position 42 is Asp, Glu or Thr

 <400> 97
 Cys Xaa Xaa Xaa Xaa Xaa Xaa Gln Xaa Xaa Xaa Leu Tyr Xaa Xaa Leu
 1 5 10 15
 Xaa Xaa Tyr Xaa Xaa Ala Leu Gly Xaa Gly Gly Xaa Lys Xaa Xaa Xaa
 20 25 30
 Ser Gly Phe Gly Xaa Asp Gln Phe Asp Xaa
 35 40

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 <220>
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 <223> Xaa in position 6 is any or no amino acid

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 <223> Xaa in position 8 is any or no amino acid

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 <223> Xaa in position 11 is Phe or Tyr

 <220>
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 <223> Xaa in position 13 is Lys or Arg

 <220>
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 <223> Xaa in position 14 to 15 is any amino acid

 <220>
 <221> Variant

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<222> (19)..(19)
<223> Xaa in position 19 is Ile, Leu, Met or Val

<220>
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<223> Xaa in position 20 is Thr or Val

<220>
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<223> Xaa in position 21 is any amino acid

<220>
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<223> Xaa in position 22 is Phe, Ile or Val

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<222> (23)..(23)
<223> Xaa in position 23 is any amino acid

<220>
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<223> Xaa in position 29 is Ala or Ser

<220>
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<223> Xaa in position 30 to 32 is any amino acid

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<223> Xaa in position 34 to 39 is any amino acid

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1      5      10      15
Ser Pro Xaa Xaa Xaa Xaa Xaa Xaa Val Xaa Xaa Ala Xaa Xaa Xaa Xaa
      20      25      30
Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa
      35      40

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<211> 32

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<212> PRT
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<220>
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<220>
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<223> Xaa in position 25 is Phe, Leu or Val

<220>
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<222> (26)..(27)

<223> Xaa in position 26 to 27 is any amino acid

<220>

<221> Variant

<222> (28)..(28)

<223> Xaa in position 28 is Phe or Tyr

<220>

<221> Variant

<222> (29)..(31)

<223> Xaa in position 29 to 31 is any amino acid

<220>

<221> Variant

<222> (32)..(32)

<223> Xaa in position 32 is Ala or Ser

<400> 99

Leu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Arg	Leu	Xaa	Xaa	Phe	Tyr	Trp	Xaa
1				5					10					15	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asn	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			20				25						30		

<210> 100

<211> 31

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<220>

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<220>

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<222> (3)..(3)

<223> Xaa in position 3 is any amino acid

<220>

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<222> (4)..(4)

<223> Xaa in position 4 is Asp or Asn

<220>

<221> Variant

<222> (5)..(5)

<223> Xaa in position 5 is Phe or Tyr

<220>

<221> Variant

<222> (6)..(6)

<223> Xaa in position 6 is any amino acid

<220>

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<222> (8)..(8)

<223> Xaa in position 8 is any amino acid

<220>

<221> Variant

<222> (11)..(11)

<223> Xaa in position 11 is any amino acid

<220>

<221> Variant

<222> (12)..(12)

<223> Xaa in position 12 is Lys or Arg

<220>

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<223> Xaa in position 13 is Ala or Ser

<220>
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<223> Xaa in position 26 is Ile or Val

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<223> Xaa in position 28 is Cys, Gly or Val

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<220>
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Xaa Xaa Gly Xaa Xaa Xaa Xaa Ala Xaa Xaa Leu Xaa Xaa Glu Xaa
      20      25      30

<210> 101
<211> 28
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<220>
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<223> Xaa in position 8 to 9 is any amino acid

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<220>
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<223> Xaa in position 14 is Ala, Gly or Ser

<220>
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<220>
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<222> (24)..(24)
<223> Xaa in position 24 is any amino acid

<220>
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<223> Xaa in position 26 to 27 is any amino acid

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PF59082SeqList_PF59082.txt

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 1 5 10 15
 Xaa Met Xaa Xaa Xaa Ala Xaa Xaa Glu Xaa Xaa Arg
 20 25

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 <222> (11)..(11)
 <223> Xaa in position 11 is Thr or Val

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<220>

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<222> (22)..(22)

<223> Xaa in position 22 is Glu, Gly or Ser

<220>

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<222> (23)..(23)

<223> Xaa in position 23 is Phe, Leu or Met

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<222> (24)..(24)

<223> Xaa in position 24 is any amino acid

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<222> (26)..(26)

<223> Xaa in position 26 is Ala or Pro

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<222> (27)..(27)

<223> Xaa in position 27 is any amino acid

<400> 102

Ile	Xaa	Xaa	Ala	Xaa	Xaa	Xaa	Xaa	Gly	Xaa	Xaa	Xaa	Leu	Xaa	Xaa
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Xaa	Thr	Xaa	Xaa	Pro	Xaa	Xaa	Xaa	Pro	Xaa	Xaa	Cys			
			20					25						

<210> 103

<211> 13

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<222> (6)..(6)

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<220>

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PF59082SeqList_PF59082.txt

<222> (7)..(7)

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<222> (9)..(9)

<223> Xaa in position 9 is Asp or Glu

<220>

<221> Variant

<222> (10)..(10)

<223> Xaa in position 10 is His or Lys

<400> 103

His Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Ala Ala Ile
1 5 10

<210> 104

<211> 1110

<212> DNA

<213> Arabidopsis thaliana

<220>

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<222> (1)..(1110)

<400> 104

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Met	Ala	Ser	Ser	Val	Phe	Leu	Ser	Ser	Phe	Ser	Ser	Ser	Ser	Ser	Leu	
1				5					10					15		
caa	ctc	tgc	tct	tcc	ttt	cac	ggc	gag	tac	tta	gct	ccg	tcg	aga	tgc	96
Gln	Leu	Cys	Ser	Ser	Phe	His	Gly	Glu	Tyr	Leu	Ala	Pro	Ser	Arg	Cys	
			20				25					30				
ttt	ctc	gga	gct	ccg	gtc	act	tcc	tct	tct	tta	tca	ctc	tcc	ggg	aag	144
Phe	Leu	Gly	Ala	Pro	Val	Thr	Ser	Ser	Ser	Leu	Ser	Leu	Ser	Gly	Lys	
		35					40					45				
aag	aac	tca	tat	tct	ccg	aga	cag	ttc	cat	gtt	tct	gcc	aag	aaa	ggt	192
Lys	Asn	Ser	Tyr	Ser	Pro	Arg	Gln	Phe	His	Val	Ser	Ala	Lys	Lys	Val	
	50					55				60						
tct	ggg	tta	gag	gaa	gcc	att	aga	atc	aga	aaa	atg	aga	gag	ctt	gaa	240
Ser	Gly	Leu	Glu	Glu	Ala	Ile	Arg	Ile	Arg	Lys	Met	Arg	Glu	Leu	Glu	
	65				70					75					80	
act	aaa	tca	aaa	ggt	agg	aga	aat	cca	cca	tta	aga	cgt	gga	aga	gta	288
Thr	Lys	Ser	Lys	Val	Arg	Arg	Asn	Pro	Pro	Leu	Arg	Arg	Gly	Arg	Val	
				85					90					95		
tcg	cct	cgt	ctt	ctt	gta	cct	gat	cac	att	cca	agg	cct	cct	tat	ggt	336
Ser	Pro	Arg	Leu	Leu	Val	Pro	Asp	His	Ile	Pro	Arg	Pro	Pro	Tyr	Val	
			100				105					110				
gag	tct	ggt	gta	tta	ccg	gat	ata	tca	agt	gag	ttc	cag	att	cct	ggt	384
Glu	Ser	Gly	Val	Leu	Pro	Asp	Ile	Ser	Ser	Glu	Phe	Gln	Ile	Pro	Gly	
		115				120					125					
cct	gaa	ggc	att	gcg	aaa	atg	aga	gct	gct	tgc	gag	ctt	gct	gct	cgg	432
Pro	Glu	Gly	Ile	Ala	Lys	Met	Arg	Ala	Ala	Cys	Glu	Leu	Ala	Ala	Arg	
	130					135				140						
gtt	tta	aac	tat	gct	gga	act	ttg	gtt	aag	cca	tct	gtt	acg	act	aat	480
Val	Leu	Asn	Tyr	Ala	Gly	Thr	Leu	Val	Lys	Pro	Ser	Val	Thr	Thr	Asn	
	145				150					155					160	
gaa	atc	gat	aaa	gct	gtg	cat	gat	atg	att	att	gaa	gct	ggg	gct	tat	528
Glu	Ile	Asp	Lys	Ala	Val	His	Asp	Met	Ile	Ile	Glu	Ala	Gly	Ala	Tyr	
			165						170					175		
cct	tca	cct	ctt	gga	tat	ggg	gga	ttt	cct	aaa	agt	gtg	tgt	act	tca	576
Pro	Ser	Pro	Leu	Gly	Tyr	Gly	Gly	Phe	Pro	Lys	Ser	Val	Cys	Thr	Ser	
			180				185						190			
gtt	aat	gag	tgt	atg	tgt	cac	gga	ata	cca	gat	tct	cgc	cag	cta	cag	624
Val	Asn	Glu	Cys	Met	Cys	His	Gly	Ile	Pro	Asp	Ser	Arg	Gln	Leu	Gln	
		195					200					205				
agc	ggg	gat	ata	atc	aac	atc	gat	gtc	acg	gtt	tac	ttg	gat	ggg	tac	672
Ser	Gly	Asp	Ile	Ile	Asn	Ile	Asp	Val	Thr	Val	Tyr	Leu	Asp	Gly	Tyr	
	210					215					220					

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225					230					235					240	
ttc	aaa	cga	ctt	gtg	aag	ggt	acg	gaa	gaa	tgt	ttg	gag	aga	ggt	att	768
Phe	Lys	Arg	Leu	Val	Lys	Val	Thr	Glu	Glu	Cys	Leu	Glu	Arg	Gly	Ile	
				245					250					255		
gca	ggt	tgt	aaa	gac	gga	gca	agc	ttc	aag	aaa	atc	ggg	aaa	aga	atc	816
Ala	Val	Cys	Lys	Asp	Gly	Ala	Ser	Phe	Lys	Lys	Ile	Gly	Lys	Arg	Ile	
				260				265					270			
agt	gag	cat	gcg	gaa	aag	ttc	ggc	tac	aac	ggt	gtg	gag	cgg	ttt	ggt	864
Ser	Glu	His	Ala	Glu	Lys	Phe	Gly	Tyr	Asn	Val	Val	Glu	Arg	Phe	Val	
		275					280					285				
ggg	cat	ggt	ggt	gga	cca	gta	ttc	cac	tcc	gaa	cct	ctt	ata	tat	cat	912
Gly	His	Gly	Val	Gly	Pro	Val	Phe	His	Ser	Glu	Pro	Leu	Ile	Tyr	His	
	290					295					300					
tac	cga	aat	gat	gag	cct	gga	cta	atg	ggt	gag	gga	cag	aca	ttc	aca	960
Tyr	Arg	Asn	Asp	Glu	Pro	Gly	Leu	Met	Val	Glu	Gly	Gln	Thr	Phe	Thr	
305					310					315					320	
att	gaa	ccg	att	ctc	acg	att	gga	acc	aca	gaa	tgt	gta	aca	tgg	cca	1008
Ile	Glu	Pro	Ile	Leu	Thr	Ile	Gly	Thr	Thr	Glu	Cys	Val	Thr	Trp	Pro	
				325				330						335		
gac	aac	tgg	act	act	ctg	aca	gca	gat	ggg	ggc	gtc	gct	gct	cag	ttt	1056
Asp	Asn	Trp	Thr	Thr	Leu	Thr	Ala	Asp	Gly	Gly	Val	Ala	Ala	Gln	Phe	
				340				345					350			
gag	cat	acc	att	ctg	att	act	aga	act	ggg	tca	gag	att	ctt	acc	aaa	1104
Glu	His	Thr	Ile	Leu	Ile	Thr	Arg	Thr	Gly	Ser	Glu	Ile	Leu	Thr	Lys	
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tg	taa															1110
Cys																

<210> 105

<211> 369

<212> PRT

<213> Arabidopsis thaliana

<400> 105

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			20					25					30			
Phe	Leu	Gly	Ala	Pro	Val	Thr	Ser	Ser	Ser	Leu	Ser	Leu	Ser	Gly	Lys	
		35					40					45				
Lys	Asn	Ser	Tyr	Ser	Pro	Arg	Gln	Phe	His	Val	Ser	Ala	Lys	Lys	Val	
	50					55				60						
Ser	Gly	Leu	Glu	Glu	Ala	Ile	Arg	Ile	Arg	Lys	Met	Arg	Glu	Leu	Glu	
65					70					75				80		
Thr	Lys	Ser	Lys	Val	Arg	Arg	Asn	Pro	Pro	Leu	Arg	Arg	Gly	Arg	Val	
				85					90					95		
Ser	Pro	Arg	Leu	Leu	Val	Pro	Asp	His	Ile	Pro	Arg	Pro	Pro	Tyr	Val	
			100					105					110			
Glu	Ser	Gly	Val	Leu	Pro	Asp	Ile	Ser	Ser	Glu	Phe	Gln	Ile	Pro	Gly	
		115					120					125				
Pro	Glu	Gly	Ile	Ala	Lys	Met	Arg	Ala	Ala	Cys	Glu	Leu	Ala	Ala	Arg	
	130					135					140					
Val	Leu	Asn	Tyr	Ala	Gly	Thr	Leu	Val	Lys	Pro	Ser	Val	Thr	Thr	Asn	
145					150					155					160	
Glu	Ile	Asp	Lys	Ala	Val	His	Asp	Met	Ile	Ile	Glu	Ala	Gly	Ala	Tyr	
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Pro	Ser	Pro	Leu	Gly	Tyr	Gly	Gly	Phe	Pro	Lys	Ser	Val	Cys	Thr	Ser	
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Val	Asn	Glu	Cys	Met	Cys	His	Gly	Ile	Pro	Asp	Ser	Arg	Gln	Leu	Gln	
		195					200					205				
Ser	Gly	Asp	Ile	Ile	Asn	Ile	Asp	Val	Thr	Val	Tyr	Leu	Asp	Gly	Tyr	
	210					215					220					
His	Gly	Asp	Thr	Ser	Arg	Thr	Phe	Phe	Cys	Gly	Glu	Val	Asp	Glu	Gly	
225					230					235					240	
Phe	Lys	Arg	Leu	Val	Lys	Val	Thr	Glu	Glu	Cys	Leu	Glu	Arg	Gly	Ile	
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PF59082SeqList_PF59082.txt

Ala Val Cys Lys Asp Gly Ala Ser Phe Lys Lys Ile Gly Lys Arg Ile
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 Ser Glu His Ala Glu Lys Phe Gly Tyr Asn Val Val Glu Arg Phe Val
 275 280 285
 Gly His Gly Val Gly Pro Val Phe His Ser Glu Pro Leu Ile Tyr His
 290 295 300
 Tyr Arg Asn Asp Glu Pro Gly Leu Met Val Glu Gly Gln Thr Phe Thr
 305 310 315 320
 Ile Glu Pro Ile Leu Thr Ile Gly Thr Thr Glu Cys Val Thr Trp Pro
 325 330 335
 Asp Asn Trp Thr Thr Leu Thr Ala Asp Gly Gly Val Ala Ala Gln Phe
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 Glu His Thr Ile Leu Ile Thr Arg Thr Gly Ser Glu Ile Leu Thr Lys
 355 360 365
 Cys

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 <213> Brassica napus

<220>
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 caa ctc cgt tct tct ttc aac ggc gag tac gta tcc tcc tcg agg agc 96
 Gln Leu Arg Ser Ser Phe Asn Gly Glu Tyr Val Ser Ser Ser Arg Ser
 20 25 30
 ttc atc gga gca gct ccg ttc gct tcc tct tct cta tcg ctg ctc tcc 144
 Phe Ile Gln Ala Ala Pro Phe Ala Ser Ser Ser Leu Ser Leu Ser
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 ggt cag aag aac tca tat cct cag aga aaa ctc cac gtg tcc gcc aag 192
 Gly Gln Lys Asn Ser Tyr Pro Gln Arg Lys Leu His Val Ser Ala Lys
 50 55 60
 aaa gtt tct gga tta gag gaa att aga atc aga agg atg aga gag 240
 Lys Val Ser Gly Leu Glu Glu Ala Ile Arg Ile Arg Arg Met Arg Glu
 65 70 75 80
 ctt gag aaa act tca aaa gtt agg aga aac cca ccg tta cga cgt gga 288
 Leu Glu Lys Thr Ser Lys Val Arg Arg Asn Pro Pro Leu Arg Arg Gly
 85 90 95
 aga gtc tcc cct cgt ctc ctc gtc cct gac cac ata cca agg cct cct 336
 Arg Val Ser Pro Arg Leu Leu Val Pro Asp His Ile Pro Arg Pro Pro
 100 105 110
 tac gtt gag tct ggc gtg tta cct gat ata tct cct gag ttc cag att 384
 Tyr Val Glu Ser Gly Val Leu Pro Asp Ile Ser Pro Glu Phe Gln Ile
 115 120 125
 cct ggt cct gaa ggc att gtg aag atg aga gct gct tgc gag ctc gct 432
 Pro Gly Pro Glu Gly Ile Val Lys Met Arg Ala Ala Cys Glu Leu Ala
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 gct cgg gtt cta aac ttt gca gga act ttg gtt aaa cca tct gtg acg 480
 Ala Arg Val Leu Asn Phe Ala Gly Thr Leu Val Lys Pro Ser Val Thr
 145 150 155 160
 act aat gaa ata gac aaa gcg gtg cat gat atg att gtt gaa gct ggt 528
 Thr Asn Glu Ile Asp Lys Ala Val His Asp Met Ile Val Glu Ala Gly
 165 170 175
 gct tat cct tcg cct ctt ggg tat ggt ggg ttc cct aaa agt gtg tgt 576
 Ala Tyr Pro Ser Pro Leu Gly Tyr Gly Gly Phe Pro Lys Ser Val Cys
 180 185 190
 acg tca gtg aac gag tgt atg tgt cat ggg ata cca gat tct cga cag 624
 Thr Ser Val Asn Glu Cys Met Cys His Gly Ile Pro Asp Ser Arg Gln
 195 200 205
 ctg cag agt ggg gat ata ata aac atc gat gtc aca gtt tac ttg gat 672
 Leu Gln Ser Gly Asp Ile Ile Asn Ile Asp Val Thr Val Tyr Leu Asp
 210 215 220

PF59082SeqList_PF59082.txt

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gaa	ggt	ttt	aaa	cga	ctt	gta	aag	ggt	acg	gag	gaa	tgc	ttg	gag	aga	768
Glu	Gly	Phe	Lys	Arg	Leu	Val	Lys	Val	Thr	Glu	Glu	Cys	Leu	Glu	Arg	
			245						250					255		
ggt	ata	gcc	ggt	tgc	aaa	gat	gga	gca	agc	ttc	aag	aaa	atc	ggc	aag	816
Gly	Ile	Ala	Val	Cys	Lys	Asp	Gly	Ala	Ser	Phe	Lys	Lys	Ile	Gly	Lys	
			260					265					270			
aga	ata	agc	gag	cat	gct	gaa	aag	aac	ggc	tac	aac	gtg	gtg	gag	cgc	864
Arg	Ile	Ser	Glu	His	Ala	Glu	Lys	Asn	Gly	Tyr	Asn	Val	Val	Glu	Arg	
			275					280					285			
ttt	ggt	ggg	cat	ggt	ggt	gga	cca	gtg	ttc	cac	tca	gaa	ccc	ttg	att	912
Phe	Val	Gly	His	Gly	Val	Gly	Pro	Val	Phe	His	Ser	Glu	Pro	Leu	Ile	
290						295					300					
tat	cat	tac	cga	aat	gat	ggg	cct	ggg	caa	atg	ggt	gag	gga	caa	aca	960
Tyr	His	Tyr	Arg	Asn	Asp	Gly	Pro	Gly	Gln	Met	Val	Glu	Gly	Gln	Thr	
305					310					315					320	
ttc	aca	att	gaa	ccg	att	ctg	acg	att	gga	acc	acg	gaa	tgt	gta	aca	1008
Phe	Thr	Ile	Glu	Pro	Ile	Leu	Thr	Ile	Gly	Thr	Thr	Glu	Cys	Val	Thr	
				325					330					335		
tgg	cca	gac	aac	tgg	act	act	cta	aca	gct	gat	ggt	ggg	gta	gcc	gca	1056
Trp	Pro	Asp	Asn	Trp	Thr	Thr	Leu	Thr	Ala	Asp	Gly	Gly	Val	Ala	Ala	
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cag	tgt	gaa	cat	aca	att	ctg	ata	act	aga	act	ggt	gca	gag	att	ctt	1104
Gln	Cys	Glu	His	Thr	Ile	Leu	Ile	Thr	Arg	Thr	Gly	Ala	Glu	Ile	Leu	
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Thr	Lys	Cys														
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<212> PRT

<213> Brassica napus

<400> 107

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			20				25					30				
Phe	Ile	Gly	Ala	Ala	Pro	Phe	Ala	Ser	Ser	Ser	Leu	Ser	Leu	Leu	Ser	
		35				40						45				
Gly	Gln	Lys	Asn	Ser	Tyr	Pro	Gln	Arg	Lys	Leu	His	Val	Ser	Ala	Lys	
	50					55					60					
Lys	Val	Ser	Gly	Leu	Glu	Glu	Ala	Ile	Arg	Ile	Arg	Arg	Met	Arg	Glu	
65				70					75					80		
Leu	Glu	Lys	Thr	Ser	Lys	Val	Arg	Arg	Asn	Pro	Pro	Leu	Arg	Arg	Gly	
				85					90					95		
Arg	Val	Ser	Pro	Arg	Leu	Leu	Val	Pro	Asp	His	Ile	Pro	Arg	Pro	Pro	
			100					105					110			
Tyr	Val	Glu	Ser	Gly	Val	Leu	Pro	Asp	Ile	Ser	Pro	Glu	Phe	Gln	Ile	
		115					120					125				
Pro	Gly	Pro	Glu	Gly	Ile	Val	Lys	Met	Arg	Ala	Ala	Cys	Glu	Leu	Ala	
					135						140					
Ala	Arg	Val	Leu	Asn	Phe	Ala	Gly	Thr	Leu	Val	Lys	Pro	Ser	Val	Thr	
145				150						155					160	
Thr	Asn	Glu	Ile	Asp	Lys	Ala	Val	His	Asp	Met	Ile	Val	Glu	Ala	Gly	
				165					170					175		
Ala	Tyr	Pro	Ser	Pro	Leu	Gly	Tyr	Gly	Phe	Pro	Lys	Ser	Val	Cys		
			180					185				190				
Thr	Ser	Val	Asn	Glu	Cys	Met	Cys	His	Gly	Ile	Pro	Asp	Ser	Arg	Gln	
		195					200					205				
Leu	Gln	Ser	Gly	Asp	Ile	Ile	Asn	Ile	Asp	Val	Thr	Val	Tyr	Leu	Asp	
					215						220					
Gly	Tyr	His	Gly	Asp	Thr	Ser	Arg	Thr	Phe	Phe	Cys	Gly	Glu	Val	Asp	
225				230					235						240	
Glu	Gly	Phe	Lys	Arg	Leu	Val	Lys	Val	Thr	Glu	Glu	Cys	Leu	Glu	Arg	
				245					250					255		

PF59082SeqList_PF59082.txt

Gly Ile Ala Val Cys Lys Asp Gly Ala Ser Phe Lys Lys Ile Gly Lys
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 Arg Ile Ser Glu His Ala Glu Lys Asn Gly Tyr Asn Val Val Glu Arg
 275 280 285
 Phe Val Gly His Gly Val Gly Pro Val Phe His Ser Glu Pro Leu Ile
 290 295 300
 Tyr His Tyr Arg Asn Asp Gly Pro Gly Gln Met Val Glu Gly Gln Thr
 305 310 315 320
 Phe Thr Ile Glu Pro Ile Leu Thr Ile Gly Thr Thr Glu Cys Val Thr
 325 330 335
 Trp Pro Asp Asn Trp Thr Leu Thr Ala Asp Gly Gly Val Ala Ala
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 Thr Lys Cys
 370

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 <223> n is a, g, c or t

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 Ser Pro Arg Leu Leu Ser Ser Phe Leu Gly Asp Arg Leu Leu Ser Ala
 10 15 20
 agc gcc agg ccg ctc ctc cgc ggg gcc gct cca gga agc agg cgg gcc 151
 Ser Ala Arg Pro Leu Leu Arg Gly Ala Ala Pro Gly Ser Arg Arg Ala
 25 30 35
 gcg tat cag gcg acg aga acg ctc tgc aac ctg gtg gat atc ctc ttc 199
 Ala Tyr Gln Ala Thr Arg Thr Leu Cys Asn Leu Val Asp Ile Leu Phe
 40 45 50
 aac aga ggt cag agt gac aaa ccg gaa gat aac cct aga cgc cta cgg 247
 Asn Arg Gly Gln Ser Asp Lys Pro Glu Asp Asn Pro Arg Arg Leu Arg
 55 60 65
 cct ggg aaa gta tct cct cgt cta agc gtt ccc aaa cat ata cag cgg 295
 Pro Gly Lys Val Ser Pro Arg Leu Ser Val Pro Lys His Ile Gln Arg
 70 75 80 85
 cca cca tat gtc aat gct cgt caa aga cct gga ttg cac aat gga cct 343
 Pro Pro Tyr Val Asn Ala Arg Gln Arg Pro Gly Leu His Asn Gly Pro
 90 95 100
 gaa ata cat gat gag aga ggg atc gaa tgc atg agg gct tct gga aag 391
 Glu Ile His Asp Glu Arg Gly Ile Glu Cys Met Arg Ala Ser Gly Lys
 105 110 115
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 Leu Ala Ala Gln Val Leu Lys Phe Ala Gly Thr Leu Val Glu Pro Gly
 120 125 130
 ata aca act gat gag att gat aaa gcg gtg cac caa atg ata gta gat 487
 Ile Thr Thr Asp Glu Ile Asp Lys Ala Val His Gln Met Ile Val Asp
 135 140 145
 aat gga gca tac cct tcg cca ctt ggt tat tgc ggt ttt cca aag agt 535
 Asn Gly Ala Tyr Pro Ser Pro Leu Gly Tyr Cys Gly Phe Pro Lys Ser
 150 155 160 165
 gtc tgc acc tca gtg aat gag tgc atc tgt cat ggt ata cct gat tct 583
 Val Cys Thr Ser Val Asn Glu Cys Ile Cys His Gly Ile Pro Asp Ser
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PF59082SeqList_PF59082.txt

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Leu	Asn	Gly	Tyr	His	Gly	Asp	Thr	Ser	Ala	Thr	Phe	Leu	Cys	Gly	Asn	
		200					205					210				
ggt	gat	gac	aaa	gct	aag	aaa	tta	ggt	cag	gta	aca	aga	gaa	tgt	ctc	727
Val	Asp	Asp	Lys	Ala	Lys	Lys	Leu	Val	Gln	Val	Thr	Arg	Glu	Cys	Leu	
		215				220					225					
gac	aag	gct	ata	tca	atc	tgc	gcc	cct	ggg	gtg	gag	atc	aaa	cgt	att	775
Asp	Lys	Ala	Ile	Ser	Ile	Cys	Ala	Pro	Gly	Val	Glu	Ile	Lys	Arg	Ile	
		230			235					240					245	
ggt	cga	act	ata	cag	gac	cat	gca	gat	aaa	ttc	aag	ttt	ggt	gta	ggt	823
Gly	Arg	Thr	Ile	Gln	Asp	His	Ala	Asp	Lys	Phe	Lys	Phe	Gly	Val	Val	
			250					255						260		
cga	cag	ttc	gtc	ggt	cat	ggg	ggt	gga	caa	gtg	ttt	cat	gct	gaa	cct	871
Arg	Gln	Phe	Val	Gly	His	Gly	Val	Gln	Val	Phe	His	Ala	Glu	Pro		
			265				270						275			
gtg	gtg	ctt	cat	ttc	cga	aac	aat	gaa	tgg	ggc	cgt	atg	aca	ttg	aac	919
Val	Val	Leu	His	Phe	Arg	Asn	Asn	Glu	Trp	Gly	Arg	Met	Thr	Leu	Asn	
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caa	aca	ttt	act	ata	gag	ccc	atg	cta	acc	gtg	ggg	agc	gta	aat	cca	967
Gln	Thr	Phe	Thr	Ile	Glu	Pro	Met	Leu	Thr	Val	Gly	Ser	Val	Asn	Pro	
		295				300					305					
ggt	ata	tgg	tcc	gat	gac	tgg	aca	gcg	gtg	act	gaa	gac	ggc	agc	ttg	1015
Val	Ile	Trp	Ser	Asp	Asp	Trp	Thr	Ala	Val	Thr	Glu	Asp	Gly	Ser	Leu	
		310			315					320					325	
tca	gca	cag	ttt	gag	cac	aca	ata	ctg	att	aca	gag	gat	ggc	gcg	gag	1063
Ser	Ala	Gln	Phe	Glu	His	Thr	Ile	Leu	Ile	Thr	Glu	Asp	Gly	Ala	Glu	
			330					335						340		
ata	ctg	acg	cag	tgt	taagggcgga	cgaggattag	aggcgagtaa	tgacagtgat								1118
Ile	Leu	Thr	Gln	Cys												
			345													
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 35 40 45
 Val Asp Ile Leu Phe Asn Arg Gly Gln Ser Asp Lys Pro Glu Asp Asn
 50 55 60
 Pro Arg Arg Leu Arg Pro Gly Lys Val Ser Pro Arg Leu Ser Val Pro
 65 70 75 80
 Lys His Ile Gln Arg Pro Pro Tyr Val Asn Ala Arg Gln Arg Pro Gly
 85 90 95
 Leu His Asn Gly Pro Glu Ile His Asp Glu Arg Gly Ile Glu Cys Met
 100 105 110
 Arg Ala Ser Gly Lys Leu Ala Ala Gln Val Leu Lys Phe Ala Gly Thr
 115 120 125
 Leu Val Glu Pro Gly Ile Thr Thr Asp Glu Ile Asp Lys Ala Val His
 130 135 140

PF59082SeqList_PF59082.txt

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 145 150 155 160
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 165 170 175
 Gly Ile Pro Asp Ser Arg Pro Leu Glu Asp Gly Asp Ile Ile Asn Ile
 180 185 190
 Asp Val Thr Val Tyr Leu Asn Gly Tyr His Gly Asp Thr Ser Ala Thr
 195 200 205
 Phe Leu Cys Gly Asn Val Asp Asp Lys Ala Lys Lys Leu Val Gln Val
 210 215 220
 Thr Arg Glu Cys Leu Asp Lys Ala Ile Ser Ile Cys Ala Pro Gly Val
 225 230 235 240
 Glu Ile Lys Arg Ile Gly Arg Thr Ile Gln Asp His Ala Asp Lys Phe
 245 250 255
 Lys Phe Gly Val Val Arg Gln Phe Val Gly His Gly Val Gly Gln Val
 260 265 270
 Phe His Ala Glu Pro Val Val Leu His Phe Arg Asn Asn Glu Trp Gly
 275 280 285
 Arg Met Thr Leu Asn Gln Thr Phe Thr Ile Glu Pro Met Leu Thr Val
 290 295 300
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<220>
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 Met Ala Val Arg Val Pro Ser Met Glu
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 Leu His Arg Pro Pro Ser Val Ser Gly Val Arg Gly Lys Ser Cys
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 ctt caa aag cct ttc ctt gtc caa gca aag aga tta gag gga ttg gag 208
 Leu Gln Lys Pro Phe Leu Val Gln Ala Lys Arg Leu Glu Gly Leu Glu
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 aag gca aac cca agg tca cga gga aag caa agt ttg gaa caa gtg aag 256
 Lys Ala Asn Pro Arg Ser Arg Gly Lys Gln Ser Leu Glu Gln Val Lys
 45 50 55
 aaa aga gca cca ctg atc cgt ggg aca gtg agt cca cct cta cca gta 304
 Lys Arg Ala Pro Leu Ile Arg Gly Thr Val Ser Pro Pro Leu Pro Val
 60 65 70
 cca ggt cac ata act caa cct cct tac gtt ggt aaa aag gat gct tca 352
 Pro Gly His Ile Thr Gln Pro Pro Tyr Val Gly Lys Lys Asp Ala Ser
 75 80 85
 gag ata gca agt gag ata caa atg cat gac aaa gtg agc att att cac 400
 Glu Ile Ala Ser Glu Ile Gln Met His Asp Lys Val Ser Ile Ile His
 90 95 100 105
 atg aaa gct gca tgt gag ctt gct gct cgt gtt ctt gaa tac gct gga 448
 Met Lys Ala Ala Cys Glu Leu Ala Ala Arg Val Leu Glu Tyr Ala Gly
 110 115 120
 act tta gtg aaa ccc tct gta aca aca gaa att gat aaa gca gtg 496
 Thr Leu Val Lys Pro Ser Val Thr Thr Asp Glu Ile Asp Lys Ala Val
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 His Lys Met Ile Ile Asp Ala Gly Ala Tyr Pro Ser Pro Leu Gly Tyr

PF59082SeqList_PF59082.txt

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Gly Gly Phe Pro Lys Ser Val Cys Thr Ser Val Asn Glu Cys Ile Cys			
155	160	165	
cat gga att cct gat tct cgt gaa ctt cag gat gga gac ata att aat			640
His Gly Ile Pro Asp Ser Arg Glu Leu Gln Asp Gly Asp Ile Ile Asn			
170	175	180	
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Ile Asp Val Thr Val Tyr Leu Asn Gly Tyr His Gly Asp Thr Ser Lys			
190	195	200	
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Thr Phe Leu Cys Gly Glu Val Asp Glu Ala Ser Lys Arg Leu Val Lys			
205	210	215	
gtt act gaa gag tgc atg ctc agg gct ata tca gct tgc aaa cat ggt			784
Val Thr Glu Glu Cys Met Leu Arg Ala Ile Ser Ala Cys Lys His Gly			
220	225	230	
acc agc ttg aag aaa att ggc aga aga ata agc gag cat gct gag agg			832
Thr Ser Leu Lys Lys Ile Gly Arg Arg Ile Ser Glu His Ala Glu Arg			
235	240	245	
cac gga ttt ggt gtt gtg gat cgt ttt gtt ggg cat gga gtt ggg aga			880
His Gly Phe Gly Val Val Asp Arg Phe Val Gly His Gly Val Gly Arg			
250	255	260	
ata ttt cat tca gaa cca atg ata tat cac cag cgt aat aat atg cca			928
Ile Phe His Ser Glu Pro Met Ile Tyr His Gln Arg Asn Asn Met Pro			
270	275	280	
ggt caa atg gtt gaa ggc cag aca ttc aca ata gaa ccg gcc cta tcc			976
Gly Gln Met Val Glu Gly Gln Thr Phe Thr Ile Glu Pro Ala Leu Ser			
285	290	295	
atg gga agc att gat tgc gac atg tgg gac gac ggc tgg acg gcc gtc			1024
Met Gly Ser Ile Asp Cys Asp Met Trp Asp Asp Gly Trp Thr Ala Val			
300	305	310	
acg acg gac ggc agc cta gcc gcg cag ttc gag cac acg ata ctg att			1072
Thr Thr Asp Gly Ser Leu Ala Ala Gln Phe Glu His Thr Ile Leu Ile			
315	320	325	
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Thr Lys Thr Gly Ala Glu Ile Leu Thr Lys Cys			
330	335	340	
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atgccgttga cttttt			1261

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 <212> PRT
 <213> Oryza sativa

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 Gln Ala Lys Arg Leu Glu Gly Leu Glu Lys Ala Asn Pro Arg Ser Arg
 35 40 45
 Gly Lys Gln Ser Leu Glu Gln Val Lys Lys Arg Ala Pro Leu Ile Arg
 50 55 60
 Gly Thr Val Ser Pro Pro Leu Pro Val Pro Gly His Ile Thr Gln Pro
 65 70 75 80
 Pro Tyr Val Gly Lys Asp Ala Ser Glu Ile Ala Ser Glu Ile Gln
 85 90 95
 Met His Asp Lys Val Ser Ile Ile His Met Lys Ala Ala Cys Glu Leu
 100 105 110
 Ala Ala Arg Val Leu Glu Tyr Ala Gly Thr Leu Val Lys Pro Ser Val
 115 120 125

PF59082SeqList_PF59082.txt

Thr Thr Asp Glu Ile Asp Lys Ala Val His Lys Met Ile Ile Asp Ala
 130 135 140
 Gly Ala Tyr Pro Ser Pro Leu Gly Tyr Gly Gly Phe Pro Lys Ser Val
 145 150 155 160
 Cys Thr Ser Val Asn Glu Cys Ile Cys His Gly Ile Pro Asp Ser Arg
 165 170 175
 Glu Leu Gln Asp Gly Asp Ile Ile Asn Ile Asp Val Thr Val Tyr Leu
 180 185 190
 Asn Gly Tyr His Gly Asp Thr Ser Lys Thr Phe Leu Cys Gly Glu Val
 195 200 205
 Asp Glu Ala Ser Lys Arg Leu Val Lys Val Thr Glu Glu Cys Met Leu
 210 215 220
 Arg Ala Ile Ser Ala Cys Lys His Gly Thr Ser Leu Lys Lys Ile Gly
 225 230 235 240
 Arg Arg Ile Ser Glu His Ala Glu Arg His Gly Phe Gly Val Val Asp
 245 250 255
 Arg Phe Val Gly His Gly Val Gly Arg Ile Phe His Ser Glu Pro Met
 260 265 270
 Ile Tyr His Gln Arg Asn Asn Met Pro Gly Gln Met Val Glu Gly Gln
 275 280 285
 Thr Phe Thr Ile Glu Pro Ala Leu Ser Met Gly Ser Ile Asp Cys Asp
 290 295 300
 Met Trp Asp Asp Gly Trp Thr Ala Val Thr Thr Asp Gly Ser Leu Ala
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 325 330 335
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 Met Ala Thr Ser Ser Ser Pro Arg Leu Leu Ser Ser Phe Leu Gly Asp
 1 5 10 15
 cgc ctc ctc tcc gcc agc gcc agg ccg ctc ctc cgc ggg gcc gct cca 157
 Arg Leu Leu Ser Ala Ser Ala Arg Pro Leu Leu Arg Gly Ala Ala Pro
 20 25 30
 gga agc agg cgg gcc gcg tat cag gcg acg aga acg ctc tgc aac ctg 205
 Gly Ser Arg Arg Ala Ala Tyr Gln Ala Thr Arg Thr Leu Cys Asn Leu
 35 40 45
 gtg gat atc ctc ttc aac aga ggt cag agt gac aaa ccg gaa gat aac 253
 Val Asp Ile Leu Phe Asn Arg Gly Gln Ser Asp Lys Pro Glu Asp Asn
 50 55 60
 cct aga cgc cta cgg cct ggg aaa gta tct cct cgt cta agc gtt ccc 301
 Pro Arg Arg Leu Arg Pro Gly Lys Val Ser Pro Arg Leu Ser Val Pro
 65 70 75 80
 aaa cat ata cag cgg cca cca tat gtc aat gct cgt caa aga cct gga 349
 Lys His Ile Gln Arg Pro Pro Tyr Val Asn Ala Arg Gln Arg Pro Gly
 85 90 95
 ttg cac aat gga cct gaa ata cat gat gag aga ggg atc gaa tgc atg 397
 Leu His Asn Gly Pro Glu Ile His Asp Glu Arg Gly Ile Glu Cys Met
 100 105 110
 agg gct tct gga aag ctt gct gca caa gtt ttg aag ttt gcc ggg act 445
 Arg Ala Ser Gly Lys Leu Ala Gln Val Leu Lys Phe Ala Gly Thr
 115 120 125
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 Leu Val Glu Pro Gly Ile Thr Thr Asp Glu Ile Asp Lys Ala Val His
 130 135 140

PF59082SeqList_PF59082.txt

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Gln Met Ile Val Asp Asn Gly Ala Tyr Pro Ser Pro Leu Gly Tyr Cys	
145 150 155 160	
ggt ttt cca agg agt gtc tgc acc tca gtg aat gag tgc atc tgt cat	589
Gly Phe Pro Arg Ser Val Cys Thr Ser Val Asn Glu Cys Ile Cys His	
165 170 175	
ggt ata cct gat tct cgt cct ctt gaa gat ggt gac att atc aac att	637
Gly Ile Pro Asp Ser Arg Pro Leu Glu Asp Gly Asp Ile Ile Asn Ile	
180 185 190	
gat gtt act gtt tat ctc aat aga gtg ttt cta tgc atc tcc tcc tta	685
Asp Val Thr Val Tyr Leu Asn Arg Val Phe Leu Cys Ile Ser Ser Leu	
195 200 205	
tat ttg cat aaa tgt caa agt atg aca atg gtg gct gga cag ctg ggt	733
Tyr Leu His Lys Cys Gln Ser Met Thr Met Val Ala Gly Gln Leu Gly	
210 215 220	
tac cac ggt gat aca tct gct aca ttt cta tgt ggt aat gtt gat gac	781
Tyr His Gly Asp Thr Ser Ala Thr Phe Leu Cys Gly Asn Val Asp Asp	
225 230 235 240	
aaa gct aag aaa tta gtt cag gta aca aga gaa tgt ctc gac aag gct	829
Lys Ala Lys Lys Leu Val Gln Val Thr Arg Glu Cys Leu Asp Lys Ala	
245 250 255	
ata tca atc tgc gcc cct ggg gtg gag atc aaa cgt att ggt cga act	877
Ile Ser Ile Cys Ala Pro Gly Val Glu Ile Lys Arg Ile Gly Arg Thr	
260 265 270	
ata cag gac cat gca gat aaa ttc aag ttt ggt gta gtt cga cag ttc	925
Ile Gln Asp His Ala Asp Lys Phe Lys Phe Gly Val Val Arg Gln Phe	
275 280 285	
gtc ggt cat ggg gtt gga caa gtg ttt cat gct gaa cct gtg gtg ctt	973
Val Gly His Gly Val Gly Gln Val Phe His Ala Glu Pro Val Val Leu	
290 295 300	
cat ttc cga aac aat gaa tgg ggc cgt atg aca ttg aac caa aca ttt	1021
His Phe Arg Asn Asn Glu Trp Gly Arg Met Thr Leu Asn Gln Thr Phe	
305 310 315 320	
act ata gag ccc atg cta acc gtg ggg agc gta aat cca gtt ata tgg	1069
Thr Ile Glu Pro Met Leu Thr Val Gly Ser Val Asn Pro Val Ile Trp	
325 330 335	
tcc gat gac tgg aca gcg gtg act gaa gac ggc agc ttg tca gca cag	1117
Ser Asp Asp Trp Thr Ala Val Thr Glu Asp Gly Ser Leu Ser Ala Gln	
340 345 350	
ttt gag cac aca ata ctg att aca gag gat ggc gcg gag ata ctg acg	1165
Phe Glu His Thr Ile Leu Ile Thr Glu Asp Gly Ala Glu Ile Leu Thr	
355 360 365	
cag tgt taagggcgga cgaggattag aggcgagtaa tgacagtgat tctatttcta	1221
Gln Cys 370	
taagtggctg gctggagatg gaatcctaca tttttttgga caaatgatcc aacttgaagt	1281
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ggtttttagaa gtc	1354

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 <213> Oryza sativa

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 Gly Ser Arg Arg Ala Ala Tyr Gln Ala Thr Arg Thr Leu Cys Asn Leu
 35 40 45
 Val Asp Ile Leu Phe Asn Arg Gly Gln Ser Asp Lys Pro Glu Asp Asn
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PF59082SeqList_PF59082.txt

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Lys His Ile Gln Arg Pro Pro Tyr Val Asn Ala Arg Gln Arg Pro Gly
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Leu His Asn Gly Pro Glu Ile His Asp Glu Arg Gly Ile Glu Cys Met
100 105 110
Arg Ala Ser Gly Lys Leu Ala Ala Gln Val Leu Lys Phe Ala Gly Thr
115 120 125
Leu Val Glu Pro Gly Ile Thr Thr Asp Glu Ile Asp Lys Ala Val His
130 135 140
Gln Met Ile Val Asp Asn Gly Ala Tyr Pro Ser Pro Leu Gly Tyr Cys
145 150 155 160
Gly Phe Pro Arg Ser Val Cys Thr Ser Val Asn Glu Cys Ile Cys His
165 170 175
Gly Ile Pro Asp Ser Arg Pro Leu Glu Asp Gly Asp Ile Ile Asn Ile
180 185 190
Asp Val Thr Val Tyr Leu Asn Arg Val Phe Leu Cys Ile Ser Ser Leu
195 200 205
Tyr Leu His Lys Cys Gln Ser Met Thr Met Val Ala Gly Gln Leu Gly
210 215 220
Tyr His Gly Asp Thr Ser Ala Thr Phe Leu Cys Gly Asn Val Asp Asp
225 230 235 240
Lys Ala Lys Lys Leu Val Gln Val Thr Arg Glu Cys Leu Asp Lys Ala
245 250 255
Ile Ser Ile Cys Ala Pro Gly Val Glu Ile Lys Arg Ile Gly Arg Thr
260 265 270
Ile Gln Asp His Ala Asp Lys Phe Lys Phe Gly Val Val Arg Gln Phe
275 280 285
Val Gly His Gly Val Gly Gln Val Phe His Ala Glu Pro Val Val Leu
290 295 300
His Phe Arg Asn Asn Glu Trp Gly Arg Met Thr Leu Asn Gln Thr Phe
305 310 315 320
Thr Ile Glu Pro Met Leu Thr Val Gly Ser Val Asn Pro Val Ile Trp
325 330 335
Ser Asp Asp Trp Thr Ala Val Thr Glu Asp Gly Ser Leu Ser Ala Gln
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Gln Cys
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Met Ala Ser

ggc gcc tca ccg caa ctg caa atg agg ttg aag tcc tct ttc atc gga 163
Gly Ala Ser Pro Gln Leu Gln Met Arg Leu Lys Ser Ser Phe Ile Gly

gat cgt ctc tta cgc tgt tca act tca agg cac caa cct ctt cct caa 211
Asp Arg Leu Leu Arg Cys Ser Thr Ser Arg His Gln Pro Leu Pro Gln

cta ttc cgt tac aac cct gga acc aag cat gtt tcg atg cag tta tct 259
Leu Phe Arg Tyr Asn Pro Gly Thr Lys His Val Ser Met Gln Leu Ser

aga aca ctt tct ggc ttg acc aat ctc ttt ttt aat aga aga aat ttg 307
Arg Thr Leu Ser Gly Leu Thr Asn Leu Phe Phe Asn Arg Arg Asn Leu

PF59082SeqList_PF59082.txt

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		70						75				80							
tct	ccg	cgg	cga	cag	gtg	ccg	aag	aat	ata	ccg	agg	cct	ccg	tat	gtg	403			
Ser	Pro	Arg	Arg	Gln	Val	Pro	Lys	Asn	Ile	Pro	Arg	Pro	Pro	Tyr	Val				
	85					90				95									
aat	tct	atg	att	cct	cca	ggg	att	gcc	agt	gga	gct	gaa	gtg	cat	gac	451			
Asn	Ser	Met	Ile	Pro	Pro	Gly	Ile	Ala	Ser	Gly	Ala	Glu	Val	His	Asp				
100				105				110							115				
aag	aaa	ggg	ata	gaa	tgc	atg	aga	gct	tct	gga	agg	ctt	gca	gcg	cag	499			
Lys	Lys	Gly	Ile	Glu	Cys	Met	Arg	Ala	Ser	Gly	Arg	Leu	Ala	Ala	Gln				
			120					125						130					
gtt	ctt	caa	tat	gct	ggc	acc	tta	gtt	aag	cca	ggc	ata	aca	aca	gat	547			
Val	Leu	Gln	Tyr	Ala	Gly	Thr	Leu	Val	Lys	Pro	Gly	Ile	Thr	Thr	Asp				
		135					140					145							
gaa	att	gac	caa	gca	gtt	cac	caa	atg	ata	att	gat	aat	ggg	gca	tac	595			
Glu	Ile	Asp	Gln	Ala	Val	His	Gln	Met	Ile	Ile	Asp	Asn	Gly	Ala	Tyr				
		150				155					160								
cca	tct	cct	ctc	ggc	tat	ggg	agt	ttt	cct	aag	agt	gtc	tgc	aca	tct	643			
Pro	Ser	Pro	Leu	Gly	Tyr	Gly	Ser	Phe	Pro	Lys	Ser	Val	Cys	Thr	Ser				
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Val	Asn	Glu	Cys	Ile	Cys	His	Gly	Ile	Pro	Asp	Ser	Arg	Ala	Leu	Glu				
180				185				190							195				
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Asp	Gly	Asp	Ile	Ile	Asn	Ile	Asp	Val	Thr	Val	Tyr	Leu	Asn	Gly	Tyr				
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cat	ggg	gac	aca	tca	gca	act	ttc	tat	tgt	gga	gat	gtt	gat	gat	gaa	787			
His	Gly	Asp	Thr	Ser	Ala	Thr	Phe	Tyr	Cys	Gly	Asp	Val	Asp	Asp	Glu				
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gct	aaa	aaa	cta	gtt	cag	gta	act	aaa	gaa	tgc	cta	gat	aaa	gca	ata	835			
Ala	Lys	Lys	Leu	Val	Gln	Val	Thr	Lys	Glu	Cys	Leu	Asp	Lys	Ala	Ile				
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tca	ata	tgt	gca	cca	gga	gtg	gag	ttc	aag	aaa	att	ggc	aaa	aca	att	883			
Ser	Ile	Cys	Ala	Pro	Gly	Val	Glu	Phe	Lys	Lys	Ile	Gly	Lys	Thr	Ile				
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His	Asp	His	Ala	Asp	Lys	Tyr	Arg	Tyr	Gly	Val	Val	Arg	Gln	Phe	Val				
260				265				270							275				
ggc	cat	gga	gta	gga	agt	gtt	ttt	cat	gct	gaa	cct	gtt	att	ctt	cac	979			
Gly	His	Gly	Val	Gly	Ser	Val	Phe	His	Ala	Glu	Pro	Val	Ile	Leu	His				
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Asp	Asp	Trp	Thr	Val	Val	Thr	Glu	Asp	Gly	Ser	Leu	Ser	Ala	Gln	Phe				
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gaa	cac	acc	att	ctg	ata	aca	cct	gac	ggg	gct	gag	att	atg	act	caa	1171			
Glu	His	Thr	Ile	Leu	Ile	Thr	Pro	Asp	Gly	Ala	Glu	Ile	Met	Thr	Gln				
340				345				350							355				
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Cys																			
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tct	ctt	ccgt	gtct	caattg	ata	attttt	ttt	catt	cctt	atg	ggggg	gaga	aa	ta	agtcc		1344		
gg	tgt	ggc	tt	gag	cat	gtt	gag	ag	ccgga	aaaa	aata	at	ttt	ctg	ctt	g	aggcgcagtt	1404	
cat	ga	attt	c	acg	cg	ggg	cc	att	g	act	g	at	agg	ac	act	at	ttatg	ctaaa	1464

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atttactatc 1534

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 35 40 45
 Gln Leu Ser Arg Thr Leu Ser Gly Leu Thr Asn Leu Phe Phe Asn Arg
 50 55 60
 Arg Asn Leu Asp Glu Leu Pro Asn Ser Lys Arg Lys Arg Leu Arg Pro
 65 70 75 80
 Gly Lys Val Ser Pro Arg Arg Gln Val Pro Lys Asn Ile Pro Arg Pro
 85 90 95
 Pro Tyr Val Asn Ser Met Ile Pro Pro Gly Ile Ala Ser Gly Ala Glu
 100 105 110
 Val His Asp Lys Lys Gly Ile Glu Cys Met Arg Ala Ser Gly Arg Leu
 115 120 125
 Ala Ala Gln Val Leu Gln Tyr Ala Gly Thr Leu Val Lys Pro Gly Ile
 130 135 140
 Thr Thr Asp Glu Ile Asp Gln Ala Val His Gln Met Ile Ile Asp Asn
 145 150 155 160
 Gly Ala Tyr Pro Ser Pro Leu Gly Tyr Gly Ser Phe Pro Lys Ser Val
 165 170 175
 Cys Thr Ser Val Asn Glu Cys Ile Cys His Gly Ile Pro Asp Ser Arg
 180 185 190
 Ala Leu Glu Asp Gly Asp Ile Ile Asn Ile Asp Val Thr Val Tyr Leu
 195 200 205
 Asn Gly Tyr His Gly Asp Thr Ser Ala Thr Phe Tyr Cys Gly Asp Val
 210 215 220
 Asp Asp Glu Ala Lys Lys Leu Val Gln Val Thr Lys Glu Cys Leu Asp
 225 230 235 240
 Lys Ala Ile Ser Ile Cys Ala Pro Gly Val Glu Phe Lys Lys Ile Gly
 245 250 255
 Lys Thr Ile His Asp His Ala Asp Lys Tyr Arg Tyr Gly Val Val Arg
 260 265 270
 Gln Phe Val Gly His Gly Val Gly Ser Val Phe His Ala Glu Pro Val
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 Ile Leu His Tyr Arg Asn Asn Glu Ser Gly Arg Met Val Leu Asn Gln
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 Thr Phe Thr Ile Glu Pro Met Leu Thr Ile Gly Ser Ile Asn Pro Val
 305 310 315 320
 Met Trp Asn Asp Asp Trp Thr Val Val Thr Glu Asp Gly Ser Leu Ser
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 Met Thr Gln Cys
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Ser Pro Ser Leu Leu 10 Ser Ser Phe Leu Gly 15 Asp Arg Leu Ala Leu Ser 20

act agg cct ctc ctt ctc cgc tcc gct gtc cca ggc agc agg cgg ctg      211
Thr Arg Pro Leu Leu 25 Leu Arg Ser Ala Val Pro Gly Ser Arg Arg Leu 30 35

gcg tat caa gca acg aga acg cta tgc aac ttg gtg gat atc cta ttt      259
Ala Tyr Gln Ala Thr Arg Thr Leu 40 Cys Asn Leu Val Asp 50 Ile Leu Phe 55

aac agg aga aat cag gat gat gca cca gaa aac aac cct aga cgc ctg      307
Asn Arg Arg Asn Gln Asp Asp Ala Pro Glu Asn Asn Pro Arg Arg Leu 60 65

cgt cct ggg aaa gta tct tct cca cgc ctt agt gtt ccc aat cat ata caa      355
Arg Pro Gly Lys Val Ser 70 Pro Arg Leu Ser Val 80 Pro Asn His Ile Gln 85

cgg cct cca tat gtc aat tct cgt caa caa cga cct ggt atg aat aat      403
Arg Pro Pro Tyr Val 90 Asn Ser Arg Gln Gln 95 Arg Pro Gly Met Asn Asn 100

gga cct gaa ata cat gat gag aac ggg atc gag tgc atg aga gct tct      451
Gly Pro Glu Ile His Asp Glu Asn Gly Ile Glu Cys Met Arg Ala Ser 105 110 115

gga aag ctt gct gca cag gtt ttg aaa ttt gct ggg act ctt gta aag      499
Gly Lys 120 Leu Ala Ala Gln Val 125 Leu Lys Phe Ala Gly Thr Leu Val Lys 130

cca ggc ata acg act gat gaa att gat aaa gca gtg cac caa atg ata      547
Pro Gly Ile Thr Thr Asp Glu 135 Ile Asp Lys Ala Val 140 Val His Gln Met Ile 145

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aag agt gtc tgc act tca gtg aat gaa tgc atc tgt cat ggg att ccg      643
Lys Ser Val Cys Thr 170 Ser Val Asn Glu Cys 175 Ile Cys His Gly Ile Pro 180

gat tct cgt ccc ctt gag gat gga gat atc atc aat att gat gtt act      691
Asp Ser Arg Pro Leu Glu Asp Gly Asp Ile Ile Asn Ile Asp Val Thr 185 190 195

gtc tac ctc aat ggc tac cat ggt gat aca tct gct aca ttt ctt tgc      739
Val Tyr 200 Leu Asn Gly Tyr His 205 Gly Asp Thr Ser Ala Thr Phe Leu Cys 210

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Gly Asp Val Asp Asp Glu 215 Ala Lys Lys Leu Val 220 Lys Val Thr Arg Glu 225

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Cys Leu Asp Lys Ala Ile 230 Ser Ile Cys Ser Pro 240 Gly Val Glu Ile Lys 245

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Gln Ile Gly Arg Thr 250 Gln Asp His Ala Asp Lys Phe Lys Phe Gly 255 260 265

gta gtt aga cag ttt gtt ggc cat ggg gtt ggc aaa gtt ttt cat gct      931
Val Val Arg Gln Phe Val Gly His Gly Val Gly Lys Val Phe His Ala 265 270 275

gag cct gtt gtg ctt cat ttc aga aac aat gaa tgg gga cgt atg atg      979
Glu Pro Val Val Leu His Phe 280 Arg Asn Asn Glu Trp Gly Arg Met Met 285 290 295

ttg aat caa aca ttt act ata gag ccc atg cta acc ata ggg agc atc      1027
Leu Asn Gln Thr Phe Thr Ile Glu Pro Met Leu Thr 300 Ile Gly Ser Ile 305 310 315

aac cct gtc atg tgg tcc gat gac tgg acc gca gtg aca gaa gac ggc      1075
Asn Pro Val Met Trp Ser Asp Asp Trp Thr Ala Val Thr Glu Asp Gly 310 315 320 325

agc ttg tca gca cag ttt gag cac acg ata ctt att acc gaa gat ggc      1123
Ser Leu Ser Ala Gln Phe Glu His Thr Ile Leu Ile Thr Glu Asp Gly 325 330 335

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PF59082SeqList_PF59082.txt

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          330          335          340
cct gaa ata ctg aca cag tgt taatggaagg ccaaataaca aagaacaatc      1174
Pro Glu Ile Leu Thr Gln Cys
          345
gtagtcagc tggcaagatc ctgcatttct ttttggggac taattggtcc aacctaaact      1234

ctgatgcaaa atggcaaact cacattgtaa tctcggttca tcggtacaac gatatatgta      1294

tagaaaattgt actattttcg aagttatatt tgagaaaaaa atttgctggt gcccgcggac      1354

gctggg                                                                1360

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<210> 117
 <211> 348
 <212> PRT
 <213> Zea mays

<400> 117

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Met Ala Ser Leu Ser Ser Pro Ser Leu Leu Ser Ser Phe Leu Gly Asp
1      5      10      15
Arg Leu Ala Leu Ser Thr Arg Pro Leu Leu Leu Arg Ser Ala Val Pro
      20      25      30
Gly Ser Arg Arg Leu Ala Tyr Gln Ala Thr Arg Thr Leu Cys Asn Leu
      35      40      45
Val Asp Ile Leu Phe Asn Arg Arg Asn Gln Asp Asp Ala Pro Glu Asn
      50      55      60
Asn Pro Arg Arg Leu Arg Pro Gly Lys Val Ser Pro Arg Leu Ser Val
      65      70      75      80
Pro Asn His Ile Gln Arg Pro Pro Tyr Val Asn Ser Arg Gln Gln Arg
      85      90      95
Pro Gly Met Asn Asn Gly Pro Glu Ile His Asp Glu Asn Gly Ile Glu
      100      105      110
Cys Met Arg Ala Ser Gly Lys Leu Ala Ala Gln Val Leu Lys Phe Ala
      115      120      125
Gly Thr Leu Val Lys Pro Gly Ile Thr Thr Asp Glu Ile Asp Lys Ala
      130      135      140
Val His Gln Met Ile Ile Asp Asn Gly Ala Tyr Pro Ser Pro Leu Gly
      145      150      155      160
Tyr Cys Gly Tyr Pro Lys Ser Val Cys Thr Ser Val Asn Glu Cys Ile
      165      170      175
Cys His Gly Ile Pro Asp Ser Arg Pro Leu Glu Asp Gly Asp Ile Ile
      180      185      190
Asn Ile Asp Val Thr Val Tyr Leu Asn Gly Tyr His Gly Asp Thr Ser
      195      200      205
Ala Thr Phe Leu Cys Gly Asp Val Asp Asp Glu Ala Lys Lys Leu Val
      210      215      220
Lys Val Thr Arg Glu Cys Leu Asp Lys Ala Ile Ser Ile Cys Ser Pro
      225      230      235      240
Gly Val Glu Ile Lys Gln Ile Gly Arg Thr Ile Gln Asp His Ala Asp
      245      250      255
Lys Phe Lys Phe Gly Val Val Arg Gln Phe Val Gly His Gly Val Gly
      260      265      270
Lys Val Phe His Ala Glu Pro Val Val Leu His Phe Arg Asn Asn Glu
      275      280      285
Trp Gly Arg Met Met Leu Asn Gln Thr Phe Thr Ile Glu Pro Met Leu
      290      295      300
Thr Ile Gly Ser Ile Asn Pro Val Met Trp Ser Asp Asp Trp Thr Ala
      305      310      315      320
Val Thr Glu Asp Gly Ser Leu Ser Ala Gln Phe Glu His Thr Ile Leu
      325      330      335
Ile Thr Glu Asp Gly Pro Glu Ile Leu Thr Gln Cys
      340      345

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<210> 118

PF59082SeqList_PF59082.txt

<211> 1734
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<213> Zea mays

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<222> (4)..(4)
<223> n is a, g, c or t

<220>
<221> misc_feature
<222> (1713)..(1713)
<223> n is a, g, c or t

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ggcctgtatc cctctcccc atg gct gct gga ctg gga gcg cgc ccc tcc gcc 172
Met Ala Ala Gly Leu Gly Ala Arg Pro Ser Ala
1 5 10

acc ttc gag gcc gga agg ttc cgg cct ctc gct gcc cct ctc cgc ccc 220
Thr Phe Glu Ala Gly Arg Phe Arg Pro Leu Ala Ala Pro Leu Arg Pro
15 20 25

gtc cgc tcc gga aaa ttc gta gtg cct aag cga tgc ttc act gtg tca 268
Val Arg Ser Gly Lys Phe Val Val Pro Lys Arg Cys Phe Thr Val Ser
30 35 40

agt agg ctt gca tgg gtg gaa gat gag ctt atg gag ata aaa aag tca 316
Ser Arg Leu Ala Trp Val Glu Asp Glu Leu Met Glu Ile Lys Lys Ser
45 50 55

caa gag caa agt tca gta aaa tca aag aaa aga cca cct ttg agg cgt 364
Gln Glu Gln Ser Ser Val Lys Ser Lys Lys Arg Pro Pro Leu Arg Arg
60 65 70 75

gga aag gtc tcc cca caa ctt cct gta cca ggg cac att cca aga cca 412
Gly Lys Val Ser Pro Gln Leu Pro Val Pro Gly His Ile Pro Arg Pro
80 85 90

tct tat gtt ggt tca aaa gga ttg cca gaa cta tgc aag ggc caa tta 460
Ser Tyr Val Gly Ser Lys Gly Leu Pro Glu Leu Cys Lys Gly Gln Leu
95 100 105

cac gat gct caa gga att gct gga atg aga gct gct tgc aaa ctt gct 508
His Asp Ala Gln Gly Ile Ala Gly Met Arg Ala Ala Cys Lys Leu Ala
110 115 120

gcc cgt gtt ctt gat ttt gct ggg act tta gtt aag cca tcc att act 556
Ala Arg Val Leu Asp Phe Ala Gly Thr Leu Val Lys Pro Ser Ile Thr
125 130 135

aca aat gaa att gac gaa gca gtc cat aat atg atc att gaa gct ggt 604
Thr Asn Glu Ile Asp Glu Ala Val His Asn Met Ile Ile Glu Ala Gly
140 145 150 155

gct tat cct tct cca ctt ggc tat cat gga ttt cct aaa agt ata tgt 652
Ala Tyr Pro Ser Pro Leu Gly Tyr His Gly Phe Pro Lys Ser Ile Cys
160 165 170

aca tca gta aat gag tgt gtc tgt cat ggg gta cct gat tca act cag 700
Thr Ser Val Asn Glu Cys Val Cys His Gly Val Pro Asp Ser Thr Gln
175 180 185

ctg cag aat ggg gat att ata aat att gat gta aat gtg ttc ctg aat 748
Leu Gln Asn Gly Asp Ile Ile Asn Ile Asp Val Asn Val Phe Leu Asn
190 195 200

gga tac cat ggg ggt acc tcc aga aca ttt gca tgt gga caa gtt gat 796
Gly Tyr His Gly Gly Thr Ser Arg Thr Phe Ala Cys Gly Gln Val Asp
205 210 215

gat tct atc aaa cat ttt ctc aat gca gct gaa gaa tgc ttg gag aaa 844
Asp Ser Ile Lys His Phe Leu Asn Ala Ala Glu Glu Cys Leu Glu Lys

PF59082SeqList_PF59082.txt

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220          225          230          235
ggc att tct atc tgc agg gat ggt gtg aac tac aga aag att ggc aag      892
Gly Ile Ser Ile Cys Arg Asp Gly Val Asn Tyr Arg Lys Ile Gly Lys
          240          245          250
aaa ata agc aag ctt gcc tat ttt tat ggc tat tat gtg gtg gaa cgc      940
Lys Ile Ser Lys Leu Ala Tyr Phe Tyr Gly Tyr Tyr Val Val Glu Arg
          255          260          265
ttt gtt ggc cat ggg att gga act atg tat cat tct gag cca ctt atc      988
Phe Val Gly His Gly Ile Gly Thr Met Tyr His Ser Glu Pro Leu Ile
          270          275          280
cta cat cat gcc aac gaa aac tca ggg cgt atg gtt gag ggc caa aca      1036
Leu His His Ala Asn Glu Asn Ser Gly Arg Met Val Glu Gly Gln Thr
          285          290          295
ttt aca att gaa cct ata ctc aca atg gag aaa aca gag tgt gtt aca      1084
Phe Thr Ile Glu Pro Ile Leu Thr Met Glu Lys Thr Glu Cys Val Thr
          300          305          310          315
tgg gaa gat gga tgg acg act gtc act gct gat ggt agc tgg gct gcg      1132
Trp Glu Asp Gly Trp Thr Thr Val Thr Ala Asp Gly Ser Trp Ala Ala
          320          325          330
cag ttt gag cat acc ata ctg gtg act agg gac ggt gca gaa ata ctg      1180
Gln Phe Glu His Thr Ile Leu Val Thr Arg Asp Gly Ala Glu Ile Leu
          335          340          345
acg aaa gtt tgagctattc tcctgcccga taattcttgt cagaactctc agctatgggt      1239
Thr Lys Val
          350
cctgtcccaa gtcatcctgg tcatgtccgt tgctcgtcgc aatactcatt tcagagtttt      1299

gagatctgct gcaggccgac atacgggaaa ggtttcccc atgtagcagc aacttgagg      1359

tgataggtga gggcacacac acacacagag acacggctgc atctctgtga ttaacacatt      1419

actggtctcc tgcagcctgc ttagtggtg tttgctgtgc ctttgattc tagaagacat      1479

tctgtatata aaacagcact cctaacagtt cagtctagaa cctagaagta gaaactgtta      1539

ttgttatgat acggaagcac tttaggggaa cagttggaga cacattttta tgtttttcaa      1599

aaaaaaaaatg atttagaaaa gacttatagg gagctcttgg aaatgctcta ataaaaacat      1659

ctcctaaagt ttttgacgt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aacncgaggg      1719

ggagaacggt accca      1734

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<210> 119
 <211> 350
 <212> PRT
 <213> Zea mays

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 Arg Phe Arg Pro Leu Ala Ala Pro Leu Arg Pro Val Arg Ser Gly Lys
 20 25 30
 Phe Val Val Pro Lys Arg Cys Phe Thr Val Ser Ser Arg Leu Ala Trp
 35 40 45
 Val Glu Asp Glu Leu Met Glu Ile Lys Lys Ser Gln Glu Gln Ser Ser
 50 55 60
 Val Lys Ser Lys Lys Arg Pro Pro Leu Arg Arg Gly Lys Val Ser Pro
 65 70 75 80

PF59082SeqList_PF59082.txt

Gln Leu Pro Val Pro Gly His Ile Pro Arg Pro Ser Tyr Val Gly Ser
 85 90 95
 Lys Gly Leu Pro Glu Leu Cys Lys Gly Gln Leu His Asp Ala Gln Gly
 100 105 110
 Ile Ala Gly Met Arg Ala Ala Cys Lys Leu Ala Ala Arg Val Leu Asp
 115 120 125
 Phe Ala Gly Thr Leu Val Lys Pro Ser Ile Thr Thr Asn Glu Ile Asp
 130 135 140
 Glu Ala Val His Asn Met Ile Ile Glu Ala Gly Ala Tyr Pro Ser Pro
 145 150 155 160
 Leu Gly Tyr His Gly Phe Pro Lys Ser Ile Cys Thr Ser Val Asn Glu
 165 170 175
 Cys Val Cys His Gly Val Pro Asp Ser Thr Gln Leu Gln Asn Gly Asp
 180 185 190
 Ile Ile Asn Ile Asp Val Asn Val Phe Leu Asn Gly Tyr His Gly Gly
 195 200 205
 Thr Ser Arg Thr Phe Ala Cys Gly Gln Val Asp Asp Ser Ile Lys His
 210 215 220
 Phe Leu Asn Ala Ala Glu Glu Cys Leu Glu Lys Gly Ile Ser Ile Cys
 225 230 235 240
 Arg Asp Gly Val Asn Tyr Arg Lys Ile Gly Lys Lys Ile Ser Lys Leu
 245 250 255
 Ala Tyr Phe Tyr Gly Tyr Tyr Val Val Glu Arg Phe Val Gly His Gly
 260 265 270
 Ile Gly Thr Met Tyr His Ser Glu Pro Leu Ile Leu His His Ala Asn
 275 280 285
 Glu Asn Ser Gly Arg Met Val Glu Gly Gln Thr Phe Thr Ile Glu Pro
 290 295 300
 Ile Leu Thr Met Glu Lys Thr Glu Cys Val Thr Trp Glu Asp Gly Trp
 305 310 315 320
 Thr Thr Val Thr Ala Asp Gly Ser Trp Ala Ala Gln Phe Glu His Thr
 325 330 335
 Ile Leu Val Thr Arg Asp Gly Ala Glu Ile Leu Thr Lys Val
 340 345 350

<210> 120

<211> 1389

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (184)..(1209)

<400> 120

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tccaaactgg cgacgaccct gctgccaccc cacagcagat ttgaggagcg gacgcccggtt 180

taa atg gct att gga gtc cca tcc atg gag ctc cac cgc tcc tca ccg 228
 Met Ala Ile Gly Val Pro Ser Met Glu Leu His Arg Ser Ser Pro 15

ttg ctc tcg ggt ggc cga gga gga aat aca tgc cta cag aag aag ccc 276
 Leu Leu Ser Gly Gly Arg Gly Gly Asn Thr Cys Leu Gln Lys Lys Pro 30

ttc ttt gtc caa gca aag aga cta gtg ggg atg gag aaa gca agt acg 324
 Phe Phe Val Gln Ala Lys Arg Leu Val Gly Met Glu Lys Ala Ser Thr 45

agg cca gga aca caa gag tct gga cag aca aag aaa aga gca ccc ctg 372
 Arg Pro Gly Thr Gln Glu Ser Gly Gln Thr Lys Lys Arg Ala Pro Leu 60

gtt cgt gga act gtt agc cca cct ctt cca gta cca gga aac ata cct 420
 Val Arg Gly Thr Val Ser Pro Pro Leu Pro Val Pro Gly Asn Ile Pro 75

PF59082SeqList_PF59082.txt

cgg	cct	cct	tat	gtc	ggc	aca	gaa	tat	gta	cca	gag	ata	gca	aaa	gag	468
Arg	Pro	Pro	Tyr	Val	Gly	Thr	Glu	Tyr	Val	Pro	Glu	Ile	Ala	Lys	Glu	
80					85				90						95	
ata	caa	atg	cat	gac	aaa	gag	ggc	att	gtc	cac	atg	aga	gct	gct	tgc	516
Ile	Gln	Met	His	Asp	Lys	Glu	Gly	Ile	Val	His	Met	Arg	Ala	Ala	Cys	
				100				105						110		
gag	ctc	gcg	gct	cgt	gtt	ctt	gac	tat	gca	gga	acg	tta	gtg	aaa	ccc	564
Glu	Leu	Ala	Ala	Arg	Val	Leu	Asp	Tyr	Ala	Gly	Thr	Leu	Val	Lys	Pro	
			115					120					125			
tct	gta	aca	aca	gac	gaa	att	gat	aaa	gca	gtg	cac	aag	atg	atc	atc	612
Ser	Val	Thr	Thr	Asp	Glu	Ile	Asp	Lys	Ala	Val	His	Lys	Met	Ile	Ile	
			130				135					140				
gat	gct	gga	gcc	tat	cca	tca	cca	ctt	gga	tat	ggt	ggg	ttt	cca	aaa	660
Asp	Ala	Gly	Ala	Tyr	Pro	Ser	Pro	Leu	Gly	Tyr	Gly	Gly	Phe	Pro	Lys	
	145					150					155					
agt	gta	tgc	acc	tca	gtg	aat	gag	tgc	atg	tgc	cat	gga	att	cct	gat	708
Ser	Val	Cys	Thr	Ser	Val	Asn	Glu	Cys	Met	Cys	His	Gly	Ile	Pro	Asp	
				165				170							175	
tca	cgc	gag	cta	cag	gat	gga	gac	ata	att	aac	att	gat	gtc	act	gtc	756
Ser	Arg	Glu	Leu	Gln	Asp	Gly	Asp	Ile	Ile	Asn	Ile	Asp	Val	Thr	Val	
				180				185						190		
tac	ttg	aat	ggt	tat	cat	ggg	gat	acc	tca	aaa	aca	ttt	ctt	tgt	gga	804
Tyr	Leu	Asn	Gly	Tyr	His	Gly	Asp	Thr	Ser	Lys	Thr	Phe	Leu	Cys	Gly	
			195				200						205			
gaa	gtc	gat	gaa	gcc	agt	aaa	cga	ctt	gtg	aag	gtt	act	gaa	gag	tgc	852
Glu	Val	Asp	Glu	Ala	Ser	Lys	Arg	Leu	Val	Lys	Val	Thr	Glu	Glu	Cys	
		210					215					220				
ttg	ctc	agg	ggc	ata	tca	aca	tgc	aaa	cat	ggt	acc	agc	ttt	aag	aag	900
Leu	Leu	Arg	Gly	Ile	Ser	Thr	Cys	Lys	His	Gly	Thr	Ser	Phe	Lys	Lys	
	225					230					235					
att	ggc	aga	aga	ata	agt	gag	cat	gct	gag	agg	aac	ggt	ttt	ggt	gtt	948
Ile	Gly	Arg	Arg	Ile	Ser	Glu	His	Ala	Glu	Arg	Asn	Gly	Phe	Gly	Val	
	240				245				250					255		
gtg	gag	tgt	ttt	gtt	ggg	cat	gga	gtc	ggc	agg	gta	ttt	cac	tca	gaa	996
Val	Glu	Cys	Phe	Val	Gly	His	Gly	Val	Gly	Arg	Val	Phe	His	Ser	Glu	
				260				265						270		
cca	att	atc	tat	cac	cag	agg	aac	aac	aga	ccg	ggc	cag	atg	att	gaa	1044
Pro	Ile	Ile	Tyr	His	Gln	Arg	Asn	Asn	Arg	Pro	Gly	Gln	Met	Ile	Glu	
			275				280						285			
ggg	cag	act	ttc	aca	ata	gag	ccg	atc	ata	tcc	atg	ggg	agc	atc	gag	1092
Gly	Gln	Thr	Phe	Thr	Ile	Glu	Pro	Ile	Ile	Ser	Met	Gly	Ser	Ile	Glu	
		290					295					300				
tgc	gac	atg	tgg	gac	gac	ggc	tgg	act	gcc	gtg	acg	acg	gac	ggc	agc	1140
Cys	Asp	Met	Trp	Asp	Asp	Gly	Trp	Thr	Ala	Val	Thr	Thr	Asp	Gly	Ser	
	305					310					315					
ttg	gcg	gcg	cag	ttc	gag	cac	acc	ata	ctg	atc	acc	agg	acc	gga	gcc	1188
Leu	Ala	Ala	Gln	Phe	Glu	His	Thr	Ile	Leu	Ile	Thr	Arg	Thr	Gly	Ala	
				325				330						335		
gag	atc	ctc	acc	aag	tgc	taggaggaaa	ggaaatcgca	tgtgcccgat								1236
Glu	Ile	Leu	Thr	Lys	Cys											
			340													
agccgacggt	aggtaatctg	tattcgtgag	gtggtgagga	tgcttgaggt	gacctat	tttt										1296
gtctcgcaaa	atgggcgtgc	tacagaatag	tgaagaaaag	ggttgagaga	ttgcaaatgg											1356
caggtttggg	caaagagggc	caagttctag	gcc													1389

<210> 121

<211> 341

<212> PRT

<213> Zea mays

<400> 121

Met Ala Ile Gly Val Pro Ser Met Glu Leu His Arg Ser Ser Pro Leu
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PF59082SeqList_PF59082.txt

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 Phe Val Gln Ala Lys Arg Leu Val Gly Met Glu Lys Ala Ser Thr Arg
 35 40 45
 Pro Gly Thr Gln Glu Ser Gly Gln Thr Lys Lys Arg Ala Pro Leu Val
 50 55 60
 Arg Gly Thr Val Ser Pro Pro Leu Pro Val Pro Gly Asn Ile Pro Arg
 65 70 75 80
 Pro Pro Tyr Val Gly Thr Glu Tyr Val Pro Glu Ile Ala Lys Glu Ile
 85 90 95
 Gln Met His Asp Lys Glu Gly Ile Val His Met Arg Ala Ala Cys Glu
 100 105 110
 Leu Ala Ala Arg Val Leu Asp Tyr Ala Gly Thr Leu Val Lys Pro Ser
 115 120 125
 Val Thr Thr Asp Glu Ile Asp Lys Ala Val His Lys Met Ile Ile Asp
 130 135 140
 Ala Gly Ala Tyr Pro Ser Pro Leu Gly Tyr Gly Gly Phe Pro Lys Ser
 145 150 155 160
 Val Cys Thr Ser Val Asn Glu Cys Met Cys His Gly Ile Pro Asp Ser
 165 170 175
 Arg Glu Leu Gln Asp Gly Asp Ile Ile Asn Ile Asp Val Thr Val Tyr
 180 185 190
 Leu Asn Gly Tyr His Gly Asp Thr Ser Lys Thr Phe Leu Cys Gly Glu
 195 200 205
 Val Asp Glu Ala Ser Lys Arg Leu Val Lys Val Thr Glu Glu Cys Leu
 210 215 220
 Leu Arg Gly Ile Ser Thr Cys Lys His Gly Thr Ser Phe Lys Lys Ile
 225 230 235 240
 Gly Arg Arg Ile Ser Glu His Ala Glu Arg Asn Gly Phe Gly Val Val
 245 250 255
 Glu Cys Phe Val Gly His Gly Val Gly Arg Val Phe His Ser Glu Pro
 260 265 270
 Ile Ile Tyr His Gln Arg Asn Asn Arg Pro Gly Gln Met Ile Glu Gly
 275 280 285
 Gln Thr Phe Thr Ile Glu Pro Ile Ile Ser Met Gly Ser Ile Glu Cys
 290 295 300
 Asp Met Trp Asp Asp Gly Trp Thr Ala Val Thr Thr Asp Gly Ser Leu
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 325 330 335
 Ile Leu Thr Lys Cys
 340

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<212> DNA

<213> Triticum aestivum

<220>

<221> CDS

<222> (131)..(1168)

<400> 122

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120

cactgctccg atg gcg gtc aga gtt ccg tcc atg gag ctg aac cgc tcc
 Met Ala Val Arg Val Pro Ser Met Glu Leu Asn Arg Ser

169

ccg ccg ctc ctc tcc ggc ggc aga ggc aaa aca tgc ctt cag aag cct
 Pro Pro Leu Leu Ser Gly Gly Arg Gly Lys Thr Cys Leu Gln Lys Pro

217

ttc att gtc caa gca aag aga tca ggt gga ttg gag aaa gca aat act
 Phe Ile Val Gln Ala Lys Arg Ser Gly Gly Leu Glu Lys Ala Asn Thr

265

agc agg tca cga gga ccg caa gct tct gaa aaa ctc aag aaa aga gaa

313

PF59082SeqList_PF59082.txt

Ser	Arg	Ser	Arg	Gly	Pro	Gln	Ala	Ser	Glu	Lys	Leu	Lys	Lys	Arg	Glu		
ccc	ctg	act	cgt	ggg	act	gtt	agt	gcg	cct	ctt	ccg	gta	cca	gga	cac	361	
Pro	Leu	Thr	Arg	Gly	Thr	Val	Ser	Ala	Pro	Leu	Pro	Val	Pro	Gly	His		
			65					70					75				
ata	cct	cga	cct	cct	tac	gtt	gga	tca	aac	aaa	atg	ccc	gag	ata	tcg	409	
Ile	Pro	Arg	Pro	Pro	Tyr	Val	Gly	Ser	Asn	Lys	Met	Pro	Glu	Ile	Ser		
		80					85					90					
agt	gag	aga	caa	atg	cag	gac	aaa	gac	acc	atc	gtg	cac	atg	aaa	gct	457	
Ser	Glu	Arg	Gln	Met	Gln	Asp	Lys	Asp	Thr	Ile	Val	His	Met	Lys	Ala		
		95				100					105						
gca	tgt	gag	ctt	gct	gct	cgt	gtt	ctt	caa	aat	gca	ggg	aaa	tta	gtc	505	
Ala	Cys	Glu	Leu	Ala	Ala	Arg	Val	Leu	Gln	Asn	Ala	Gly	Lys	Leu	Val		
110				115					120						125		
aaa	ccc	tct	gta	aca	gac	gaa	att	gat	aaa	gca	gtg	cac	aag	atg		553	
Lys	Pro	Ser	Val	Thr	Asp	Glu	Ile	Asp	Lys	Ala	Val	His	Lys	Met			
			130					135					140				
atc	att	gat	gct	gga	gcc	tat	cca	tcc	ccg	ctt	gga	tac	ggg	ggg	ttt	601	
Ile	Ile	Asp	Ala	Gly	Ala	Tyr	Pro	Ser	Pro	Leu	Gly	Tyr	Gly	Gly	Phe		
			145					150					155				
cca	aaa	agt	gta	tgc	aca	tca	gtg	aac	gaa	tgc	atg	tgc	cat	ggg	att	649	
Pro	Lys	Ser	Val	Cys	Thr	Ser	Val	Asn	Glu	Cys	Met	Cys	His	Gly	Ile		
		160					165					170					
cct	gat	tca	cga	gaa	cta	aag	gat	gga	gac	ata	att	aac	atc	gat	gtc	697	
Pro	Asp	Ser	Arg	Glu	Leu	Lys	Asp	Gly	Asp	Ile	Ile	Asn	Ile	Asp	Val		
		175				180					185						
act	gtc	tac	ttg	aac	ggg	ttt	cat	ggg	gat	acc	tct	aaa	acg	ttt	ttc	745	
Thr	Val	Tyr	Leu	Asn	Gly	Phe	His	Gly	Asp	Thr	Ser	Lys	Thr	Phe	Phe		
190				195				200						205			
tgt	gga	gaa	gtt	gac	gaa	gct	gct	aaa	aga	ctt	gtg	aag	gtt	act	gaa	793	
Cys	Gly	Glu	Val	Asp	Glu	Ala	Ala	Lys	Arg	Leu	Val	Lys	Val	Thr	Glu		
			210					215						220			
gag	tgc	atg	ctt	agg	ggc	ata	tca	tcc	tgc	aaa	cac	ggg	gtg	agc	ttt	841	
Glu	Cys	Met	Leu	Arg	Gly	Ile	Ser	Ser	Cys	Lys	His	Gly	Val	Ser	Phe		
			225					230					235				
aag	aaa	atc	ggc	aga	aga	ata	agc	gag	cat	gct	gag	agg	aat	gga	ttt	889	
Lys	Lys	Ile	Gly	Arg	Arg	Ile	Ser	Glu	His	Ala	Glu	Arg	Asn	Gly	Phe		
		240					245					250					
ggg	gtc	gtg	gag	caa	ttt	gtt	ggg	cat	gga	gtt	ggc	aga	gtt	ttt	cat	937	
Gly	Val	Val	Glu	Gln	Phe	Val	Gly	His	Gly	Val	Gly	Arg	Val	Phe	His		
		255				260					265						
tca	caa	cca	att	ata	tat	cac	cag	cgc	aac	aac	atg	cca	ggg	cag	atg	985	
Ser	Gln	Pro	Ile	Ile	Tyr	His	Gln	Arg	Asn	Asn	Met	Pro	Gly	Gln	Met		
270				275					280					285			
gtt	gaa	ggc	cag	acg	ttc	aca	ata	gag	ccg	atc	ctg	acc	atg	gga	agc	1033	
Val	Glu	Gly	Gln	Thr	Phe	Thr	Ile	Glu	Pro	Ile	Leu	Thr	Met	Gly	Ser		
			290					295						300			
aac	agc	aac	agc	atc	gag	tgc	gac	atg	tgg	gag	gac	ggc	tgg	acg	gcg	1081	
Asn	Ser	Asn	Ser	Ile	Glu	Cys	Asp	Met	Trp	Glu	Asp	Gly	Trp	Thr	Ala		
			305				310						315				
gtg	acg	acg	gac	ggc	agc	ctg	gcg	gcg	cag	ttc	gag	cac	acc	atc	ctc	1129	
Val	Thr	Thr	Asp	Gly	Ser	Leu	Ala	Ala	Gln	Phe	Glu	His	Thr	Ile	Leu		
		320				325						330					
atc	acc	agg	acc	ggc	gca	gag	atc	cta	acc	aaa	tgc	tag	caa	agcc		1175	
Ile	Thr	Arg	Thr	Gly	Ala	Glu	Ile	Leu	Thr	Lys	Cys						
		335				340					345						
agcgctgaag	gcgtacggat	cctgaccgcg	tagatcacgt	gatttcttct	tatgttgtat											1235	
gccaaagcat	cactggaaca	gctgcttacg	tataaccgat	gattttttggc	agcggcaaag											1295	
agctccaggc	ttcctctggc	acact														1320	

<210> 123
 <211> 345
 <212> PRT

PF59082SeqList_PF59082.txt

<213> Triticum aestivum

<400> 123

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Leu Ser Gly Gly Arg Gly Lys Thr Cys Leu Gln Lys Pro Phe Ile Val
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Gln Ala Lys Arg Ser Gly Gly Leu Glu Lys Ala Asn Thr Ser Arg Ser
      35      40      45
Arg Gly Pro Gln Ala Ser Glu Lys Leu Lys Lys Arg Glu Pro Leu Thr
      50      55      60
Arg Gly Thr Val Ser Ala Pro Leu Pro Val Pro Gly His Ile Pro Arg
65      70      75      80
Pro Pro Tyr Val Gly Ser Asn Lys Met Pro Glu Ile Ser Ser Glu Arg
      85      90      95
Gln Met Gln Asp Lys Asp Thr Ile Val His Met Lys Ala Ala Cys Glu
      100      105      110
Leu Ala Ala Arg Val Leu Gln Asn Ala Gly Lys Leu Val Lys Pro Ser
      115      120      125
Val Thr Thr Asp Glu Ile Asp Lys Ala Val His Lys Met Ile Ile Asp
130      135      140
Ala Gly Ala Tyr Pro Ser Pro Leu Gly Tyr Gly Gly Phe Pro Lys Ser
145      150      155      160
Val Cys Thr Ser Val Asn Glu Cys Met Cys His Gly Ile Pro Asp Ser
      165      170      175
Arg Glu Leu Lys Asp Gly Asp Ile Ile Asn Ile Asp Val Thr Val Tyr
      180      185      190
Leu Asn Gly Phe His Gly Asp Thr Ser Lys Thr Phe Phe Cys Gly Glu
      195      200      205
Val Asp Glu Ala Ala Lys Arg Leu Val Lys Val Thr Glu Glu Cys Met
210      215      220
Leu Arg Gly Ile Ser Ser Cys Lys His Gly Val Ser Phe Lys Lys Ile
225      230      235      240
Gly Arg Arg Ile Ser Glu His Ala Glu Arg Asn Gly Phe Gly Val Val
      245      250      255
Glu Gln Phe Val Gly His Gly Val Gly Arg Val Phe His Ser Gln Pro
      260      265      270
Ile Ile Tyr His Gln Arg Asn Asn Met Pro Gly Gln Met Val Glu Gly
      275      280      285
Gln Thr Phe Thr Ile Glu Pro Ile Leu Thr Met Gly Ser Asn Ser Asn
290      295      300
Ser Ile Glu Cys Asp Met Trp Glu Asp Gly Trp Thr Ala Val Thr Thr
305      310      315      320
Asp Gly Ser Leu Ala Gln Phe Glu His Thr Ile Leu Ile Thr Arg
      325      330      335
Thr Gly Ala Glu Ile Leu Thr Lys Cys
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<210> 124

<211> 1320

<212> DNA

<213> Triticum aestivum

<220>

<221> CDS

<222> (152)..(1168)

<400> 124

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cactgctccg atggcgggtca gagttccgtc c atg gag ctg aac cgc tcc ccg      172
                               Met Glu Leu Asn Arg Ser Pro
                               1      5
ccg ctc ctc tcc ggc ggc aga ggc aaa aca tgc ctt cag aag cct ttc      220
Pro Leu Leu Ser Gly Gly Arg Gly Lys Thr Cys Leu Gln Lys Pro Phe
                               Seite 158

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PF59082SeqList_PF59082.txt

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Ile	Val	Gln	Ala	Lys	Arg	Ser	Gly	Gly	Leu	Glu	Lys	Ala	Asn	Thr	Ser			
	25					30					35							
agg	tca	cga	gga	ccg	caa	gct	tct	gaa	aaa	ctc	aag	aaa	aga	gaa	ccc			316
Arg	Ser	Arg	Gly	Pro	Gln	Ala	Ser	Glu	Lys	Leu	Lys	Lys	Arg	Glu	Pro			
	40				45					50					55			
ctg	act	cgt	ggg	act	gtt	agt	gcg	cct	ctt	ccg	gta	cca	gga	cac	ata			364
Leu	Thr	Arg	Gly	Thr	Val	Ser	Ala	Pro	Leu	Pro	Val	Pro	Gly	His	Ile			
				60					65					70				
cct	cga	cct	cct	tac	gtt	gga	tca	aac	aaa	atg	ccc	gag	ata	tcg	agt			412
Pro	Arg	Pro	Pro	Tyr	Val	Gly	Ser	Asn	Lys	Met	Pro	Glu	Ile	Ser	Ser			
				75				80					85					
gag	aga	caa	atg	cag	gac	aaa	gac	acc	atc	gtg	cac	atg	aaa	gct	gca			460
Glu	Arg	Gln	Met	Gln	Asp	Lys	Asp	Thr	Ile	Val	His	Met	Lys	Ala	Ala			
		90					95					100						
tgt	gag	ctt	gct	gct	cgt	gtt	ctt	caa	aat	gca	ggg	aaa	tta	gtc	aaa			508
Cys	Glu	Leu	Ala	Ala	Arg	Val	Leu	Gln	Asn	Ala	Gly	Lys	Leu	Val	Lys			
	105					110				115								
ccc	tct	gta	aca	aca	gac	gaa	att	gat	aaa	gca	gtg	cac	aag	atg	atc			556
Pro	Ser	Val	Thr	Thr	Asp	Glu	Ile	Asp	Lys	Ala	Val	His	Lys	Met	Ile			
	120				125					130					135			
att	gat	gct	gga	gcc	tat	cca	tcc	ccg	ctt	gga	tac	ggg	ggg	ttt	cca			604
Ile	Asp	Ala	Gly	Ala	Tyr	Pro	Ser	Pro	Leu	Gly	Tyr	Gly	Gly	Phe	Pro			
				140					145					150				
aaa	agt	gta	tgc	aca	tca	gtg	aac	gaa	tgc	atg	tgc	cat	ggg	att	cct			652
Lys	Ser	Val	Cys	Thr	Ser	Val	Asn	Glu	Cys	Met	Cys	His	Gly	Ile	Pro			
		155					160					165						
gat	tca	cga	gaa	cta	aag	gat	gga	gac	ata	att	aac	atc	gat	gtc	act			700
Asp	Ser	Arg	Glu	Leu	Lys	Asp	Gly	Asp	Ile	Ile	Asn	Ile	Asp	Val	Thr			
		170					175					180						
gtc	tac	ttg	aac	ggg	ttt	cat	ggg	gat	acc	tct	aaa	acg	ttt	ttc	tgt			748
Val	Tyr	Leu	Asn	Gly	Phe	His	Gly	Asp	Thr	Ser	Lys	Thr	Phe	Phe	Cys			
	185				190					195								
gga	gaa	gtt	gac	gaa	gct	aaa	aga	ctt	gtg	aag	gtt	act	gaa	gag				796
Gly	Glu	Val	Asp	Glu	Ala	Lys	Arg	Leu	Val	Lys	Val	Thr	Glu	Glu				
	200				205				210					215				
tgc	atg	ctt	agg	ggc	ata	tca	tcc	tgc	aaa	cac	ggg	gtg	agc	ttt	aag			844
Cys	Met	Leu	Arg	Gly	Ile	Ser	Ser	Cys	Lys	His	Gly	Val	Ser	Phe	Lys			
				220					225					230				
aaa	atc	ggc	aga	aga	ata	agc	gag	cat	gct	gag	agg	aat	gga	ttt	ggg			892
Lys	Ile	Gly	Arg	Arg	Ile	Ser	Glu	His	Ala	Glu	Arg	Asn	Gly	Phe	Gly			
		235					240					245						
gtc	gtg	gag	caa	ttt	gtt	ggg	cat	gga	gtt	ggc	aga	gtt	ttt	cat	tca			940
Val	Val	Gln	Phe	Val	Gly	His	Gly	Val	Gly	Arg	Val	Phe	His	Ser				
		250			255						260							
caa	cca	att	ata	tat	cac	cag	cgc	aac	aac	atg	cca	ggg	cag	atg	gtt			988
Gln	Pro	Ile	Ile	Tyr	His	Gln	Arg	Asn	Asn	Met	Pro	Gly	Gln	Met	Val			
	265				270					275								
gaa	ggc	cag	acg	ttc	aca	ata	gag	ccg	atc	ctg	acc	atg	gga	agc	aac			1036
Glu	Gly	Gln	Thr	Phe	Thr	Ile	Glu	Pro	Ile	Leu	Thr	Met	Gly	Ser	Asn			
	280				285					290				295				
agc	aac	agc	atc	gag	tgc	gac	atg	tgg	gag	gac	ggc	tgg	acg	gcg	gtg			1084
Ser	Asn	Ser	Ile	Glu	Cys	Asp	Met	Trp	Glu	Asp	Gly	Trp	Thr	Ala	Val			
				300					305					310				
acg	acg	gac	ggc	agc	ctg	gcg	gcg	cag	ttc	gag	cac	acc	atc	ctc	atc			1132
Thr	Thr	Asp	Gly	Ser	Leu	Ala	Ala	Gln	Phe	Glu	His	Thr	Ile	Leu	Ile			
		315						320					325					
acc	agg	acc	ggc	gca	gag	atc	cta	acc	aaa	tgc	tag	caa	agc	agc	gct	gaag		1185
Thr	Arg	Thr	Gly	Ala	Glu	Ile	Leu	Thr	Lys	Cys								
		330				335												
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cactggaaca	gctgcttacg	tataaccgat	gattttttggc	agcggcaaaag	agctccaggc													1305
ttcctctggc	acact																	1320

PF59082SeqList_PF59082.txt

<210> 125
 <211> 338
 <212> PRT
 <213> Triticum aestivum

<400> 125
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 Leu Glu Lys Ala Asn Thr Ser Arg Ser Arg Gly Pro Gln Ala Ser Glu
 35 40 45
 Lys Leu Lys Lys Arg Glu Pro Leu Thr Arg Gly Thr Val Ser Ala Pro
 50 55 60
 Leu Pro Val Pro Gly His Ile Pro Arg Pro Pro Tyr Val Gly Ser Asn
 65 70 75 80
 Lys Met Pro Glu Ile Ser Ser Glu Arg Gln Met Gln Asp Lys Asp Thr
 85 90 95
 Ile Val His Met Lys Ala Ala Cys Glu Leu Ala Ala Arg Val Leu Gln
 100 105 110
 Asn Ala Gly Lys Leu Val Lys Pro Ser Val Thr Thr Asp Glu Ile Asp
 115 120 125
 Lys Ala Val His Lys Met Ile Ile Asp Ala Gly Ala Tyr Pro Ser Pro
 130 135 140
 Leu Gly Tyr Gly Gly Phe Pro Lys Ser Val Cys Thr Ser Val Asn Glu
 145 150 155 160
 Cys Met Cys His Gly Ile Pro Asp Ser Arg Glu Leu Lys Asp Gly Asp
 165 170 175
 Ile Ile Asn Ile Asp Val Thr Val Tyr Leu Asn Gly Phe His Gly Asp
 180 185 190
 Thr Ser Lys Thr Phe Phe Cys Gly Glu Val Asp Glu Ala Ala Lys Arg
 195 200 205
 Leu Val Lys Val Thr Glu Glu Cys Met Leu Arg Gly Ile Ser Ser Cys
 210 215 220
 Lys His Gly Val Ser Phe Lys Lys Ile Gly Arg Arg Ile Ser Glu His
 225 230 235 240
 Ala Glu Arg Asn Gly Phe Gly Val Val Glu Gln Phe Val Gly His Gly
 245 250 255
 Val Gly Arg Val Phe His Ser Gln Pro Ile Ile Tyr His Gln Arg Asn
 260 265 270
 Asn Met Pro Gly Gln Met Val Glu Gly Gln Thr Phe Thr Ile Glu Pro
 275 280 285
 Ile Leu Thr Met Gly Ser Asn Ser Asn Ser Ile Glu Cys Asp Met Trp
 290 295 300
 Glu Asp Gly Trp Thr Ala Val Thr Thr Asp Gly Ser Leu Ala Ala Gln
 305 310 315 320
 Phe Glu His Thr Ile Leu Ile Thr Arg Thr Gly Ala Glu Ile Leu Thr
 325 330 335
 Lys Cys

<210> 126
 <211> 1317
 <212> DNA
 <213> Zea mays subsp. mays

<220>
 <221> CDS
 <222> (155)..(1159)

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ggactaccaa tccaaactgg cgacgaccct gctgccaccc cacagcagat ttgaggagcg 120

PF59082SeqList_PF59082.txt

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ccg ttg ctc tcg ggt ggc cga gga gga aat aca tgc cta cag aag aag	223
Pro Leu Leu Ser Gly Gly Arg Gly Gly Asn Thr Cys Leu Gln Lys Lys	
10 15 20	
ccc ttc ttt gtc caa gca aag aga cta gtg ggg atg gag aaa gca agt	271
Pro Phe Phe Val Gln Ala Lys Arg Leu Val Gly Met Glu Lys Ala Ser	
25 30 35	
acg agg cca gga aca caa gag tct gga cag aca aag aaa aga gca ccc	319
Thr Arg Pro Gly Thr Gln Glu Ser Gly Gln Thr Lys Lys Arg Ala Pro	
40 45 50 55	
ctg gtt cgt gga act gtt agc cca cct ctt cca gta cca gga aac ata	367
Leu Val Arg Gly Thr Val Ser Pro Pro Leu Pro Val Pro Gly Asn Ile	
60 65 70	
cct cgg cct cct tat gtc ggc aca gaa tat gta cca gag ata gca aaa	415
Pro Arg Pro Pro Tyr Val Gly Thr Glu Tyr Val Pro Glu Ile Ala Lys	
75 80 85	
gag ata caa atg cat gac aaa gag ggc att gtc cac atg aga gct gct	463
Glu Ile Gln Met His Asp Lys Glu Gly Ile Val His Met Arg Ala Ala	
90 95 100	
tgc gag ctc gcg gct cgt gtt ctt gac tat gca gga acg tta gtg aaa	511
Cys Glu Leu Ala Ala Arg Val Leu Asp Tyr Ala Gly Thr Leu Val Lys	
105 110 115	
ccc tct gta aca aca gac gaa att gat aaa gca gtg cac aag atg atc	559
Pro Ser Val Thr Thr Asp Glu Ile Asp Lys Ala Val His Lys Met Ile	
120 125 130 135	
atc gat gct gga gcc tat cca tca cca ctt gga tat ggt ggg ttt cca	607
Ile Asp Ala Gly Ala Tyr Pro Ser Pro Leu Gly Tyr Gly Gly Phe Pro	
140 145 150	
aaa agt gta tgc acc tca gtg aat gag tgc atg tgc cat gga att cct	655
Lys Ser Val Cys Thr Ser Val Asn Glu Cys Met Cys His Gly Ile Pro	
155 160 165	
gat tca cgc gag cta cag gat gga gac ata att aac att gat gtc act	703
Asp Ser Arg Glu Leu Gln Asp Gly Asp Ile Ile Asn Ile Asp Val Thr	
170 175 180	
gtc tac ttg aat ggt tat cat ggg gat acc tca aaa aca ttt ctt tgt	751
Val Tyr Leu Asn Gly Tyr His Gly Asp Thr Ser Lys Thr Phe Leu Cys	
185 190 195	
gga gaa gtc gat gaa gcc agt aaa cga ctt gtg aag gtt act gaa gag	799
Gly Glu Val Asp Glu Ala Ser Lys Arg Leu Val Lys Val Thr Glu Glu	
200 205 210 215	
tgc ttg ctc agg ggc ata tca aca tgc aaa cat ggt acc agc ttt aag	847
Cys Leu Leu Arg Gly Ile Ser Thr Cys Lys His Gly Thr Ser Phe Lys	
220 225 230	
aag att ggc aga aga ata agt gag cat gct gag agg aac ggt ttt ggt	895
Lys Ile Gly Arg Arg Ile Ser Glu His Ala Glu Arg Asn Gly Phe Gly	
235 240 245	
gtt gtg gag tgt ttt gtt ggg cat gga gtc ggc agg gta ttt cac tca	943
Val Val Glu Cys Phe Val Gly His Gly Val Gly Arg Val Phe His Ser	
250 255 260	
gaa cca att atc tat cac cag agg aac aac aga ccg ggc cag atg att	991
Glu Pro Ile Ile Tyr His Gln Arg Asn Asn Arg Pro Gly Gln Met Ile	
265 270 275	
gaa ggg cag act ttc aca ata gag ccg atc ata tcg atg ggg agc atc	1039
Glu Gly Gln Thr Phe Thr Ile Glu Pro Ile Ile Ser Met Gly Ser Ile	
280 285 290 295	
gag tgc gac atg tgg gac gac ggc tgg act gcc gtg acg acg gac ggc	1087
Glu Cys Asp Met Trp Asp Asp Gly Trp Thr Ala Val Thr Thr Asp Gly	
300 305 310	
agc ttg gcg gcg cag ttc gag cac acc ata ctg atc acc agg acc gga	1135
Ser Leu Ala Ala Gln Phe Glu His Thr Ile Leu Ile Thr Arg Thr Gly	
315 320 325	
gcc gag atc ctc acc aag tgc taggaggaaa ggaaatcgca tgtgcccgat	1186
Ala Glu Ile Leu Thr Lys Cys	
330	
agccgacggt aggtaatctg tattcgtgag gtggtgagga tgcttgaggt gacctat	1246

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<210> 127

<211> 334

<212> PRT

<213> Zea mays subsp. mays

<400> 127

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Val Gly Met Glu Lys Ala Ser Thr Arg Pro Gly Thr Gln Glu Ser Gly
35     40     45
Gln Thr Lys Lys Arg Ala Pro Leu Val Arg Gly Thr Val Ser Pro Pro
50     55     60
Leu Pro Val Pro Gly Asn Ile Pro Arg Pro Pro Tyr Val Gly Thr Glu
65     70     75     80
Tyr Val Pro Glu Ile Ala Lys Glu Ile Gln Met His Asp Lys Glu Gly
85     90     95
Ile Val His Met Arg Ala Ala Cys Glu Leu Ala Ala Arg Val Leu Asp
100    105    110
Tyr Ala Gly Thr Leu Val Lys Pro Ser Val Thr Thr Asp Glu Ile Asp
115    120    125
Lys Ala Val His Lys Met Ile Ile Asp Ala Gly Ala Tyr Pro Ser Pro
130    135    140
Leu Gly Tyr Gly Gly Phe Pro Lys Ser Val Cys Thr Ser Val Asn Glu
145    150    155    160
Cys Met Cys His Gly Ile Pro Asp Ser Arg Glu Leu Gln Asp Gly Asp
165    170    175
Ile Ile Asn Ile Asp Val Thr Val Tyr Leu Asn Gly Tyr His Gly Asp
180    185    190
Thr Ser Lys Thr Phe Leu Cys Gly Glu Val Asp Glu Ala Ser Lys Arg
195    200    205
Leu Val Lys Val Thr Glu Glu Cys Leu Leu Arg Gly Ile Ser Thr Cys
210    215    220
Lys His Gly Thr Ser Phe Lys Lys Ile Gly Arg Arg Ile Ser Glu His
225    230    235    240
Ala Glu Arg Asn Gly Phe Gly Val Val Glu Cys Phe Val Gly His Gly
245    250    255
Val Gly Arg Val Phe His Ser Glu Pro Ile Ile Tyr His Gln Arg Asn
260    265    270
Asn Arg Pro Gly Gln Met Ile Glu Gly Gln Thr Phe Thr Ile Glu Pro
275    280    285
Ile Ile Ser Met Gly Ser Ile Glu Cys Asp Met Trp Asp Asp Gly Trp
290    295    300
Thr Ala Val Thr Thr Asp Gly Ser Leu Ala Ala Gln Phe Glu His Thr
305    310    315    320
Ile Leu Ile Thr Arg Thr Gly Ala Glu Ile Leu Thr Lys Cys
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<210> 128

<211> 1317

<212> DNA

<213> Zea mays subsp. mays

<220>

<221> CDS

<222> (257)..(1159)

<400> 128

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PF59082SeqList_PF59082.txt

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gctctcgggt ggccgaggag gaaatacatg cctacagaag aagcccttct ttgtccaagc	240
aaagagacta gtgggg atg gag aaa gca agt acg agg cca gga aca caa gag	292
Met Glu Lys Ala Ser Thr Arg Pro Gly Thr Gln Glu	
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tct gga cag aca aag aaa aga gca ccc ctg gtt cgt gga act gtt agc	340
Ser Gly Gln Thr Lys Lys Arg Ala Pro Leu Val Arg Gly Thr Val Ser	
15 20 25	
cca cct ctt cca gta cca gga aac ata cct cgg cct cct tat gtc ggc	388
Pro Pro Leu Pro Val Pro Gly Asn Ile Pro Arg Pro Pro Tyr Val Gly	
30 35 40	
aca gaa tat gta cca gag ata gca aaa gag ata caa atg cat gac aaa	436
Thr Glu Tyr Val Pro Glu Ile Ala Lys Glu Ile Gln Met His Asp Lys	
45 50 55 60	
gag ggc att gtc cac atg aga gct gct tgc gag ctc gcg gct cgt gtt	484
Glu Gly Ile Val His Met Arg Ala Ala Cys Glu Leu Ala Ala Arg Val	
65 70 75	
ctt gac tat gca gga acg tta gtg aaa ccc tct gta aca aca gac gaa	532
Leu Asp Tyr Ala Gly Thr Leu Val Lys Pro Ser Val Thr Thr Asp Glu	
80 85 90	
att gat aaa gca gtg cac aag atg atc atc gat gct gga gcc tat cca	580
Ile Asp Lys Ala Val His Lys Met Ile Ile Asp Ala Gly Ala Tyr Pro	
95 100 105	
tca cca ctt gga tat ggt ggg ttt cca aaa agt gta tgc acc tca gtg	628
Ser Pro Leu Gly Tyr Gly Gly Phe Pro Lys Ser Val Cys Thr Ser Val	
110 115 120	
aat gag tgc atg tgc cat gga att cct gat tca cgc gag cta cag gat	676
Asn Glu Cys Met Cys His Gly Ile Pro Asp Ser Arg Glu Leu Gln Asp	
125 130 135 140	
gga gac ata att aac att gat gtc act gtc tac ttg aat ggt tat cat	724
Gly Asp Ile Ile Asn Ile Asp Val Thr Val Tyr Leu Asn Gly Tyr His	
145 150 155	
ggg gat acc tca aaa aca ttt ctt tgt gga gaa gtc gat gaa gcc agt	772
Gly Asp Thr Ser Lys Thr Phe Leu Cys Gly Glu Val Asp Glu Ala Ser	
160 165 170	
aaa cga ctt gtg aag gtt act gaa gag tgc ttg ctc agg ggc ata tca	820
Lys Arg Leu Val Lys Val Thr Glu Glu Cys Leu Leu Arg Gly Ile Ser	
175 180 185	
aca tgc aaa cat ggt acc agc ttt aag aag att ggc aga aga ata agt	868
Thr Cys Lys His Gly Thr Ser Phe Lys Lys Ile Gly Arg Arg Ile Ser	
190 195 200	
gag cat gct gag agg aac ggt ttt ggt gtt gtg gag tgt ttt gtt ggg	916
Glu His Ala Glu Arg Asn Gly Phe Gly Val Val Glu Cys Phe Val Gly	
205 210 215 220	
cat gga gtc ggc agg gta ttt cac tca gaa cca att atc tat cac cag	964
His Gly Val Gly Arg Val Phe His Ser Glu Pro Ile Ile Tyr His Gln	
225 230 235	
agg aac aac aga ccg ggc cag atg att gaa ggg cag act ttc aca ata	1012
Arg Asn Asn Arg Pro Gly Gln Met Ile Glu Gly Gln Thr Phe Thr Ile	
240 245 250	
gag ccg atc ata tcg atg ggg agc atc gag tgc gac atg tgg gac gac	1060
Glu Pro Ile Ile Ser Met Gly Ser Ile Glu Cys Asp Met Trp Asp Asp	
255 260 265	
ggc tgg act gcc gtg acg acg gac ggc agc ttg gcg gcg cag ttc gag	1108
Gly Trp Thr Ala Val Thr Thr Asp Gly Ser Leu Ala Ala Gln Phe Glu	
270 275 280	
cac acc ata ctg atc acc agg acc gga gcc gag atc ctc acc aag tgc	1156
His Thr Ile Leu Ile Thr Arg Thr Gly Ala Glu Ile Leu Thr Lys Cys	
285 290 295 300	
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gtgggtgagga tgcttgaggt gacctatttt gtctcgcaaa atgggcgtgc tacagaatag 1276

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<210> 129

<211> 300

<212> PRT

<213> Zea mays subsp. mays

<400> 129

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Lys Lys Arg Ala Pro Leu Val Arg Gly Thr Val Ser Pro Pro Leu Pro
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Val Pro Gly Asn Ile Pro Arg Pro Pro Tyr Val Gly Thr Glu Tyr Val
      35      40      45
Pro Glu Ile Ala Lys Glu Ile Gln Met His Asp Lys Glu Gly Ile Val
      50      55      60
His Met Arg Ala Ala Cys Glu Leu Ala Ala Arg Val Leu Asp Tyr Ala
65      70      75      80
Gly Thr Leu Val Lys Pro Ser Val Thr Thr Asp Glu Ile Asp Lys Ala
      85      90      95
Val His Lys Met Ile Ile Asp Ala Gly Ala Tyr Pro Ser Pro Leu Gly
      100      105      110
Tyr Gly Gly Phe Pro Lys Ser Val Cys Thr Ser Val Asn Glu Cys Met
      115      120      125
Cys His Gly Ile Pro Asp Ser Arg Glu Leu Gln Asp Gly Asp Ile Ile
130      135      140
Asn Ile Asp Val Thr Val Tyr Leu Asn Gly Tyr His Gly Asp Thr Ser
145      150      155      160
Lys Thr Phe Leu Cys Gly Glu Val Asp Glu Ala Ser Lys Arg Leu Val
      165      170      175
Lys Val Thr Glu Glu Cys Leu Leu Arg Gly Ile Ser Thr Cys Lys His
      180      185      190
Gly Thr Ser Phe Lys Lys Ile Gly Arg Arg Ile Ser Glu His Ala Glu
      195      200      205
Arg Asn Gly Phe Gly Val Val Glu Cys Phe Val Gly His Gly Val Gly
210      215      220
Arg Val Phe His Ser Glu Pro Ile Ile Tyr His Gln Arg Asn Asn Arg
225      230      235      240
Pro Gly Gln Met Ile Glu Gly Gln Thr Phe Thr Ile Glu Pro Ile Ile
      245      250      255
Ser Met Gly Ser Ile Glu Cys Asp Met Trp Asp Asp Gly Trp Thr Ala
260      265      270
Val Thr Thr Asp Gly Ser Leu Ala Ala Gln Phe Glu His Thr Ile Leu
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<211> 1438

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<213> Glycine max

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<222> (46)..(1146)

<400> 130

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Met Ala Leu Thr

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Ala Ser Leu Ala Asn Asn Ala Phe Leu Lys Ile Pro Thr Leu His His
5 10 15 20

ggc gaa tgc tca ctg tct tcg tca tcc ttc atc ggt tct cgg ctc aca 153

PF59082SeqList_PF59082.txt

Gly	Glu	Cys	Ser	Leu	Ser	Ser	Ser	Ser	Phe	Ile	Gly	Ser	Arg	Leu	Thr	
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Leu	Ser	Arg	Ser	Ser	Thr	Leu	Gln	Gly	Asn	Gln	Leu	Leu	Ser	Arg	Lys	
caa	ttc	gtg	ggt	ttc	gcg	agg	aag	att	tcg	ggg	ttg	gag	gag	gcc	atg	249
Gln	Phe	Val	Val	Phe	Ala	Arg	Lys	Ile	Ser	Gly	Leu	Glu	Glu	Ala	Met	
aat	atc	aga	aga	gaa	cgt	gaa	ggt	cga	ggt	gtg	cca	aag	ttt	aag	aaa	297
Asn	Ile	Arg	Arg	Glu	Arg	Glu	Val	Arg	Val	Val	Pro	Lys	Phe	Lys	Lys	
agg	cct	cca	tta	agg	cgt	ggg	aga	gta	tca	cca	cat	ctc	cct	ggt	cct	345
Arg	Pro	Pro	Leu	Arg	Arg	Gly	Arg	Val	Ser	Pro	His	Leu	Pro	Val	Pro	
gac	cac	ata	cca	agg	cct	cct	tat	gta	ggt	tca	gat	ata	ctt	cca	gaa	393
Asp	His	Ile	Pro	Arg	Pro	Pro	Tyr	Val	Gly	Ser	Asp	Ile	Leu	Pro	Glu	
att	gca	agt	gag	cat	caa	att	cat	gat	tct	gaa	ggt	ata	gct	aaa	atg	441
Ile	Ala	Ser	Glu	His	Gln	Ile	His	Asp	Ser	Glu	Gly	Ile	Ala	Lys	Met	
agg	gct	gca	ggt	gag	ctt	gca	gcg	cgt	gtc	tta	aac	ttt	gca	gga	act	489
Arg	Ala	Ala	Gly	Glu	Leu	Ala	Ala	Arg	Val	Leu	Asn	Phe	Ala	Gly	Thr	
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Met	Val	Arg	Pro	Ser	Ile	Thr	Thr	Asn	Glu	Ile	Asp	Lys	Ala	Val	His	
cag	atg	ata	att	gat	gct	ggt	gct	tat	ccc	tca	ccc	ctt	ggc	tat	ggt	585
Gln	Met	Ile	Ile	Asp	Ala	Gly	Ala	Tyr	Pro	Ser	Pro	Leu	Gly	Tyr	Gly	
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Gly	Phe	Pro	Lys	Ser	Val	Cys	Thr	Ser	Val	Asn	Glu	Cys	Met	Cys	His	
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Gly	Ile	Pro	Asp	Ser	Arg	Gln	Leu	Gln	Asn	Gly	Asp	Ile	Ile	Asn	Ile	
gat	gtg	aca	gtc	tac	ctg	gat	gga	tat	cac	gga	gac	acg	tca	aag	aca	729
Asp	Val	Thr	Val	Tyr	Leu	Asp	Gly	Tyr	His	Gly	Asp	Thr	Ser	Lys	Thr	
ttt	ttt	tgt	ggg	gaa	gtc	agt	gat	gaa	ctg	aaa	aat	ctt	ggt	aag	gta	777
Phe	Phe	Cys	Gly	Glu	Val	Ser	Asp	Glu	Leu	Lys	Asn	Leu	Val	Lys	Val	
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Thr	Glu	Glu	Cys	Leu	Glu	Lys	Gly	Ile	Ala	Ala	Cys	Lys	Asp	Gly	Ala	
ctc	ttt	agg	aaa	att	gga	aag	aga	atc	agt	gag	cat	gct	gaa	aag	tat	873
Leu	Phe	Arg	Lys	Ile	Gly	Lys	Arg	Ile	Ser	Glu	His	Ala	Glu	Lys	Tyr	
ggc	tat	ggt	gta	gtg	gag	cgt	ttt	ggt	ggg	cat	ggt	gtg	gga	aca	gtg	921
Gly	Tyr	Gly	Val	Val	Glu	Arg	Phe	Val	Gly	His	Gly	Val	Gly	Thr	Val	
ttt	cat	tct	gaa	cca	att	att	ata	cac	aat	cgc	aat	gag	aag	gca	ggc	969
Phe	His	Ser	Glu	Pro	Ile	Ile	Ile	His	Asn	Arg	Asn	Glu	Lys	Ala	Gly	
cgc	atg	ggt	gaa	ggt	caa	aca	ttt	aca	att	gag	ccg	att	ctt	tca	atg	1017
Arg	Met	Val	Glu	Gly	Gln	Thr	Phe	Thr	Ile	Glu	Pro	Ile	Leu	Ser	Met	
gga	agc	att	gat	tcc	att	aca	tgg	cca	gac	aac	tgg	aca	aca	cta	aca	1065
Gly	Ser	Ile	Asp	Ser	Ile	Thr	Trp	Pro	Asp	Asn	Trp	Thr	Thr	Leu	Thr	
gct	gat	ggt	agt	ccg	gct	gca	cag	ttt	gag	cat	acc	att	ttg	ata	act	1113
Ala	Asp	Gly	Ser	Pro	Ala	Ala	Gln	Phe	Glu	His	Thr	Ile	Leu	Ile	Thr	
aag	act	gga	gcc	gaa	att	ttg	act	aca	tgt	tgac	atg	gta	att	ctt	gtt	1163
Lys	Thr	Gly	Ala	Glu	Ile	Leu	Thr	Thr	Cys							
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tgcccttaaa	tcaatttgct	tctggaatat	tatgctctgg	caagtaaaga	ttgccttcag											1283

PF59082SeqList_PF59082.txt

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tgaattggta gtctaataaa aaaaaaaaaa aaaaa 1438

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 <211> 366
 <212> PRT
 <213> Glycine max

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 35 40 45
 Leu Ser Arg Lys Gln Phe Val Phe Ala Arg Lys Ile Ser Gly Leu
 50 55 60
 Glu Glu Ala Met Asn Ile Arg Arg Glu Arg Glu Val Arg Val Val Pro
 65 70 75 80
 Lys Phe Lys Lys Arg Pro Pro Leu Arg Arg Gly Arg Val Ser Pro His
 85 90 95
 Leu Pro Val Pro Asp His Ile Pro Arg Pro Pro Tyr Val Gly Ser Asp
 100 105 110
 Ile Leu Pro Glu Ile Ala Ser Glu His Gln Ile His Asp Ser Glu Gly
 115 120 125
 Ile Ala Lys Met Arg Ala Ala Gly Glu Leu Ala Ala Arg Val Leu Asn
 130 135 140
 Phe Ala Gly Thr Met Val Arg Pro Ser Ile Thr Thr Asn Glu Ile Asp
 145 150 155 160
 Lys Ala Val His Gln Met Ile Ile Asp Ala Gly Ala Tyr Pro Ser Pro
 165 170 175
 Leu Gly Tyr Gly Gly Phe Pro Lys Ser Val Cys Thr Ser Val Asn Glu
 180 185 190
 Cys Met Cys His Gly Ile Pro Asp Ser Arg Gln Leu Gln Asn Gly Asp
 195 200 205
 Ile Ile Asn Ile Asp Val Thr Val Tyr Leu Asp Gly Tyr His Gly Asp
 210 215 220
 Thr Ser Lys Thr Phe Phe Cys Gly Glu Val Ser Asp Glu Leu Lys Asn
 225 230 235 240
 Leu Val Lys Val Thr Glu Glu Cys Leu Glu Lys Gly Ile Ala Ala Cys
 245 250 255
 Lys Asp Gly Ala Leu Phe Arg Lys Ile Gly Lys Arg Ile Ser Glu His
 260 265 270
 Ala Glu Lys Tyr Gly Tyr Gly Val Val Glu Arg Phe Val Gly His Gly
 275 280 285
 Val Gly Thr Val Phe His Ser Glu Pro Ile Ile Ile His Asn Arg Asn
 290 295 300
 Glu Lys Ala Gly Arg Met Val Glu Gly Gln Thr Phe Thr Ile Glu Pro
 305 310 315 320
 Ile Leu Ser Met Gly Ser Ile Asp Ser Ile Thr Trp Pro Asp Asn Trp
 325 330 335
 Thr Thr Leu Thr Ala Asp Gly Ser Pro Ala Ala Gln Phe Glu His Thr
 340 345 350
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 <211> 1071
 <212> DNA
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PF59082SeqList_PF59082.txt

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<400> 132

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Phe	Ile	Gly	Asp	Arg	Leu	Leu	Arg	Cys	Ser	Thr	Ser	Arg	His	Gln	Pro	
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ctt	cct	caa	cta	ttc	cgt	tac	aac	cct	gga	acc	aag	cat	gtt	tcg	atg	144
Leu	Pro	Gln	Leu	Phe	Arg	Tyr	Asn	Pro	Gly	Thr	Lys	His	Val	Ser	Met	
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Gln	Leu	Ser	Arg	Thr	Leu	Ser	Gly	Leu	Thr	Asn	Leu	Phe	Phe	Asn	Arg	
	50					55					60					
aga	aat	ttg	gat	gaa	ttg	cct	aac	agc	aag	cgt	aaa	cgt	ctg	aga	cct	240
Arg	Asn	Leu	Asp	Glu	Leu	Pro	Asn	Ser	Lys	Arg	Lys	Arg	Leu	Arg	Pro	
	65				70				75						80	
ggg	aaa	gtt	tct	ccg	cgg	cga	cag	gtg	ccg	aag	aat	ata	ccg	agg	cct	288
Gly	Lys	Val	Ser	Pro	Arg	Arg	Gln	Val	Pro	Lys	Asn	Ile	Pro	Arg	Pro	
				85				90					95			
ccg	tat	gtg	aat	tct	atg	att	cct	cca	ggg	att	gcc	agt	gga	gct	gaa	336
Pro	Tyr	Val	Asn	Ser	Met	Ile	Pro	Pro	Gly	Ile	Ala	Ser	Gly	Ala	Glu	
			100					105					110			
gtg	cat	gac	aag	aaa	ggg	ata	gaa	tgc	atg	aga	gct	tct	gga	agg	ctt	384
Val	His	Asp	Lys	Lys	Gly	Ile	Glu	Cys	Met	Arg	Ala	Ser	Gly	Arg	Leu	
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Ala	Ala	Gln	Val	Leu	Gln	Tyr	Ala	Gly	Thr	Leu	Val	Lys	Pro	Gly	Ile	
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Thr	Thr	Asp	Glu	Ile	Asp	Gln	Ala	Val	His	Gln	Met	Ile	Ile	Asp	Asn	
	145				150				155						160	
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Gly	Ala	Tyr	Pro	Ser	Pro	Leu	Gly	Tyr	Gly	Ser	Phe	Pro	Lys	Ser	Val	
				165				170					175			
tgc	aca	tct	gta	aat	gaa	tgc	att	tgc	gga	ata	cca	gat	tcc	cgt		576
Cys	Thr	Ser	Val	Asn	Glu	Cys	Ile	Cys	His	Gly	Ile	Pro	Asp	Ser	Arg	
			180					185					190			
gcc	ctt	gag	gat	ggg	gat	ata	atc	aac	att	gat	gtt	act	gtt	tat	cta	624
Ala	Leu	Glu	Asp	Gly	Asp	Ile	Ile	Asn	Ile	Asp	Val	Thr	Val	Tyr	Leu	
		195					200					205				
aat	ggc	tat	cat	ggg	gac	aca	tca	gca	act	ttc	tat	tgt	gga	gat	gtt	672
Asn	Gly	Tyr	His	Gly	Asp	Thr	Ser	Ala	Thr	Phe	Tyr	Cys	Gly	Asp	Val	
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gat	gat	gaa	gct	aaa	aaa	cta	gtt	cag	gta	act	aaa	gaa	tgc	cta	gat	720
Asp	Asp	Glu	Ala	Lys	Lys	Leu	Val	Gln	Val	Thr	Lys	Glu	Cys	Leu	Asp	
	225				230				235					240		
aaa	gca	ata	tca	ata	tgt	gca	cca	gga	gtg	gag	ttc	aag	aaa	att	ggc	768
Lys	Ala	Ile	Ser	Ile	Cys	Ala	Pro	Gly	Val	Glu	Phe	Lys	Lys	Ile	Gly	
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aaa	aca	att	cat	gat	cat	gca	gat	aaa	tat	cgt	tat	ggg	gtt	gtc	cga	816
Lys	Thr	Ile	His	Asp	His	Ala	Asp	Lys	Tyr	Arg	Tyr	Gly	Val	Val	Arg	
			260				265						270			
cag	ttt	gtt	ggc	cat	gga	gtt	gga	agt	gtt	ttt	cat	gct	gat	cct	gtt	864
Gln	Phe	Val	Gly	His	Gly	Val	Gly	Ser	Val	Phe	His	Ala	Asp	Pro	Val	
		275					280					285				
att	ctt	cac	tat	aga	aac	aat	gaa	agt	gga	cga	atg	gtg	cta	aat	caa	912
Ile	Leu	His	Tyr	Arg	Asn	Asn	Glu	Ser	Gly	Arg	Met	Val	Leu	Asn	Gln	
	290				295						300					
acc	ttt	aca	att	gaa	cct	atg	ctg	act	att	ggc	agc	atc	aat	cct	gtg	960
Thr	Phe	Thr	Ile	Glu	Pro	Met	Leu	Thr	Ile	Gly	Ser	Ile	Asn	Pro	Val	
	305				310					315					320	
atg	tgg	aat	gac	gac	tgg	aca	gtt	gta	acg	gaa	gat	gga	agc	ctt	tca	1008
Met	Trp	Asn	Asp	Asp	Trp	Thr	Val	Val	Thr	Glu	Asp	Gly	Ser	Leu	Ser	
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PF59082SeqList_PF59082.txt

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atg act caa tgc tga 1071
Met Thr Gln Cys
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<210> 133
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<212> PRT
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Leu Pro Gln Leu Phe Arg Tyr Asn Pro Gly Thr Lys His Val Ser Met
35 40 45
Gln Leu Ser Arg Thr Leu Ser Gly Leu Thr Asn Leu Phe Phe Asn Arg
50 55 60
Arg Asn Leu Asp Glu Leu Pro Asn Ser Lys Arg Lys Arg Leu Arg Pro
65 70 75 80
Gly Lys Val Ser Pro Arg Arg Gln Val Pro Lys Asn Ile Pro Arg Pro
85 90 95
Pro Tyr Val Asn Ser Met Ile Pro Pro Gly Ile Ala Ser Gly Ala Glu
100 105 110
Val His Asp Lys Lys Gly Ile Glu Cys Met Arg Ala Ser Gly Arg Leu
115 120 125
Ala Ala Gln Val Leu Gln Tyr Ala Gly Thr Leu Val Lys Pro Gly Ile
130 135 140
Thr Thr Asp Glu Ile Asp Gln Ala Val His Gln Met Ile Ile Asp Asn
145 150 155 160
Gly Ala Tyr Pro Ser Pro Leu Gly Tyr Gly Ser Phe Pro Lys Ser Val
165 170 175
Cys Thr Ser Val Asn Glu Cys Ile Cys His Gly Ile Pro Asp Ser Arg
180 185 190
Ala Leu Glu Asp Gly Asp Ile Ile Asn Ile Asp Val Thr Val Tyr Leu
195 200 205
Asn Gly Tyr His Gly Asp Thr Ser Ala Thr Phe Tyr Cys Gly Asp Val
210 215 220
Asp Asp Glu Ala Lys Lys Leu Val Gln Val Thr Lys Glu Cys Leu Asp
225 230 235 240
Lys Ala Ile Ser Ile Cys Ala Pro Gly Val Glu Phe Lys Lys Ile Gly
245 250 255
Lys Thr Ile His Asp His Ala Asp Lys Tyr Arg Tyr Gly Val Val Arg
260 265 270
Gln Phe Val Gly His Gly Val Gly Ser Val Phe His Ala Asp Pro Val
275 280 285
Ile Leu His Tyr Arg Asn Asn Glu Ser Gly Arg Met Val Leu Asn Gln
290 295 300
Thr Phe Thr Ile Glu Pro Met Leu Thr Ile Gly Ser Ile Asn Pro Val
305 310 315 320
Met Trp Asn Asp Asp Trp Thr Val Val Thr Glu Asp Gly Ser Leu Ser
325 330 335
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340 345 350
Met Thr Gln Cys
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PF59082SeqList_PF59082.txt

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1      5      10      15
aca ctc cat cat ggc gaa tgc tca ctg tct tcg tca tcc ttc atc ggt      96
Thr Leu His His Gly Glu Cys Ser Leu Ser Ser Ser Phe Ile Gly
20      25      30
tct cgg ctc aca ctc tcg cgc tct tct act ctt caa ggg aac caa ttg      144
Ser Arg Leu Thr Leu Ser Arg Ser Ser Thr Leu Gln Gly Asn Gln Leu
35      40      45
ctt tcg aga aag caa ttc gtg gtt ttc gcg agg aag att tcg ggg ttg      192
Leu Ser Arg Lys Gln Phe Val Val Phe Ala Arg Lys Ile Ser Gly Leu
50      55      60
gag gag gcc atg aat atc aga aga gaa cgt gaa gtt cga gtt gtg cca      240
Glu Glu Ala Met Asn Ile Arg Arg Glu Arg Glu Val Arg Val Val Pro
65      70      75
aag ttt aag aaa agg cct cca tta agg cgt ggg aga gta tca cca cat      288
Lys Phe Lys Lys Arg Pro Pro Leu Arg Arg Gly Arg Val Ser Pro His
85      90      95
ctc cct gtt cct gac cac ata cca agg cct cct tat gta ggt tca gat      336
Leu Pro Val Pro Asp His Ile Pro Arg Pro Pro Tyr Val Gly Ser Asp
100      105      110
ata ctt cca gaa att gca agt gag cat caa att cat gat tct gaa ggt      384
Ile Leu Pro Glu Ile Ala Ser Glu His Gln Ile His Asp Ser Glu Gly
115      120      125
ata gct aaa atg agg gct gca ggt gag ctt gca gcg cgt gtc tta aac      432
Ile Ala Lys Met Arg Ala Ala Gly Glu Leu Ala Ala Arg Val Leu Asn
130      135      140
ttt gca gga act atg gtt agg cct tcc ata aca act aat gag att gat      480
Phe Ala Gly Thr Met Val Arg Pro Ser Ile Thr Thr Asn Glu Ile Asp
145      150      155
aaa gca gtg cac cag atg ata att gat gct ggt gct tat ccc tca ccc      528
Lys Ala Val His Gln Met Ile Ile Asp Ala Gly Ala Tyr Pro Ser Pro
165      170      175
ctt ggc tat ggt gga ttt ccg aaa agc ggt gtc aca tca gtt aat gag      576
Leu Gly Tyr Gly Gly Phe Pro Lys Ser Val Cys Thr Ser Val Asn Glu
180      185      190
tgc atg tgc cat gga ata cct gat tct cgg cag tta cag aat ggt gat      624
Cys Met Cys His Gly Ile Pro Asp Ser Arg Gln Leu Gln Asn Gly Asp
195      200      205
att att aac att gat gtg aca gtc tac ctg gat gga tat cac gga gac      672
Ile Ile Asn Ile Asp Val Thr Val Tyr Leu Asp Gly Tyr His Gly Asp
210      215      220
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225      230      235
ctt gtc aag gta act gaa gaa tgc ctg gag aag gga ata gct gcg tgc      768
Leu Val Lys Val Thr Glu Glu Cys Leu Glu Lys Gly Ile Ala Ala Cys
245      250      255
aag gac ggt gct ctc ttt agg aaa att gga aag aga atc agt gag cat      816
Lys Asp Gly Ala Leu Phe Arg Lys Ile Gly Lys Arg Ile Ser Glu His
260      265      270
gct gaa aag tat ggc tat ggt gta gtg gag cgt ttt gtt ggg cat ggt      864
Ala Glu Lys Tyr Gly Tyr Gly Val Val Glu Arg Phe Val Gly His Gly
275      280      285
gtg gga aca gtg ttc cat tct gaa cca att att ata cac aat cgc aat      912
Val Gly Thr Val Phe His Ser Glu Pro Ile Ile Ile His Asn Arg Asn
290      295      300
gag aag gca ggc cgc atg att gaa ggt caa aca ttt aca att gag ccg      960
Glu Lys Ala Gly Arg Met Ile Glu Gly Gln Thr Phe Thr Ile Glu Pro
305      310      315
att ctt tcg atg gga agc att gat tcc att aca tgg cct gac aac tgg      1008
Ile Leu Ser Met Gly Ser Ile Asp Ser Ile Thr Trp Pro Asp Asn Trp
325      330      335
aca aca ata aca gct gat ggt agt ccg gct gca cag ttt gag cat acc      1056
Thr Thr Ile Thr Ala Asp Gly Ser Pro Ala Ala Gln Phe Glu His Thr
340      345      350
att ttg ata act aag act gga gcc gaa att ttg act aaa tgt tga      1101
Ile Leu Ile Thr Lys Thr Gly Ala Glu Ile Leu Thr Lys Cys

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355

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<211> 366
<212> PRT
<213> Glycine max

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Thr Leu His His Gly Glu Cys Ser Leu Ser Ser Ser Phe Ile Gly
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Ser Arg Leu Thr Leu Ser Arg Ser Ser Thr Leu Gln Gly Asn Gln Leu
35 40 45
Leu Ser Arg Lys Gln Phe Val Phe Ala Arg Lys Ile Ser Gly Leu
50 55 60
Glu Glu Ala Met Asn Ile Arg Arg Glu Arg Glu Val Arg Val Val Pro
65 70 75 80
Lys Phe Lys Lys Arg Pro Pro Leu Arg Arg Gly Arg Val Ser Pro His
85 90 95
Leu Pro Val Pro Asp His Ile Pro Arg Pro Pro Tyr Val Gly Ser Asp
100 105 110
Ile Leu Pro Glu Ile Ala Ser Glu His Gln Ile His Asp Ser Glu Gly
115 120 125
Ile Ala Lys Met Arg Ala Ala Gly Glu Leu Ala Ala Arg Val Leu Asn
130 135 140
Phe Ala Gly Thr Met Val Arg Pro Ser Ile Thr Thr Asn Glu Ile Asp
145 150 155 160
Lys Ala Val His Gln Met Ile Ile Asp Ala Gly Ala Tyr Pro Ser Pro
165 170 175
Leu Gly Tyr Gly Gly Phe Pro Lys Ser Val Cys Thr Ser Val Asn Glu
180 185 190
Cys Met Cys His Gly Ile Pro Asp Ser Arg Gln Leu Gln Asn Gly Asp
195 200 205
Ile Ile Asn Ile Asp Val Thr Val Tyr Leu Asp Gly Tyr His Gly Asp
210 215 220
Thr Ser Lys Thr Phe Phe Cys Gly Glu Val Ser Asp Glu Leu Lys Asn
225 230 235 240
Leu Val Lys Val Thr Glu Glu Cys Leu Glu Lys Gly Ile Ala Ala Cys
245 250 255
Lys Asp Gly Ala Leu Phe Arg Lys Ile Gly Lys Arg Ile Ser Glu His
260 265 270
Ala Glu Lys Tyr Gly Tyr Gly Val Val Glu Arg Phe Val Gly His Gly
275 280 285
Val Gly Thr Val Phe His Ser Glu Pro Ile Ile Ile His Asn Arg Asn
290 295 300
Glu Lys Ala Gly Arg Met Ile Glu Gly Gln Thr Phe Thr Ile Glu Pro
305 310 315 320
Ile Leu Ser Met Gly Ser Ile Asp Ser Ile Thr Trp Pro Asp Asn Trp
325 330 335
Thr Thr Ile Thr Ala Asp Gly Ser Pro Ala Ala Gln Phe Glu His Thr
340 345 350
Ile Leu Ile Thr Lys Thr Gly Ala Glu Ile Leu Thr Lys Cys
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<210> 136
<211> 1113
<212> DNA
<213> Oryza sativa (japonica cultivar-group)

<220>
<221> CDS
<222> (1)..(1113)

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cgc ctc ctc tcc gcc agc gcc agg ccg ctc ctc cgc ggg gcc gct cca 96
Seite 170

PF59082SeqList_PF59082.txt

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Gly	Ser	Arg	Arg	Ala	Ala	Tyr	Gln	Ala	Thr	Arg	Thr	Leu	Cys	Asn	Leu	
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gtg	gat	atc	ctc	ttc	aac	aga	ggg	cag	agt	gac	aaa	ccg	gaa	gat	aac	192
Val	Asp	Ile	Leu	Phe	Asn	Arg	Gly	Gln	Ser	Asp	Lys	Pro	Glu	Asp	Asn	
	50					55					60					
cct	aga	cgc	cta	cgg	cct	ggg	aaa	gta	tct	cct	cgt	cta	agc	gtt	ccc	240
Pro	Arg	Arg	Leu	Arg	Pro	Gly	Lys	Val	Ser	Pro	Arg	Leu	Ser	Val	Pro	
	65				70					75					80	
aaa	cat	ata	cag	cgg	cca	cca	tat	gtc	aat	gct	cgt	caa	aga	cct	gga	288
Lys	His	Ile	Gln	Arg	Pro	Pro	Tyr	Val	Asn	Ala	Arg	Gln	Arg	Pro	Gly	
			85				90							95		
ttg	cac	aat	gga	cct	gaa	ata	cat	gat	gag	aga	ggg	atc	gaa	tgc	atg	336
Leu	His	Asn	Gly	Pro	Glu	Ile	His	Asp	Glu	Arg	Gly	Ile	Glu	Cys	Met	
			100				105						110			
agg	gct	tct	gga	aag	ctt	gct	gca	caa	gtt	ttg	aag	ttt	gcc	ggg	act	384
Arg	Ala	Ser	Gly	Lys	Leu	Ala	Ala	Gln	Val	Leu	Lys	Phe	Ala	Gly	Thr	
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Leu	Val	Glu	Pro	Gly	Ile	Thr	Thr	Asp	Glu	Ile	Asp	Lys	Ala	Val	His	
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caa	atg	ata	gta	gat	aat	gga	gca	tac	cct	tcg	cca	ctt	ggg	tat	tgc	480
Gln	Met	Ile	Val	Asp	Asn	Gly	Ala	Tyr	Pro	Ser	Pro	Leu	Gly	Tyr	Cys	
	145				150					155					160	
ggg	ttt	cca	aag	agt	gtc	tgc	acc	tca	gtg	aat	gag	tgc	atc	tgt	cat	528
Gly	Phe	Pro	Lys	Ser	Val	Cys	Thr	Ser	Val	Asn	Glu	Cys	Ile	Cys	His	
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Gly	Ile	Pro	Asp	Ser	Arg	Pro	Leu	Glu	Asp	Gly	Asp	Ile	Ile	Asn	Ile	
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gat	gtt	act	gtt	tat	ctc	aat	aga	gtg	ttt	cta	tgc	atc	tcc	tcc	tta	624
Asp	Val	Thr	Val	Tyr	Leu	Asn	Arg	Val	Phe	Leu	Cys	Ile	Ser	Ser	Leu	
		195					200						205			
tat	ttg	cat	aaa	tgt	caa	agt	atg	aca	atg	gtg	gct	gga	cag	ctg	ggg	672
Tyr	Leu	His	Lys	Cys	Gln	Ser	Met	Thr	Met	Val	Ala	Gly	Gln	Leu	Gly	
		210				215					220					
tac	cac	ggg	gat	aca	tct	gct	aca	ttt	cta	tgt	ggg	aat	gtt	gat	gac	720
Tyr	His	Gly	Asp	Thr	Ser	Ala	Thr	Phe	Leu	Cys	Gly	Asn	Val	Asp	Asp	
	225				230					235					240	
aaa	gct	aag	aaa	tta	gtt	cag	gta	aca	aga	gaa	tgt	ctc	gac	aag	gct	768
Lys	Ala	Lys	Lys	Leu	Val	Gln	Val	Thr	Arg	Glu	Cys	Leu	Asp	Lys	Ala	
			245					250						255		
ata	tca	atc	tgc	gcc	cct	ggg	gtg	gag	atc	aaa	cgt	att	ggg	cga	act	816
Ile	Ser	Ile	Cys	Ala	Pro	Gly	Val	Glu	Ile	Lys	Arg	Ile	Gly	Arg	Thr	
		260					265						270			
ata	cag	gac	cat	gca	gat	aaa	ttc	aag	ttt	ggg	gta	gtt	cga	cag	ttc	864
Ile	Gln	Asp	His	Ala	Asp	Lys	Phe	Lys	Phe	Gly	Val	Val	Arg	Gln	Phe	
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gtc	ggg	cat	ggg	gtt	gga	caa	gtg	ttt	cat	gct	gaa	cct	gtg	gtg	ctt	912
Val	Gly	His	Gly	Val	Gly	Gln	Val	Phe	His	Ala	Glu	Pro	Val	Val	Leu	
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cat	ttc	cga	aac	aat	gaa	tgg	ggc	cgt	atg	aca	ttg	aac	caa	aca	ttt	960
His	Phe	Arg	Asn	Asn	Glu	Trp	Gly	Arg	Met	Thr	Leu	Asn	Gln	Thr	Phe	
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act	ata	gag	ccc	atg	cta	acc	gtg	ggg	agc	gta	aat	cca	gtt	ata	tgg	1008
Thr	Ile	Glu	Pro	Met	Leu	Thr	Val	Gly	Ser	Val	Asn	Pro	Val	Ile	Trp	
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tcc	gat	gac	tgg	aca	gcg	gtg	act	gaa	gac	ggc	agc	ttg	tca	gca	cag	1056
Ser	Asp	Asp	Trp	Thr	Ala	Val	Thr	Glu	Asp	Gly	Ser	Leu	Ser	Ala	Gln	
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Phe	Glu	His	Thr	Ile	Leu	Ile	Thr	Glu	Asp	Gly	Ala	Ile	Ile	Leu	Thr	
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Gln	Cys															
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PF59082SeqList_PF59082.txt

<210> 137

<211> 370

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<400> 137

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Gly Ser Arg Arg Ala Ala Tyr Gln Ala Thr Arg Thr Leu Cys Asn Leu
35      40      45
Val Asp Ile Leu Phe Asn Arg Gly Gln Ser Asp Lys Pro Glu Asp Asn
50      55      60
Pro Arg Arg Leu Arg Pro Gly Lys Val Ser Pro Arg Leu Ser Val Pro
65      70      75      80
Lys His Ile Gln Arg Pro Pro Tyr Val Asn Ala Arg Gln Arg Pro Gly
85      90      95
Leu His Asn Gly Pro Glu Ile His Asp Glu Arg Gly Ile Glu Cys Met
100     105     110
Arg Ala Ser Gly Lys Leu Ala Ala Gln Val Leu Lys Phe Ala Gly Thr
115     120     125
Leu Val Glu Pro Gly Ile Thr Thr Asp Glu Ile Asp Lys Ala Val His
130     135     140
Gln Met Ile Val Asp Asn Gly Ala Tyr Pro Ser Pro Leu Gly Tyr Cys
145     150     155     160
Gly Phe Pro Lys Ser Val Cys Thr Ser Val Asn Glu Cys Ile Cys His
165     170     175
Gly Ile Pro Asp Ser Arg Pro Leu Glu Asp Gly Asp Ile Ile Asn Ile
180     185     190
Asp Val Thr Val Tyr Leu Asn Arg Val Phe Leu Cys Ile Ser Ser Leu
195     200     205
Tyr Leu His Lys Cys Gln Ser Met Thr Met Val Ala Gly Gln Leu Gly
210     215     220
Tyr His Gly Asp Thr Ser Ala Thr Phe Leu Cys Gly Asn Val Asp Asp
225     230     235     240
Lys Ala Lys Lys Leu Val Gln Val Thr Arg Glu Cys Leu Asp Lys Ala
245     250     255
Ile Ser Ile Cys Ala Pro Gly Val Glu Ile Lys Arg Ile Gly Arg Thr
260     265     270
Ile Gln Asp His Ala Asp Lys Phe Lys Phe Gly Val Val Arg Gln Phe
275     280     285
Val Gly His Gly Val Gly Gln Val Phe His Ala Glu Pro Val Val Leu
290     295     300
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305     310     315     320
Thr Ile Glu Pro Met Leu Thr Val Gly Ser Val Asn Pro Val Ile Trp
325     330     335
Ser Asp Asp Trp Thr Ala Val Thr Glu Asp Gly Ser Leu Ser Ala Gln
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Gln Cys
370

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<210> 138

<211> 1002

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<221> CDS

<222> (1)..(1002)

<400> 138

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agc tgc ctt caa aag cct ttc ctt gtc caa gca aag aga tta gag gga      96

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PF59082SeqList_PF59082.txt

Ser	Cys	Leu	Gln	Lys	Pro	Phe	Leu	Val	Gln	Ala	Lys	Arg	Leu	Glu	Gly		
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Leu	Glu	Lys	Ala	Asn	Pro	Arg	Ser	Arg	Gly	Lys	Gln	Ser	Leu	Glu	Gln		
		35					40					45					
gtg	aag	aaa	aga	gca	cca	ctg	atc	cgt	ggg	aca	gtg	agt	cca	cct	cta	192	
Val	Lys	Lys	Arg	Ala	Pro	Leu	Ile	Arg	Gly	Thr	Val	Ser	Pro	Pro	Leu		
		50				55					60						
cca	gta	cca	ggg	cac	ata	act	caa	cct	cct	tac	gtt	ggg	aaa	aag	gat	240	
Pro	Val	Pro	Gly	His	Ile	Thr	Gln	Pro	Pro	Tyr	Val	Gly	Lys	Lys	Asp		
		65			70					75					80		
gct	tca	gag	ata	gca	agt	gag	ata	caa	atg	cat	gac	aaa	gtg	agc	att	288	
Ala	Ser	Glu	Ile	Ala	Ser	Glu	Ile	Gln	Met	His	Asp	Lys	Val	Ser	Ile		
			85					90						95			
att	cac	atg	aaa	gct	gca	tgt	gag	ctt	gct	gct	cgt	gtt	ctt	gaa	tac	336	
Ile	His	Met	Lys	Ala	Ala	Cys	Glu	Leu	Ala	Ala	Arg	Val	Leu	Glu	Tyr		
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gct	gga	act	tta	gtg	aaa	ccc	tct	gta	aca	aca	gac	gaa	att	gat	aaa	384	
Ala	Gly	Thr	Leu	Val	Lys	Pro	Ser	Val	Thr	Thr	Asp	Glu	Ile	Asp	Lys		
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gca	gtg	cac	aag	atg	atc	att	gat	gct	gga	gcc	tat	cca	tcc	cct	ctc	432	
Ala	Val	His	Lys	Met	Ile	Ile	Asp	Ala	Gly	Ala	Tyr	Pro	Ser	Pro	Leu		
		130			135					140							
gga	tac	gga	ggg	ttt	cca	aaa	agc	gtg	tgc	aca	tct	gtg	aat	gaa	tgc	480	
Gly	Tyr	Gly	Gly	Phe	Pro	Lys	Ser	Val	Cys	Thr	Ser	Val	Asn	Glu	Cys		
					150				155					160			
atc	tgc	cat	gga	att	cct	gat	tct	cgt	gaa	ctt	cag	gat	gga	gac	ata	528	
Ile	Cys	His	Gly	Ile	Pro	Asp	Ser	Arg	Glu	Leu	Gln	Asp	Gly	Asp	Ile		
			165					170						175			
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Ile	Asn	Ile	Asp	Val	Thr	Val	Tyr	Leu	Asn	Gly	Tyr	His	Gly	Asp	Thr		
			180				185						190				
tca	aag	act	ttc	cta	tgt	gga	gaa	gtg	gat	gaa	gcc	agt	aaa	cga	ctt	624	
Ser	Lys	Thr	Phe	Leu	Cys	Gly	Glu	Val	Asp	Glu	Ala	Ser	Lys	Arg	Leu		
		195				200						205					
gtg	aag	gtt	act	gaa	gag	tgc	atg	ctc	agg	gct	ata	tca	gct	tgc	aaa	672	
Val	Lys	Val	Thr	Glu	Glu	Cys	Met	Leu	Arg	Ala	Ile	Ser	Ala	Cys	Lys		
		210			215					220							
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His	Gly	Thr	Ser	Leu	Lys	Ile	Gly	Arg	Arg	Arg	Ile	Ser	Glu	His	Ala		
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gag	agg	cac	gga	ttt	ggg	gtt	gtg	gat	cgt	ttt	gtt	ggg	cat	gga	gtt	768	
Glu	Arg	His	Gly	Phe	Gly	Val	Val	Asp	Arg	Phe	Val	Gly	His	Gly	Val		
			245					250						255			
ggg	aga	ata	ttt	cat	tca	gaa	cca	atg	ata	tat	cac	cag	cgt	aat	aat	816	
Gly	Arg	Ile	Phe	His	Ser	Glu	Pro	Met	Ile	Tyr	His	Gln	Arg	Asn	Asn		
		260				265						270					
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Met	Pro	Gly	Gln	Met	Val	Glu	Gly	Gln	Thr	Phe	Thr	Ile	Glu	Pro	Ala		
		275				280						285					
cta	tcc	atg	gga	agc	att	gat	tgc	gac	atg	tgg	gac	gac	ggc	tgg	acg	912	
Leu	Ser	Met	Gly	Ser	Ile	Asp	Cys	Asp	Met	Trp	Asp	Asp	Gly	Trp	Thr		
		290				295				300							
gcc	gtc	acg	acg	gac	ggc	agc	cta	gcc	gcg	cag	ttc	gag	cac	acg	ata	960	
Ala	Val	Thr	Thr	Asp	Gly	Ser	Leu	Ala	Ala	Gln	Phe	Glu	His	Thr	Ile		
		305			310				315						320		
ctg	att	acc	aag	aca	gga	gca	gaa	atc	ctc	acg	aaa	tgc	tag			1002	
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<210> 139

<211> 333

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<400> 139

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Ser	Cys	Leu	Gln	Lys	Pro	Phe	Leu	Val	Gln	Ala	Lys	Arg	Leu	Glu	Gly

Seite 173

PF59082SeqList_PF59082.txt

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 Leu Glu Lys Ala Asn Pro Arg Ser Arg Gly Lys Gln Ser Leu Glu Gln
 Val Lys₃₅ Lys Arg Ala Pro Leu₅₅ Ile Arg Gly Thr Val₆₀ Ser Pro Pro Leu
 Pro Val₆₅ Pro Gly His Ile₇₀ Thr Gln Pro Pro Tyr₇₅ Val Gly Lys Lys Asp₈₀
 Ala Ser Glu Ile Ala₈₅ Ser Glu Ile Gln Met₉₀ His Asp Lys Val Ser Ile₉₅
 Ile His Met Lys₁₀₀ Ala Ala Cys Glu Leu₁₀₅ Ala Ala Arg Val Leu Glu Tyr
 Ala Gly Thr Leu Val Lys Pro Ser Val Thr Thr Asp Glu Ile Asp Lys
 Ala Val₁₁₅ His Lys Met Ile Ile₁₂₀ Asp Ala Gly Ala Tyr₁₂₅ Pro Ser Pro Leu
 Gly₁₃₀ Tyr Gly Gly Phe Pro₁₃₅ Lys Ser Val Cys Thr₁₄₀ Ser Val Asn Glu Cys
 145 Ile Cys His Gly Ile₁₅₀ Pro Asp Ser Arg Glu Leu Gln Asp Gly Asp Ile₁₆₀
 Ile Asn Ile Asp₁₆₅ Val Thr Val Tyr Leu₁₇₀ Asn Gly Tyr His Gly Asp Thr
 Ser Lys Thr Phe₁₈₀ Leu Cys Gly Glu Val₁₈₅ Asp Glu Ala Ser Lys Arg Leu
 Val Lys₁₉₅ Val Thr Glu Glu Cys Met Leu Arg Ala Ile₂₀₀ Ser Ala Cys Lys
 His₂₁₀ Gly Thr Ser Leu Lys₂₁₅ Lys Ile Gly Arg Arg₂₂₀ Ile Ser Glu His Ala
 225 Glu Arg His Gly Phe₂₃₀ Gly Val Val Asp Arg Phe Val Gly His Gly Val
 Gly Arg Ile Phe₂₄₅ His Ser Glu Pro Met₂₅₀ Ile Tyr His Gln Arg Asn Asn
 Met Pro Gly Gln Met Val Glu Gly Gln Thr Phe Thr Ile Glu Pro Ala
 Leu Ser₂₇₅ Met Gly Ser Ile Asp Cys Asp Met Trp Asp₂₈₀ Asp Gly Trp Thr
 Ala Val₂₉₀ Thr Thr Asp Gly Ser Leu Ala Ala Gln₃₀₀ Phe Glu His Thr Ile
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<210> 140

<211> 1074

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<221> CDS

<222> (1)..(1074)

<400> 140

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ctc gcc ggc ggg ttc ctc gct gcc cgc cct gcc gcc gtc tct ccc atc	96
Leu Ala Gly Gly ₂₀ Phe Leu Ala Ala Arg ₂₅ Pro Ala Ala Val Ser Pro Ile ₃₀	
ccc tcc cgc tcc ggg aaa tca atc gca ccg agc cga cgc ttt atc gtg	144
Pro Ser Arg ₃₅ Ser Gly Lys Ser Ile Ala Pro Ser Arg Arg ₄₅ Phe Ile Val ₅₀	
tct aat aaa ctt gct tgg gtt gaa gat gag tta gtg gag ata aca gag	192
Ser Asn Lys Leu Ala Trp Val ₅₅ Glu Asp Glu Leu Val ₆₀ Glu Ile Thr Glu ₆₅	
tca caa gag cca agc tcc gca agt tca aag aaa agg cca cct ttg agg	240
Ser Gln Glu Pro Ser Ser ₇₀ Ala Ser Ser Lys ₇₅ Arg Pro Pro Leu Arg ₈₀	
cgt ggg aaa atc tct cca caa ctt ccg gtg cca gaa cac att ccg aga	288
Arg Gly Lys Ile Ser ₈₅ Pro Gln Leu Pro Val ₉₀ Pro Glu His Ile Pro Arg ₉₅	
cca tct tat gta ggt tcg aat aga ccg caa gaa cta tct agt gtg cgc	336

PF59082SeqList_PF59082.txt

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Gln	Ile	His	Ser	Ala	Glu	Gly	Ile	Ala	Gly	Met	Arg	Ala	Ala	Cys	Lys
		115					120					125			
ctt	gct	gcc	cgt	gct	ctg	gac	ttt	gct	gga	aca	ttg	att	aag	cca	tca
Leu	Ala	Ala	Arg	Ala	Leu	Asp	Phe	Ala	Gly	Thr	Leu	Ile	Lys	Pro	Ser
	130					135					140				
gtt	act	aca	aat	gaa	att	gac	agg	gaa	gtg	cat	aac	atg	ata	att	gag
Val	Thr	Thr	Asn	Glu	Ile	Asp	Arg	Glu	Val	His	Asn	Met	Ile	Ile	Glu
	145				150					155					160
gcc	ggt	gct	tat	cct	tct	caa	ctt	ggc	tat	ggt	gga	ttt	cct	aaa	agt
Ala	Gly	Ala	Tyr	Pro	Ser	Gln	Leu	Gly	Tyr	Gly	Gly	Phe	Pro	Lys	Ser
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Ile	Cys	Thr	Ser	Leu	Asn	Glu	Cys	Val	Cys	His	Gly	Val	Pro	Asp	Ser
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aca	caa	ctg	cag	acc	gga	gac	atc	atg	aat	gtt	gat	gta	aat	gtg	ttc
Thr	Gln	Leu	Gln	Thr	Gly	Asp	Ile	Met	Asn	Val	Asp	Val	Asn	Val	Phe
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ctg	aac	gga	tac	cat	ggg	ggt	tct	aga	aca	ttt	gta	tgt	gga	gaa	
Leu	Asn	Gly	Tyr	His	Gly	Gly	Ala	Ser	Arg	Thr	Phe	Val	Cys	Gly	Glu
	210				215					220					
gtg	gat	gac	tct	atc	agg	cat	ttt	ctg	aag	gca	gct	gaa	gaa	tgc	ttg
Val	Asp	Asp	Ser	Ile	Arg	His	Phe	Leu	Lys	Ala	Ala	Glu	Glu	Cys	Leu
	225				230					235					240
gag	aag	ggt	att	aca	gtc	tgc	agg	gat	ggt	gtc	aac	tac	aaa	aag	att
Glu	Lys	Gly	Ile	Thr	Val	Cys	Arg	Asp	Gly	Val	Asn	Tyr	Lys	Lys	Ile
			245					250						255	
ggc	aag	aaa	ata	agc	aag	ctt	gct	tat	ttt	tac	ggc	tat	tat	gtg	gtg
Gly	Lys	Lys	Ile	Ser	Lys	Leu	Ala	Tyr	Phe	Tyr	Gly	Tyr	Tyr	Val	Val
			260					265					270		
gat	cgt	ttt	gtt	gga	cat	ggg	att	gga	cct	att	tgg	cat	tct	gag	cca
Asp	Arg	Phe	Val	Gly	His	Gly	Ile	Gly	Pro	Ile	Trp	His	Ser	Glu	Pro
		275					280					285			
cta	atc	cta	cat	cat	gcc	aat	gac	aac	tct	ggg	cga	atg	gtt	gaa	ggt
Leu	Ile	Leu	His	His	Ala	Asn	Asp	Asn	Ser	Gly	Arg	Met	Val	Glu	Gly
	290				295					300					
cag	aca	ttt	aca	att	gaa	cct	att	ctt	aca	atg	gaa	aag	gct	gag	aca
Gln	Thr	Phe	Thr	Ile	Glu	Pro	Ile	Leu	Thr	Met	Glu	Lys	Ala	Glu	Thr
	305				310					315					320
gtt	aca	tgg	gaa	gat	gga	tgg	act	act	gtc	act	gcc	gat	ggc	agc	tgg
Val	Thr	Trp	Glu	Asp	Gly	Trp	Thr	Thr	Val	Thr	Ala	Asp	Gly	Ser	Trp
			325						330					335	
gct	gcg	cag	ttt	aag	cat	act	gta	cta	gtc	act	cgg	aca	ggg	gct	gaa
Ala	Ala	Gln	Phe	Lys	His	Thr	Val	Leu	Val	Thr	Arg	Thr	Gly	Ala	Glu
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Ile	Leu	Thr	Lys	Leu											
		355													

<210> 141

<211> 357

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<400> 141

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Leu	Ala	Gly	Gly	Phe	Leu	Ala	Ala	Arg	Pro	Ala	Ala	Val	Ser	Pro	Ile
			20					25					30		
Pro	Ser	Arg	Ser	Gly	Lys	Ser	Ile	Ala	Pro	Ser	Arg	Arg	Phe	Ile	Val
		35					40					45			
Ser	Asn	Lys	Leu	Ala	Trp	Val	Glu	Asp	Glu	Leu	Val	Glu	Ile	Thr	Glu
	50					55					60				
Ser	Gln	Glu	Pro	Ser	Ser	Ala	Ser	Ser	Lys	Lys	Arg	Pro	Pro	Leu	Arg
	65				70					75				80	
Arg	Gly	Lys	Ile	Ser	Pro	Gln	Leu	Pro	Val	Pro	Glu	His	Ile	Pro	Arg
				85					90					95	

PF59082SeqList_PF59082.txt

Pro Ser Tyr Val Gly Ser Asn Arg Pro Gln Glu Leu Ser Val Arg
 100 105 110
 Gln Ile His Ser Ala Glu Gly Ile Ala Gly Met Arg Ala Ala Cys Lys
 115 120 125
 Leu Ala Ala Arg Ala Leu Asp Phe Ala Gly Thr Leu Ile Lys Pro Ser
 130 135 140
 Val Thr Thr Asn Glu Ile Asp Arg Glu Val His Asn Met Ile Ile Glu
 145 150 155 160
 Ala Gly Ala Tyr Pro Ser Gln Leu Gly Tyr Gly Gly Phe Pro Lys Ser
 165 170 175
 Ile Cys Thr Ser Leu Asn Glu Cys Val Cys His Gly Val Pro Asp Ser
 180 185 190
 Thr Gln Leu Gln Thr Gly Asp Ile Met Asn Val Asp Val Asn Val Phe
 195 200 205
 Leu Asn Gly Tyr His Gly Gly Ala Ser Arg Thr Phe Val Cys Gly Glu
 210 215 220
 Val Asp Asp Ser Ile Arg His Phe Leu Lys Ala Ala Glu Glu Cys Leu
 225 230 235 240
 Glu Lys Gly Ile Thr Val Cys Arg Asp Gly Val Asn Tyr Lys Lys Ile
 245 250 255
 Gly Lys Lys Ile Ser Lys Leu Ala Tyr Phe Tyr Gly Tyr Tyr Val Val
 260 265 270
 Asp Arg Phe Val Gly His Gly Ile Gly Pro Ile Trp His Ser Glu Pro
 275 280 285
 Leu Ile Leu His His Ala Asn Asp Asn Ser Gly Arg Met Val Glu Gly
 290 295 300
 Gln Thr Phe Thr Ile Glu Pro Ile Leu Thr Met Glu Lys Ala Glu Thr
 305 310 315 320
 Val Thr Trp Glu Asp Gly Trp Thr Thr Val Thr Ala Asp Gly Ser Trp
 325 330 335
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 340 345 350
 Ile Leu Thr Lys Leu
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 <211> 1110
 <212> DNA
 <213> Arabidopsis thaliana

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 caa ctc tgc tct tcc ttt cac ggc gag tac tta gct ccg tcg aga tgc 96
 Gln Leu Cys Ser Phe His Gly Glu Tyr Leu Ala Pro Ser Arg Cys
 20 25 30
 ttt ctc gga gct ccg gtc act tcc tct tct tta tca ctc tcc ggt aag 144
 Phe Leu Gly Ala Pro Val Thr Ser Ser Ser Leu Ser Leu Ser Gly Lys
 35 40 45
 aag aac tca tat tct ccg aga cag ttc cat gtt tct gcc aag aaa gtt 192
 Lys Asn Ser Tyr Ser Pro Arg Gln Phe His Val Ser Ala Lys Lys Val
 50 55 60
 tct ggg tta gag gaa gcc att aga atc aga aaa atg aga gag ctt gaa 240
 Ser Gly Leu Glu Glu Ala Ile Arg Ile Arg Lys Met Arg Glu Leu Glu
 65 70 75 80
 act aaa tca aaa gtt agg aga aat cca cca tta aga cgt gga aga gta 288
 Thr Lys Ser Lys Val Arg Arg Asn Pro Pro Leu Arg Arg Gly Arg Val
 85 90 95
 tcg cct cgt ctt gta cct gat cac att cca agg cct cct tat gtt 336
 Ser Pro Arg Leu Val Pro Asp His Ile Pro Arg Pro Pro Tyr Val
 100 105 110
 gag tct ggt gta tta ccg gat ata tca agt gag ttc cag att cct ggt 384
 Glu Ser Gly Val Leu Pro Asp Ile Ser Ser Glu Phe Gln Ile Pro Gly
 115 120 125

PF59082SeqList_PF59082.txt

cct	gaa	ggc	att	gcg	aaa	atg	aga	gct	gct	tgc	gag	ctt	gct	gct	cgg	432
Pro	Glu	Gly	Ile	Ala	Lys	Met	Arg	Ala	Ala	Cys	Glu	Leu	Ala	Ala	Arg	
	130					135					140					
ggt	tta	aac	tat	gct	gga	act	ttg	ggt	aag	cca	tct	ggt	acg	act	aat	480
Val	Leu	Asn	Tyr	Ala	Gly	Thr	Leu	Val	Lys	Pro	Ser	Val	Thr	Thr	Asn	
	145				150					155					160	
gaa	atc	gat	aaa	gct	gtg	cat	gat	atg	att	att	gaa	gct	ggg	gct	tat	528
Glu	Ile	Asp	Lys	Ala	Val	His	Asp	Met	Ile	Ile	Glu	Ala	Gly	Ala	Tyr	
			165						170					175		
cct	tca	cct	ctt	gga	tat	ggg	gga	ttt	cct	aaa	agt	gtg	tgt	act	tca	576
Pro	Ser	Pro	Leu	Gly	Tyr	Gly	Gly	Phe	Pro	Lys	Ser	Val	Cys	Thr	Ser	
			180					185					190			
ggt	aat	gag	tgt	atg	tgt	cac	gga	ata	cca	gat	tct	cg	cag	cta	cag	624
Val	Asn	Glu	Cys	Met	Cys	His	Gly	Ile	Pro	Asp	Ser	Arg	Gln	Leu	Gln	
		195					200					205				
agc	ggg	gat	ata	atc	aac	atc	gat	gtc	acg	ggt	tac	ttg	gat	ggg	tac	672
Ser	Gly	Asp	Ile	Ile	Asn	Ile	Asp	Val	Thr	Val	Tyr	Leu	Asp	Gly	Tyr	
	210					215					220					
cat	gga	gat	acg	tcg	aga	act	ttc	ttc	tgt	gga	gaa	ggt	gac	gaa	ggg	720
His	Gly	Asp	Thr	Ser	Arg	Thr	Phe	Phe	Cys	Gly	Glu	Val	Asp	Glu	Gly	
	225				230					235					240	
ttc	aaa	cga	ctt	gtg	aag	ggt	acg	gaa	gaa	tgt	ttg	gag	aga	ggg	att	768
Phe	Lys	Arg	Leu	Val	Lys	Val	Thr	Glu	Glu	Cys	Leu	Glu	Arg	Gly	Ile	
			245					250						255		
gca	ggt	tgt	aaa	gac	gga	gca	agc	ttc	aag	aaa	atc	ggg	aaa	aga	atc	816
Ala	Val	Cys	Lys	Asp	Gly	Ala	Ser	Phe	Lys	Lys	Ile	Gly	Lys	Arg	Ile	
			260					265					270			
agt	gag	cat	gcg	gaa	aag	ttc	ggc	tac	aac	ggt	gtg	gag	cgg	ttt	ggt	864
Ser	Glu	His	Ala	Glu	Lys	Phe	Gly	Tyr	Asn	Val	Val	Glu	Arg	Phe	Val	
		275					280					285				
ggg	cat	ggg	ggt	gga	cca	gta	ttc	cac	tcc	gaa	cct	ctt	ata	tat	cat	912
Gly	His	Gly	Val	Gly	Pro	Val	Phe	His	Ser	Glu	Pro	Leu	Ile	Tyr	His	
	290					295					300					
tac	cga	aat	gat	gag	cct	gga	cta	atg	ggt	gag	gga	cag	aca	ttc	aca	960
Tyr	Arg	Asn	Asp	Glu	Pro	Gly	Leu	Met	Val	Glu	Gly	Gln	Thr	Phe	Thr	
	305				310					315					320	
att	gaa	ccg	att	ctc	acg	att	gga	acc	aca	gaa	tgt	gta	aca	tgg	cca	1008
Ile	Glu	Pro	Ile	Leu	Thr	Ile	Gly	Thr	Thr	Glu	Cys	Val	Thr	Trp	Pro	
			325					330						335		
gac	aac	tgg	act	act	ctg	aca	gca	gat	ggg	ggt	gtc	gct	gct	cag	ttt	1056
Asp	Asn	Trp	Thr	Thr	Leu	Thr	Ala	Asp	Gly	Gly	Val	Ala	Ala	Gln	Phe	
			340					345					350			
gag	cat	acc	att	ctg	att	act	aga	act	ggg	tca	gag	att	ctt	acc	aaa	1104
Glu	His	Thr	Ile	Leu	Ile	Thr	Arg	Thr	Gly	Ser	Glu	Ile	Leu	Thr	Lys	
		355					360					365				
tgc	taa															1110
Cys																

<210> 143

<211> 369

<212> PRT

<213> Arabidopsis thaliana

<400> 143

Met	Ala	Ser	Ser	Val	Phe	Leu	Ser	Ser	Phe	Ser	Ser	Ser	Ser	Ser	Leu	
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			20					25					30			
Phe	Leu	Gly	Ala	Pro	Val	Thr	Ser	Ser	Leu	Ser	Leu	Ser	Gly	Lys		
		35					40					45				
Lys	Asn	Ser	Tyr	Ser	Pro	Arg	Gln	Phe	His	Val	Ser	Ala	Lys	Lys	Val	
	50					55					60					
Ser	Gly	Leu	Glu	Glu	Ala	Ile	Arg	Ile	Arg	Lys	Met	Arg	Glu	Leu	Glu	
	65				70					75					80	
Thr	Lys	Ser	Lys	Val	Arg	Arg	Asn	Pro	Pro	Leu	Arg	Arg	Gly	Arg	Val	
			85					90						95		
Ser	Pro	Arg	Leu	Leu	Val	Pro	Asp	His	Ile	Pro	Arg	Pro	Pro	Tyr	Val	
			100					105					110			

PF59082SeqList_PF59082.txt

Glu Ser Gly Val Leu Pro Asp Ile Ser Ser Glu Phe Gln Ile Pro Gly
115 120 125
Pro Glu Gly Ile Ala Lys Met Arg Ala Ala Cys Glu Leu Ala Ala Arg
130 135 140
Val Leu Asn Tyr Ala Gly Thr Leu Val Lys Pro Ser Val Thr Thr Asn
145 150 155 160
Glu Ile Asp Lys Ala Val His Asp Met Ile Ile Glu Ala Gly Ala Tyr
165 170 175
Pro Ser Pro Leu Gly Tyr Gly Gly Phe Pro Lys Ser Val Cys Thr Ser
180 185 190
Val Asn Glu Cys Met Cys His Gly Ile Pro Asp Ser Arg Gln Leu Gln
195 200 205
Ser Gly Asp Ile Ile Asn Ile Asp Val Thr Val Tyr Leu Asp Gly Tyr
210 215 220
His Gly Asp Thr Ser Arg Thr Phe Phe Cys Gly Glu Val Asp Glu Gly
225 230 235 240
Phe Lys Arg Leu Val Lys Val Thr Glu Glu Cys Leu Glu Arg Gly Ile
245 250 255
Ala Val Cys Lys Asp Gly Ala Ser Phe Lys Lys Ile Gly Lys Arg Ile
260 265 270
Ser Glu His Ala Glu Lys Phe Gly Tyr Asn Val Val Glu Arg Phe Val
275 280 285
Gly His Gly Val Gly Pro Val Phe His Ser Glu Pro Leu Ile Tyr His
290 295 300
Tyr Arg Asn Asp Glu Pro Gly Leu Met Val Glu Gly Gln Thr Phe Thr
305 310 315 320
Ile Glu Pro Ile Leu Thr Ile Gly Thr Thr Glu Cys Val Thr Trp Pro
325 330 335
Asp Asn Trp Thr Thr Leu Thr Ala Asp Gly Gly Val Ala Ala Gln Phe
340 345 350
Glu His Thr Ile Leu Ile Thr Arg Thr Gly Ser Glu Ile Leu Thr Lys
355 360 365
Cys

<210> 144
<211> 1035
<212> DNA
<213> Arabidopsis thaliana

<220>
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ttt aag ccg tta ata tac ctc gcc gga gct ccg acg aac ttc atc tct 96
Phe Lys Pro Leu Ile Tyr Leu Ala Gly Ala Pro Thr Asn Phe Ile Ser
20 25 30
tcc cct ctc tca ggc aag aag aaa tca tct tct ctg aga att aaa agg 144
Ser Pro Leu Ser Gly Lys Lys Lys Ser Ser Ser Leu Arg Ile Lys Arg
35 40 45
ata caa caa ctt caa agt aca tta gaa gat aga ata aat cca cca cta 192
Ile Gln Gln Leu Gln Ser Thr Leu Glu Asp Arg Ile Asn Pro Pro Leu
50 55 60
gta tgt gga aca gta tcg cca cgt ctt agt gtt cct gat cat ata cta 240
Val Cys Gly Thr Val Ser Pro Arg Leu Ser Val Pro Asp His Ile Leu
65 70 75 80
aag cct cta tat gtt gag tct agc aaa gtt cca gag ata tca agt gaa 288
Lys Pro Leu Tyr Val Glu Ser Ser Lys Val Pro Glu Ile Ser Ser Glu
85 90 95
tta cag att cct gac tct ata ggc att gtg aaa atg aag aaa gcg tgt 336
Leu Gln Ile Pro Asp Ser Ile Gly Ile Val Lys Met Lys Lys Ala Cys
100 105 110
gag ctc gcg gct cgt gta tta gac tat gca gga act ttg gtt aga ccg 384
Glu Leu Ala Ala Arg Val Leu Asp Tyr Ala Gly Thr Leu Val Arg Pro
115 120 125

PF59082SeqList_PF59082.txt

ttt	ggt	act	aca	gat	gaa	att	gat	aaa	gca	gtg	cat	cag	atg	ggt	att	432
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	130					135					140					
gag	ttt	ggt	gca	tat	cct	tca	cct	ctt	gga	tat	ggt	gga	ttt	cct	aaa	480
Glu	Phe	Gly	Ala	Tyr	Pro	Ser	Pro	Leu	Gly	Tyr	Gly	Gly	Phe	Pro	Lys	
145					150					155					160	
agt	ggt	tgt	aca	tcg	ggt	aat	gaa	tgt	atg	ttt	cac	ggg	att	ccc	gat	528
Ser	Val	Cys	Thr	Ser	Val	Asn	Glu	Cys	Met	Phe	His	Gly	Ile	Pro	Asp	
				165					170					175		
tct	cgt	ccg	cta	cag	aat	gga	gat	att	ata	aac	atc	gat	ggt	gcg	ggt	576
Ser	Arg	Pro	Leu	Gln	Asn	Gly	Asp	Ile	Ile	Asn	Ile	Asp	Val	Ala	Val	
			180					185					190			
tac	ttg	gat	ggg	tat	cat	gga	gat	acg	tca	aag	act	ttc	tta	tgt	gga	624
Tyr	Leu	Asp	Gly	Tyr	His	Gly	Asp	Thr	Ser	Lys	Thr	Phe	Leu	Cys	Gly	
		195				200						205				
gac	gtc	aat	gga	agc	ctt	aaa	caa	ctt	gtc	aag	gtc	aca	gaa	gaa	tgc	672
Asp	Val	Asn	Gly	Ser	Leu	Lys	Gln	Leu	Val	Lys	Val	Thr	Glu	Glu	Cys	
	210					215					220					
ttg	gag	aaa	ggt	ata	tcg	ggt	tgt	aaa	gat	gga	gca	agc	ttc	aaa	caa	720
Leu	Glu	Lys	Gly	Ile	Ser	Val	Cys	Lys	Asp	Gly	Ala	Ser	Phe	Lys	Gln	
225					230					235					240	
atc	ggg	aag	ata	atc	agt	gag	cat	gct	gca	aag	tat	ggc	tat	aat	atg	768
Ile	Gly	Lys	Ile	Ile	Ser	Glu	His	Ala	Ala	Lys	Tyr	Gly	Tyr	Asn	Met	
				245				250						255		
gag	cga	ttc	atc	ggt	cat	ggt	gta	gga	acg	gta	tta	cac	tcg	gaa	cct	816
Glu	Arg	Phe	Ile	Gly	His	Gly	Val	Gly	Thr	Val	Leu	His	Ser	Glu	Pro	
			260					265					270			
ctt	ata	tat	ctt	cat	agt	aac	tat	gat	tat	gaa	ctt	gaa	tat	atg	att	864
Leu	Ile	Tyr	Leu	His	Ser	Asn	Tyr	Asp	Tyr	Glu	Leu	Glu	Tyr	Met	Ile	
		275					280					285				
gaa	ggt	caa	act	ttt	acg	ctc	gaa	cca	att	ctc	acc	att	gga	aca	aca	912
Glu	Gly	Gln	Thr	Phe	Thr	Leu	Glu	Pro	Ile	Leu	Thr	Ile	Gly	Thr	Thr	
	290					295					300					
gag	ttt	gta	aca	tgg	cct	gac	aaa	tgg	aca	att	gtg	acc	gca	gat	ggt	960
Glu	Phe	Val	Thr	Trp	Pro	Asp	Lys	Trp	Thr	Ile	Val	Thr	Ala	Asp	Gly	
305					310					315					320	
ggt	ccg	gcc	gca	cag	ttt	gag	cat	aca	att	ctt	att	acc	acc	act	ggt	1008
Gly	Pro	Ala	Ala	Gln	Phe	Glu	His	Thr	Ile	Leu	Ile	Thr	Thr	Thr	Gly	
				325					330					335		
gca	gaa	att	ctc	acc	ata	tca	tca	tga								1035
Ala	Glu	Ile	Leu	Thr	Ile	Ser	Ser									
			340													

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<211> 344

<212> PRT

<213> Arabidopsis thaliana

<400> 145

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			20					25					30			
Ser	Pro	Leu	Ser	Gly	Lys	Lys	Lys	Ser	Ser	Ser	Leu	Arg	Ile	Lys	Arg	
		35					40					45				
Ile	Gln	Gln	Leu	Gln	Ser	Thr	Leu	Glu	Asp	Arg	Ile	Asn	Pro	Pro	Leu	
	50					55					60					
Val	Cys	Gly	Thr	Val	Ser	Pro	Arg	Leu	Ser	Val	Pro	Asp	His	Ile	Leu	
65					70					75					80	
Lys	Pro	Leu	Tyr	Val	Glu	Ser	Ser	Lys	Val	Pro	Glu	Ile	Ser	Ser	Glu	
				85					90					95		
Leu	Gln	Ile	Pro	Asp	Ser	Ile	Gly	Ile	Val	Lys	Met	Lys	Lys	Ala	Cys	
			100					105					110			
Glu	Leu	Ala	Arg	Val	Leu	Asp	Tyr	Ala	Gly	Thr	Leu	Val	Arg	Pro		
		115				120					125					
Phe	Val	Thr	Thr	Asp	Glu	Ile	Asp	Lys	Ala	Val	His	Gln	Met	Val	Ile	
	130					135					140					
Glu	Phe	Gly	Ala	Tyr	Pro	Ser	Pro	Leu	Gly	Tyr	Gly	Gly	Phe	Pro	Lys	160
145					150					155						

PF59082SeqList_PF59082.txt

Ser Val Cys Thr Ser Val Asn Glu Cys Met Phe His Gly Ile Pro Asp
 165 170 175
 Ser Arg Pro Leu Gln Asn Gly Asp Ile Ile Asn Ile Asp Val Ala Val
 180 185 190
 Tyr Leu Asp Gly Tyr His Gly Asp Thr Ser Lys Thr Phe Leu Cys Gly
 195 200 205
 Asp Val Asn Gly Ser Leu Lys Gln Leu Val Lys Val Thr Glu Glu Cys
 210 215 220
 Leu Glu Lys Gly Ile Ser Val Cys Lys Asp Gly Ala Ser Phe Lys Gln
 225 230 235 240
 Ile Gly Lys Ile Ile Ser Glu His Ala Ala Lys Tyr Gly Tyr Asn Met
 245 250 255
 Glu Arg Phe Ile Gly His Gly Val Gly Thr Val Leu His Ser Glu Pro
 260 265 270
 Leu Ile Tyr Leu His Ser Asn Tyr Asp Tyr Glu Leu Glu Tyr Met Ile
 275 280 285
 Glu Gly Gln Thr Phe Thr Leu Glu Pro Ile Leu Thr Ile Gly Thr Thr
 290 295 300
 Glu Phe Val Thr Trp Pro Asp Lys Trp Thr Ile Val Thr Ala Asp Gly
 305 310 315 320
 Gly Pro Ala Ala Gln Phe Glu His Thr Ile Leu Ile Thr Thr Thr Gly
 325 330 335
 Ala Glu Ile Leu Thr Ile Ser Ser
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 <211> 1053
 <212> DNA
 <213> Arabidopsis thaliana

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 ggc aac aat tct att aga tca acg caa cca ctt att cat ctc ttt cgc 96
 Gly Asn Asn Ser Ile Arg Ser Thr Gln Pro Leu Ile His Leu Phe Arg
 20 25 30
 ttc gat tta gga aga aga cat gtt tcg atg caa tta tca aga acc ttt 144
 Phe Asp Leu Gly Arg Arg His Val Ser Met Gln Leu Ser Arg Thr Phe
 35 40 45
 tct gga tta acc gat ctc ctg ttt aat aga aga aat gaa gat gaa gtt 192
 Ser Gly Leu Thr Asp Leu Leu Phe Asn Arg Arg Asn Glu Asp Glu Val
 50 55 60
 att gat ggc aag aga aaa cgt ctg aga ccg gga aat gta tct cct cgt 240
 Ile Asp Gly Lys Arg Lys Arg Leu Arg Pro Gly Asn Val Ser Pro Arg
 65 70 75 80
 cgt cct gtt ccg ggt cat ata aca aaa cct cct tat gtt gat tct ctt 288
 Arg Pro Val Pro Gly His Ile Thr Lys Pro Pro Tyr Val Asp Ser Leu
 85 90 95
 caa gct ccc gga atc tca agt gga ctt gaa gtt cat gat aag aaa ggt 336
 Gln Ala Pro Gly Ile Ser Ser Gly Leu Glu Val His Asp Lys Lys Gly
 100 105 110
 ata gaa tgc atg aga gct tct gga ata ctt gca gct agg gtt cga gat 384
 Ile Glu Cys Met Arg Ala Ser Gly Ile Leu Ala Ala Arg Val Arg Asp
 115 120 125
 tac gct ggc act ttg gtt aag cca ggc gta acc act gat gaa atc gat 432
 Tyr Ala Gly Thr Leu Val Lys Pro Gly Val Thr Thr Asp Glu Ile Asp
 130 135 140
 gaa gca gtt cac aat atg att att gag aat gga gct tat cct tcg cct 480
 Glu Ala Val His Asn Met Ile Ile Glu Asn Gly Ala Tyr Pro Ser Pro
 145 150 155 160
 ctt ggt tat gga ggt ttc ccg aaa agt gtt tgc aca tct gtg aat gaa 528
 Leu Gly Tyr Gly Gly Phe Pro Lys Ser Val Cys Thr Ser Val Asn Glu
 165 170 175
 tgc att tgc cat ggt ata cca gat tca aga cca ctt gag gat ggg gat 576
 180

PF59082SeqList_PF59082.txt

Cys	Ile	Cys	His	Gly	Ile	Pro	Asp	Ser	Arg	Pro	Leu	Glu	Asp	Gly	Asp	
att	atc	aac	atc	gat	gtc	aca	ggt	tat	ttg	aat	ggt	tat	cat	ggt	gat	624
Ile	Ile	Asn	Ile	Asp	Val	Thr	Val	Tyr	Leu	Asn	Gly	Tyr	His	Gly	Asp	
		195					200					205				
act	tca	gca	act	ttc	ttc	tgt	gga	aat	ggt	gac	gag	aag	gct	aaa	aag	672
Thr	Ser	Ala	Thr	Phe	Phe	Cys	Gly	Asn	Val	Asp	Glu	Lys	Ala	Lys	Lys	
	210					215					220					
cta	gtc	gag	gtg	acg	aaa	gag	tct	ctc	gac	aaa	gca	ata	tca	ata	tgt	720
Leu	Val	Glu	Val	Thr	Lys	Glu	Ser	Leu	Asp	Lys	Ala	Ile	Ser	Ile	Cys	
	225				230					235					240	
ggt	ccc	gga	ggt	gag	tac	aag	aaa	atc	ggc	aaa	gtc	att	cat	gat	ctt	768
Gly	Pro	Gly	Val	Glu	Tyr	Lys	Lys	Ile	Gly	Lys	Val	Ile	His	Asp	Leu	
			245					250						255		
gca	gat	aaa	cat	aaa	tat	gga	ggt	ggt	cga	caa	ttt	gta	ggc	cac	ggg	816
Ala	Asp	Lys	His	Lys	Tyr	Gly	Val	Val	Arg	Gln	Phe	Val	Gly	His	Gly	
			260				265						270			
ggt	ggc	agc	gtc	ttc	cac	gct	gat	cca	ggt	ggt	ctg	cat	ttc	cgg	aac	864
Val	Gly	Ser	Val	Phe	His	Ala	Asp	Pro	Val	Val	Leu	His	Phe	Arg	Asn	
		275					280					285				
aat	gaa	gct	gga	cgt	atg	gtc	ttg	aat	caa	acc	ttc	acc	att	gaa	ccg	912
Asn	Glu	Ala	Gly	Arg	Met	Val	Leu	Asn	Gln	Thr	Phe	Thr	Ile	Glu	Pro	
	290					295					300					
atg	ctt	aca	ata	gga	agc	aga	aac	ccg	ata	atg	tgg	gat	gat	aac	tgg	960
Met	Leu	Thr	Ile	Gly	Ser	Arg	Asn	Pro	Ile	Met	Trp	Asp	Asp	Asn	Trp	
	305				310					315					320	
acc	gtg	gta	aca	gaa	gat	gca	agc	ctc	tcg	gcg	caa	ttc	gag	cat	acc	1008
Thr	Val	Val	Thr	Glu	Asp	Ala	Ser	Leu	Ser	Ala	Gln	Phe	Glu	His	Thr	
			325					330						335		
att	ctt	ata	acc	aaa	gat	ggt	gct	gag	att	cta	acc	aag	tgt	taa		1053
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<210> 147

<211> 350

<212> PRT

<213> Arabidopsis thaliana

<400> 147

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			20					25					30			
Phe	Asp	Leu	Gly	Arg	Arg	His	Val	Ser	Met	Gln	Leu	Ser	Arg	Thr	Phe	
		35					40					45				
Ser	Gly	Leu	Thr	Asp	Leu	Leu	Phe	Asn	Arg	Arg	Asn	Glu	Asp	Glu	Val	
	50				55					60						
Ile	Asp	Gly	Lys	Arg	Lys	Arg	Leu	Arg	Pro	Gly	Asn	Val	Ser	Pro	Arg	
65					70				75					80		
Arg	Pro	Val	Pro	Gly	His	Ile	Thr	Lys	Pro	Pro	Tyr	Val	Asp	Ser	Leu	
			85					90					95			
Gln	Ala	Pro	Gly	Ile	Ser	Ser	Gly	Leu	Glu	Val	His	Asp	Lys	Lys	Gly	
		100					105						110			
Ile	Glu	Cys	Met	Arg	Ala	Ser	Gly	Ile	Leu	Ala	Ala	Arg	Val	Arg	Asp	
	115						120					125				
Tyr	Ala	Gly	Thr	Leu	Val	Lys	Pro	Gly	Val	Thr	Thr	Asp	Glu	Ile	Asp	
	130					135				140						
Glu	Ala	Val	His	Asn	Met	Ile	Ile	Glu	Asn	Gly	Ala	Tyr	Pro	Ser	Pro	
145				150					155					160		
Leu	Gly	Tyr	Gly	Gly	Phe	Pro	Lys	Ser	Val	Cys	Thr	Ser	Val	Asn	Glu	
			165					170						175		
Cys	Ile	Cys	His	Gly	Ile	Pro	Asp	Ser	Arg	Pro	Leu	Glu	Asp	Gly	Asp	
		180						185					190			
Ile	Ile	Asn	Ile	Asp	Val	Thr	Val	Tyr	Leu	Asn	Gly	Tyr	His	Gly	Asp	
		195					200					205				
Thr	Ser	Ala	Thr	Phe	Phe	Cys	Gly	Asn	Val	Asp	Glu	Lys	Ala	Lys	Lys	
	210					215					220					
Leu	Val	Glu	Val	Thr	Lys	Glu	Ser	Leu	Asp	Lys	Ala	Ile	Ser	Ile	Cys	240
225					230					235						

PF59082SeqList_PF59082.txt

Gly Pro Gly Val Glu Tyr Lys Lys Ile Gly Lys Val Ile His Asp Leu
 245 250 255
 Ala Asp Lys His Lys Tyr Gly Val Val Arg Gln Phe Val Gly His Gly
 260 265 270
 Val Gly Ser Val Phe His Ala Asp Pro Val Val Leu His Phe Arg Asn
 275 280 285
 Asn Glu Ala Gly Arg Met Val Leu Asn Gln Thr Phe Thr Ile Glu Pro
 290 295 300
 Met Leu Thr Ile Gly Ser Arg Asn Pro Ile Met Trp Asp Asp Asn Trp
 305 310 315 320
 Thr Val Val Thr Glu Asp Ala Ser Leu Ser Ala Gln Phe Glu His Thr
 325 330 335
 Ile Leu Ile Thr Lys Asp Gly Ala Glu Ile Leu Thr Lys Cys
 340 345 350

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 <212> DNA
 <213> Zea mays

<220>
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 Arg Phe Arg Pro Leu Ala Ala Pro Leu Arg Pro Val Arg Ser Gly Lys
 20 25 30
 ttc gtt gtg cca aag cga tgc ttc att gta tca agc agg ctt gca tgg 144
 Phe Val Val Pro Lys Arg Cys Phe Ile Val Ser Ser Arg Leu Ala Trp
 35 40 45
 gtg gaa gat gag ctt atg gag ata caa aag tca caa gag caa agt tca 192
 Val Glu Asp Glu Leu Met Glu Ile Gln Lys Ser Gln Glu Gln Ser Ser
 50 55 60
 gta aaa tca aag aaa agg cca cct ttg agg cgt gga aag gtc tcc cca 240
 Val Lys Ser Lys Lys Arg Pro Pro Leu Arg Arg Gly Lys Val Ser Pro
 65 70 75 80
 caa ctt cct gta cca ggg cac att cca aga cca tct tat gtt ggt gcg 288
 Gln Leu Pro Val Pro Gly His Ile Pro Arg Pro Ser Tyr Val Gly Ala
 85 90 95
 aaa gga ttg cct gaa cta tgc aag ggc caa tta cat gat gct caa gga 336
 Lys Gly Leu Pro Glu Leu Cys Lys Gly Gln Leu His Asp Ala Gln Gly
 100 105 110
 att act gga atg aga gct gct tgc aaa ctt gct gcc cgt gtt ctt gac 384
 Ile Thr Gly Met Arg Ala Ala Cys Lys Leu Ala Ala Arg Val Leu Asp
 115 120 125
 ttc gct ggg act tta gtt aag cca tcc att act aca aat gaa att gac 432
 Phe Ala Gly Thr Leu Val Lys Pro Ser Ile Thr Thr Asn Glu Ile Asp
 130 135 140
 gca gca gtc cat aat atg atc att gag gct ggt gct tat cct tct cca 480
 Ala Ala Val His Asn Met Ile Ile Glu Ala Gly Ala Tyr Pro Ser Pro
 145 150 155 160
 ctt ggc tat cat gga ttt cct aag agt ata tgt aca tca gta aat gag 528
 Leu Gly Tyr His Gly Phe Pro Lys Ser Ile Cys Thr Ser Val Asn Glu
 165 170 175
 tgt gtc tgt cat ggg gta cct gat tca act cag ctg cag aat ggg gat 576
 Cys Val Cys His Gly Val Pro Asp Ser Thr Gln Leu Gln Asn Gly Asp
 180 185 190
 att ata aat att gat gta aat gtg ttc ctg aat gga tac cat ggg ggt 624
 Ile Ile Asn Ile Asp Val Asn Val Phe Leu Asn Gly Tyr His Gly Gly
 195 200 205
 acc tcc aga aca ttt gca tgt gga caa gtg gat gat tct atc aaa cat 672
 Thr Ser Arg Thr Phe Ala Cys Gly Gln Val Asp Asp Ser Ile Lys His
 210 215 220
 ttt ctg aat gca gct gaa gaa tgc ttg gag aaa ggc att tct atc tgc 720
 Phe Leu Asn Ala Ala Glu Glu Cys Leu Glu Lys Gly Ile Ser Ile Cys

PF59082SeqList_PF59082.txt

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					245					250					255		
	gcc	tat	ttt	tat	ggc	tat	tat	gtg	gtg	gaa	cgc	ttt	gtt	ggc	cat	ggg	816
	Ala	Tyr	Phe	Tyr	Gly	Tyr	Tyr	Val	Val	Glu	Arg	Phe	Val	Gly	His	Gly	
					260					265					270		
	att	gga	act	atg	tat	cat	tct	gag	cca	cta	att	cta	cat	cat	gcc	aac	864
	Ile	Gly	Thr	Met	Tyr	His	Ser	Glu	Pro	Leu	Ile	Leu	His	His	Ala	Asn	
					275					280					285		
	gaa	aac	tca	ggg	cgt	atg	gtt	gag	ggc	caa	aca	ttt	aca	att	gaa	cct	912
	Glu	Asn	Ser	Gly	Arg	Met	Val	Glu	Gly	Gln	Thr	Phe	Thr	Ile	Glu	Pro	
							295								300		
	ata	ctc	aca	atg	gag	aaa	aca	gag	tgt	gtt	aca	tgg	gaa	gat	gga	tgg	960
	Ile	Leu	Thr	Met	Glu	Lys	Thr	Glu	Cys	Val	Thr	Trp	Glu	Asp	Gly	Trp	
						310									320		
	acg	act	gtc	act	gct	gat	ggg	agc	tgg	gct	gcg	cag	ttt	gag	cat	acc	1008
	Thr	Thr	Val	Thr	Ala	Asp	Gly	Ser	Trp	Ala	Ala	Gln	Phe	Glu	His	Thr	
					325					330					335		
	ata	ctg	gtg	act	agg	gac	ggg	gca	gaa	ata	ctg	acg	aaa	gtt	tga		1053
	Ile	Leu	Val	Thr	Arg	Asp	Gly	Ala	Glu	Ile	Leu	Thr	Lys	Val			
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<210> 149
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 <212> PRT
 <213> Zea mays

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 35 40 45
 Val Glu Asp Glu Leu Met Glu Ile Gln Lys Ser Gln Glu Gln Ser Ser
 50 55 60
 Val Lys Ser Lys Lys Arg Pro Pro Leu Arg Arg Gly Lys Val Ser Pro
 65 70 75 80
 Gln Leu Pro Val Pro Gly His Ile Pro Arg Pro Ser Tyr Val Gly Ala
 85 90 95
 Lys Gly Leu Pro Glu Leu Cys Lys Gly Gln Leu His Asp Ala Gln Gly
 100 105 110
 Ile Thr Gly Met Arg Ala Ala Cys Lys Leu Ala Ala Arg Val Leu Asp
 115 120 125
 Phe Ala Gly Thr Leu Val Lys Pro Ser Ile Thr Thr Asn Glu Ile Asp
 130 135 140
 Ala Ala Val His Asn Met Ile Ile Glu Ala Gly Ala Tyr Pro Ser Pro
 145 150 155 160
 Leu Gly Tyr His Gly Phe Pro Lys Ser Ile Cys Thr Ser Val Asn Glu
 165 170 175
 Cys Val Cys His Gly Val Pro Asp Ser Thr Gln Leu Gln Asn Gly Asp
 180 185 190
 Ile Ile Asn Ile Asp Val Asn Val Phe Leu Asn Gly Tyr His Gly Gly
 195 200 205
 Thr Ser Arg Thr Phe Ala Cys Gly Gln Val Asp Asp Ser Ile Lys His
 210 215 220
 Phe Leu Asn Ala Ala Glu Glu Cys Leu Glu Lys Gly Ile Ser Ile Cys
 225 230 235 240
 Arg Asp Gly Val Asn Tyr Arg Lys Ile Gly Lys Lys Ile Ser Lys Leu
 245 250 255
 Ala Tyr Phe Tyr Gly Tyr Tyr Val Val Glu Arg Phe Val Gly His Gly
 260 265 270
 Ile Gly Thr Met Tyr His Ser Glu Pro Leu Ile Leu His His Ala Asn
 275 280 285
 Glu Asn Ser Gly Arg Met Val Glu Gly Gln Thr Phe Thr Ile Glu Pro
 290 295 300
 Ile Leu Thr Met Glu Lys Thr Glu Cys Val Thr Trp Glu Asp Gly Trp
 305 310 315 320

PF59082SeqList_PF59082.txt

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 325 330
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 <212> DNA
 <213> Zea mays

<220>
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 <222> (1)..(1047)

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 cgc ctc gca ctc tcc act agg cct ctc ctt ctc cgc tcc gct gtc cca 96
 Arg Leu Ala Leu Ser Thr Arg Pro Leu Leu Leu Arg Ser Ala Val Pro
 20 25 30
 ggc agc agg cgg ctg gcg tat caa gca acg aga acg cta tgc aac ttg 144
 Gly Ser Arg Arg Leu Ala Tyr Gln Ala Thr Arg Thr Leu Cys Asn Leu
 35 40 45
 gtg gat atc cta ttt aac agg aga aat cag gat gat gca cca gaa aac 192
 Val Asp Ile Leu Phe Asn Arg Arg Asn Gln Asp Asp Ala Pro Glu Asn
 50 55 60
 aac cct aga cgc ctg cgt cct ggg aaa gta tct cca cgc ctt agt gtt 240
 Asn Pro Arg Arg Leu Arg Pro Gly Lys Val Ser Pro Arg Leu Ser Val
 65 70 75 80
 ccc aat cat ata caa cgg cct cca tat gtc aat tct cgt caa caa cga 288
 Pro Asn His Ile Gln Arg Pro Pro Tyr Val Asn Ser Arg Gln Gln Arg
 85 90 95
 cct ggt atg aat aat gga cct gaa ata cat gat gag aac ggg atc gag 336
 Pro Gly Met Asn Asn Gly Pro Glu Ile His Asp Glu Asn Gly Ile Glu
 100 105 110
 tgc atg aga gct tct gga aag ctt gct gca cag gtt ttg aaa ttt gct 384
 Cys Met Arg Ala Ser Gly Lys Leu Ala Ala Gln Val Leu Lys Phe Ala
 115 120 125
 ggg act ctt gta aag cca ggc ata acg act gat gaa att gat aaa gca 432
 Gly Thr Leu Val Lys Pro Gly Ile Thr Thr Asp Glu Ile Asp Lys Ala
 130 135 140
 gtg cac caa atg ata att gat aat gga gca cat cct tca cct ctt ggt 480
 Val His Gln Met Ile Ile Asp Asn Gly Ala His Pro Ser Pro Leu Gly
 145 150 155 160
 tat tgt gga tac cca aag agt gtc tgc act tca gtg aat gaa tgc atc 528
 Tyr Cys Gly Tyr Pro Lys Ser Val Cys Thr Ser Val Asn Glu Cys Ile
 165 170 175
 tgt cat ggg att ccg gat tct cgt ccc ctt gag gat gga gat atc atc 576
 Cys His Gly Ile Pro Asp Ser Arg Pro Leu Glu Asp Gly Asp Ile Ile
 180 185 190
 aat att gat gtt act gtc tac ctc aat ggc tac cat ggt gat aca tct 624
 Asn Ile Asp Val Thr Val Tyr Leu Asn Gly Tyr His Gly Asp Thr Ser
 195 200 205
 gct aca ttt ctt tgc ggt gat gtt gat gac gaa gct aag aaa tta gtt 672
 Ala Thr Phe Leu Cys Gly Asp Val Asp Asp Glu Ala Lys Lys Leu Val
 210 215 220
 aag gtg aca aga gaa tgt ctc gac aag gct ata tcg att tgt cca cct 720
 Lys Val Thr Arg Glu Cys Leu Asp Lys Ala Ile Ser Ile Cys Pro Pro
 225 230 235 240
 ggg gtg gag atc aaa caa att ggt aga act ata cag gat cat gca gac 768
 Gly Val Glu Ile Lys Gln Ile Gly Arg Thr Ile Gln Asp His Ala Asp
 245 250 255
 aag ttc aag ttt ggt gta gtt aga cag ttt gtt ggc cat ggg gtt ggc 816
 Lys Phe Lys Phe Gly Val Val Arg Gln Phe Val Gly His Gly Val Gly
 260 265 270
 aaa gtt ttt cat gct gag cct gtt gtg ctt cat ttc aga aac aat gaa 864
 Lys Val Phe His Ala Glu Pro Val Val Leu His Phe Arg Asn Asn Glu
 275 280 285

PF59082SeqList_PF59082.txt

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acc	ata	ggg	agc	atc	aac	cct	gtc	atg	tgg	tcc	gat	gac	tgg	acc	gca	960
Thr	Ile	Gly	Ser	Ile	Asn	Pro	Val	Met	Trp	Ser	Asp	Asp	Trp	Thr	Ala	
305					310					315					320	
gtg	aca	gaa	gac	ggc	agc	ttg	tca	gca	cag	ttt	gag	cac	acg	ata	ctt	1008
Val	Thr	Glu	Asp	Gly	Ser	Leu	Ser	Ala	Gln	Phe	Glu	His	Thr	Ile	Leu	
				325					330					335		
att	acc	gaa	gat	ggc	cct	gaa	ata	ctg	aca	cag	tgt	taa				1047
Ile	Thr	Glu	Asp	Gly	Pro	Glu	Ile	Leu	Thr	Gln	Cys					
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<210> 151
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 <212> PRT
 <213> Zea mays

<400> 151

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			20					25					30			
Gly	Ser	Arg	Arg	Leu	Ala	Tyr	Gln	Ala	Thr	Arg	Thr	Leu	Cys	Asn	Leu	
		35				40						45				
Val	Asp	Ile	Leu	Phe	Asn	Arg	Arg	Asn	Gln	Asp	Asp	Ala	Pro	Glu	Asn	
	50					55				60						
Asn	Pro	Arg	Arg	Leu	Arg	Pro	Gly	Lys	Val	Ser	Pro	Arg	Leu	Ser	Val	
65					70				75						80	
Pro	Asn	His	Ile	Gln	Arg	Pro	Pro	Tyr	Val	Asn	Ser	Arg	Gln	Gln	Arg	
			85					90					95			
Pro	Gly	Met	Asn	Asn	Gly	Pro	Glu	Ile	His	Asp	Glu	Asn	Gly	Ile	Glu	
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Cys	Met	Arg	Ala	Ser	Gly	Lys	Leu	Ala	Ala	Gln	Val	Leu	Lys	Phe	Ala	
	115					120					125					
Gly	Thr	Leu	Val	Lys	Pro	Gly	Ile	Thr	Thr	Asp	Glu	Ile	Asp	Lys	Ala	
	130					135				140						
Val	His	Gln	Met	Ile	Ile	Asp	Asn	Gly	Ala	His	Pro	Ser	Pro	Leu	Gly	
145				150					155					160		
Tyr	Cys	Gly	Tyr	Pro	Lys	Ser	Val	Cys	Thr	Ser	Val	Asn	Glu	Cys	Ile	
			165					170					175			
Cys	His	Gly	Ile	Pro	Asp	Ser	Arg	Pro	Leu	Glu	Asp	Gly	Asp	Ile	Ile	
		180						185				190				
Asn	Ile	Asp	Val	Thr	Val	Tyr	Leu	Asn	Gly	Tyr	His	Gly	Asp	Thr	Ser	
	195					200					205					
Ala	Thr	Phe	Leu	Cys	Gly	Asp	Val	Asp	Asp	Glu	Ala	Lys	Lys	Leu	Val	
	210					215				220						
Lys	Val	Thr	Arg	Glu	Cys	Leu	Asp	Lys	Ala	Ile	Ser	Ile	Cys	Pro	Pro	
225					230				235					240		
Gly	Val	Glu	Ile	Lys	Gln	Ile	Gly	Arg	Thr	Ile	Gln	Asp	His	Ala	Asp	
			245					250						255		
Lys	Phe	Lys	Phe	Gly	Val	Val	Arg	Gln	Phe	Val	Gly	His	Gly	Val	Gly	
		260					265					270				
Lys	Val	Phe	His	Ala	Glu	Pro	Val	Val	Leu	His	Phe	Arg	Asn	Asn	Glu	
	275					280					285					
Trp	Gly	Arg	Met	Met	Leu	Asn	Gln	Thr	Phe	Thr	Ile	Glu	Pro	Met	Leu	
	290					295					300					
Thr	Ile	Gly	Ser	Ile	Asn	Pro	Val	Met	Trp	Ser	Asp	Asp	Trp	Thr	Ala	
305					310					315					320	
Val	Thr	Glu	Asp	Gly	Ser	Leu	Ser	Ala	Gln	Phe	Glu	His	Thr	Ile	Leu	
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Ile	Thr	Glu	Asp	Gly	Pro	Glu	Ile	Leu	Thr	Gln	Cys					
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 <213> Zea mays

PF59082SeqList_PF59082.txt

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<221> CDS

<222> (1)..(1053)

<400> 152

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Arg Phe Arg Pro Leu Ala Ala Pro Leu Arg Pro Val Arg Ser Gly Lys	
20 25 30	
ttc gtt gtg cca aag cga tgc ttc att gta tca agc agg ctt gca tgg	144
Phe Val Val Pro Lys Arg Cys Phe Ile Val Ser Ser Arg Leu Ala Trp	
35 40 45	
gtg gaa gat gag ctt atg gag ata caa aag tca caa gag caa agt tca	192
Val Glu Asp Glu Leu Met Glu Ile Gln Lys Ser Gln Glu Gln Ser Ser	
50 55 60	
gta aaa tca aag aaa agg cca cct ttg agg cgt gga aag gtc tcc cca	240
Val Lys Ser Lys Lys Arg Pro Pro Leu Arg Arg Gly Lys Val Ser Pro	
65 70 75 80	
caa ctt cct gta cca ggg cac att cca aga cca tct tat gtt ggt gcg	288
Gln Leu Pro Val Pro Gly His Ile Pro Arg Pro Ser Tyr Val Gly Ala	
85 90 95	
aaa gga ttg cct gaa cta tgc aag ggc caa tta cat gat gct caa gga	336
Lys Gly Leu Pro Glu Leu Cys Lys Gly Gln Leu His Asp Ala Gln Gly	
100 105 110	
att act gga atg aga gct gct tgc aaa ctt gct gcc cgt gtt ctt gac	384
Ile Thr Gly Met Arg Ala Ala Cys Lys Leu Ala Ala Arg Val Leu Asp	
115 120 125	
ttc gct ggg act tta gtt aag cca tcc att act aca aat gaa att gac	432
Phe Ala Gly Thr Leu Val Lys Pro Ser Ile Thr Thr Asn Glu Ile Asp	
130 135 140	
gca gca gtc cat aat atg atc att gag gct ggt gct tat cct tct cca	480
Ala Ala Val His Asn Met Ile Ile Glu Ala Gly Ala Tyr Pro Ser Pro	
145 150 155 160	
ctt ggc tat cat gga ttt cct aag agt ata tgt aca tca gta aat gag	528
Leu Gly Tyr His Gly Phe Pro Lys Ser Ile Cys Thr Ser Val Asn Glu	
165 170 175	
tgt gtc tgt cat ggg gta cct gat tca act cag ctg cag aat ggg gat	576
Cys Val Cys His Gly Val Pro Asp Ser Thr Gln Leu Gln Asn Gly Asp	
180 185 190	
att ata aat att gat gta aat gtg ttc ctg aat gga tac cat ggg ggt	624
Ile Ile Asn Ile Asp Val Asn Val Phe Leu Asn Gly Tyr His Gly Gly	
195 200 205	
acc tcc aga aca ttt gca tgt gga caa gtg gat gat tct atc aaa cat	672
Thr Ser Arg Thr Phe Ala Cys Gly Gln Val Asp Asp Ser Ile Lys His	
210 215 220	
ttt ctc aat gca gct gaa gaa tgc ttg gag aaa ggc att tct atc tgc	720
Phe Leu Asn Ala Ala Glu Glu Cys Leu Glu Lys Gly Ile Ser Ile Cys	
225 230 235 240	
agg gat ggt gtg aac tac aga aag att ggc aag aaa ata agc aag ctt	768
Arg Asp Gly Val Asn Tyr Arg Lys Ile Gly Lys Lys Ile Ser Lys Leu	
245 250 255	
gcc tat ttt tat ggc tat tat gtg gtg gaa cgc ttt gtt ggg cat ggg	816
Ala Tyr Phe Tyr Gly Tyr Tyr Val Val Glu Arg Phe Val Gly His Gly	
260 265 270	
att gaa act atg tat cat tct gag cca cta att cta cat cat gcc aac	864
Ile Glu Thr Met Tyr His Ser Glu Pro Leu Ile Leu His His Ala Asn	
275 280 285	
gaa aac tca ggg cgt atg gtt gag ggc caa aca ttt aca att gaa cct	912
Glu Asn Ser Gly Arg Met Val Glu Gly Gln Thr Phe Thr Ile Glu Pro	
290 295 300	
ata ctc aca atg gag aaa aca gag tgt gtt aca tgg gaa gat gga tgg	960
Ile Leu Thr Met Glu Lys Thr Glu Cys Val Thr Trp Glu Asp Gly Trp	
305 310 315 320	
acg act gtc act gct gat ggt agc tgg gct gcg cag ttt gag cat acc	1008
Thr Thr Val Thr Ala Asp Gly Ser Trp Ala Ala Gln Phe Glu His Thr	
325 330 335	
ata ctg gtg act agg gac ggt gca gaa ata ctg acg aaa gtc tga	1053

PF59082SeqList_PF59082.txt

	20	25	30	
cgc ttc cat tta ggg aga cgg cat gtt tcg atg caa ttg tca aga acc	144			
Arg Phe His Leu Gly Arg Arg His Val Ser Met Gln Leu Ser Arg Thr				
ttg tct gga tta acc aat ctt ctc ttt aat aca aga aac gtt gat gaa	192			
Leu Ser Gly Leu Thr Asn Leu Phe Asn Thr Arg Asn Val Asp Glu				
gtg att gat gcc aag aga aaa cgt ctg aaa cca gga cac gtg tct cct	240			
Val Ile Asp Ala Lys Arg Lys Arg Leu Lys Pro Gly His Val Ser Pro				
cgc cgc cct gtc cct gcc cac ata acc aaa cct tac gtt gag tct	288			
Arg Arg Pro Val Pro Ala His Ile Thr Lys Pro Pro Tyr Val Glu Ser				
tta aac gtc ccc gga atc tcg agt gga ctt gag att cac gac gag gat	336			
Leu Asn Val Gly Ile Ser Ser Gly Leu Glu Ile His Asp Glu Asp				
ggg gta gag agg atg aga gct tct ggg agg ctt gca gct aga gtt cgt	384			
Gly Val Glu Arg Met Arg Ala Ser Gly Arg Leu Ala Ala Arg Val Arg				
gaa tac gct ggg act ttg gtt aag ccc ggt gtg act aca gat gag att	432			
Glu Tyr Ala Gly Thr Leu Val Lys Pro Gly Val Thr Thr Asp Glu Ile				
gat gag gct gtt cac aac atg atc atc gag aac gga gct tat cct tcg	480			
Asp Glu Ala Val His Asn Met Ile Ile Glu Asn Gly Ala Tyr Pro Ser				
cca ctt ggc tat gga ggt ttc cct aag agt gtt tgc acg tct gtg aat	528			
Pro Leu Gly Tyr Gly Gly Phe Pro Lys Ser Val Cys Thr Ser Val Asn				
gag tgc att tgc cat gga atc ccc gat tca cga ccg ctt gag gat gga	576			
Glu Cys Ile Cys His Gly Ile Pro Asp Ser Arg Pro Leu Glu Asp Gly				
gat ata atc aac att gat gtc aca gtt tat ttg aac ggc tat cac ggt	624			
Asp Ile Ile Asn Ile Asp Val Thr Val Tyr Leu Asn Gly Tyr His Gly				
gat act tca gct act ttc ttc gga gat gtc gac gag aaa gct aaa	672			
Asp Thr Ser Ala Thr Phe Phe Cys Gly Asp Val Asp Glu Lys Ala Lys				
aag cta gtc cag gtg act aaa gag tct ctt gac aaa gct ata tcg ata	720			
Lys Leu Val Gln Val Thr Lys Glu Ser Leu Asp Lys Ala Ile Ser Ile				
tgt gga cct ggt gtt gag tac aag aaa atc ggc aaa atc att cat gat	768			
Cys Gly Pro Gly Val Glu Tyr Lys Lys Ile Gly Lys Ile Ile His Asp				
cat gca gat aaa tat aaa tat gga gtg gtt aga caa ttt gta ggc cac	816			
His Ala Asp Lys Tyr Lys Tyr Gly Val Val Arg Gln Phe Val Gly His				
ggg att gga cgt gtc ttc cat gct gat cct gtt gtt cta cac ttc cgg	864			
Gly Ile Gly Arg Val Phe His Ala Asp Pro Val Val Leu His Phe Arg				
aac aat gaa gct gga cgt atg gtt ttg aat caa acc ttc acc ata gaa	912			
Asn Asn Glu Ala Gly Arg Met Val Leu Asn Gln Thr Phe Thr Ile Glu				
ccg atg cta acc ata gga agc aga aaa ccg att atg tgg gat gat aat	960			
Pro Met Leu Thr Ile Gly Ser Arg Lys Pro Ile Met Trp Asp Asp Asn				
tgg acc gtg gtt aca gaa gat gca agc ctc tct gcg caa ttc gag cat	1008			
Trp Thr Val Val Thr Glu Asp Ala Ser Leu Ser Ala Gln Phe Glu His				
acc att ctt ata acc aaa gat gga gct gag ata ctc acc gac tgt	1053			
Thr Ile Leu Thr Lys Asp Gly Ala Glu Ile Leu Thr Asp Cys				
tag	1056			

<210> 155

<211> 351

<212> PRT

<213> Brassica napus

PF59082SeqList_PF59082.txt

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<400> 155
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1      5      10      15
Gly Asn Asn Ser Ile Leu Val Ser Thr Gln Pro Leu Pro His Leu Phe
20      25      30
Arg Phe His Leu Gly Arg Arg His Val Ser Met Gln Leu Ser Arg Thr
35      40      45
Leu Ser Gly Leu Thr Asn Leu Leu Phe Asn Thr Arg Asn Val Asp Glu
50      55      60
Val Ile Asp Ala Lys Arg Lys Arg Leu Lys Pro Gly His Val Ser Pro
65      70      75
Arg Arg Pro Val Pro Ala His Ile Thr Lys Pro Pro Tyr Val Glu Ser
85      90      95
Leu Asn Val Pro Gly Ile Ser Ser Gly Leu Glu Ile His Asp Glu Asp
100     105
Gly Val Glu Arg Met Arg Ala Ser Gly Arg Leu Ala Ala Arg Val Arg
115     120     125
Glu Tyr Ala Gly Thr Leu Val Lys Pro Gly Val Thr Thr Asp Glu Ile
130     135     140
Asp Glu Ala Val His Asn Met Ile Ile Glu Asn Gly Ala Tyr Pro Ser
145     150     155
Pro Leu Gly Tyr Gly Gly Phe Pro Lys Ser Val Cys Thr Ser Val Asn
165     170     175
Glu Cys Ile Cys His Gly Ile Pro Asp Ser Arg Pro Leu Glu Asp Gly
180     185     190
Asp Ile Ile Asn Ile Asp Val Thr Val Tyr Leu Asn Gly Tyr His Gly
195     200     205
Asp Thr Ser Ala Thr Phe Phe Cys Gly Asp Val Asp Glu Lys Ala Lys
210     215     220
Lys Leu Val Gln Val Thr Lys Glu Ser Leu Asp Lys Ala Ile Ser Ile
225     230     235
Cys Gly Pro Gly Val Glu Tyr Lys Lys Ile Gly Lys Ile Ile His Asp
245     250     255
His Ala Asp Lys Tyr Lys Tyr Gly Val Val Arg Gln Phe Val Gly His
260     265     270
Gly Ile Gly Arg Val Phe His Ala Asp Pro Val Val Leu His Phe Arg
275     280     285
Asn Asn Glu Ala Gly Arg Met Val Leu Asn Gln Thr Phe Thr Ile Glu
290     295     300
Pro Met Leu Thr Ile Gly Ser Arg Lys Pro Ile Met Trp Asp Asp Asn
305     310     315
Trp Thr Val Val Thr Glu Asp Ala Ser Leu Ser Ala Gln Phe Glu His
325     330     335
Thr Ile Leu Ile Thr Lys Asp Gly Ala Glu Ile Leu Thr Asp Cys
340     345     350

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<210> 156
<211> 1071
<212> DNA
<213> Glycine max

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<220>
<221> CDS
<222> (1)..(1071)

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<400> 156
atg gcg agc ggc gcc tca ccg caa ctg caa atg agg ttg aag tcc tct      48
Met Ala Ser Gly Ala Ser Pro Gln Leu Gln Met Arg Leu Lys Ser Ser
1      5      10      15
ttc atc gga gat cgt ctc tta cgc tgt tca act tca agg cac caa cct      96
Phe Ile Gly Asp Arg Leu Leu Arg Cys Ser Thr Ser Arg His Gln Pro
20      25      30
ctt cct caa cta ttc cgt tac aac cct gga acc aag cat gtt tcg atg      144
Leu Pro Gln Leu Phe Arg Tyr Asn Pro Gly Thr Lys His Val Ser Met
35      40      45
cag tta tct aga aca ctt tct ggc ttg acc aat ctc ttt ttt aat aga      192
Gln Leu Ser Arg Thr Leu Ser Gly Leu Thr Asn Leu Phe Phe Asn Arg
50      55      60

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PF59082SeqList_PF59082.txt

aga	aat	ttg	gat	gaa	ttg	cct	aac	agc	aag	cgt	aaa	cgt	ctg	aga	cct	240
Arg	Asn	Leu	Asp	Glu	Leu	Pro	Asn	Ser	Lys	Arg	Lys	Arg	Leu	Arg	Pro	
65					70					75					80	
ggg	aaa	gtt	tct	ccg	cgg	cga	cag	gtg	ccg	aag	aat	ata	ccg	agg	cct	288
Gly	Lys	Val	Ser	Pro	Arg	Arg	Gln	Val	Pro	Lys	Asn	Ile	Pro	Arg	Pro	
				85					90					95		
ccg	tat	gtg	aat	tct	atg	att	cct	cca	ggg	att	gcc	agt	gga	gct	gaa	336
Pro	Tyr	Val	Asn	Ser	Met	Ile	Pro	Pro	Gly	Ile	Ala	Ser	Gly	Ala	Glu	
			100				105				110					
gtg	cat	gac	aag	aaa	ggg	ata	gaa	tgc	atg	aga	gct	tct	gga	agg	ctt	384
Val	His	Asp	Lys	Lys	Gly	Ile	Glu	Cys	Met	Arg	Ala	Ser	Gly	Arg	Leu	
		115				120					125					
gca	gcg	cag	gtt	ctt	caa	tat	gct	ggc	acc	tta	gtt	aag	cca	ggc	ata	432
Ala	Ala	Gln	Val	Leu	Gln	Tyr	Ala	Gly	Thr	Leu	Val	Lys	Pro	Gly	Ile	
	130					135					140					
aca	aca	gat	gaa	att	gac	caa	gca	gtt	cac	caa	atg	ata	att	gat	aat	480
Thr	Thr	Asp	Glu	Ile	Asp	Gln	Ala	Val	His	Gln	Met	Ile	Ile	Asp	Asn	
	145				150				155						160	
ggg	gca	tac	cca	tct	cct	ctc	ggc	tat	ggg	agt	ttt	cct	aag	agt	gtc	528
Gly	Ala	Tyr	Pro	Ser	Pro	Leu	Gly	Tyr	Gly	Ser	Phe	Pro	Lys	Ser	Val	
			165					170						175		
tgc	aca	tct	gta	aat	gaa	tgc	att	tgc	cat	gga	ata	cca	gaa	tcc	cgt	576
Cys	Thr	Ser	Val	Asn	Glu	Cys	Ile	Cys	His	Gly	Ile	Pro	Glu	Ser	Arg	
		180				185						190				
gcc	ctt	gag	gat	ggg	gat	ata	atc	aac	att	gat	gtt	act	gtt	tat	cta	624
Ala	Leu	Glu	Asp	Gly	Asp	Ile	Ile	Asn	Ile	Asp	Val	Thr	Val	Tyr	Leu	
		195				200						205				
aat	ggc	tat	cat	ggg	gac	aca	tca	gca	act	ttc	tat	tgt	gga	gat	gtt	672
Asn	Gly	Tyr	His	Gly	Asp	Thr	Ser	Ala	Thr	Phe	Tyr	Cys	Gly	Asp	Val	
	210				215						220					
gat	gat	gaa	gct	aaa	aaa	cta	gtt	cag	gta	act	aaa	gaa	tgc	cta	gat	720
Asp	Asp	Glu	Ala	Lys	Lys	Leu	Val	Gln	Val	Thr	Lys	Glu	Cys	Leu	Asp	
	225				230				235					240		
aaa	gca	ata	tca	ata	tgt	gca	cca	gga	gtg	gag	ttc	aag	aaa	att	ggc	768
Lys	Ala	Ile	Ser	Ile	Cys	Ala	Pro	Gly	Val	Glu	Phe	Lys	Lys	Ile	Gly	
			245					250						255		
aaa	aca	att	cat	gat	cat	gca	gat	aaa	tat	cgt	tat	ggg	gtt	gtc	cga	816
Lys	Thr	Ile	His	Asp	His	Ala	Asp	Lys	Tyr	Arg	Tyr	Gly	Val	Val	Arg	
		260					265						270			
cag	ttt	gtt	ggc	cat	gga	gtt	gga	agt	gtt	ttt	cat	gct	gat	cct	gtt	864
Gln	Phe	Val	Gly	His	Gly	Val	Gly	Ser	Val	Phe	His	Ala	Asp	Pro	Val	
		275				280						285				
att	ctt	cac	tat	aga	aac	aat	gaa	agt	gga	cga	atg	gtg	cta	aat	caa	912
Ile	Leu	His	Tyr	Arg	Asn	Asn	Glu	Ser	Gly	Arg	Met	Val	Leu	Asn	Gln	
	290				295						300					
acc	ttt	aca	att	gaa	cct	atg	ctg	act	att	ggc	agc	atc	aat	cct	gtg	960
Thr	Phe	Thr	Ile	Glu	Pro	Met	Leu	Thr	Ile	Gly	Ser	Ile	Asn	Pro	Val	
	305				310				315					320		
atg	tgg	aat	gac	gac	tgg	aca	gtt	gta	acg	gaa	gat	gga	agc	ctt	tca	1008
Met	Trp	Asn	Asp	Asp	Trp	Thr	Val	Val	Thr	Glu	Asp	Gly	Ser	Leu	Ser	
			325					330						335		
gca	cag	ttt	gaa	cac	acc	att	ctg	ata	aca	cct	gac	ggg	gct	gag	att	1056
Ala	Gln	Phe	Glu	His	Thr	Ile	Leu	Ile	Thr	Pro	Asp	Gly	Ala	Glu	Ile	
			340				345						350			
atg	act	caa	tgc	tga												1071
Met	Thr	Gln	Cys													
		355														

<210> 157

<211> 356

<212> PRT

<213> Glycine max

<400> 157

Met	Ala	Ser	Gly	Ala	Ser	Pro	Gln	Leu	Gln	Met	Arg	Leu	Lys	Ser	Ser
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Phe	Ile	Gly	Asp	Arg	Leu	Leu	Arg	Cys	Ser	Thr	Ser	Arg	His	Gln	Pro
			20					25					30		
Leu	Pro	Gln	Leu	Phe	Arg	Tyr	Asn	Pro	Gly	Thr	Lys	His	Val	Ser	Met

PF59082SeqList_PF59082.txt

35 40 45
 Gln Leu Ser Arg Thr Leu Ser Gly Leu Thr Asn Leu Phe Phe Asn Arg
 50 55 60
 Arg Asn Leu Asp Glu Leu Pro Asn Ser Lys Arg Lys Arg Leu Arg Pro
 65 70 75
 Gly Lys Val Ser Pro Arg Arg Gln Val Pro Lys Asn Ile Pro Arg Pro
 85 90 95
 Pro Tyr Val Asn Ser Met Ile Pro Pro Gly Ile Ala Ser Gly Ala Glu
 100 105 110
 Val His Asp Lys Lys Gly Ile Glu Cys Met Arg Ala Ser Gly Arg Leu
 115 120 125
 Ala Ala Gln Val Leu Gln Tyr Ala Gly Thr Leu Val Lys Pro Gly Ile
 130 135 140
 Thr Thr Asp Glu Ile Asp Gln Ala Val His Gln Met Ile Ile Asp Asn
 145 150 155
 Gly Ala Tyr Pro Ser Pro Leu Gly Tyr Gly Ser Phe Pro Lys Ser Val
 165 170 175
 Cys Thr Ser Val Asn Glu Cys Ile Cys His Gly Ile Pro Glu Ser Arg
 180 185 190
 Ala Leu Glu Asp Gly Asp Ile Ile Asn Ile Asp Val Thr Val Tyr Leu
 195 200 205
 Asn Gly Tyr His Gly Asp Thr Ser Ala Thr Phe Tyr Cys Gly Asp Val
 210 215 220
 Asp Asp Glu Ala Lys Lys Leu Val Gln Val Thr Lys Glu Cys Leu Asp
 225 230 235
 Lys Ala Ile Ser Ile Cys Ala Pro Gly Val Glu Phe Lys Lys Ile Gly
 245 250 255
 Lys Thr Ile His Asp His Ala Asp Lys Tyr Arg Tyr Gly Val Val Arg
 260 265 270
 Gln Phe Val Gly His Gly Val Gly Ser Val Phe His Ala Asp Pro Val
 275 280 285
 Ile Leu His Tyr Arg Asn Asn Glu Ser Gly Arg Met Val Leu Asn Gln
 290 295 300
 Thr Phe Thr Ile Glu Pro Met Leu Thr Ile Gly Ser Ile Asn Pro Val
 305 310 315
 Met Trp Asn Asp Asp Trp Thr Val Val Thr Glu Asp Gly Ser Leu Ser
 325 330 335
 Ala Gln Phe Glu His Thr Ile Leu Ile Thr Pro Asp Gly Ala Glu Ile
 340 345 350
 Met Thr Gln Cys
 355

<210> 158
 <211> 1101
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (1)..(1101)

<400> 158	
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Met Ala Leu Thr Ala Ser Leu Ala Asn Asn Ala Phe Leu Lys Ile Pro	
1 5 10 15	
aca ctc cat cat ggc gaa tgc tca ctg tct tcg tca tcc ttc atc ggt	96
Thr Leu His His Gly Glu Cys Ser Leu Ser Ser Ser Ser Phe Ile Gly	
20 25 30	
tct cgg ctc aca ctc tcg cgc tct tgt act ctt caa ggg aac caa ttg	144
Ser Arg Leu Thr Leu Ser Arg Cys Thr Leu Gln Gly Asn Gln Leu	
35 40 45	
ctt tcg aga aag caa ttc gtg gtt ttc gcg agg aag att tcg ggg ttg	192
Leu Ser Arg Lys Gln Phe Val Val Phe Ala Arg Lys Ile Ser Gly Leu	
50 55 60	
gag gag gcc atg aat atc aga aga gaa cgt gaa gtt gtt cca	240
Glu Glu Ala Met Asn Ile Arg Arg Glu Arg Glu Val Arg Val Val Pro	
65 70 75 80	
aag ttt aag aaa agg cct cca tta agg cgt ggg aga gta tca cca cat	288
Lys Phe Lys Lys Arg Pro Pro Leu Arg Arg Gly Arg Val Ser Pro His	

PF59082SeqList_PF59082.txt

	85	90	95	
ctc cct gtt cct gac cac ata cca agg cct cct tat gta ggt tca gat	336			
Leu Pro Val Pro Asp His Ile Pro Arg Pro Pro Tyr Val Gly Ser Asp				
ata ctt cca gaa att gca agt gag cat caa att cat gat tct gaa ggt	384			
Ile Leu Pro Glu Ile Ala Ser Glu His Gln Ile His Asp Ser Glu Gly				
ata gct aaa atg agg gct gca ggt gag ctt gca gcg cat gtc tta aac	432			
Ile Ala Lys Met Arg Ala Ala Gly Glu Leu Ala Ala His Val Leu Asn				
ttt gca gga act atg gtt agg cct tcc ata aca act aat gag att gat	480			
Phe Ala Gly Thr Met Val Arg Pro Ser Ile Thr Thr Asn Glu Ile Asp				
aaa gca gtg cac cag atg ata att gat gcc ggt gct tat ccc tca ccc	528			
Lys Ala Val His Gln Met Ile Ile Asp Ala Gly Ala Tyr Pro Ser Pro				
ctt ggc tat ggt gga ttt ccg aaa agc gtg tgc aca tca gtt aat gag	576			
Leu Gly Tyr Gly Gly Phe Pro Lys Ser Val Cys Thr Ser Val Asn Glu				
tgc atg tgc cat gga ata cct gat tct cgg cag tta cag aat ggt gat	624			
Cys Met Cys His Gly Ile Pro Asp Ser Arg Gln Leu Gln Asn Gly Asp				
att att aac att gat gtg aca gtc tac ctg gat gga tat cat gga gac	672			
Ile Ile Asn Ile Asp Val Thr Val Tyr Leu Asp Gly Tyr His Gly Asp				
aca tca aag aca ttt ttt tgt ggg gaa gtc ggt gat gaa ctc aaa aat	720			
Thr Ser Lys Thr Phe Phe Cys Gly Glu Val Gly Asp Glu Leu Lys Asn				
ctt gtt aag gta act gaa gag tgc ctg gag aag gga ata gct gcg tgc	768			
Leu Val Lys Val Thr Glu Glu Cys Leu Glu Lys Gly Ile Ala Ala Cys				
aag gac ggt gct ctc ttt agg aaa att gga aag aga atc agt gag cat	816			
Lys Asp Gly Ala Leu Phe Arg Lys Ile Gly Lys Arg Ile Ser Glu His				
gct gaa aag tat ggc tat ggt gta gtg gag cgt ttt gtt ggg cat ggt	864			
Ala Glu Lys Tyr Gly Tyr Gly Val Val Glu Arg Phe Val Gly His Gly				
gtg gga aca gtg ttc cat tct gaa cca att att atg cac aat cgc aat	912			
Val Gly Thr Val Phe His Ser Glu Pro Ile Ile Met His Asn Arg Asn				
gag aag gca ggt cgc atg att gaa ggt caa aca ttt aca att gag ccg	960			
Glu Lys Ala Gly Arg Met Ile Glu Gly Gln Thr Phe Thr Ile Glu Pro				
att ctt tcg atg gga agc att gat tcc att aca tgg cct gac aac tgg	1008			
Ile Leu Ser Met Gly Ser Ile Asp Ser Ile Thr Trp Pro Asp Asn Trp				
aca aca ata aca gct gat ggt agt ccg gct gca cag ttt gag cat acc	1056			
Thr Thr Ile Thr Ala Asp Gly Ser Pro Ala Ala Gln Phe Glu His Thr				
att ttg ata act aag act gga gcc gaa att ttg act aaa tgt tga	1101			
Ile Leu Ile Thr Lys Thr Gly Ala Glu Ile Leu Thr Lys Cys				

<210> 159
 <211> 366
 <212> PRT
 <213> Glycine max

<400> 159
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 1 5 10 15
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 20 25 30
 Ser Arg Leu Thr Leu Ser Arg Ser Cys Thr Leu Gln Gly Asn Gln Leu
 35 40 45
 Leu Ser Arg Lys Gln Phe Val Val Phe Ala Arg Lys Ile Ser Gly Leu
 50 55 60
 Glu Glu Ala Met Asn Ile Arg Arg Glu Arg Val Arg Val Val Pro
 65 70 75 80

PF59082SeqList_PF59082.txt

Lys Phe Lys Lys Arg Pro Pro Leu Arg Arg Gly Arg Val Ser Pro His
 85 90 95
 Leu Pro Val Pro Asp His Ile Pro Arg Pro Pro Tyr Val Gly Ser Asp
 100 105 110
 Ile Leu Pro Glu Ile Ala Ser Glu His Gln Ile His Asp Ser Glu Gly
 115 120 125
 Ile Ala Lys Met Arg Ala Ala Gly Glu Leu Ala Ala His Val Leu Asn
 130 135 140
 Phe Ala Gly Thr Met Val Arg Pro Ser Ile Thr Thr Asn Glu Ile Asp
 145 150 155 160
 Lys Ala Val His Gln Met Ile Ile Asp Ala Gly Ala Tyr Pro Ser Pro
 165 170 175
 Leu Gly Tyr Gly Gly Phe Pro Lys Ser Val Cys Thr Ser Val Asn Glu
 180 185 190
 Cys Met Cys His Gly Ile Pro Asp Ser Arg Gln Leu Gln Asn Gly Asp
 195 200 205
 Ile Ile Asn Ile Asp Val Thr Val Tyr Leu Asp Gly Tyr His Gly Asp
 210 215 220
 Thr Ser Lys Thr Phe Phe Cys Gly Glu Val Gly Asp Glu Leu Lys Asn
 225 230 235 240
 Leu Val Lys Val Thr Glu Glu Cys Leu Glu Lys Gly Ile Ala Ala Cys
 245 250 255
 Lys Asp Gly Ala Leu Phe Arg Lys Ile Gly Lys Arg Ile Ser Glu His
 260 265 270
 Ala Glu Lys Tyr Gly Tyr Gly Val Glu Arg Phe Val Gly His Gly
 275 280 285
 Val Gly Thr Val Phe His Ser Glu Pro Ile Ile Met His Asn Arg Asn
 290 295 300
 Glu Lys Ala Gly Arg Met Ile Glu Gly Gln Thr Phe Thr Ile Glu Pro
 305 310 315 320
 Ile Leu Ser Met Gly Ser Ile Asp Ser Ile Thr Trp Pro Asp Asn Trp
 325 330 335
 Thr Thr Ile Thr Ala Asp Gly Ser Pro Ala Ala Gln Phe Glu His Thr
 340 345 350
 Ile Leu Ile Thr Lys Thr Gly Ala Glu Ile Leu Thr Lys Cys
 355 360 365

<210> 160
 <211> 1101
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (1)..(1101)

<400> 160
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 Met Ala Leu Thr Ala Ser Leu Ala Asn Asn Ala Phe Leu Lys Ile Pro
 1 5 10 15
 aca ctc cat cat ggc gaa tgc tca ctg tct tcg tca tcc ttc atc ggt 96
 Thr Leu His His Gly Glu Cys Ser Leu Ser Ser Ser Phe Ile Gly
 20 25 30
 tct cgg ctc aca ctc tcg cgc tct tgt act ctt caa ggg aac caa ttg 144
 Ser Arg Leu Thr Leu Ser Arg Ser Cys Thr Leu Gln Gly Asn Gln Leu
 35 40 45
 ctt tcg aga aag caa ttc gtg gtt ttc gcg agg aag att tcg ggg ttg 192
 Leu Ser Arg Lys Gln Phe Val Val Phe Ala Arg Lys Ile Ser Gly Leu
 50 55 60
 gag gag gcc atg aat atc aga aga gaa cgt gaa gtt gtt cca 240
 Glu Glu Ala Met Asn Ile Arg Arg Glu Arg Glu Val Arg Val Val Pro
 65 70 75 80
 aag ttt aag aaa agg cct cca tta agg cgt ggg aga gta tca cca cat 288
 Lys Phe Lys Lys Arg Pro Pro Leu Arg Arg Gly Arg Val Ser Pro His
 85 90 95
 ctc cct gtt cct gac cac ata cca agg cct cct tat gta ggt tca gat 336
 Leu Pro Val Pro Asp His Ile Pro Arg Pro Pro Tyr Val Gly Ser Asp
 100 105 110
 ata ctt cca gaa att gca agt gag cat caa att cat gat tct gaa ggt 384

PF59082SeqList_PF59082.txt

Ile	Leu	Pro	Glu	Ile	Ala	Ser	Glu	His	Gln	Ile	His	Asp	Ser	Glu	Gly	
ata	gct	aaa	atg	agg	gct	gca	ggg	gag	ctt	gca	gcg	cat	gtc	tta	aac	432
Ile	Ala	Lys	Met	Arg	Ala	Ala	Gly	Glu	Leu	Ala	Ala	His	Val	Leu	Asn	
130						135				140						
ttt	gca	gga	act	atg	gtt	agg	cct	tct	gta	aca	act	aat	gag	att	gat	480
Phe	Ala	Gly	Thr	Met	Val	Arg	Pro	Ser	Val	Thr	Thr	Asn	Glu	Ile	Asp	
145					150					155					160	
aaa	gca	gtg	cac	cag	atg	ata	att	gat	gcc	ggg	gct	tat	ccc	tca	ccc	528
Lys	Ala	Val	His	Gln	Met	Ile	Ile	Asp	Ala	Gly	Ala	Tyr	Pro	Ser	Pro	
				165					170					175		
ctt	ggc	tat	ggg	gga	ttt	ccg	aaa	agc	gtg	tgc	aca	tca	ggt	aat	gag	576
Leu	Gly	Tyr	Gly	Gly	Phe	Pro	Lys	Ser	Val	Cys	Thr	Ser	Val	Asn	Glu	
			180					185					190			
tgc	atg	tgc	cat	gga	ata	cct	gat	tct	cgg	cag	tta	cag	aat	ggg	gat	624
Cys	Met	Cys	His	Gly	Ile	Pro	Asp	Ser	Arg	Gln	Leu	Gln	Asn	Gly	Asp	
		195				200						205				
att	att	aac	att	gat	gtg	aca	gtc	tac	ctg	gat	gga	tat	cac	gga	gac	672
Ile	Ile	Asn	Ile	Asp	Val	Thr	Val	Tyr	Leu	Asp	Gly	Tyr	His	Gly	Asp	
210						215					220					
aca	tca	aag	aca	ttt	ttt	tgt	ggg	gaa	gtc	agt	gat	gaa	ctg	aaa	aat	720
Thr	Ser	Lys	Thr	Phe	Phe	Cys	Gly	Glu	Val	Ser	Asp	Glu	Leu	Lys	Asn	
225				230				235						240		
ctt	gtc	aag	gta	act	gaa	gaa	tgc	ctg	gag	aag	gga	ata	gct	gcg	tgc	768
Leu	Val	Lys	Val	Thr	Glu	Glu	Cys	Leu	Glu	Lys	Gly	Ile	Ala	Ala	Cys	
				245				250						255		
aag	gac	ggg	gct	ctc	ttt	agg	aaa	att	gga	aag	aga	atc	agt	gag	cat	816
Lys	Asp	Gly	Ala	Leu	Phe	Arg	Lys	Ile	Gly	Lys	Arg	Ile	Ser	Glu	His	
			260			265						270				
gct	gaa	aag	tat	ggc	tat	ggg	gta	gtg	gag	cgt	ttt	gtt	ggg	cat	ggg	864
Ala	Glu	Lys	Tyr	Gly	Tyr	Gly	Val	Val	Glu	Arg	Phe	Val	Gly	His	Gly	
		275				280						285				
gtg	gga	aca	gtg	ttc	cat	tct	gaa	cca	att	att	atg	cac	aat	cg	aat	912
Val	Gly	Thr	Val	Phe	His	Ser	Glu	Pro	Ile	Ile	Met	His	Asn	Arg	Asn	
290						295					300					
gag	aag	gca	ggg	cg	atg	att	gaa	ggg	caa	aca	ttt	aca	att	gag	ccg	960
Glu	Lys	Ala	Gly	Arg	Met	Ile	Glu	Gly	Gln	Thr	Phe	Thr	Ile	Glu	Pro	
305				310				315						320		
att	ctt	tcg	atg	gga	agc	att	gat	tcc	att	aca	tgg	cct	gac	aac	tgg	1008
Ile	Leu	Ser	Met	Gly	Ser	Ile	Asp	Ser	Ile	Thr	Trp	Pro	Asp	Asn	Trp	
				325				330						335		
aca	aca	ata	aca	gct	gat	ggg	agt	ccg	gct	gca	cag	ttt	gag	cat	acc	1056
Thr	Thr	Ile	Thr	Ala	Asp	Gly	Ser	Pro	Ala	Ala	Gln	Phe	Glu	His	Thr	
			340			345						350				
att	ttg	ata	act	aag	act	gga	gcc	gaa	att	ttg	act	aaa	tgt	tga		1101
Ile	Leu	Ile	Thr	Lys	Thr	Gly	Ala	Glu	Ile	Leu	Thr	Lys	Cys			
		355				360						365				

<210> 161
 <211> 366
 <212> PRT
 <213> Glycine max

<400> 161
 Met Ala Leu Thr Ala Ser Leu Ala Asn Asn Ala Phe Leu Lys Ile Pro
 1 5 10 15
 Thr Leu His His Gly Glu Cys Ser Leu Ser Ser Ser Phe Ile Gly
 20 25 30
 Ser Arg Leu Thr Leu Ser Arg Ser Cys Thr Leu Gln Gly Asn Gln Leu
 35 40 45
 Leu Ser Arg Lys Gln Phe Val Val Phe Ala Arg Lys Ile Ser Gly Leu
 50 55 60
 Glu Glu Ala Met Asn Ile Arg Arg Glu Arg Val Arg Val Val Pro
 65 70 75
 Lys Phe Lys Lys Arg Pro Pro Leu Arg Arg Gly Arg Val Ser Pro His
 85 90 95
 Leu Pro Val Pro Asp His Ile Pro Arg Pro Pro Tyr Val Gly Ser Asp
 100 105 110
 Ile Leu Pro Glu Ile Ala Ser Glu His Gln Ile His Asp Ser Glu Gly
 Seite 194

PF59082SeqList_PF59082.txt

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115      120      125
Ile Ala Lys Met Arg Ala Ala Gly Glu Leu Ala Ala His Val Leu Asn
130      135      140
Phe Ala Gly Thr Met Val Arg Pro Ser Val Thr Thr Asn Glu Ile Asp
145      150      155
Lys Ala Val His Gln Met Ile Ile Asp Ala Gly Ala Tyr Pro Ser Pro
165      170
Leu Gly Tyr Gly Gly Phe Pro Lys Ser Val Cys Thr Ser Val Asn Glu
180      185
Cys Met Cys His Gly Ile Pro Asp Ser Arg Gln Leu Gln Asn Gly Asp
195      200
Ile Ile Asn Ile Asp Val Thr Val Tyr Leu Asp Gly Tyr His Gly Asp
210      215      220
Thr Ser Lys Thr Phe Phe Cys Gly Glu Val Ser Asp Glu Leu Lys Asn
225      230      235
Leu Val Lys Val Thr Glu Cys Leu Glu Lys Gly Ile Ala Ala Cys
245      250
Lys Asp Gly Ala Leu Phe Arg Lys Ile Gly Lys Arg Ile Ser Glu His
260      265
Ala Glu Lys Tyr Gly Tyr Gly Val Glu Arg Phe Val Gly His Gly
275      280      285
Val Gly Thr Val Phe His Ser Glu Pro Ile Ile Met His Asn Arg Asn
290      295      300
Glu Lys Ala Gly Arg Met Ile Glu Gly Gln Thr Phe Thr Ile Glu Pro
305      310      315
Ile Leu Ser Met Gly Ser Ile Asp Ser Ile Thr Trp Pro Asp Asn Trp
325      330
Thr Thr Ile Thr Ala Asp Gly Ser Pro Ala Ala Gln Phe Glu His Thr
340      345      350
Ile Leu Ile Thr Lys Thr Gly Ala Glu Ile Leu Thr Lys Cys
355      360      365

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<210> 162
 <211> 1011
 <212> DNA
 <213> Hordeum vulgare

<220>
 <221> CDS
 <222> (1)..(1011)

```

<400> 162
atg gcg gtc aga gtc cag tcc atg gag ctg aac cgc tcc ccg acg ctc      48
Met Ala Val Arg Val Gln Ser Met Glu Leu Asn Arg Ser Pro Thr Leu
1      5      10      15
ctc tcc ggc ggc cga ggc aaa aca tgc ccg ttc att ata caa gca aag      96
Leu Ser Gly Gly Arg Gly Lys Thr Cys Pro Phe Ile Ile Gln Ala Lys
20      25      30
aga tca ggg gga tta gag aaa gca aat aca agg tcg caa gct tct gaa      144
Arg Ser Gly Gly Leu Glu Lys Ala Asn Thr Arg Ser Gln Ala Ser Glu
35      40      45
aaa ctc aag aaa aga gaa ccc ctg acc cgt ggg att gtt agt gca cct      192
Lys Leu Lys Lys Arg Glu Pro Leu Thr Arg Gly Ile Val Ser Ala Pro
50      55      60
ctt ccg gta cca ggc cat ata cct cga cct cct tat gtt gga tca aac      240
Leu Pro Val Pro Gly His Ile Pro Arg Pro Pro Tyr Val Gly Ser Asn
65      70      75      80
aaa atg cca gag ata tcg agt gag aga caa atg cag gac aaa gag agc      288
Lys Met Pro Glu Ile Ser Ser Glu Arg Gln Met Gln Asp Lys Glu Ser
85      90      95
atc gtg cac atg aaa gct tca tgt gag ctt gct gct cgt gtt ctt gaa      336
Ile Val His Met Lys Ala Ser Cys Glu Leu Ala Ala Arg Val Leu Glu
100      105      110
aat gca ggg aaa tta gtc aaa cct tct gta aca acc gac gaa att gat      384
Asn Ala Gly Lys Leu Val Lys Pro Ser Val Thr Thr Asp Glu Ile Asp
115      120      125
aaa gca gtg cac aag atg atc att gat gct gga gcc tat cca tcc ccg      432
Lys Ala Val His Lys Met Ile Ile Asp Ala Gly Ala Tyr Pro Ser Pro
130      135      140

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PF59082SeqList_PF59082.txt

ctt gga tac ggc ggg ttt cca aaa agt gta tgc aca tca gtg aac gaa	480
Leu Gly Tyr Gly Gly Phe Pro Lys Ser Val Cys Thr Ser Val Asn Glu	
145 150 155 160	
tgc atg tgc cat ggt att cct gat tca cga gaa cta aag gat gga gac	528
Cys Met Cys His Gly Ile Pro Asp Ser Arg Glu Leu Lys Asp Gly Asp	
165 170 175	
ata ata aac att gac gtc act gtc tac ttg aat ggt ttt cat ggg gat	576
Ile Ile Asn Ile Asp Val Thr Val Tyr Leu Asn Gly Phe His Gly Asp	
180 185 190	
acc tct aaa acg ttt ttc tgt gga gaa gtt gac gaa gct act aaa aga	624
Thr Ser Lys Thr Phe Phe Cys Gly Glu Val Asp Glu Ala Thr Lys Arg	
195 200 205	
ctt gtg aag gtt act gaa gaa tgc atg ctt agg ggc ata tca gcc tgc	672
Leu Val Lys Val Thr Glu Glu Cys Met Leu Arg Gly Ile Ser Ala Cys	
210 215 220	
aaa cat ggt gtg agc ttt aag aaa att ggc aga aga ata agc gag cat	720
Lys His Gly Val Ser Phe Lys Lys Ile Gly Arg Arg Ile Ser Glu His	
225 230 235 240	
gct gag agg cat ggc ttt ggt gtt gtg gag caa ttt gtt ggg cat gga	768
Ala Glu Arg His Gly Phe Gly Val Val Glu Gln Phe Val Gly His Gly	
245 250 255	
gtt ggc aga gta ttc cat tca cag cca att ata tat cac cag cgc aac	816
Val Gly Arg Val Phe His Ser Gln Pro Ile Ile Tyr His Gln Arg Asn	
260 265 270	
aac atg ccg ggg cag atg gta gaa ggc cag acg ttc aca ata gag ccg	864
Asn Met Pro Gly Gln Met Val Glu Gly Gln Thr Phe Thr Ile Glu Pro	
275 280 285	
atc ctg acc atg gga cgc agc agc atc gag tgc gac atg tgg gag gac	912
Ile Leu Thr Met Gly Arg Ser Ser Ile Glu Cys Asp Met Trp Glu Asp	
290 295 300	
ggc tgg acg gcg gtg acg agc gac ggc agc ctg gcg gcg cag ttc gag	960
Gly Trp Thr Ala Val Thr Thr Asp Gly Ser Leu Ala Ala Gln Phe Glu	
305 310 315 320	
cac acc atc ctc atc acc agg acc ggc gcg gag atc ctc acc aaa tgc	1008
His Thr Ile Leu Ile Thr Arg Thr Gly Ala Glu Ile Leu Thr Lys Cys	
325 330 335	
tag	1011

<210> 163
 <211> 336
 <212> PRT
 <213> Hordeum vulgare

<400> 163
 Met Ala Val Arg Val Gln Ser Met Glu Leu Asn Arg Ser Pro Thr Leu
 1 5 10 15
 Leu Ser Gly Gly Arg Gly Lys Thr Cys Pro Phe Ile Ile Gln Ala Lys
 20 25 30
 Arg Ser Gly Gly Leu Glu Lys Ala Asn Thr Arg Ser Gln Ala Ser Glu
 35 40 45
 Lys Leu Lys Lys Arg Glu Pro Leu Thr Arg Gly Ile Val Ser Ala Pro
 50 55 60
 Leu Pro Val Pro Gly His Ile Pro Arg Pro Pro Tyr Val Gly Ser Asn
 65 70 75 80
 Lys Met Pro Glu Ile Ser Ser Glu Arg Gln Met Gln Asp Lys Glu Ser
 85 90 95
 Ile Val His Met Lys Ala Ser Cys Glu Leu Ala Ala Arg Val Leu Glu
 100 105 110
 Asn Ala Gly Lys Leu Val Lys Pro Ser Val Thr Thr Asp Glu Ile Asp
 115 120 125
 Lys Ala Val His Lys Met Ile Ile Asp Ala Gly Ala Tyr Pro Ser Pro
 130 135 140
 Leu Gly Tyr Gly Gly Phe Pro Lys Ser Val Cys Thr Ser Val Asn Glu
 145 150 155 160
 Cys Met Cys His Gly Ile Pro Asp Ser Arg Glu Leu Lys Asp Gly Asp
 165 170 175
 Ile Ile Asn Ile Asp Val Thr Val Tyr Leu Asn Gly Phe His Gly Asp

PF59082SeqList_PF59082.txt

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      180      185      190
Thr Ser Lys Thr Phe Phe Cys Gly Glu Val Asp Glu Ala Thr Lys Arg
      195      200      205
Leu Val Lys Val Thr Glu Glu Cys Met Leu Arg Gly Ile Ser Ala Cys
      210      215      220
Lys His Gly Val Ser Phe Lys Lys Ile Gly Arg Arg Ile Ser Glu His
      225      230      235
Ala Glu Arg His Gly Phe Gly Val Val Glu Gln Phe Val Gly His Gly
      240      245      250
Val Gly Arg Val Phe His Ser Gln Pro Ile Ile Tyr His Gln Arg Asn
      255      260      265
Asn Met Pro Gly Gln Met Val Glu Gly Gln Thr Phe Thr Ile Glu Pro
      270      275      280
Ile Leu Thr Met Gly Arg Ser Ser Ile Glu Cys Asp Met Trp Glu Asp
      285      290      295
Gly Trp Thr Ala Val Thr Thr Asp Gly Ser Leu Ala Gln Phe Glu
      300      305      310
His Thr Ile Leu Ile Thr Arg Thr Gly Ala Glu Ile Leu Thr Lys Cys
      315      320      325
      330      335

```

<210> 164
 <211> 1026
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (1)..(1026)

```

<400> 164
atg gct att gga gtc cca tcc atg gag ctc cac cgc tcc tca ccg ttg      48
Met Ala Ile Gly Val Pro Ser Met Glu Leu His Arg Ser Ser Pro Leu
      1      5      10
ctc tcg ggt ggc cga gga gga aat aca tgc cta cag aag aag ccc ttc      96
Leu Ser Gly Gly Arg Gly Gly Asn Thr Cys Leu Gln Lys Lys Pro Phe
      15      20      25
ttt gtc caa gca aag aga cta gtg ggg atg gag aaa gca agt acg agg      144
Phe Val Gln Ala Lys Arg Leu Val Gly Met Glu Lys Ala Ser Thr Arg
      30      35      40
cca gga aca caa gag tct gga cag aca aag aaa aga gca ccc ctg gtt      192
Pro Gly Thr Gln Glu Ser Gly Gln Thr Lys Lys Arg Ala Pro Leu Val
      45      50      55
cgt gga act gtt agc cca cct ctt cca gta cca gga aac ata cct cgg      240
Arg Gly Thr Val Ser Pro Pro Leu Pro Val Pro Gly Asn Ile Pro Arg
      60      65      70
cct cct tat gtc ggc aca gaa tat gta cca gag ata gca aaa gag ata      288
Pro Pro Tyr Val Gly Thr Glu Tyr Val Pro Glu Ile Ala Lys Glu Ile
      75      80      85
caa atg cat gac aaa gag ggc att gtc cac atg aga gct gct tgc gag      336
Gln Met His Asp Lys Glu Gly Ile Val His Met Arg Ala Ala Cys Glu
      90      95      100
ctc gcg gct cgt gtt ctt gac tat gca gga acg tta gtg aaa ccc tct      384
Leu Ala Ala Arg Val Leu Asp Tyr Ala Gly Thr Leu Val Lys Pro Ser
      105      110      115
gta aca aca gac gaa att gat aaa gca gtg cac aag atg atc atc gat      432
Val Thr Thr Asp Glu Ile Asp Lys Ala Val His Lys Met Ile Ile Asp
      120      125      130
gct gga gcc tat cca tca cca ctt gga tat ggt ggg ttt cca aaa agt      480
Ala Gly Ala Tyr Pro Ser Pro Leu Gly Tyr Gly Gly Phe Pro Lys Ser
      135      140      145
gta tgc acc tca gtg aat gag tgc atg tgc cat gga att cct gat tca      528
Val Cys Thr Ser Val Asn Glu Cys Met Cys His Gly Ile Pro Asp Ser
      150      155      160
cgc gag cta cag gat gga gac ata att aac att gat gtc act gtc tac      576
Arg Glu Leu Gln Asp Gly Asp Ile Ile Asn Ile Asp Val Thr Val Tyr
      165      170      175
ttg aat ggt tat cat ggg gat acc tca aaa aca ttt ctt tgt gga gaa      624
Leu Asn Gly Tyr His Gly Asp Thr Ser Lys Thr Phe Leu Cys Gly Glu
      180      185      190
      195      200      205

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PF59082SeqList_PF59082.txt

gtc	gat	gaa	gcc	agt	aaa	cga	ctt	gtg	aag	gtt	act	gaa	gag	tgc	ttg	672
Val	Asp	Glu	Ala	Ser	Lys	Arg	Leu	Val	Lys	Val	Thr	Glu	Glu	Cys	Leu	
	210					215					220					
ctc	agg	ggc	ata	tca	aca	tgc	aaa	cat	ggt	acc	agc	ttt	aag	aag	att	720
Leu	Arg	Gly	Ile	Ser	Thr	Cys	Lys	His	Gly	Thr	Ser	Phe	Lys	Lys	Ile	
225					230				235						240	
ggc	aga	aga	ata	agt	gag	cat	gct	gag	agg	aac	ggt	ttt	ggt	gtt	gtg	768
Gly	Arg	Arg	Ile	Ser	Glu	His	Ala	Glu	Arg	Asn	Gly	Phe	Gly	Val	Val	
				245					250					255		
gag	tgt	ttt	gtt	ggg	cat	gga	gtc	ggc	agg	gta	ttt	cac	tca	gaa	cca	816
Glu	Cys	Phe	Val	Gly	His	Gly	Val	Gly	Arg	Val	Phe	His	Ser	Glu	Pro	
			260					265					270			
att	atc	tat	cac	cag	agg	aac	aac	aga	ccg	ggc	cag	atg	att	gaa	ggg	864
Ile	Ile	Tyr	His	Gln	Arg	Asn	Asn	Arg	Pro	Gly	Gln	Met	Ile	Glu	Gly	
		275				280						285				
cag	act	ttc	aca	ata	gag	ccg	atc	ata	tcc	atg	ggg	agc	atc	gag	tgc	912
Gln	Thr	Phe	Thr	Ile	Glu	Pro	Ile	Ile	Ser	Met	Gly	Ser	Ile	Glu	Cys	
	290					295					300					
gac	atg	tgg	gac	gac	ggc	tgg	act	gcc	gtg	acg	acg	gac	ggc	agc	ttg	960
Asp	Met	Trp	Asp	Asp	Gly	Trp	Thr	Ala	Val	Thr	Thr	Asp	Gly	Ser	Leu	
305					310					315					320	
gcg	gcg	cag	ttc	gag	cac	acc	ata	ctg	atc	acc	agg	acc	gga	gcc	gag	1008
Ala	Ala	Gln	Phe	Glu	His	Thr	Ile	Leu	Ile	Thr	Arg	Thr	Gly	Ala	Glu	
				325					330					335		
atc	ctc	acc	aag	tgc	tag											1026
Ile	Leu	Thr	Lys	Cys												
			340													

<210> 165
 <211> 341
 <212> PRT
 <213> Zea mays

<400> 165
 Met Ala Ile Gly Val Pro Ser Met Glu Leu His Arg Ser Ser Pro Leu
 1 5 10 15
 Leu Ser Gly Gly Arg Gly Gly Asn Thr Cys Leu Gln Lys Lys Pro Phe
 20 25 30
 Phe Val Gln Ala Lys Arg Leu Val Gly Met Glu Lys Ala Ser Thr Arg
 35 40 45
 Pro Gly Thr Gln Glu Ser Gly Gln Thr Lys Lys Arg Ala Pro Leu Val
 50 55 60
 Arg Gly Thr Val Ser Pro Pro Leu Pro Val Pro Gly Asn Ile Pro Arg
 65 70 75 80
 Pro Pro Tyr Val Gly Thr Glu Tyr Val Pro Glu Ile Ala Lys Glu Ile
 85 90 95
 Gln Met His Asp Lys Glu Gly Ile Val His Met Arg Ala Ala Cys Glu
 100 105 110
 Leu Ala Ala Arg Val Leu Asp Tyr Ala Gly Thr Leu Val Lys Pro Ser
 115 120 125
 Val Thr Thr Asp Glu Ile Asp Lys Ala Val His Lys Met Ile Ile Asp
 130 135 140
 Ala Gly Ala Tyr Pro Ser Pro Leu Gly Tyr Gly Gly Phe Pro Lys Ser
 145 150 155 160
 Val Cys Thr Ser Val Asn Glu Cys Met Cys His Gly Ile Pro Asp Ser
 165 170 175
 Arg Glu Leu Gln Asp Gly Asp Ile Ile Asn Ile Asp Val Thr Val Tyr
 180 185 190
 Leu Asn Gly Tyr His Gly Asp Thr Ser Lys Thr Phe Leu Cys Gly Glu
 195 200 205
 Val Asp Glu Ala Ser Lys Arg Leu Val Lys Val Thr Glu Glu Cys Leu
 210 215 220
 Leu Arg Gly Ile Ser Thr Cys Lys His Gly Thr Ser Phe Lys Lys Ile
 225 230 235 240
 Gly Arg Arg Ile Ser Glu His Ala Glu Arg Asn Gly Phe Gly Val Val
 245 250 255
 Glu Cys Phe Val Gly His Gly Val Gly Arg Val Phe His Ser Glu Pro
 260 265 270
 Ile Ile Tyr His Gln Arg Asn Asn Arg Pro Gly Gln Met Ile Glu Gly

PF59082SeqList_PF59082.txt

275
 Gln Thr Phe Thr Ile Glu Pro Ile Ile Ser Met Gly Ser Ile Glu Cys
 290 280 285
 Asp Met Trp Asp Asp Gly Trp Thr Ala Val Thr Thr Asp Gly Ser Leu
 305 310 315
 Ala Ala Gln Phe Glu His Thr Ile Leu Ile Thr Arg Thr Gly Ala Glu
 325 330 335
 Ile Leu Thr Lys Cys
 340

<210> 166
 <211> 1035
 <212> DNA
 <213> Triticum aestivum

<220>
 <221> CDS
 <222> (1)..(1035)

<400> 166
 atg gcg gtc aga gtt ccg tcc atg gag ctg aac cgc tcc ccg ccg ctc 48
 Met Ala Val Arg Val Pro Ser Met Glu Leu Asn Arg Ser Pro Pro Leu
 1 5 10 15
 ctc tcc ggc ggc aga ggc aaa aca tgc ctt cag aag cct ttc att gtc 96
 Leu Ser Gly Gly Arg Gly Lys Thr Cys Leu Gln Lys Pro Phe Ile Val
 20 25 30
 caa gca aag aga tca ggt gga ttg gag aaa gca aat act agg tca cga 144
 Gln Ala Lys Arg Ser Gly Gly Leu Glu Lys Ala Asn Thr Arg Ser Arg
 35 40 45
 gga ccg caa gct tct gaa aaa ctc aag aaa aga gaa ccc ctg act cgt 192
 Gly Pro Gln Ala Ser Glu Lys Leu Lys Lys Arg Glu Pro Leu Thr Arg
 50 55 60
 ggg act gtt agt gcg cct ctt ccg gta cca gga cac ata cct cga cct 240
 Gly Thr Val Ser Ala Pro Leu Pro Val Pro Gly His Ile Pro Arg Pro
 65 70 75 80
 cct tac gtt gga tca aac aaa atg ccc gag ata tcg agt gag aga caa 288
 Pro Tyr Val Gly Ser Asn Lys Met Pro Glu Ile Ser Ser Glu Arg Gln
 85 90 95
 atg cag gac aaa gac acc atc gtg cac atg aaa gct gca tgt gag ctt 336
 Met Gln Asp Lys Asp Thr Ile Val His Met Lys Ala Ala Cys Glu Leu
 100 105 110
 gct gct cgt gtt ctt caa aat gca ggg aaa tta gtc aaa ccc tct gta 384
 Ala Ala Arg Val Leu Gln Asn Ala Gly Lys Leu Val Lys Pro Ser Val
 115 120 125
 aca aca gac gaa att gat aaa gca gtg cac aag atg atc atc gat gct 432
 Thr Thr Asp Glu Ile Asp Lys Ala Val His Lys Met Ile Ile Asp Ala
 130 135 140
 gga gcc tat cca tcc ccg ctt gga tac ggt ggg ttt cca aaa agt gta 480
 Gly Ala Tyr Pro Ser Pro Leu Gly Tyr Gly Gly Phe Pro Lys Ser Val
 145 150 155 160
 tgc aca tca gtg aac gaa tgc atg tgc cat ggt att cct gat tca cga 528
 Cys Thr Ser Val Asn Glu Cys Met Cys His Gly Ile Pro Asp Ser Arg
 165 170 175
 gaa cta aag gat gga gac ata att aac atc gat gtc act gtc tac ttg 576
 Glu Leu Lys Asp Gly Asp Ile Ile Asn Ile Asp Val Thr Val Tyr Leu
 180 185 190
 aac ggt ttt cat gga gat acc tct aaa aca ttc ttc tgt gga gaa gtt 624
 Asn Gly Phe His Gly Asp Thr Ser Lys Thr Phe Phe Cys Gly Glu Val
 195 200 205
 gac gaa gct gct aaa aga ctt gtg aag gtt act gaa gag tgc atg ctt 672
 Asp Glu Ala Ala Lys Arg Leu Val Lys Val Thr Glu Glu Cys Met Leu
 210 215 220
 agg ggc ata tca tcc tgc aaa cat ggt gtg agc ttt aag aaa att ggc 720
 Arg Gly Ile Ser Ser Cys Lys His Gly Val Ser Phe Lys Lys Ile Gly
 225 230 235 240
 aga aga ata agc gag cat gct gag aag cat gga ttt ggt gtc gtg gag 768
 Arg Arg Ile Ser Glu His Ala Glu Lys His Gly Phe Gly Val Val Glu
 245 250 255
 caa ttt gtt ggg cat gga gtt ggc aga gtt ttt cat tca caa ccg att 816

PF59082SeqList_PF59082.txt

Gln	Phe	Val	Gly	His	Gly	Val	Gly	Arg	Val	Phe	His	Ser	Gln	Pro	Ile	
			260				265					270				
ata	tat	cac	cag	cgc	aac	aac	atg	ccg	ggg	cag	atg	gtg	gaa	ggg	cag	864
Ile	Tyr	His	Gln	Arg	Asn	Asn	Met	Pro	Gly	Gln	Met	Val	Glu	Gly	Gln	
		275					280					285				
aca	ttc	aca	ata	gag	ccg	atc	ctg	acc	atg	gga	agc	aac	agc	aac	agc	912
Thr	Phe	Thr	Ile	Glu	Pro	Ile	Leu	Thr	Met	Gly	Ser	Asn	Ser	Asn	Ser	
	290					295					300					
atc	gag	tcg	gac	atg	tgg	gag	gac	ggc	tgg	acg	gcg	gtg	acg	acg	gac	960
Ile	Glu	Cys	Asp	Met	Trp	Glu	Asp	Gly	Trp	Thr	Ala	Val	Thr	Thr	Asp	
305					310					315					320	
ggc	agc	ctg	gcg	gcg	cag	ttc	gag	cac	acc	atc	ctc	atc	acc	agg	acc	1008
Gly	Ser	Leu	Ala	Ala	Gln	Phe	Glu	His	Thr	Ile	Leu	Ile	Thr	Arg	Thr	
			325						330					335		
ggc	gca	gag	atc	cta	acc	aaa	tgc	tag								1035
Gly	Ala	Glu	Ile	Leu	Thr	Lys	Cys									
			340													

<210> 167

<211> 344

<212> PRT

<213> Triticum aestivum

<400> 167

Met	Ala	Val	Arg	Val	Pro	Ser	Met	Glu	Leu	Asn	Arg	Ser	Pro	Pro	Leu	
1				5				10						15		
Leu	Ser	Gly	Gly	Arg	Gly	Lys	Thr	Cys	Leu	Gln	Lys	Pro	Phe	Ile	Val	
			20					25					30			
Gln	Ala	Lys	Arg	Ser	Gly	Gly	Leu	Glu	Lys	Ala	Asn	Thr	Arg	Ser	Arg	
		35					40					45				
Gly	Pro	Gln	Ala	Ser	Glu	Lys	Leu	Lys	Lys	Arg	Glu	Pro	Leu	Thr	Arg	
	50					55					60					
Gly	Thr	Val	Ser	Ala	Pro	Leu	Pro	Val	Pro	Gly	His	Ile	Pro	Arg	Pro	
65					70					75					80	
Pro	Tyr	Val	Gly	Ser	Asn	Lys	Met	Pro	Glu	Ile	Ser	Ser	Glu	Arg	Gln	
				85					90					95		
Met	Gln	Asp	Lys	Asp	Thr	Ile	Val	His	Met	Lys	Ala	Ala	Cys	Glu	Leu	
			100					105					110			
Ala	Ala	Arg	Val	Leu	Gln	Asn	Ala	Gly	Lys	Leu	Val	Lys	Pro	Ser	Val	
			115					120					125			
Thr	Thr	Asp	Glu	Ile	Asp	Lys	Ala	Val	His	Lys	Met	Ile	Ile	Asp	Ala	
	130					135					140					
Gly	Ala	Tyr	Pro	Ser	Pro	Leu	Gly	Tyr	Gly	Gly	Phe	Pro	Lys	Ser	Val	
145					150					155					160	
Cys	Thr	Ser	Val	Asn	Glu	Cys	Met	Cys	His	Gly	Ile	Pro	Asp	Ser	Arg	
				165					170					175		
Glu	Leu	Lys	Asp	Gly	Asp	Ile	Ile	Asn	Ile	Asp	Val	Thr	Val	Tyr	Leu	
			180					185						190		
Asn	Gly	Phe	His	Gly	Asp	Thr	Ser	Lys	Thr	Phe	Phe	Cys	Gly	Glu	Val	
		195					200					205				
Asp	Glu	Ala	Ala	Lys	Arg	Leu	Val	Lys	Val	Thr	Glu	Glu	Cys	Met	Leu	
	210					215					220					
Arg	Gly	Ile	Ser	Ser	Cys	Lys	His	Gly	Val	Ser	Phe	Lys	Lys	Ile	Gly	
225					230					235					240	
Arg	Arg	Ile	Ser	Glu	His	Ala	Glu	Lys	His	Gly	Phe	Gly	Val	Val	Glu	
				245					250					255		
Gln	Phe	Val	Gly	His	Gly	Val	Gly	Arg	Val	Phe	His	Ser	Gln	Pro	Ile	
			260					265						270		
Ile	Tyr	His	Gln	Arg	Asn	Asn	Met	Pro	Gly	Gln	Met	Val	Glu	Gly	Gln	
		275					280						285			
Thr	Phe	Thr	Ile	Glu	Pro	Ile	Leu	Thr	Met	Gly	Ser	Asn	Ser	Asn	Ser	
	290					295					300					
Ile	Glu	Cys	Asp	Met	Trp	Glu	Asp	Gly	Trp	Thr	Ala	Val	Thr	Thr	Asp	
305					310					315					320	
Gly	Ser	Leu	Ala	Ala	Gln	Phe	Glu	His	Thr	Ile	Leu	Ile	Thr	Arg	Thr	
				325					330					335		
Gly	Ala	Glu	Ile	Leu	Thr	Lys	Cys									
			340													

PF59082SeqList_PF59082.txt

<210> 168
<211> 1026
<212> DNA
<213> Zea mays

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<221> CDS
<222> (1)..(1026)

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ctc tcg ggt ggc cga gga gga aat aca tgc cta cag aag aag ccc ttc      96
Leu Ser Gly Gly Arg Gly Gly Asn Thr Cys Leu Gln Lys Lys Pro Phe
          20          25          30
ttt gtc caa gca aag aga cta gtg ggg atg gag aaa gca agt acg agg      144
Phe Val Gln Ala Lys Arg Leu Val Gly Met Glu Lys Ala Ser Thr Arg
          35          40          45
cca gga aca caa gag tct gga cag aca aag aaa aga gca ccc ctg gtt      192
Pro Gly Thr Gln Glu Ser Gly Gln Thr Lys Lys Arg Ala Pro Leu Val
          50          55          60
cgt gga act gtt agc cca cct ctt cca gta cca gga aac ata cct cgg      240
Arg Gly Thr Val Ser Pro Pro Leu Pro Val Pro Gly Asn Ile Pro Arg
          65          70          75
cct cct tat gtc ggc aca gaa tat gta cca gag ata gca aaa gag ata      288
Pro Pro Tyr Val Gly Thr Glu Tyr Val Pro Glu Ile Ala Lys Glu Ile
          80          85          90
caa atg cat gac aaa gag ggc att gtc cac atg aga gct gct tgc gag      336
Gln Met His Asp Lys Glu Gly Ile Val His Met Arg Ala Ala Cys Glu
          100          105          110
ctc gcg gct cgt gtt ctt gac tat gca gga acg tta gtg aaa ccc tct      384
Leu Ala Ala Arg Val Leu Asp Tyr Ala Gly Thr Leu Val Lys Pro Ser
          115          120          125
gta aca aca gac gaa att gat aaa gca gtg cac aag atg atc atc gat      432
Val Thr Thr Asp Glu Ile Asp Lys Ala Val His Lys Met Ile Ile Asp
          130          135          140
gct gga gcc tat cca tca cca ctt gga tat ggt ggg ttt cca aaa agt      480
Ala Gly Ala Tyr Pro Ser Pro Leu Gly Tyr Gly Gly Phe Pro Lys Ser
          145          150          155
gta tgc acc tca gtg aat gag tgc atg tgc cat gga att cct gat tca      528
Val Cys Thr Ser Val Asn Glu Cys Met Cys His Gly Ile Pro Asp Ser
          160          165          170
cgc gag cta cag gat gga gac ata att aac att gat gtc act gtc tac      576
Arg Glu Leu Gln Asp Gly Asp Ile Ile Asn Ile Asp Val Thr Val Tyr
          175          180          185
ttg aat ggt tat cat ggg gat acc tca aaa aca ttt ctt tgt gga gaa      624
Leu Asn Gly Tyr His Gly Asp Thr Ser Lys Thr Phe Leu Cys Gly Glu
          190          200          205
gtc gat gaa gcc agt aaa cga ctt gtg aag gtt act gaa gag tgc ttg      672
Val Asp Glu Ala Ser Lys Arg Leu Val Lys Val Thr Glu Glu Cys Leu
          210          215          220
ctc agg ggc ata tca aca tgc aaa cat ggt acc agc ttt aag aag att      720
Leu Arg Gly Ile Ser Thr Cys Lys His Gly Thr Ser Phe Lys Lys Ile
          225          230          235
ggc aga aga ata agt gag cat gct gag agg aac ggt ttt ggt gtt gtg      768
Gly Arg Arg Ile Ser Glu His Ala Glu Arg Asn Gly Phe Gly Val Val
          240          245          250
gag tgt ttt gtt ggg cat gga gtc ggc agg gta ttt cac tca gaa cca      816
Glu Cys Phe Val Gly His Gly Val Gly Arg Val Phe His Ser Glu Pro
          255          260          265
att atc tat cac cag agg aac aac aga ccg ggc cag atg att gaa ggg      864
Ile Ile Tyr His Gln Arg Asn Asn Arg Pro Gly Gln Met Ile Glu Gly
          270          275          280
cag act ttc aca ata gag ccg atc ata tcg atg ggg agc atc gag tgc      912
Gln Thr Phe Thr Ile Glu Pro Ile Ile Ser Met Gly Ser Ile Glu Cys
          285          290          295
gac atg tgg gac gac ggc tgg act gcc gtg acg acg gac ggc agc ttg      960
Asp Met Trp Asp Asp Gly Trp Thr Ala Val Thr Thr Asp Gly Ser Leu
          300

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PF59082SeqList_PF59082.txt

305 310 315 320
gcg gcg cag ttc gag cac acc ata ctg atc acc agg acc gga gcc gag 1008
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atc ctc acc aag tgc tag 1026
Ile Leu Thr Lys Cys
340

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<212> PRT
<213> Zea mays

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Leu Ser Gly Gly Arg Gly Gly Asn Thr Cys Leu Gln Lys Lys Pro Phe
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Phe Val Gln Ala Lys Arg Leu Val Gly Met Glu Lys Ala Ser Thr Arg
35 40 45
Pro Gly Thr Gln Glu Ser Gly Gln Thr Lys Lys Arg Ala Pro Leu Val
50 55 60
Arg Gly Thr Val Ser Pro Pro Leu Pro Val Pro Gly Asn Ile Pro Arg
65 70 75 80
Pro Pro Tyr Val Gly Thr Glu Tyr Val Pro Glu Ile Ala Lys Glu Ile
85 90 95
Gln Met His Asp Lys Glu Gly Ile Val His Met Arg Ala Ala Cys Glu
100 105 110
Leu Ala Ala Arg Val Leu Asp Tyr Ala Gly Thr Leu Val Lys Pro Ser
115 120 125
Val Thr Thr Asp Glu Ile Asp Lys Ala Val His Lys Met Ile Ile Asp
130 135 140
Ala Gly Ala Tyr Pro Ser Pro Leu Gly Tyr Gly Gly Phe Pro Lys Ser
145 150 155 160
Val Cys Thr Ser Val Asn Glu Cys Met Cys His Gly Ile Pro Asp Ser
165 170 175
Arg Glu Leu Gln Asp Gly Asp Ile Ile Asn Ile Asp Val Thr Val Tyr
180 185 190
Leu Asn Gly Tyr His Gly Asp Thr Ser Lys Thr Phe Leu Cys Gly Glu
195 200 205
Val Asp Glu Ala Ser Lys Arg Leu Val Lys Val Thr Glu Glu Cys Leu
210 215 220
Leu Arg Gly Ile Ser Thr Cys Lys His Gly Thr Ser Phe Lys Lys Ile
225 230 235 240
Gly Arg Arg Ile Ser Glu His Ala Glu Arg Asn Gly Phe Gly Val Val
245 250 255
Glu Cys Phe Val Gly His Gly Val Gly Arg Val Phe His Ser Glu Pro
260 265 270
Ile Ile Tyr His Gln Arg Asn Asn Arg Pro Gly Gln Met Ile Glu Gly
275 280 285
Gln Thr Phe Thr Ile Glu Pro Ile Ile Ser Met Gly Ser Ile Glu Cys
290 295 300
Asp Met Trp Asp Asp Gly Trp Thr Ala Val Thr Thr Asp Gly Ser Leu
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Ala Ala Gln Phe Glu His Thr Ile Leu Ile Thr Arg Thr Gly Ala Glu
325 330 335
Ile Leu Thr Lys Cys
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<212> DNA
<213> Zea mays

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<222> (1)..(1053)

<400> 170

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1				5					10					15		
agg	ttc	cgg	cct	ctc	gct	gcc	cct	ctc	cgc	ccc	gtc	cgc	tcc	ggc	aag	96
Arg	Phe	Arg	Pro	Leu	Ala	Ala	Pro	Leu	Arg	Pro	Val	Arg	Ser	Gly	Lys	
			20					25					30			
ttc	gtt	gtg	cca	aag	cga	tgc	ttc	att	gta	tca	agc	agg	ctt	gca	tgg	144
Phe	Val	Val	Pro	Lys	Arg	Cys	Phe	Ile	Val	Ser	Ser	Arg	Leu	Ala	Trp	
			35				40					45				
gtg	gaa	gat	gag	ctt	atg	gag	ata	caa	aag	tca	caa	gag	caa	agt	tca	192
Val	Glu	Asp	Glu	Leu	Met	Glu	Ile	Gln	Lys	Ser	Gln	Glu	Gln	Ser	Ser	
	50					55					60					
gta	aaa	tca	aag	aaa	agg	cca	cct	ttg	agg	cgt	gga	aag	gtc	tcc	cca	240
Val	Lys	Ser	Lys	Lys	Arg	Pro	Pro	Leu	Arg	Arg	Gly	Lys	Val	Ser	Pro	
	65				70					75					80	
caa	ctt	cct	gta	cca	ggg	cac	att	cca	aga	cca	tct	tat	gtt	ggc	gcg	288
Gln	Leu	Pro	Val	Pro	Gly	His	Ile	Pro	Arg	Pro	Ser	Tyr	Val	Gly	Ala	
				85				90						95		
aaa	gga	ttg	cct	gaa	cta	tgc	aag	ggc	caa	tta	cat	gat	gct	caa	gga	336
Lys	Gly	Leu	Pro	Glu	Leu	Cys	Lys	Gly	Gln	Leu	His	Asp	Ala	Gln	Gly	
			100					105					110			
att	act	gga	atg	aga	gct	gct	tgc	aaa	ctt	gct	gcc	cgt	gtt	ctt	gac	384
Ile	Thr	Gly	Met	Arg	Ala	Ala	Cys	Lys	Leu	Ala	Ala	Arg	Val	Leu	Asp	
			115				120					125				
ttc	gct	ggg	act	tta	gtt	aag	cca	tcc	att	act	aca	aat	gaa	att	gac	432
Phe	Ala	Gly	Thr	Leu	Val	Lys	Pro	Ser	Ile	Thr	Thr	Asn	Glu	Ile	Asp	
	130					135					140					
gca	gca	gtc	cat	aat	atg	atc	att	gag	gct	ggt	gct	tat	cct	tct	cca	480
Ala	Ala	Val	His	Asn	Met	Ile	Ile	Glu	Ala	Gly	Ala	Tyr	Pro	Ser	Pro	
	145				150					155					160	
ctt	ggc	tat	cat	gga	ttt	cct	aag	agt	ata	tgt	aca	tca	gta	aat	gag	528
Leu	Gly	Tyr	His	Gly	Phe	Pro	Lys	Ser	Ile	Cys	Thr	Ser	Val	Asn	Glu	
				165					170					175		
tgt	gtc	tgt	cat	ggg	gta	cct	gat	tca	act	cag	ctg	cag	aat	ggg	gat	576
Cys	Val	Cys	His	Gly	Val	Pro	Asp	Ser	Thr	Gln	Leu	Gln	Asn	Gly	Asp	
			180					185					190			
att	ata	aat	att	gat	gta	aat	gtg	ttc	ctg	aat	gga	tac	cat	ggg	ggt	624
Ile	Ile	Asn	Ile	Asp	Val	Asn	Val	Phe	Leu	Asn	Gly	Tyr	His	Gly	Gly	
			195				200					205				
acc	tcc	aga	aca	ttt	gca	tgt	gga	caa	gtg	gat	gat	tct	atc	aaa	cat	672
Thr	Ser	Arg	Thr	Phe	Ala	Cys	Gly	Gln	Val	Asp	Asp	Ser	Ile	Lys	His	
	210					215					220					
ttt	ctc	aat	gca	gct	gaa	gaa	tgc	ttg	gag	aaa	ggc	att	tct	atc	tgc	720
Phe	Leu	Asn	Ala	Ala	Glu	Glu	Cys	Leu	Glu	Lys	Gly	Ile	Ser	Ile	Cys	
	225				230					235					240	
agg	gat	ggt	gtg	aac	tac	aga	aag	att	ggc	aag	aaa	ata	agc	aag	ctt	768
Arg	Asp	Gly	Val	Asn	Tyr	Arg	Lys	Ile	Gly	Lys	Lys	Ile	Ser	Lys	Leu	
				245					250					255		
gcc	tat	ttt	tat	ggc	tat	tat	gtg	gtg	gaa	cgc	ttt	gtt	ggg	cat	ggg	816
Ala	Tyr	Phe	Tyr	Gly	Tyr	Tyr	Val	Val	Glu	Arg	Phe	Val	Gly	His	Gly	
			260				265						270			
att	gga	act	atg	tat	cat	tct	gag	cca	cta	att	cta	cat	cat	gcc	aac	864
Ile	Gly	Thr	Met	Tyr	His	Ser	Glu	Pro	Leu	Ile	Leu	His	His	Ala	Asn	
			275				280					285				
gaa	aac	tca	ggg	cgt	atg	gtt	gag	ggc	caa	aca	ttt	aca	att	gaa	cct	912
Glu	Asn	Ser	Gly	Arg	Met	Val	Glu	Gly	Gln	Thr	Phe	Thr	Ile	Glu	Pro	
	290					295					300					
ata	ctc	aca	atg	gag	aaa	aca	gag	tgt	gtt	aca	tgg	gaa	gat	gga	tgg	960
Ile	Leu	Thr	Met	Glu	Lys	Thr	Glu	Cys	Val	Thr	Trp	Glu	Asp	Gly	Trp	
	305				310					315				320		
acg	act	gtc	act	gct	gat	ggt	agc	tgg	gct	gcg	cag	ttt	gag	cat	acc	1008
Thr	Thr	Val	Thr	Ala	Asp	Gly	Ser	Trp	Ala	Ala	Gln	Phe	Glu	His	Thr	
				325					330					335		
ata	ctg	gtg	act	agg	gac	ggt	gca	gaa	ata	ctg	acg	aaa	gtc	tga		1053
Ile	Leu	Val	Thr	Arg	Asp	Gly	Ala	Glu	Ile	Leu	Thr	Lys	Val			
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PF59082SeqList_PF59082.txt

<212> PRT

<213> Zea mays

<400> 171

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      20      25      30
Phe Val Val Pro Lys Arg Cys Phe Ile Val Ser Ser Arg Leu Ala Trp
      35      40      45
Val Glu Asp Glu Leu Met Glu Ile Gln Lys Ser Gln Glu Gln Ser Ser
      50      55      60
Val Lys Ser Lys Lys Arg Pro Pro Leu Arg Arg Gly Lys Val Ser Pro
65      70      75      80
Gln Leu Pro Val Pro Gly His Ile Pro Arg Pro Ser Tyr Val Gly Ala
      85      90      95
Lys Gly Leu Pro Glu Leu Cys Lys Gly Gln Leu His Asp Ala Gln Gly
      100      105      110
Ile Thr Gly Met Arg Ala Ala Cys Lys Leu Ala Ala Arg Val Leu Asp
      115      120      125
Phe Ala Gly Thr Leu Val Lys Pro Ser Ile Thr Thr Asn Glu Ile Asp
130      135      140
Ala Ala Val His Asn Met Ile Ile Glu Ala Gly Ala Tyr Pro Ser Pro
145      150      155      160
Leu Gly Tyr His Gly Phe Pro Lys Ser Ile Cys Thr Ser Val Asn Glu
      165      170      175
Cys Val Cys His Gly Val Pro Asp Ser Thr Gln Leu Gln Asn Gly Asp
      180      185      190
Ile Ile Asn Ile Asp Val Asn Val Phe Leu Asn Gly Tyr His Gly Gly
195      200      205
Thr Ser Arg Thr Phe Ala Cys Gly Gln Val Asp Asp Ser Ile Lys His
210      215      220
Phe Leu Asn Ala Ala Glu Glu Cys Leu Glu Lys Gly Ile Ser Ile Cys
225      230      235      240
Arg Asp Gly Val Asn Tyr Arg Lys Ile Gly Lys Lys Ile Ser Lys Leu
      245      250      255
Ala Tyr Phe Tyr Gly Tyr Tyr Val Val Glu Arg Phe Val Gly His Gly
      260      265      270
Ile Gly Thr Met Tyr His Ser Glu Pro Leu Ile Leu His His Ala Asn
275      280      285
Glu Asn Ser Gly Arg Met Val Glu Gly Gln Thr Phe Thr Ile Glu Pro
290      295      300
Ile Leu Thr Met Glu Lys Thr Glu Cys Val Thr Trp Glu Asp Gly Trp
305      310      315      320
Thr Thr Val Thr Ala Asp Gly Ser Trp Ala Ala Gln Phe Glu His Thr
      325      330      335
Ile Leu Val Thr Arg Asp Gly Ala Glu Ile Leu Thr Lys Val
340      345      350

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<210> 172

<211> 1026

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<213> Zea mays

<220>

<221> CDS

<222> (1)..(1026)

<400> 172

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Met Ala Ile Gly Val Pro Ser Met Glu Leu His Arg Ser Ser Pro Leu
1      5      10      15
ctc tcg ggt ggc cga gga gga aat aca tgc cta cag aag aag ccc ttc      96
Leu Ser Gly Gly Arg Gly Gly Asn Thr Cys Leu Gln Lys Lys Pro Phe
      20      25      30
ttt gtc caa gca aag aga cta gtg ggg atg gag aaa gca agt acg agg      144
Phe Val Gln Ala Lys Arg Leu Val Gly Met Glu Lys Ala Ser Thr Arg
      35      40      45
cca gga aca caa gag tct gga cag aca aag aaa aga gca ccc ctg gtt      192
      340      345      350

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PF59082SeqList_PF59082.txt

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	65				70					75					80		
cct	cct	tat	gtc	ggc	aca	gaa	tat	gta	cca	gag	ata	gca	aaa	gag	ata	288	
Pro	Pro	Tyr	Val	Gly	Thr	Glu	Tyr	Val	Pro	Glu	Ile	Ala	Lys	Glu	Ile		
				85					90					95			
caa	atg	cat	gac	aaa	gag	ggc	att	gtc	cac	atg	agg	gct	gct	tgc	gag	336	
Gln	Met	His	Asp	Lys	Glu	Gly	Ile	Val	His	Met	Arg	Ala	Ala	Cys	Glu		
			100					105					110				
ctc	gcg	gct	cgt	gtt	ctt	gac	tat	gca	gga	acg	tta	gtg	aaa	ccc	tct	384	
Leu	Ala	Ala	Arg	Val	Leu	Asp	Tyr	Ala	Gly	Thr	Leu	Val	Lys	Pro	Ser		
	115						120					125					
gta	aca	aca	gac	gaa	att	gat	aaa	gca	gtg	cac	aag	atg	atc	atc	gat	432	
Val	Thr	Thr	Asp	Glu	Ile	Asp	Lys	Ala	Val	His	Lys	Met	Ile	Ile	Asp		
	130					135					140						
gct	gga	gcc	tat	cca	tca	cca	ctt	gga	tat	ggt	ggg	ttt	cca	aaa	agt	480	
Ala	Gly	Ala	Tyr	Pro	Ser	Pro	Leu	Gly	Tyr	Gly	Gly	Phe	Pro	Lys	Ser		
	145				150					155					160		
gta	tgc	acc	tca	gtg	aat	gag	tgc	atg	tgc	cat	gga	att	cct	gat	tca	528	
Val	Cys	Thr	Ser	Val	Asn	Glu	Cys	Met	Cys	His	Gly	Ile	Pro	Asp	Ser		
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cgc	gag	cta	cag	gat	gga	gac	ata	att	aac	att	gat	gtc	act	gtc	tac	576	
Arg	Glu	Leu	Gln	Asp	Gly	Asp	Ile	Ile	Asn	Ile	Asp	Val	Thr	Val	Tyr		
			180				185						190				
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Leu	Asn	Gly	Tyr	His	Gly	Asp	Thr	Ser	Lys	Thr	Phe	Leu	Cys	Gly	Glu		
	195					200						205					
gtc	gat	gag	gcc	agt	aaa	cga	ctt	gtg	aag	gtt	act	gaa	gag	tgc	ttg	672	
Val	Asp	Glu	Ala	Ser	Lys	Arg	Leu	Val	Lys	Val	Thr	Glu	Glu	Cys	Leu		
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Leu	Arg	Gly	Ile	Ser	Thr	Cys	Lys	His	Gly	Thr	Ser	Phe	Lys	Lys	Ile		
	225				230				235						240		
ggc	aga	aga	ata	agt	gag	cat	gct	gag	agg	aac	ggt	ttt	ggt	gtt	gtg	768	
Gly	Arg	Arg	Ile	Ser	Glu	His	Ala	Glu	Arg	Asn	Gly	Phe	Gly	Val	Val		
			245					250					255				
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Glu	Cys	Phe	Val	Gly	His	Val	Val	Gly	Arg	Val	Phe	His	Ser	Glu	Pro		
			260				265						270				
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Ile	Ile	Tyr	His	Gln	Arg	Asn	Asn	Arg	Pro	Gly	Gln	Met	Ile	Glu	Gly		
		275				280						285					
cag	act	ttc	aca	ata	gag	ccg	atc	ata	tcg	atg	ggg	agc	atc	gag	tgc	912	
Gln	Thr	Phe	Thr	Ile	Glu	Pro	Ile	Ile	Ser	Met	Gly	Ser	Ile	Glu	Cys		
	290					295					300						
gac	atg	tgg	gac	gac	ggc	tgg	act	gcc	gtg	acg	acg	gac	ggc	agc	ttg	960	
Asp	Met	Trp	Asp	Asp	Gly	Trp	Thr	Ala	Val	Thr	Thr	Asp	Gly	Ser	Leu		
	305				310					315					320		
gcg	gct	cag	ttc	gag	cac	acc	ata	ctg	atc	acc	agg	acc	gga	gcc	gag	1008	
Ala	Ala	Gln	Phe	Glu	His	Thr	Ile	Leu	Ile	Thr	Arg	Thr	Gly	Ala	Glu		
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atc	ctc	acc	aag	tgc	tag											1026	
Ile	Leu	Thr	Lys	Cys													
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 20 25 30
 Phe Val Gln Ala Lys Arg Leu Val Gly Met Glu Lys Ala Ser Thr Arg
 35 40 45

PF59082SeqList_PF59082.txt

Pro Gly Thr Gln Glu Ser Gly Gln Thr Lys Lys Arg Ala Pro Leu Val
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Arg Gly Thr Val Ser Pro Pro Leu Pro Val Pro Gly Asn Ile Pro Arg
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Pro Pro Tyr Val Gly Thr Glu Tyr Val Pro Glu Ile Ala Lys Glu Ile
85 90 95
Gln Met His Asp Lys Glu Gly Ile Val His Met Arg Ala Ala Cys Glu
100 105 110
Leu Ala Ala Arg Val Leu Asp Tyr Ala Gly Thr Leu Val Lys Pro Ser
115 120 125
Val Thr Thr Asp Glu Ile Asp Lys Ala Val His Lys Met Ile Ile Asp
130 135 140
Ala Gly Ala Tyr Pro Ser Pro Leu Gly Tyr Gly Gly Phe Pro Lys Ser
145 150 155 160
Val Cys Thr Ser Val Asn Glu Cys Met Cys His Gly Ile Pro Asp Ser
165 170 175
Arg Glu Leu Gln Asp Gly Asp Ile Ile Asn Ile Asp Val Thr Val Tyr
180 185 190
Leu Asn Gly Tyr His Gly Asp Thr Ser Lys Thr Phe Leu Cys Gly Glu
195 200 205
Val Asp Glu Ala Ser Lys Arg Leu Val Lys Val Thr Glu Glu Cys Leu
210 215 220
Leu Arg Gly Ile Ser Thr Cys Lys His Gly Thr Ser Phe Lys Lys Ile
225 230 235 240
Gly Arg Arg Ile Ser Glu His Ala Glu Arg Asn Gly Phe Gly Val Val
245 250 255
Glu Cys Phe Val Gly His Val Val Gly Arg Val Phe His Ser Glu Pro
260 265 270
Ile Ile Tyr His Gln Arg Asn Asn Arg Pro Gly Gln Met Ile Glu Gly
275 280 285
Gln Thr Phe Thr Ile Glu Pro Ile Ile Ser Met Gly Ser Ile Glu Cys
290 295 300
Asp Met Trp Asp Asp Gly Trp Thr Ala Val Thr Thr Asp Gly Ser Leu
305 310 315 320
Ala Ala Gln Phe Glu His Thr Ile Leu Ile Thr Arg Thr Gly Ala Glu
325 330 335
Ile Leu Thr Lys Cys
340

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Met Ala Ala Gly Leu Gly Ala Arg Pro Ser Ala Thr Phe Glu Ala Gly
1 5 10 15
agg ttc cgg cct ctg gct gcc cct ctg cgc ccc gtc cgc tcc gga aaa 96
Arg Phe Arg Pro Leu Ala Ala Pro Leu Arg Pro Val Arg Ser Gly Lys
20 25 30
ttc gta gtg cct aag cga tgc ttc act gtg tca agt agg ctt gca tgg 144
Phe Val Val Pro Lys Arg Cys Phe Thr Val Ser Ser Arg Leu Ala Trp
35 40 45
gtg gaa gat gag ctt atg gag ata aaa aag tca caa gag caa agt tca 192
Val Glu Asp Glu Leu Met Glu Ile Lys Lys Ser Gln Glu Gln Ser Ser
50 55 60
gta aaa tca aag aaa aga cca cct ttg agg cgt gga aag gtc tcc cca 240
Val Lys Ser Lys Lys Arg Pro Pro Leu Arg Arg Gly Lys Val Ser Pro
65 70 75 80
caa ctt cct gta cca ggg cac att cca aga cca tct tat gtt ggt tca 288
Gln Leu Pro Val Pro Gly His Ile Pro Arg Pro Ser Tyr Val Gly Ser
85 90 95
aaa gga ttg cca gaa cta tgc aag ggc caa tta cac gat gct caa gga 336
Lys Gly Leu Pro Glu Leu Cys Lys Gly Gln Leu His Asp Ala Gln Gly

PF59082SeqList_PF59082.txt

	100		105		110												
att gct gga atg aga gct gct tgc aaa ctt gct gcc cgt gtt ctt gat	Ile Ala Gly Met Arg Ala Ala Cys Lys Leu Ala Ala Arg Val Leu Asp	384															
ttt gct ggg act tta gtt aag cca tcc att act aca aat gaa att gac	Phe Ala Gly Thr Leu Val Lys Pro Ser Ile Thr Asn Glu Ile Asp	432															
gaa gca gtc cat aat atg atc att gaa gct ggt gct tat cct tct cca	Glu Ala Val His Asn Met Ile Ile Glu Ala Gly Ala Tyr Pro Ser Pro	480															
ctt ggc tat cat gga ttt cct aaa agt ata tgt aca tca gta aat gag	Leu Gly Tyr His Gly Phe Pro Lys Ser Ile Cys Thr Ser Val Asn Glu	528															
tgt gtc tgt cat ggg gta cct gat tca act cag ctg cag aat ggg gat	Cys Val Cys His Gly Val Pro Asp Ser Thr Gln Leu Gln Asn Gly Asp	576															
att ata aat att gat gta aat gtg ttc ctg aat gga tac cat ggg ggt	Ile Ile Asn Ile Asp Val Asn Val Phe Leu Asn Gly Tyr His Gly Gly	624															
acc tcc aga aca ttt gca tgt gga caa gtt gat gat tct atc aaa cat	Thr Ser Arg Thr Phe Ala Cys Gly Gln Val Asp Asp Ser Ile Lys His	672															
ttt ctc aat gca gct gaa gaa tgc ttg gag aaa ggc att tct atc tgc	Phe Leu Asn Ala Ala Glu Glu Cys Leu Glu Lys Gly Ile Ser Ile Cys	720															
agg gat ggt gtg aac tac aga aag att ggc aag aaa ata agc aag ctt	Arg Asp Gly Val Asn Tyr Arg Lys Ile Gly Lys Lys Ile Ser Lys Leu	768															
gcc tat ttt tat ggc tat tat gtg gtg gaa cgc ttt gtt ggc cat ggg	Ala Tyr Phe Tyr Gly Tyr Tyr Val Val Glu Arg Phe Val Gly His Gly	816															
att gga act atg tat cat tct gag cca ctt atc cta cat cat gcc aac	Ile Gly Thr Met Tyr His Ser Glu Pro Leu Ile Leu His His Ala Asn	864															
gaa aac tca ggg cgt atg gtt gag ggc caa aca ttt aca att gaa cct	Glu Asn Ser Gly Arg Met Val Glu Gly Gln Thr Phe Thr Ile Glu Pro	912															
ata ctc aca atg gag aaa aca gag tgt gtt aca tgg gaa gat gga tgg	Ile Leu Thr Met Glu Lys Thr Glu Cys Val Thr Trp Glu Asp Gly Trp	960															
acg act gtc act gct gat ggt agc tgg gct gcg cag ttt gag cat acc	Thr Thr Val Thr Ala Asp Gly Ser Trp Ala Ala Gln Phe Glu His Thr	1008															
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 1 Arg Phe Arg Pro Leu Ala Ala Pro Leu Arg Pro Val Arg Ser Gly Lys
 20 Phe Val Val Pro Lys Arg Cys Phe Thr Val Ser Ser Arg Leu Ala Trp
 35 Val Glu Asp Glu Leu Met Glu Ile Lys Lys Ser Gln Glu Gln Ser Ser
 50 Val Lys Ser Lys Lys Arg Pro Pro Leu Arg Arg Gly Lys Val Ser Pro
 65 Gln Leu Pro Val Pro Gly His Ile Pro Arg Pro Ser Tyr Val Gly Ser
 80 Lys Gly Leu Pro Glu Leu Cys Lys Gly Gln Leu His Asp Ala Gln Gly
 100 Ile Ala Gly Met Arg Ala Ala Cys Lys Leu Ala Ala Arg Val Leu Asp
 115 120 125

PF59082SeqList_PF59082.txt

Phe Ala Gly Thr Leu Val Lys Pro Ser Ile Thr Thr Asn Glu Ile Asp
130 135 140
Glu Ala Val His Asn Met Ile Ile Glu Ala Gly Ala Tyr Pro Ser Pro
145 150 155 160
Leu Gly Tyr His Gly Phe Pro Lys Ser Ile Cys Thr Ser Val Asn Glu
165 170 175
Cys Val Cys His Gly Val Pro Asp Ser Thr Gln Leu Gln Asn Gly Asp
180 185 190
Ile Ile Asn Ile Asp Val Asn Val Phe Leu Asn Gly Tyr His Gly Gly
195 200 205
Thr Ser Arg Thr Phe Ala Cys Gly Gln Val Asp Asp Ser Ile Lys His
210 215 220
Phe Leu Asn Ala Ala Glu Glu Cys Leu Glu Lys Gly Ile Ser Ile Cys
225 230 235 240
Arg Asp Gly Val Asn Tyr Arg Lys Ile Gly Lys Lys Ile Ser Lys Leu
245 250 255
Ala Tyr Phe Tyr Gly Tyr Tyr Val Val Glu Arg Phe Val Gly His Gly
260 265 270
Ile Gly Thr Met Tyr His Ser Glu Pro Leu Ile Leu His His Ala Asn
275 280 285
Glu Asn Ser Gly Arg Met Val Glu Gly Gln Thr Phe Thr Ile Glu Pro
290 295 300
Ile Leu Thr Met Glu Lys Thr Glu Cys Val Thr Trp Glu Asp Gly Trp
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Thr Thr Val Thr Ala Asp Gly Ser Trp Ala Gln Phe Glu His Thr
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28

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<400> 177
ataccgga atacaccaga ctcaacataa gg

32

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<400> 178
atggcgtctt cggtttttct atc

23

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PF59082SeqList_PF59082.txt

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<223> Xaa in position 282 is any amino acid

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<222> (285)..(285)

<223> Xaa in position 285 is any amino acid

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<221> Variant

<222> (289)..(290)

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<221> Variant

<222> (301)..(302)

<223> Xaa in position 301 to 302 is any amino acid

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<223> Xaa in position 309 is any amino acid

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Leu Xaa Xaa Gly Xaa Val Ser Pro Xaa Leu Xaa Val Pro Xaa Xaa Ile
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Xaa Arg Pro Pro Tyr Val Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa
      20      25      30
Xaa Xaa Xaa Xaa Xaa Xaa Asp Xaa Xaa Gly Ile Xaa Xaa Met Arg Ala
      35      40      45
Xaa Xaa Xaa Leu Ala Ala Xaa Val Leu Xaa Xaa Ala Gly Thr Leu Val
      50      55      60
Xaa Pro Xaa Xaa Thr Thr Xaa Glu Ile Asp Xaa Ala Val His Xaa Met
65      70      75      80
Ile Ile Xaa Xaa Gly Ala Tyr Pro Ser Pro Leu Gly Tyr Xaa Gly Phe
      85      90      95
Pro Lys Ser Val Cys Thr Ser Val Asn Glu Cys Xaa Cys His Gly Ile
      100     105     110
Pro Asp Ser Arg Xaa Leu Xaa Xaa Gly Asp Ile Ile Asn Ile Asp Val
      115     120     125
Thr Val Tyr Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Tyr His
130     135     140     145
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Tyr His
145     150     155     160
Gly Asp Thr Ser Xaa Thr Phe Xaa Cys Gly Xaa Val Asp Xaa Xaa Xaa
      165     170     175
Lys Xaa Leu Val Xaa Val Thr Xaa Glu Cys Leu Xaa Xaa Xaa Ile Xaa
      180     185     190
Xaa Cys Xaa Xaa Gly Xaa Xaa Xaa Xaa Lys Ile Gly Xaa Xaa Ile Xaa
      195     200     205
Xaa His Ala Xaa Xaa Xaa Xaa Xaa Val Val Xaa Xaa Phe Val Gly
210     215     220
His Gly Val Gly Xaa Xaa Phe His Xaa Xaa Pro Xaa Ile Xaa His Xaa
225     230     235     240
Arg Asn Xaa Xaa Xaa Xaa Gly Xaa Met Xaa Xaa Xaa Gln Thr Phe
      245     250     255
Thr Ile Glu Pro Xaa Leu Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa
      260     265     270
Xaa Xaa Xaa Trp Xaa Asp Xaa Trp Thr Xaa Val Thr Xaa Asp Gly Ser
      275     280     285
Xaa Xaa Ala Gln Phe Glu His Thr Ile Leu Ile Thr Xaa Xaa Gly Ala
290     295     300
Glu Ile Leu Thr Xaa Cys
305     310

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<210> 185

<211> 60

<212> PRT

<213> Artificial sequence

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<220>
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<222> (8)..(8)
<223> Xaa in position 8 is Ala or Asn

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<222> (38)..(38)
<223> Xaa in position 38 is Asp or Glu

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<222> (40)..(41)
<223> Xaa in position 40 to 41 is any amino acid

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<222> (43)..(43)
<223> Xaa in position 43 is any amino acid

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PF59082SeqList_PF59082.txt

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 <223> Xaa in position 55 is Phe or Tyr

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 <222> (57)..(57)
 <223> Xaa in position 57 is Asp or Asn

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 1 5 10 15
 Tyr Xaa Xaa Xaa Pro Lys Ser Xaa Cys Thr Ser Val Asn Glu Cys Xaa
 20 25 30
 Cys His Gly Xaa Pro Xaa Ser Xaa Xaa Leu Xaa Xaa Gly Asp Ile Ile
 35 40 45
 Asn Ile Asp Val Xaa Val Xaa Leu Xaa Gly Xaa His
 50 55 60

 <210> 186
 <211> 30
 <212> PRT
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 <220>
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 <222> (3)..(3)
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 <222> (5)..(6)
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 <222> (7)..(7)
 <223> Xaa in position 7 is any or no amino acid

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 <222> (11)..(11)
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PF59082SeqList_PF59082.txt

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<223> Xaa in position 21 is Glu, Lys or Arg

<220>
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<223> Xaa in position 23 is any amino acid

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<220>
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Gly Thr Xaa Val Xaa Pro Xaa Xaa Thr Thr Xaa Glu Ile Asp
      20      25      30

<210> 187
<211> 29
<212> PRT
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PF59082SeqList_PF59082.txt

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<223> Xaa in position 17 is Asp, Glu or Gln

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<223> Xaa in position 21 is any amino acid

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<222> (23)..(24)
<223> Xaa in position 23 to 24 is any amino acid

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<222> (26)..(26)
<223> Xaa in position 26 is Asp, Glu or Asn

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<222> (27)..(28)
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Val Val Xaa Xaa Phe Val Gly His Gly Xaa Gly Xaa Xaa Xaa His Xaa
1      5      10      15
Xaa Pro Xaa Xaa Xaa His Xaa Xaa Asn Xaa Xaa Xaa Gly
      20      25

<210> 188
<211> 38
<212> PRT
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<220>
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<223> Xaa in position 5 is Asp, Glu, Asn or Gln

<220>

<221> Variant

<222> (8)..(8)

<223> Xaa in position 8 is Asp or Glu

<220>

<221> Variant

<222> (9)..(10)

<223> Xaa in position 9 to 10 is any amino acid

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<222> (12)..(12)

<223> Xaa in position 12 is any amino acid

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<221> Variant

<222> (13)..(13)

<223> Xaa in position 13 is any or no amino acid

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<222> (19)..(19)

<223> Xaa in position 19 is any or no amino acid

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<221> Variant

<222> (21)..(21)

<223> Xaa in position 21 is Cys or Ser

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<222> (22)..(22)

<223> Xaa in position 22 is Leu or Met

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<222> (23)..(23)

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<222> (24)..(24)

<223> Xaa in position 24 is Lys or Arg

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<221> Variant

<222> (25)..(25)

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<221> Variant

<222> (27)..(27)

<223> Xaa in position 27 is Ala or Ser

<220>

<221> Variant

<222> (28)..(28)

<223> Xaa in position 28 is any amino acid

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<222> (30)..(31)
 <223> Xaa in position 30 to 31 is any amino acid

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 <222> (33)..(33)
 <223> Xaa in position 33 is Ala, Thr or Val

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 <222> (34)..(34)
 <223> Xaa in position 34 is Glu, Asn or Ser

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 <222> (35)..(35)
 <223> Xaa in position 35 is any amino acid

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 <223> Xaa in position 36 is Lys or Arg

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 20 25 30
 Xaa Xaa Xaa Xaa Xaa Ile
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 <213> Artificial sequence

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Thr Asn Phe Ala Pro Leu Leu Gly Ala Leu Ile Ser Asp Ala Tyr Ile
      20      25      30
ggc cgt ttc aag acc atc gct tac gca tcc ctc ttc tca att cta gga      144
Gly Arg Phe Lys Thr Ile Ala Tyr Ala Ser Leu Phe Ser Ile Leu Gly
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cta atg acg gtg aca ctc acc gcc tgc ctg cct caa ctc cac cca cca      192
Leu Met Thr Val Thr Leu Thr Ala Cys Leu Pro Gln Leu His Pro Pro
      50      55      60
ccg tgc aac aac cct cat cca gac gaa tgc gac gat ccg aac aag ctc      240
Pro Cys Asn Asn Pro His Pro Asp Glu Cys Asp Asp Pro Asn Lys Leu
      65      70      75
cag ctc ggg att cta ttc ctc ggt ctc ggc ttt ctc tcc atc ggt agc      288
Gln Leu Gly Ile Leu Phe Leu Gly Leu Gly Phe Leu Ser Ile Gly Ser
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ggc gga atc cgg cct tgc agc att cca ttc gga gtt gat cag ttt gac      336
Gly Gly Ile Arg Pro Cys Ser Ile Pro Phe Gly Val Asp Gln Phe Asp
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Gln Arg Thr Glu Gln Gly Leu Lys Gly Val Ala Ser Phe Phe Asn Trp
      115      120      125
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Tyr Tyr Leu Thr Leu Thr Met Val Leu Ile Phe Ser His Thr Val Val
      130      135      140
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Val Tyr Leu Gln Thr Val Ser Trp Val Ile Gly Phe Ser Ile Pro Thr
      145      150      155
agt tta atg gct tgt gca gtg gtt ctg ttc ttt gtc ggt atg cgg ttt      528
Ser Leu Met Ala Cys Ala Val Val Leu Phe Phe Val Gly Met Arg Phe
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Tyr Val Tyr Val Lys Pro Glu Gly Ser Val Phe Ser Gly Ile Ala Arg
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Val Ile Val Ala Ala Arg Lys Lys Arg Asp Leu Lys Ile Ser Leu Val
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Asp Asp Gly Thr Glu Glu Tyr Tyr Glu Pro Pro Val Lys Pro Gly Val
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Leu Ser Lys Leu Pro Leu Thr Asp Gln Phe Lys Phe Leu Asp Lys Ala
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Ala Val Ile Leu Asp Gly Asp Leu Thr Ser Glu Gly Val Pro Ala Asn
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aag tgg cgg cta tgt agc atc caa gaa gtt gaa gag gtc aag tgc ctg      816
Lys Trp Arg Leu Cys Ser Ile Gln Glu Val Glu Glu Val Lys Cys Leu
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Ile Arg Val Val Pro Val Trp Ser Ala Gly Ile Ile Ser Ile Val Ala
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caa cgg atg ggg ata ggg atc gtc ttc gcc att ctc tcc atg ttc act				Gln Arg Met Gly Ile Gly Ile Val Phe Ala Ile Leu Ser Met Phe Thr											1104
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				405				410						415	
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				435				440						445	
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				450				455						460	
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				465				470						475	
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				485				490						495	
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 Gln Leu Gly Ile Leu Phe Leu Gly Leu Gly Phe Leu Ser Ile Gly Ser
 85 90 95
 Gly Gly Ile Arg Pro Cys Ser Ile Pro Phe Gly Val Asp Gln Phe Asp
 100 105 110
 Gln Arg Thr Glu Gln Gly Leu Lys Gly Val Ala Ser Phe Phe Asn Trp
 115 120 125
 Tyr Tyr Leu Thr Leu Thr Met Val Leu Ile Phe Ser His Thr Val Val
 130 135 140
 Val Tyr Leu Gln Thr Val Ser Trp Val Ile Gly Phe Ser Ile Pro Thr
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 Ser Leu Met Ala Cys Ala Val Val Leu Phe Phe Val Gly Met Arg Phe
 165 170 175

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225 230 235 240
Ala Val Ile Leu Asp Gly Asp Leu Thr Ser Glu Gly Val Pro Ala Asn
245 250 255
Lys Trp Arg Leu Cys Ser Ile Gln Glu Val Glu Glu Val Lys Cys Leu
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Ala Gly Phe Val Glu Gly Val Arg Arg Thr Arg Ala Thr Glu Met Thr
370 375 380
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385 390 395 400
Cys Glu Ser Phe Asn Phe Ile Gly Leu Ile Glu Phe Phe Asn Ser Gln
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Phe Pro Glu His Met Arg Ser Ile Ala Asn Ser Leu Phe Pro Leu Ser
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465 470 475 480
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Met Val Leu Met Asp Gly Arg Asp
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10 15 20

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Asn	Ile	Trp	Phe	Gly	Phe	Thr	Asn	Leu	Thr	Pro	Leu	Val	Gly	Ala	Phe	
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Ile	Ser	Asp	Ala	Tyr	Val	Gly	Arg	Phe	Lys	Thr	Ile	Ala	Phe	Ala	Ser	
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Phe	Ala	Thr	Leu	Leu	Gly	Leu	Val	Thr	Leu	Thr	Leu	Thr	Ala	Ser	Leu	
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Val Phe Ala Ile Leu Ser Met Ile Val Ala Gly Leu Val Glu Arg Val
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Phe Ser Gly Gly His Asp Arg Pro Asp Trp Leu Asp Lys Asn Leu Asn
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Ala Gly Lys Leu Asp Tyr Phe Tyr Tyr Leu Ile Ala Ile Leu Gly Val
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Val Asn Leu Val Tyr Phe Trp Tyr Cys Ala Arg Gly Tyr Arg Tyr Lys
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Leu Leu Ser Asn Phe Met Val Tyr Leu Thr Arg Val Phe His Leu Glu
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Gln Val Lys Ala Ala Asn Val Ile Asn Ile Trp Phe Gly Phe Thr Asn
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PF59082SeqList_PF59082.txt

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Val	Ile	Lys	Glu	Gly	Asp	Leu	Thr	Ser	Glu	Gly	Val	Pro	Ala	Asn	Lys
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Ser	Leu	Leu	Thr	Ile	Gly	Ile	Phe	Leu	Pro	Ile	Tyr	Asp	Arg	Val	Leu
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Val	Pro	Phe	Leu	Arg	Arg	Ile	Thr	Gly	His	Lys	Ser	Gly	Ile	Thr	Arg
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Val	Ala	Gly	Leu	Val	Glu	Arg	Val	Arg	Arg	Thr	Arg	Ser	Ile	Lys	Ser
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Gln	Leu	Ile	Leu	Met	Gly	Leu	Cys	Glu	Ala	Leu	Asn	Ile	Ile	Gly	Gln
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Asn	Ala	Leu	Phe	Ser	Leu	Ser	Phe	Ala	Gly	Ser	Ser	Tyr	Leu	Ser	Ser
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Phe	Leu	Val	Thr	Val	Val	His	Lys	Phe	Ser	Gly	Gly	His	Asp	Arg	Pro
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Asp	Trp	Leu	Asp	Lys	Asn	Leu	Asn	Ala	Gly	Lys	Leu	Asp	Tyr	Phe	Tyr
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Tyr	Leu	Ile	Ala	Ile	Leu	Gly	Val	Val	Asn	Leu	Val	Tyr	Phe	Trp	Tyr
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PF59082SeqList_PF59082.txt

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Tyr Lys Gly Phe Pro Ala Asp Arg Ser Lys Thr Gly Gly Trp Val Pro
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Ala Ala Leu Ile Leu Gly Ile Glu Ile Val Glu Arg Leu Ser Thr Met
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Arg Tyr Lys Thr Ile Gly Ile Phe Ala Ser Ile Gln Thr Leu Gly Thr
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gct aca tta gca atc tca aca aaa ttg cca ggg cta cgt cca cca cct      445
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Cys His Ala Asn Ser Asp Ser Cys Lys Gln Ala Asn Gly Phe Gln Met
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ctc aag tcc agt gtt tca gga ttt ggt tct gac caa ttc gat gag aaa      589
Leu Lys Ser Ser Val Ser Gly Phe Gly Ser Asp Gln Phe Asp Glu Lys
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gat gag aag gag aaa tcg caa atg gcc tat ttt ttc aac agg ttt ttc      637
Asp Glu Lys Glu Lys Ser Gln Met Ala Tyr Phe Phe Asn Arg Phe Phe
175          180          185          190
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Ser Met Ile Ile Ala Ile Ile Val Phe Leu Ser Gly Thr Lys Arg Tyr
          225          230          235
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Arg Tyr Lys Arg Ser Leu Gly Ser Pro Ile Val His Ile Phe Gln Val
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Ile Ala Ala Ser Ile Lys Lys Arg Lys Met Gln Leu Pro Tyr Asn Val
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          275          280          285
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          290          295          300
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Phe Glu Thr Asn Leu Cys Gly Ser Gly Pro Asn Pro Trp Lys Leu Cys
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tca cta aca agg gta gag gag gtg aaa atg atg gtg aga ctt ctg cca      1069
Ser Leu Thr Arg Val Glu Glu Val Lys Met Met Val Arg Leu Leu Pro
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PF59082SeqList_PF59082.txt

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ttc	caa	atc	cct	gca	ggc	tct	gtc	aca	gtc	ttt	ttt	gtg	gct	gca	ata	1213									
Phe	Gln	Ile	Pro	Ala	Gly	Ser	Val	Thr	Val	Phe	Phe	Val	Ala	Ala	Ile										
cta	atc	act	ctg	gct	gtc	tat	gac	cga	ctc	atc	atg	ccc	ctt	tgg	aaa	1261									
Leu	Ile	Thr 385	Leu	Ala	Val	Tyr	Asp 390	Arg	Leu	Ile	Met	Pro	Leu	Trp	Lys										
aag	tgg	aac	ggc	aaa	cca	ggt	ttc	act	gac	cta	caa	agg	ata	gca	att	1309									
Lys	Trp	Asn	Gly	Lys	Pro	Gly 405	Phe	Thr	Asp	Leu	Gln	Arg	Ile	Ala	Ile										
ggg	ctt	gta	ttt	tcc	att	ttt	gga	atg	gcg	gct	gct	tct	gta	tgc	gag	1357									
Gly 415	Leu	Val	Phe	Ser	Ile 420	Phe	Gly	Met	Ala	Ala 425	Ala	Ser	Val	Cys	Glu 430										
agg	aaa	cgg	tta	tcc	gtt	gca	aaa	agt	gtt	agt	ggc	ggc	aac	caa	gca	1405									
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Phe 495	Leu	Thr	Thr	Leu	Ser 500	Leu	Gly	Phe	Phe	Phe	Ser	Ser	Phe	Leu	Val 510										
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PF59082SeqList_PF59082.txt

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Leu	Cys	Leu	Leu	Gly	Gly	Phe	Leu	Ala	Asp	Ser	Phe	Leu	Gly	Arg	Tyr
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Lys	Thr	Ile	Gly	Ile	Phe	Ala	Ser	Ile	Gln	Thr	Leu	Gly	Thr	Ala	Thr
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Ser	Ser	Val	Ser	Gly	Phe	Gly	Ser	Asp	Gln	Phe	Asp	Glu	Lys	Asp	Glu
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Lys	Glu	Lys	Ser	Gln	Met	Ala	Tyr	Phe	Phe	Asn	Arg	Phe	Phe	Phe	Phe
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210						215					220				
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Leu	Tyr	Glu	Asp	Thr	Pro	Glu	Ala	Ser	Arg	Ile	Glu	His	Thr	Glu	Gln
		275					280					285			
Phe	Arg	Phe	Leu	Glu	Lys	Ala	Ala	Ile	Val	Ala	Glu	Asp	Asp	Phe	Glu
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Thr	Asn	Leu	Cys	Gly	Ser	Gly	Pro	Asn	Pro	Trp	Lys	Leu	Cys	Ser	Leu
305					310					315					320
Thr	Arg	Val	Glu	Glu	Val	Lys	Met	Met	Val	Arg	Leu	Leu	Pro	Val	Trp
				325					330					335	
Ala	Thr	Thr	Ile	Ile	Phe	Trp	Thr	Ile	Tyr	Ala	Gln	Leu	Ile	Thr	Phe
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Ile	Pro	Ala	Gly	Ser	Val	Thr	Val	Phe	Phe	Val	Ala	Ala	Ile	Leu	Ile
370						375					380				
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Asn	Gly	Lys	Pro	Gly	Phe	Thr	Asp	Leu	Gln	Arg	Ile	Ala	Ile	Gly	Leu
				405					410					415	
Val	Phe	Ser	Ile	Phe	Gly	Met	Ala	Ala	Ala	Ser	Val	Cys	Glu	Arg	Lys
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		435					440					445			
Thr	Leu	Pro	Ile	Ser	Val	Phe	Leu	Leu	Ile	Pro	Gln	Phe	Phe	Leu	Val
	450					455					460				
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Ser	Ile	Asn	Lys	Gly	Arg	Leu	Asp	Leu	Phe	Tyr	Ala	Leu	Leu	Thr	Ile
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Ile Ala Gly Asn Leu Ile Thr Tyr Leu Thr Thr Lys Leu His Gln Gly	
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Leu Thr Pro Leu Ile Gly Ala Val Leu Ala Asp Ala Tyr Trp Gly Arg	
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Tyr Trp Thr Ile Ala Cys Phe Ser Gly Ile Tyr Phe Ile Gly Met Ser	
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130 135 140	
ctt ggc acc ttc tgt cct tca gca acg cca gct cag tac gca atg ttc	540
Leu Gly Thr Phe Cys Pro Ser Ala Thr Pro Ala Gln Tyr Ala Met Phe	
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Cys Val Ser Ser Phe Gly Ala Asp Gln Phe Asp Asp Thr Asp Ser Arg	
180 185 190	
gaa cga gtc aga aaa gct tcc ttc ttc aac tgg ttt tac ttc tcc atc	684
Glu Arg Val Arg Lys Ala Ser Phe Phe Asn Trp Phe Tyr Phe Ser Ile	
195 200 205	
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Asn Arg Gly Trp Gly Leu Gly Phe Gly Ile Pro Thr Val Phe Met Gly	
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Lys Pro Gly Gly Ser Pro Ile Thr Arg Ile Ser Gln Val Val Val Ala	
260 265 270	
tcc ttc cgt aaa tcg act ctc aaa gtc cct gaa gac gct gca ctt ttg	924
Ser Phe Arg Lys Ser Thr Leu Lys Val Pro Glu Asp Ala Ala Leu Leu	
275 280 285	
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Asp Glu Glu Ser Lys Ser Gly Asp Phe Ser Asn Ser Trp Arg Leu Cys
325          330          335
acg gtc act caa gtc gaa gaa ctc aag att ctg atc cgt atg ttc cca 1116
Thr Val Thr Gln Val Glu Glu Leu Lys Ile Leu Ile Arg Met Phe Pro
340          345          350
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Ile Trp Ala Ser Gly Ile Ile Phe Ser Ala Val Tyr Ala Gln Met Ser
355          360          365
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370          375          380
ttc cag ctt cct cca gcg gca cta ggg aca ttc gac acc gct agc gtc 1260
Phe Gln Leu Pro Pro Ala Ala Leu Gly Thr Phe Asp Thr Ala Ser Val
385          390          395
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Arg Phe Thr Gly Val Asp Lys Gly Phe Thr Glu Ile Gln Arg Met Gly
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Ile Gly Leu Phe Val Ser Val Leu Cys Met Ala Ala Ala Ala Ile Ile
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Glu Ile Ile Arg Leu Arg Leu Thr Asp Glu Leu Gly Leu Val Glu Ser
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Gly Ala Pro Val Pro Ile Ser Val Leu Trp Gln Ile Pro Gln Tyr Phe
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Ile Leu Gly Ala Ala Glu Val Phe Tyr Phe Ile Gly Gln Leu Glu Phe
485          490          495
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Phe Tyr Asp Gln Ser Pro Asp Thr Met Arg Ser Leu Cys Ser Ala Leu
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Ala Leu Leu Thr Asn Ala Leu Gly Asn Tyr Leu Ser Ser Leu Ile Leu
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PF59082SeqList_PF59082.txt

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Phe Ser Gly Leu Tyr Leu Ile Ala Leu Gly Thr Gly Gly Ile Lys Pro
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Cys Val Ser Ser Phe Gly Ala Asp Gln Phe Asp Asp Thr Asp Ser Arg
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385     390     395     400
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PF59082SeqList_PF59082.txt

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PF59082SeqList_PF59082.txt																
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PF59082SeqList_PF59082.txt

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Asp Glu Pro Glu Val
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Ile Ala Thr Phe Gly Ala Asp Gln Phe Asp Glu Glu His Ser Lys Glu
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PF59082SeqList_PF59082.txt

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 Ala Ser Leu Phe Val Glu Gln Gly Ala Ala Met Lys Thr Lys Val Ser
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 465 470 475 480
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 Val Ser Val Val Met Lys Ile Ser Thr Glu Asp His Met Pro Gly Trp
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 Met Ser Asn Leu Pro Thr Thr Gln Gly Lys Ala Ile Pro Asp Ala
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110

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 Ser Asp Tyr Lys Gly Arg Pro Ala Glu Arg Ser Lys Thr Gly Gly Trp
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158

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 Thr Ala Ser Ala Met Ile Leu Gly Glu Val Met Glu Arg Leu Thr
 35 40 45

206

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254

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 65 70 75

302

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Trp	Phe	Tyr	Phe	Val	Ser	Ile	Gly	Ser	Leu	Ala	Ala	Thr	Thr	Val		
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Cys	Ala	Gly	Ala	Ile	Val	Val	Ala	Leu	Leu	Val	Phe	Leu	Ser	Gly	Thr	
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Thr	Leu	Thr	Asp	Val	Glu	Glu	Val	Lys	Met	Ile	Leu	Arg	Met	Leu	Pro	
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Ile	Trp	Ala	Thr	Thr	Ile	Met	Phe	Trp	Thr	Ile	His	Ala	Gln	Met	Thr	
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Thr	Phe	Ser	Val	Ser	Gln	Ala	Thr	Thr	Met	Asp	Arg	His	Ile	Gly	Lys	
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Thr	Phe	Gln	Met	Pro	Ala	Ala	Ser	Met	Thr	Val	Phe	Leu	Ile	Gly	Thr	
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Ile	Leu	Leu	Thr	Val	Pro	Phe	Tyr	Asp	Arg	Phe	Ile	Val	Pro	Val	Ala	
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Lys	Lys	Val	Leu	Lys	Asn	Pro	His	Gly	Phe	Thr	Pro	Leu	Gln	Arg	Ile	
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Gly	Val	Gly	Leu	Val	Leu	Ser	Val	Val	Ser	Met	Val	Val	Gly	Ala	Leu	
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Ile	Glu	Ile	Lys	Arg	Leu	Arg	Tyr	Ala	Gln	Ser	His	Gly	Leu	Val	Asp	
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aag	cca	gaa	gca	aag	atc	cct	atg	acc	gtg	ttt	tgg	ttg	ata	cca	cag	1454
Lys	Pro	Glu	Ala	Lys	Ile	Pro	Met	Thr	Val	Phe	Trp	Leu	Ile	Pro	Gln	

PF59082SeqList_PF59082.txt

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gac ttt ttc ctt aga gag tgt ccc aaa ggg atg aaa aca atg agc acg      1550
Asp Phe Phe Leu Arg Glu Cys Pro Lys Gly Met Lys Thr Met Ser Thr
480      485      490
gga ttg ttc ttg agc aca ctc tct ttg ggg ttt ttc ttt agc acc ttg      1598
Gly Leu Phe Leu Ser Thr Leu Ser Leu Gly Phe Phe Phe Ser Thr Leu
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Leu Val Ser Ile Val Asn Lys Met Thr Ala His Gly Arg Pro Trp Leu
515      520      525
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Ala Asp Asn Leu Asn Gln Gly Arg Leu Tyr Asp Phe Tyr Trp Leu Leu
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gct ata ttg agt gct ata aat gtg gtc tta tac ttg gtt tgt gct aag      1742
Ala Ile Leu Ser Ala Ile Asn Val Val Leu Tyr Leu Val Cys Ala Lys
545      550      555
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Trp Tyr Val Tyr Lys Glu Lys Arg Leu Ala Glu Glu Cys Ile Glu Leu
560      565      570      575
gaa gaa gca gat gct gct gct ttc cat ggc cat tga atcttctccc      1836
Glu Glu Ala Asp Ala Ala Ala Phe His Gly His
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gccaaccttt tctcttgttt ctctcttttt tcttttcttt tttttaaaat ttttttcaaa      1896

atcccccttg cttgtatcaa aatgttaaac aagtatttcc acacgaaaaa aagaaatgcc      1956

tagcatctgg ttaccataa ttataaataa gcttgtaaga tgtaaccatt ttctatgtgt      2016

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Leu Gly Ile Ala Val Asn Leu Val Thr Tyr Leu Thr Gly Thr Met His
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Leu Gly Asn Ala Ala Ser Ala Asn Val Val Thr Asn Phe Leu Gly Thr
65      70      75      80
Ser Phe Met Leu Cys Leu Leu Gly Gly Phe Leu Ala Asp Thr Phe Leu
85      90      95
Gly Arg Tyr Arg Thr Ile Ala Ile Phe Ala Ala Val Gln Ala Thr Gly
100      105      110
Val Thr Ile Leu Thr Ile Ser Thr Ile Ile Pro Ser Leu His Pro Pro
115      120      125
Lys Cys Asn Gly Asp Thr Val Pro Pro Cys Val Arg Ala Asn Glu Lys
130      135      140
Gln Leu Thr Val Leu Tyr Leu Ala Leu Tyr Val Thr Ala Leu Gly Thr
145      150      155      160
Gly Gly Leu Lys Ser Val Ser Gly Phe Gly Ser Asp Gln Phe Asp
165      170      175

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PF59082SeqList_PF59082.txt

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 Val Tyr Val Gln Asp Asn Ile Gly Arg Gly Trp Gly Tyr Gly Ile Cys
 210 215 220
 Ala Gly Ala Ile Val Val Ala Leu Leu Val Phe Leu Ser Gly Thr Arg
 225 230 235 240
 Lys Tyr Arg Phe Lys Lys Leu Val Gly Ser Pro Leu Thr Gln Phe Ala
 245 250 255
 Glu Val Phe Val Ala Ala Leu Arg Lys Arg Asn Met Glu Leu Pro Ser
 260 265 270
 Asp Ser Ser Leu Leu Phe Asn Asp Tyr Asp Pro Lys Lys Gln Thr Leu
 275 280 285
 Pro His Ser Lys Gln Phe Arg Phe Leu Asp Lys Ala Ala Ile Met Asp
 290 295 300
 Ser Ser Glu Cys Gly Gly Gly Met Lys Arg Lys Trp Tyr Leu Cys Thr
 305 310 315 320
 Leu Thr Asp Val Glu Glu Val Lys Met Ile Leu Arg Met Leu Pro Ile
 325 330 335
 Trp Ala Thr Thr Ile Met Phe Trp Thr Ile His Ala Gln Met Thr Thr
 340 345 350
 Phe Ser Val Ser Gln Ala Thr Thr Met Asp Arg His Ile Gly Lys Thr
 355 360 365
 Phe Gln Met Pro Ala Ala Ser Met Thr Val Phe Leu Ile Gly Thr Ile
 370 375 380
 Leu Leu Thr Val Pro Phe Tyr Asp Arg Phe Ile Val Pro Val Ala Lys
 385 390 395 400
 Lys Val Leu Lys Asn Pro His Gly Phe Thr Pro Leu Gln Arg Ile Gly
 405 410 415
 Val Gly Leu Val Leu Ser Val Val Ser Met Val Val Gly Ala Leu Ile
 420 425 430
 Glu Ile Lys Arg Leu Arg Tyr Ala Gln Ser His Gly Leu Val Asp Lys
 435 440 445
 Pro Glu Ala Lys Ile Pro Met Thr Val Phe Trp Leu Ile Pro Gln Asn
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 485 490 495
 Leu Phe Leu Ser Thr Leu Ser Leu Gly Phe Phe Phe Ser Thr Leu Leu
 500 505 510
 Val Ser Ile Val Asn Lys Met Thr Ala His Gly Arg Pro Trp Leu Ala
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 Ile Leu Ser Ala Ile Asn Val Val Leu Tyr Leu Val Cys Ala Lys Trp
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113

PF59082SeqList_PF59082.txt

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Lys	Gly	Leu	Pro	Val	Leu	Arg	Ser	Thr	Ser	Gly	Gly	Trp	Lys	Ala	Ala	
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Ala	Phe	Ile	Ile	Thr	Val	Glu	Val	Ala	Glu	Arg	Phe	Ala	Tyr	Tyr	Gly	
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Ile	Asn	Ser	Asn	Leu	Ile	Asn	Tyr	Leu	Thr	Gly	Pro	Leu	Gly	Gln	Ser	
	60				65					70					75	
acg	gta	acg	gca	gca	gag	aac	gtc	aac	ctc	tgg	tct	gga	aca	gcg	tca	353
Thr	Val	Thr	Ala	Ala	Glu	Asn	Val	Asn	Leu	Trp	Ser	Gly	Thr	Ala	Ser	
			80						85					90		
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Leu	Leu	Pro	Leu	Leu	Gly	Ala	Phe	Leu	Ala	Asp	Ser	Phe	Leu	Gly	Arg	
			95					100					105			
tac	cgc	acc	atc	gtt	tta	gct	tcc	ctt	att	tat	gtt	ctg	gga	ctg	agc	449
Tyr	Arg	Thr	Ile	Val	Leu	Ala	Leu	Ile	Tyr	Val	Val	Leu	Gly	Leu	Ser	
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Leu	Leu	Thr	Phe	Ser	Thr	Ile	Leu	Pro	Val	Thr	Thr	Ser	Asp	Gly	Glu	
	125					130					135					
gtt	gct	cgt	ccc	caa	tta	ata	ttc	ttc	ttc	ttt	tct	cta	tat	ctc	gtt	545
Val	Ala	Arg	Pro	Gln	Leu	Ile	Phe	Phe	Phe	Phe	Ser	Leu	Tyr	Leu	Val	
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Asp	Gln	Phe	Asp	Val	Asn	Asp	Pro	Glu	Glu	Cys	Lys	Ala	Arg	Ser	Ser	
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Phe	Phe	Asn	Trp	Trp	Tyr	Phe	Ala	Phe	Ser	Ala	Gly	Leu	Phe	Val	Thr	
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ctt	ttc	atc	ttg	aac	tat	gtc	cag	gat	aat	gtc	ggt	tgg	gtt	ctt	gga	737
Leu	Phe	Ile	Leu	Asn	Tyr	Val	Gln	Asp	Asn	Val	Gly	Trp	Val	Leu	Gly	
	205					210					215					
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Phe	Gly	Ile	Pro	Cys	Ile	Ala	Met	Leu	Thr	Ala	Leu	Val	Ile	Phe	Leu	
	220				225					230					235	
att	gga	act	tgg	act	tac	cgg	ttt	agc	att	cgg	agg	gag	gaa	cga	ggc	833
Ile	Gly	Thr	Trp	Thr	Tyr	Arg	Phe	Ser	Ile	Arg	Arg	Glu	Glu	Arg	Gly	
		240							245					250		
cct	ttt	ttg	agg	att	ggt	agg	gtg	ttt	att	gtt	gca	gtg	aac	aat	tgg	881
Pro	Phe	Leu	Arg	Ile	Gly	Arg	Val	Phe	Ile	Val	Ala	Val	Asn	Asn	Trp	
		255						260					265			
cga	att	acc	cct	tca	gct	gtc	act	tct	gaa	gag	gaa	gct	tgt	ggc	act	929
Arg	Ile	Thr	Pro	Ser	Ala	Val	Thr	Ser	Glu	Glu	Glu	Ala	Cys	Gly	Thr	
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Leu	Pro	Cys	His	Gly	Ser	Asp	Gln	Phe	Ser	Phe	Leu	Asn	Lys	Ala	Leu	
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Ile	Ala	Ser	Asn	Gly	Ser	Lys	Glu	Glu	Gly	Glu	Val	Cys	Ser	Ala	Ala	
	300				305				310						315	
gaa	gtt	gaa	gaa	gca	aag	gca	gtc	ctc	agg	ctt	gtt	cca	ata	tgg	gct	1073
Glu	Val	Glu	Glu	Ala	Lys	Ala	Val	Leu	Arg	Leu	Val	Pro	Ile	Trp	Ala	
				320					325					330		
aca	tgt	tta	att	ttt	gct	att	gtg	ttt	gct	cag	tct	tct	act	ttc	ttt	1121
Thr	Cys	Leu	Ile	Phe	Ala	Ile	Val	Phe	Ala	Gln	Ser	Ser	Thr	Phe	Phe	
		335						340					345			
aca	aaa	caa	ggt	gtt	acg	atg	gac	agg	gaa	att	ttg	cct	ggg	ttt	tat	1169
Thr	Lys	Gln	Gly	Val	Thr	Met	Asp	Arg	Glu	Ile	Leu	Pro	Gly	Phe	Tyr	
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gta	ccc	cct	gct	tct	ctt	caa	tcc	att	atc	agc	ctc	tcc	att	gtt	ctt	1217
Val	Pro	Pro	Ala	Ser	Leu	Gln	Ser	Ile	Ile	Ser	Leu	Ser	Ile	Val	Leu	
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act ggc aaa ccc tct ggc atc aca atg ctg cag aga att gga act gga	1313
Thr Gly Lys Pro Ser Gly Ile Thr Met Leu Gln Arg Ile Gly Thr Gly	
400 405 410	
atg ctt ctt tct gca att tct atg gta att gca gct ttt gtg gag atg	1361
Met Leu Leu Ser Ala Ile Ser Met Val Ile Ala Ala Phe Val Glu Met	
415 420 425	
aaa aga ctc aaa gtg gct cgt gac tgt ggg cta att gac atg cct aat	1409
Lys Arg Leu Lys Val Ala Arg Asp Cys Gly Leu Ile Asp Met Pro Asn	
430 435 440	
gtg aca att cca atg agc atc tgg tgg tta gtt cct caa tat gcc ttg	1457
Val Thr Ile Pro Met Ser Ile Trp Trp Leu Val Pro Gln Tyr Ala Leu	
445 450 455	
ttt gga att gct gat gtc ttt gca atg gtg ggt ctg caa gag ttt ttc	1505
Phe Gly Ile Ala Asp Val Phe Ala Met Val Gly Leu Gln Glu Phe Phe	
460 465 470 475	
tat gat caa gtc cca cag gaa tta aga agt gtg ggt ctt tct ctc tat	1553
Tyr Asp Gln Val Pro Gln Glu Leu Arg Ser Val Gly Leu Ser Leu Tyr	
480 485 490	
cta agt att ttt ggg gtc ggg agc ttt ctg agt ggc ttt ctc atc tct	1601
Leu Ser Ile Phe Gly Val Gly Ser Phe Leu Ser Gly Phe Leu Ile Ser	
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gct att gaa aat gtc acg ggt aaa gat aat cgt cat agc tgg ttt tct	1649
Ala Ile Glu Asn Val Thr Gly Lys Asp Asn Arg His Ser Trp Phe Ser	
510 515 520	
agt aat ctc aat cgt gcg cat ctt gat tat ttc tat gcc ctt cta gct	1697
Ser Asn Leu Asn Arg Ala His Leu Asp Tyr Phe Tyr Ala Leu Leu Ala	
525 530 535	
gct ctc agt gca gtg gag tta tct gtc ttc tgg ttc ttt tcc aaa tct	1745
Ala Leu Ser Ala Val Glu Leu Ser Val Phe Trp Phe Phe Ser Lys Ser	
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Tyr Val Tyr Lys Thr Arg Ser Thr	
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ttctaagacg agatgcaaag gatccaaatt accttgcaaa ctcaaattgga atcatatata	1912
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 35 40 45
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 50 55 60
 Ile Asn Tyr Leu Thr Gly Pro Leu Gly Gln Ser Thr Val Thr Ala Ala
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 Glu Asn Val Asn Leu Trp Ser Gly Thr Ala Ser Leu Leu Pro Leu Leu
 Seite 241

PF59082SeqList_PF59082.txt

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Thr	Ile	Leu	Pro	Val	Thr	Thr	Ser	Asp	Gly	Glu	Val	Ala	Arg	Pro	Gln
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Leu	Ile	Phe	Phe	Phe	Phe	Ser	Leu	Tyr	Leu	Val	Ala	Leu	Ala	Gln	Gly
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Gly	His	Lys	Pro	Cys	Val	Gln	Ala	Phe	Gly	Ala	Asp	Gln	Phe	Asp	Val
				165					170					175	
Asn	Asp	Pro	Glu	Glu	Cys	Lys	Ala	Arg	Ser	Ser	Phe	Phe	Asn	Trp	Trp
			180					185					190		
Tyr	Phe	Ala	Phe	Ser	Ala	Gly	Leu	Phe	Val	Thr	Leu	Phe	Ile	Leu	Asn
			195					200					205		
Tyr	Val	Gln	Asp	Asn	Val	Gly	Trp	Val	Leu	Gly	Phe	Gly	Ile	Pro	Cys
			210					215					220		
Ile	Ala	Met	Leu	Thr	Ala	Leu	Val	Ile	Phe	Leu	Ile	Gly	Thr	Trp	Thr
225															240
Tyr	Arg	Phe	Ser	Ile	Arg	Arg	Glu	Glu	Arg	Gly	Pro	Phe	Leu	Arg	Ile
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Gly	Arg	Val	Phe	Ile	Val	Ala	Val	Asn	Asn	Trp	Arg	Ile	Thr	Pro	Ser
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Ala	Val	Thr	Ser	Glu	Glu	Glu	Ala	Cys	Gly	Thr	Leu	Pro	Cys	His	Gly
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Ser	Asp	Gln	Phe	Ser	Phe	Leu	Asn	Lys	Ala	Leu	Ile	Ala	Ser	Asn	Gly
			290					295					300		
Ser	Lys	Glu	Glu	Gly	Glu	Val	Cys	Ser	Ala	Ala	Glu	Val	Glu	Glu	Ala
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Lys	Ala	Val	Leu	Arg	Leu	Val	Pro	Ile	Trp	Ala	Thr	Cys	Leu	Ile	Phe
				325					330					335	
Ala	Ile	Val	Phe	Ala	Gln	Ser	Ser	Thr	Phe	Phe	Thr	Lys	Gln	Gly	Val
			340					345					350		
Thr	Met	Asp	Arg	Glu	Ile	Leu	Pro	Gly	Phe	Tyr	Val	Pro	Pro	Ala	Ser
			355					360					365		
Leu	Gln	Ser	Ile	Ile	Ser	Leu	Ser	Ile	Val	Leu	Phe	Ile	Pro	Ile	Tyr
			370					375					380		
Asp	Arg	Ile	Ile	Val	Pro	Val	Ala	Arg	Ala	Phe	Thr	Gly	Lys	Pro	Ser
385															400
Gly	Ile	Thr	Met	Leu	Gln	Arg	Ile	Gly	Thr	Gly	Met	Leu	Leu	Ser	Ala
				405					410					415	
Ile	Ser	Met	Val	Ile	Ala	Ala	Phe	Val	Glu	Met	Lys	Arg	Leu	Lys	Val
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<222> (73)..(1908)

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Ala Met Gly Lys Glu Lys Thr Lys Ala Val Lys Ala Val Ser Glu Glu
              15          20          25
gct gag tcg tcg tcc tcg gat gcc ggc gac gac ggc gag gag gcg gcg      207
Ala Glu Ser Ser Ser Ser Asp Ala Gly Asp Asp Gly Glu Glu Ala Ala
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ggc gcc gtc cac aac cac cgc gga tgg aag gcc atg ccg tac gtc ata      255
Gly Ala Val His Asn His Arg Gly Trp Lys Ala Met Pro Tyr Val Ile
              50          55          60
ggg aac gag acg ttc gag aag ctc ggg acg atc gcc acg ctg tcg aac      303
Gly Asn Glu Thr Phe Glu Lys Leu Gly Thr Ile Gly Thr Leu Ser Asn
              65          70          75
atg ttg gtg tac ctg acg acg gtg tac cac atg cca agc gtc aac gcc      351
Met Leu Val Tyr Leu Thr Thr Val Tyr His Met Pro Ser Val Asn Ala
              80          85          90
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Ala Thr Leu Leu Asn Val Phe Ser Gly Thr Ser Asn Leu Ala Thr Val
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ttc ggc gcc tac gtc agc gac acc tac ctc ggc cgc tac acc acc atc      447
Phe Gly Ala Tyr Val Ser Asp Thr Tyr Leu Gly Arg Tyr Thr Thr Ile
              110          115          120          125
gca gcc gcc acc atg tcc tcc ttc atc ggc atg ctc atc ctc acg ctc      495
Ala Ala Ala Thr Met Ser Ser Phe Ile Gly Met Leu Ile Leu Thr Leu
              130          135          140
acg gcc gct atc cac acc ctc cat cct ccg gcg tgc aac gcg tcc aag      543
Thr Ala Ala Ile His Thr Leu His Pro Ala Cys Asn Ala Ser Lys
              145          150          155
ggg caa caa tgt gag ggt ccc act ggc tcc cag cta gcc gcc atc ctg      591
Gly Gln Gln Cys Glu Gly Pro Thr Gly Ser Gln Leu Ala Ala Ile Leu
              160          165          170
gtg tcc ttc ttc ttc ctg gtc ggt gct gga ggc atc cgg ccc tgc      639
Val Ser Phe Phe Phe Leu Val Val Gly Ala Gly Gly Ile Arg Pro Cys
              175          180          185
aac ctc gcc ttc ggg gcc gac cag ttc aac cca cgc aca gcc gat ggt      687
Asn Leu Ala Phe Gly Ala Asp Gln Phe Asn Pro Arg Thr Ala Asp Gly
              190          195          200          205
cgc cgc ggc atc gcc agc ttc ttc aac tgg tac tac ttc acc ttc aca      735
Arg Arg Gly Ile Ala Ser Phe Phe Asn Trp Tyr Tyr Phe Thr Phe Thr
              210          215          220
gtc gcc atg atg ctc tcg gca act gtc atc atc tac ctc cag agc aac      783
Val Ala Met Leu Ser Ala Thr Val Ile Ile Tyr Leu Gln Ser Asn
              225          230          235
gtt aat tgg gcg cta ggg ctc gcc gtg ccc gcc gcg ctc atg ggc ctc      831
Val Asn Trp Ala Leu Gly Leu Ala Val Pro Ala Ala Leu Met Gly Leu
              240          245          250
tca tgc gcc gtc ttc ttc atg ggc aca cgc ctt tat gtc cgt gta cgc      879
Ser Cys Ala Val Phe Phe Met Gly Thr Arg Leu Tyr Val Arg Val Arg
              255          260          265
ccc gag ggc agc ccc ttc aca agc ttc gcc caa gtc ctc gtc gcc gca      927
Pro Glu Gly Ser Pro Phe Thr Ser Phe Ala Gln Val Leu Val Ala Ala
              270          275          280          285
gcc cgc aag cgc cat ctc cgt cga gct cgc ggc gat gcc gag ctg ttc      975
Ala Arg Lys Arg His Leu Arg Arg Ala Arg Gly Asp Ala Glu Leu Phe
              290          295          300          305
gac ccg cca cac cag agt aag ctc gtc tcc aag ctg gca tac acc gac      1023
Asp Pro Pro His Gln Ser Lys Leu Val Ser Lys Leu Ala Tyr Thr Asp
              310          315
cag ttc gcg tgc ctc gat aaa gcg gcc gtg cgg acc ccc gac gac gcg      1071
Gln Phe Ala Cys Leu Asp Lys Ala Ala Val Arg Thr Pro Asp Asp Ala
              320          325          330

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PF59082SeqList_PF59082.txt

ttg tgc atc gac ggg aag aca ccg gca gac cca tgg cgg ttg tgc acg	1119
Leu Cys Ile Asp Gly Lys Thr Pro Ala Asp Pro Trp Arg Leu Cys Thr	
335 340 345	
gtg cag cag gtg gag gag gtc aag tgc cta gcg cgc atc att ccg gtg	1167
Val Gln Gln Val Glu Glu Val Lys Cys Leu Ala Arg Ile Ile Pro Val	
350 355 360	
tgg tcg tcg ggg atc gtc tac ttc atc gtg ctc acc cag ctg ggc acc	1215
Trp Ser Ser Gly Ile Val Tyr Phe Ile Val Leu Thr Gln Leu Gly Thr	
370 375 380	
tac gtc gtg ctc cag gct gcg cag atg gac cgc cga atc agc aac tcc	1263
Tyr Val Val Leu Gln Ala Ala Gln Met Asp Arg Arg Ile Ser Asn Ser	
385 390 395	
agc agc ttc cag atc ccg caa ggc tcc ttc gtc gtc ttc cag atg ctc	1311
Ser Ser Phe Gln Ile Pro Gln Gly Ser Phe Val Val Phe Gln Met Leu	
400 405 410	
gcc ctt acg acg tgg atc cct gtc tac gac cgg ttc gtg gtg ccg acg	1359
Ala Leu Thr Thr Trp Ile Pro Val Tyr Asp Arg Phe Val Val Pro Thr	
415 420 425	
ctc cgc cgc ttc acg aag cgc gag ggc ggc atc acc ctg ctc cag ccg	1407
Leu Arg Arg Phe Thr Lys Arg Glu Gly Gly Ile Thr Leu Leu Gln Arg	
430 435 440 445	
atc ggt gtc ggg ttg gcg ttg tcc gtg gcg acg atg gtg gtg tcg gcg	1455
Ile Gly Val Gly Leu Ala Leu Ser Val Ala Thr Met Val Val Ser Ala	
450 455 460	
gcc gtg gag cag cga cga cga agg atc ggc tcg tcg atg tca tgc ttc	1503
Ala Val Glu Gln Arg Arg Arg Arg Ile Gly Ser Ser Met Ser Cys Phe	
465 470 475	
tgg ctg gtg ccg cag cag ctg ttg gcg ggc ttg tca gag gcg ttc ggc	1551
Trp Leu Val Pro Gln Gln Leu Leu Ala Gly Leu Ser Glu Ala Phe Gly	
480 485 490	
gcc atc ggg cag att gaa ttc tac tac cgg cag ttc ccg gag aac atg	1599
Ala Ile Gly Gln Ile Glu Phe Tyr Tyr Arg Gln Phe Pro Glu Asn Met	
495 500 505	
cgg agc gtg gcg ggg gcg ctc tac ttc ctg ggg ttc gcc atg gcg agc	1647
Arg Ser Val Ala Gly Ala Leu Tyr Phe Leu Gly Phe Ala Met Ala Ser	
510 515 520 525	
tac gca agc ggg ctg atg gtg atg gtg gtg cac cgg gcg acg cgc ggc	1695
Tyr Ala Ser Gly Leu Met Val Met Val Val His Arg Ala Thr Arg Gly	
530 535 540	
cgg gac ggt cag cct gac tgg ctg gcg cag gac ctg gac gag ggt agg	1743
Arg Asp Gly Gln Pro Asp Trp Leu Ala Gln Asp Leu Asp Glu Gly Arg	
545 550 555	
gtg gac cta ttc tac ctg gtc acc gcc gcc atc gcc gcc gtg aac ctc	1791
Val Asp Leu Phe Tyr Leu Val Thr Ala Ala Ile Ala Ala Val Asn Leu	
560 565 570	
gtc tac ttt gtg atc tgc gca cgg tgg tac agg ttc aag aag tcc gac	1839
Val Tyr Phe Val Ile Cys Ala Arg Trp Tyr Arg Phe Lys Lys Ser Asp	
575 580 585	
gat gcc ggc gcc gga gat gtg gag ctc gac gac gac agc ccg aag aag	1887
Asp Ala Gly Ala Gly Asp Val Glu Leu Asp Asp Ser Pro Lys Lys	
590 595 600 605	
gct ggc gct ggt tta gct tag ttattattat tattctttcc ttttggggct	1938
Ala Gly Ala Gly Leu Ala	
610	
tcataactc cgatgcacgc atagaatggt agagtctaag ggatatatgt gcatatatag	1998
ctcatcgatc gatcccgagg aatctatgta atagggattt ggaatcgatc aaaacagaac	2058
aggggagatt gaagaaaaaa aaaaaaaa	2086

<210> 205
 <211> 611
 <212> PRT
 <213> Triticum aestivum

PF59082SeqList_PF59082.txt

<400> 205

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      20      25      30
Ser Ser Ser Asp Ala Gly Asp Asp Gly Glu Glu Ala Ala Gly Ala Val
      35      40      45
His Asn His Arg Gly Trp Lys Ala Met Pro Tyr Val Ile Gly Asn Glu
      50      55      60
Thr Phe Glu Lys Leu Gly Thr Ile Gly Thr Leu Ser Asn Met Leu Val
65      70      75      80
Tyr Leu Thr Thr Val Tyr His Met Pro Ser Val Asn Ala Ala Thr Leu
      85      90      95
Leu Asn Val Phe Ser Gly Thr Ser Asn Leu Ala Thr Val Phe Gly Ala
      100      105      110
Tyr Val Ser Asp Thr Tyr Leu Gly Arg Tyr Thr Thr Ile Ala Ala Ala
      115      120      125
Thr Met Ser Ser Phe Ile Gly Met Leu Ile Leu Thr Leu Thr Ala Ala
130      135      140
Ile His Thr Leu His Pro Pro Ala Cys Asn Ala Ser Lys Gly Gln Gln
145      150      155      160
Cys Glu Gly Pro Thr Gly Ser Gln Leu Ala Ala Ile Leu Val Ser Phe
      165      170      175
Phe Phe Leu Val Gly Ala Gly Gly Ile Arg Pro Cys Asn Leu Ala
      180      185      190
Phe Gly Ala Asp Gln Phe Asn Pro Arg Thr Ala Asp Gly Arg Arg Gly
195      200      205
Ile Ala Ser Phe Phe Asn Trp Tyr Tyr Phe Thr Phe Thr Val Ala Met
210      215      220
Met Leu Ser Ala Thr Val Ile Ile Tyr Leu Gln Ser Asn Val Asn Trp
225      230      235      240
Ala Leu Gly Leu Ala Val Pro Ala Ala Leu Met Gly Leu Ser Cys Ala
      245      250      255
Val Phe Phe Met Gly Thr Arg Leu Tyr Val Arg Val Arg Pro Glu Gly
260      265      270
Ser Pro Phe Thr Ser Phe Ala Gln Val Leu Val Ala Ala Arg Lys
275      280      285
Arg His Leu Arg Arg Ala Arg Gly Asp Ala Glu Leu Phe Asp Pro Pro
290      295      300
His Gln Ser Lys Leu Val Ser Lys Leu Ala Tyr Thr Asp Gln Phe Ala
305      310      315      320
Cys Leu Asp Lys Ala Ala Val Arg Thr Pro Asp Asp Ala Leu Cys Ile
      325      330      335
Asp Gly Lys Thr Pro Ala Asp Pro Trp Arg Leu Cys Thr Val Gln Gln
340      345      350
Val Glu Glu Val Lys Cys Leu Ala Arg Ile Ile Pro Val Trp Ser Ser
355      360      365
Gly Ile Val Tyr Phe Ile Val Leu Thr Gln Leu Gly Thr Tyr Val Val
370      375      380
Leu Gln Ala Ala Gln Met Asp Arg Arg Ile Ser Asn Ser Ser Ser Phe
385      390      395      400
Gln Ile Pro Gln Gly Ser Phe Val Val Phe Gln Met Leu Ala Leu Thr
      405      410      415
Thr Trp Ile Pro Val Tyr Asp Arg Phe Val Val Pro Thr Leu Arg Arg
420      425      430
Phe Thr Lys Arg Glu Gly Gly Ile Thr Leu Leu Gln Arg Ile Gly Val
435      440      445
Gly Leu Ala Leu Ser Val Ala Thr Met Val Val Ser Ala Ala Val Glu
450      455      460
Gln Arg Arg Arg Arg Ile Gly Ser Ser Met Ser Cys Phe Trp Leu Val
465      470      475      480
Pro Gln Gln Leu Leu Ala Gly Leu Ser Glu Ala Phe Gly Ala Ile Gly
      485      490      495
Gln Ile Glu Phe Tyr Tyr Arg Gln Phe Pro Glu Asn Met Arg Ser Val
500      505      510
Ala Gly Ala Leu Tyr Phe Leu Gly Phe Ala Met Ala Ser Tyr Ala Ser
515      520      525
Gly Leu Met Val Met Val Val His Arg Ala Thr Arg Gly Arg Asp Gly
530      535      540

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PF59082SeqList_PF59082.txt

Gln Pro Asp Trp Leu Ala Gln Asp Leu Asp Glu Gly Arg Val Asp Leu
 545 550 555 560
 Phe Tyr Leu Val Thr Ala Ala Ile Ala Ala Val Asn Leu Val Tyr Phe
 565 570 575
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 580 585 590
 Ala Gly Asp Val Glu Leu Asp Asp Ser Pro Lys Lys Ala Gly Ala
 595 600 605
 Gly Leu Ala
 610

<210> 206
 <211> 1940
 <212> DNA
 <213> Hordeum vulgare

<220>
 <221> CDS
 <222> (47)..(1747)

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 Glu Ala Gly Glu Ala Pro Leu Leu Ser His Gln Arg Asn Ser Asn Gln
 5 10 15
 gtt tcc tcg tca aat tac aac tgc aaa ccc ttc aac tgg aaa gct cct 151
 Val Ser Ser Ser Asn Tyr Asn Cys Lys Pro Phe Asn Trp Lys Ala Pro
 20 25 30 35
 gct att atc ttg gca ttt gag ttc ttg gag agc att gca tac gct ggt 199
 Ala Ile Ile Leu Ala Phe Glu Phe Leu Glu Ser Ile Ala Tyr Ala Gly
 40 45 50
 att gcc ctc aac ttg gta gta tat ctt ggg aag gtc ctt cat gga acc 247
 Ile Ala Leu Asn Leu Val Val Tyr Leu Gly Lys Val Leu His Gly Thr
 55 60 65
 act gct tca aat gct gcg aat gtt gat aca tgg aac ggc acc acg ttc 295
 Thr Ala Ser Asn Ala Ala Asn Val Asp Thr Trp Asn Gly Thr Thr Phe
 70 75 80
 ctc atg ccc gtc ctt gga gca ttt ctt gct gat aca tac tgg ggg aag 343
 Leu Met Pro Val Leu Gly Ala Phe Leu Ala Asp Thr Tyr Trp Gly Lys
 85 90 95
 tac aag acc gtg gct atc tcc gta ata ttt tat ctt aca ggg ttg ctc 391
 Tyr Lys Thr Val Ala Ile Ser Val Ile Phe Tyr Leu Thr Gly Leu Leu
 100 105 110 115
 atc att act gct tcg gcg atc att cca tct tta caa ccc gcc ccg tgt 439
 Ile Ile Thr Ala Ser Ala Ile Ile Pro Ser Leu Gln Pro Ala Pro Cys
 120 125 130
 gaa gga aat tca tgc cct cct gcc aca ggg ttt cag tat ttt gtc ttg 487
 Glu Gly Asn Ser Cys Pro Pro Ala Thr Gly Phe Gln Tyr Phe Val Leu
 135 140 145
 ttt gct tca cta tac ctt gtc tcg att ggg acc gga ggg gtt aaa tca 535
 Phe Ala Ser Leu Tyr Leu Val Ser Ile Gly Thr Gly Gly Val Lys Ser
 150 155 160
 gct ttg ctc ccc ctt ggg gct gat cag tat gat gat tca aac ctt gaa 583
 Ala Leu Leu Pro Leu Gly Ala Asp Gln Tyr Asp Asp Ser Asn Leu Glu
 165 170 175
 cag agt aaa aag aag caa gcc ttc ttt agc tgg ttc ttc att gcc att 631
 Gln Ser Lys Lys Lys Gln Ala Phe Phe Ser Trp Phe Phe Ile Ala Ile
 180 185 190 195
 aac ctt ggc gtc ttc atc tca ggg acc gtt gtt gta tgg ata cag caa 679
 Asn Leu Gly Val Phe Ile Ser Gly Thr Val Val Val Trp Ile Gln Gln
 200 205 210 215
 aat gtt gct tgg tct ctt gga ttc ggc atc tca tca gta tgc att att 727
 Asn Val Ala Trp Ser Leu Gly Phe Gly Ile Ser Ser Val Cys Ile Ile
 215 220 225
 att gcc aca gtt gcc ttc ttg gca gga aca cca atc tac agg gtt caa 775
 Ile Ala Thr Val Ala Phe Leu Ala Gly Thr Pro Ile Tyr Arg Val Gln
 230 235 240

PF59082SeqList_PF59082.txt

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Leu	Pro	Thr	Gly	Ser	Pro	Leu	Lys	Ser	Leu	Ile	Ala	Val	Phe	Val	Ala	
	245					250					255					
tca	ttt	aaa	aag	aga	aaa	gtg	gag	gtt	cct	gct	gat	agc	tca	ata	ttg	871
Ser	Phe	Lys	Lys	Arg	Lys	Val	Glu	Val	Pro	Ala	Asp	Ser	Ser	Ile	Leu	
260					265					270					275	
ttt	gat	ggg	aat	gat	gct	gat	tta	acc	aat	gaa	gca	cca	aac	aaa	ttg	919
Phe	Asp	Gly	Asn	Asp	Ala	Asp	Leu	Thr	Asn	Glu	Ala	Pro	Asn	Lys	Leu	
			280						285					290		
gca	cat	act	gaa	gga	ttc	agg	tgc	tta	gat	aag	gct	gct	gtg	gtg	tta	967
Ala	His	Thr	Glu	Gly	Phe	Arg	Cys	Leu	Asp	Lys	Ala	Ala	Val	Val	Leu	
			295					300					305			
ggg	gac	caa	gag	ata	aag	gag	agc	ctt	tcc	ggg	cgt	cca	tgg	atg	cta	1015
Gly	Asp	Gln	Glu	Ile	Lys	Glu	Ser	Leu	Ser	Gly	Arg	Pro	Trp	Met	Leu	
		310					315					320				
tgc	act	gta	act	cag	gtg	gag	gaa	gtg	aag	atc	ctt	gtc	cgg	atg	ctt	1063
Cys	Thr	Val	Thr	Gln	Val	Glu	Glu	Val	Lys	Ile	Leu	Val	Arg	Met	Leu	
		325				330					335					
cca	ata	tgg	ttc	acc	agc	gtg	ttc	tat	gca	gca	tcg	atg	tgc	caa	aca	1111
Pro	Ile	Trp	Phe	Thr	Ser	Val	Phe	Tyr	Ala	Ala	Ser	Met	Cys	Gln	Thr	
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gcc	acc	act	ttc	atc	caa	cag	ggg	aac	aaa	atg	aac	aca	aag	atc	gga	1159
Ala	Thr	Thr	Phe	Ile	Gln	Gln	Gly	Asn	Lys	Met	Asn	Thr	Lys	Ile	Gly	
			360				365							370		
tcc	ttc	tct	gtc	cct	cct	gct	tcc	atg	aac	tcg	gcc	tcg	gtg	gtc	ttc	1207
Ser	Phe	Ser	Val	Pro	Pro	Ala	Ser	Met	Asn	Ser	Ala	Ser	Val	Val	Phe	
			375					380					385			
atg	atg	atc	ttc	gtc	gtg	atc	cag	gac	agc	att	gtg	atc	cca	ata	gcc	1255
Met	Met	Ile	Phe	Val	Val	Ile	Gln	Asp	Ser	Ile	Val	Ile	Pro	Ile	Ala	
		390					395					400				
agg	cga	tac	acg	gga	aac	gtc	gct	ggg	ctc	acg	cag	ctg	cag	cgg	atg	1303
Arg	Arg	Tyr	Thr	Gly	Asn	Val	Ala	Gly	Leu	Thr	Gln	Leu	Gln	Arg	Met	
	405					410					415					
ggc	gtc	ggc	cgg	ttc	cta	gcg	gtc	ccg	gcg	ctg	gcc	gcg	gcg	gca	ctg	1351
Gly	Val	Gly	Arg	Phe	Leu	Ala	Val	Pro	Ala	Ala	Ala	Ala	Ala	Ala	Leu	
420					425					430					435	
gtt	gag	atg	tgg	agg	ctg	cgc	agc	gtc	ggg	gcc	ggc	cac	aac	ctg	agc	1399
Val	Glu	Met	Trp	Arg	Leu	Arg	Ser	Val	Gly	Ala	Gly	His	Asn	Leu	Ser	
			440					445						450		
ata	gcg	tgg	cag	ctc	ccc	cag	ttc	atg	ctc	atc	gcc	tgc	tct	gac	gtg	1447
Ile	Ala	Trp	Gln	Leu	Pro	Gln	Phe	Met	Leu	Ile	Ala	Cys	Ser	Asp	Val	
			455					460					465			
ttc	tgc	ggc	ata	gcc	cag	ctc	gag	ttc	ttc	tac	tcg	gaa	gcc	ccc	atg	1495
Phe	Cys	Gly	Ile	Ala	Gln	Leu	Glu	Phe	Phe	Tyr	Ser	Glu	Ala	Pro	Met	
		470					475					480				
tcg	atg	cgg	agc	cta	tgc	tcg	gca	ttc	tcg	ttc	ctg	gcg	atg	tcg	ctt	1543
Ser	Met	Arg	Ser	Leu	Cys	Ser	Ala	Phe	Ser	Phe	Leu	Ala	Met	Ser	Leu	
		485				490					495					
ggg	tac	tac	ctg	aac	tcc	atg	atc	atc	tcg	gcc	atc	gct	gct	ctg	tca	1591
Gly	Tyr	Tyr	Leu	Asn	Ser	Met	Ile	Ile	Ser	Ala	Ile	Ala	Ala	Leu	Ser	
500					505					510					515	
aag	agc	ggc	ggc	ggg	aag	ggc	tgg	ctt	ccc	gcc	gac	ttg	aac	gac	ggg	1639
Lys	Ser	Gly	Gly	Gly	Lys	Gly	Trp	Leu	Pro	Ala	Asp	Leu	Asn	Asp	Gly	
			520						525					530		
cat	ctt	gac	tac	tac	ttc	tgg	ctg	tgg	gct	gtg	atc	ggc	gcg	gtg	aac	1687
His	Leu	Asp	Tyr	Tyr	Phe	Trp	Leu	Trp	Ala	Val	Ile	Gly	Ala	Val	Asn	
			535					540					545			
ttc	gtt	gtg	tac	acg	gcc	ttc	gcg	aag	aat	tat	aca	gtg	aag	aaa	gtc	1735
Phe	Val	Val	Tyr	Thr	Ala	Phe	Ala	Lys	Asn	Tyr	Thr	Val	Lys	Lys	Val	
			550				555					560				
gag	ctc	cgg	tga	acacggtttg	ctgttggtca	caagcgtaca	gttcttatcc									1787
Glu	Leu	Arg														
	565															
tctttgttgt	gtatgtacta	tctacaatac	agctttggtg	taattaaata	tcgctcaa	aat										1847
tcctgtagtt	gtgtccattt	gaataaaatg	ttcctttgaa	acacaaatga	agcaaagcta											1907

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1940

<210> 207

<211> 566

<212> PRT

<213> Hordeum vulgare

<400> 207

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      20      25      30
Lys Ala Pro Ala Ile Ile Leu Ala Phe Glu Phe Leu Glu Ser Ile Ala
      35      40      45
Tyr Ala Gly Ile Ala Leu Asn Leu Val Val Tyr Leu Gly Lys Val Leu
      50      55      60
His Gly Thr Thr Ala Ser Asn Ala Ala Asn Val Asp Thr Trp Asn Gly
65      70      75      80
Thr Thr Phe Leu Met Pro Val Leu Gly Ala Phe Leu Ala Asp Thr Tyr
      85      90      95
Trp Gly Lys Tyr Lys Thr Val Ala Ile Ser Val Ile Phe Tyr Leu Thr
      100      105      110
Gly Leu Leu Ile Ile Thr Ala Ser Ala Ile Ile Pro Ser Leu Gln Pro
      115      120      125
Ala Pro Cys Glu Gly Asn Ser Cys Pro Pro Ala Thr Gly Phe Gln Tyr
      130      135      140
Phe Val Leu Phe Ala Ser Leu Tyr Leu Val Ser Ile Gly Thr Gly Gly
145      150      155      160
Val Lys Ser Ala Leu Leu Pro Leu Gly Ala Asp Gln Tyr Asp Asp Ser
      165      170      175
Asn Leu Glu Gln Ser Lys Lys Lys Gln Ala Phe Phe Ser Trp Phe Phe
      180      185      190
Ile Ala Ile Asn Leu Gly Val Phe Ile Ser Gly Thr Val Val Val Trp
      195      200      205
Ile Gln Gln Asn Val Ala Trp Ser Leu Gly Phe Gly Ile Ser Ser Val
      210      215      220
Cys Ile Ile Ile Ala Thr Val Ala Phe Leu Ala Gly Thr Pro Ile Tyr
225      230      235      240
Arg Val Gln Leu Pro Thr Gly Ser Pro Leu Lys Ser Leu Ile Ala Val
      245      250      255
Phe Val Ala Ser Phe Lys Lys Arg Lys Val Glu Val Pro Ala Asp Ser
      260      265      270
Ser Ile Leu Phe Asp Gly Asn Asp Ala Asp Leu Thr Asn Glu Ala Pro
      275      280      285
Asn Lys Leu Ala His Thr Glu Gly Phe Arg Cys Leu Asp Lys Ala Ala
290      295      300
Val Val Leu Gly Asp Gln Glu Ile Lys Glu Ser Leu Ser Gly Arg Pro
305      310      315      320
Trp Met Leu Cys Thr Val Thr Gln Val Glu Glu Val Lys Ile Leu Val
      325      330      335
Arg Met Leu Pro Ile Trp Phe Thr Ser Val Phe Tyr Ala Ala Ser Met
      340      345      350
Cys Gln Thr Ala Thr Thr Phe Ile Gln Gln Gly Asn Lys Met Asn Thr
      355      360      365
Lys Ile Gly Ser Phe Ser Val Pro Pro Ala Ser Met Asn Ser Ala Ser
      370      375      380
Val Val Phe Met Met Ile Phe Val Val Ile Gln Asp Ser Ile Val Ile
385      390      395      400
Pro Ile Ala Arg Arg Tyr Thr Gly Asn Val Ala Gly Leu Thr Gln Leu
      405      410      415
Gln Arg Met Gly Val Gly Arg Phe Leu Ala Val Pro Ala Leu Ala Ala
      420      425      430
Ala Ala Leu Val Glu Met Trp Arg Leu Arg Ser Val Gly Ala Gly His
      435      440      445
Asn Leu Ser Ile Ala Trp Gln Leu Pro Gln Phe Met Leu Ile Ala Cys
450      455      460
Ser Asp Val Phe Cys Gly Ile Ala Gln Leu Glu Phe Phe Tyr Ser Glu

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PF59082SeqList_PF59082.txt

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Ala Leu Ser Lys Ser Gly Gly Gly Lys Gly Trp Leu Pro Ala Asp Leu
Asn Asp Gly His Leu Asp Tyr Tyr Phe Trp Leu Trp Ala Val Ile Gly
Ala Val Asn Phe Val Val Tyr Thr Ala Phe Ala Lys Asn Tyr Thr Val
Lys Lys Val Glu Leu Arg
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<211> 1837
<212> DNA
<213> glycine max

<220>
<221> CDS
<222> (1)..(1764)

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gat gaa gag aaa tgg gtc cat gat gca tct gtg gat tac aag gga aga 96
Asp Glu Glu Lys Trp Val His Asp Ala Ser Val Asp Tyr Lys Gly Arg
20 25 30
atc cct ctc cgt gct tcc acg ggt gta tgg aaa gct tcg ctt ttt gtc 144
Ile Pro Leu Arg Ala Ser Thr Gly Val Trp Lys Ala Ser Leu Phe Val
35 40 45
ctt gca att gaa ttt agt gaa agg ata tgc cac ttt ggg ata gcc act 192
Leu Ala Ile Glu Phe Ser Glu Arg Ile Cys His Phe Gly Ile Ala Thr
50 55 60
aat ctt atc atg tac ctg act aaa gta atg cat gaa gat ctc aaa aca 240
Asn Leu Ile Met Tyr Leu Thr Lys Val Met His Glu Asp Leu Lys Thr
65 70 75 80
gcg acc aag aat gta aac tac tgg gta gga gca aca act ttg atg cct 288
Ala Thr Lys Asn Val Asn Tyr Trp Val Gly Ala Thr Thr Leu Met Pro
85 90 95
cta att gga gga ttt gtt gct gat gcc tac act ggt cga ttt cgt atg 336
Leu Ile Gly Gly Phe Val Ala Asp Ala Tyr Thr Gly Arg Phe Arg Met
100 105 110
gtc ctc ttt tct tcc ctc tta tac ctc aag gga tta agc ctc ttg acc 384
Val Leu Phe Ser Ser Leu Leu Tyr Leu Lys Gly Leu Ser Leu Leu Thr
115 120 125
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Met Ser Gln Phe Ile Pro Ser Leu Lys Pro Cys Asn Asn Glu Ile Cys
130 135 140
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His Trp Pro Arg Lys Val His Glu Val Val Leu Phe Leu Ala Leu Tyr
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Cys Val Ala Leu Gly Thr Gly Gly Phe Lys Pro Cys Leu Gln Ser Phe
165 170 175
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Gly Ala Asp Gln Phe Asp Asp Asp His Leu Glu Glu Arg Lys Lys Lys
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Met Ser Phe Phe Asn Trp Trp Asn Phe Thr Leu Cys Thr Ala Met Leu
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Leu Gly Ala Thr Val Ile Val Tyr Val Gln Asp Phe Val Ser Trp Gly
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PF59082SeqList_PF59082.txt

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 180 185 190
 Met Ser Phe Phe Asn Trp Trp Asn Phe Thr Leu Cys Thr Ala Met Leu
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 Leu Gly Ala Thr Val Ile Val Tyr Val Gln Asp Phe Val Ser Trp Gly
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 Glu Tyr Phe Tyr Asp Glu Val Pro Asp Ser Met Arg Ser Ile Gly Met
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PF59082SeqList_PF59082.txt

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530 535 540
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Met Lys
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cag gaa atg gag aag aga aag cgt gga aaa agt gaa gaa aaa gga gaa 165
Gln Glu Met Glu Lys Arg Lys Arg Gly Lys Ser Glu Glu Lys Gly Glu
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gag aaa tgg gtg cat gat gca tct gtg gat tat aag ggc aga gtt cct 213
Glu Lys Trp Val His Asp Ala Ser Val Asp Tyr Lys Gly Arg Val Pro
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ctc cgt gct tcc aca ggt gta tgg aaa gcg tcg ctt ttt gtc ctt gca 261
Leu Arg Ala Ser Thr Gly Val Trp Lys Ala Ser Leu Phe Val Leu Ala
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Ile Glu Phe Ser Glu Arg Ile Cys His Phe Gly Ile Ala Thr Asn Leu
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Ile Met Tyr Leu Thr Lys Val Met His Glu Asp Leu Lys Thr Ala Thr
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Lys Asn Val Asn Tyr Trp Val Gly Ala Thr Thr Leu Met Pro Leu Ile
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Gly Gly Phe Val Ala Asp Ala Tyr Thr Gly Arg Phe Arg Met Val Leu
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Pro Arg Lys Val His Glu Val Val Phe Leu Ala Leu Tyr Cys Val
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Ala Leu Gly Thr Gly Gly Phe Lys Pro Cys Leu Gln Ser Phe Gly Ala
165 170 175
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Asp Gln Phe Asp Asp Asp His Leu Glu Glu Arg Lys Lys Lys Met Ser
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PF59082SeqList_PF59082.txt

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Asn	Leu	Lys	Ile	Ile	Asn	Ser	Phe	Lys	Ile	Pro	Pro	Ala	Ser	Met	Thr	
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Met	Val	Val	Ala	Ala	Leu	Val	Glu	Thr	Lys	Arg	Leu	Arg	Met	Val	Glu	
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Gly	Arg	Ile	Glu	Glu	Ser	Asp	Glu	Glu	Lys	Trp	Val	His	Asp	Ala	Ser	
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Val	Asp	Tyr	Lys	Gly	Arg	Ile	Pro	Leu	Arg	Ala	Ser	Thr	Gly	Val	Trp	
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Lys	Ala	Ser	Leu	Phe	Val	Leu	Ala	Ile	Glu	Phe	Ser	Glu	Arg	Ile	Ala	
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His	Phe	Gly	Ile	Ser	Ser	Asn	Leu	Ile	Met	Tyr	Leu	Thr	Glu	Val	Met	
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His	Glu	Asp	Leu	Lys	Thr	Ala	Thr	Asn	Asn	Ala	Asn	Leu	Trp	Lys	Gly	
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gca	aca	acc	ttg	ttg	cct	atg	att	ggg	gga	ttt	ctt	ggg	gat	gcc	tac	401
Ala	Thr	Thr	Leu	Leu	Pro	Met	Ile	Gly	Gly	Phe	Leu	Gly	Asp	Ala	Tyr	
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acc	ggt	cga	ttt	cgt	atg	gta	gtc	ttt	tct	tcc	ctc	gta	tac	ttc	aag	449
Thr	Gly	Arg	Phe	Arg	Met	Val	Val	Phe	Ser	Ser	Leu	Val	Tyr	Phe	Lys	
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Gly	Leu	Ser	Leu	Leu	Thr	Met	Ser	Gln	Phe	Ile	Pro	Asn	Leu	Lys	Pro	
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Cys	Asn	Asn	Asp	Ile	Cys	His	Gln	Pro	Arg	Lys	Val	His	Glu	Val	Val	
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Phe	Phe	Leu	Ala	Leu	Tyr	Cys	Ile	Ala	Leu	Gly	Thr	Gly	Gly	Phe	Lys	
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cca	tgc	tta	gaa	agt	ttt	gga	ggg	gat	caa	ttt	gat	ggg	gac	aac	ctt	641
Pro	Cys	Leu	Glu	Ser	Phe	Gly	Gly	Asp	Gln	Phe	Asp	Gly	Asp	Asn	Leu	
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gaa	gaa	cga	aag	aag	aag	atg	tct	ttc	ttc	aac	tgg	tgg	acc	ttt	aca	689
Glu	Glu	Arg	Lys	Lys	Lys	Met	Ser	Phe	Phe	Asn	Trp	Trp	Thr	Phe	Thr	
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Phe	Ser	Ile	Ala	Leu	Leu	Leu	Ala	Thr	Thr	Val	Val	Val	Tyr	Val	Gln	
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Asp	Phe	Val	Ser	Trp	Gly	Val	Ala	Tyr	Leu	Ile	Leu	Ala	Met	Phe	Met	
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gct	ctc	act	atc	att	gct	ttc	tat	gtg	ggg	ata	cct	ttt	tac	agg	tac	833
Ala	Leu	Thr	Ile	Ile	Ala	Phe	Tyr	Val	Gly	Ile	Pro	Phe	Tyr	Arg	Tyr	
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Arg	Met	Arg	Pro	Asn	Ala	Asn	Pro	Phe	Ile	Pro	Ile	Leu	Gln	Val	Leu	
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att	gca	tcc	ata	agg	aaa	agg	aat	ttg	tct	tgt	cct	tca	aat	cct	gct	929
Ile	Ala	Ser	Ile	Arg	Lys	Arg	Asn	Leu	Ser	Cys	Pro	Ser	Asn	Pro	Ala	
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Leu	Leu	Cys	Glu	Val	Pro	Met	Ser	Glu	Asn	Ser	Gln	Gly	Arg	Leu	Leu	
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Asn	His	Thr	Ser	Arg	Leu	Arg	Phe	Leu	Asp	Lys	Ala	Ala	Ile	Val	Glu	
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gaa	aag	tat	att	gag	aag	gct	ggc	cca	tgg	aga	tta	gca	aca	gtg		1073
Glu	Lys	Tyr	Ile	Glu	Lys	Lys	Ala	Gly	Pro	Trp	Arg	Leu	Ala	Thr	Val	
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Thr	Arg	Val	Glu	Glu	Thr	Lys	Leu	Ile	Leu	Asn	Val	Val	Pro	Ile	Trp	
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cta	act	tca	tta	atg	att	ggg	gta	tgc	ata	gca	caa	ggg	tcg	aca	ctc	1169
Leu	Thr	Ser	Leu	Met	Ile	Gly	Val	Cys	Ile	Ala	Gln	Gly	Ser	Thr	Leu	
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Lys Ile Pro Pro Ala Ser Met Ala Ser Leu Ser Ala Phe Ser Thr Ile	
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Ile Ser Val Pro Ile Tyr Asp Arg Ile Ile Val Pro Ile Leu Arg Lys	
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Val Arg Gly Asn Glu Arg Gly Ile Ser Ile Leu Gly Arg Ile Gly Ile	
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Gly Leu Ile Phe Leu Val Ile Leu Met Val Val Ala Ala Leu Val Glu	
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Asn Met Arg Leu Arg Met Pro Gly His Glu Thr Met Ser Val Met Trp	
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Phe Tyr Trp Met Leu Ala Val Ile Ser Ala Leu Asn Leu Cys Leu Phe	
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cta ttc ttg gca aag agg ttt act tat aag acc gca cgg agg aaa gct	1793
Leu Phe Leu Ala Lys Arg Phe Thr Tyr Lys Thr Ala Arg Arg Lys Ala	
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Thr Glu Ile Asp Cys Ser Asn Cys Asp Gly Val Asp Thr Val Ala	
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PF59082SeqList_PF59082.txt

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 35 40 45
 Leu Ala Ile Glu Phe Ser Glu Arg Ile Ala His Phe Gly Ile Ser Ser
 50 55 60
 Asn Leu Ile Met Tyr Leu Thr Glu Val Met His Glu Asp Leu Lys Thr
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 Ala Thr Asn Asn Ala Asn Leu Trp Lys Gly Ala Thr Thr Leu Leu Pro
 85 90 95
 Met Ile Gly Gly Phe Leu Gly Asp Ala Tyr Thr Gly Arg Phe Arg Met
 100 105 110
 Val Val Phe Ser Ser Leu Val Tyr Phe Lys Gly Leu Ser Leu Leu Thr
 115 120 125
 Met Ser Gln Phe Ile Pro Asn Lys Pro Cys Asn Asn Asp Ile Cys
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 His Gln Pro Arg Lys Val His Glu Val Val Phe Phe Leu Ala Leu Tyr
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 Cys Ile Ala Leu Gly Thr Gly Gly Phe Lys Pro Cys Leu Glu Ser Phe
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 Gly Gly Asp Gln Phe Asp Gly Asp Asn Leu Glu Glu Arg Lys Lys Lys
 180 185 190
 Met Ser Phe Phe Asn Trp Trp Thr Phe Thr Phe Ser Ile Ala Leu Leu
 195 200 205
 Leu Ala Thr Thr Val Val Val Tyr Val Gln Asp Phe Val Ser Trp Gly
 210 215 220
 Val Ala Tyr Leu Ile Leu Ala Met Phe Met Ala Leu Thr Ile Ile Ala
 225 230 235 240
 Phe Tyr Val Gly Ile Pro Phe Tyr Arg Tyr Arg Met Arg Pro Asn Ala
 245 250 255
 Asn Pro Phe Ile Pro Ile Leu Gln Val Leu Ile Ala Ser Ile Arg Lys
 260 265 270
 Arg Asn Leu Ser Cys Pro Ser Asn Pro Ala Leu Leu Cys Glu Val Pro
 275 280 285
 Met Ser Glu Asn Ser Gln Gly Arg Leu Leu Asn His Thr Ser Arg Leu
 290 295 300
 Arg Phe Leu Asp Lys Ala Ala Ile Val Glu Glu Lys Tyr Ile Glu Lys
 305 310 315 320
 Lys Ala Gly Pro Trp Arg Leu Ala Thr Val Thr Arg Val Glu Glu Thr
 325 330 335
 Lys Leu Ile Leu Asn Val Val Pro Ile Trp Leu Thr Ser Leu Met Ile
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 Gly Val Cys Ile Ala Gln Gly Ser Thr Leu Phe Val Lys Gln Ala Ala
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 Ala Met Asn Leu Lys Ile Ser Asp Asn Phe Lys Ile Pro Pro Ala Ser
 370 375 380
 Met Ala Ser Leu Ser Ala Phe Ser Thr Ile Ile Ser Val Pro Ile Tyr
 385 390 395 400
 Asp Arg Ile Ile Val Pro Ile Leu Arg Lys Val Arg Gly Asn Glu Arg
 405 410 415
 Gly Ile Ser Ile Leu Gly Arg Ile Gly Ile Gly Leu Ile Phe Leu Val
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 Ile Leu Met Val Val Ala Ala Leu Val Glu Asn Met Arg Leu Arg Met
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 Pro Gly His Glu Thr Met Ser Val Met Trp Leu Ile Pro Gln Tyr Leu
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 465 470 475 480

PF59082SeqList_PF59082.txt

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 Lys Asp Val Asn Ser Ser Arg Leu Asp Lys Phe Tyr Trp Met Leu Ala
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 gag gaa ttt aac gat gag atg aaa tgg gtt cgt gat tct tca ttg gat 160
 Glu Glu Phe Asn Asp Glu Met Lys Trp Val Arg Asp Ser Ser Leu Asp
 15 20 25
 cac aaa gga aga gtt cct ctc cga gct act ggt tct tgg aaa gct 208
 His Lys Gly Arg Val Pro Leu Arg Ala Ser Thr Gly Ser Trp Lys Ala
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 tct atc ttc att att gca att gag ttt agt gag aga ttg agc tat ttt 256
 Ser Ile Phe Ile Ile Ala Ile Glu Phe Ser Glu Arg Leu Ser Tyr Phe
 45 50 55
 gga ata gca act agc ttg gtc att tac ctt aca aaa gtt ctt cat caa 304
 Gly Ile Ala Thr Ser Leu Val Ile Tyr Leu Thr Lys Val Leu His Gln
 60 65 70
 gac ctt aag aca gca gtt aag aat gtg aac tat tgg tct ggt gtc acc 352
 Asp Leu Lys Thr Ala Val Lys Asn Val Asn Trp Ser Gly Val Thr
 75 80 85 90
 act ttg atg cca ttg tta gga gga ttc cta gct gat gct tac tta ggc 400
 Thr Leu Met Pro Leu Leu Gly Gly Phe Leu Ala Asp Ala Tyr Leu Gly
 95 100 105
 cgt tac acc act gtg ata aca tca tgc atc gtt tat ctc atg ggt ttg 448
 Arg Tyr Thr Thr Val Ile Thr Ser Cys Ile Val Tyr Leu Met Gly Leu
 110 115 120
 gtt ctg ctt tct ttg tca tgg ttc ata cca ggt ttc aaa cca tgt gat 496
 Val Leu Leu Ser Leu Ser Trp Phe Ile Pro Gly Phe Lys Pro Cys Asp
 125 130 135
 cat act agt aca tgc acc gaa cct agg agg att cat gag gtg gtt ttc 544
 His Thr Ser Thr Cys Thr Glu Pro Arg Arg Ile His Glu Val Val Phe
 140 145 150
 ttc cta ggc atc tat tta ata tca gta gga act gga ggg cat aaa cct 592
 Phe Leu Gly Ile Tyr Leu Ile Ser Val Gly Thr Gly Gly His Lys Pro
 155 160 165 170
 tcc ttg gag agc tct ggt gct gat caa ttt gat gat aat aat gcc aaa 640
 Ser Leu Glu Ser Ser Gly Ala Asp Gln Phe Asp Asp Asn Asn Ala Lys
 175 180 185
 gaa aga agt cag aaa atg tcc ttt ttc aac tgg tgg aac agt ggt ttg 688
 Glu Arg Ser Gln Lys Met Ser Phe Phe Asn Trp Trp Asn Ser Gly Leu
 190 195 200
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 Cys Ser Gly Ile Ile Leu Gly Val Thr Val Ile Tyr Val Gln Asp

PF59082SeqList_PF59082.txt

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His	Val	Asn	Trp	Gly	Val	Ala	Asp	Ile	Val	Leu	Thr	Gly	Val	Met	Ala		
	220					225				230							
gct	tca	ttg	ctc	ata	ttc	ttg	att	gga	agg	tct	tct	tat	cgt	tac	agg		832
Val	Ser	Leu	Leu	Ile	Phe	Leu	Ile	Gly	Arg	Ser	Ser	Tyr	Arg	Tyr	Arg		
	235				240					245					250		
aca	cca	att	ggg	agc	ccc	ttg	act	cct	atg	ttg	caa	ggt	att	ggt	gct		880
Thr	Pro	Ile	Gly	Ser	Pro	Leu	Thr	Pro	Met	Leu	Gln	Val	Ile	Val	Ala		
			255						260					265			
gct	att	tcc	aaa	aga	aag	ctt	cca	tat	cct	tcc	aat	cca	act	caa	ttg		928
Ala	Ile	Ser	Lys	Arg	Lys	Leu	Pro	Tyr	Pro	Ser	Asn	Pro	Thr	Gln	Leu		
			270					275					280				
tat	gaa	ggt	tcc	aag	tct	gag	ggc	aac	agt	gaa	aga	ttt	ctg	gct	cac		976
Tyr	Glu	Val	Ser	Lys	Ser	Glu	Gly	Asn	Ser	Glu	Arg	Phe	Leu	Ala	His		
		285					290					295					
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Thr	Lys	Lys	Leu	Lys	Phe	Leu	Asp	Lys	Ala	Ala	Ile	Leu	Glu	Asn	Glu		
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Gly	Asn	Ile	Ala	Glu	Lys	Gln	Ser	Pro	Trp	Arg	Leu	Ala	Thr	Val	Thr		
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aag	ggt	gaa	gaa	ctg	aag	ctt	atc	atc	aac	atg	atc	ccc	att	tgg	gtg		1120
Lys	Val	Glu	Glu	Leu	Lys	Leu	Ile	Ile	Asn	Met	Ile	Pro	Ile	Trp	Val		
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ttc	aca	tta	cca	ttt	gga	atc	tgt	gct	tcc	caa	acc	tcc	act	ttc	ttc		1168
Phe	Thr	Leu	Pro	Phe	Gly	Ile	Cys	Ala	Ser	Gln	Thr	Ser	Thr	Phe	Phe		
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atc	aaa	caa	ggt	gcc	atc	atg	aac	aga	aat	ata	ggc	aat	aat	gga	ttt		1216
Ile	Lys	Gln	Gly	Ala	Ile	Met	Asn	Arg	Asn	Ile	Gly	Asn	Asn	Gly	Phe		
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gtg	ggt	ccc	cca	gct	tca	att	ttc	act	ctt	gca	gcc	ggt	ggg	atg	ata		1264
Val	Val	Pro	Pro	Ala	Ser	Ile	Phe	Thr	Leu	Ala	Ala	Val	Gly	Met	Ile		
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Leu	Ser	Val	Thr	Ile	Tyr	Asp	Lys	Leu	Leu	Val	Pro	Val	Leu	Arg	Lys		
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cta	aca	gga	aat	gac	aga	gga	atc	agc	atc	ctc	caa	agg	att	ggt	att		1360
Leu	Thr	Gly	Asn	Asp	Arg	Gly	Ile	Ser	Ile	Leu	Gln	Arg	Ile	Gly	Ile		
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gga	atg	gct	ttc	tca	gtc	atc	aca	atg	ata	gtg	gca	gct	ttg	gtg	gaa		1408
Gly	Met	Val	Phe	Ser	Val	Ile	Thr	Met	Ile	Val	Ala	Ala	Leu	Val	Glu		
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aaa	aag	agg	ctt	gag	gca	ggt	gaa	atg	aat	ggc	cca	tta	aag	ggt	tct		1456
Lys	Lys	Arg	Leu	Glu	Ala	Val	Glu	Met	Asn	Gly	Pro	Leu	Lys	Gly	Ser		
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Leu	Ser	Met	Ser	Ala	Leu	Trp	Leu	Ala	Pro	Gln	Phe	Met	Ile	Ile	Gly		
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Phe	Gly	Asp	Gly	Phe	Ala	Leu	Val	Gly	Leu	Gln	Glu	Tyr	Phe	Tyr	Asp		
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caa	gtg	cct	gac	tca	atg	aga	agc	ctt	gga	ata	gca	ctt	tac	ctt	agt		1600
Gln	Val	Pro	Asp	Ser	Met	Arg	Ser	Leu	Gly	Ile	Ala	Leu	Tyr	Leu	Ser		
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Val	Ile	Gly	Ala	Ala	Ser	Phe	Leu	Ser	Ser	Leu	Leu	Ile	Thr	Ile	Val		
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gat	cat	gtc	act	ggt	aag	att	ggg	aag	agt	tgg	att	ggt	aag	gat	ttg		1696
Asp	His	Val	Thr	Gly	Lys	Ile	Gly	Lys	Ser	Trp	Ile	Gly	Lys	Asp	Leu		
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aat	agt	agc	cgc	ttg	gac	aaa	ttt	tac	tgg	ctt	ctt	gca	gcc	atc	acc		1744
Asn	Ser	Ser	Arg	Leu	Asp	Lys	Phe	Tyr	Trp	Leu	Leu	Ala	Ala	Ile	Thr		
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Thr	Leu	Asn	Leu	Phe	Met	Phe	Val	Ile	Phe	Ala	Arg	Lys	Tyr	Asn	Tyr		
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aag	aat	gtg	caa	aag	gtg	gca	gcg	gct	gat	tgc	tac	gaa	ggc	aaa	agt		1840
Lys	Asn	Val	Gln	Lys	Val	Ala	Ala	Ala	Asp	Cys	Tyr	Glu	Gly	Lys	Ser		

PF59082SeqList_PF59082.txt

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tctactatta gaatccttaa gttttatcct tagcaaagcg ttgataactt gtgctcctaa      2007

ccaagagttt ttgtttgggt tagttgttta tgggtgtccat gtaatatgac aataaaaatta      2067

tgtatgcgat tgtcatttca aaaggagtca ttcatgtttt catcttatta tctcgtgttt      2127

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          35          40          45
Ile Glu Phe Ser Glu Arg Leu Ser Tyr Phe Gly Ile Ala Thr Ser Leu
          50          55          60
Val Ile Tyr Leu Thr Lys Val Leu His Gln Asp Leu Lys Thr Ala Val
65          70          75          80
Lys Asn Val Asn Tyr Trp Ser Gly Val Thr Leu Met Pro Leu Leu
          85          90          95
Gly Gly Phe Leu Ala Asp Ala Tyr Leu Gly Arg Tyr Thr Thr Val Ile
          100          105          110
Thr Ser Cys Ile Val Tyr Leu Met Gly Leu Val Leu Leu Ser Leu Ser
          115          120          125
Trp Phe Ile Pro Gly Phe Lys Pro Cys Asp His Thr Ser Thr Cys Thr
130          135          140          145
Glu Pro Arg Arg Ile His Glu Val Val Phe Phe Leu Gly Ile Tyr Leu
145          150          155          160
Ile Ser Val Gly Thr Gly Gly His Lys Pro Ser Leu Glu Ser Ser Gly
          165          170          175
Ala Asp Gln Phe Asp Asp Asn Asn Ala Lys Glu Arg Ser Gln Lys Met
          180          185          190
Ser Phe Phe Asn Trp Trp Asn Ser Gly Leu Cys Ser Gly Ile Ile Leu
          195          200          205
Gly Val Thr Val Ile Val Tyr Val Gln Asp His Val Asn Trp Gly Val
210          215          220          225
Ala Asp Ile Val Leu Thr Gly Val Met Ala Val Ser Leu Leu Ile Phe
225          230          235          240
Leu Ile Gly Arg Ser Tyr Arg Tyr Arg Thr Pro Ile Gly Ser Pro
          245          250          255
Leu Thr Pro Met Leu Gln Val Ile Val Ala Ala Ile Ser Lys Arg Lys
          260          265          270
Leu Pro Tyr Pro Ser Asn Pro Thr Gln Leu Tyr Glu Val Ser Lys Ser
          275          280          285
Glu Gly Asn Ser Glu Arg Phe Leu Ala His Thr Lys Lys Leu Lys Phe
290          295          300          305
Leu Asp Lys Ala Ala Ile Leu Glu Asn Glu Gly Asn Ile Ala Glu Lys
305          310          315          320

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PF59082SeqList_PF59082.txt

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 Met Asn Arg Asn Ile Gly Asn Asn Gly Phe Val Val Pro Pro Ala Ser
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 385 390 400
 Asp Lys Leu Leu Val Pro Val Leu Arg Lys Leu Thr Gly Asn Asp Arg
 405 410 415
 Gly Ile Ser Ile Leu Gln Arg Ile Gly Ile Gly Met Val Phe Ser Val
 420 425 430
 Ile Thr Met Ile Val Ala Ala Leu Val Glu Lys Lys Arg Leu Glu Ala
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 485 490 495
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112

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 Glu Glu Val Ile Ser Met Glu Lys Gln Gln Gln Pro Gly Glu Lys Lys
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160

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 Ile Thr Gly Gly Glu Glu Glu Glu Glu Glu Val Ile Ser Ser Val
 30 35 40

208

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 Arg Tyr Arg Gly Trp Lys Ser Met Pro Tyr Val Ile Gly Asn Glu Thr
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256

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 Phe Glu Lys Leu Gly Thr Ile Gly Thr Thr Ala Asn Leu Leu Val Tyr
 65 70 75

304

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 Leu Thr Thr Val Tyr His Leu Pro Ser Val Arg Ala Ala Thr Leu Leu
 80 85 90

352

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400

PF59082SeqList_PF59082.txt

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Leu	Ser	Asp	Thr	Phe	Leu	Gly	Arg	Tyr	Thr	Thr	Ile	Ala	Ala	Ala	Ser	
ctc	gcc	tcc	tgc	ctc	ggc	atg	ctt	gtg	ctt	acc	ctc	acc	gcc	gcc	atc	496
Leu	Ala	Ser	Cys	Leu	Gly	Met	Leu	Val	Leu	Thr	Leu	Thr	Ala	Ala	Ile	
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Pro	Ser	Leu	His	Pro	Pro	Pro	Cys	Thr	Ala	Ser	Ser	Ser	Ser	Ser	Ser	
tgc	cag	ggc	ccc	aca	cac	ggc	cag	ctc	gcc	gct	ctc	ctc	gcc	gcc	ttc	592
Cys	Gln	Gly	Pro	Thr	His	Gly	Gln	Leu	Ala	Ala	Leu	Leu	Ala	Ala	Phe	
gcc	ttc	ctc	gtc	gtc	ggc	ggc	ggc	ggc	atc	cgc	ccc	tgc	aac	ctc	gcc	640
Ala	Phe	Leu	Val	Val	Gly	Ala	Gly	Gly	Ile	Arg	Pro	Cys	Asn	Leu	Ala	
ttc	ggc	ggc	gac	cag	ttc	gac	ccg	cgc	acc	gac	tcc	ggc	cgc	cgc	ggc	688
Phe	Gly	Ala	Asp	Gln	Phe	Asp	Pro	Arg	Thr	Asp	Ser	Gly	Arg	Arg	Gly	
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Ile	Ala	Ser	Phe	Phe	Asn	Trp	Tyr	Tyr	Phe	Thr	Phe	Thr	Val	Ala	Met	
atg	ctc	tcc	gcc	acc	ctc	atc	atc	tac	ctc	cag	agc	aac	gtc	agc	tgg	784
Met	Leu	Ser	Ala	Thr	Leu	Ile	Ile	Tyr	Leu	Gln	Ser	Asn	Val	Ser	Trp	
gcg	atc	gga	ctc	gcc	gtc	ccc	gcc	gcc	ctc	atg	gcc	atc	tcc	tgc	gcg	832
Ala	Ile	Gly	Leu	Ala	Val	Pro	Ala	Ala	Leu	Met	Ala	Ile	Ser	Cys	Ala	
ctc	ttc	ttc	atg	ggc	acc	cgc	ctc	tac	gtc	cgc	gtc	cgc	ccc	gag	ggc	880
Leu	Phe	Phe	Met	Gly	Thr	Arg	Leu	Tyr	Val	Arg	Val	Arg	Pro	Glu	Gly	
agc	ccc	ttc	acc	agc	ttc	gcc	cgg	gtc	atc	gtc	gcc	gcc	gtc	cgc	aag	928
Ser	Pro	Phe	Thr	Ser	Phe	Ala	Arg	Val	Ile	Val	Ala	Ala	Val	Arg	Lys	
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Arg	Arg	Val	Pro	Ala	Pro	Ala	Ser	Ala	Asp	Asp	Leu	Phe	Asp	Pro	Pro	
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His	Gln	Ser	Lys	Leu	Val	Ala	Lys	Ile	Ala	Tyr	Thr	Asp	Gln	Phe	Arg	
tgc	ctg	gac	aag	gcc	gcc	gtg	gtg	acg	ccg	gag	tcg	aga	tcg	agc	ccg	1072
Cys	Leu	Asp	Lys	Ala	Ala	Val	Val	Thr	Pro	Glu	Ser	Arg	Ser	Ser	Pro	
tgg	cgg	ctg	tgc	acg	gtg	cag	cag	gtg	gag	gag	gtg	aag	tgc	ctg	gcg	1120
Trp	Arg	Leu	Cys	Thr	Val	Gln	Gln	Val	Glu	Glu	Val	Lys	Cys	Leu	Ala	
cgg	atc	atc	ccg	gtg	tgg	tcg	gcg	ggg	atc	gtg	tac	ttc	atc	gtg	gta	1168
Arg	Ile	Ile	Pro	Val	Trp	Ser	Ala	Gly	Ile	Val	Tyr	Phe	Ile	Val	Val	
acg	cag	ctg	ggc	acg	ttc	gtg	gtg	ctc	cag	gcg	ctc	cag	atg	gac	cgg	1216
Thr	Gln	Leu	Gly	Thr	Phe	Val	Val	Leu	Gln	Ala	Leu	Gln	Met	Asp	Arg	
cgg	ctg	acg	agg	tgg	tgg	gcg	ttc	gag	gtg	ccg	gcg	ggg	tcg	atg	gtg	1264
Arg	Leu	Thr	Arg	Trp	Trp	Ala	Phe	Glu	Val	Pro	Ala	Gly	Ser	Met	Val	
gtg	ttc	aac	atg	atg	gcg	atg	acg	gtg	tgg	atc	ccg	gtg	tac	gac	cgg	1312
Val	Phe	Asn	Met	Met	Ala	Met	Thr	Val	Trp	Ile	Pro	Val	Tyr	Asp	Arg	
gtg	gtg	gtg	ccg	gcg	ctg	cgg	cgg	gtg	acg	ggg	aag	gag	ggc	ggg	atc	1360
Val	Val	Val	Pro	Ala	Leu	Arg	Arg	Val	Thr	Gly	Lys	Glu	Gly	Gly	Ile	
agc	cag	ctg	cag	cgc	atc	ggg	gtg	ggg	ctg	gtg	ctg	tcg	gtg	gcg	acg	1408
Ser	Gln	Leu	Gln	Arg	Ile	Gly	Val	Gly	Leu	Val	Leu	Ser	Val	Ala	Thr	
atg	gtg	gtg	gcg	gcg	gcg	gtg	gag	cag	cgg	cgg	cgc	cgg	ctg	ggc	gcg	1456
Met	Val	Val	Ala	Ala	Ala	Val	Glu	Gln	Arg	Arg	Arg	Arg	Leu	Gly	Ala	
gtg	gga	gtg	aag	atg	tcg	ttc	ctg	tgg	ctg	gtg	ccg	cag	cag	gtg	gcg	1504

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Ala	Gly	Met	Ser	Glu	Ala	Phe	Ala	Ala	Ile	Gly	Gln	Thr	Glu	Leu	Tyr	
			480					485					490			
tac	agg	cag	ttc	ccg	gag	aac	atg	agg	agc	gtg	gcg	ggg	gcg	ctc	ttc	1600
Tyr	Arg	Gln	Phe	Pro	Glu	Asn	Met	Arg	Ser	Val	Ala	Gly	Ala	Leu	Phe	
		495					500					505				
ttc	ctg	gcg	ttc	gcg	ctg	gcc	aac	tac	gcg	agc	ggc	ttc	atg	gtg	gcg	1648
Phe	Leu	Ala	Phe	Ala	Leu	Ala	Asn	Tyr	Ala	Ser	Gly	Phe	Met	Val	Ala	
	510					515					520					
gcg	gtg	cac	cgg	acc	acg	ggg	tgg	ctg	gcg	cag	gat	ctg	aac	cac	gcc	1696
Ala	Val	His	Arg	Thr	Thr	Gly	Trp	Leu	Ala	Gln	Asp	Leu	Asn	His	Ala	
	525				530				535						540	
cgc	ctc	gac	ctc	ttc	tac	cta	acc	gtc	gcg	gcc	atc	gcg	gcg	gcc	aac	1744
Arg	Leu	Asp	Leu	Phe	Tyr	Leu	Thr	Val	Ala	Ile	Ala	Ala	Ala	Ala	Asn	
				545				550						555		
gtc	tgc	tac	ttc	ctc	ctc	tgc	gcc	cgc	tgg	tac	agg	ttc	aag	aac	acc	1792
Val	Cys	Tyr	Phe	Leu	Leu	Cys	Ala	Arg	Trp	Tyr	Arg	Phe	Lys	Asn	Thr	
			560				565						570			
acc	atc	gcc	gac	cac	gtc	gag	ctg	ccg	gat	tat	cat	cat	cat	cag	ccc	1840
Thr	Ile	Ala	Asp	His	Val	Glu	Leu	Pro	Asp	Tyr	His	His	His	Gln	Pro	
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gga	acc	gcc	aac	acc	ata	gcc	tcc	aag	gtt	taattaattt	tattatcaca					1890
Gly	Thr	Ala	Asn	Thr	Ile	Ala	Ser	Lys	Val							
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<400> 219

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Glu	Glu	Glu	Glu	Glu	Glu	Glu	Val	Ile	Ser	Ser	Val	Arg	Tyr	Arg	Gly	
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Tyr	His	Leu	Pro	Ser	Val	Arg	Ala	Ala	Thr	Leu	Leu	Asn	Phe	Phe	Ser	
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Phe	Leu	Gly	Arg	Tyr	Thr	Thr	Ile	Ala	Ala	Ala	Ser	Leu	Ala	Ser	Cys	
		115				120						125				
Leu	Gly	Met	Leu	Val	Leu	Thr	Leu	Thr	Ala	Ala	Ile	Pro	Ser	Leu	His	
	130					135					140					
Pro	Pro	Pro	Cys	Thr	Ala	Ser	Ser	Ser	Ser	Ser	Ser	Cys	Gln	Gly	Pro	
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Thr	His	Gly	Gln	Leu	Ala	Ala	Leu	Leu	Ala	Ala	Phe	Ala	Phe	Leu	Val	
			165					170						175		
Val	Gly	Ala	Gly	Ile	Arg	Pro	Cys	Asn	Leu	Ala	Phe	Gly	Ala	Asp		
			180				185					190				
Gln	Phe	Asp	Pro	Arg	Thr	Asp	Ser	Gly	Arg	Arg	Gly	Ile	Ala	Ser	Phe	
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Phe	Asn	Trp	Tyr	Tyr	Phe	Thr	Phe	Thr	Val	Ala	Met	Met	Leu	Ser	Ala	

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 Ala Val Pro Ala Ala Leu Met Ala Ile Ser Cys Ala Leu Phe Phe Met
 245 250 255
 Gly Thr Arg Leu Tyr Val Arg Val Arg Pro Glu Gly Ser Pro Phe Thr
 260 265 270
 Ser Phe Ala Arg Val Ile Val Ala Ala Val Arg Lys Arg Arg Val Pro
 275 280 285
 Ala Pro Ala Ser Ala Asp Asp Leu Phe Asp Pro Pro His Gln Ser Lys
 290 295 300
 Leu Val Ala Lys Ile Ala Tyr Thr Asp Gln Phe Arg Cys Leu Asp Lys
 305 310 315 320
 Ala Ala Val Val Thr Pro Glu Ser Arg Ser Ser Pro Trp Arg Leu Cys
 325 330 335
 Thr Val Gln Gln Val Glu Glu Val Lys Cys Leu Ala Arg Ile Ile Pro
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 Val Trp Ser Ala Gly Ile Val Tyr Phe Ile Val Val Thr Gln Leu Gly
 355 360 365
 Thr Phe Val Val Leu Gln Ala Leu Gln Met Asp Arg Arg Leu Thr Arg
 370 375 380
 Trp Trp Ala Phe Glu Val Pro Ala Gly Ser Met Val Val Phe Asn Met
 385 390 395 400
 Met Ala Met Thr Val Trp Ile Pro Val Tyr Asp Arg Val Val Pro
 405 410 415
 Ala Leu Arg Arg Val Thr Gly Lys Glu Gly Gly Ile Ser Gln Leu Gln
 420 425 430
 Arg Ile Gly Val Gly Leu Val Leu Ser Val Ala Thr Met Val Val Ala
 435 440 445
 Ala Ala Val Glu Gln Arg Arg Arg Arg Leu Gly Ala Val Gly Val Lys
 450 455 460
 Met Ser Phe Leu Trp Leu Val Pro Gln Gln Val Ala Ala Gly Met Ser
 465 470 475 480
 Glu Ala Phe Ala Ala Ile Gly Gln Thr Glu Leu Tyr Tyr Arg Gln Phe
 485 490 495
 Pro Glu Asn Met Arg Ser Val Ala Gly Ala Leu Phe Phe Leu Ala Phe
 500 505 510
 Ala Leu Ala Asn Tyr Ala Ser Gly Phe Met Val Ala Ala Val His Arg
 515 520 525
 Thr Thr Gly Trp Leu Ala Gln Asp Leu Asn His Ala Arg Leu Asp Leu
 530 535 540
 Phe Tyr Leu Thr Val Ala Ala Ile Ala Ala Ala Asn Val Cys Tyr Phe
 545 550 555 560
 Leu Leu Cys Ala Arg Trp Tyr Arg Phe Lys Asn Thr Thr Ile Ala Asp
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 His Val Glu Leu Pro Asp Tyr His His His Gln Pro Gly Thr Ala Asn
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 Thr Ile Ala Ser Lys Val
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cagggcacag caa atg gtt tcc ggt gcg ggt cat ggt ggg tac ggc ggc 169
 Met Val Ser Gly Ala Gly His Gly Gly Tyr Gly Gly
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tcg	agg	acc	gga	ggc	tgg	ctg	ggc	gcc	ggg	ctg	atc	ctg	ggc	acg	gag	265
Ser	Arg	Thr	Gly	Gly	Trp	Leu	Gly	Ala	Gly	Leu	Ile	Leu	Gly	Thr	Glu	
	30					35					40					
ctg	gcg	gag	cgt	gtg	tgc	gtg	atg	ggc	atc	tcg	atg	aac	ctg	gtg	acg	313
Leu	Ala	Glu	Arg	Val	Cys	Val	Met	Gly	Ile	Ser	Met	Asn	Leu	Val	Thr	
	45				50					55					60	
tac	ctc	gtc	ggc	gag	ctg	cac	ctc	tcc	aac	tcc	aag	tcc	gcc	acc	gtg	361
Tyr	Leu	Val	Gly	Glu	Leu	His	Leu	Ser	Asn	Ser	Lys	Ser	Ala	Thr	Val	
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gtg	acc	aac	ttc	atg	ggc	acg	ctc	aac	ctg	ctc	gcc	ctc	gtc	ggc	ggc	409
Val	Thr	Asn	Phe	Met	Gly	Thr	Leu	Asn	Leu	Leu	Ala	Leu	Val	Gly	Gly	
			80					85					90			
ttc	ctc	gcc	gac	ggc	aag	ctc	ggc	cgc	tac	ctc	acc	atc	gcc	atc	tcc	457
Phe	Leu	Ala	Asp	Ala	Lys	Leu	Gly	Arg	Tyr	Leu	Thr	Ile	Ala	Ile	Ser	
		95					100					105				
gcc	aca	atc	ggc	ggc	acg	ggc	gtg	agc	ttg	ctg	acg	gtg	gac	acg	acg	505
Ala	Thr	Ile	Ala	Ala	Thr	Val	Val	Ser	Leu	Leu	Thr	Val	Asp	Thr	Thr	
	110					115					120					
gtg	ccg	agc	atg	cgt	cca	ccg	gcg	tgc	ctg	gac	gcc	cgc	ggg	ccg	cgc	553
Val	Pro	Ser	Met	Arg	Pro	Pro	Ala	Cys	Leu	Asp	Ala	Arg	Gly	Pro	Arg	
	125				130					135				140		
gcg	cac	gag	tgc	gtg	ccg	gcg	cgc	ggc	ggg	cag	ctg	gcg	ctt	ctg	tac	601
Ala	His	Glu	Cys	Val	Pro	Ala	Arg	Gly	Gly	Gln	Leu	Ala	Leu	Leu	Tyr	
				145				150						155		
gcg	gcg	ctg	tac	acg	gtg	gcg	gcg	ggg	gcc	ggc	ggg	ctc	aag	gcg	aac	649
Ala	Ala	Leu	Tyr	Thr	Val	Ala	Ala	Gly	Ala	Gly	Gly	Leu	Lys	Ala	Asn	
			160					165					170			
gtg	tcc	ggg	ttc	ggg	tcg	gac	cag	ttc	gac	ggg	cgc	gac	ccg	gcg	gag	697
Val	Ser	Gly	Phe	Gly	Ser	Asp	Gln	Phe	Asp	Gly	Arg	Asp	Pro	Arg	Glu	
		175					180					185				
gag	cgc	ggc	atg	gtg	ttc	ttc	ttc	aac	cgc	ttc	tac	ttc	tgc	gtc	agc	745
Glu	Arg	Ala	Met	Val	Phe	Phe	Phe	Asn	Arg	Phe	Tyr	Phe	Cys	Val	Ser	
	190				195						200					
ctg	ggg	tcg	ctg	ttc	gcg	gtc	acc	gtg	ctg	gtg	tac	gtg	cag	gac	aac	793
Leu	Gly	Ser	Leu	Phe	Ala	Val	Thr	Val	Leu	Val	Tyr	Val	Gln	Asp	Asn	
	205				210					215					220	
gtg	ggg	cgg	ggc	tgg	gtg	tac	ggc	gtc	tcc	gca	gtc	gcc	atg	gcg	ctc	841
Val	Gly	Arg	Gly	Trp	Gly	Tyr	Gly	Val	Ser	Ala	Val	Ala	Met	Ala	Leu	
				225				230						235		
gcc	gtc	gcc	gtg	ctc	gtg	gcc	ggc	acg	ccc	cgg	tac	agg	tac	cgc	cgc	889
Ala	Val	Ala	Val	Leu	Val	Ala	Gly	Thr	Pro	Arg	Tyr	Arg	Tyr	Arg	Arg	
			240					245					250			
ccg	cag	ggc	agc	ccg	ctg	acg	gcg	gtc	ggc	cgg	gtg	ctc	gcc	gcg	gcg	937
Pro	Gln	Gly	Ser	Pro	Leu	Thr	Ala	Val	Gly	Arg	Val	Leu	Ala	Ala	Ala	
		255					260					265				
tgg	agg	aag	cgc	cgg	ctg	ccg	ctg	ccc	gcc	gac	gcc	gcc	gag	ctc	cac	985
Trp	Arg	Lys	Arg	Arg	Leu	Pro	Leu	Pro	Ala	Asp	Ala	Ala	Glu	Leu	His	
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ggg	ttc	gcc	gcg	ggc	aag	gtc	gcc	cac	act	gac	agg	ctc	agg	tgg	ctt	1033
Gly	Phe	Ala	Ala	Ala	Lys	Val	Ala	His	Thr	Asp	Arg	Leu	Arg	Trp	Leu	
	285				290					295					300	
gac	aag	gcc	gcg	atc	gtg	gag	gcc	gag	ctg	ggc	ggg	aag	cag	cgg	gcg	1081
Asp	Lys	Ala	Ala	Ile	Val	Glu	Ala	Glu	Leu	Ala	Gly	Lys	Gln	Arg	Ala	
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agc	gcg	gcg	gca	gcg	tcg	acg	gtg	acg	gag	gtc	gag	gag	gtg	aag	atg	1129
Ser	Ala	Ala	Ala	Ala	Ser	Thr	Val	Thr	Glu	Val	Glu	Glu	Val	Lys	Met	
			320					325					330			
gtg	gcg	aag	ctg	ctg	ccc	atc	tgg	ttc	acg	tgc	atc	ctc	ttc	tgg	acg	1177
Val	Ala	Lys	Leu	Leu	Pro	Ile	Trp	Phe	Thr	Cys	Ile	Leu	Phe	Trp	Thr	
		335					340					345				
gtc	tac	tcc	cag	atg	acc	acc	ttc	tcg	gtg	gag	cag	gcc	acg	cgc	atg	1225
Val	Tyr	Ser	Gln	Met	Thr	Thr	Phe	Ser	Val	Glu	Gln	Ala	Thr	Arg	Met	
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gac	cgc	cac	ctc	cgc	ccg	ggc	tcc	ggc	gcc	ggc	gcc	ggc	ggc	ttc	gcc	1273
Asp	Arg	His	Leu	Arg	Pro	Gly	Ser	Gly	Ala	Gly	Ala	Gly	Gly	Phe	Ala	
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Phe	Thr	Ser	Leu	Asn	Glu	Arg	Leu	Val	Pro	Leu	Ala	Ala	Arg	Leu		
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acg	ggc	cgc	ccg	cag	ggg	ctc	acc	tcg	ctg	cag	cgc	gtc	ggg	gcc	ggg	1417
Thr	Gly	Arg	Pro	Gln	Gly	Leu	Thr	Ser	Leu	Gln	Arg	Val	Gly	Ala	Gly	
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ctc	gcg	ctc	tcc	gtc	gcc	gcc	atg	gcc	gtc	tcc	gcg	ctc	gta	gag	agg	1465
Leu	Ala	Leu	Ser	Val	Ala	Ala	Met	Ala	Val	Ser	Ala	Leu	Val	Glu	Arg	
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aag	cgg	cgc	gac	gcg	gcc	aac	ggg	ccg	gac	cac	gtc	gcc	gtc	agc	gcc	1513
Lys	Arg	Arg	Asp	Ala	Ala	Asn	Gly	Pro	Asp	His	Val	Ala	Val	Ser	Ala	
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gcc	tac	gtg	ggc	cag	ctg	gag	ttc	ttc	atc	cgc	gag	gcg	ccc	gag	cgg	1609
Ala	Tyr	Val	Gly	Gln	Leu	Glu	Phe	Phe	Ile	Arg	Glu	Ala	Pro	Glu	Arg	
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Tyr	Trp	Met	Leu	Ala	Leu	Leu	Gly	Val	Ala	Asn	Phe	Ala	Val	Phe	Val	
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gtc	ttc	gcc	agg	cgg	cac	cag	tac	aag	gcc	acc	agc	ttg	ccg	gcg	tcg	1849
Val	Phe	Ala	Arg	Arg	His	Gln	Tyr	Lys	Ala	Thr	Ser	Leu	Pro	Ala	Ser	
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gtg	gcg	ccc	gac	ggc	acc	ggg	cac	aag	gag	atg	gac	gac	ttc	gtc	gca	1897
Val	Ala	Pro	Asp	Gly	Thr	Gly	His	Lys	Glu	Met	Asp	Asp	Phe	Val	Ala	
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Val	Thr	Glu	Ala	Val	Glu	Gly	Val	Asp	Val							
			590			595										
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tatggcggaag	ttttctttct	cttgccagtt	tccagtttgc	tgctacttcg	gcctgctctc											2067
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 Val Cys Val Met Gly Ile Ser Met Asn Leu Val Thr Tyr Leu Val Gly
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Ala	Lys	Leu	Gly 100	Arg	Tyr	Leu	Thr	Ile 105	Ala	Ile	Ser	Ala	Thr 110	Ile	Ala
Ala	Thr	Gly 115	Val	Ser	Leu	Leu	Thr 120	Val	Asp	Thr	Thr	Val 125	Pro	Ser	Met
Arg	Pro 130	Pro	Ala	Cys	Leu	Asp 135	Ala	Arg	Gly	Pro	Arg 140	Ala	His	Glu	Cys
Val 145	Pro	Ala	Arg	Gly	Gly 150	Gln	Leu	Ala	Leu	Leu 155	Tyr	Ala	Ala	Leu	Tyr 160
Thr	Val	Ala	Ala	Gly 165	Ala	Gly	Gly	Leu	Lys 170	Ala	Asn	Val	Ser	Gly 175	Phe
Gly	Ser	Asp 180	Gln	Phe	Asp	Gly	Arg	Asp 185	Pro	Arg	Glu	Glu	Arg 190	Ala	Met
Val	Phe 195	Phe	Phe	Asn	Arg	Phe	Tyr 200	Phe	Cys	Val	Ser	Leu	Gly 205	Ser	Leu
Phe	Ala 210	Val	Thr	Val	Leu	Val 215	Tyr	Val	Gln	Asp	Asn 220	Val	Gly	Arg	Gly
Trp 225	Gly	Tyr	Gly	Val	Ser 230	Ala	Val	Ala	Met	Ala 235	Leu	Ala	Val	Ala	Val 240
Leu	Val	Ala	Gly	Thr 245	Pro	Arg	Tyr	Arg	Tyr 250	Arg	Arg	Pro	Gln	Gly 255	Ser
Pro	Leu	Thr	Ala 260	Val	Gly	Arg	Val	Leu 265	Ala	Ala	Ala	Trp	Arg 270	Lys	Arg
Arg	Leu	Pro 275	Leu	Pro	Ala	Asp	Ala 280	Ala	Glu	Leu	His	Gly 285	Phe	Ala	Ala
Ala	Lys 290	Val	Ala	His	Thr	Asp 295	Arg	Leu	Arg	Trp	Leu	Asp	Lys	Ala	Ala
Ile 305	Val	Glu	Ala	Glu	Leu 310	Ala	Gly	Lys	Gln	Arg 315	Ala	Ser	Ala	Ala	Ala 320
Ala	Ser	Thr	Val	Thr 325	Glu	Val	Glu	Glu	Val 330	Lys	Met	Val	Ala	Lys 335	Leu
Leu	Pro	Ile 340	Trp	Phe	Thr	Cys	Ile	Leu 345	Phe	Trp	Thr	Val	Tyr 350	Ser	Gln
Met	Thr 355	Thr	Phe	Ser	Val	Glu	Gln 360	Ala	Thr	Arg	Met	Asp 365	Arg	His	Leu
Arg	Pro 370	Gly	Ser	Gly	Ala	Gly 375	Ala	Gly	Gly	Phe	Ala 380	Val	Pro	Ala	Gly
Ser 385	Phe	Ser	Val	Phe	Leu 390	Phe	Leu	Ser	Ile	Leu 395	Leu	Phe	Thr	Ser	Leu 400
Asn	Glu	Arg	Leu	Leu 405	Val	Pro	Leu	Ala	Ala 410	Arg	Leu	Thr	Gly	Arg 415	Pro
Gln	Gly	Leu	Thr 420	Ser	Leu	Gln	Arg	Val 425	Gly	Ala	Gly	Leu	Ala 430	Leu	Ser
Val	Ala 435	Ala	Met	Ala	Val	Ser	Ala 440	Leu	Val	Glu	Arg	Lys 445	Arg	Arg	Asp
Ala	Ala 450	Asn	Gly	Pro	Asp	His 455	Val	Ala	Val	Ser	Ala 460	Phe	Trp	Leu	Val
Pro 465	Gln	Tyr	Phe	Leu	Val 470	Gly	Ala	Gly	Glu	Ala 475	Phe	Ala	Tyr	Val	Gly 480
Gln	Leu	Glu	Phe	Phe 485	Ile	Arg	Glu	Ala	Pro 490	Glu	Arg	Met	Lys	Ser 495	Met
Ser	Thr	Gly	Leu 500	Phe	Leu	Val	Thr	Leu 505	Ser	Met	Gly	Phe	Phe 510	Leu	Ser
Ser	Phe 515	Leu	Val	Phe	Ala	Val	Asp 520	Ala	Ala	Thr	Ala	Gly 525	Ala	Trp	Ile
Arg	Asn 530	Asn	Leu	Asp	Arg	Gly 535	Arg	Leu	Asp	Leu	Phe 540	Tyr	Trp	Met	Leu
Ala 545	Leu	Leu	Gly	Val	Ala 550	Asn	Phe	Ala	Val	Phe 555	Val	Val	Phe	Ala	Arg 560
Arg	His	Gln	Tyr	Lys 565	Ala	Thr	Ser	Leu	Pro 570	Ala	Ser	Val	Ala	Pro 575	Asp
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ccccttgccc accacgcgcg accggtatcc ggcgctagga gctgcggctg acagctcggg 180

cgacaagcgg gtccccgaca gcgggagaca aggccccgtt ctcgattaac ccaagccaaa 240

gggtccgtttt ctctctgaga ccgtttacat cagttttttt tcttttcttc aaaatatatg 300

tgtgaacgaa caatagtttg cagtacacga ccgaaacaca atatttcatt gattccttcc 360

ttgtcttctc acctctgacg attctgtttc tgaaatctgc ttcctgcaaa atggttccat 420

ggtcacggaa ttcgccatgg tcagagtcag agggagagag agagagagag tcgtactggt 480

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ccc Pro	aag Lys	agg Arg	gat Asp 20	cgc Arg	ggc Gly	atc Ile	tcc Ser	tgg Trp 25	gcc Ala	tgc Cys	gtc Val	ttc Phe	atc Ile 30	ctg Leu	gcg Ala	636
agt Ser	aac Asn	tgc Cys 35	ttc Phe	cag Gln	ttc Phe	atc Ile	gcc Ala 40	tac Tyr	ttc Phe	gcc Ala	gtg Val	tcg Ser 45	acg Thr	aac Asn	ctg Leu	684
gtg Val	aac Asn 50	tac Tyr	ctc Leu	aag Lys	gac Asp	cgc Arg 55	ctg Leu	cac His	cag Gln	ggc Gly	agc Ser 60	aaa Lys	gcc Ala	gcc Ala	gcg Ala	732
aac Asn 65	ggc Gly	gtc Val	acc Thr	aac Asn 70	tgg Trp	atg Met	ggc Gly	acg Thr	agc Ser	gcc Ala 75	atc Ile	acg Thr	ccg Pro	ctc Leu	gtc Val 80	780
gcc Ala	gcc Ala	ttc Phe	ctc Leu	gcc Ala 85	gac Asp	gcc Ala	ttc Phe	ctc Leu	ggc Gly 90	aga Arg	tac Tyr	tgg Trp	acc Thr	atc Ile 95	gcg Ala	828
ctc Leu	ttc Phe	ctg Leu	gtc Val 100	atc Ile	tcc Ser	gtc Val	ctg Leu	gcc Ala 105	tac Tyr	gtg Val	gtg Val	ctc Leu 110	acg Thr	gtg Val	agc Ser	876
gcg Ala	gcg Ala	gcg Ala 115	gag Ala	ctg Leu	gag Glu	agc Ser	gcg Ala 120	ttc Phe	tac Tyr	gcg Ala	ggg Gly 125	ctg Leu	tac Tyr	ctg Leu	ctg Leu	924
ctg Leu 130	gcg Ala	ctg Leu	ggc Gly	ggg Gly	gag Ala	ctg Leu 135	cag Gln	ccg Pro	gtg Val	ctg Leu	tcg Ser 140	tcg Ser	ttc Phe	ggc Gly	gcc Ala	972
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tgg Trp	ttc Phe	tac Tyr	ctc Leu	tcc Ser 165	atc Ile	aac Asn	gtc Val	ggc Gly	tcg Ser 170	ctg Leu	ctc Leu	ggc Gly	ggc Gly	acc Thr 175	gtg Val	1068
ctg Leu	gtg Val	tgg Trp 180	gtg Val	cag Gln	tcc Ser	agc Ser	gtc Val	agc Ser 185	tgg Trp	ggg Gly	ctc Leu	ggg Gly	tac Tyr 190	ggc Gly	atc Ile	1116
ccg Pro	gag Ala	ctc Leu 195	ttc Phe	agc Ser	gag Ala	ctg Leu	gcc Ala 200	gtc Val	gag Ala	gag Ala	ttc Phe	ctg Leu 205	gcc Ala	ggc Gly	acc Thr	1164
gcc Ala	acg Thr 210	tac Tyr	cgc Arg	cgc Arg	cac His	cag Gln 215	ccg Pro	ccg Pro	gcc Ala	ggc Gly	agc Ser 220	ccg Pro	ctc Leu	acc Thr	agg Arg	1212
gtc Val 225	gag Ala	cag Gln	gtc Val	gtc Val	gtc Val 230	gcc Ala	gag Ala	tgc Cys	agg Arg	aag Lys 235	tgc Cys	ggc Gly	gtc Val	cac His	gcg Ala 240	1260
tcc Ser	gag Glu	gac Asp	gag Ala 245	tgg Trp	gag Ala	gac Asp	gag Ala	tgg Trp 250	gtg Val	gac Asp	agc Ser	ggc Gly	ggc Gly	atg Met 255	tcc Ser	1308
gag Ala	ata Ile	cag Gln 260	ggg Gly	agc Ser	cgc Arg	cgc Arg	ctc Leu	gag Ala 265	cac His	acc Thr	gat Asp	cag Gln 270	ttc Phe	agg Arg	ttc Phe	1356
ctg Leu	gac Asp	aag Lys 275	gca Ala	gag Ala	tcg Ser	gtg Val	gag Glu 280	cca Pro	tcg Ser	gac Asp	gac Asp	aag Lys 285	tcg Ser	cgt Arg	ccg Pro	1404
gag Ala	agc Ser 290	gag Ala	tgg Trp	cgt Arg	ctg Leu	tgc Cys 295	acg Thr	gtg Val	acg Thr	cag Gln	gtg Val 300	gag Glu	gag Glu	ctc Leu	aag Lys	1452
tgc Cys 305	gtg Val	ctc Leu	cgg Arg	ctg Leu	ctg Leu 310	ccg Pro	gtg Val	tgg Trp	gag Ala	agc Ser 315	ggg Gly	atc Ile	gtg Val	ttc Phe	gcg Ala 320	1500
gag Ala	gag Ala	tac Tyr	acg Thr	cag Gln 325	atg Met	acc Thr	acc Thr	acc Thr	ttc Phe 330	gtc Val	ctg Leu	cag Gln	ggc Gly	gac Asp 335	acg Thr	1548
ctg Leu	gac Asp	ccg Pro	tac Tyr 340	gtg Val	ggc Gly	ggc Gly	ttc Phe	cgc Arg 345	gtg Val	ccc Pro	gcc Ala	gcc Ala	gtg Val 350	ctc Leu	tcc Ser	1596

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Leu	Val	Val	Pro	Leu	Ala	Arg	Arg	Ala	Thr	Gly	His	Asp	Arg	Gly	Phe	
	370					375					380					
acg	cag	ctg	gcg	cgc	atg	ggc	gtg	ggc	ctc	gtc	gtg	ctc	acc	gcc	gcc	1740
Thr	Gln	Leu	Ala	Arg	Met	Gly	Val	Gly	Leu	Val	Val	Leu	Thr	Ala	Ala	
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Arg	Tyr	Gly	Met	Tyr	Asp	Thr	Asn	Thr	Gly	Ala	Gly	Gly	Asp	Gly	Ala	
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Tyr	Leu	Pro	Leu	Ser	Ile	Phe	Trp	Gln	Val	Pro	Gln	Tyr	Val	Val	Val	
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gac	cag	gcg	ccc	gac	gcg	atg	cgg	agc	ctc	tgc	tgc	ggg	ctc	tcc	atg	1980
Asp	Gln	Ala	Pro	Asp	Ala	Met	Arg	Ser	Leu	Cys	Ser	Gly	Leu	Ser	Met	
465					470					475					480	
acg	tcc	ttc	gcg	ctc	ggg	aac	tac	gtc	agc	tcc	gcg	ctc	gtc	acc	gtg	2028
Thr	Ser	Phe	Ala	Leu	Gly	Asn	Tyr	Val	Ser	Ser	Ala	Leu	Val	Thr	Val	
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gtg	gcg	cgc	gcc	acc	gcg	cgg	ggc	ggg	cgg	gac	ggc	tgg	atc	ccc	gac	2076
Val	Ala	Arg	Ala	Thr	Ala	Arg	Gly	Gly	Arg	Asp	Gly	Trp	Ile	Pro	Asp	
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gac	atc	aac	cgg	gcg	cac	ctc	gac	aac	ttc	ttc	tgg	ctg	ctg	gcc	atg	2124
Asp	Ile	Asn	Arg	Ala	His	Leu	Asp	Asn	Phe	Phe	Trp	Leu	Leu	Ala	Met	
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ctc	tgc	gcc	gga	aac	ttc	ggc	gtc	tac	ctg	ctc	atc	gcg	cgg	tgg	tac	2172
Leu	Cys	Ala	Gly	Asn	Phe	Gly	Val	Tyr	Leu	Leu	Ile	Ala	Arg	Trp	Tyr	
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Thr	Tyr	Lys	Lys	Thr	Val	Asp										
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 Val Asn Tyr Leu Lys Asp Arg Leu His Gln Gly Ser Lys Ala Ala Ala
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 Asn Gly Val Thr Asn Trp Met Gly Thr Ser Ala Ile Thr Pro Leu Val
 65 70 75 80
 Ala Ala Phe Leu Ala Asp Ala Phe Leu Gly Arg Tyr Trp Thr Ile Ala
 85 90 95
 Leu Phe Leu Val Ile Ser Val Leu Ala Tyr Val Val Leu Thr Val Ser
 100 105 110
 Ala Ala Ala Ala Leu Glu Ser Ala Ala Phe Tyr Ala Gly Leu Tyr Leu
 115 120 125
 Leu Ala Leu Gly Gly Ala Leu Gln Pro Val Leu Ser Ser Phe Gly Ala
 Seite 304

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 Pro Ala Leu Phe Ser Ala Leu Ala Val Ala Ala Phe Leu Ala Gly Thr
 195 200 205
 Ala Thr Tyr Arg Arg His Gln Pro Pro Ala Gly Ser Pro Leu Thr Arg
 210 215 220
 Val Ala Gln Val Val Val Ala Ala Cys Arg Lys Cys Gly Val His Ala
 225 230 235 240
 Ser Glu Asp Ala Trp Ala Asp Ala Trp Val Asp Ser Gly Gly Met Ser
 245 250 255
 Ala Ile Gln Gly Ser Arg Arg Leu Ala His Thr Asp Gln Phe Arg Phe
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 Leu Asp Lys Ala Ala Ser Val Glu Pro Ser Asp Asp Lys Ser Arg Pro
 275 280 285
 Ala Ser Ala Trp Arg Leu Cys Thr Val Thr Gln Val Glu Leu Lys
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 Cys Val Leu Arg Leu Leu Pro Val Trp Ala Ser Gly Ile Val Phe Ala
 305 310 315 320
 Ala Ala Tyr Thr Gln Met Thr Thr Thr Phe Val Leu Gln Gly Asp Thr
 325 330 335
 Leu Asp Pro Tyr Val Gly Gly Phe Arg Val Pro Ala Ala Val Leu Ser
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 Leu Val Val Pro Leu Ala Arg Arg Ala Thr Gly His Asp Arg Gly Phe
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 450 455 460
 Asp Gln Ala Pro Asp Ala Met Arg Ser Leu Cys Ser Gly Leu Ser Met
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PF59082SeqList_PF59082.txt

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tgccgccgcc gatcagggct tcgcctcccc tgttctcgcg aagatccgat tgctttcgcc	420
cgccacccgc atg gct ccg gcg tcc gag acg gag ctg caa gca cca cca	469
Met Ala Pro Ala Ser Glu Thr Glu Leu Gln Ala Pro Pro	
cca cca ccg gcg tcg gct aag gag atc aag tcg ccg gag gtg ctg ccg	517
Pro Pro Pro Ala Ser Ala Lys Glu Ile Lys Ser Pro Glu Val Leu Pro	
gag cca ggc tcg ctg tca gcg ctg cag cgc aag aag ctg ggt gcg cac	565
Glu Pro Gly Ser Leu Ser Ala Leu Gln Arg Lys Lys Leu Gly Ala His	
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Phe Met Glu Ser Asp Glu Arg Arg Val Ser Arg Ala Arg Thr Pro Leu	
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Gly Ala Ala Tyr Glu Pro Pro Ser Ala Ala Ala Gly Gly Gly Gly Thr	
acg ccg gtc aac atc cgc ggc gag ccc atc cag gac ctg tcg agg acc	709
Thr Pro Val Asn Ile Arg Gly Glu Pro Ile Gln Asp Leu Ser Arg Thr	
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Gly Gly Trp Val Ala Ala Phe Phe Ile Phe Gly Asn Glu Met Ala Glu	
cgc atg gcc tac ttc ggc ctc tcc gtc aac atg gtc atc ttc atg ttc	805
Arg Met Ala Tyr Phe Gly Leu Ser Val Asn Met Val Ile Phe Met Phe	
aag gtg atg cac cgc ccg ttc gcc agc tcc gcc aac gcc gtc aac aac	853
Lys Val Met His Arg Pro Phe Ala Ser Ser Ala Asn Ala Val Asn Asn	
ttc ctc ggc atc tcc cag gcg tcc tcc gtg ctg ggt ggc ttc ctc gcc	901
Phe Leu Gly Ile Ser Gln Ala Ser Val Leu Gly Gly Phe Leu Ala	
gac gcc tac ctg ggg cgc tac tgg acc atc gcc atc ttc acc acc atg	949
Asp Ala Tyr Leu Gly Arg Tyr Trp Thr Ile Ala Ile Phe Thr Thr Met	
tac ctg ctg ggg ctc atc gcg ctc acc gtg agc gcc agc gtg ccg gcg	997
Tyr Leu Leu Gly Leu Ile Ala Leu Thr Val Ser Ala Ser Val Pro Ala	
ctc gtg ccg ccg cag gag ggc tgc gac aag ctg gcc atg ctg ctg ggc	1045
Leu Val Pro Pro Gln Glu Gly Cys Asp Lys Leu Ala Met Leu Leu Gly	
gcc tgc gcg ccc gcg gcg ccc tgg cag atg gcc tac ctc cag acg gcg	1093
Ala Cys Ala Pro Ala Ala Pro Trp Gln Met Ala Tyr Leu Gln Thr Ala	
ctc tac gtg acg gcg ttg ggc gcg gcg ggg atc cgg ccc tgc gtc tcc	1141
Leu Tyr Val Thr Ala Leu Gly Ala Ala Gly Ile Arg Pro Cys Val Ser	
tcc ttc ggc gcc gac cag ttc gac gag cgc agc ccc ggg tac aag cgc	1189
Ser Phe Gly Ala Asp Gln Phe Asp Glu Arg Ser Pro Gly Tyr Lys Arg	
cgg ctc gac cgc ttc ttc aac ctc ttc tac ctc gcc gtc acg ctc ggc	1237
Arg Leu Asp Arg Phe Phe Asn Leu Phe Tyr Leu Ala Val Thr Leu Gly	
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Ala Ile Ala Ala Phe Thr Ala Val Val Tyr Ile Met Gln His Gly	

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gc	ctc	ttc	ttc	gtg	ggc	acg	ccg	ctg	tac	cgc	cac	cgg	ctg	ccg	ggg			1381	
Ala	Leu	Phe	Phe	Val	Gly	Thr	Pro	Leu	Tyr	Arg	His	Arg	Leu	Pro	Gly				
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Gly	Ser	Pro	Leu	Thr	Arg	Val	Ala	Gln	Val	Leu	Val	Ala	Ala	Phe	Arg				
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Lys	Arg	Asp	Ala	Ala	Phe	Asp	Ser	Gly	Asp	Phe	Val	Gly	Leu	Tyr	Glu				
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Val	Ala	Gly	Ala	Lys	Ser	Ala	Ile	Arg	Gly	Ser	Ala	Lys	Ile	Asp	His				
	350				355					360					365				
acc	gac	gac	ttc	aga	tgg	ctc	gac	aag	gcc	gc	ctg	cag	ctg	gag	ggt			1573	
Thr	Asp	Asp	Phe	Arg	Trp	Leu	Asp	Lys	Ala	Ala	Leu	Gln	Leu	Glu	Gly				
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gac	ctc	gcc	ggc	gag	gag	gac	gag	gag	gc	gtg	aac	ccg	tgg	cgt	ctg			1621	
Asp	Leu	Ala	Gly	Gly	Glu	Asp	Glu	Glu	Ala	Val	Asn	Pro	Trp	Arg	Leu				
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Cys	Thr	Val	Thr	Gln	Val	Glu	Glu	Val	Lys	Ile	Leu	Leu	Arg	Leu	Leu				
		400					405					410							
ccg	gtg	ccg	gc	tgc	acg	gtg	atg	ctg	agc	gtg	gtc	ctc	acc	gag	ttc			1717	
Pro	Val	Pro	Ala	Cys	Thr	Val	Met	Leu	Ser	Val	Val	Leu	Thr	Glu	Phe				
	415				420						425								
ctc	acg	ctg	tcg	gtg	cag	gcc	tac	acg	ctg	aac	acc	cgc	gtg	gc				1765	
Leu	Thr	Leu	Ser	Val	Gln	Ala	Tyr	Thr	Leu	Asn	Thr	Arg	Val	Ala					
				435					440					445					
gc	ctg	cac	ctg	ccc	gtg	acg	tgc	atg	ccg	gtg	ttc	ccc	tgc	ctg	gcc			1813	
Ala	Leu	His	Leu	Pro	Val	Thr	Cys	Met	Pro	Val	Phe	Pro	Cys	Leu	Ala				
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Ile	Phe	Leu	Ile	Leu	Ala	Leu	Tyr	Tyr	Gln	Thr	Phe	Ala	Pro	Leu	Ala				
			465				470					475							
cgc	cgc	ctg	acg	ggc	cac	ccg	cac	ggc	gcc	tcc	cag	ctg	cag	cgc	gtc			1909	
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Gly	Leu	Gly	Leu	Phe	Phe	Ser	Ile	Leu	Ser	Val	Ala	Trp	Ala	Gly	Leu				
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Phe	Glu	Arg	Tyr	Arg	Arg	Gly	Tyr	Ala	Val	Arg	His	Gly	Tyr	Leu	Gly				
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Leu	Phe	Leu	Thr	Pro	Met	Pro	Asp	Leu	Ser	Ala	Tyr	Trp	Leu	Leu	Ile				
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cag	tac	tgc	ctc	atc	ggc	gtg	gcc	gag	gtg	ttc	tgc	ctc	gtc	gc	ctc			2101	
Gln	Tyr	Cys	Leu	Ile	Gly	Val	Ala	Glu	Val	Phe	Cys	Leu	Val	Ala	Leu				
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Ser	Ala	Tyr	Ala	Ala	Val	Ala	Gly	Gly	Leu	Gly	Cys	Phe	Val	Ala	Ser				
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Ala	Ile	Asn	Thr	Ala	Val	Asp	Ala	Ala	Thr	Arg	Asp	Asp	Glu	Glu	Gly				
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Arg	Pro	Ser	Trp	Leu	Ala	Gln	Asn	Ile	Asn	Val	Gly	Arg	Phe	Asp	Tyr				
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ctg	tac	tgg	ctg	ctc	gcc	gtg	ctc	agc	aca	gtc	aac	ctg	ctc	gtt	ttc			2341	
Leu	Tyr	Trp	Leu	Leu	Ala	Val	Leu	Ser	Thr	Val	Asn	Leu	Leu	Val	Phe				
			625				630					635							
gtc	ttc	ttt	gcc	aag	cgg	tac	aag	tac	agg	gtc	agg	gtc	gac	gtg	ccg			2389	
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PF59082SeqList_PF59082.txt

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ccgtcgcggc aatagaatag accagccgga actggtgcct ggtggagtgg gagcttcagc      2563

cttgggcctc catctggaga tcaagtatcc ggtgactgct gccagctcag gagcgtgata      2623

gcatgatgaa ccacatcgta ctgctgactg ttcatcagta attccccagt tgcttttagct      2683

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Ser Asp Glu Arg Arg Val Ser Arg Ala Arg Thr Pro Leu Gly Ala Ala
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Tyr Glu Pro Pro Ser Ala Ala Ala Gly Gly Gly Gly Thr Thr Pro Val
65      70      75      80
Asn Ile Arg Gly Glu Pro Ile Gln Asp Leu Ser Arg Thr Gly Gly Trp
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Tyr Phe Gly Leu Ser Val Asn Met Val Ile Phe Met Phe Lys Val Met
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His Arg Pro Phe Ala Ser Ser Ala Asn Ala Val Asn Asn Phe Leu Gly
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Ile Ser Gln Ala Ser Ser Val Leu Gly Gly Phe Leu Ala Asp Ala Tyr
145     150     155     160
Leu Gly Arg Tyr Trp Thr Ile Ala Ile Phe Thr Thr Met Tyr Leu Leu
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Gly Leu Ile Ala Leu Thr Val Ser Ala Ser Val Pro Ala Leu Val Pro
        180     185     190
Pro Gln Glu Gly Cys Asp Lys Leu Ala Met Leu Leu Gly Ala Cys Ala
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Thr Ala Leu Gly Ala Ala Gly Ile Arg Pro Cys Val Ser Ser Phe Gly
225     230     235     240
Ala Asp Gln Phe Asp Glu Arg Ser Pro Gly Tyr Lys Arg Arg Leu Asp
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Arg Phe Phe Asn Leu Phe Tyr Leu Ala Val Thr Leu Gly Ala Ile Ala
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Ala Phe Gly Thr Leu Ala Leu Ala Met Gly Thr Ser Asn Ala Leu Phe
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PF59082SeqList_PF59082.txt

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 Phe Arg Trp Leu Asp Lys Ala Ala Leu Gln Leu Glu Gly Asp Leu Ala
 370 375 380
 Gly Gly Glu Asp Glu Glu Ala Val Asn Pro Trp Arg Leu Cys Thr Val
 385 390 400
 Thr Gln Val Glu Glu Val Lys Ile Leu Leu Arg Leu Leu Pro Val Pro
 405 410 415
 Ala Cys Thr Val Met Leu Ser Val Val Leu Thr Glu Phe Leu Thr Leu
 420 425 430
 Ser Val Gln Gln Ala Tyr Thr Leu Asn Thr Arg Val Ala Ala Leu His
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 Ile Leu Ala Leu Tyr Tyr Gln Thr Phe Ala Pro Leu Ala Arg Arg Leu
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 Thr Gly His Pro His Gly Ala Ser Gln Leu Gln Arg Val Gly Leu Gly
 485 490 495
 Leu Phe Phe Ser Ile Leu Ser Val Ala Trp Ala Gly Leu Phe Glu Arg
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 Tyr Arg Arg Gly Tyr Ala Val Arg His Gly Tyr Leu Gly Leu Phe Leu
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 Thr Pro Met Pro Asp Leu Ser Ala Tyr Trp Leu Leu Ile Gln Tyr Cys
 530 535 540
 Leu Ile Gly Val Ala Glu Val Phe Cys Leu Val Ala Leu Leu Glu Phe
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 Leu Tyr Gln Glu Ala Pro Asp Ala Met Arg Ser Val Gly Ser Ala Tyr
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 Ala Ala Val Ala Gly Gly Leu Gly Cys Phe Val Ala Ser Ala Ile Asn
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 Thr Ala Val Asp Ala Ala Thr Arg Asp Asp Glu Glu Gly Arg Pro Ser
 595 600 605
 Trp Leu Ala Gln Asn Ile Asn Val Gly Arg Phe Asp Tyr Leu Tyr Trp
 610 615 620
 Leu Leu Ala Val Leu Ser Thr Val Asn Leu Leu Val Phe Val Phe Phe
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 tatcctcctt cccttcttgt gcccttgctt ggaccatata cctgaagtag cagcttcctt 240
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PF59082SeqList_PF59082.txt

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Pro	His	His	Pro	Pro	Ser	Gln	Thr	Gln	Val	Ser	Ser	Ala	Asn	Gln	
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tat	aac	aaa	ccc	ttc	agc	tgg	aag	gcc	cca	gcc	att	att	ttg	gcc	445
Tyr	Asn	Lys	Pro	Phe	Ser	Trp	Lys	Ala	Pro	Ala	Ile	Ile	Leu	Ala	
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Glu	Phe	Leu	Glu	Ser	Ile	Ala	Tyr	Ser	Gly	Ile	Ala	Leu	Asn	Leu	
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Val	Tyr	Leu	Gly	Thr	Val	Leu	His	Gly	Thr	Thr	Ala	Ser	Asn	Ala	
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aac	gtc	gat	gcg	tgg	aac	ggc	gcc	acg	ttt	ctt	acg	ccg	gtc	ctt	589
Asn	Val	Asp	Ala	Trp	Asn	Gly	Ala	Thr	Phe	Leu	Thr	Pro	Val	Leu	
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Pro	Ala	Thr	Gly	Phe	Gln	Tyr	Phe	Val	Leu	Phe	Gly	Ser	Leu	Tyr	
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Ala	Asp	Gln	Tyr	Asn	Asp	Ala	Asn	Ala	Glu	Glu	Ser	Lys	Ser	Lys	
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Gly	Phe	Gly	Ile	Ser	Ser	Ile	Cys	Leu	Val	Ile	Ala	Ala	Val	Ala	
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Leu	Lys	Ser	Ile	Val	Met	Val	Phe	Val	Ala	Ser	Tyr	Lys	Lys	Arg	
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Val	Ala	Val	Pro	Ala	Asp	Ser	Thr	Leu	Leu	Phe	Glu	Gly	Asn	Glu	
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His	Arg	Pro	Trp	Leu	Leu	Cys	Thr	Val	Thr	Gln	Val	Glu	Glu	Val	
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Ile	Leu	Ile	Arg	Met	Leu	Pro	Ile	Trp	Phe	Thr	Cys	Val	Phe	Tyr	
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cagccccaac ccgccgttct ctgcgcgcc gatcggaccg gaggctcgcc gttccacc 238

atg gca gag gcc ggc gac ccc acc ctg gag cag ggg ctc ctc gct gac 286

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Pro Glu Glu Ser Asn Gln Leu Thr Tyr Thr Gly Asp Gly Ser Val Asp
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Phe Ser Gly Asn Pro Val Val Lys Glu Lys Thr Gly Arg Trp Lys Ala
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Cys Pro Phe Ile Leu Gly Asn Glu Cys Cys Glu Arg Leu Ala Tyr Tyr
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Gly Asn Ser Ser Ala Ala Arg Asn Val Thr Thr Trp Gln Gly Thr Cys
85 90 95

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115 120 125

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Gln	Lys	Pro	Gly	Gly	Ser	Pro	Ile	Thr	Arg	Val	Cys	Gln	Val	Val	Ala	
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gcc	act	ttg	cgc	aag	tgg	aat	gca	cat	gtt	cca	gag	gac	agc	tct	ctc	1102
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Thr	Asp	Leu	Asp	Val	Lys	Glu	Asp	Ser	Phe	Asn	Asn	Pro	Trp	Arg	Val	
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Cys	Thr	Val	Thr	Gln	Val	Glu	Glu	Lys	Lys	Ile	Leu	Val	Arg	Met	Phe	
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Pro	Val	Trp	Ala	Thr	Thr	Ile	Val	Phe	Ser	Ala	Val	Tyr	Ala	Gln	Met	
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Ser	Thr	Met	Phe	Val	Glu	Gln	Gly	Met	Val	Leu	Asp	Pro	Thr	Ile	Gly	
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Ser	Phe	Lys	Ile	Pro	Pro	Ala	Ser	Leu	Ser	Thr	Phe	Asp	Val	Val	Ser	
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Val	Ile	Ile	Trp	Val	Pro	Ile	Tyr	Asp	Ser	Ile	Leu	Val	Pro	Ile	Ala	
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Gly	Ile	Gly	Leu	Val	Ile	Ser	Ile	Leu	Ala	Met	Ser	Ala	Ala	Ala	Val	
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Leu	Glu	Ile	Lys	Arg	Leu	Ala	Ile	Ala	Arg	Glu	Ala	His	Leu	Val	Asp	
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cag	aac	gtc	ccg	gtt	ccg	ctg	agc	atc	ctg	tgg	caa	atc	cct	cag	tac	1678
Gln	Asn	Val	Pro	Val	Pro	Leu	Ser	Ile	Leu	Trp	Gln	Ile	Pro	Gln	Tyr	
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Phe	Phe	Tyr	Asp	Gln	Ser	Pro	Asp	Ala	Met	Arg	Ser	Leu	Cys	Ser	Ala	
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ctg	cag	ctc	atc	acc	acc	gcg	ctc	ggg	aac	tac	ctc	agc	gcc	ttc	atc	1822
Leu	Gln	Leu	Ile	Thr	Thr	Ala	Leu	Gly	Asn	Tyr	Leu	Ser	Ala	Phe	Ile	
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ctc	acg	atg	gtc	gcc	tac	ttc	acg	acc	agg	gga	ggg	aga	ccc	ggg	tgg	1870
Leu	Thr	Met	Val	Ala	Tyr	Phe	Thr	Thr	Arg	Gly	Gly	Arg	Pro	Gly	Trp	
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atc	ccc	gac	aac	ctg	aac	gag	ggg	cgt	ctc	gat	tac	ttc	ttc	tgg	ctg	1918
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ctc	gcg	ggg	ctc	agc	ttt	ctc	aac	ttt	ttg	gtg	tac	gtg	ctg	tgc	gcc	1966
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Asn	Arg	Phe	Lys	Ser	Lys	Lys	Ala	Ala								
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PF59082SeqList_PF59082.txt

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Gly Ile Ser Thr Asn Leu Val Thr Tyr Leu Thr Lys Lys Leu His Asp
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Gly Asn Ser Ser Ala Ala Arg Asn Val Thr Thr Trp Gln Gly Thr Cys
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Tyr Leu Thr Pro Leu Ile Gly Ala Ile Leu Ala Asp Ala Tyr Trp Gly
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Arg Tyr Trp Thr Ile Ala Thr Phe Ser Thr Ile Tyr Phe Ile Gly Met
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Ser Val Leu Thr Leu Ser Ala Ser Val Pro Met Leu Met Pro Pro Ser
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Phe Phe Leu Gly Leu Tyr Leu Ile Ala Leu Gly Thr Gly Gly Ile Lys
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Pro Cys Val Ser Ser Phe Gly Ala Asp Gln Phe Asp Asp Thr Asp Pro
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Ala Glu Arg Ile Gln Lys Gly Ser Phe Phe Asn Trp Phe Tyr Phe Ser
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Ile Asn Ile Gly Ala Leu Ile Ser Ser Ser Phe Leu Val Trp Val Gln
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Asp Asn Leu Gly Trp Gly Leu Gly Phe Gly Ile Pro Thr Val Phe Met
225 230 235 240
Gly Leu Ala Ile Ile Ser Phe Phe Ala Gly Thr Ser Leu Tyr Arg Phe
245 250 255
Gln Lys Pro Gly Gly Ser Pro Ile Thr Arg Val Cys Gln Val Val Ala
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Ala Thr Leu Arg Lys Trp Asn Ala His Val Pro Glu Asp Ser Ser Leu
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Leu Glu His Thr Asp Glu Leu Arg Cys Leu Asp Arg Ala Ala Thr Ile
305 310 315 320
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Cys Thr Val Thr Gln Val Glu Glu Leu Lys Ile Leu Val Arg Met Phe
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PF59082SeqList_PF59082.txt

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 Met Glu Lys Gly Ser Met Glu Asn Asn Glu Lys His
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112

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 Val Thr Glu Asn Asp Pro Lys Ile Asp Tyr Arg Gly Trp Lys Ala Met
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160

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208

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 Thr Leu Ala Asn Leu Leu Val Tyr Leu Thr Thr Val Phe Asn Leu Lys
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256

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304

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 80 85 90

352

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 Tyr Lys Thr Ile Gly Phe Cys Thr Phe Thr Ser Phe Leu Gly Leu Leu
 95 100 105

400

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 Val Ile Gln Leu Thr Ala Val Phe Lys Asn Leu His Pro Pro His Cys
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448

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496

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Phe	Leu	Val	Ser	Gly 145	Phe	Gly	Leu	Leu	Leu	Ile	Gly	Ala	Ala	Gly 155	Val	
aga	cca	tgt	aac	ttg	gct	ttt	gga	gct	gat	caa	ttc	aat	ccc	aat	aca	592
Arg	Pro	Cys	Asn	Leu	Ala	Phe	Gly	Ala	Asp	Gln	Phe	Asn	Pro	Asn	Thr	
gat	tca	gga	aaa	aaa	ggg	atc	aac	agt	ttc	ttc	aat	tgg	tat	ttt	ttt	640
Asp	Ser	Gly 175	Lys	Lys	Gly	Ile	Asn	Ser	Phe	Phe	Asn	Trp	Tyr	Phe	Phe	
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Thr	Phe	Thr	Phe	Ala	Gln	Met 195	Val	Ser	Leu	Thr	Leu	Ile	Val	Tyr	Val	
cag	tca	aat	gtg	agc	tgg	gca	ata	ggg	ttg	gga	att	cct	gct	gct	ttg	736
Gln	Ser	Asn	Val	Ser	Trp 210	Ala	Ile	Gly	Leu	Gly 215	Ile	Pro	Ala	Ala	Leu	
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Met	Leu	Ile	Ser	Cys 225	Val	Val	Tyr	Phe	Met 230	Gly	Ser	Lys	Ile	Tyr 235	Val	
aaa	gtt	gaa	cct	agt	ggt	agt	ccc	ata	gct	ggt	att	gtg	caa	gtt	ttt	832
Lys	Val	Glu	Pro	Ser	Gly	Ser	Pro	Ile	Ala	Gly	Ile	Val	Gln	Val	Phe	
gtg	gtt	gca	gta	aaa	aaa	agg	agt	ata	aaa	cta	cct	gca	gag	cat	cca	880
Val	Val	Ala 255	Val	Lys	Lys	Arg	Ser	Ile	Lys	Leu	Pro	Ala	Glu	His	Pro	
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Leu	Pro	Tyr	Thr	Phe	Gln 290	Phe	Arg	Leu	Leu	Asp 295	Lys	Ala	Ala	Ile	Val	
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Thr	Pro	Lys	Asp	Lys 305	Ile	Lys	Pro	Asp	Gly 310	Ser	Ala	Ala	Asp	Pro	Trp	
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Asn	Leu	Cys	Ser	Ile	Gln	Gln	Val	Glu	Glu	Ala	Lys	Cys	Val	Val	Arg	
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Val	Leu	Pro 335	Ile	Trp	Phe	Ala	Ile	Val	Tyr	His	Leu	Val	Ile	Val		
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Gln	Met 350	His	Thr	Leu	Leu	Val 355	Phe	Gln	Ala	Leu	Gln	Ser	Asp	Arg	Arg	
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Ile	Val 430	Ala	Gly	Val	Val	Glu 435	Glu	His	Arg	Arg	Ser	Leu	Ala	Leu	Thr	
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Ser	Ser	Tyr	Leu	Ser	Thr	Leu	Leu	Ile	Ser	Ile	Val	His	Asn	Thr	Ser		
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Glu	Lys	Ser	Ala	Thr	Gly	Asn	Trp	Leu	Pro	Glu	Asp	Leu	Asn	Lys	Gly		
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Ile	Gly	Ala	Phe	Leu	Ser	Asp	Thr	Tyr	Phe	Gly	Arg	Tyr	Lys	Thr	Ile		
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Lys	Thr	Cys	Lys	Gly	Pro	Thr	Ala	Gly	Gln	Met	Ala	Phe	Leu	Val	Ser		
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 Seite 319

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Ala	Val	Val	Gly	Phe 35	Asn	Thr	Asn	Met	Ile 40	Ser	Tyr	Leu	Thr	Thr 45	Gln	
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Leu	His	Met	Pro	Leu	Thr	Lys	Ala	Ala	Asn	Thr	Leu	Thr	Asn	Phe	Gly	
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Tyr	Ala	Gly	Lys	Phe	Trp	Thr	Val	Thr	Leu	Ala	Ser	Ile	Ile	Tyr	Gln	
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Ile	Gly	Met	Ile	Ser	Leu	Thr	Leu	Ser	Ala	Val 105	Leu	Pro	Gln	Phe	Arg	
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Pro	Pro	Pro	Cys	Lys 115	Gly	Glu	Glu	Val	Cys 120	Gln	Gln	Ala	Ser	Ala 125	Gly	
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Gln	Leu	Ala	Ile	Leu	Tyr	Ile	Ser	Leu	Leu	Leu	Gly	Ala	Leu	Gly	Ser	
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Gly	Gly	Ile	Arg	Pro	Cys	Ile	Val 150	Ala	Phe	Gly	Ala	Asp	Gln	Phe	Asp	
gag	tct	gat	ccc	aag	cag	aca	aca	agg	aca	tgg	acc	tac	ttc	aac	tgg	708
Glu	Ser	Asp	Pro	Lys	Gln	Thr	Thr	Arg	Thr	Trp	Thr	Tyr	Phe	Asn	Trp	
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Tyr	Tyr	Phe	Val	Met	Gly 180	Val	Ala	Ile	Leu	Val 185	Ala	Val	Thr	Val	Leu	
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Gln	Val 240	Ala	Val	Ala	Ala	Phe 245	Arg	Lys	Arg	Lys	Val 250	Pro	Asn	Val	Ser	
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His	Pro	Ser	Leu	Leu	Tyr 260	Gln	Asn	Asp	Glu	Leu	Asp	Ala	Ser	Ile	Ser	
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Met	Gly	Gly	Lys	Leu 275	Leu	His	Ser	Gly	Gln 280	Met	Lys	Phe	Leu	Asp 285	Lys	
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Ala	Ala	Ile	Val	Thr	Glu	Glu	Asp	Asp	Asn	Lys	Thr	Pro	Asn	Leu	Trp	
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Arg	Leu	Asn	Thr	Ile	His	Arg	Val 310	Glu	Glu	Leu	Lys	Ser	Ile	Ile	Arg	
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Gln	Gln	Asn	Thr	Phe	Ser 340	Leu	Gln	Gln	Ala	Lys 345	Thr	Met	Asp	Arg	His	
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Leu	Thr	Lys	Thr	Phe 355	Gln	Ile	Pro	Ala	Gly 360	Ser	Met	Ser	Val	Phe 365	Thr	
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Ile	Leu	Thr	Met	Leu	Thr	Thr	Thr	Ala	Phe	Tyr	Asp	Arg	Val	Phe	Ile	
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His Arg Met Gly Ile Gly Phe Val Ile Ser Thr Leu Ala Thr Leu Val	
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Ala Gly Phe Val Glu Met Lys Arg Lys Lys Ala Ala Leu Ala His Gly	
415 420 425	
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Leu Phe Asp His Pro His Ala Ile Ile Pro Ile Ser Val Phe Trp Leu	
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Val Pro Gln Tyr Ser Leu His Gly Met Ala Glu Ala Phe Met Ser Ile	
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Gly His Leu Glu Phe Phe Tyr Asp Gln Ala Pro Glu Ser Met Arg Ser	
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Thr Ala Met Ala Leu Phe Trp Thr Ala Ile Ala Ala Gly Asn Tyr Val	
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Ser Thr Ile Met Val Thr Leu Val His Lys Phe Ser Ala Gly Ser Asn	
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Gly Ser Asn Trp Leu Pro Asp Asn Asn Leu Asn Lys Gly Lys Leu Glu	
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Thr Val	
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 35 40 45
 Met Pro Leu Thr Lys Ala Ala Asn Thr Leu Thr Asn Phe Gly Gly Thr
 50 55 60
 Ala Ser Leu Thr Pro Leu Leu Gly Ala Phe Ile Ala Asp Ser Tyr Ala
 65 70 75 80
 Gly Lys Phe Trp Thr Val Thr Leu Ala Ser Ile Ile Tyr Gln Ile Gly
 85 90 95
 Met Ile Ser Leu Thr Leu Ser Ala Val Leu Pro Gln Phe Arg Pro Pro
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 Pro Cys Lys Gly Glu Glu Val Cys Gln Ala Ser Ala Gly Gln Leu

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Asp	Pro	Lys	Gln	Thr	Thr	Arg	Thr	Trp	Thr	Tyr	Phe	Asn	Trp	Tyr	Tyr
				165					170					175	
Phe	Val	Met	Gly	Val	Ala	Ile	Leu	Val	Ala	Val	Thr	Val	Leu	Val	Tyr
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Ala	Val	Ala	Ala	Phe	Arg	Lys	Arg	Lys	Val	Pro	Asn	Val	Ser	His	Pro
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Ser	Leu	Leu	Tyr	Gln	Asn	Asp	Glu	Leu	Asp	Ala	Ser	Ile	Ser	Met	Gly
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Pro	Ile	Trp	Ala	Ser	Gly	Ile	Leu	Leu	Ile	Thr	Ala	Tyr	Ala	Gln	Gln
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Ala	Arg	Arg	Phe	Thr	Gly	Leu	Asp	Arg	Gly	Ile	Ser	Phe	Leu	His	Arg
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Phe	Val	Glu	Met	Lys	Arg	Lys	Lys	Ala	Ala	Leu	Ala	His	Gly	Leu	Phe
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Asp	His	Pro	His	Ala	Ile	Ile	Pro	Ile	Ser	Val	Phe	Trp	Leu	Val	Pro
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Gln	Tyr	Ser	Leu	His	Gly	Met	Ala	Glu	Ala	Phe	Met	Ser	Ile	Gly	His
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Met	Ala	Leu	Phe	Trp	Thr	Ala	Ile	Ala	Ala	Gly	Asn	Tyr	Val	Ser	Thr
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Ile	Met	Val	Thr	Leu	Val	His	Lys	Phe	Ser	Ala	Gly	Ser	Asn	Gly	Ser
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Asn	Trp	Leu	Pro	Asp	Asn	Asn	Leu	Asn	Lys	Gly	Lys	Leu	Glu	Tyr	Phe
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atg gcc ggc gcc gag cgc gcg gag gcg gtc gct ctg gag gaa ggg ctc	348
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Leu Ala Pro Glu Glu Ser Asn Gln Val Val Tyr Thr Gly Asp Gly Ser	
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Trp Gly Arg Tyr Trp Thr Ile Ala Thr Phe Ser Thr Val Tyr Phe Ile	
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Gly Met Ser Ile Leu Thr Leu Ser Ala Ser Val Pro Met Leu Met Pro	
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Pro Ser Cys Glu Gly Ser Phe Cys Pro Gln Ala Ser Pro Phe Gln Tyr	
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Thr Val Phe Phe Leu Gly Leu Tyr Leu Ile Ala Leu Gly Thr Gly Gly	
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Ile Lys Pro Cys Val Ser Ser Phe Gly Ala Asp Gln Phe Asp Asp Thr	
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Asp Pro Ala Glu Arg Ile Gln Lys Gly Ser Phe Phe Asn Trp Phe Tyr	
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Val Gln Asp Asn Val Gly Trp Gly Leu Gly Phe Gly Ile Pro Thr Val	
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Arg Phe Gln Lys Pro Gly Gly Ser Pro Ile Thr Arg Val Cys Gln Val	
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Arg	Gln	Ile	Glu	His	Thr	Asp	Glu	Leu	Arg	Cys	Leu	Asp	Lys	Ala	Ala	
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Thr	Val	Thr	Glu	Val	Asp	Val	Lys	Met	Ala	Asp	Phe	Ser	Asn	Pro	Trp	
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Arg	Ile	Cys	Thr	Val	Thr	Gln	Val	Glu	Glu	Leu	Lys	Ile	Leu	Val	Arg	
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Leu	Ser	Val	Ile	Val	Cys	Val	Pro	Met	Tyr	Asp	Tyr	Ile	Val	Val	Pro	
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Ile	Ala	Arg	Arg	Phe	Thr	Gly	Asn	Glu	Arg	Gly	Phe	Thr	Glu	Leu	Gln	
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Arg	Met	Gly	Ile	Gly	Leu	Val	Ile	Ser	Ile	Leu	Ala	Met	Ser	Val	Ala	
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Gln	Tyr	Phe	Leu	Ile	Gly	Leu	Ala	Glu	Ile	Phe	Thr	Phe	Ile	Gly	Ala	
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Phe	Ile	Leu	Thr	Met	Val	Ala	Tyr	Phe	Thr	Thr	Arg	Gly	Gly	Asn	Pro	
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Trp	Leu	Leu	Ala	Gly	Leu	Ser	Phe	Leu	Asn	Leu	Ile	Val	Tyr	Val	Ile	
				565					570					575		
tgt	gct	ggc	aaa	tac	aag	ggc	aag	aag	gca	gct	tgagttgtga	agg	tcaggaa			2081
Cys	Ala	Gly	Lys	Tyr	Lys	Gly	Lys	Lys	Ala	Ala						
				580					585							
ctggacggct	cgccatgttt	ccttggacac	ttattaactt	caacaatctg	tatatatggt											2141
tcccacattc	actctagctg	aagcaacgat	ctgtaattgt	tgggaagctt	ttatttctca											2201
ttttactgta	ctaaattgat	tttacattcg	tacttccact	ttctgtatat	attgctgaat											2261
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PF59082SeqList_PF59082.txt

<210> 235

<211> 587

<212> PRT

<213> Sorghum bicolor

<400> 235

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      20      25      30
Val Asp Phe Ser Gly Asn Pro Val Val Lys Glu Thr Thr Gly Arg Trp
      35      40      45
Lys Ala Cys Pro Phe Ile Leu Gly Asn Glu Cys Cys Glu Arg Leu Ala
      50      55      60
Tyr Tyr Gly Ile Ser Thr Asn Leu Val Thr Tyr Leu Thr Lys Lys Leu
65      70      75      80
His Ala Gly Asn Ala Ser Ala Ala Ser Asn Val Thr Thr Trp Gln Gly
      85      90      95
Thr Cys Tyr Leu Thr Pro Leu Ile Gly Ala Ile Leu Ala Asp Ala Tyr
      100      105      110
Trp Gly Arg Tyr Trp Thr Ile Ala Thr Phe Ser Thr Val Tyr Phe Ile
      115      120      125
Gly Met Ser Ile Leu Thr Leu Ser Ala Ser Val Pro Met Leu Met Pro
      130      135      140
Pro Ser Cys Glu Gly Ser Phe Cys Pro Gln Ala Ser Pro Phe Gln Tyr
145      150      155      160
Thr Val Phe Phe Leu Gly Leu Tyr Leu Ile Ala Leu Gly Thr Gly Gly
      165      170      175
Ile Lys Pro Cys Val Ser Ser Phe Gly Ala Asp Gln Phe Asp Asp Thr
      180      185      190
Asp Pro Ala Glu Arg Ile Gln Lys Gly Ser Phe Phe Asn Trp Phe Tyr
      195      200      205
Phe Ser Ile Asn Ile Gly Ala Leu Ile Ser Ser Ser Phe Leu Val Trp
      210      215      220
Val Gln Asp Asn Val Gly Trp Gly Leu Gly Phe Gly Ile Pro Thr Val
225      230      235      240
Phe Met Gly Leu Ala Ile Ile Ser Phe Phe Ser Gly Thr Ser Leu Tyr
      245      250      255
Arg Phe Gln Lys Pro Gly Gly Ser Pro Ile Thr Arg Val Cys Gln Val
      260      265      270
Ile Val Ala Ser Leu Arg Lys Trp Asn Val Pro Ala Pro Glu Asp Ser
      275      280      285
Ser Leu Leu Tyr Glu Leu Pro Asn Gly Val Ser Thr Ile Glu Gly Ser
      290      295      300
Arg Gln Ile Glu His Thr Asp Glu Leu Arg Cys Leu Asp Lys Ala Ala
305      310      315      320
Thr Val Thr Glu Val Asp Val Lys Met Ala Asp Phe Ser Asn Pro Trp
      325      330      335
Arg Ile Cys Thr Val Thr Gln Val Glu Leu Lys Ile Leu Val Arg
      340      345      350
Met Phe Pro Val Trp Ala Thr Thr Ile Val Phe Ser Ala Val Tyr Ala
      355      360      365
Gln Met Ser Thr Met Phe Val Glu Gln Gly Met Val Leu Asp Pro Ser
      370      375      380
Leu Gly Ser Phe Lys Ile Pro Pro Ala Ser Leu Ser Thr Phe Asp Thr
385      390      395      400
Leu Ser Val Ile Val Cys Val Pro Met Tyr Asp Tyr Ile Val Val Pro
      405      410      415
Ile Ala Arg Arg Phe Thr Gly Asn Glu Arg Gly Phe Thr Glu Leu Gln
      420      425      430
Arg Met Gly Ile Gly Leu Val Ile Ser Ile Leu Ala Met Ser Val Ala
      435      440      445
Ala Ile Leu Glu Ile Lys Arg Leu Ala Val Ala Arg Glu Ala His Leu
450      455      460
Val Asp Gln Asn Val Pro Val Pro Leu Ser Ile Phe Trp Gln Ile Pro
465      470      475      480
Gln Tyr Phe Leu Ile Gly Leu Ala Glu Ile Phe Thr Phe Ile Gly Ala
      485      490      495
Leu Glu Phe Phe Tyr Asp Gln Ser Pro Asp Ala Met Arg Ser Leu Cys

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PF59082SeqList_PF59082.txt

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 530 535 540
 Gly Trp Ile Pro Asp Asn Leu Asn Glu Gly His Leu Asp Tyr Phe Phe
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 Cys Ala Gly Lys Tyr Lys Gly Lys Lys Ala Ala
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 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (249)..(2033)

<400> 236
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 acatgatatg ttttcataaa taagtggagt ggaggcaggc agcgaggggac gctaggcacc 180

 gttgtggctg tgcggaactg cacaagagcg tttcgccctg gccaccacga acggagaagg 240

 cggcagcc atg gcc atg gag gaa gcg ggg aag atg acg tgc agg aag aag 290
 Met Ala Met Glu Glu Ala Gly Lys Met Thr Cys Arg Lys Lys
 1 5 10
 ggt ggt ctg aga aca atg ccc ttc atc ttc gcc aac gag gtg gcg gag 338
 Gly Gly Leu Arg Thr Met Pro Phe Ile Phe Ala Asn Glu Val Ala Glu
 15 20 25 30
 aag ctc gcc gtg gtg ggt ttc tcg acc aac atg ctg acg tac ctg acc 386
 Lys Leu Ala Val Val Gly Phe Ser Thr Asn Met Leu Thr Tyr Leu Thr
 35 40 45
 act cag ctg cac atg ccg cta gcg aag gcc gcc acc acg ctc acc aac 434
 Thr Gln Leu His Met Pro Leu Ala Lys Ala Ala Thr Thr Leu Thr Asn
 50 55 60
 ttc ggc ggc acc tcc gcc gcg acg ccc ctc atc ggt gcc ttc ctc gcc 482
 Phe Gly Gly Thr Ser Ala Ala Thr Pro Leu Ile Gly Ala Phe Leu Ala
 65 70 75
 gac gcc tgc atc ggc cgg ttc tgg acc atc gcc gcc tcc gtc gtc 530
 Asp Ala Cys Ile Gly Arg Phe Trp Thr Ile Ala Ala Ala Ser Val Val
 80 85 90
 tac caa gcc ggc atg gcg ctc ctg acg gtg tca gcg gcg ctg ccg ccg 578
 Tyr Gln Ala Gly Met Ala Leu Leu Thr Val Ser Ala Ala Leu Pro Arg
 95 100 105 110
 ttc cgg ccg gcg ccg tgc aag ccg ggc ggc gcg gtg gca tgc cag gag 626
 Phe Arg Pro Ala Pro Cys Lys Pro Gly Gly Ala Val Ala Cys Gln Glu
 115 120 125
 gcc gcg ccg tgg cag ctg gcg gtg ctg tac gtg tcc ctg ctc ctg aac 674
 Ala Ala Pro Trp Gln Leu Ala Val Tyr Val Ser Leu Leu Leu Asn
 130 135 140
 gcg gtg ggc gcg ggc ggg tac cgc ccc tgc atc gtg gcg ttc ggg gcg 722
 Ala Val Gly Ala Gly Tyr Arg Pro Cys Ile Val Ala Phe Gly Ala
 145 150 155
 gac cag ttc gac gag tcg ccg gcg gcg gag cgc gcg agc tgg ggc 770
 Asp Gln Phe Asp Glu Ser Arg Ala Ala Glu Arg Ala Arg Ser Trp Gly
 160 165 170
 ttc ttc aac tgg tac tac ttc tgc aac ggc gcg tcc atg ctg ctg gcc 818
 Phe Phe Asn Trp Tyr Tyr Phe Cys Asn Gly Ala Ser Met Leu Leu Ala

PF59082SeqList_PF59082.txt

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	ctc	ggc	gtg	ccg	gcc	ttc	tgc	atg	ggc	gtc	tcc	gtc	gcc	gcc	ttc	gtg	914
	Leu	Gly	Val	Pro	Ala	Phe	Cys	Met	Gly	Val	Ser	Val	Ala	Ala	Phe	Val	
				210					215					220			
	gcc	ggg	tac	ccg	atg	tac	cgg	agg	ctg	gag	ccc	gcg	ggg	agc	ccg	ttc	962
	Ala	Gly	Tyr	Pro	Met	Tyr	Arg	Arg	Leu	Glu	Pro	Ala	Gly	Ser	Pro	Phe	
			225					230					235				
	acg	cgg	ctc	gcg	cag	gtt	gtc	gtc	gcc	gct	gtc	aag	aag	cgg	cgg	ctg	1010
	Thr	Arg	Leu	Ala	Gln	Val	Val	Val	Ala	Ala	Val	Lys	Lys	Arg	Arg	Leu	
		240				245						250					
	ccg	gcg	gcg	gac	gtc	aac	ccc	gcg	ttg	ctg	tac	gag	gac	gac	gag	ctc	1058
	Pro	Ala	Ala	Asp	Val	Asn	Pro	Ala	Leu	Leu	Tyr	Glu	Asp	Asp	Glu	Leu	
	255					260					265					270	
	gac	gcg	ccc	atc	tcc	atg	tac	ggc	aag	ctt	gtg	cac	acg	gat	cag	ctc	1106
	Asp	Ala	Pro	Ile	Ser	Met	Tyr	Gly	Lys	Leu	Val	His	Thr	Asp	Gln	Leu	
				275					280						285		
	agc	ttc	ttt	gac	cgc	gcg	gcg	atc	gtc	acc	gac	ggc	gac	ctg	gtc	acg	1154
	Ser	Phe	Phe	Asp	Arg	Ala	Ala	Ile	Val	Thr	Asp	Gly	Asp	Leu	Val	Thr	
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	ctg	acg	gac	gcg	gac	tcc	ggc	aag	ccg	tcg	acg	gcc	ccc	gtc	ccg	gac	1202
	Leu	Thr	Asp	Ala	Asp	Ser	Gly	Lys	Pro	Ser	Thr	Ala	Pro	Val	Pro	Asp	
			305					310					315				
	ctg	tgg	cgc	ctg	agc	acc	gtg	cac	gcg	gtg	gag	gag	ctc	aag	tcg	gtg	1250
	Leu	Trp	Arg	Leu	Ser	Thr	Val	His	Arg	Val	Glu	Glu	Leu	Lys	Ser	Val	
		320				325						330					
	atc	cgc	atg	ggt	cct	atc	tgg	gcg	gcg	ggc	atc	ctg	gtg	atc	acg	ggg	1298
	Ile	Arg	Met	Gly	Pro	Ile	Trp	Ala	Ala	Gly	Ile	Leu	Val	Ile	Thr	Gly	
	335					340					345					350	
	tcg	tcg	acg	cag	aac	acc	ttc	tct	ctg	cag	cag	gcg	agc	acc	atg	gac	1346
	Ser	Ser	Thr	Gln	Asn	Thr	Phe	Ser	Leu	Gln	Gln	Ala	Ser	Thr	Met	Asp	
				355					360						365		
	cgc	cgc	ctc	gcg	ccg	ggc	ctc	tcc	acg	ttc	gag	atc	ccc	gcg	ggg	tcc	1394
	Arg	Arg	Leu	Ala	Pro	Gly	Leu	Ser	Thr	Phe	Glu	Ile	Pro	Ala	Gly	Ser	
				370					375					380			
	atg	acc	gtc	ttc	ggg	ctg	ctg	gcc	atg	ctc	ttc	acc	ctc	ttc	gtc	tac	1442
	Met	Thr	Val	Phe	Gly	Leu	Leu	Ala	Met	Leu	Phe	Thr	Leu	Phe	Val	Tyr	
			385					390					395				
	gac	cgc	gcg	ctc	atc	cgc	gtg	gcg	gcg	gcg	ttc	acg	ggg	ctg	gac	cgc	1490
	Asp	Arg	Ala	Leu	Ile	Arg	Val	Ala	Arg	Arg	Phe	Thr	Gly	Leu	Asp	Arg	
		400					405					410					
	ggc	atc	tcc	ttc	ctg	cac	cgc	atg	ggc	gtc	ggc	ttc	gcc	atc	agc	gtg	1538
	Gly	Ile	Ser	Phe	Leu	His	Arg	Met	Gly	Val	Gly	Phe	Ala	Ile	Ser	Val	
	415					420					425					430	
	ctc	gcc	acc	ctg	gtc	gct	gga	ttc	gtg	gag	cgg	cac	cgc	agg	gac	gcg	1586
	Leu	Ala	Thr	Leu	Val	Ala	Gly	Phe	Val	Glu	Arg	His	Arg	Arg	Asp	Ala	
				435					440						445		
	gcg	gcg	gcg	gcc	ggc	gcc	acg	gac	gcc	acg	tcc	ccg	ctg	tcg	gcc		1634
	Ala	Ala	Ala	Ala	Gly	Ala	Thr	Asp	Ala	Gly	Thr	Ser	Pro	Leu	Ser	Ala	
				450				455					460				
	tac	tgg	ctg	gtg	ccg	cag	tac	gca	ctg	cac	ggc	gtg	gcc	gag	gcg	ttc	1682
	Tyr	Trp	Leu	Val	Pro	Gln	Tyr	Ala	Leu	His	Gly	Val	Ala	Glu	Ala	Phe	
			465					470					475				
	acc	tcc	gtg	ggg	cac	ctc	gag	ttc	atg	tac	gac	cag	gcg	ccc	gag	agc	1730
	Thr	Ser	Val	Gly	His	Leu	Glu	Phe	Met	Tyr	Asp	Gln	Ala	Pro	Glu	Ser	
		480					485					490					
	atg	cgc	agc	acg	gcg	acg	gcg	ctc	ttc	tgg	ctg	tcc	atc	tcg	ctg	gga	1778
	Met	Arg	Ser	Thr	Ala	Thr	Ala	Leu	Phe	Trp	Leu	Ser	Ile	Ser	Leu	Gly	
	495					500					505					510	
	agc	tac	gcg	agc	acg	ctg	ctg	gtg	gac	gct	gtg	cac	cgc	tgg	agc	gcg	1826
	Ser	Tyr	Ala	Ser	Thr	Leu	Leu	Val	Asp	Ala	Val	His	Arg	Trp	Ser	Ala	
				515						520					525		
	ggg	ccc	ggc	ggc	gcc	aac	tgg	ctg	ccg	gac	aac	atc	aat	cac	ggc	aag	1874
	Gly	Pro	Gly	Gly	Ala	Asn	Trp	Leu	Pro	Asp	Asn	Ile	Asn	His	Gly	Lys	
				530					535					540			
	ctg	gat	tac	ttt	tac	tgg	gtc	gtc	acg	gta	ctg	cag	gtc	atg	aac	ctt	1922
	Leu	Asp	Tyr	Phe	Tyr	Trp	Val	Val	Thr	Val	Leu	Gln	Val	Met	Asn	Leu	

PF59082SeqList_PF59082.txt

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Val Tyr Tyr Ala Ile Cys Ala Lys Arg Phe Thr Phe Lys Pro Val Gln			
560	565	570	
ctc cac aag aaa gag gag gaa gaa ggc ggc aag gca ctt gtg gag ttg			2018
Leu His Lys Lys Glu Glu Glu Glu Gly Gly Lys Ala Leu Val Glu Leu			
575	580	585	590
caa gag aag gtt taatttgagc agcatgcact ttcatacagtg ctaggaagat			2070
Gln Glu Lys Val			
cctcagaaaa actcccaagg tattactata taaatctatg tgagcatctg tattagtcaa			2130
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tcctgagact tggcacaggt caaaaacaca actcgactat atttgtaact agaaagcagg			2250
cacgaggcac atgtctgaac tctgaaactt gacgttaatg catagtactg tataagactc			2310
tgtttgtaca ttagagtcta gggataaaca cacagatatt gttcaggcaa cagtcttcga			2370
aaagttgtca cgcaacacat ctctcagaga cagaaatatt tcgatctgaa tcctggcata			2430
gcttattaat attccgactt ggacactagg tagtaaggaa acaggtttgc acccacaatc			2490
tggcatgaat tccaacccaa gcagatagcg gagcttttca ggtaaacaga ctacggtaca			2550
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gatctcgaac ccggtggacg gatccacggg ctcggccgtg gacgggacga cggcggtgac			2730
ggtggcggct ggggggcca cggggaggcg gcgggttatc atgtcttcga tcttcgcggg			2790
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accgagcgac tcggccgtgg acgccgtcca gtcgcggaac cccacccccg tgacgtcccc			2910
cttcaccacc acgcggactg cttccgtgc gggctccggc tgcggcgcgg atggtggcgt			2970
ggcggcatcg ggatcggcgg aggacgccat ggcgcgggtg tgctggtacg gttgtggact			3030
tgtggaagca gcgagactgg agaccggaga cggagaggga cgaccggacg agacgagacg			3090
gccgaagcaa ggaactgctc cccggccggc cccgaggtac ccaa			3134

<210> 237
 <211> 594
 <212> PRT
 <213> Zea mays

PF59082SeqList_PF59082.txt

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Ala Val Val Gly Phe Ser Thr Asn Met Leu Thr Tyr Leu Thr Thr Gln
      35      40      45
Leu His Met Pro Leu Ala Lys Ala Ala Thr Thr Leu Thr Asn Phe Gly
      50      55      60
Gly Thr Ser Ala Ala Thr Pro Leu Ile Gly Ala Phe Leu Ala Asp Ala
65      70      75      80
Cys Ile Gly Arg Phe Trp Thr Ile Ala Ala Ala Ser Val Val Tyr Gln
      85      90      95
Ala Gly Met Ala Leu Leu Thr Val Ser Ala Ala Leu Pro Arg Phe Arg
      100      105      110
Pro Ala Pro Cys Lys Pro Gly Gly Ala Val Ala Cys Gln Glu Ala Ala
      115      120      125
Pro Trp Gln Leu Ala Val Leu Tyr Val Ser Leu Leu Leu Asn Ala Val
      130      135      140
Gly Ala Gly Gly Tyr Arg Pro Cys Ile Val Ala Phe Gly Ala Asp Gln
145      150      155      160
Phe Asp Glu Ser Arg Ala Ala Glu Arg Ala Arg Ser Trp Gly Phe Phe
      165      170      175
Asn Trp Tyr Tyr Phe Cys Asn Gly Ala Ser Met Leu Leu Ala Val Thr
      180      185      190
Ala Val Val Tyr Val Gln Asp Asn Val Gly Trp Gly Trp Gly Leu Gly
      195      200      205
Val Pro Ala Phe Cys Met Gly Val Ser Val Ala Ala Phe Val Ala Gly
210      215      220
Tyr Pro Met Tyr Arg Arg Leu Glu Pro Ala Gly Ser Pro Phe Thr Arg
225      230      235      240
Leu Ala Gln Val Val Val Ala Ala Val Lys Lys Arg Arg Leu Pro Ala
      245      250      255
Ala Asp Val Asn Pro Ala Leu Leu Tyr Glu Asp Asp Glu Leu Asp Ala
      260      265      270
Pro Ile Ser Met Tyr Gly Lys Leu Val His Thr Asp Gln Leu Ser Phe
      275      280      285
Phe Asp Arg Ala Ala Ile Val Thr Asp Gly Asp Leu Val Thr Leu Thr
290      295      300
Asp Ala Asp Ser Gly Lys Pro Ser Thr Ala Pro Val Pro Asp Leu Trp
305      310      315      320
Arg Leu Ser Thr Val His Arg Val Glu Glu Leu Lys Ser Val Ile Arg
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Met Gly Pro Ile Trp Ala Ala Gly Ile Leu Val Ile Thr Gly Ser Ser
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      355      360      365
Leu Ala Pro Gly Leu Ser Thr Phe Glu Ile Pro Ala Gly Ser Met Thr
370      375      380
Val Phe Gly Leu Leu Ala Met Leu Phe Thr Leu Phe Val Tyr Asp Arg
385      390      395      400
Ala Leu Ile Arg Val Ala Arg Arg Phe Thr Gly Leu Asp Arg Gly Ile
      405      410      415
Ser Phe Leu His Arg Met Gly Val Gly Phe Ala Ile Ser Val Leu Ala
      420      425      430
Thr Leu Val Ala Gly Phe Val Glu Arg His Arg Arg Asp Ala Ala Ala
      435      440      445
Ala Ala Gly Ala Thr Asp Ala Gly Thr Ser Pro Leu Ser Ala Tyr Trp
450      455      460
Leu Val Pro Gln Tyr Ala Leu His Gly Val Ala Glu Ala Phe Thr Ser
465      470      475      480
Val Gly His Leu Glu Phe Met Tyr Asp Gln Ala Pro Glu Ser Met Arg
      485      490      495
Ser Thr Ala Thr Ala Leu Phe Trp Leu Ser Ile Ser Leu Gly Ser Tyr
      500      505      510
Ala Ser Thr Leu Leu Val Asp Ala Val His Arg Trp Ser Ala Gly Pro
515      520      525
Gly Gly Ala Asn Trp Leu Pro Asp Asn Ile Asn His Gly Lys Leu Asp

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PF59082SeqList_PF59082.txt

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 Lys Lys Glu Glu Glu Gly Gly Lys Ala Leu Val Glu Leu Gln Glu
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 Lys Val

<210> 238
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<220>
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 <222> (1305)..(3074)

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 cactcccgcg tccccggaga agcggcgaga tgtacggcat cctgacctcc ccctgccctc 240

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 cctggttccc caacatcccc tgggaccgcc agcccttctc ggccctgcgc gacctctgcg 600

 accccttcct cgccctgtgc cgtgaggta tgcccccggt gttcgggcgc aagctcgacc 660

 tcagcccgtg tgttgcatc atggctattg acatcatcat catgatcctg cgcccgcagc 720

 cacgcatgtg atgactccct gcagcagtgg gtttgacga tgtatgttgg tatgttaggc 780

 tctgactgca ggaacaagga tctaaggctg ttttcggtca tcagatggca aagaaagggtg 840

 ctgtgccgct cacctgtatc agtacacaag tgcgggtggtt ggttgatta gttttgcgat 900

 cttagcatag cggttatgga ggggttaatg caatataaat gatttcgatg tggcttcatt 960

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PF59082SeqList_PF59082.txt

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aaaaaaaaaa aaaaaaaaaa aaaaaaaac atgtaccgcc cggcggggcg gggattactg	1140
acaagcgcca gagcagagag ggagagatag aacacacaag gggagagggg tggggaaggg	1200
aaggcgaagg gaggcgcact cgtcccgtct ggtgctctgg tatcgtctcc ccccggcagg	1260
gaaggagtag aaggaaggag agtacgtagg aggaggaggg gaga atg cgt gtc ggc Met Arg Val Gly	1316
ggc ggg cgg gac gac gac gac gag gtg tcc cgg aag ctc aag agc atg Gly Gly Arg Asp Asp Asp Asp Glu Val Ser Arg Lys Leu Lys Ser Met	1364
gac gtg gac aag ctg gag aac ggc ggc agg gag agc ccg cgg ccc Asp Val Asp Lys Leu Glu Asn Gly Gly Arg Glu Glu Ser Pro Arg Pro	1412
gcc gtc aag tac cac ggc tgg aag gcc atg ccg ttc atc atc ggg aac Ala Val Lys Tyr His Gly Trp Lys Ala Met Pro Phe Ile Ile Gly Asn	1460
gag acg ttc gag aag ctg ggg acg cta ggc acg tcg gcg aac ctg ctg Glu Thr Phe Glu Lys Leu Gly Thr Leu Gly Thr Ser Ala Asn Leu Leu	1508
gtg tac ctg acg cag gtg ttc cac atg cgg agc gtg gac gcg gcg acg Val Tyr Leu Thr Gln Val Phe His Met Arg Ser Val Asp Ala Ala Thr	1556
cta ctc aac ggg ctc aac ggc acc acc agc ctc gcc ccc atc atc ggc Leu Leu Asn Gly Leu Asn Gly Thr Thr Ser Leu Ala Pro Ile Ile Gly	1604
gcc ttc ctc tcc gac gcc tac ctc ggc cgc tac ctc gcg ctc gcc atc Ala Phe Leu Ser Asp Ala Tyr Leu Gly Arg Tyr Leu Ala Leu Ala Ile	1652
gcc tcc gtc gcc tcc ctc atc ggc atg ttc ctg ctg acg atg acg gcc Ala Ser Val Ala Ser Leu Ile Gly Met Phe Leu Leu Thr Met Thr Ala	1700
ggc gcg aac agc ctg cac ccg ccg gag tgc agc gtg ggc gag acc tgc Gly Ala Asn Ser Leu His Pro Pro Glu Cys Ser Val Gly Glu Thr Cys	1748
gag aag gcg acg tcg tac cag ggc ggc gtg ctc ttc gtg gcc ttc gcg Glu Lys Ala Thr Ser Tyr Gln Phe Ala Val Leu Phe Val Ala Phe Ala	1796
ttc ctg gtg ctg ggc tcg gcg ggc atc cgc ccc tgc agc atg ccc ttc Phe Leu Val Leu Gly Ser Ala Gly Ile Arg Pro Cys Ser Met Pro Phe	1844
ggc gcc gac cag ttc gac ccc aac acg gag tct ggc aag cgc ggc atc Gly Ala Asp Gln Phe Asp Pro Asn Thr Glu Ser Gly Lys Arg Gly Ile	1892
aac agc ttc ttc aac tgg tac tac ttc acc ttc acg gcc gcc atg atg Asn Ser Phe Phe Asn Trp Tyr Tyr Phe Thr Phe Thr Ala Ala Met Met	1940
atc tcc gcc acc gtc atc atc tac gtg cag agc aac gtg agc tgg ccc Ile Ser Ala Thr Val Ile Ile Tyr Val Gln Ser Asn Val Ser Trp Pro	1988
atc ggc ctg ggc atc ccc acg gca ctc atg ttc ctg gca tgc gtg ctc Ile Gly Leu Gly Ile Pro Thr Ala Leu Met Phe Leu Ala Cys Val Leu	2036
ttc ttc gtg ggc acg cgc cta tac gtg cgg gtg acg ccc gag ggg agc Phe Phe Val Gly Thr Arg Leu Tyr Val Arg Val Thr Pro Glu Gly Ser	2084
ccc ttc acc agc gtc gtg cag gtg cta tcg gcc gcg ctc aag aag cgg Pro Phe Thr Ser Val Val Gln Val Leu Ser Ala Ala Leu Lys Lys Arg	2132
tcg ctg aag cag ccc aag gac ccg aag cag gac ctc ttc gac ccg ccg	2180

PF59082SeqList_PF59082.txt

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cac	acc	agc	gcc	atc	gtc	acc	aag	ttg	gcg	cac	acg	gac	cag	ttc	cg	2228
His	Thr	Ser	Ala	Ile	Val	Thr	Lys	Leu	Ala	His	Thr	Asp	Gln	Phe	Arg	
		295					300					305				
tgc	ctc	gac	aag	gcg	gcc	atc	gtg	gca	tcc	ccg	gac	gag	gtg	cgt	tcc	2276
Cys	Leu	Asp	Lys	Ala	Ala	Ile	Val	Ala	Ser	Pro	Asp	Glu	Val	Arg	Ser	
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ggc	ggc	ggc	gcg	ccc	gcg	gac	ccc	tgg	agg	ctc	tgc	agc	gtg	cag	cag	2324
Gly	Gly	Gly	Ala	Pro	Ala	Asp	Pro	Trp	Arg	Leu	Cys	Ser	Val	Gln	Gln	
	325				330					335					340	
gtg	gag	gag	gtc	aag	tgc	ctc	atc	cg	atc	gtg	ccc	gtc	tgg	tcc	acg	2372
Val	Glu	Glu	Val	Lys	Cys	Leu	Ile	Arg	Ile	Val	Pro	Val	Trp	Ser	Thr	
			345					350						355		
ggg	atc	atc	tac	tac	gtc	gcc	gtg	gtg	cag	cag	tcc	acg	tac	gtg	gtg	2420
Gly	Ile	Ile	Tyr	Tyr	Val	Ala	Val	Val	Gln	Gln	Ser	Thr	Tyr	Val	Val	
			360				365						370			
ctc	tcg	gcg	ctg	cag	tcc	gac	cg	cac	ctc	ggc	ggc	gcc	ggc	ttc	cag	2468
Leu	Ser	Ala	Leu	Gln	Ser	Asp	Arg	His	Leu	Gly	Gly	Ala	Gly	Phe	Gln	
		375				380						385				
atc	ccc	gcc	gcg	tcc	ttc	acc	ctc	ttc	gcc	atg	ctc	gcg	cag	acg	ctg	2516
Ile	Pro	Ala	Ala	Ser	Phe	Thr	Val	Phe	Ala	Met	Leu	Ala	Gln	Thr	Leu	
	390					395					400					
tgg	atc	ccg	ttc	tac	gac	cg	ctc	ctg	ctg	ccc	aag	ctc	cg	aag	ata	2564
Trp	Ile	Pro	Phe	Tyr	Asp	Arg	Leu	Leu	Leu	Pro	Lys	Leu	Arg	Lys	Ile	
	405				410					415					420	
acc	ggc	aag	gaa	gag	ggg	ttc	acg	ctg	ctc	cag	cg	cag	ggc	atc	ggc	2612
Thr	Gly	Lys	Glu	Glu	Gly	Phe	Thr	Leu	Leu	Gln	Arg	Gln	Gly	Ile	Gly	
			425					430						435		
atc	gcg	ctc	tcc	acc	gtc	gcc	atg	gtc	atc	tct	gcc	atc	gtc	gag	gac	2660
Ile	Ala	Leu	Ser	Thr	Val	Ala	Met	Val	Ile	Ser	Ala	Ile	Val	Glu	Asp	
			440				445						450			
cg	cg	cgt	gcc	atc	gcg	ctc	agc	cag	ccg	aca	ctc	gga	acc	acc	atc	2708
Arg	Arg	Arg	Ala	Ile	Ala	Leu	Ser	Gln	Pro	Thr	Leu	Gly	Thr	Thr	Ile	
		455				460						465				
acc	ggc	ggg	gcc	atc	tcg	gcc	atg	tcc	agc	ctg	tgg	atg	gtg	ccg	cag	2756
Thr	Gly	Gly	Ala	Ile	Ser	Ala	Met	Ser	Ser	Leu	Trp	Met	Val	Pro	Gln	
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ctc	atg	atc	ctg	ggc	cta	tcg	gag	gca	ttc	aac	ctc	atc	agc	cag	att	2804
Leu	Met	Ile	Leu	Gly	Leu	Ser	Glu	Ala	Phe	Asn	Leu	Ile	Ser	Gln	Ile	
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gag	ttc	tac	tac	aag	gag	atc	ccg	gag	cac	atg	cg	agc	gtg	gcg	ggg	2852
Glu	Phe	Tyr	Tyr	Lys	Glu	Ile	Pro	Glu	His	Met	Arg	Ser	Val	Ala	Gly	
			505					510						515		
gcg	ctc	gca	ttc	tgc	aac	ctg	gcg	ctc	ggc	aac	tac	ctc	agc	ggc	ttc	2900
Ala	Leu	Ala	Phe	Cys	Asn	Leu	Ala	Leu	Gly	Asn	Tyr	Leu	Ser	Gly	Phe	
			520				525						530			
ctg	gtg	acc	atc	gtg	cac	cg	acc	acg	ggg	tcc	ggg	cag	aac	tgg	ctg	2948
Leu	Val	Thr	Ile	Val	His	Arg	Thr	Thr	Gly	Ser	Gly	Gln	Asn	Trp	Leu	
		535				540						545				
gcg	cag	gac	ctc	aac	aag	ggc	cg	ctc	gac	ctc	ttc	tac	tgg	acc	atc	2996
Ala	Gln	Asp	Leu	Asn	Lys	Gly	Arg	Leu	Asp	Leu	Phe	Tyr	Trp	Thr	Ile	
	550					555					560					
gca	ggc	atc	ggc	gtc	ttt	aat	ctc	atc	tac	ttt	gtc	atc	tgc	gcc	agg	3044
Ala	Gly	Ile	Gly	Val	Phe	Asn	Leu	Ile	Tyr	Phe	Val	Ile	Cys	Ala	Arg	
	565				570				575						580	
tgg	tac	agg	ttc	aag	ggg	acc	agc	aac	tgatccgcca	ggttcatggt						3091
Trp	Tyr	Arg	Phe	Lys	Gly	Thr	Ser	Asn								
			585													
tg	gacaggtt	ggtggggttg	gataattatg	ttatggcctc	tctctttttt	gtttattact										3151
ttataccttt	gttactggtc	ctttcatttg	aatctatagg	atgatcaagt	ggctgatgaa											3211
agaggagaaa	gaaacaaaat	agttggtttc	ttgtaatttg	taagtgggta	aactgaaata											3271
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3334

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 <213> Zea mays

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 35 40 45
 Ile Ile Gly Asn Glu Thr Phe Glu Lys Leu Gly Thr Leu Gly Thr Ser
 50 55 60
 Ala Asn Leu Leu Val Tyr Leu Thr Gln Val Phe His Met Arg Ser Val
 65 70 75 80
 Asp Ala Ala Thr Leu Leu Asn Gly Leu Asn Gly Thr Thr Ser Leu Ala
 85 90 95
 Pro Ile Ile Gly Ala Phe Leu Ser Asp Ala Tyr Leu Gly Arg Tyr Leu
 100 105 110
 Ala Leu Ala Ile Ala Ser Val Ala Ser Leu Ile Gly Met Phe Leu Leu
 115 120 125
 Thr Met Thr Ala Gly Ala Asn Ser Leu His Pro Pro Glu Cys Ser Val
 130 135 140
 Gly Glu Thr Cys Glu Lys Ala Thr Ser Tyr Gln Phe Ala Val Leu Phe
 145 150 155 160
 Val Ala Phe Ala Phe Leu Val Leu Gly Ser Ala Gly Ile Arg Pro Cys
 165 170 175
 Ser Met Pro Phe Gly Ala Asp Gln Phe Asp Pro Asn Thr Glu Ser Gly
 180 185 190
 Lys Arg Gly Ile Asn Ser Phe Phe Asn Trp Tyr Tyr Phe Thr Phe Thr
 195 200 205
 Ala Ala Met Met Ile Ser Ala Thr Val Ile Ile Tyr Val Gln Ser Asn
 210 215 220
 Val Ser Trp Pro Ile Gly Leu Gly Ile Pro Thr Ala Leu Met Phe Leu
 225 230 235 240
 Ala Cys Val Leu Phe Phe Val Gly Thr Arg Leu Tyr Val Arg Val Thr
 245 250 255
 Pro Glu Gly Ser Pro Phe Thr Ser Val Val Gln Val Leu Ser Ala Ala
 260 265 270
 Leu Lys Lys Arg Ser Leu Lys Gln Pro Lys Asp Pro Lys Gln Asp Leu
 275 280 285
 Phe Asp Pro Pro His Thr Ser Ala Ile Val Thr Lys Leu Ala His Thr
 290 295 300
 Asp Gln Phe Arg Cys Leu Asp Lys Ala Ala Ile Val Ala Ser Pro Asp
 305 310 315 320
 Glu Val Arg Ser Gly Gly Gly Ala Pro Ala Asp Pro Trp Arg Leu Cys
 325 330 335
 Ser Val Gln Gln Val Glu Glu Val Lys Cys Leu Ile Arg Ile Val Pro
 340 345 350
 Val Trp Ser Thr Gly Ile Ile Tyr Tyr Val Ala Val Val Gln Gln Ser
 355 360 365
 Thr Tyr Val Val Leu Ser Ala Leu Gln Ser Asp Arg His Leu Gly Gly
 370 375 380
 Ala Gly Phe Gln Ile Pro Ala Ala Ser Phe Thr Val Phe Ala Met Leu
 385 390 395 400
 Ala Gln Thr Leu Trp Ile Pro Phe Tyr Asp Arg Leu Leu Leu Pro Lys
 405 410 415
 Leu Arg Lys Ile Thr Gly Lys Glu Glu Gly Phe Thr Leu Leu Gln Arg
 420 425 430
 Gln Gly Ile Gly Ile Ala Leu Ser Thr Val Ala Met Val Ile Ser Ala
 435 440 445
 Ile Val Glu Asp Arg Arg Arg Ala Ile Ala Leu Ser Gln Pro Thr Leu

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 Gly Thr Thr Ile Thr Gly Gly Ala Ile Ser Ala Met Ser Ser Leu Trp
 465 470 475 480
 Met Val Pro Gln Leu Met Ile Leu Gly Leu Ser Glu Ala Phe Asn Leu
 485 490 495
 Ile Ser Gln Ile Glu Phe Tyr Tyr Lys Glu Ile Pro Glu His Met Arg
 500 505 510
 Ser Val Ala Gly Ala Leu Ala Phe Cys Asn Leu Ala Leu Gly Asn Tyr
 515 520 525
 Leu Ser Gly Phe Leu Val Thr Ile Val His Arg Thr Thr Gly Ser Gly
 530 535 540
 Gln Asn Trp Leu Ala Gln Asp Leu Asn Lys Gly Arg Leu Asp Leu Phe
 545 550 555 560
 Tyr Trp Thr Ile Ala Gly Ile Gly Val Phe Asn Leu Ile Tyr Phe Val
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 Ile Cys Ala Arg Trp Tyr Arg Phe Lys Gly Thr Ser Asn
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120

ggcgcgctcc tctgcctcg cctgcctcc cccggggaag aagaggagga gagggagctg

180

agcagcagcc ggccgacgcg gga atg ctc gtc ggc ggc ggg cgg gac gac gag
 Met Leu Val Gly Gly Gly Arg Asp Asp Glu
 1 5 10

233

gag gtg ctc cgg aag ctc aag agc atg gac gtg gac aag ctg gag aac
 Glu Val Leu Arg Lys Leu Lys Ser Met Asp Val Asp Lys Leu Glu Asn
 15 20 25

281

ggc gga ggc ggc ggc gac gcg gag agc ccg cgc ccc gtc gtc aag tac
 Gly Gly Gly Gly Gly Asp Ala Glu Ser Pro Arg Pro Val Val Lys Tyr
 30 35 40

329

cac ggc tgg aag gcc atg ccc ttc atc atc ggg aac gag acg ttc gag
 His Gly Trp Lys Ala Met Pro Phe Ile Ile Gly Asn Glu Thr Phe Glu
 45 50 55

377

aag ctg ggc acg ctg ggc acg tcg gcc aac ctg ctg gtg tac ctg acg
 Lys Leu Gly Thr Leu Gly Thr Ser Ala Asn Leu Leu Val Tyr Leu Thr
 60 65 70

425

cag gtg ttc cac atg cgg agc gtg gac gcg gcc acg ctg ctc aac ggc
 Gln Val Phe His Met Arg Ser Val Asp Ala Ala Thr Leu Leu Asn Gly
 75 80 85 90

473

ctc aac ggc acc acc agc ctc gcc ccc atc gtc ggc gcc ttc ctc tcc
 Leu Asn Gly Thr Thr Ser Leu Ala Pro Ile Val Gly Ala Phe Leu Ser
 95 100 105

521

gac gcc tac ctc ggc cgc tac ctc gcg ctc gcc atc gcc tcc atc gcc

569

PF59082SeqList_PF59082.txt

Asp	Ala	Tyr	Leu	Gly	Arg	Tyr	Leu	Ala	Ile	Ala	Ser	Ile	Ala	
tcc	ctc	atc	ggc	atg	ttc	ctg	ctg	acg	ctt	acg	gcc	ggc	gac	agc
Ser	Leu	Ile	Gly	Met	Phe	Leu	Leu	Thr	Leu	Thr	Ala	Gly	Ala	Ser
		125					130					135		
ctg	cac	ccg	gaa	tgc	ggc	gtg	ggc	gag	gcc	tgc	gag	aag	gac	acg
Leu	His	Pro	Pro	Glu	Cys	Gly	Val	Gly	Glu	Ala	Cys	Glu	Lys	Thr
	140					145				150				
tcg	tac	cag	ttc	gcg	gtg	ctc	ttc	gtc	gcc	ttc	gag	ttc	ctg	ctg
Ser	Tyr	Gln	Phe	Ala	Val	Leu	Phe	Val	Ala	Phe	Ala	Phe	Leu	Val
155					160				165					170
ggc	tcg	gag	ggg	atc	cgc	ccc	tgc	agc	atg	ccc	ttc	ggc	gac	cag
Gly	Ser	Ala	Gly	Ile	Arg	Pro	Cys	Ser	Met	Pro	Phe	Gly	Ala	Asp
			175					180					185	
ttc	gac	ccc	cac	acg	gag	tcc	ggc	aag	cgc	ggc	atc	aac	agc	ttc
Phe	Asp	Pro	His	Thr	Glu	Ser	Gly	Lys	Arg	Gly	Ile	Asn	Ser	Phe
			190					195				200		
aac	tgg	tac	tac	ttc	acg	ttc	acg	gag	gcc	atg	atg	atc	tcc	gcc
Asn	Trp	Tyr	Tyr	Phe	Thr	Phe	Thr	Ala	Ala	Met	Met	Ile	Ser	Ala
	205						210					215		
gtc	atc	atc	tac	gtg	cag	agc	aac	gtg	agc	tgg	ccc	atc	ggg	ctg
Val	Ile	Ile	Tyr	Val	Gln	Ser	Asn	Val	Ser	Trp	Pro	Ile	Gly	Leu
	220					225					230			
atc	ccc	acg	gag	ctc	atg	ttc	ctg	gcc	tgc	gtg	ctc	ttc	ttc	atg
Ile	Pro	Thr	Ala	Leu	Met	Phe	Leu	Ala	Cys	Val	Leu	Phe	Phe	Met
235					240				245					250
acg	cgc	ctc	tac	gtg	cgg	gtg	acg	ccc	gag	ggg	agc	ccc	ttc	acc
Thr	Arg	Leu	Tyr	Val	Arg	Val	Thr	Pro	Glu	Gly	Ser	Pro	Phe	Thr
			255					260					265	
gtc	gtg	cag	gtg	ctg	tcg	gcc	gag	ctc	aag	cgg	tcg	ctg	aag	cag
Val	Val	Gln	Val	Leu	Ser	Ala	Ala	Leu	Lys	Lys	Arg	Ser	Leu	Lys
			270					275					280	
ccc	aag	gac	ccg	aag	cag	gac	ctc	ttc	gac	ccg	ccg	cac	acc	agc
Pro	Lys	Asp	Pro	Lys	Gln	Asp	Leu	Phe	Asp	Pro	Pro	His	Thr	Ser
		285					290					295		
atc	gtc	acc	cag	ctc	gag	cac	acg	gac	cag	ttc	cgc	tgc	ctc	gac
Ile	Val	Thr	Gln	Leu	Ala	His	Thr	Asp	Gln	Phe	Arg	Cys	Leu	Asp
	300					305					310			
gag	gcc	atc	gtg	gag	tcc	cag	gac	gag	ttg	cgc	ccc	ggc	ggc	gcc
Ala	Ala	Ile	Val	Ala	Ser	Gln	Asp	Glu	Leu	Arg	Pro	Gly	Gly	Ala
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ccc	gag	gac	ccc	tgg	agg	ctc	tgc	agc	gtg	cag	cag	gtg	gag	gag
Pro	Ala	Asp	Pro	Trp	Arg	Leu	Cys	Ser	Val	Gln	Gln	Val	Glu	Glu
				335					340				345	
aag	tgc	ctc	atc	cgc	atc	gtg	ccc	gtc	tgg	tcc	acg	ggg	atc	tac
Lys	Cys	Leu	Ile	Arg	Ile	Val	Pro	Val	Trp	Ser	Thr	Gly	Ile	Ile
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Tyr	Val	Ala	Val	Val	Gln	Gln	Ser	Thr	Tyr	Val	Val	Leu	Ser	Ala
		365					370					375		
cag	tcc	gac	cgc	cac	ctc	ggc	ggc	gcc	ggc	ttc	cag	atc	ccc	gag
Gln	Ser	Asp	Arg	His	Leu	Gly	Gly	Ala	Gly	Phe	Gln	Ile	Pro	Ala
	380					385					390			
tcc	ttc	acc	gtc	ttc	gcc	atg	ctc	gag	cag	acg	ctg	tgg	atc	ccg
Ser	Phe	Thr	Val	Phe	Ala	Met	Leu	Ala	Gln	Thr	Leu	Trp	Ile	Pro
395					400				405					410
tac	gac	cgc	ctc	ctg	ctg	ccc	aag	ctc	cgg	aag	ata	acc	ggc	aag
Tyr	Asp	Arg	Leu	Leu	Leu	Pro	Lys	Leu	Arg	Lys	Ile	Thr	Gly	Lys
			415						420				425	
gag	ggg	ttc	acg	ctg	ctc	cag	cgc	cag	ggc	atc	ggc	atc	gag	ctc
Glu	Gly	Phe	Thr	Leu	Leu	Gln	Arg	Gln	Gly	Ile	Gly	Ile	Ala	Leu
			430					435				440		
acc	gtc	gcc	atg	gtc	atc	tct	gcc	atc	gtc	gag	gac	cgg	cgc	cggt
Thr	Val	Ala	Met	Val	Ile	Ser	Ala	Ile	Val	Glu	Asp	Arg	Arg	Ala
		445					450					455		
atc	gag	ctc	agc	cag	ccg	acg	ctc	gga	acc	acc	atc	acc	ggc	ggg
Ile	Ala	Leu	Ser	Gln	Pro	Thr	Leu	Gly	Thr	Thr	Ile	Thr	Gly	Gly
	460					465					470			
atc	tcg	gcc	atg	tcc	agc	ctg	tgg	atg	gtg	ccg	cag	ctc	atg	atc
														ctg

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495 500 505
aag gag atc ccg gag cac atg cgg agc gtg gcg ggg gcg ctc gca ttc 1769
Lys Glu Ile Pro Glu His Met Arg Ser Val Ala Gly Ala Leu Ala Phe
510 515 520
tgc aac ctg gca ctc ggc aac tac ctc agt ggc ttc ctg gtg acc atc 1817
Cys Asn Leu Ala Leu Gly Asn Tyr Leu Ser Gly Phe Leu Val Thr Ile
525 530 535
gtg cac cgg acc acg ggg tcc ggg cag aac tgg ctg gcg cag gac ctc 1865
Val His Arg Thr Thr Gly Ser Gly Gln Asn Trp Leu Ala Gln Asp Leu
540 545 550
aac aag ggc cgc ctc gac ctc ttc tac tgg acc atc gca ggc atc ggc 1913
Asn Lys Gly Arg Leu Asp Leu Phe Tyr Trp Thr Ile Ala Gly Ile Gly
555 560 565 570
gtc ttt aat ctc atc tac ttc gtc atc tgc gcc agg tgg tac agg ttc 1961
Val Phe Asn Leu Ile Tyr Phe Val Ile Cys Ala Arg Trp Tyr Arg Phe
575 580 585
aag gga acc agc aac tgatccgccg aggtgacat atatcgtctc tctcatggtt 2016
Lys Gly Thr Ser Asn
590
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ttataaccttt gttactggtc ctttcatttg aatctatagg atgatcaagt ggctgatgaa 2136

agaggagaaa gaaacaaaat agttggtttt ttgtaatttg taagtgggta aactgaaata 2196

caaatggatg taagcttgaa tgaaagttta gcacagttac cgaccagctt atgattgccca 2256

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35 40 45
Pro Phe Ile Ile Gly Asn Glu Thr Phe Glu Lys Leu Gly Thr Leu Gly
50 55 60
Thr Ser Ala Asn Leu Leu Val Tyr Leu Thr Gln Val Phe His Met Arg
65 70 75 80
Ser Val Asp Ala Ala Thr Leu Leu Asn Gly Leu Asn Gly Thr Thr Ser
85 90 95
Leu Ala Pro Ile Val Gly Ala Phe Leu Ser Asp Ala Tyr Leu Gly Arg
100 105 110
Tyr Leu Ala Leu Ala Ile Ala Ser Ile Ala Ser Leu Ile Gly Met Phe
115 120 125
Leu Leu Thr Leu Thr Ala Gly Ala Asp Ser Leu His Pro Pro Glu Cys
130 135 140
Gly Val Gly Glu Ala Cys Glu Lys Ala Thr Ser Tyr Gln Phe Ala Val
145 150 155 160
Leu Phe Val Ala Phe Ala Phe Leu Val Leu Gly Ser Ala Gly Ile Arg
165 170 175
Pro Cys Ser Met Pro Phe Gly Ala Asp Gln Phe Asp Pro His Thr Glu
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PF59082SeqList_PF59082.txt

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 210 215 220
 Ser Asn Val Ser Trp Pro Ile Gly Leu Gly Ile Pro Thr Ala Leu Met
 225 230 235 240
 Phe Leu Ala Cys Val Leu Phe Phe Met Gly Thr Arg Leu Tyr Val Arg
 245 250 255
 Val Thr Pro Glu Gly Ser Pro Phe Thr Ser Val Val Gln Val Leu Ser
 260 265 270
 Ala Ala Leu Lys Lys Arg Ser Leu Lys Gln Pro Lys Asp Pro Lys Gln
 275 280 285
 Asp Leu Phe Asp Pro Pro His Thr Ser Ala Ile Val Thr Gln Leu Ala
 290 295 300
 His Thr Asp Gln Phe Arg Cys Leu Asp Lys Ala Ala Ile Val Ala Ser
 305 310 315 320
 Gln Asp Glu Leu Arg Pro Gly Gly Ala Ala Pro Ala Asp Pro Trp Arg
 325 330 335
 Leu Cys Ser Val Gln Gln Val Glu Glu Val Lys Cys Leu Ile Arg Ile
 340 345 350
 Val Pro Val Trp Ser Thr Gly Ile Ile Tyr Tyr Val Ala Val Val Gln
 355 360 365
 Gln Ser Thr Tyr Val Val Leu Ser Ala Leu Gln Ser Asp Arg His Leu
 370 375 380
 Gly Gly Ala Gly Phe Gln Ile Pro Ala Ala Ser Phe Thr Val Phe Ala
 385 390 395 400
 Met Leu Ala Gln Thr Leu Trp Ile Pro Phe Tyr Asp Arg Leu Leu Leu
 405 410 415
 Pro Lys Leu Arg Lys Ile Thr Gly Lys Glu Glu Gly Phe Thr Leu Leu
 420 425 430
 Gln Arg Gln Gly Ile Gly Ile Ala Leu Ser Thr Val Ala Met Val Ile
 435 440 445
 Ser Ala Ile Val Glu Asp Arg Arg Arg Ala Ile Ala Leu Ser Gln Pro
 450 455 460
 Thr Leu Gly Thr Thr Ile Thr Gly Gly Ala Ile Ser Ala Met Ser Ser
 465 470 475 480
 Leu Trp Met Val Pro Gln Leu Met Ile Leu Gly Leu Ser Glu Ala Phe
 485 490 495
 Asn Leu Ile Ser Gln Ile Glu Phe Tyr Lys Glu Ile Pro Glu His
 500 505 510
 Met Arg Ser Val Ala Gly Ala Leu Ala Phe Cys Asn Leu Ala Leu Gly
 515 520 525
 Asn Tyr Leu Ser Gly Phe Leu Val Thr Ile Val His Arg Thr Thr Gly
 530 535 540
 Ser Gly Gln Asn Trp Leu Ala Gln Asp Leu Asn Lys Gly Arg Leu Asp
 545 550 555 560
 Leu Phe Tyr Trp Thr Ile Ala Gly Ile Gly Val Phe Asn Leu Ile Tyr
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 Phe Val Ile Cys Ala Arg Trp Tyr Arg Phe Lys Gly Thr Ser Asn
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 <212> DNA
 <213> Zea mays

<220>
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<400> 242
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 Lys Gly Asn Pro Ala Val Lys Lys Gly Thr Gly Asn Trp Arg Ala Cys
 20 25 30
 ccc tac atc ctc gcg aac gag tgc tgc gag agg ctg gct tac tat ggc 144
 Pro Tyr Ile Leu Ala Asn Glu Cys Cys Glu Arg Leu Ala Tyr Tyr Gly
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atg	agc	acc	aac	ctg	gtg	aac	tac	atg	aag	acc	cga	ctt	ggc	cag	gtg	192
Met	Ser	Thr	Asn	Leu	Val	Asn	Tyr	Met	Lys	Thr	Arg	Leu	Gly	Gln	Val	
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aac	tcc	gtt	gcc	tcc	aac	aac	gtc	acc	aac	tgg	caa	ggg	acg	tgc	tac	240
Asn	Ser	Val	Ala	Ser	Asn	Asn	Val	Thr	Asn	Trp	Gln	Gly	Thr	Cys	Tyr	
65					70				75						80	
atc	acg	ccg	ctc	atc	ggc	gcc	ttc	ttc	gcc	gac	gcg	tac	atg	ggg	agg	288
Ile	Thr	Pro	Leu	Ile	Gly	Ala	Phe	Phe	Ala	Asp	Ala	Tyr	Met	Gly	Arg	
				85					90					95		
ttc	tgg	acc	atc	gcc	atc	ttc	atg	atc	atc	tac	att	ttc	ggc	ctg	gcg	336
Phe	Trp	Thr	Ile	Ala	Ile	Phe	Met	Ile	Ile	Tyr	Ile	Phe	Gly	Leu	Ala	
			100				105						110			
ctg	ctg	acg	atg	gct	tcg	tcg	gtg	aag	ggg	ctg	gtg	cct	acg	tcg	tgc	384
Leu	Leu	Thr	Met	Ala	Ser	Ser	Val	Lys	Gly	Leu	Val	Pro	Thr	Ser	Cys	
		115					120					125				
ggc	gac	aag	gat	gtg	tgc	cac	ccg	acg	gac	gcg	cag	ggc	ggc	gtg	gtg	432
Gly	Asp	Lys	Asp	Val	Cys	His	Pro	Thr	Asp	Ala	Gln	Ala	Ala	Val	Val	
	130					135					140					
ttc	gtg	gcg	ctg	tac	ctc	atc	gcg	ctg	ggc	acg	ggc	ggg	atc	aag	ccg	480
Phe	Val	Ala	Leu	Tyr	Leu	Ile	Ala	Leu	Gly	Thr	Gly	Gly	Ile	Lys	Pro	
145					150				155						160	
tgc	gtg	tcc	tcc	ttc	ggc	gcc	gac	cag	ttc	gac	gag	aac	gac	gag	cgg	528
Cys	Val	Ser	Ser	Phe	Gly	Ala	Asp	Gln	Phe	Asp	Glu	Asn	Asp	Glu	Arg	
				165					170					175		
gag	aag	aag	agc	aag	agc	tcc	ttc	ttc	aac	tgg	ttc	tac	ttc	tcc	atc	576
Glu	Lys	Lys	Ser	Lys	Ser	Ser	Phe	Phe	Asn	Trp	Phe	Tyr	Phe	Ser	Ile	
			180				185						190			
aac	atc	ggc	ggc	ctg	gtg	gcg	tcc	aca	gtg	ctg	gtg	tac	gtg	cag	acg	624
Asn	Ile	Gly	Ala	Leu	Val	Ala	Ser	Thr	Val	Leu	Val	Tyr	Val	Gln	Thr	
		195					200					205				
cac	gtg	ggc	tgg	ggc	tgg	ggc	ttc	ggc	atc	ccc	gcc	gtg	gtc	atg	gcc	672
His	Val	Gly	Trp	Gly	Trp	Gly	Phe	Gly	Ile	Pro	Ala	Val	Val	Met	Ala	
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Ile	Ala	Val	Gly	Ser	Phe	Phe	Val	Gly	Thr	Pro	Leu	Tyr	Arg	His	Gln	
225					230					235					240	
aag	ccc	ggg	ggc	agc	ccg	ctg	acg	cgc	atc	gcg	cag	gtg	ctc	gtc	gcg	768
Lys	Pro	Gly	Gly	Ser	Pro	Leu	Thr	Arg	Ile	Ala	Gln	Val	Leu	Val	Ala	
				245					250					255		
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Cys	Ala	Arg	Lys	Trp	Asn	Val	Ala	Val	Pro	Ala	Asp	Lys	Ser	Arg	Leu	
			260				265						270			
cac	gag	acg	gtg	gac	ggg	gag	tcc	gtc	atc	gag	ggg	agc	cgc	aag	ctg	864
His	Glu	Thr	Val	Asp	Gly	Glu	Ser	Val	Ile	Glu	Gly	Ser	Arg	Lys	Leu	
		275					280					285				
gag	cac	tcg	gag	cag	ctg	gcg	tgc	ctc	gac	agg	gct	gcc	gtg	gtg	acg	912
Glu	His	Ser	Glu	Gln	Leu	Ala	Cys	Leu	Asp	Arg	Ala	Ala	Val	Val	Thr	
	290					295					300					
gcc	gag	gac	ggc	gcg	gag	gcg	agc	ccg	tgg	cgc	ctg	tgc	tcg	gtg	acg	960
Ala	Glu	Asp	Gly	Ala	Glu	Ala	Ser	Pro	Trp	Arg	Leu	Cys	Ser	Val	Thr	
305					310					315					320	
cag	gtg	gag	gag	ctc	aag	agc	gtg	atc	cgg	ctg	ctg	ccc	atc	tgg	gcc	1008
Gln	Val	Glu	Glu	Leu	Lys	Ser	Val	Ile	Arg	Leu	Leu	Pro	Ile	Trp	Ala	
				325					330					335		
agc	ggg	atc	gtg	ttc	gcg	gcg	gtg	tac	tcg	cag	atg	agc	acc	atg	ttc	1056
Ser	Gly	Ile	Val	Phe	Ala	Ala	Val	Tyr	Ser	Gln	Met	Ser	Thr	Met	Phe	
			340				345						350			
gtg	ctg	cag	ggt	aac	acg	ctg	gac	cag	agc	atg	ggg	ccc	cgg	ttc	aag	1104
Val	Leu	Gln	Gly	Asn	Thr	Leu	Asp	Gln	Ser	Met	Gly	Pro	Arg	Phe	Lys	
		355					360					365				
atc	ccc	tcg	gcg	acg	ctg	tcc	atg	gtg	gac	act	atc	agc	gtc	atc	gtc	1152
Ile	Pro	Ser	Ala	Thr	Leu	Ser	Met	Val	Asp	Thr	Ile	Ser	Val	Ile	Val	
	370					375					380					
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Trp	Val	Pro	Val	Tyr	Asp	Arg	Ala	Ile	Val	Pro	Leu	Val	Arg	Ser	Tyr	
385					390				395						400	
acc	ggg	agg	ccg	cgc	ggg	ttc	acg	cag	ctg	cag	cgc	atg	ggc	atc	ggc	1248
Thr	Gly	Arg	Pro	Arg	Gly	Phe	Thr	Gln	Leu	Gln	Arg	Met	Gly	Ile	Gly	

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gtg	cgg	ctg	cgc	435	gcc	atc	gcg	cgg	cac	ggc	ctg	tac	ggc	gag	aac	gac
Val	Arg	Leu	Arg	440	Ala	Ile	Ala	Arg	His	Gly	Leu	Tyr	Gly	Glu	Asn	Asp
atc	gtg	ccc	atc	455	tcc	atc	tcc	tgg	cag	ata	ccg	cag	tac	ttc	atc	atc
Ile	Val	Pro	Ile	470	Ser	Ile	Phe	Trp	Gln	Ile	Pro	Gln	Tyr	Phe	Ile	Ile
gga	tgc	gcg	gag	485	gtg	tcc	acc	gtg	ggg	cag	ctg	gag	ttc	ttc	tac	1440
Gly	Cys	Ala	Glu	495	Val	Phe	Thr	Phe	Val	Gly	Gln	Leu	Glu	Phe	Phe	Tyr
gac	cag	gcg	ccc	510	gac	gcc	atg	agg	agc	atg	tgc	tcc	gcg	ctg	tcg	ctc
Asp	Gln	Ala	Pro	525	Asp	Ala	Met	Arg	Ser	Met	Cys	Ser	Ala	Leu	Ser	Leu
acc	acc	gtc	gcg	540	ctc	ggc	aac	tac	ctc	agc	acg	gtc	ctg	gtg	acc	atc
Thr	Thr	Val	Ala	555	Leu	Gly	Asn	Tyr	Leu	Ser	Thr	Val	Leu	Val	Thr	Ile
gtc	acc	cac	atc	570	acc	agg	cac	ggc	cgc	atc	ggg	tgg	atc	ccg	gag	1584
Val	Thr	His	Ile	580	Thr	Arg	His	Gly	Arg	Ile	Gly	Trp	Ile	Pro	Glu	
aac	ctc	aac	cgc	600	ggc	cac	ctc	gac	tac	ttc	ttc	tgg	ctg	ctc	gcc	gtg
Asn	Leu	Asn	Arg	615	Gly	His	Leu	Asp	Tyr	Phe	Phe	Trp	Leu	Leu	Ala	Val
ctc	agc	ctt	ctc	630	aac	tcc	ctt	gcc	tac	ctc	gtc	atc	gcc	agc	tgg	tac
Leu	Ser	Leu	Leu	645	Asn	Phe	Leu	Ala	Tyr	Leu	Val	Ile	Ala	Ser	Trp	Tyr
aag	tac	aag	aag	660	acc	gcc	gat	gat	tac	cct	ggc	gcc	aaa	ggg	gag	cac
Lys	Tyr	Lys	Lys	675	Thr	Ala	Asp	Asp	Tyr	Pro	Gly	Ala	Lys	Gly	Glu	His
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 <212> PRT
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	Pro	Tyr	Ile	Leu	Ala	Asn	Glu	Cys	Cys	Glu	Arg	Leu	Ala	Tyr	Tyr	Gly
	Met	Ser	Thr	Asn	Leu	Val	Asn	Tyr	Met	Lys	Thr	Arg	Leu	Gly	Gln	Val
	Asn	Ser	Val	Ala	Ser	Asn	Val	Thr	Asn	Trp	Gln	Gly	Thr	Cys	Tyr	
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	Phe	Trp	Thr	Ile	Ala	Ile	Phe	Met	Ile	Ile	Tyr	Ile	Phe	Gly	Leu	Ala
	Leu	Leu	Thr	Met	Ala	Ser	Ser	Val	Lys	Gly	Leu	Val	Pro	Thr	Ser	Cys
	Gly	Asp	Lys	Asp	Val	Cys	His	Pro	Thr	Asp	Ala	Gln	Ala	Ala	Val	Val
	Phe	Val	Ala	Leu	Tyr	Leu	Ile	Ala	Leu	Gly	Thr	Gly	Gly	Ile	Lys	Pro
145	Cys	Val	Ser	Ser	Phe	Gly	Ala	Asp	Gln	Phe	Asp	Glu	Asn	Asp	Glu	Arg
	Glu	Lys	Lys	Ser	Lys	Ser	Ser	Phe	Phe	Asn	Trp	Phe	Tyr	Phe	Ser	Ile
	Asn	Ile	Gly	Ala	Leu	Val	Ala	Ser	Thr	Val	Leu	Val	Tyr	Val	Gln	Thr
	His	Val	Gly	Trp	Gly	Trp	Gly	Phe	Gly	Ile	Pro	Ala	Val	Val	Met	Ala
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PF59082SeqList_PF59082.txt

Ile Ala Val Gly Ser Phe Phe Val Gly Thr Pro Leu Tyr Arg His Gln
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 Lys Pro Gly Gly Ser Pro Leu Thr Arg Ile Ala Gln Val Leu Val Ala
 245 250 255
 Cys Ala Arg Lys Trp Asn Val Ala Val Pro Ala Asp Lys Ser Arg Leu
 260 265 270
 His Glu Thr Val Asp Gly Glu Ser Val Ile Glu Gly Ser Arg Lys Leu
 275 280 285
 Glu His Ser Glu Gln Leu Ala Cys Leu Asp Arg Ala Ala Val Val Thr
 290 295 300
 Ala Glu Asp Gly Ala Glu Ala Ser Pro Trp Arg Leu Cys Ser Val Thr
 305 310 315 320
 Gln Val Glu Glu Leu Lys Ser Val Ile Arg Leu Leu Pro Ile Trp Ala
 325 330 335
 Ser Gly Ile Val Phe Ala Ala Val Tyr Ser Gln Met Ser Thr Met Phe
 340 345 350
 Val Leu Gln Gly Asn Thr Leu Asp Gln Ser Met Gly Pro Arg Phe Lys
 355 360 365
 Ile Pro Ser Ala Thr Leu Ser Met Val Asp Thr Ile Ser Val Ile Val
 370 375 380
 Trp Val Pro Val Tyr Asp Arg Ala Ile Val Pro Leu Val Arg Ser Tyr
 385 390 395 400
 Thr Gly Arg Pro Arg Gly Phe Thr Gln Leu Gln Arg Met Gly Ile Gly
 405 410 415
 Leu Val Val Ser Ile Phe Ser Met Val Ala Ala Gly Val Leu Asp Ile
 420 425 430
 Val Arg Leu Arg Ala Ile Ala Arg His Gly Leu Tyr Gly Glu Asn Asp
 435 440 445
 Ile Val Pro Ile Ser Ile Phe Thr Phe Val Gly Gln Leu Glu Phe Phe Tyr
 450 455 460 465 470 475 480
 Gly Cys Ala Glu Val Phe Thr Phe Val Gly Gln Leu Glu Phe Phe Tyr
 465 470 475 480
 Asp Gln Ala Pro Asp Ala Met Arg Ser Met Cys Ser Ala Leu Ser Leu
 485 490 495
 Thr Thr Val Ala Leu Gly Asn Tyr Leu Ser Thr Val Leu Val Thr Ile
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 Val Thr His Ile Thr Thr Arg His Gly Arg Ile Gly Trp Ile Pro Glu
 515 520 525
 Asn Leu Asn Arg Gly His Leu Asp Tyr Phe Phe Trp Leu Leu Ala Val
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 Leu Ser Leu Leu Asn Phe Leu Ala Tyr Leu Val Ile Ala Ser Trp Tyr
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 Gly Thr Glu His
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<212> DNA

<213> Triticum aestivum

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<222> (85)..(1908)

<400> 244

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 Met Asp Ala Pro Arg Gln Gln Gln Glu

111

gag gag cgc aag gag aag acg aag gcg gtg aag gcc gtc tcc gag gag
 Glu Glu Arg Lys Glu Lys Thr Lys Ala Val Lys Ala Val Ser Glu Glu
 10 15 20 25

159

gcc ggg tcg tcg tcc tcg gac acc ggc gac gat ggc gag gag gag gcg
 Ala Gly Ser Ser Ser Ser Asp Thr Gly Asp Asp Gly Glu Glu Glu Ala
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207

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Gly	Asn	Glu	Thr	Phe	Glu	Lys	Leu	Gly	Thr	Ile	Gly	Thr	Leu	Ser	Asn	
		60					65					70				
atg	ctg	gtg	tac	ctg	aca	acg	gtg	tac	cac	atg	ccg	agc	gtc	aac	gcc	351
Met	Leu	Val	Tyr	Leu	Thr	Thr	Val	Tyr	His	Met	Pro	Ser	Val	Asn	Ala	
	75					80					85					
gcc	acc	ctc	ctc	aat	gta	ttc	tcc	ggc	acc	agc	aac	ctc	gcc	act	gtc	399
Ala	Thr	Leu	Leu	Asn	Val	Phe	Ser	Gly	Thr	Ser	Asn	Leu	Ala	Thr	Val	
	90				95					100					105	
ttc	ggc	gcc	tac	gtg	agc	gac	acc	tac	ctc	ggc	cgc	tac	acc	acc	atc	447
Phe	Gly	Ala	Tyr	Val	Ser	Asp	Thr	Tyr	Leu	Gly	Arg	Tyr	Thr	Thr	Ile	
				110					115					120		
gcc	gcc	gcc	acc	atg	tcc	tcc	ttc	ata	ggc	atg	ctc	atc	ctc	acg	ctc	495
Ala	Ala	Ala	Thr	Met	Ser	Ser	Phe	Ile	Gly	Met	Leu	Ile	Leu	Thr	Leu	
			125					130					135			
acg	gcc	gct	atc	cac	acc	ctc	cat	cct	ccc	gcg	tgc	aac	gcg	tcc	aag	543
Thr	Ala	Ala	Ile	His	Thr	Leu	His	Pro	Pro	Ala	Cys	Asn	Ala	Ser	Lys	
		140					145					150				
ggg	caa	cat	tgt	gag	ggt	ccc	act	ggc	tcc	cag	ctc	gcc	gcc	atc	cta	591
Gly	Gln	His	Cys	Glu	Gly	Pro	Thr	Gly	Ser	Gln	Leu	Ala	Ala	Ile	Leu	
	155					160					165					
gtg	tcc	ttc	ttc	ttc	cta	gtc	atc	ggt	gct	gga	ggc	atc	cgg	ccc	tgc	639
Val	Ser	Phe	Phe	Phe	Leu	Val	Ile	Gly	Ala	Gly	Gly	Ile	Arg	Pro	Cys	
	170				175					180					185	
aac	ctt	gcc	ttt	ggg	gcc	gac	cag	ttc	aac	cca	cac	act	gct	gat	ggt	687
Asn	Leu	Ala	Phe	Gly	Ala	Asp	Gln	Phe	Asn	Pro	His	Thr	Ala	Asp	Gly	
				190					195					200		
cgc	cgc	ggc	atc	gcc	agc	ttc	ttc	aac	tgg	tac	tac	ttc	acc	ttc	aca	735
Arg	Arg	Gly	Ile	Ala	Ser	Phe	Phe	Asn	Trp	Tyr	Tyr	Phe	Thr	Phe	Thr	
			205					210					215			
gtc	gcc	atg	atg	ctc	tcg	gca	acc	gtc	atc	atc	tac	ctc	cag	agc	aac	783
Val	Ala	Met	Met	Leu	Ser	Ala	Thr	Val	Ile	Ile	Tyr	Leu	Gln	Ser	Asn	
		220					225					230				
gtt	aat	tgg	gcg	cta	ggg	ctc	gca	gtg	cct	gcc	gcg	ctc	atg	ggc	ctc	831
Val	Asn	Trp	Ala	Leu	Gly	Leu	Ala	Val	Pro	Ala	Ala	Leu	Met	Gly	Leu	
	235					240					245					
tca	tgt	gcc	gtc	ttc	ttc	atg	ggc	aca	cgc	ctc	tat	gtc	cgt	gta	cgc	879
Ser	Cys	Ala	Val	Phe	Phe	Met	Gly	Thr	Arg	Leu	Tyr	Val	Arg	Val	Arg	
	250				255					260					265	
ccc	gag	ggc	agc	ccc	ttc	aca	agc	ttc	gcc	caa	gtc	ctc	gtc	gcc	gcc	927
Pro	Glu	Gly	Ser	Pro	Phe	Thr	Ser	Phe	Ala	Gln	Val	Leu	Val	Ala	Ala	
				270					275					280		
gcc	cgc	aag	cgc	cac	atc	cgg	cga	gct	cgc	ggc	gat	gcc	gag	ctg	ttt	975
Ala	Arg	Lys	Arg	His	Ile	Arg	Arg	Ala	Arg	Gly	Asp	Ala	Glu	Leu	Phe	
			285					290				295				
gac	cca	ccg	cac	cag	agt	aag	ctc	gtc	tcc	aag	ctg	gca	tac	acc	gac	1023
Asp	Pro	Pro	His	Gln	Ser	Lys	Leu	Val	Ser	Lys	Leu	Ala	Tyr	Thr	Asp	
		300					305					310				
cag	ttt	gcg	tgc	ctt	gat	aag	gcg	gcc	gtg	cgg	acc	cct	gac	gac	gcg	1071
Gln	Phe	Ala	Cys	Leu	Asp	Lys	Ala	Ala	Val	Arg	Thr	Pro	Asp	Asp	Ala	
	315					320					325					
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Leu	Cys	Ile	Asp	Gly	Lys	Thr	Pro	Ala	Asp	Pro	Trp	Arg	Leu	Cys	Thr	
					335					340					345	
gtg	caa	cag	gtg	gag	gag	gtc	aag	tgc	cta	gcg	cgc	atc	att	ccg	gtg	1167
Val	Gln	Gln	Val	Glu	Glu	Val	Lys	Cys	Leu	Ala	Arg	Ile	Ile	Pro	Val	
				350					355					360		
tgg	tcg	tcg	ggg	atc	gtc	tac	ttc	atc	gtg	ctc	acc	cag	ctg	ggc	acc	1215
Trp	Ser	Ser	Gly	Ile	Val	Tyr	Phe	Ile	Val	Leu	Thr	Gln	Leu	Gly	Thr	
			365					370					375			
tat	gtc	gtg	ctc	cag	gct	gcg	cag	atg	gac	cgc	cga	atc	agc	aag	tcc	1263
Tyr	Val	Val	Leu	Gln	Ala	Ala	Gln	Met	Asp	Arg	Arg	Ile	Ser	Lys	Ser	
		380					385					390				
agc	agc	ttc	cag	atc	ccg	caa	ggc	tcc	ttc	gtc	gtc	ttc	cag	atg	ctc	1311
Ser	Ser	Phe	Gln	Ile	Pro	Gln	Gly	Ser	Phe	Val	Val	Phe	Gln	Met	Leu	
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410					415				420						425	
ctt	cgc	cgc	ttc	aca	aag	cgc	gag	ggc	ggc	atc	acc	ctg	ctc	caa	cgg	1407
Leu	Arg	Arg	Phe	Thr	Lys	Arg	Glu	Gly	Gly	Ile	Thr	Leu	Leu	Gln	Arg	
				430					435					440		
atc	ggc	gtc	ggg	ttg	gcg	ttg	tct	gtg	gcg	aca	atg	gtg	gtg	tca	gcg	1455
Ile	Gly	Val	Gly	Leu	Ala	Leu	Ser	Val	Ala	Thr	Met	Val	Val	Ser	Ala	
			445					450					455			
gct	gtg	gag	cag	cga	cga	cga	aag	atc	ggc	tcg	tcg	atg	tcg	tgc	ttc	1503
Ala	Val	Glu	Gln	Arg	Arg	Arg	Lys	Ile	Gly	Ser	Ser	Met	Ser	Cys	Phe	
		460					465					470				
tgg	ctg	gtg	ccg	cag	caa	ctg	ctg	gcg	ggc	ctg	tcg	gag	gcg	ttc	ggc	1551
Trp	Leu	Val	Pro	Gln	Gln	Leu	Leu	Ala	Gly	Leu	Ser	Glu	Ala	Phe	Gly	
	475					480					485					
gcc	atc	ggg	cag	att	gag	ttc	tac	tac	cgg	cag	ttc	ccg	gag	aac	atg	1599
Ala	Ile	Gly	Gln	Ile	Glu	Phe	Tyr	Tyr	Arg	Gln	Phe	Pro	Glu	Asn	Met	
490					495				500						505	
cgg	agc	gtg	gcg	ggg	gcg	ctc	tac	ttc	ctg	ggg	ttc	gcg	atg	gcg	agc	1647
Arg	Ser	Val	Ala	Gly	Ala	Leu	Tyr	Phe	Leu	Gly	Phe	Ala	Met	Ala	Ser	
				510					515					520		
tac	gca	agc	ggg	ctg	atg	gtg	atg	gtg	gtg	cac	cgg	gcg	acg	cg	ggg	1695
Tyr	Ala	Ser	Gly	Leu	Met	Val	Met	Val	Val	His	Arg	Ala	Thr	Arg	Gly	
			525					530					535			
cgg	ggc	ggc	cag	cct	gac	tgg	ctg	gcg	cag	gac	ctg	gac	gag	ggc	agg	1743
Arg	Gly	Gly	Gln	Pro	Asp	Trp	Leu	Ala	Gln	Asp	Leu	Asp	Glu	Gly	Arg	
		540				545						550				
gtg	gac	ctg	ttc	tac	ctg	gtc	acc	gcc	gcc	atc	gcc	act	gtg	aac	ctc	1791
Val	Asp	Leu	Phe	Tyr	Leu	Val	Thr	Ala	Ala	Ile	Ala	Thr	Val	Asn	Leu	
	555				560						565					
gtc	tac	ttt	gtg	atc	tgt	gca	cgg	tgg	tac	agg	ttc	aag	aag	tcc	gac	1839
Val	Tyr	Phe	Val	Ile	Cys	Ala	Arg	Trp	Tyr	Arg	Phe	Lys	Lys	Ser	Asp	
570					575				580						585	
gat	gcc	ggc	gcc	gga	gat	gtt	gag	ctc	gac	gac	gac	agc	ccg	aag	aag	1887
Asp	Ala	Gly	Ala	Gly	Asp	Val	Glu	Leu	Asp	Asp	Asp	Ser	Pro	Lys	Lys	
				590				595						600		
gct	agt	gct	ggc	tta	gct	tagttattat	tgccctcctt	tggggcttaa								1935
Ala	Ser	Ala	Gly	Leu	Ala											
			605													
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tgctcatcga	tcgatcccg	ggaatgtatg	taatacagat	ttggaactaa	tcaaaaagcc											2055
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<211> 607

<212> PRT

<213> Triticum aestivum

<400> 245

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Thr	Gly	Asp	Gly	Glu	Glu	Glu	Ala	Gly	Ala	Val	His	Asn	His	Arg		
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Gly	Trp	Lys	Ala	Met	Pro	Tyr	Val	Ile	Gly	Asn	Glu	Thr	Phe	Glu	Lys	
	50					55				60						
Leu	Gly	Thr	Ile	Gly	Thr	Leu	Ser	Asn	Met	Leu	Val	Tyr	Leu	Thr	Thr	
65					70					75					80	
Val	Tyr	His	Met	Pro	Ser	Val	Asn	Ala	Ala	Thr	Leu	Leu	Asn	Val	Phe	
				85					90					95		
Ser	Gly	Thr	Ser	Asn	Leu	Ala	Thr	Val	Phe	Gly	Ala	Tyr	Val	Ser	Asp	
			100					105					110			

PF59082SeqList_PF59082.txt

Thr	Tyr	Leu	Gly	Arg	Tyr	Thr	Thr	Ile	Ala	Ala	Ala	Thr	Met	Ser	Ser
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Phe	Ile	Gly	Met	Leu	Ile	Leu	Thr	Leu	Thr	Ala	Ala	Ile	His	Thr	Leu
	130					135					140				
His	Pro	Pro	Ala	Cys	Asn	Ala	Ser	Lys	Gly	Gln	His	Cys	Glu	Gly	Pro
	145				150					155					160
Thr	Gly	Ser	Gln	Leu	Ala	Ala	Ile	Leu	Val	Ser	Phe	Phe	Phe	Leu	Val
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Ile	Gly	Ala	Gly	Gly	Ile	Arg	Pro	Cys	Asn	Leu	Ala	Phe	Gly	Ala	Asp
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Gln	Phe	Asn	Pro	His	Thr	Ala	Asp	Gly	Arg	Arg	Gly	Ile	Ala	Ser	Phe
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Phe	Asn	Trp	Tyr	Tyr	Phe	Thr	Phe	Thr	Val	Ala	Met	Met	Leu	Ser	Ala
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Thr	Val	Ile	Ile	Tyr	Leu	Gln	Ser	Asn	Val	Asn	Trp	Ala	Leu	Gly	Leu
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Ala	Val	Pro	Ala	Ala	Leu	Met	Gly	Leu	Ser	Cys	Ala	Val	Phe	Phe	Met
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Gly	Thr	Arg	Leu	Tyr	Val	Arg	Val	Arg	Pro	Glu	Gly	Ser	Pro	Phe	Thr
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Ser	Phe	Ala	Gln	Val	Leu	Val	Ala	Ala	Arg	Lys	Arg	His	Ile	Arg	
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Leu	Val	Ser	Lys	Leu	Ala	Tyr	Thr	Asp	Gln	Phe	Ala	Cys	Leu	Asp	Lys
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Ala	Ala	Val	Arg	Thr	Pro	Asp	Asp	Ala	Leu	Cys	Ile	Asp	Gly	Lys	Thr
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Pro	Ala	Asp	Pro	Trp	Arg	Leu	Cys	Thr	Val	Gln	Gln	Val	Glu	Glu	Val
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Lys	Cys	Leu	Ala	Arg	Ile	Ile	Pro	Val	Trp	Ser	Ser	Gly	Ile	Val	Tyr
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Phe	Ile	Val	Leu	Thr	Gln	Leu	Gly	Thr	Tyr	Val	Val	Leu	Gln	Ala	Ala
	370					375					380				
Gln	Met	Asp	Arg	Arg	Ile	Ser	Lys	Ser	Ser	Ser	Phe	Gln	Ile	Pro	Gln
	385				390					395					400
Gly	Ser	Phe	Val	Val	Phe	Gln	Met	Leu	Ala	Leu	Thr	Met	Trp	Ile	Pro
				405					410					415	
Val	Tyr	Asp	Arg	Phe	Val	Val	Pro	Ala	Leu	Arg	Arg	Phe	Thr	Lys	Arg
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Glu	Gly	Gly	Ile	Thr	Leu	Leu	Gln	Arg	Ile	Gly	Val	Gly	Leu	Ala	Leu
			435				440					445			
Ser	Val	Ala	Thr	Met	Val	Val	Ser	Ala	Ala	Val	Glu	Gln	Arg	Arg	Arg
	450					455					460				
Lys	Ile	Gly	Ser	Ser	Met	Ser	Cys	Phe	Trp	Leu	Val	Pro	Gln	Gln	Leu
	465				470					475					480
Leu	Ala	Gly	Leu	Ser	Glu	Ala	Phe	Gly	Ala	Ile	Gly	Gln	Ile	Glu	Phe
				485					490					495	
Tyr	Tyr	Arg	Gln	Phe	Pro	Glu	Asn	Met	Arg	Ser	Val	Ala	Gly	Ala	Leu
			500					505					510		
Tyr	Phe	Leu	Gly	Phe	Ala	Met	Ala	Ser	Tyr	Ala	Ser	Gly	Leu	Met	Val
		515					520					525			
Met	Val	Val	His	Arg	Ala	Thr	Arg	Gly	Arg	Gly	Gly	Gln	Pro	Asp	Trp
	530					535					540				
Leu	Ala	Gln	Asp	Leu	Asp	Glu	Gly	Arg	Val	Asp	Leu	Phe	Tyr	Leu	Val
	545				550					555					560
Thr	Ala	Ala	Ile	Ala	Thr	Val	Asn	Leu	Val	Tyr	Phe	Val	Ile	Cys	Ala
				565					570					575	
Arg	Trp	Tyr	Arg	Phe	Lys	Lys	Ser	Asp	Asp	Ala	Gly	Ala	Gly	Asp	Val
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Glu	Leu	Asp	Asp	Asp	Ser	Pro	Lys	Lys	Ala	Ser	Ala	Gly	Leu	Ala	
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<212> DNA

<213> Triticum aestivum

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PF59082SeqList_PF59082.txt

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<222> (122)..(1888)

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c atg gaa gtc tgc gcc atg gag gaa gcc gcc gtt cgt gtc cct gtc cct 169

Met Glu Val Ser Ala Met Glu Glu Ala Ala Val Arg Val Pro Val Pro
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gcg gcg agg agg aag ggc ggc ctc aga acc ata ccg ttc atc atc tcg 217

Ala Ala Arg Arg Lys Gly Gly Leu Arg Thr Ile Pro Phe Ile Ile Ser
20 25 30

aac gag atc ttc gag aag gtg gcg acg tac ggg ctg caa gcg aac atg 265

Asn Glu Ile Phe Glu Lys Val Ala Thr Tyr Gly Leu Gln Ala Asn Met
35 40 45

gtc gta tac ctc acc aag cgg tac aac atg acg ccg gcc gcc agc gcc 313

Val Val Tyr Leu Thr Lys Arg Tyr Asn Met Thr Pro Ala Ala Ser Ala
50 55 60

atg gtg ctc tac ctt tgg tcc gcc ctc acc aac ttc ctg ccc atc ggc 361

Met Val Leu Tyr Leu Trp Ser Ala Leu Thr Asn Phe Leu Pro Ile Gly
65 70 75 80

ggc ggc gtg ttg tgc gac gtt ttc ttc ggc cgg ttc ccg gtc atc gcc 409

Gly Gly Val Leu Ser Asp Val Phe Phe Gly Arg Phe Pro Val Ile Ala
85 90 95

gtg gga tgc gtc gtc agc ctc tgc ggg atg tgc ctg cta ttg gtg act 457

Val Gly Cys Val Val Ser Leu Ser Gly Met Cys Leu Leu Val Thr
100 105 110

gcg atc ctg ccg gtg tac aag aag act ctg ggg tgc gac ccg gcc aac 505

Ala Ile Leu Pro Val Tyr Lys Lys Thr Leu Gly Cys Asp Pro Ala Asn
115 120 125

ccg agc gcg tgc acg atg ctg ccg tgc cag ctg ccg cta ctg ttc acg 553

Pro Ser Ala Cys Thr Met Leu Pro Cys Gln Leu Pro Leu Phe Thr
130 135 140

tcg ttc atg ctc atg tgc ctc ggg gcg ggc ggc atc ccg ccg tgc gcg 601

Ser Phe Met Leu Met Ser Leu Gly Ala Gly Gly Ile Arg Pro Cys Ala
145 150 155 160

ctg gcg ttc gga gcg gac cag ctg gac aag ccg gac aac agc acc aag 649

Leu Ala Phe Gly Ala Asp Gln Leu Asp Lys Arg Asp Asn Ser Thr Lys
165 170 175

aac gtg agg agg ctg cag acc ttc ttc aac tgg tac tac acc gtg ctg 697

Asn Val Arg Arg Leu Gln Thr Phe Phe Asn Trp Tyr Tyr Thr Val Leu
180 185 190

ggg ctc tcc ctc gtc gtt gcc gtc ctc gtc atc gtc tac ata cag gac 745

Gly Leu Ser Leu Val Val Ala Val Leu Val Ile Val Tyr Ile Gln Asp
195 200 205

cac atg ggg tgg gtc gtc ggc ttc tcc gtg ccc gtc gtg ctc atg ctc 793

His Met Gly Trp Val Val Gly Phe Ser Val Pro Val Val Leu Met Leu
210 215 220

gcc gct ctc atg ctc ttc ctg gcc ggc tgc cct ttg tac ctc aag gcg 841

Ala Ala Leu Met Leu Phe Leu Ala Gly Ser Pro Leu Tyr Leu Lys Ala
225 230 235 240

gag gcc gac agg agc gtg ctg gtg ggc atc gtg cag gtg ctc gtc gcc 889

Glu Ala Asp Arg Ser Val Leu Val Gly Ile Val Gln Val Leu Val Ala
245 250 255

agc tac aag aac cgg cgc gag ctg ttg ccg ccg gac acg gcc gaa gcg 937

Ser Tyr Lys Asn Arg Arg Glu Leu Leu Pro Pro Asp Thr Ala Glu Ala
260 265 270

tcg tgc ttt cac aac aaa gct ggc tcc agg ccc aga gtt ccc acc aag 985

Ser Cys Phe His Asn Lys Ala Gly Ser Arg Pro Arg Val Pro Thr Lys
275 280 285

aag atg gtg tct atg aac cgg gcg tgc gtg ctc agg aac ccg agc aag 1033

Lys Met Val Ser Met Asn Arg Ala Cys Val Leu Arg Asn Pro Ser Lys
290 295 300

gag ctc aac agc gac ggg tgc gcg tgt gac ccg tgg cgg ctg tgc acg 1081

Glu Leu Asn Ser Asp Gly Ser Ala Cys Asp Pro Trp Arg Leu Cys Thr
305 310 315 320 325 330 335 340 344

PF59082SeqList_PF59082.txt

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Val	Gln	Gln	Val	Glu	Asp	Ala	Lys	Ala	Val	Ile	Arg	Val	Leu	Pro	Ile	1129
			325						330					335		
tgg	tcc	acg	ggg	atc	ata	ccg	ggc	gtg	atc	gtc	gcc	cag	gtg	atg	ttc	1177
Trp	Ser	Thr	Gly	Ile	Ile	Pro	Gly	Val	Ile	Val	Ala	Gln	Val	Met	Phe	
			340					345					350			
ccc	gtg	ctg	caa	gca	ggt	acg	atg	gat	cgg	cag	atg	ggc	aag	gtg	gag	1225
Pro	Val	Leu	Gln	Ala	Gly	Thr	Met	Asp	Arg	Gln	Met	Gly	Lys	Val	Glu	
		355					360					365				
gtc	ccc	gcc	gca	tcc	tac	agc	gtc	ttc	ggc	atc	atc	acg	ctc	acc	gtc	1273
Val	Pro	Ala	Ala	Ser	Tyr	Ser	Val	Phe	Gly	Ile	Ile	Thr	Leu	Thr	Val	
	370					375					380					
tgg	gtg	gcc	ttg	tac	gac	cg	gtg	ctt	gtg	cgg	ccc	ctc	tcg	cgg	ctc	1321
Trp	Val	Ala	Leu	Tyr	Asp	Arg	Val	Leu	Val	Arg	Pro	Leu	Ser	Arg	Leu	
	385				390					395					400	
acc	ggc	cac	gcg	cg	ggg	ctc	agc	ctg	cga	cag	cg	atg	gga	gcc	ggg	1369
Thr	Gly	His	Ala	Arg	Gly	Leu	Ser	Leu	Arg	Gln	Arg	Met	Gly	Ala	Gly	
			405					410						415		
ctg	gcg	gtc	ttc	gcc	gtg	gcc	atg	gct	gtg	gcc	gcg	cga	acc	gag	gcc	1417
Leu	Ala	Val	Phe	Ala	Val	Ala	Met	Ala	Val	Ala	Ala	Arg	Thr	Glu	Ala	
			420					425					430			
ctc	cg	cg	ggc	gcg	gcc	atc	gcg	gag	ggc	ttc	cag	gac	caa	aag	cat	1465
Leu	Arg	Arg	Gly	Ala	Ala	Ile	Ala	Glu	Gly	Phe	Gln	Asp	Gln	Lys	His	
		435				440						445				
gcg	gtg	gta	cac	atg	tcg	gcg	atg	cgg	ctt	gtg	ccg	cag	cac	tgc	ctc	1513
Ala	Val	Val	His	Met	Ser	Ala	Met	Arg	Leu	Val	Pro	Gln	His	Cys	Leu	
	450					455					460					
atc	ggg	ctc	gcc	gac	gcg	ttg	aac	ctg	atc	ggg	cag	atc	gag	ttc	tac	1561
Ile	Gly	Leu	Ala	Asp	Ala	Leu	Asn	Leu	Ile	Gly	Gln	Ile	Glu	Phe	Tyr	
	465				470				475						480	
tac	tcc	gag	ttc	ccc	aag	acc	atg	tcc	agc	atc	ggg	gtg	tcg	ctg	ctc	1609
Tyr	Ser	Glu	Phe	Pro	Lys	Thr	Met	Ser	Ser	Ile	Gly	Val	Ser	Leu	Leu	
			485					490						495		
gcc	ctc	ggc	gtg	ggc	ttc	ggc	gcc	gtg	ctg	ggg	agc	gcc	atc	gtg	ggg	1657
Ala	Leu	Gly	Val	Gly	Phe	Gly	Ala	Val	Leu	Gly	Ser	Ala	Ile	Val	Gly	
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atc	atg	aac	agc	gcc	acc	ggg	agg	gac	ggg	cg	gac	agc	tgg	ttg	tcc	1705
Ile	Met	Asn	Ser	Ala	Thr	Gly	Arg	Asp	Gly	Arg	Asp	Ser	Trp	Leu	Ser	
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agc	aac	ctc	aac	agg	ggc	cg	tac	gac	tac	tac	tat	ctg	gtt	ctc	gcg	1753
Ser	Asn	Leu	Asn	Arg	Gly	Arg	Tyr	Asp	Tyr	Tyr	Tyr	Leu	Val	Leu	Ala	
	530				535						540					
gcg	ctg	tcc	gtg	gcc	aac	ttg	gtg	tac	ttc	atc	tgg	tgc	agc	tgg	gcg	1801
Ala	Leu	Ser	Val	Ala	Asn	Leu	Val	Tyr	Phe	Ile	Trp	Cys	Ser	Trp	Ala	
	545				550					555					560	
tac	ggc	gag	gaa	ggg	cag	atc	aga	att	atg	gcg	ttg	gcg	gct	gag	gag	1849
Tyr	Gly	Glu	Glu	Gly	Gln	Ile	Arg	Ile	Met	Ala	Leu	Ala	Ala	Glu	Glu	
			565					570						575		
gcg	gag	gag	gaa	gag	acc	aaa	caa	gaa	cag	cac	aaa	tgataggcaa				1895
Ala	Glu	Glu	Glu	Glu	Thr	Lys	Gln	Glu	Gln	His	Lys					
		580					585									
ggcattcgcc	gggcagtgac	gcagtgctgt	gttgctgtcg	tttgaccttg	cgcgcgctt											1955
tctctcttgc	gaattgctga	attgtgaatt	gtgatattga	tgtgctacgt	tagttagtaa											2015
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ttgcatcaaa	aaaaaaaaaa	aaa														2098

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 <212> PRT
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PF59082SeqList_PF59082.txt

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35      40      45
Val Val Tyr Leu Thr Lys Arg Tyr Asn Met Thr Pro Ala Ala Ser Ala
50      55      60
Met Val Leu Tyr Leu Trp Ser Ala Leu Thr Asn Phe Leu Pro Ile Gly
65      70      75      80
Gly Gly Val Leu Ser Asp Val Phe Phe Gly Arg Phe Pro Val Ile Ala
85      90      95
Val Gly Cys Val Val Ser Leu Ser Gly Met Cys Leu Leu Val Thr
100      105      110
Ala Ile Leu Pro Val Tyr Lys Lys Thr Leu Gly Cys Asp Pro Ala Asn
115      120      125
Pro Ser Ala Cys Thr Met Leu Pro Cys Gln Leu Pro Leu Leu Phe Thr
130      135      140
Ser Phe Met Leu Met Ser Leu Gly Ala Gly Gly Ile Arg Pro Cys Ala
145      150      155      160
Leu Ala Phe Gly Ala Asp Gln Leu Asp Lys Arg Asp Asn Ser Thr Lys
165      170      175
Asn Val Arg Arg Leu Gln Thr Phe Phe Asn Trp Tyr Tyr Thr Val Leu
180      185      190
Gly Leu Ser Leu Val Val Ala Val Leu Val Ile Val Tyr Ile Gln Asp
195      200      205
His Met Gly Trp Val Val Gly Phe Ser Val Pro Val Val Leu Met Leu
210      215      220
Ala Ala Leu Met Leu Phe Leu Ala Gly Ser Pro Leu Tyr Leu Lys Ala
225      230      235      240
Glu Ala Asp Arg Ser Val Leu Val Gly Ile Val Gln Val Leu Val Ala
245      250      255
Ser Tyr Lys Asn Arg Arg Glu Leu Leu Pro Pro Asp Thr Ala Glu Ala
260      265      270
Ser Cys Phe His Asn Lys Ala Gly Ser Arg Pro Arg Val Pro Thr Lys
275      280      285
Lys Met Val Ser Met Asn Arg Ala Cys Val Leu Arg Asn Pro Ser Lys
290      295      300
Glu Leu Asn Ser Asp Gly Ser Ala Cys Asp Pro Trp Arg Leu Cys Thr
305      310      315      320
Val Gln Gln Val Glu Asp Ala Lys Ala Val Ile Arg Val Leu Pro Ile
325      330      335
Trp Ser Thr Gly Ile Ile Pro Gly Val Ile Val Ala Gln Val Met Phe
340      345      350
Pro Val Leu Gln Ala Gly Thr Met Asp Arg Gln Met Gly Lys Val Glu
355      360      365
Val Pro Ala Ala Ser Tyr Ser Val Phe Gly Ile Ile Thr Leu Thr Val
370      375      380
Trp Val Ala Leu Tyr Asp Arg Val Leu Val Arg Pro Leu Ser Arg Leu
385      390      395      400
Thr Gly His Ala Arg Gly Leu Ser Leu Arg Gln Arg Met Gly Ala Gly
405      410      415
Leu Ala Val Phe Ala Val Ala Met Ala Val Ala Ala Arg Thr Glu Ala
420      425      430
Leu Arg Arg Gly Ala Ala Ile Ala Glu Gly Phe Gln Asp Gln Lys His
435      440      445
Ala Val Val His Met Ser Ala Met Arg Leu Val Pro Gln His Cys Leu
450      455      460
Ile Gly Leu Ala Asp Ala Leu Asn Leu Ile Gly Gln Ile Glu Phe Tyr
465      470      475      480
Tyr Ser Glu Phe Pro Lys Thr Met Ser Ser Ile Gly Val Ser Leu Leu
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Ala Leu Gly Val Gly Phe Gly Ala Val Leu Gly Ser Ala Ile Val Gly
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Ile Met Asn Ser Ala Thr Gly Arg Asp Gly Arg Asp Ser Trp Leu Ser
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PF59082SeqList_PF59082.txt

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atg aaa tgg gtt cgt gat tct tca ttg gat cac aaa gga aga gtt cct 96
Met Lys Trp Val Arg Asp Ser Ser Leu Asp His Lys Gly Arg Val Pro
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Leu Arg Ala Ser Thr Gly Ser Trp Lys Ala Ser Leu Phe Ile Ile Ala
35 40 45
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Ile Glu Phe Ser Glu Arg Leu Ser Tyr Phe Gly Ile Ala Thr Ser Leu
50 55 60
gtc att tac ctt acg aaa gtt ctt cat caa gac ctt aag aca gca gtt 240
Val Ile Tyr Leu Thr Lys Val Leu His Gln Asp Leu Lys Thr Ala Val
65 70 75 80
aaa aat gtg aac tat tgg tct ggt gtc acc acc ttg ata cca ttg tta 288
Lys Asn Val Asn Tyr Trp Ser Gly Val Thr 90 95
gga gga ttc cta gct gat gct tac tta ggc cgt tac acc gct gtg ata 336
Gly Gly Phe Leu Ala Asp Ala Tyr Leu Gly Arg Tyr Thr Ala Val Ile
100 105 110
gca tca tgc att gtt tat ctc atg ggt ttg gtt ctg ctt tct ttg tca 384
Ala Ser Cys Ile Val Tyr Leu Met Gly Leu Val Leu Leu Ser Leu Ser
115 120 125
tgg ttc tta cca ggt ttc aaa cct tgt gat cat acc agt aca tgc acc 432
Trp Phe Leu Pro Gly Phe Lys Pro Cys Asp His Thr Ser Thr Cys Thr
130 135 140
gaa cct agg agg att cat gag gtg ggt ttc ttc cta ggc atc tat tta 480
Glu Pro Arg Arg Ile His Glu Val Gly Phe Phe Leu Gly Ile Tyr Leu
145 150 155 160
ata tca gta gga act gga ggc cat aaa cct tcc ttg gag agc tct ggt 528
Ile Ser Val Gly Thr 165 170 175
gct gat caa ttt gat gat aat aat gcc aaa gaa aga agt cag aaa atg 576
Ala Asp Gln Phe Asp Asp Asn Asn Ala Lys Glu Arg Ser Gln Lys Met
180 185 190
tcc ttt ttc aac tgg tgg aac agt ggt tcg tgt agt gga atc att cta 624
Ser Phe Phe Asn Trp Trp Asn Ser Gly Ser Cys Ser Gly Ile Ile Leu
195 200 205
cga gtg act gtg att gtg tat gtt caa gac cat gtc aat tgg ggg gtt 672
Arg Val Thr Val Ile Val Tyr Val Gln Asp His Val Asn Trp Gly Val
210 215 220
gct gat atc gtc ctc aca ggg gtc atg gct gtc tca ttg ctc ata ttc 720
Ala Asp Ile Val Leu Thr Gly Val Met Ala Val Ser Leu Leu Ile Phe
225 230 235 240
ttg att gga agg tct tct tat cgt tac agg aca cca att ggg agc ccc 768
Leu Ile Gly Arg Ser Tyr Arg Tyr Thr Pro Ile Gly Ser Pro
245 250 255
ttg act cct atg ttg caa gtt att gtt gct gct att tcc aaa aga aag 816
Leu Thr Pro Met Leu Gln Val Ile Val Ala Ala Ile Ser Lys Arg Lys
260 265 270

PF59082SeqList_PF59082.txt

ctt	cca	tat	cct	tcc	aat	cca	act	caa	ttg	tat	gaa	gtt	tcc	aag	tct	864
Leu	Pro	Tyr	Pro	Ser	Asn	Pro	Thr	Gln	Leu	Tyr	Glu	Val	Ser	Lys	Ser	
		275					280					285				
gag	ggc	aac	agt	gaa	aga	ttt	ctg	gct	cac	acc	aag	aaa	ctc	aaa	ttt	912
Glu	Gly	Asn	Ser	Glu	Arg	Phe	Leu	Ala	His	Thr	Lys	Lys	Leu	Lys	Phe	
	290					295					300					
ctt	gac	aag	gca	gca	atc	ctt	gaa	aat	gaa	ggg	aac	ata	gca	gag	aaa	960
Leu	Asp	Lys	Ala	Ala	Ile	Leu	Glu	Asn	Glu	Gly	Asn	Ile	Ala	Glu	Lys	
305					310					315					320	
cag	agt	cca	tgg	aga	ctt	gca	aca	gta	acc	aag	gtt	gaa	gaa	ctg	aag	1008
Gln	Ser	Pro	Trp	Arg	Leu	Ala	Thr	Val	Thr	Lys	Val	Glu	Glu	Leu	Lys	
				325				330						335		
ctt	atc	atc	aac	atg	atc	ccc	att	tgg	gtg	ttc	aca	tta	cca	ttt	gga	1056
Leu	Ile	Ile	Asn	Met	Ile	Pro	Ile	Trp	Val	Phe	Thr	Leu	Pro	Phe	Gly	
			340					345					350			
atc	tgt	gct	tcc	caa	acc	tcc	act	ttc	atc	aaa	caa	ggg	gcc	atc		1104
Ile	Cys	Ala	Ser	Gln	Thr	Ser	Thr	Phe	Phe	Ile	Lys	Gln	Gly	Ala	Ile	
		355					360					365				
atg	aac	aga	aat	ata	ggc	aat	aat	gga	ttt	gtg	gtt	ccc	cca	gct	tca	1152
Met	Asn	Arg	Asn	Ile	Gly	Asn	Asn	Gly	Phe	Val	Val	Pro	Pro	Ala	Ser	
	370					375					380					
att	ttc	act	ctt	gca	gcc	gtt	ggg	atg	ata	ctt	tca	gtg	acc	atc	tat	1200
Ile	Phe	Thr	Leu	Ala	Ala	Val	Gly	Met	Ile	Leu	Ser	Val	Thr	Ile	Tyr	
385					390					395					400	
gac	aag	ctc	ctt	gtg	cca	gtg	cta	aga	aaa	cta	aca	gga	aat	gac	aga	1248
Asp	Lys	Leu	Leu	Val	Pro	Val	Leu	Arg	Lys	Leu	Thr	Gly	Asn	Asp	Arg	
				405					410					415		
gga	atc	agc	atc	ctc	caa	agg	att	ggg	att	gga	atg	gtc	ttc	tca	gtc	1296
Gly	Ile	Ser	Ile	Leu	Gln	Arg	Ile	Gly	Ile	Gly	Met	Val	Phe	Ser	Val	
			420					425					430			
atc	aca	atg	ata	gtg	gca	gct	ttg	gtg	gaa	aaa	aag	agg	ctt	gag	gca	1344
Ile	Thr	Met	Ile	Val	Ala	Ala	Leu	Val	Glu	Lys	Lys	Arg	Leu	Glu	Ala	
		435					440					445				
gtt	gaa	atg	aat	ggc	cca	tta	aag	ggg	tct	ttg	tcc	atg	agt	gcc	ctt	1392
Val	Glu	Met	Asn	Gly	Pro	Leu	Lys	Gly	Ser	Leu	Ser	Met	Ser	Ala	Leu	
	450					455					460					
tgg	ttg	gcc	cca	caa	ttt	atg	atc	att	gga	ttt	ggg	gat	ggg	ttt	gct	1440
Trp	Leu	Ala	Pro	Gln	Phe	Met	Ile	Ile	Gly	Phe	Gly	Asp	Gly	Phe	Ala	
465					470					475					480	
ctt	gtg	ggc	ttg	caa	gag	tat	ttc	tat	gac	caa	gtg	cct	gac	tca	atg	1488
Leu	Val	Gly	Leu	Gln	Glu	Tyr	Phe	Tyr	Asp	Gln	Val	Pro	Asp	Ser	Met	
				485					490					495		
aga	agc	ctt	gga	ata	gca	ctt	tac	ctt	agt	gtc	att	ggg	gct	gca	agt	1536
Arg	Ser	Leu	Gly	Ile	Ala	Leu	Tyr	Leu	Ser	Val	Ile	Gly	Ala	Ala	Ser	
			500					505					510			
ttt	ctt	agt	agt	tta	tta	ata	aca	att	gtg	gat	cat	gtc	act	ggg	aag	1584
Phe	Leu	Ser	Ser	Leu	Leu	Ile	Thr	Ile	Val	Asp	His	Val	Thr	Gly	Lys	
		515					520					525				
att	ggg	aag	agt	tgg	att	ggg	aag	gat	ttg	aat	agt	agc	cgc	ttg	gac	1632
Ile	Gly	Lys	Ser	Trp	Ile	Gly	Lys	Asp	Leu	Asn	Ser	Ser	Arg	Leu	Asp	
	530					535					540					
aaa	ttt	tac	tgg	ctt	ctt	gca	gcc	atc	acc	aca	ttg	aac	ttg	ttc	atg	1680
Lys	Phe	Tyr	Trp	Leu	Leu	Ala	Ala	Ile	Thr	Thr	Leu	Asn	Leu	Phe	Met	
545					550					555					560	
ttt	gtg	atc	ttt	gct	cgc	aag	tat	aac	tac	aag	aat	gtg	caa	aag	gtg	1728
Phe	Val	Ile	Phe	Ala	Arg	Lys	Tyr	Asn	Tyr	Lys	Asn	Val	Gln	Lys	Val	
				565					570					575		
gca	gcg	gct	gat	tgc	tac	gaa	ggc	aaa	agt	gag	gat	gat	gga	tca	gag	1776
Ala	Ala	Ala	Asp	Cys	Tyr	Glu	Gly	Lys	Ser	Glu	Asp	Asp	Gly	Ser	Glu	
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act	tgg	gtt	tga													1788
Thr	Trp	Val														
		595														

<210> 249
 <211> 595
 <212> PRT
 <213> Glycine max

PF59082SeqList_PF59082.txt

<400> 249

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      20      25      30
Leu Arg Ala Ser Thr Gly Ser Trp Lys Ala Ser Leu Phe Ile Ile Ala
      35      40      45
Ile Glu Phe Ser Glu Arg Leu Ser Tyr Phe Gly Ile Ala Thr Ser Leu
      50      55      60
Val Ile Tyr Leu Thr Lys Val Leu His Gln Asp Leu Lys Thr Ala Val
65      70      75      80
Lys Asn Val Asn Tyr Trp Ser Gly Val Thr Thr Leu Ile Pro Leu Leu
      85      90      95
Gly Gly Phe Leu Ala Asp Ala Tyr Leu Gly Arg Tyr Thr Ala Val Ile
      100      105      110
Ala Ser Cys Ile Val Tyr Leu Met Gly Leu Val Leu Leu Ser Leu Ser
      115      120      125
Trp Phe Leu Pro Gly Phe Lys Pro Cys Asp His Thr Ser Thr Cys Thr
130      135      140
Glu Pro Arg Arg Ile His Glu Val Gly Phe Phe Leu Gly Ile Tyr Leu
145      150      155      160
Ile Ser Val Gly Thr Gly Gly His Lys Pro Ser Leu Glu Ser Ser Gly
      165      170      175
Ala Asp Gln Phe Asp Asp Asn Asn Ala Lys Glu Arg Ser Gln Lys Met
180      185      190
Ser Phe Phe Asn Trp Trp Asn Ser Gly Ser Cys Ser Gly Ile Ile Leu
195      200      205
Arg Val Thr Val Ile Val Tyr Val Gln Asp His Val Asn Trp Gly Val
210      215      220
Ala Asp Ile Val Leu Thr Gly Val Met Ala Val Ser Leu Leu Ile Phe
225      230      235      240
Leu Ile Gly Arg Ser Ser Tyr Arg Tyr Arg Thr Pro Ile Gly Ser Pro
      245      250      255
Leu Thr Pro Met Leu Gln Val Ile Val Ala Ala Ile Ser Lys Arg Lys
260      265      270
Leu Pro Tyr Pro Ser Asn Pro Thr Gln Leu Tyr Glu Val Ser Lys Ser
275      280      285
Glu Gly Asn Ser Glu Arg Phe Leu Ala His Thr Lys Lys Leu Lys Phe
290      295      300
Leu Asp Lys Ala Ala Ile Leu Glu Asn Glu Gly Asn Ile Ala Glu Lys
305      310      315      320
Gln Ser Pro Trp Arg Leu Ala Thr Val Thr Lys Val Glu Glu Leu Lys
      325      330      335
Leu Ile Ile Asn Met Ile Pro Ile Trp Val Phe Thr Leu Pro Phe Gly
340      345      350
Ile Cys Ala Ser Gln Thr Ser Thr Phe Phe Ile Lys Gln Gly Ala Ile
355      360      365
Met Asn Arg Asn Ile Gly Asn Asn Gly Phe Val Val Pro Pro Ala Ser
370      375      380
Ile Phe Thr Leu Ala Ala Val Gly Met Ile Leu Ser Val Thr Ile Tyr
385      390      395      400
Asp Lys Leu Leu Val Pro Val Leu Arg Lys Leu Thr Gly Asn Asp Arg
      405      410      415
Gly Ile Ser Ile Leu Gln Arg Ile Gly Ile Gly Met Val Phe Ser Val
      420      425      430
Ile Thr Met Ile Val Ala Ala Leu Val Glu Lys Lys Arg Leu Glu Ala
435      440      445
Val Glu Met Asn Gly Pro Leu Lys Gly Ser Leu Ser Met Ser Ala Leu
450      455      460
Trp Leu Ala Pro Gln Phe Met Ile Ile Gly Phe Gly Asp Gly Phe Ala
465      470      475      480
Leu Val Gly Leu Gln Glu Tyr Phe Tyr Asp Gln Val Pro Asp Ser Met
      485      490      495
Arg Ser Leu Gly Ile Ala Leu Tyr Leu Ser Val Ile Gly Ala Ala Ser
500      505      510
Phe Leu Ser Ser Leu Leu Ile Thr Ile Val Asp His Val Thr Gly Lys
515      520      525
Ile Gly Lys Ser Trp Ile Gly Lys Asp Leu Asn Ser Ser Arg Leu Asp
530      535      540

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PF59082SeqList_PF59082.txt

Lys Phe Tyr Trp Leu Leu Ala Ala Ile Thr Thr Leu Asn Leu Phe Met
 545 550 555 560
 Phe Val Ile Phe Ala Arg Lys Tyr Asn Tyr Lys Asn Val Gln Lys Val
 565 570 575
 Ala Ala Ala Asp Cys Tyr Glu Gly Lys Ser Glu Asp Asp Gly Ser Glu
 580 585 590
 Thr Trp Val
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 <211> 1851
 <212> DNA
 <213> Glycine max

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 <222> (1)..(1851)

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 cag cac att tca caa cca cag aag cgc aag ggt ggt ctt gtt acc atg 96
 Gln His Ile Ser Gln Pro Gln Lys Arg Lys Gly Gly Leu Val Thr Met
 20 25 30
 cct ttc atc att gca aat gag gca ctt gcg agg gtg gca agt ttg ggc 144
 Pro Phe Ile Ile Ala Asn Glu Ala Leu Ala Arg Val Ala Ser Leu Gly
 35 40 45
 ctt ttg ccc aac atg ata ctg tat ttg atg ggg acc tac agg ctt cac 192
 Leu Leu Pro Asn Met Ile Leu Tyr Leu Met Gly Thr Tyr Arg Leu His
 50 55 60
 ctt gcc caa gca acc cag ata ctt ctc tcg tcc cat gct acc agc aat 240
 Leu Ala Gln Ala Thr Gln Ile Leu Leu Ser Ser His Ala Thr Ser Asn
 65 70 75 80
 ttc aca cct gtg gtg ggt gct ttc att gct gat tct tat ctg ggt cga 288
 Phe Thr Pro Val Val Gly Ala Phe Ile Ala Asp Ser Tyr Leu Gly Arg
 85 90 95
 ttc ctc gct gtt ggg ttg ggt tcg gcc atc act ttt ctg gga atg aca 336
 Phe Leu Ala Val Gly Leu Gly Ser Ala Ile Thr Phe Leu Gly Met Thr
 100 105 110
 ctg ctg tgg tta aca gct atg atc cca cag gca cgg cct ccc act tgc 384
 Leu Leu Trp Leu Thr Ala Met Ile Pro Gln Ala Arg Pro Pro Thr Cys
 115 120 125
 agt agc aat aaa gct gga ggc tgt aaa tcg gca aca gga ggg caa atg 432
 Ser Ser Asn Lys Ala Gly Cys Lys Ser Ala Thr Gly Gly Gln Met
 130 135 140
 gca atc tta atc tct gcc ctt gct ctc atg tct gtt gga aat ggt ggt 480
 Ala Ile Leu Ile Ser Ala Leu Ala Leu Met Ser Val Gly Asn Gly Gly
 145 150 155 160
 ctt tca tgc tcc tta gca ttt ggt gca gac cag gtg aac aga aaa gat 528
 Leu Ser Cys Ser Leu Ala Phe Gly Ala Asp Gln Val Asn Arg Lys Asp
 165 170 175
 aac ccc aac aac aga agg gtc ttg gaa ata ttc ttc agc tgg tat tat 576
 Asn Pro Asn Asn Arg Arg Val Leu Glu Ile Phe Phe Ser Trp Tyr Tyr
 180 185 190
 gct tct gct gct att tct gtc ata att gct ctc aca gga ata gtt tat 624
 Ala Ser Ala Ala Ile Ser Val Ile Ile Ala Leu Thr Gly Ile Val Tyr
 195 200 205
 atc caa gat cat ctt gga tgg aaa gtg ggt tat gga gtt cca gca gca 672
 Ile Gln Asp His Leu Gly Trp Lys Val Gly Tyr Gly Val Pro Ala Ala
 210 215 220
 ctc atg ctt tta tct act gtc tcc ttc ctc ctt gcc tct cca ctt tat 720
 Leu Met Leu Leu Ser Thr Val Ser Phe Leu Leu Ala Ser Pro Leu Tyr
 225 230 235 240
 gta aag aat aaa gta gaa tcc agc ttg ttc gga ttt gta caa gtg 768
 Val Lys Asn Lys Val Glu Ser Ser Leu Phe Thr Gly Phe Val Gln Val
 245 250 255
 att gtt gtt gcc tac aag aac aga aaa ctt cca tta cca cca aac aac 816
 Ile Val Val Ala Tyr Lys Asn Arg Lys Leu Pro Leu Pro Pro Asn Asn

PF59082SeqList_PF59082.txt

	260	265	270	
tcc cct gaa cat tac cat cat aag aag gag tca gac ctt gtc gtt cca	Ser Pro Glu His Tyr His His Lys Lys Glu Ser Asp Leu Val Val Pro	864		
acc gat aaa cta agt ttc ctg aat aga gcc tgt gtt atc aaa gat cgg	Thr Asp Lys Leu Ser Phe Leu Asn Arg Ala Cys Val Ile Lys Asp Arg	912		
gaa caa gaa ata gcc tcg gat ggt tca gca tca aat cca tgg aaa ctc	Glu Gln Glu Ile Ala Ser Asp Gly Ser Ala Ser Asn Pro Trp Lys Leu	960		
tgc aca gta gat caa gta gag gaa cta aaa gcc att att aaa gtg att	Cys Thr Val Asp Gln Val Glu Glu Leu Lys Ala Ile Ile Lys Val Ile	1008		
ccc ttg tgg tct aca ggg atc atg atg tca gtt aac att gga ggc tca	Pro Leu Trp Thr Gly Ile Met Met Ser Val Asn Ile Gly Gly Ser	1056		
ttt gga ttg ctg caa gct aag tcc ctg gac aga cac atc acc tca cac	Phe Gly Leu Leu Gln Ala Lys Ser Leu Asp Arg His Ile Thr Ser His	1104		
ttc caa gtg cca cct ggc tct ttt agt gta gtc atg gta ctt aca ata	Phe Gln Val Pro Pro Gly Ser Phe Ser Val Val Met Val Leu Thr Ile	1152		
ttt tta tgg ata gct ctc tat gac cga gcc att ctt cct tta gca tca	Phe Leu Trp Ile Ala Leu Tyr Asp Arg Ala Ile Leu Pro Leu Ala Ser	1200		
aag ata aga ggc aaa ccg gtt agg atc agt gca aag aga aga atg gga	Lys Ile Arg Gly Lys Pro Val Arg Ile Ser Ala Lys Arg Arg Met Gly	1248		
ctt ggc ttg ttt ttc tct ttt atc cac ttg gta act tcg gct att gtc	Leu Gly Leu Phe Ser Phe Ile His Leu Val Thr Ser Ala Ile Val	1296		
gaa tcc gta agg cga agg aga gca atc aag gag gga tat ctt aac aat	Glu Ser Val Arg Arg Arg Arg Ala Ile Lys Glu Gly Tyr Leu Asn Asn	1344		
gcc aat ggt gtg ttg cat atg tct gca atg tgg ctt ttc cca caa ctt	Ala Asn Gly Val Leu His Met Ser Ala Met Trp Leu Phe Pro Gln Leu	1392		
tgc ttg ggt gga ata gct gaa gca ttc aat gca ata ggc caa aat gag	Cys Leu Gly Gly Ile Ala Glu Ala Phe Asn Ala Ile Gly Gln Asn Glu	1440		
ttc tat tac aca gag ttt cct agg acc atg tcc agt gtt gct gct tcc	Phe Tyr Tyr Thr Glu Phe Pro Arg Thr Met Ser Ser Val Ala Ala Ser	1488		
ctt tct gga ctg gga atg gct gca gga aac ttg gtg tct agt ttt gtc	Leu Ser Gly Leu Gly Met Ala Ala Gly Asn Leu Val Ser Phe Val	1536		
ttc agc gtt gta caa aat gct act tca aga ggg ggg aaa gaa ggt tgg	Phe Ser Val Val Gln Asn Ala Thr Ser Arg Gly Gly Lys Glu Gly Trp	1584		
gtt ttg gat aac att aac aag ggt cgt tat gac aag tac tgg gtt	Val Leu Asp Asn Ile Asn Lys Gly Arg Tyr Asp Lys Tyr Tyr Trp Val	1632		
att tct gga ctc agt gct ctt aat ata gtg tat tat cta ata tgc agt	Ile Ser Gly Leu Ser Ala Leu Asn Ile Val Tyr Tyr Leu Ile Cys Ser	1680		
tgg gct tat gga cct acc gtt gag caa gta caa gta cgt aag tta ggt	Trp Ala Tyr Gly Pro Thr Val Glu Gln Val Gln Val Arg Lys Leu Gly	1728		
gaa gaa aat ggc tca agg gaa tta gaa cct tca act gaa ttt agg aat	Glu Glu Asn Gly Ser Arg Glu Leu Leu Glu Pro Ser Thr Glu Phe Arg Asn	1776		
ggg agt cag gtt gac aaa gaa ttc cag att agt aaa gaa aat ggc tca	Gly Ser Gln Val Asp Lys Glu Phe Gln Ile Ser Lys Glu Asn Gly Ser	1824		
aag gag gaa gag tta act agg tga	Lys Glu Glu Glu Leu Thr Arg	1851		

PF59082SeqList_PF59082.txt

<211> 616

<212> PRT

<213> Glycine max

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      20      25      30
Pro Phe Ile Ile Ala Asn Glu Ala Leu Ala Arg Val Ala Ser Leu Gly
      35      40      45
Leu Leu Pro Asn Met Ile Leu Tyr Leu Met Gly Thr Tyr Arg Leu His
      50      55      60
Leu Ala Gln Ala Thr Gln Ile Leu Leu Ser Ser His Ala Thr Ser Asn
65      70      75      80
Phe Thr Pro Val Val Gly Ala Phe Ile Ala Asp Ser Tyr Leu Gly Arg
      85      90      95
Phe Leu Ala Val Gly Leu Gly Ser Ala Ile Thr Phe Leu Gly Met Thr
      100      105      110
Leu Leu Trp Leu Thr Ala Met Ile Pro Gln Ala Arg Pro Pro Thr Cys
      115      120      125
Ser Ser Asn Lys Ala Gly Gly Cys Lys Ser Ala Thr Gly Gly Gln Met
130      135      140
Ala Ile Leu Ile Ser Ala Leu Ala Leu Met Ser Val Gly Asn Gly Gly
145      150      155      160
Leu Ser Cys Ser Leu Ala Phe Gly Ala Asp Gln Val Asn Arg Lys Asp
      165      170      175
Asn Pro Asn Asn Arg Arg Val Leu Glu Ile Phe Phe Ser Trp Tyr Tyr
      180      185      190
Ala Ser Ala Ala Ile Ser Val Ile Ala Leu Thr Gly Ile Val Tyr
      195      200      205
Ile Gln Asp His Leu Gly Trp Lys Val Gly Tyr Gly Val Pro Ala Ala
210      215      220
Leu Met Leu Leu Ser Thr Val Ser Phe Leu Leu Ala Ser Pro Leu Tyr
225      230      235      240
Val Lys Asn Lys Val Glu Ser Ser Leu Phe Thr Gly Phe Val Gln Val
      245      250      255
Ile Val Val Ala Tyr Lys Asn Arg Lys Leu Pro Leu Pro Pro Asn Asn
      260      265      270
Ser Pro Glu His Tyr His His Lys Lys Glu Ser Asp Leu Val Val Pro
      275      280      285
Thr Asp Lys Leu Ser Phe Leu Asn Arg Ala Cys Val Ile Lys Asp Arg
290      295      300
Glu Gln Glu Ile Ala Ser Asp Gly Ser Ala Ser Asn Pro Trp Lys Leu
305      310      315      320
Cys Thr Val Asp Gln Val Glu Glu Leu Lys Ala Ile Ile Lys Val Ile
      325      330      335
Pro Leu Trp Ser Thr Gly Ile Met Met Ser Val Asn Ile Gly Gly Ser
      340      345      350
Phe Gly Leu Leu Gln Ala Lys Ser Leu Asp Arg His Ile Thr Ser His
      355      360      365
Phe Gln Val Pro Pro Gly Ser Phe Ser Val Val Met Val Leu Thr Ile
370      375      380
Phe Leu Trp Ile Ala Leu Tyr Asp Arg Ala Ile Leu Pro Leu Ala Ser
385      390      395      400
Lys Ile Arg Gly Lys Pro Val Arg Ile Ser Ala Lys Arg Arg Met Gly
      405      410      415
Leu Gly Leu Phe Phe Ser Phe Ile His Leu Val Thr Ser Ala Ile Val
      420      425      430
Glu Ser Val Arg Arg Arg Ala Ile Lys Glu Gly Tyr Leu Asn Asn
      435      440      445
Ala Asn Gly Val Leu His Met Ser Ala Met Trp Leu Phe Pro Gln Leu
450      455      460
Cys Leu Gly Gly Ile Ala Glu Ala Phe Asn Ala Ile Gly Gln Asn Glu
465      470      475      480
Phe Tyr Tyr Thr Glu Phe Pro Arg Thr Met Ser Ser Val Ala Ala Ser
      485      490      495
Leu Ser Gly Leu Gly Met Ala Ala Gly Asn Leu Val Ser Ser Phe Val
500      505      510

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PF59082SeqList_PF59082.txt

Phe Ser Val Val Gln Asn Ala Thr Ser Arg Gly Gly Lys Glu Gly Trp
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Val Leu Asp Asn Ile Asn Lys Gly Arg Tyr Asp Lys Tyr Tyr Trp Val
530 535 540
Ile Ser Gly Leu Ser Ala Leu Asn Ile Val Tyr Tyr Leu Ile Cys Ser
545 550 555 560
Trp Ala Tyr Gly Pro Thr Val Glu Gln Val Gln Val Arg Lys Leu Gly
565 570 575
Glu Glu Asn Gly Ser Arg Glu Leu Glu Pro Ser Thr Glu Phe Arg Asn
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Gly Ser Gln Val Asp Lys Glu Phe Gln Ile Ser Lys Glu Asn Gly Ser
595 600 605
Lys Glu Glu Glu Glu Leu Thr Arg
610 615

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Gln His Ile Ser Gln Pro Gln Lys Arg Lys Gly Gly Leu Val Thr Met 20 30
20 25 30
cct ttc atc att gca aat gag gca ctt gcg agg gtg gca agt ttg ggc 144
Pro Phe Ile Ile Ala Asn Glu Ala Leu Ala Arg Val Ala Ser Leu Gly 35 40 45
35 40 45
ctt ttg ccc aac atg ata ctg tat ttg atg ggg acc tac agg ctt cac 192
Leu Leu Pro Asn Met Ile Leu Tyr Leu Met Gly Thr Tyr Arg Leu His 50 55 60
50 55 60
ctt gcc caa gca acc cag ata ctt ctc tgg tcc cat gct acc agc aat 240
Leu Ala Gln Ala Thr Gln Ile Leu Leu Trp Ser His Ala Thr Ser Asn 65 70 75 80
65 70 75 80
ttc aca cct gtg gtg ggt gct ttc att gct gat tct tat ctg ggt cga 288
Phe Thr Pro Val Val Gly Ala Phe Ile Ala Asp Ser Tyr Leu Gly Arg 85 90 95
85 90 95
ttc ctc gct gtt ggg ttg ggt tcg gcc atc act ttt ctg gga atg aca 336
Phe Leu Ala Val Gly Leu Gly Ser Ala Ile Thr Phe Leu Gly Met Thr 100 105 110
100 105 110
ctg ctg tgg tta aca gct atg atc cca cag gca cgg cct ccc act tgc 384
Leu Leu Trp Leu Thr Ala Met Ile Pro Gln Ala Arg Pro Pro Thr Cys 115 120 125
115 120 125
agt agc aat aaa gct gga ggc tgt aaa tcg gca aca gga ggg caa atg 432
Ser Ser Asn Lys Ala Gly Gly Cys Lys Ser Ala Thr Gly Gly Gln Met 130 135 140
130 135 140
gca atc tta atc tct gcc ctt gct ctc atg tct gtt gga aat ggt ggt 480
Ala Ile Leu Ile Ser Ala Leu Ala Leu Met Ser Val Gly Asn Gly Gly 145 150 155 160
145 150 155 160
ctt tca tgc tcc tta gca ttt ggt gca gac cag gtg aac aga aaa gat 528
Leu Ser Cys Ser Leu Ala Phe Gly Ala Asp Gln Val Asn Arg Lys Asp 165 170 175
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aac ccc aac aac aga agg gtc ttg gaa ata ttc ttc agc tgg tat tat 576
Asn Pro Asn Asn Arg Arg Val Leu Glu Ile Phe Phe Ser Trp Tyr Tyr 180 185 190
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gct tct gct gct att tct gtc ata att gct ctc aca gga ata gtt tat 624
Ala Ser Ala Ala Ile Ser Val Ile Ile Ala Leu Thr Gly Ile Val Tyr 195 200 205
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atc caa gat cat ttt gga tgg aaa gtg ggt tat gga gtt cca gca gca 672
Ile Gln Asp His Phe Gly Trp Lys Val Gly Tyr Gly Val Pro Ala Ala 210 215 220
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ctc atg ctt tta tct act gtc tcc ttc ctc ctt gcc tct cca ctt tat 720
Leu Met Leu Leu Ser Thr Val Ser Phe Leu Leu Ala Ser Pro Leu Tyr 220 225 230
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	Ile	Val	Val	Ala	Tyr	Lys	Asn	Arg	Lys	Leu	Pro	Leu	Pro	Pro	Asn	Asn	
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	Thr	Asp	Lys	Leu	Ser	Phe	Leu	Asn	Arg	Ala	Cys	Val	Ile	Lys	Asp	Arg	
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	Glu	Gln	Glu	Ile	Ala	Ser	Asp	Gly	Ser	Ala	Ser	Asn	Pro	Trp	Lys	Leu	
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	tgc	aca	gta	gat	caa	gta	gag	gaa	cta	aaa	gcc	att	att	aaa	gtg	att	1008
	Cys	Thr	Val	Asp	Gln	Val	Glu	Glu	Leu	Lys	Ala	Ile	Ile	Lys	Val	Ile	
				325						330					335		
	ccc	ttg	tgg	tct	aca	ggg	atc	atg	atg	tca	gtt	aac	att	gga	ggc	tca	1056
	Pro	Leu	Trp	Ser	Thr	Gly	Ile	Met	Met	Ser	Val	Asn	Ile	Gly	Gly	Ser	
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	ttt	gga	ttg	ctg	caa	gct	aag	tcc	ctg	gac	aga	cac	atc	acc	tca	cac	1104
	Phe	Gly	Leu	Leu	Gln	Ala	Lys	Ser	Leu	Asp	Arg	His	Ile	Thr	Ser	His	
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	Phe	Gln	Val	Pro	Pro	Gly	Ser	Phe	Ser	Val	Val	Met	Val	Leu	Thr	Ile	
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	Phe	Leu	Trp	Ile	Ala	Leu	Tyr	Asp	Arg	Ala	Ile	Leu	Pro	Leu	Ala	Ser	
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	Lys	Ile	Arg	Gly	Lys	Pro	Val	Arg	Ile	Ser	Ala	Lys	Arg	Arg	Met	Gly	
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	Leu	Gly	Leu	Phe	Phe	Ser	Phe	Ile	His	Leu	Val	Thr	Ser	Ala	Ile	Val	
				420				425						430			
	gaa	tcc	gta	agg	cga	agg	aga	gca	atc	aag	gag	gga	tat	ctt	aac	aat	1344
	Glu	Ser	Val	Arg	Arg	Arg	Arg	Ala	Ile	Lys	Glu	Gly	Tyr	Leu	Asn	Asn	
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	Ala	Asn	Gly	Val	Leu	His	Met	Ser	Ala	Met	Trp	Leu	Phe	Pro	Gln	Leu	
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	Cys	Leu	Gly	Gly	Ile	Ala	Glu	Ala	Phe	Asn	Ala	Ile	Gly	Gln	Asn	Glu	
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	ttc	tat	tac	aca	gag	ttt	cct	agg	acc	atg	tcc	agt	gtt	gct	gct	tcc	1488
	Phe	Tyr	Tyr	Thr	Glu	Phe	Pro	Arg	Thr	Met	Ser	Ser	Val	Ala	Ala	Ser	
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	ctt	tct	gga	ctg	gga	atg	gct	gca	gga	aac	ttg	gtg	tct	agt	ttt	gtc	1536
	Leu	Ser	Gly	Leu	Gly	Met	Ala	Ala	Gly	Asn	Leu	Val	Ser	Ser	Phe	Val	
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	ttc	agc	gtt	gta	caa	aat	gct	act	tca	aga	ggg	ggg	aaa	gaa	ggg	tgg	1584
	Phe	Ser	Val	Val	Gln	Asn	Ala	Thr	Ser	Arg	Gly	Gly	Lys	Glu	Gly	Trp	
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	gtt	ttg	gat	aac	att	aac	aag	ggg	cgt	tat	gac	aag	tac	tac	tgg	gtt	1632
	Val	Leu	Asp	Asn	Ile	Asn	Lys	Gly	Arg	Tyr	Asp	Lys	Tyr	Tyr	Trp	Val	
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	Ile	Ser	Gly	Leu	Ser	Ala	Leu	Asn	Ile	Val	Tyr	Tyr	Leu	Ile	Cys	Ser	
	545					550					555					560	
	tgg	gct	tat	gga	cct	acc	gtt	gag	caa	gta	caa	gta	cgt	aag	tta	ggg	1728
	Trp	Ala	Tyr	Gly	Pro	Thr	Val	Glu	Gln	Val	Gln	Val	Arg	Lys	Leu	Gly	
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	Glu	Glu	Asn	Gly	Ser	Arg	Glu	Leu	Glu	Pro	Ser	Thr	Glu	Phe	Arg	Asn	
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	ggg	agt	cag	gtt	gac	aaa	gaa	ttc	cag	att	agt	aaa	gaa	aat	ggc	tca	1824
	Gly	Ser	Gln	Val	Asp	Lys	Glu	Phe	Gln	Ile	Ser	Lys	Glu	Asn	Gly	Ser	

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605

1851

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35 40 45
Leu Leu Pro Asn Met Ile Leu Tyr Leu Met Gly Thr Tyr Arg Leu His
50 55 60
Leu Ala Gln Ala Thr Gln Ile Leu Leu Trp Ser His Ala Thr Ser Asn
65 70 75 80
Phe Thr Pro Val Val Gly Ala Phe Ile Ala Asp Ser Tyr Leu Gly Arg
85 90 95
Phe Leu Ala Val Gly Leu Gly Ser Ala Ile Thr Phe Leu Gly Met Thr
100 105 110
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115 120 125
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130 135 140
Ala Ile Leu Ile Ser Ala Leu Ala Leu Met Ser Val Gly Asn Gly Gly
145 150 155 160
Leu Ser Cys Ser Leu Ala Phe Gly Ala Asp Gln Val Asn Arg Lys Asp
165 170 175
Asn Pro Asn Asn Arg Arg Val Leu Glu Ile Phe Phe Ser Trp Tyr Tyr
180 185 190
Ala Ser Ala Ala Ile Ser Val Ile Ile Ala Leu Thr Gly Ile Val Tyr
195 200 205
Ile Gln Asp His Phe Gly Trp Lys Val Gly Tyr Gly Val Pro Ala Ala
210 215 220
Leu Met Leu Leu Ser Thr Val Ser Phe Leu Leu Ala Ser Pro Leu Tyr
225 230 235 240
Val Lys Asn Lys Val Glu Ser Ser Leu Phe Thr Gly Phe Val Gln Val
245 250 255
Ile Val Val Ala Tyr Lys Asn Arg Lys Leu Pro Leu Pro Pro Asn Asn
260 265 270
Ser Pro Glu His Tyr His His Lys Lys Glu Ser Asp Leu Val Val Pro
275 280 285
Thr Asp Lys Leu Ser Phe Leu Asn Arg Ala Cys Val Ile Lys Asp Arg
290 295 300
Glu Gln Glu Ile Ala Ser Asp Gly Ser Ala Ser Asn Pro Trp Lys Leu
305 310 315 320
Cys Thr Val Asp Gln Val Glu Glu Leu Lys Ala Ile Ile Lys Val Ile
325 330 335
Pro Leu Trp Ser Thr Gly Ile Met Met Ser Val Asn Ile Gly Gly Ser
340 345 350
Phe Gly Leu Leu Gln Ala Lys Ser Leu Asp Arg His Ile Thr Ser His
355 360 365
Phe Gln Val Pro Pro Gly Ser Phe Ser Val Val Met Val Leu Thr Ile
370 375 380
Phe Leu Trp Ile Ala Leu Tyr Asp Arg Ala Ile Leu Pro Leu Ala Ser
385 390 395 400
Lys Ile Arg Gly Lys Pro Val Arg Ile Ser Ala Lys Arg Arg Met Gly
405 410 415
Leu Gly Leu Phe Ser Phe Ile His Leu Val Thr Ser Ala Ile Val
420 425 430
Glu Ser Val Arg Arg Arg Arg Ala Ile Lys Glu Gly Tyr Leu Asn Asn
435 440 445
Ala Asn Gly Val Leu His Met Ser Ala Met Trp Leu Phe Pro Gln Leu
450 455 460

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 485 490 495
 Leu Ser Gly Leu Gly Met Ala Ala Gly Asn Leu Val Ser Ser Phe Val
 500 505 510
 Phe Ser Val Val Gln Asn Ala Thr Ser Arg Gly Gly Lys Glu Gly Trp
 515 520 525
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 530 535 540
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 545 550 555 560
 Trp Ala Tyr Gly Pro Thr Val Glu Gln Val Gln Val Arg Lys Leu Gly
 565 570 575
 Glu Glu Asn Gly Ser Arg Glu Leu Glu Pro Ser Thr Glu Phe Arg Asn
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Glu Thr Phe Glu Lys Leu Gly Ile Val Gly Ser Ser Ser Asn Leu Val	
35 40 45	
ata tac tta acg acg gtt ttc aac atg aag agc atc acg gct gcg aaa	192
Ile Tyr Leu Thr Thr Val Phe Asn Met Lys Ser Ile Thr Ala Ala Lys	
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gtc gtc aac atc tac ggt ggc aca agc aac ttt ggc acc atc gtc gct	240
Val Val Asn Ile Tyr Gly Gly Thr Ser Asn Phe Gly Thr Ile Val Ala	
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gct ttc ctc tgt gac tcc tac ttt ggc cgc tac aag acc cta tct ttc	288
Ala Phe Leu Cys Asp Ser Tyr Phe Gly Arg Tyr Lys Thr Leu Ser Phe	
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gcc atg atc gct tgc ttt ctc ggt tcg gtg gca atg gat cta acg gct	336
Ala Met Ile Ala Cys Phe Leu Gly Ser Val Ala Met Asp Leu Thr Ala	
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Val Ile His Pro Leu His Pro Ala Gln Cys Ala Lys Glu Ile Gly Ser	
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Val Cys Asn Gly Pro Ser Ile Gly Gln Ile Met Phe Leu Ala Gly Ala	
130 135 140	
atg gtt ttg ctg gtg atc gga gcc ggt ggg att agg cca tgc aat ctt	480
Met Val Leu Leu Val Ile Gly Ala Gly Gly Ile Arg Pro Cys Asn Leu	
145 150 155 160	
cca ttt ggt gct gat cag ttc gat ccg aag aca aaa gaa ggg aaa cga	528
Pro Phe Gly Ala Asp Gln Phe Asp Pro Lys Thr Lys Glu Gly Lys Arg	
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Gly Ile Glu Ser Phe Phe Asn Trp Tyr Phe Phe Thr Phe Thr Phe Ala	
180 185 190	
cag atg gtg tcg tta acc ctc atc gtc tat gtt cag tca aac gtg agc	624
Gln Met Val Ser Leu Thr Leu Ile Val Tyr Val Gln Ser Asn Val Ser	

205

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720	atc	ata	ttc	ttc	gct	ggt	tct	aag	ctc	tat	gtc	aag	gtt	aaa	gct	agt
	ile	ile	phe	phe	ala	gly	ser	lys	leu	tyr	val	lys	val	lys	ala	ser
768	ggc	agt	ccc	att	cac	agc	ata	act	cgt	gtc	att	gtt	gtc	gcg	atc	aag
	gly	ser	pro	ile	his	ser	ile	thr	arg	val	ile	val	val	ala	ile	lys
816	aag	agg	cgg	tta	aag	ccc	gtt	ggg	cct	aac	gag	ctt	tac	aac	tac	atc
	lys	arg	arg	leu	lys	pro	val	gly	pro	asn	glu	leu	tyr	asn	tyr	ile
864	gcc	agt	gat	ttc	aag	aac	tcg	aaa	ttg	ggc	cat	aca	gag	cag	ttc	agg
	ala	ser	asp	phe	lys	asn	ser	lys	leu	gly	his	thr	glu	gln	phe	arg
912	ttt	ctt	gac	aaa	tcg	gca	atc	caa	aca	caa	gac	gac	aag	ctg	aac	aaa
	phe	leu	asp	lys	ser	ala	ile	gln	thr	gln	asp	asp	lys	leu	asn	lys
960	gat	ggg	tcg	ccg	gtg	gat	gca	tgg	aaa	ctc	tgc	agt	atg	caa	caa	gtg
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	gln	ser	leu	gln	ser	asp	arg	arg	leu	gly	pro	gly	ser	phe	gln	ile
1152	ccg	gcc	ggt	tct	tat	acc	gtc	ttc	cta	atg	ctt	gga	atg	acg	ata	ttc
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1296	ttt	cta	tgc	atc	aca	agt	atg	atg	gtg	tct	gca	att	gta	gaa	caa	tac
	phe	leu	cys	ile	thr	ser	met	met	val	ser	ala	ile	val	glu	gln	tyr
1344	aga	aga	aag	gta	gct	ctc	aca	aaa	ccg	acg	cta	ggg	ttg	gcc	cca	aga
	arg	arg	lys	val	ala	leu	thr	lys	pro	thr	leu	gly	leu	ala	pro	arg
1392	aaa	ggc	gca	atc	tct	tcg	atg	tcc	ggt	atg	tgg	ttg	att	cct	cag	cta
	lys	gly	ala	ile	ser	ser	met	ser	gly	met	trp	leu	ile	pro	gln	leu
1440	gtg	cta	atg	ggt	atc	gcg	gac	gcc	ctc	gct	gga	gtt	gga	caa	atg	gag
	val	leu	met	gly	ile	ala	asp	ala	leu	ala	gly	val	gly	gln	met	glu
1488	ttt	tac	tac	aaa	cag	ttt	cca	gag	aac	atg	cga	agt	ttt	gct	ggt	tct
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1536	ctg	tat	tat	tgt	gga	atc	gga									

PF59082SeqList_PF59082.txt

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1764

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35 40 45
Ile Tyr Leu Thr Thr Val Phe Asn Met Lys Ser Ile Thr Ala Ala Lys
50 55 60
Val Val Asn Ile Tyr Gly Gly Thr Ser Asn Phe Gly Thr Ile Val Ala
65 70 75 80
Ala Phe Leu Cys Asp Ser Tyr Phe Gly Arg Tyr Lys Thr Leu Ser Phe
85 90 95
Ala Met Ile Ala Cys Phe Leu Gly Ser Val Ala Met Asp Leu Thr Ala
100 105 110
Val Ile His Pro Leu His Pro Ala Gln Cys Ala Lys Glu Ile Gly Ser
115 120 125
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130 135 140
Met Val Leu Leu Val Ile Gly Ala Gly Gly Ile Arg Pro Cys Asn Leu
145 150 155 160
Pro Phe Gly Ala Asp Gln Phe Asp Pro Lys Thr Lys Glu Gly Lys Arg
165 170 175
Gly Ile Glu Ser Phe Phe Asn Trp Tyr Phe Phe Thr Phe Thr Phe Ala
180 185 190
Gln Met Val Ser Leu Thr Leu Ile Val Tyr Val Gln Ser Asn Val Ser
195 200 205
Trp Ser Ile Gly Leu Ala Ile Pro Ala Ile Leu Met Leu Leu Gly Cys
210 215 220
Ile Ile Phe Phe Ala Gly Ser Lys Leu Tyr Val Lys Val Lys Ala Ser
225 230 235 240
Gly Ser Pro Ile His Ser Ile Thr Arg Val Ile Val Val Ala Ile Lys
245 250 255
Lys Arg Arg Leu Lys Pro Val Gly Pro Asn Glu Leu Tyr Asn Tyr Ile
260 265 270
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275 280 285
Phe Leu Asp Lys Ser Ala Ile Gln Thr Gln Asp Asp Lys Leu Asn Lys
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Asp Gly Ser Pro Val Asp Ala Trp Lys Leu Cys Ser Met Gln Gln Val
305 310 315 320
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325 330 335
Ala Leu Phe Tyr Leu Ala Tyr Ile Gln Thr Thr Tyr Thr Ile Phe
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Gln Ser Leu Gln Ser Asp Arg Arg Leu Gly Pro Gly Ser Phe Gln Ile
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Pro Ala Gly Ser Tyr Thr Val Phe Leu Met Leu Gly Met Thr Ile Phe
370 375 380
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385 390 395 400
Gly Arg Asp Gly Gly Ile Thr Gln Leu Gln Arg Val Gly Ala Gly Leu
405 410 415
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420 425 430
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<213> Arabidopsis thaliana

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Ala Asn Met Ile Ser Tyr Leu Thr Thr Gln Leu His Leu Pro Leu Thr	
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Lys Ala Ala Asn Thr Leu Thr Asn Phe Ala Gly Thr Ser Ser Leu Thr	
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cct ctc ctt ggt gcc ttt atc gcc gac tct ttc gcc ggc cga ttt tgg	288
Pro Leu Leu Gly Ala Phe Ile Ala Asp Ser Phe Ala Gly Arg Phe Trp	
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acg ata tcg gca ata ata cca acg cta agg cca cca cca tgt aaa gga	384
Thr Ile Ser Ala Ile Ile Pro Thr Leu Arg Pro Pro Pro Cys Lys Gly	
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Ala Ala Val Leu Leu Ala Val Thr Val Leu Val Trp Ile Gln Asp Asn	
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gaa Glu	gat Asp	agt Ser	agt Ser 580	ccg Pro	gtt Val	aag Lys	gag Glu	gaa Glu 585	ttg Leu	cag Gln	ttg Leu	tca Ser	aat Asn 590	agg Arg	agt Ser	1776

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 Lys Ala Ala Asn Thr Leu Thr Asn Phe Ala Gly Thr Ser Ser Leu Thr
 65 70 75 80
 Pro Leu Leu Gly Ala Phe Ile Ala Asp Ser Phe Ala Gly Arg Phe Trp
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 Thr Ile Ser Ala Ile Ile Pro Thr Leu Arg Pro Pro Cys Lys Gly
 115 120 125
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 Val Gly Trp Gly Leu Gly Leu Gly Ile Pro Thr Val Ala Met Phe Leu
 210 215 220
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 225 230 235 240
 Pro Ala Gly Ser Pro Phe Thr Arg Leu Ile Gln Val Gly Val Ala Ala
 245 250 255
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 260 265 270
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 275 280 285
 His Thr Lys His Met Ser Phe Leu Asp Lys Ala Ala Ile Val Thr Glu
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 Glu Asp Asn Leu Lys Pro Gly Gln Ile Pro Asn His Trp Arg Leu Ser
 305 310 315 320
 Thr Val His Arg Val Glu Glu Leu Lys Ser Val Ile Arg Met Gly Pro
 325 330 335
 Ile Gly Ala Ser Gly Ile Leu Leu Ile Thr Ala Tyr Ala Gln Gln Gly
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 Thr Phe Ser Leu Gln Gln Ala Lys Thr Met Asn Arg His Leu Thr Asn
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 Ser Phe Gln Ile Pro Ala Gly Ser Met Ser Val Phe Thr Thr Val Ala
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 385 390 395 400
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 405 410 415
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 Val Glu Val Lys Arg Lys Ser Val Ala Ile Glu His Gly Leu Leu Asp
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 Lys Pro His Thr Ile Val Pro Ile Ser Phe Leu Trp Leu Ile Pro Gln
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 Seite 361

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 aca ttg gag agg ctt gcc aca ttc ggt ttg atg gcg aat ttc atg gtg 144
 Thr Leu Glu Arg Leu Ala Thr Phe Gly Leu Met Ala Asn Phe Met Val 35
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 Tyr Met Val Arg Glu Tyr His Met Asp Gln Val Gln Ala Val Thr Leu 50
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 Ile Asn Thr Trp Ser Ala Leu Thr Asn Phe Ala Pro Ile Ile Gly Ala 65
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 Phe Ile Ser Asp Ser Tyr Thr Gly Lys Phe Asn Thr Ile Val Phe Gly 85
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 Val Pro Asn Leu Arg Pro Pro Pro Cys Thr Ala Asp Gln Ile Thr Gly 115
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 Gln Cys Ile Pro Tyr Ser Tyr Ser Gln Leu Tyr Val Leu Leu Ser Gly 130
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 Gln Leu Val Ser Met Thr Leu Val Leu Tyr Val Gln Asn Asn Ile Ser 195
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	Ser	Thr	Met	Leu	Ile	Ser	Gly	Ile	Val	Glu	Arg	Lys	Arg	Arg	Asp	Leu	
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Ser Thr Met Leu Ile Ser Gly Ile Val Glu Arg Lys Arg Arg Asp Leu
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Trp	Thr	Ile	Ala	Thr	Phe	Val	Phe	Ile	Tyr	Val	Ser	Gly	Met	Thr	Leu	
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Leu	Thr	Leu	Ser	Ala	Ser	Val	Pro	Gly	Leu	Lys	Pro	Gly	Asn	Cys	Asn	
	115					120					125					
gct	gat	act	tgt	cat	cca	aat	tct	agt	cag	act	gct	ggt	ttc	ttt	gtc	432
Ala	Asp	Thr	Cys	His	Pro	Asn	Ser	Ser	Gln	Thr	Ala	Val	Phe	Phe	Val	
	130				135					140						
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Ala	Leu	Tyr	Met	Ile	Ala	Leu	Gly	Thr	Gly	Gly	Ile	Lys	Pro	Cys	Val	
145				150				155						160		
tcg	tcc	ttt	gga	gct	gat	cag	ttt	gat	gag	aat	gat	gag	aat	gag	aag	528
Ser	Ser	Phe	Gly	Ala	Asp	Gln	Phe	Asp	Glu	Asn	Asp	Glu	Asn	Glu	Lys	
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Ile	Lys	Lys	Ser	Ser	Phe	Phe	Asn	Trp	Phe	Tyr	Phe	Ser	Ile	Asn	Val	
		180					185					190				
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Gly	Trp	Gly	Trp	Gly	Phe	Gly	Val	Pro	Thr	Val	Ala	Met	Val	Ile	Ala	
	210				215						220					
gtt	tgc	ttt	ttc	ttc	ttc	gga	agc	cgt	ttt	tac	aga	ctt	cag	aga	cct	720
Val	Cys	Phe	Phe	Phe	Phe	Gly	Ser	Arg	Phe	Tyr	Arg	Leu	Gln	Arg	Pro	
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Gly	Gly	Ser	Pro	Leu	Thr	Arg	Ile	Phe	Gln	Val	Ile	Val	Ala	Ala	Phe	
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cgg	aag	ata	agt	gtt	aag	gtt	cca	gag	gac	aag	tct	ctg	ctc	ttt	gaa	816
Arg	Lys	Ile	Ser	Val	Lys	Val	Pro	Glu	Asp	Lys	Ser	Leu	Leu	Phe	Glu	
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Thr	Ala	Asp	Asp	Glu	Ser	Asn	Ile	Lys	Gly	Ser	Arg	Lys	Leu	Val	His	
		275					280				285					
aca	gat	aac	tta	aag	ttt	ttt	gac	aag	gca	gcg	gtt	gag	agt	caa	tct	912

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Asp	Ser	Ile	Lys	Asp	Gly	Glu	Val	Asn	Pro	Trp	Arg	Leu	Cys	Ser	Val	
305					310					315					320	
act	caa	gtt	gaa	gaa	ctt	aag	tca	ata	atc	aca	ctt	ctt	cca	gtt	tgg	1008
Thr	Gln	Val	Glu	Glu	Leu	Lys	Ser	Ile	Ile	Thr	Leu	Leu	Pro	Val	Trp	
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gcc	aca	gga	ata	gtc	ttc	gcc	aca	gtg	tac	agc	caa	atg	agc	aca	atg	1056
Ala	Thr	Gly	Ile	Val	Phe	Ala	Thr	Val	Tyr	Ser	Gln	Met	Ser	Thr	Met	
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ttt	gtg	tta	caa	gga	aac	aca	atg	gac	caa	cac	atg	gga	aaa	aac	ttt	1104
Phe	Val	Leu	Gln	Gly	Asn	Thr	Met	Asp	Gln	His	Met	Gly	Lys	Asn	Phe	
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gaa	atc	cca	tca	gct	tca	ctc	tca	ctt	ttc	gac	act	gtc	agt	gta	ctc	1152
Glu	Ile	Pro	Ser	Ala	Ser	Leu	Ser	Leu	Phe	Asp	Thr	Val	Ser	Val	Leu	
	370					375					380					
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Phe	Thr	Arg	Asn	Glu	Arg	Gly	Phe	Thr	Gln	Leu	Gln	Arg	Met	Gly	Ile	
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ggg	ctt	gtg	gtc	tcc	atc	ttt	gcc	atg	atc	act	gca	gga	gtc	ttg	gag	1296
Gly	Leu	Val	Val	Ser	Ile	Phe	Ala	Met	Ile	Thr	Ala	Gly	Val	Leu	Glu	
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Val	Val	Arg	Leu	Asp	Tyr	Val	Lys	Thr	His	Asn	Ala	Tyr	Asp	Gln	Lys	
		435				440					445					
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Gln	Ile	His	Met	Ser	Ile	Phe	Trp	Gln	Ile	Pro	Gln	Tyr	Leu	Leu	Ile	
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Asp	Gln	Ala	Pro	Asp	Ala	Met	Arg	Ser	Leu	Cys	Ser	Ala	Leu	Ser	Leu	
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acc	acg	gtt	gcg	ttg	ggg	aac	tat	ttg	agc	aca	gtt	ctt	gtg	acg	gtt	1536
Thr	Thr	Val	Ala	Leu	Gly	Asn	Tyr	Leu	Ser	Thr	Val	Leu	Val	Thr	Val	
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Val	Met	Lys	Ile	Thr	Lys	Lys	Asn	Gly	Lys	Pro	Gly	Trp	Ile	Pro	Asp	
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Asn	Leu	Asn	Arg	Gly	His	Leu	Asp	Tyr	Phe	Phe	Tyr	Leu	Leu	Ala	Thr	
	530					535					540					
ctc	agt	ttc	ctc	aac	ttc	tta	gtg	tac	ctc	tgg	att	tca	aaa	cgc	tac	1680
Leu	Ser	Phe	Leu	Asn	Phe	Leu	Val	Tyr	Leu	Trp	Ile	Ser	Lys	Arg	Tyr	
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aaa	tac	aag	aaa	gct	gtt	ggg	cga	gca	cat	tga						1713
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<211> 570

<212> PRT

<213> Arabidopsis thaliana

<400> 261

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Phe	Ile	Leu	Gly	Asn	Glu	Cys	Cys	Glu	Arg	Leu	Ala	Tyr	Tyr	Gly	Met	
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Gly	Thr	Asn	Leu	Val	Asn	Tyr	Leu	Glu	Ser	Arg	Leu	Asn	Gln	Gly	Asn	
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PF59082SeqList_PF59082.txt

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Leu	Thr	Leu	Ser	Ala	Ser	Val	Pro	Gly	Leu	Lys	Pro	Gly	Asn	Cys	Asn		
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Ala	Leu	Tyr	Met	Ile	Ala	Leu	Gly	Thr	Gly	Gly	Ile	Lys	Pro	Cys	Val		
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Ser	Ser	Phe	Gly	Ala	Asp	Gln	Phe	Asp	Glu	Asn	Asp	Glu	Asn	Glu	Lys		
			165					170						175			
Ile	Lys	Lys	Ser	Ser	Phe	Phe	Asn	Trp	Phe	Tyr	Phe	Ser	Ile	Asn	Val		
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Val	Cys	Phe	Phe	Phe	Phe	Gly	Ser	Arg	Phe	Tyr	Arg	Leu	Gln	Arg	Pro		
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Thr	Asp	Asn	Leu	Lys	Phe	Phe	Asp	Lys	Ala	Ala	Val	Glu	Ser	Gln	Ser		
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Asp	Ser	Ile	Lys	Asp	Gly	Glu	Val	Asn	Pro	Trp	Arg	Leu	Cys	Ser	Val		
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	370				375						380						
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Phe	Thr	Arg	Asn	Glu	Arg	Gly	Phe	Thr	Gln	Leu	Gln	Arg	Met	Gly	Ile		
			405					410						415			
Gly	Leu	Val	Val	Ser	Ile	Phe	Ala	Met	Ile	Thr	Ala	Gly	Val	Leu	Glu		
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Val	Val	Arg	Leu	Asp	Tyr	Val	Lys	Thr	His	Asn	Ala	Tyr	Asp	Gln	Lys		
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Gln	Ile	His	Met	Ser	Ile	Phe	Trp	Gln	Ile	Pro	Gln	Tyr	Leu	Leu	Ile		
	450				455						460						
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	465				470				475						480		
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Thr	Thr	Val	Ala	Leu	Gly	Asn	Tyr	Leu	Ser	Thr	Val	Leu	Val	Thr	Val		
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Val	Met	Lys	Ile	Thr	Lys	Lys	Asn	Gly	Lys	Pro	Gly	Trp	Ile	Pro	Asp		
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Asn	Leu	Asn	Arg	Gly	His	Leu	Asp	Tyr	Phe	Phe	Tyr	Leu	Leu	Ala	Thr		
	530				535						540						
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<211> 1686

<212> DNA

<213> Arabidopsis thaliana

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Phe Glu Lys Leu Ala Ser Met Ser Leu Ile Gly Asn Leu Ser Val Tyr	
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Leu Met Thr Lys Tyr Asn Leu Gly Gly Val Phe Leu Val Asn Val Ile	
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aac ata tgg ttt ggt tct tgc aac att ctt aca ctc gct ggt gct ttt	240
Asn Ile Trp Phe Gly Ser Cys Asn Ile Leu Thr Leu Ala Gly Ala Phe	
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Val Ser Asp Ala Tyr Leu Gly Arg Phe Trp Thr Leu Leu Leu Gly Ser	
85 90 95	
atc gcc tcc ttt ata gga atg gga ata ttt gct cta acc gct gct ctc	336
Ile Ala Ser Phe Ile Gly Met Gly Ile Phe Ala Leu Thr Ala Ala Leu	
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Pro Ser Leu Arg Pro Asp Ala Cys Ile Asp Pro Ser Asn Cys Ser Asn	
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Gln Pro Ala Lys Trp Gln Leu Gly Val Leu Phe Ser Gly Leu Gly Leu	
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Leu Ala Ile Gly Ala Gly Gly Val Arg Pro Cys Asn Ile Ala Phe Gly	
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Thr Phe Phe Asn Trp Trp Tyr Phe Ser Phe Thr Val Ala Leu Val Ile	
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Ala Leu Thr Gly Val Val Tyr Ile Gln Thr Asn Ile Ser Trp Val Ile	
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210 215 220	
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Phe Ala Asp Ile Val Lys Val Val Thr Ala Ala Cys Lys Lys Arg Lys	
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Val Lys Pro Gly Ser Asp Ile Thr Phe Tyr Ile Gly Pro Ser Asn Asp	
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Gly Ser Pro Thr Leu Val Arg Asp Lys His Arg Leu Arg Phe Phe	
275 280 285	
gac aaa gca tct atc gta acg aat ccg aac gag tta aac gaa gac ggt	912
Asp Lys Ala Ser Ile Val Thr Asn Pro Asn Glu Leu Asn Glu Asp Gly	
290 295 300	
aac gcg aag tac aaa tgg aga tta tgt agt gtg cag cag gtg aaa aac	960
Asn Ala Lys Tyr Lys Trp Arg Leu Cys Ser Val Gln Gln Val Lys Asn	
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Leu Lys Cys Val Thr Ala Ile Leu Pro Val Trp Val Thr Gly Ile Ala	
325 330 335	
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Gly	Ile	Ile	Cys	Met	Ile	Val	Ala	Gly	Phe	Gln	Glu	Lys	Lys	Arg	Arg	
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Ala	Ser	Ala	Leu	Lys	Asn	Gly	Ser	Phe	Val	Ser	Pro	Val	Ser	Ile	Val	
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<211> 561

<212> PRT

<213> Arabidopsis thaliana

<400> 263

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PF59082SeqList_PF59082.txt

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 Thr 300 Phe 305 Phe 310 Asn 315 Trp 320 Trp 325 Tyr 330 Phe 335 Ser 340 Phe 345 Thr 350 Val 355 Ala 360 Leu 365 Val 370 Ile 375
 Ala 380 Leu 385 Thr 390 Gly 395 Val 400 Val 405 Tyr 410 Ile 415 Gln 420 Thr 425 Asn 430 Ile 435 Ser 440 Trp 445 Val 450 Ile 455
 Gly 460 Phe 465 Val 470 Ile 475 Pro 480 Thr 485 Tyr 490 Cys 495 Ala 500 Lys 505 Thr 510 Ser 515 Trp 520 Leu 525 Gly 530 Asn 535
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 Seite 370

PF59082SeqList_PF59082.txt

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Gln	Pro	Trp	Leu	Asn	Leu	Tyr	Asn	Tyr	Tyr	Pro	Pro	Lys	Tyr	Ala	Asn		
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Val	Asn	Phe	Ala	Tyr	Phe	Leu	Val	Met	Ser	Arg	Trp	Tyr	Arg	Tyr	Lys	
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Gly	Ser	Asp	Asp	Glu	Val	Thr	Thr	Tyr	Glu	Thr	Asn	Glu	Asn	Ile	Ile	
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Gln	Pro	Trp	Leu	Asn	Leu	Tyr	Asn	Tyr	Tyr	Pro	Pro	Lys	Tyr	Ala	Asn
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Ile	Leu	Thr	Pro	Glu	Asp	Lys	Leu	Gln	Pro	Asp	Gly	Lys	Pro	Ala	Asp
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Pro	Trp	Lys	Leu	Cys	Thr	Met	Gln	Gln	Val	Glu	Glu	Val	Lys	Cys	Ile
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Val	Phe	Leu	Met	Thr	Gly	Met	Thr	Val	Phe	Ile	Val	Val	Tyr	Asp	Arg
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Thr	Leu	Leu	Gln	Arg	Ile	Gly	Thr	Gly	Ile	Phe	Phe	Ala	Thr	Ala	Ser
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Val Tyr Leu Thr Lys Val Phe His Leu Glu Gln Val Asp Ala Ala Asn
85      90      95
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Val Ile Asn Ile Trp Ser Gly Phe Thr Asn Leu Thr Pro Leu Val Gly
100      105      110
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Ala Tyr Ile Ser Asp Thr Tyr Val Gly Arg Phe Lys Thr Ile Ala Phe
115      120      125
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Val Met Phe Phe Ala Gly Met Lys Arg Tyr Val Tyr Val Lys Pro Glu
260      265      270
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Gly Ser Ile Phe Ser Gly Ile Ala Gln Val Ile Val Ala Ala Arg Lys
275      280      285
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Lys Arg Lys Leu Lys Leu Pro Ala Glu Asp Asp Gly Thr Val Thr Tyr
290      295      300
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Tyr Asp Pro Ala Ile Lys Ser Ser Val Leu Ser Lys Leu His Arg Ser
305      310      315
aac caa ttc agg tgt ctt gac aaa gcc gcg gtg gtt ata gaa ggt gac      1008
Asn Gln Phe Arg Cys Leu Asp Lys Ala Ala Val Val Ile Glu Gly Asp
325      330      335
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PF59082SeqList_PF59082.txt

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	370					375					380					
acg	gtc	tct	caa	gct	ttg	aaa	atg	gat	cga	aac	tta	ggg	cct	aaa	ttc	1200
Thr	Val	Ser	Gln	Ala	Leu	Lys	Met	Asp	Arg	Asn	Leu	Gly	Pro	Lys	Phe	
	385				390					395					400	
gag	att	ccg	gct	ggg	tca	ctc	tcc	gtc	atc	tct	ctc	ctc	aca	atc	ggc	1248
Glu	Ile	Pro	Ala	Gly	Ser	Leu	Ser	Val	Ile	Ser	Leu	Leu	Thr	Ile	Gly	
			405					410						415		
atc	ttt	ctt	ccc	ttc	tac	gac	cgc	gtt	ttt	gta	cca	ttc	atg	cgg	cga	1296
Ile	Phe	Leu	Pro	Phe	Tyr	Asp	Arg	Val	Phe	Val	Pro	Phe	Met	Arg	Arg	
			420				425						430			
atc	acc	ggc	cat	aaa	tcc	gga	atc	aca	ctc	ctc	caa	agg	ata	gga	aca	1344
Ile	Thr	Gly	His	Lys	Ser	Gly	Ile	Thr	Leu	Leu	Gln	Arg	Ile	Gly	Thr	
		435				440						445				
ggg	atc	gtt	ttc	gcg	atc	ttt	tct	atg	atc	gtt	gcg	ggc	att	gtg	gag	1392
Gly	Ile	Val	Phe	Ala	Ile	Phe	Ser	Met	Ile	Val	Ala	Gly	Ile	Val	Glu	
	450					455					460					
cgt	atg	aga	cgc	ata	cgc	tcc	atc	aat	gcc	gga	gat	cca	acg	gga	atg	1440
Arg	Met	Arg	Arg	Ile	Arg	Ser	Ile	Asn	Ala	Gly	Asp	Pro	Thr	Gly	Met	
	465				470				475						480	
act	cca	atg	tcg	gtg	ttt	tgg	ctt	tcg	ccg	cag	cta	att	ctc	atg	gga	1488
Thr	Pro	Met	Ser	Val	Phe	Trp	Leu	Ser	Pro	Gln	Leu	Ile	Leu	Met	Gly	
				485					490					495		
cta	tgt	gaa	gca	ttc	aat	atc	atc	gga	caa	att	gag	ttc	ttc	aac	agt	1536
Leu	Cys	Glu	Ala	Phe	Asn	Ile	Ile	Gly	Gln	Ile	Glu	Phe	Phe	Asn	Ser	
			500					505					510			
cag	ttt	cca	gag	cac	atg	aga	agt	atc	gct	aac	tct	ctc	ttc	tct	tta	1584
Gln	Phe	Pro	Glu	His	Met	Arg	Ser	Ile	Ala	Asn	Ser	Leu	Phe	Ser	Leu	
		515				520						525				
tcg	ttc	gcc	ggg	tcg	agc	tac	ctt	agt	agt	ttc	ctt	gtg	act	gtc	gtt	1632
Ser	Phe	Ala	Gly	Ser	Ser	Tyr	Leu	Ser	Ser	Phe	Leu	Val	Thr	Val	Val	
	530					535					540					
cat	aaa	ttc	tcc	ggg	ggg	cat	gat	cg	ccg	gat	tgg	cta	aac	aag	aat	1680
His	Lys	Phe	Ser	Gly	Gly	His	Asp	Arg	Pro	Asp	Trp	Leu	Asn	Lys	Asn	
				550					555						560	
ctc	aac	gcg	gga	aaa	ttg	gat	tac	ttc	tat	tat	ctg	att	gcg	gtt	ttg	1728
Leu	Asn	Ala	Gly	Lys	Leu	Asp	Tyr	Phe	Tyr	Tyr	Leu	Ile	Ala	Val	Leu	
				565					570					575		
ggg	gtg	gtt	aat	ctg	gtt	tac	ttt	tgg	tat	tgt	gct	cg	gga	tac	cg	1776
Gly	Val	Val	Asn	Leu	Val	Tyr	Phe	Trp	Tyr	Cys	Ala	Arg	Gly	Tyr	Arg	
			580					585					590			
tac	aag	gtc	ggg	tta	ccg	att	gaa	gac	ttt	gag	gag	gac	aag	tcc	tcc	1824
Tyr	Lys	Val	Gly	Leu	Pro	Ile	Glu	Asp	Phe	Glu	Glu	Asp	Lys	Ser	Ser	
		595					600					605				
gat	gat	gtt	gag	atg	act	tcg	aag	aaa	tcg	atg	aaa	tga				1863
Asp	Asp	Val	Glu	Met	Thr	Ser	Lys	Lys	Ser	Met	Lys					
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<210> 267

<211> 620

<212> PRT

<213> Arabidopsis thaliana

<400> 267

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		20						25					30		
Tyr	Lys	Arg	Ile	Ser	Ser	Pro	Gly	Ser	Ile	Leu	Asp	Ala	Glu	Lys	Val
		35					40					45			
Glu	Lys	Lys	Pro	Gly	Gly	Trp	Arg	Ala	Val	Ser	Phe	Ile	Leu	Gly	Asn
	50					55					60				
Glu	Thr	Leu	Glu	Arg	Leu	Gly	Ser	Ile	Gly	Leu	Leu	Ala	Asn	Phe	Met
					70					75					80
Val	Tyr	Leu	Thr	Lys	Val	Phe	His	Leu	Glu	Gln	Val	Asp	Ala	Ala	Asn
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PF59082SeqList_PF59082.txt

Val	Ile	Asn	Ile	Trp	Ser	Gly	Phe	Thr	Asn	Leu	Thr	Pro	Leu	Val	Gly
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Ala	Tyr	Ile	Ser	Asp	Thr	Tyr	Val	Gly	Arg	Phe	Lys	Thr	Ile	Ala	Phe
		115					120					125			
Ala	Ser	Phe	Ala	Thr	Leu	Leu	Gly	Leu	Ile	Thr	Ile	Thr	Leu	Thr	Ala
		130					135					140			
Ser	Phe	Pro	Gln	Leu	His	Pro	Ala	Ser	Cys	Asn	Ser	Gln	Asp	Pro	Leu
145					150					155					160
Ser	Cys	Gly	Gly	Pro	Asn	Lys	Leu	Gln	Ile	Gly	Val	Leu	Leu	Leu	Gly
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Leu	Cys	Phe	Leu	Ser	Val	Gly	Ser	Gly	Gly	Ile	Arg	Pro	Cys	Ser	Ile
			180					185					190		
Pro	Phe	Gly	Val	Asp	Gln	Phe	Asp	Gln	Arg	Thr	Glu	Glu	Gly	Val	Lys
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Gly	Val	Ala	Ser	Phe	Phe	Asn	Trp	Tyr	Tyr	Met	Thr	Phe	Thr	Val	Val
		210				215					220				
Leu	Ile	Ile	Thr	Gln	Thr	Val	Val	Val	Tyr	Ile	Gln	Asp	Gln	Val	Ser
225					230					235					240
Trp	Ile	Ile	Gly	Phe	Ser	Ile	Pro	Thr	Gly	Leu	Met	Ala	Leu	Ala	Val
				245					250					255	
Val	Met	Phe	Phe	Ala	Gly	Met	Lys	Arg	Tyr	Val	Tyr	Val	Lys	Pro	Glu
			260					265					270		
Gly	Ser	Ile	Phe	Ser	Gly	Ile	Ala	Gln	Val	Ile	Val	Ala	Ala	Arg	Lys
		275					280					285			
Lys	Arg	Lys	Leu	Lys	Leu	Pro	Ala	Glu	Asp	Asp	Gly	Thr	Val	Thr	Tyr
		290				295					300				
Tyr	Asp	Pro	Ala	Ile	Lys	Ser	Ser	Val	Leu	Ser	Lys	Leu	His	Arg	Ser
305					310					315					320
Asn	Gln	Phe	Arg	Cys	Leu	Asp	Lys	Ala	Ala	Val	Val	Ile	Glu	Gly	Asp
				325					330					335	
Leu	Thr	Pro	Glu	Gly	Pro	Pro	Ala	Asp	Lys	Trp	Arg	Leu	Cys	Ser	Val
			340					345					350		
Gln	Glu	Val	Glu	Glu	Val	Lys	Cys	Leu	Ile	Arg	Ile	Val	Pro	Ile	Trp
		355					360					365			
Ser	Ala	Gly	Ile	Ile	Ser	Leu	Ala	Ala	Met	Thr	Thr	Gln	Gly	Thr	Phe
		370				375					380				
Thr	Val	Ser	Gln	Ala	Leu	Lys	Met	Asp	Arg	Asn	Leu	Gly	Pro	Lys	Phe
385					390					395					400
Glu	Ile	Pro	Ala	Gly	Ser	Leu	Ser	Val	Ile	Ser	Leu	Leu	Thr	Ile	Gly
				405					410					415	
Ile	Phe	Leu	Pro	Phe	Tyr	Asp	Arg	Val	Phe	Val	Pro	Phe	Met	Arg	Arg
			420					425					430		
Ile	Thr	Gly	His	Lys	Ser	Gly	Ile	Thr	Leu	Leu	Gln	Arg	Ile	Gly	Thr
		435					440					445			
Gly	Ile	Val	Phe	Ala	Ile	Phe	Ser	Met	Ile	Val	Ala	Gly	Ile	Val	Glu
		450				455					460				
Arg	Met	Arg	Arg	Ile	Arg	Ser	Ile	Asn	Ala	Gly	Asp	Pro	Thr	Gly	Met
465					470				475						480
Thr	Pro	Met	Ser	Val	Phe	Trp	Leu	Ser	Pro	Gln	Leu	Ile	Leu	Met	Gly
				485					490					495	
Leu	Cys	Glu	Ala	Phe	Asn	Ile	Ile	Gly	Gln	Ile	Glu	Phe	Phe	Asn	Ser
			500					505					510		
Gln	Phe	Pro	Glu	His	Met	Arg	Ser	Ile	Ala	Asn	Ser	Leu	Phe	Ser	Leu
		515					520					525			
Ser	Phe	Ala	Gly	Ser	Ser	Tyr	Leu	Ser	Ser	Phe	Leu	Val	Thr	Val	Val
		530				535					540				
His	Lys	Phe	Ser	Gly	Gly	His	Asp	Arg	Pro	Asp	Trp	Leu	Asn	Lys	Asn
545					550					555					560
Leu	Asn	Ala	Gly	Lys	Leu	Asp	Tyr	Phe	Tyr	Tyr	Leu	Ile	Ala	Val	Leu
				565					570					575	
Gly	Val	Val	Asn	Leu	Val	Tyr	Phe	Trp	Tyr	Cys	Ala	Arg	Gly	Tyr	Arg
			580					585					590		
Tyr	Lys	Val	Gly	Leu	Pro	Ile	Glu	Asp	Phe	Glu	Glu	Asp	Lys	Ser	Ser
		595					600					605			
Asp	Asp	Val	Glu	Met	Thr	Ser	Lys	Lys	Ser	Met	Lys				
		610				615					620				

<210> 268
<211> 1743

PF59082SeqList_PF59082.txt

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<221> CDS

<222> (1)..(1743)

<400> 268

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gtc aag ggc aac ccg gcc acc aag aag aac acc ggc aac tgg cgt gcc	96
Val Lys Gly Asn Pro Ala Thr Lys Lys Asn Thr Gly Asn Trp Arg Ala	
20 25 30	
tgc ccc tac atc ctc gct aac gag tgc tgc gag agg ctg gcc tac tat	144
Cys Pro Tyr Ile Leu Ala Asn Glu Cys Cys Glu Arg Leu Ala Tyr Tyr	
35 40 45	
ggc atg agc acc aac ctc gtg aac tac atg aag acg cgg ctc ggg cag	192
Gly Met Ser Thr Asn Leu Val Asn Tyr Met Lys Thr Arg Leu Gly Gln	
50 55 60	
gag agc gcc att gcc gcc aac aat gtc acc aac tgg tcg ggg act tgc	240
Glu Ser Ala Ile Ala Ala Asn Asn Val Thr Asn Trp Ser Gly Thr Cys	
65 70 75 80	
tac atc acc ccc ctt ctc ggt gcc ttc ttg gct gat gcc tac atg ggc	288
Tyr Ile Thr Pro Leu Leu Gly Ala Phe Leu Ala Asp Ala Tyr Met Gly	
85 90 95	
agg ttc tgg acc att gcc agc ttc atg atc atc tac atc ctg ggt ttg	336
Arg Phe Trp Thr Ile Ala Ser Phe Met Ile Ile Tyr Ile Leu Gly Leu	
100 105 110	
gcg ttg ctg aca atg gcg tcg tcg gtg aag ggg ctg gtg ccg gcg tgc	384
Ala Leu Leu Thr Met Ala Ser Ser Val Lys Gly Leu Val Pro Ala Cys	
115 120 125	
gac gga gga gcg tgt cac ccg acg gag gcg cag acg ggg gtg gtg ttc	432
Asp Gly Gly Ala Cys His Pro Thr Glu Ala Gln Thr Gly Val Val Phe	
130 135 140	
ttg gcg ctg tac ctg ata gcg ctg ggc acc ggc ggg atc aag ccg tgc	480
Leu Ala Leu Tyr Leu Ile Ala Leu Gly Thr Gly Gly Ile Lys Pro Cys	
145 150 155 160	
gtg tcg tcg ttt ggc gcg gac cag ttc gag gag aac gac gag ggg gag	528
Val Ser Ser Phe Gly Ala Asp Gln Phe Asp Glu Asn Asp Glu Gly Glu	
165 170 175	
aag cgg agc aag agc agc ttc ttc aac tgg ttc tac ttc tcc atc aac	576
Lys Arg Ser Lys Ser Ser Phe Phe Asn Trp Phe Tyr Phe Ser Ile Asn	
180 185 190	
atc ggc gcg ctg gtg gcg tcg tcg ctg gtg tac gtg cag acg cac	624
Ile Gly Ala Leu Val Ala Ser Ser Val Leu Val Tyr Val Gln Thr His	
195 200 205	
gtc ggg tgg ggg tgg ggg ttc ggc atc ccg gcc gtc gtc atg gcc gtc	672
Val Gly Trp Gly Trp Gly Phe Gly Ile Pro Ala Val Val Met Ala Val	
210 215 220	
gcc gtc gcc agc ttc ttc gtc ggc acg ccg ctg tac agg cac cag ccg	720
Ala Val Ala Ser Phe Phe Val Gly Thr Pro Leu Tyr Arg His Gln Arg	
225 230 235 240	
ccc ggg ggc agc ccg ctg acg agg atc gcg cag gtg ctc gtc gcg tcg	768
Pro Gly Gly Ser Pro Leu Thr Arg Ile Ala Gln Val Leu Val Ala Ser	
245 250 255	
gcg agg aag tgg ggc gtc gag gtc ccc gcc gac ggg tcg cgg ctg cac	816
Ala Arg Lys Trp Gly Val Glu Val Pro Ala Asp Gly Ser Arg Leu His	
260 265 270	
gag acg ctc gac agg gag tcc ggc atc gag ggc agc cgc aag ctg gag	864
Glu Thr Leu Asp Arg Glu Ser Gly Ile Glu Gly Ser Arg Lys Leu Glu	
275 280 285	
cac acc ggg cag ttc gcg tgc ctc gac agg gcg gcg gtg gag acg ccg	912
His Thr Gly Gln Phe Ala Cys Leu Asp Arg Ala Val Glu Thr Pro	
290 295 300	
gag gac agg tcg gcg gcg aac gcg tcg gcg tgg cgg ctg tgc acg gtg	960
Glu Asp Arg Ser Ala Ala Asn Ala Ser Ala Trp Arg Leu Cys Thr Val	
305 310 315 320	
acg cag gtg gag gag ctg aag agc gtg gtg cgg ctg ctg ccg atc tgg	1008

PF59082SeqList_PF59082.txt

Thr	Gln	Val	Glu	Glu	Leu	Lys	Ser	Val	Val	Arg	Leu	Leu	Pro	Ile	Trp	
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gcg	agc	ggg	atc	gtg	ttc	gcg	acg	gtg	tac	ggg	cag	atg	agc	acc	atg	1056
Ala	Ser	Gly	Ile	Val	Phe	Ala	Thr	Val	Tyr	Gly	Gln	Met	Ser	Thr	Met	
			340					345					350			
ttc	gtc	ctc	cag	ggg	aac	acg	ctc	gac	gcc	agc	atg	ggg	ccg	cac	ttc	1104
Phe	Val	Leu	Gln	Gly	Asn	Thr	Leu	Asp	Ala	Ser	Met	Gly	Pro	His	Phe	
		355					360					365				
tcc	atc	ccg	gcg	gcg	tcg	ctc	tcc	atc	ttc	gac	acc	ctc	agc	gtc	atc	1152
Ser	Ile	Pro	Ala	Ala	Ser	Leu	Ser	Ile	Phe	Asp	Thr	Leu	Ser	Val	Ile	
	370					375					380					
gtc	tgg	gtg	ccg	gtg	tac	gac	cgc	ctc	atc	gtg	ccg	gcg	gtg	cgc	gcc	1200
Val	Trp	Val	Pro	Val	Tyr	Asp	Arg	Leu	Ile	Val	Pro	Ala	Val	Arg	Ala	
385					390					395					400	
gtg	acg	ggg	cgc	cca	cgc	ggg	ttc	acc	cag	ctg	cag	cgg	atg	ggc	atc	1248
Val	Thr	Gly	Arg	Pro	Arg	Gly	Phe	Thr	Gln	Leu	Gln	Arg	Met	Gly	Ile	
				405					410					415		
ggc	ctc	gtc	atc	tcc	gtc	ttc	tcc	atg	ctc	gcc	gcc	ggc	gtg	ctc	gac	1296
Gly	Leu	Val	Ile	Ser	Val	Phe	Ser	Met	Leu	Ala	Ala	Gly	Val	Leu	Asp	
			420					425					430			
gtc	gtc	agg	ctg	cgc	gcc	atc	gct	cgc	cac	ggg	ctc	tac	ggc	gac	aag	1344
Val	Val	Arg	Leu	Arg	Ala	Ile	Ala	Arg	His	Gly	Leu	Tyr	Gly	Asp	Lys	
		435					440					445				
gac	gtc	gtg	ccc	atc	tcc	atc	ttc	tgg	cag	gtg	ccg	cag	tac	ttc	atc	1392
Asp	Val	Val	Pro	Ile	Ser	Ile	Phe	Trp	Gln	Val	Pro	Gln	Tyr	Phe	Ile	
	450					455					460					
atc	ggc	gcc	gcc	gag	gtg	ttc	acg	ttc	gtc	ggg	cag	ctg	gag	ttc	ttc	1440
Ile	Gly	Ala	Ala	Glu	Val	Phe	Thr	Phe	Val	Gly	Gln	Leu	Glu	Phe	Phe	
465				470						475				480		
tac	gac	cag	gct	ccc	gac	gcc	atg	cgc	agc	atg	tgc	tcg	gcg	ctg	tcg	1488
Tyr	Asp	Gln	Ala	Pro	Asp	Ala	Met	Arg	Ser	Met	Cys	Ser	Ala	Leu	Ser	
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ctc	acc	acc	gtc	gcg	cta	ggc	aac	tac	ctc	agc	acg	ctg	ctc	gtg	acc	1536
Leu	Thr	Thr	Val	Ala	Leu	Gly	Asn	Tyr	Leu	Ser	Thr	Leu	Leu	Val	Thr	
			500					505					510			
atc	gtt	acc	cat	gtc	acc	acc	cgg	aac	ggc	gcc	gtc	ggg	tgg	atc	ccg	1584
Ile	Val	Thr	His	Val	Thr	Thr	Arg	Asn	Gly	Ala	Val	Gly	Trp	Ile	Pro	
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gac	aac	ctc	aac	cgc	ggc	cac	ctc	gac	tac	ttc	ttc	tgg	ctg	ctc	gcc	1632
Asp	Asn	Leu	Asn	Arg	Gly	His	Leu	Asp	Tyr	Phe	Trp	Leu	Leu	Ala		
	530					535					540					
gtg	ctc	agc	ctc	atc	aac	ttc	ggc	gtc	tac	ctc	gtc	atc	gcc	agc	tgg	1680
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545					550					555					560	
tac	acc	tac	aag	aag	acg	gcg	gat	tca	ccg	gac	aag	gcc	gag	cac		1728
Tyr	Thr	Tyr	Lys	Lys	Thr	Ala	Asp	Ser	Pro	Asp	Asp	Lys	Ala	Glu	His	
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gcc	gga	gca	aac	tga												1743
Ala	Gly	Ala	Asn													
			580													

<210> 269

<211> 580

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<400> 269

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Val	Lys	Gly	Asn	Pro	Ala	Thr	Lys	Lys	Asn	Thr	Gly	Asn	Trp	Arg	Ala	
			20					25					30			
Cys	Pro	Tyr	Ile	Leu	Ala	Asn	Glu	Cys	Cys	Glu	Arg	Leu	Ala	Tyr	Tyr	
		35					40					45				
Gly	Met	Ser	Thr	Asn	Leu	Val	Asn	Tyr	Met	Lys	Thr	Arg	Leu	Gly	Gln	
	50					55					60					
Glu	Ser	Ala	Ile	Ala	Ala	Asn	Asn	Val	Thr	Asn	Trp	Ser	Gly	Thr	Cys	
65					70					75					80	
Tyr	Ile	Thr	Pro	Leu	Leu	Gly	Ala	Phe	Leu	Ala	Asp	Ala	Tyr	Met	Gly	
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PF59082SeqList_PF59082.txt

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 115 120 125
 Asp Gly Gly Ala Cys His Pro Thr Glu Ala Gln Thr Gly Val Val Phe
 130 135 140
 Leu Ala Leu Tyr Leu Ile Ala Leu Gly Thr Gly Gly Ile Lys Pro Cys
 145 150 155 160
 Val Ser Ser Phe Gly Ala Asp Gln Phe Asp Glu Asn Asp Glu Gly Glu
 165 170 175
 Lys Arg Ser Lys Ser Ser Phe Phe Asn Trp Phe Tyr Phe Ser Ile Asn
 180 185 190
 Ile Gly Ala Leu Val Ala Ser Ser Val Leu Val Tyr Val Gln Thr His
 195 200 205
 Val Gly Trp Gly Trp Gly Phe Gly Ile Pro Ala Val Val Met Ala Val
 210 215 220
 Ala Val Ala Ser Phe Phe Val Gly Thr Pro Leu Tyr Arg His Gln Arg
 225 230 235 240
 Pro Gly Gly Ser Pro Leu Thr Arg Ile Ala Gln Val Leu Val Ala Ser
 245 250 255
 Ala Arg Lys Trp Gly Val Glu Val Pro Ala Asp Gly Ser Arg Leu His
 260 265 270
 Glu Thr Leu Asp Arg Glu Ser Gly Ile Glu Gly Ser Arg Lys Leu Glu
 275 280 285
 His Thr Gly Gln Phe Ala Cys Leu Asp Arg Ala Ala Val Glu Thr Pro
 290 295 300
 Glu Asp Arg Ser Ala Ala Asn Ala Ser Ala Trp Arg Leu Cys Thr Val
 305 310 315 320
 Thr Gln Val Glu Glu Leu Lys Ser Val Val Arg Leu Leu Pro Ile Trp
 325 330 335
 Ala Ser Gly Ile Val Phe Ala Thr Val Tyr Gly Gln Met Ser Thr Met
 340 345 350
 Phe Val Leu Gln Gly Asn Thr Leu Asp Ala Ser Met Gly Pro His Phe
 355 360 365
 Ser Ile Pro Ala Ala Ser Leu Ser Ile Phe Asp Thr Leu Ser Val Ile
 370 375 380
 Val Trp Val Pro Val Tyr Asp Arg Leu Ile Val Pro Ala Val Arg Ala
 385 390 395 400
 Val Thr Gly Arg Pro Arg Gly Phe Thr Gln Leu Gln Arg Met Gly Ile
 405 410 415
 Gly Leu Val Ile Ser Val Phe Ser Met Leu Ala Ala Gly Val Leu Asp
 420 425 430
 Val Val Arg Leu Arg Ala Ile Ala Arg His Gly Leu Tyr Gly Asp Lys
 435 440 445
 Asp Val Val Pro Ile Ser Ile Phe Trp Gln Val Pro Gln Tyr Phe Ile
 450 455 460
 Ile Gly Ala Ala Glu Val Phe Thr Phe Val Gly Gln Leu Glu Phe Phe
 465 470 475 480
 Tyr Asp Gln Ala Pro Asp Ala Met Arg Ser Met Cys Ser Ala Leu Ser
 485 490 495
 Leu Thr Thr Val Ala Leu Gly Asn Tyr Leu Ser Thr Leu Leu Val Thr
 500 505 510
 Ile Val Thr His Val Thr Thr Arg Asn Gly Ala Val Gly Trp Ile Pro
 515 520 525
 Asp Asn Leu Asn Arg Gly His Leu Asp Tyr Phe Phe Trp Leu Leu Ala
 530 535 540
 Val Leu Ser Leu Ile Asn Phe Gly Val Tyr Leu Val Ile Ala Ser Trp
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<210> 270

<211> 1758

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

PF59082SeqList_PF59082.txt

<221> CDS

<222> (1)..(1758)

<400> 270

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ggc	gac	gag	agg	tgg	gtg	gag	gac	tcg	tcg	gtg	gat	tac	caa	ggg	cgg	96
Gly	Asp	Glu	Arg	Trp	Val	Glu	Asp	Ser	Ser	Val	Asp	Tyr	Gln	Gly	Arg	
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Pro	Pro	Leu	Arg	Ala	Ala	Thr	Gly	Ser	Trp	Lys	Ala	Ala	Met	Phe	Ile	
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atc	ttg	att	gag	ttc	agc	gag	agg	ctg	agc	tac	ttc	ggg	cta	gcg	acg	192
Ile	Leu	Ile	Glu	Phe	Ser	Glu	Arg	Leu	Ser	Tyr	Phe	Gly	Leu	Ala	Thr	
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Ser	Leu	Met	Ile	Tyr	Leu	Thr	Lys	Val	Leu	Gln	Glu	Glu	Met	Lys	Phe	
					70					75					80	
gcc	gcc	aag	aat	gtc	aac	tac	tgg	acc	agc	gtc	acc	acc	ctc	atg	ccc	288
Ala	Ala	Lys	Asn	Val	Asn	Tyr	Trp	Thr	Ser	Val	Thr	Thr	Leu	Met	Pro	
				85				90						95		
ctc	gtc	ggc	ggc	ttc	ctc	gcc	gac	ggc	tac	ctc	ggc	cgc	ttc	tcc	act	336
Leu	Val	Gly	Gly	Phe	Leu	Ala	Asp	Gly	Tyr	Leu	Gly	Arg	Phe	Ser	Thr	
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Val	Leu	Phe	Ser	Thr	Leu	Ile	Tyr	Leu	Ser	Gly	Leu	Ile	Leu	Leu	Ala	
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Ile	Ser	Gln	Leu	Ser	Pro	Arg	Leu	Lys	Pro	Glu	Arg	Asn	Leu	His	Leu	
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Gly	Gly	His	Lys	Pro	Ala	Leu	Glu	Ser	Phe	Gly	Ala	Asp	Gln	Phe	Asp	
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Trp	Asn	Cys	Ala	Leu	Cys	Ala	Gly	Val	Leu	Leu	Gly	Val	Thr	Val	Ile	
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gtc	tac	ctc	cag	gag	aag	gtc	ggc	tgg	ggc	gcc	gcc	gcc	gtc	gtg	ctc	672
Val	Tyr	Leu	Gln	Glu	Lys	Val	Gly	Trp	Gly	Ala	Ala	Ala	Val	Val	Leu	
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gcc	gcc	gtc	atg	gcc	gcc	tcc	ctc	gcc	gtc	ttc	ctc	gcc	ggc	tgg	cgc	720
Ala	Ala	Val	Met	Ala	Ala	Ser	Leu	Ala	Val	Phe	Leu	Ala	Gly	Trp	Arg	
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His	Tyr	Arg	Tyr	Arg	Val	Pro	Glu	Gly	Ser	Pro	Leu	Thr	Pro	Leu	Val	
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cgc	gtc	ctc	gtc	gcc	gcc	gcg	agg	aag	agg	cac	ctc	cac	ctc	ccc	gcc	816
Arg	Val	Leu	Val	Ala	Ala	Ala	Arg	Lys	Arg	His	Leu	His	Leu	Pro	Ala	
			260					265					270			
gac	gcc	aac	gag	ctc	tac	gag	gtg	aag	ccg	cag	aat	atc	aag	agg	cgg	864
Asp	Ala	Asn	Glu	Leu	Tyr	Glu	Val	Lys	Pro	Gln	Asn	Ile	Lys	Arg	Arg	
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Leu	Leu	Cys	His	Thr	Asp	Gln	Leu	Arg	Phe	Leu	Asp	Lys	Ala	Ala	Val	
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Val	Glu	His	Asp	Gly	Gly	Glu	Glu	Arg	Arg	Gly	Ala	Trp	Arg	Leu	Ala	
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Thr	Val	Thr	Gln	Val	Glu	Glu	Thr	Lys	Leu	Val	Leu	Ala	Met	Val	Pro	
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atc	tgg	gtg	gcg	acg	ctg	ccg	ttc	ggc	atc	acg	gcg	gcg	cag	gtg	tcc	1056
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Met	Ile	Val	Ala	Val	Ala	Val	Tyr	Asp	Lys	Val	Leu	Glu	Pro	Tyr	Leu		
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Gly	Val	Gly	Ile	Ala	Phe	Thr	Ile	Val	Ala	Met	Ala	Val	Ala	Ala	Thr		
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Val	Glu	Arg	Gln	Arg	Leu	Arg	Ser	Ala	Ser	Pro	Ala	Ser	Met	Ser	Val		
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Ser	Phe	Leu	Ser	Ser	Gln	Leu	Ile	Thr	Ala	Val	Asp	Arg	Val	Thr	Ser		
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<213> 0ry

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Pro	Pro	Leu	Arg	Ala	Ala	Thr	Gly	Ser	Trp	Lys	Ala	Ala	Met	Phe	Ile
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Ser	Leu	Met	Ile	Tyr	Leu	Thr	Lys	Val	Leu	Gln	Glu	Glu	Met	Lys	Phe
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Gly	Val	Gly	Ile	Ala	Phe	Thr	Ile	Val	Ala	Met	Ala	Val	Ala	Ala	Thr
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Val	Glu	Arg	Gln	Arg	Leu	Arg	Ser	Ala	Ser	Pro	Ala	Ser	Met	Ser	Val
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Ser	Phe	Leu	Ser	Ser	Gln	Leu	Ile	Thr	Ala	Val	Asp	Arg	Val	Thr	Ser
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His	Gly	Gly	Ala	Ala	Ala	Gly	Trp	Phe	Gly	Lys	Asp	Leu	Asn	Ser	Ser
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Arg	Leu	Asp	Leu	Phe	Tyr	Trp	Leu	Leu	Ala	Cys	Ile	Gly	Val	Ala	Asn
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Leu	Val	Phe	Tyr	Val	Val	Ile	Ala	Thr	Arg	Tyr	Ser	Tyr	Lys	Thr	Val
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<210> 272

<211> 1776

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<221> CDS

<222> (1)..(1776)

<400> 272

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Asn	Ser	Tyr	Tyr	Asn	Trp	Tyr	Tyr	Gly	Thr	Ser	Thr	Ala	Ala	Leu	Val	
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Val	Gln	Gln	Ile	Glu	Glu	Val	Lys	Cys	Leu	Ile	Arg	Ile	Val	Pro	Val	
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Pro Glu Asn Met Gln Thr Leu Ala Gly Ser Leu Phe Phe Cys Thr Ile	
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gct gga gca aac tac ctg agt act gct ctg gca aac atc atg aga aag	1536
Ala Gly Ala Asn Tyr Leu Ser Thr Ala Leu Ala Asn Ile Met Arg Lys	
500 505 510	
gtc acg acc aga gat ggt cac tca agc tgg tta aca gac aac att aat	1584
Val Thr Thr Arg Asp Gly His Ser Ser Trp Leu Thr Asp Asn Ile Asn	
515 520 525	
ctt ggc aaa ctc gac tat tac ttc tat ttt att gcc ctt atg gga gtc	1632
Leu Gly Lys Leu Asp Tyr Tyr Phe Tyr Phe Ile Ala Leu Met Gly Val	
530 535 540	
ctg aac ctt att tat ttt ctt ata tgc tca cac ttc tac caa tat aag	1680
Leu Asn Leu Ile Tyr Phe Leu Ile Cys Ser His Phe Tyr Gln Tyr Lys	
545 550 555 560	
gta atg tca ctc cat tct gaa gaa tcc atc aaa ata cct acc aag gaa	1728
Val Met Ser Leu His Ser Glu Glu Ser Ile Lys Ile Pro Thr Lys Glu	
565 570 575 580	
gaa gaa gcc aca gag atc gac att gac aca gat gca cct agc aaa	1773
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<210> 273

<211> 591

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<400> 273

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35 40 45	
Lys Arg Phe Asn Ile Gly Gln Ile Glu Ala Ala Asn Ile Thr Asn Ile	
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Phe Phe Gly Thr Leu Asn Phe Ala Pro Leu Leu Gly Ala Phe Ile Ser	
65 70 75 80	
Asp Val Tyr Leu Gly Arg Phe Lys Thr Leu Ala Tyr Gly Cys Phe Ala	
85 90 95	
Ser Leu Leu Gly Met Leu Gly Met Thr Tyr Ala Ser Leu Pro Ala	
100 105 110	
Leu Lys Pro Pro Ile Cys His Glu Lys Thr Arg Leu Gly Gly Gly Cys	
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Asn Ser Pro Ser Thr Leu Gln Leu Ser Val Leu Tyr Leu Ser Leu Gly	

PF59082SeqList_PF59082.txt

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165      170      175
Asn Ser Tyr Tyr Asn Trp Tyr Tyr Gly Thr Ser Thr Ala Ala Leu Val
180      185      190
Leu Ser Met Ile Val Ile Ile Tyr Ile Gln Asn Asn Val Ser Trp Pro
195      200      205
Ile Gly Phe Gly Ile Pro Thr Leu Leu Met Phe Leu Ala Ile Ile Met
210      215      220
Leu Phe Leu Gly Thr Asn Leu Tyr Val His Val Gln Pro Glu Gly Ser
225      230      235      240
Ile Phe Ala Gly Ile Ala Gln Val Leu Val Ala Ser Phe Lys Lys Arg
245      250      255
Asn Leu Lys Leu Pro Cys Pro His Asp Ile Asn Gln Gln Gly Leu Met
260      265      270
Leu Tyr Asn Pro Pro Ser Lys Gly Asn Arg Val Phe Arg Leu Pro Leu
275      280      285
Thr Ser Gln Phe Arg Phe Leu Asn Lys Gly Ala Ile Val Met Gly Asp
290      295      300
Asp Ile Asn Val Asp Gly Ser Ala Arg Asn Ser Trp Glu Leu Cys Asn
305      310      315      320
Val Gln Gln Ile Glu Val Lys Cys Leu Ile Arg Ile Val Pro Val
325      330      335
Cys Ile Ser Gly Val Leu Cys Phe Val Ala Leu Ala Gln Gln Phe Thr
340      345      350
Tyr Ile Ile Leu Gln Thr Phe Thr Met Asp Cys His Phe Gly Thr His
355      360      365
Phe Glu Ile Pro Ala Gly Ser Val Val Ser Ile Ser Leu Ile Ala Leu
370      375      380
Thr Leu Phe Ile Pro Ile Tyr Asp Arg Ile Leu Val Pro Ile Ala Arg
385      390      395      400
Gly Phe Thr Gly Val Glu Ser Gly Ile Thr Leu Leu Gln Arg Gln Gly
405      410      415
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420      425      430
Glu Arg Lys Arg Arg Asn Ser Ala Leu Ser Asn Gly Gly Ile Ser Pro
435      440      445
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450      455      460
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465      470      475      480
Pro Glu Asn Met Gln Thr Leu Ala Gly Ser Leu Phe Phe Cys Thr Ile
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500      505      510
Val Thr Thr Arg Asp Gly His Ser Ser Trp Leu Thr Asp Asn Ile Asn
515      520      525
Leu Gly Lys Leu Asp Tyr Tyr Phe Tyr Phe Ile Ala Leu Met Gly Val
530      535      540
Leu Asn Leu Ile Tyr Phe Leu Ile Cys Ser His Phe Tyr Gln Tyr Lys
545      550      555      560
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<210> 274

<211> 1638

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<221> CDS

<222> (1)..(1638)

<400> 274

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Arg	Arg	Lys	Ser	Asn	Arg	Arg	Asn	Arg	Trp	Ala	Cys	Thr	Phe	Ile	Leu
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gcg	aac	aat	ttc	ttc	caa	aac	atg	gcc	tac	ttc	ggc	gtg	tcg	acg	aac
Ala	Asn	Asn	Phe	Phe	Gln	Asn	Met	Ala	Tyr	Phe	Gly	Val	Ser	Thr	Asn
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ctg	gtg	aac	tac	ctc	aag	tac	agg	ctg	cac	gag	ggc	agc	aag	tcg	gcg
Leu	Val	Asn	Tyr	Leu	Lys	Tyr	Arg	Leu	His	Glu	Gly	Ser	Lys	Ser	Ala
	50					55				60					
gcg	aac	aac	gtc	acc	aac	tgg	gag	ggc	acc	ggc	tcc	att	gcg	ccg	ctc
Ala	Asn	Asn	Val	Thr	Asn	Trp	Glu	Gly	Thr	Gly	Ser	Ile	Ala	Pro	Leu
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gtc	gcc	ggc	tac	ctc	gcc	gac	gcc	ttc	ctc	ggc	cga	tac	tgg	acc	atc
Val	Ala	Gly	Tyr	Leu	Ala	Asp	Ala	Phe	Leu	Gly	Arg	Tyr	Trp	Thr	Ile
			85					90						95	
gtg	ctc	tcc	atg	gtc	atc	tcc	gcc	gtg	gta	cgt	tcg	tcg	ccg	ccg	ccg
Val	Leu	Ser	Met	Val	Ile	Ser	Ala	Val	Val	Arg	Ser	Ser	Pro	Pro	Pro
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Ala	Met	Gln	Gly	Tyr	Gly	Val	Leu	Ala	Ala	Ser	Ala	Ser	Val	Ile	Arg
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Leu	Glu	Ser	Ala	Ala	Leu	Tyr	Ala	Gly	Met	Tyr	Leu	Val	Ala	Leu	Gly
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Gly	Val	Leu	Glu	Pro	Ile	Met	Ala	Pro	Phe	Gly	Ala	Asp	Gln	Phe	Asp
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Asp	Gly	Glu	Asp	Asp	Gln	Arg	Gly	Arg	Arg	Gln	Ser	Ser	Phe	Phe	Asn
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Trp	Phe	Tyr	Leu	Ser	Leu	Asn	Cys	Gly	Ser	Leu	Val	Gly	Gly	Thr	Val
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Leu	Val	Trp	Val	Gln	Thr	Ser	Val	Gly	Trp	Gly	Val	Gly	Tyr	Gly	Val
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Ala	Thr	Tyr	Arg	Arg	Asp	Gln	Pro	Pro	Gly	Gly	Ser	Pro	Leu	Thr	Arg
225					230				235					240	
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Ile	Ala	Gln	Val	Val	Val	Ala	Ala	Val	Arg	Lys	Phe	Asp	Val	Glu	Ile
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Pro	Ser	Asp	Ser	Ser	Met	Leu	Tyr	Glu	Ser	Asp	Ala	Val	Asp	Gly	Met
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Pro	Ala	Ile	His	Gly	Arg	Arg	Arg	Leu	Leu	His	Thr	Gly	Gln	Phe	Arg
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Phe	Leu	Asp	Arg	Ala	Thr	Val	Lys	Thr	Ala	Gly	Glu	Lys	Ala	Ala	Gln
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Ser	Pro	Trp	Arg	Leu	Cys	Thr	Val	Thr	Gln	Val	Glu	Glu	Leu	Lys	Cys
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Val	Leu	Arg	Leu	Leu	Pro	Val	Trp	Ala	Thr	Gly	Ile	Ile	Tyr	Ala	Ala
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Ala	Tyr	Thr	Gln	Val	Thr	Thr	Thr	Phe	Ile	Leu	Gln	Gly	Asp	Thr	Leu
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Asp	Arg	Ser	Leu	Gly	Arg	Phe	Lys	Val	Pro	Ala	Ala	Ala	Leu	Ser	Ile
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Gln	Leu	Ala	Arg	Met	Gly	Val	Gly	Leu	Val	Ile	Leu	Thr	Val	Ala	Met	
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gcc	gcc	gcc	ggc	gcg	ctc	gag	gcg	gcg	cgc	cgc	cgg	ctg	atc	gcg	cgg	1296
Ala	Ala	Ala	Gly	Ala	Leu	Glu	Ala	Ala	Arg	Arg	Arg	Leu	Ile	Ala	Arg	
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Pro	Ser	Val	Phe	Trp	Gln	Val	Pro	Gln	Tyr	Ala	Val	Val	Gly	Ala	Ser	
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Glu	Val	Phe	Thr	Leu	Ile	Gly	Gln	Met	Glu	Phe	Phe	Tyr	Asp	Gln	Ala	
	450					455					460					
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Pro	Asp	Ala	Met	Arg	Ser	Leu	Cys	Ser	Ala	Leu	Ser	Ser	Thr	Ser	Phe	
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Ala	Leu	Gly	Asp	Tyr	Ala	Ser	Ser	Ala	Leu	Val	Val	Val	Ala	Ala	Arg	
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Arg	Gly	Gly	Ala	Pro	Gly	Trp	Ile	Pro	Asp	Asp	Ile	Asn	Arg	Gly	His	
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Leu	Asp	Tyr	Phe	Phe	Trp	Leu	Leu	Thr	Ala	Leu	Cys	Val	Ala	Asn	Phe	
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gcc	gcc	tac	ctc	ctc	atc	gca	cgc	tgg	tac	acg	tat	aag	aag	acc	gta	1632
Ala	Ala	Tyr	Leu	Leu	Ile	Ala	Arg	Trp	Tyr	Thr	Tyr	Lys	Lys	Thr	Val	
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Asp																
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<210> 275

<211> 545

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<400> 275

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Ala	Met	Gln	Gly	Tyr	Gly	Val	Leu	Ala	Ala	Ser	Ala	Ser	Val	Ile	Arg	
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Gly	Val	Leu	Glu	Pro	Ile	Met	Ala	Pro	Phe	Gly	Ala	Asp	Gln	Phe	Asp	
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			165					170						175		
Trp	Phe	Tyr	Leu	Ser	Leu	Asn	Cys	Gly	Ser	Leu	Val	Gly	Gly	Thr	Val	
			180					185					190			
Leu	Val	Trp	Val	Gln	Thr	Ser	Val	Gly	Trp	Gly	Val	Gly	Tyr	Gly	Val	
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PF59082SeqList_PF59082.txt

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 Pro Ser Asp Ser Met Leu Tyr Glu Ser Asp Ala Val Asp Gly Met
 260 265 270
 Pro Ala Ile His Gly Arg Arg Arg Leu Leu His Thr Gly Gln Phe Arg
 275 280 285
 Phe Leu Asp Arg Ala Thr Val Lys Thr Ala Gly Glu Lys Ala Ala Gln
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 Ser Pro Trp Arg Leu Cys Thr Val Thr Gln Val Glu Glu Leu Lys Cys
 305 310 315 320
 Val Leu Arg Leu Leu Pro Val Trp Ala Thr Gly Ile Ile Tyr Ala Ala
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 Asp Arg Ser Leu Gly Arg Phe Lys Val Pro Ala Ala Ala Leu Ser Ile
 355 360 365
 Phe His Thr Leu Ser Val Ile Leu Trp Val Ala Leu Tyr Asp Arg Ala
 370 375 380
 Ile Val Pro Leu Ala Arg Arg Val Thr Arg His Asp Gly Gly Phe Thr
 385 390 395 400
 Gln Leu Ala Arg Met Gly Val Gly Leu Val Ile Leu Thr Val Ala Met
 405 410 415
 Ala Ala Ala Gly Ala Leu Glu Ala Ala Arg Arg Leu Ile Ala Arg
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 Pro Ser Val Phe Trp Gln Val Pro Gln Tyr Ala Val Val Gly Ala Ser
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 Glu Val Phe Thr Leu Ile Gly Gln Met Glu Phe Phe Tyr Asp Gln Ala
 450 455 460
 Pro Asp Ala Met Arg Ser Leu Cys Ser Ala Leu Ser Ser Thr Ser Phe
 465 470 475 480
 Ala Leu Gly Asp Tyr Ala Ser Ser Ala Leu Val Val Val Ala Ala Arg
 485 490 495
 Arg Gly Gly Ala Pro Gly Trp Ile Pro Asp Asp Ile Asn Arg Gly His
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<210> 276

<211> 1785

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<221> CDS

<222> (1)..(1785)

<400> 276

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ggc	tgc	gcg	gcg	atg	atc	ctc	ggg	gcg	gag	ctg	ttc	gag	cgg	atg	acg	144
Gly	Cys	Ala	Ala	Met	Ile	Leu	Gly	Ala	Glu	Leu	Phe	Glu	Arg	Met	Thr	
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acg	ctg	ggc	atc	gcc	gtc	aac	ctg	gtg	ccg	tac	atg	acc	ggg	acg	atg	192
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PF59082SeqList_PF59082.txt

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Leu	Gly	Arg	Tyr	Leu	Thr	Ile	Ala	Ile	Phe	Glu	Ala	Val	Gln	Ala	Thr	
			100					105					110			
ggc	gtg	atg	ata	ctc	acg	atc	tcc	acg	gcg	gcg	ccg	ggg	ctg	cgg	ccg	384
Gly	Val	Met	Ile	Leu	Thr	Ile	Ser	Thr	Ala	Ala	Pro	Gly	Leu	Arg	Pro	
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Pro	Ala	Cys	Gly	Asp	Pro	Lys	Gly	Ala	Ser	Ala	Glu	Cys	Val	Ala	Ala	
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Leu	Gly	Thr	Gly	Gly	Leu	Lys	Ser	Ser	Val	Ser	Gly	Phe	Gly	Ser	Asp	
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cag	ttc	gac	gag	tcc	gac	gtc	gac	ggc	gag	agg	aag	aag	atg	atg	cgc	576
Gln	Phe	Asp	Glu	Ser	Asp	Val	Asp	Gly	Glu	Arg	Lys	Lys	Met	Met	Arg	
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		195					200					205				
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Val	Thr	Val	Leu	Val	Tyr	Val	Gln	Asp	Asn	Val	Gly	Arg	Arg	Trp	Gly	
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tcc	ggg	acc	agg	agg	tac	agg	ttc	aag	aag	ctg	gtg	ggg	agc	ccc	ctc	768
Ser	Gly	Thr	Arg	Arg	Tyr	Arg	Phe	Lys	Lys	Leu	Val	Gly	Ser	Pro	Leu	
			245					250						255		
acc	cag	gtc	gcc	gcc	gtc	acc	gcc	gcc	gcc	tgg	agc	aag	agg	tgc	ctg	816
Thr	Gln	Val	Ala	Ala	Val	Thr	Ala	Ala	Ala	Trp	Ser	Lys	Arg	Ser	Leu	
			260				265						270			
ccg	ctg	ccg	tcc	gac	cca	gac	atg	ctc	tac	gac	gtc	gac	gac	gcc	gcc	864
Pro	Leu	Pro	Ser	Asp	Pro	Asp	Met	Leu	Tyr	Asp	Val	Asp	Asp	Ala	Ala	
		275					280					285				
gcc	gcc	ggc	cat	gac	gtc	aag	ggc	aag	cag	agg	atg	cca	cac	agc	aag	912
Ala	Ala	Gly	His	Asp	Val	Lys	Gly	Lys	Gln	Arg	Met	Pro	His	Ser	Lys	
	290					295					300					
gag	tgc	cgg	ttc	ctg	gac	cat	gcg	gcg	atc	atc	gac	agg	tcg	gcg	gcg	960
Glu	Cys	Arg	Phe	Leu	Asp	His	Ala	Ala	Ile	Ile	Asp	Arg	Ser	Ala	Ala	
				310					315						320	
gag	tcg	ccg	gcg	acg	gcg	agc	aag	tgg	agg	ctg	tgc	acg	agg	acg	gac	1008
Glu	Ser	Pro	Ala	Thr	Ala	Ser	Lys	Trp	Arg	Leu	Cys	Thr	Arg	Thr	Asp	
			325						330					335		
gtg	gag	gag	gtg	aag	cag	gtg	gtg	cgg	atg	ctc	ccc	atc	tgg	gcg	acc	1056
Val	Glu	Glu	Val	Lys	Gln	Val	Val	Arg	Met	Leu	Pro	Ile	Trp	Ala	Thr	
			340				345						350			
acc	atc	atg	ttc	tgg	acc	atc	cac	gcc	cag	atg	acc	acc	ttc	gcc	gtc	1104
Thr	Ile	Met	Phe	Trp	Thr	Ile	His	Ala	Gln	Met	Thr	Thr	Phe	Ala	Val	
		355					360					365				
gcg	cag	gcc	gag	ctc	atg	gac	cgc	ctc	gcc	ggc	ggc	ttc	ctc	atc		1152
Ala	Gln	Ala	Glu	Leu	Met	Asp	Arg	Arg	Leu	Ala	Gly	Gly	Phe	Leu	Ile	
		370				375					380					
ccg	gcg	ggc	tcc	ctc	acc	gtc	ttc	ctc	atc	gcc	tcc	atc	ctc	ctc	acc	1200
Pro	Ala	Gly	Ser	Leu	Thr	Val	Phe	Leu	Ile	Ala	Ser	Ile	Leu	Leu	Thr	
				390						395					400	
gtc	ccc	ttc	tac	gac	cgc	ctc	gtc	gtc	ccc	gtc	gcg	cgc	cgc	gcc	acg	1248
Val	Pro	Phe	Tyr	Asp	Arg	Leu	Val	Val	Pro	Val	Ala	Arg	Arg	Ala	Thr	
			405						410					415		
gcc	aac	ccg	cac	ggc	ctc	acc	ccg	ctc	cag	cgc	gtc	ttc	gtg	ggc	ctc	1296
Ala	Asn	Pro	His	Gly	Leu	Thr	Pro	Leu	Gln	Arg	Val	Phe	Val	Gly	Leu	
			420					425					430			
tcc	ctc	tcc	atc	gcc	ggc	atg	gcc	gtc	gcc	gcg	gcc	gtc	gag	cgc	cac	1344
Ser	Leu	Ser	Ile	Ala	Gly	Met	Ala	Val	Ala	Ala	Ala	Val	Glu	Arg	His	
		435					440					445				

PF59082SeqList_PF59082.txt

cg	gcc	acc	gcc	tcc	gcc	tcc	gcc	gcc	gcc	gcc	gcg	ccc	acg	gtg	ttc	1392
Arg	Ala	Thr	Ala	Ser	Ala	Ser	Ala	Ala	Ala	Ala	Ala	Pro	Thr	Val	Phe	
	450					455				460						
ctc	ctc	atg	ccg	cag	ttc	ctc	ctc	gtc	ggc	gcc	ggc	gag	gcg	ttc	acc	1440
Leu	Leu	Met	Pro	Gln	Phe	Leu	Leu	Val	Gly	Ala	Gly	Glu	Ala	Phe	Thr	
	465				470				475						480	
tac	atg	ggc	cag	ctc	gac	ttc	ttc	ctc	cg	gag	tgc	ccc	aag	ggg	atg	1488
Tyr	Met	Gly	Gln	Leu	Asp	Phe	Phe	Leu	Arg	Glu	Cys	Pro	Lys	Gly	Met	
				485					490					495		
aag	acc	atg	agc	acg	ggc	ctc	ttc	ctc	agc	acc	tgc	gcc	atc	ggc	ttc	1536
Lys	Thr	Met	Ser	Thr	Gly	Leu	Phe	Leu	Ser	Thr	Cys	Ala	Ile	Gly	Phe	
			500					505					510			
ttc	ttc	agc	acg	ctg	ctc	gtc	acc	atc	gtc	cac	aag	gtc	acc	ggc	cat	1584
Phe	Phe	Ser	Thr	Leu	Leu	Val	Thr	Ile	Val	His	Lys	Val	Thr	Gly	His	
		515				520						525				
ggc	gcc	cg	ggc	ggc	ggc	tgg	ctc	gcc	gac	aac	ctc	gac	gac	ggc	agg	1632
Gly	Ala	Arg	Gly	Gly	Gly	Trp	Leu	Ala	Asp	Asn	Leu	Asp	Asp	Gly	Arg	
	530					535					540					
ctc	gac	tac	ttc	tac	tgg	ctg	ctc	gcc	gtc	atc	agc	gcc	atc	aac	ctc	1680
Leu	Asp	Tyr	Phe	Tyr	Trp	Leu	Leu	Ala	Val	Ile	Ser	Ala	Ile	Asn	Leu	
	545				550					555					560	
gtc	ctc	ttc	acc	gtc	gcc	gcc	agg	ggg	tac	gtc	tac	aag	gag	aag	cg	1728
Val	Leu	Phe	Thr	Val	Ala	Ala	Arg	Gly	Tyr	Val	Tyr	Lys	Glu	Lys	Arg	
				565				570						575		
ctc	gcc	gac	ggc	ggc	atc	gag	ctc	gcc	gac	gag	gag	acc	atc	gcc	gtc	1776
Leu	Ala	Asp	Ala	Gly	Ile	Glu	Leu	Ala	Asp	Glu	Glu	Thr	Ile	Ala	Val	
			580					585					590			
ggc	cac	taa														1785
Gly	His															

<210> 277

<211> 594

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<400> 277

Met	Val	Leu	Pro	Glu	Thr	Ala	Ala	Glu	Gly	Lys	Ala	Leu	Thr	Asp	Ala	
1				5					10					15		
Trp	Asp	Tyr	Lys	Gly	Arg	Pro	Ala	Gly	Arg	Ala	Ala	Thr	Gly	Gly	Trp	
			20					25					30			
Gly	Cys	Ala	Ala	Met	Ile	Leu	Gly	Ala	Glu	Leu	Phe	Glu	Arg	Met	Thr	
		35					40					45				
Thr	Leu	Gly	Ile	Ala	Val	Asn	Leu	Val	Pro	Tyr	Met	Thr	Gly	Thr	Met	
		50				55					60					
His	Leu	Gly	Asn	Ala	Ala	Ala	Ala	Asn	Thr	Val	Thr	Asn	Phe	Ile	Gly	
				70					75					80		
Thr	Ser	Phe	Met	Leu	Cys	Leu	Leu	Gly	Gly	Phe	Val	Ala	Asp	Thr	Tyr	
			85					90					95			
Leu	Gly	Arg	Tyr	Leu	Thr	Ile	Ala	Ile	Phe	Glu	Ala	Val	Gln	Ala	Thr	
			100					105					110			
Gly	Val	Met	Ile	Leu	Thr	Ile	Ser	Thr	Ala	Ala	Pro	Gly	Leu	Arg	Pro	
		115					120					125				
Pro	Ala	Cys	Gly	Asp	Pro	Lys	Gly	Ala	Ser	Ala	Glu	Cys	Val	Ala	Ala	
		130				135					140					
Asp	Gly	Thr	Gln	Leu	Gly	Val	Leu	Tyr	Leu	Gly	Leu	Tyr	Leu	Thr	Ala	
				150					155					160		
Leu	Gly	Thr	Gly	Gly	Leu	Lys	Ser	Ser	Val	Ser	Gly	Phe	Gly	Ser	Asp	
			165					170						175		
Gln	Phe	Asp	Glu	Ser	Asp	Val	Asp	Gly	Glu	Arg	Lys	Lys	Met	Met	Arg	
			180					185					190			
Phe	Phe	Asn	Trp	Phe	Tyr	Phe	Phe	Val	Ser	Leu	Gly	Ala	Leu	Leu	Ala	
		195					200					205				
Val	Thr	Val	Leu	Val	Tyr	Val	Gln	Asp	Asn	Val	Gly	Arg	Arg	Trp	Gly	
		210				215					220					
Tyr	Gly	Ile	Cys	Ala	Ala	Gly	Ile	Leu	Ala	Gly	Leu	Ala	Val	Phe	Leu	
				230					235					240		
Ser	Gly	Thr	Arg	Arg	Tyr	Arg	Phe	Lys	Lys	Leu	Val	Gly	Ser	Pro	Leu	
				245					250					255		

PF59082SeqList_PF59082.txt

Thr Gln Val Ala Ala Val Thr Ala Ala Ala Trp Ser Lys Arg Ser Leu
 260 265 270
 Pro Leu Pro Ser Asp Pro Asp Met Leu Tyr Asp Val Asp Asp Ala Ala
 275 280 285
 Ala Ala Gly His Asp Val Lys Gly Lys Gln Arg Met Pro His Ser Lys
 290 300
 Glu Cys Arg Phe Leu Asp His Ala Ala Ile Ile Asp Arg Ser Ala Ala
 305 310 315 320
 Glu Ser Pro Ala Thr Ala Ser Lys Trp Arg Leu Cys Thr Arg Thr Asp
 325 330 335
 Val Glu Glu Val Lys Gln Val Val Arg Met Leu Pro Ile Trp Ala Thr
 340 345 350
 Thr Ile Met Phe Trp Thr Ile His Ala Gln Met Thr Thr Phe Ala Val
 355 360 365
 Ala Gln Ala Glu Leu Met Asp Arg Arg Leu Ala Gly Gly Phe Leu Ile
 370 375 380
 Pro Ala Gly Ser Leu Thr Val Phe Leu Ile Ala Ser Ile Leu Leu Thr
 385 390 395 400
 Val Pro Phe Tyr Asp Arg Leu Val Val Pro Val Ala Arg Arg Ala Thr
 405 410 415
 Ala Asn Pro His Gly Leu Thr Pro Leu Gln Arg Val Phe Val Gly Leu
 420 425 430
 Ser Leu Ser Ile Ala Gly Met Ala Val Ala Ala Ala Val Glu Arg His
 435 440 445
 Arg Ala Thr Ala Ser Ala Ser Ala Ala Ala Ala Ala Pro Thr Val Phe
 450 455 460
 Leu Leu Met Pro Gln Phe Leu Leu Val Gly Ala Gly Glu Ala Phe Thr
 465 470 475 480
 Tyr Met Gly Gln Leu Asp Phe Phe Leu Arg Glu Cys Pro Lys Gly Met
 485 490 495
 Lys Thr Met Ser Thr Gly Leu Phe Leu Ser Thr Cys Ala Ile Gly Phe
 500 505 510
 Phe Phe Ser Thr Leu Leu Val Thr Ile Val His Lys Val Thr Gly His
 515 520 525
 Gly Ala Arg Gly Gly Gly Trp Leu Ala Asp Asn Leu Asp Asp Gly Arg
 530 535 540
 Leu Asp Tyr Phe Tyr Trp Leu Leu Ala Val Ile Ser Ala Ile Asn Leu
 545 550 555 560
 Val Leu Phe Thr Val Ala Ala Arg Gly Tyr Val Tyr Lys Glu Lys Arg
 565 570 575
 Leu Ala Asp Ala Gly Ile Glu Leu Ala Asp Glu Glu Thr Ile Ala Val
 580 585 590
 Gly His

<210> 278

<211> 1755

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<221> CDS

<222> (1)..(1755)

<400> 278

atg gct cca act gct gtc gat tcg aaa agg att tct gac atc act gaa	48
Met Ala Pro Thr Ala Val Asp Ser Lys Arg Ile Ser Asp Ile Thr Glu	
1 5 10 15	
gat gga tca atg gac agg cga gga aat ccg gca gtt aaa gca aaa act	96
Asp Gly Ser Met Asp Arg Arg Gly Asn Pro Ala Val Lys Ala Lys Thr	
20 25 30	
ggg aat tgg aga tct tcc atc ctc ttg cta gtc aac tat ggg ctc gtg	144
Gly Asn Trp Arg Ser Ser Ile Leu Leu Leu Val Asn Tyr Gly Leu Val	
35 40 45	
aca tgc gcc ttc ttc ggc gtc ggg gtg aac ctt gtg gtg ttc ctg cgg	192
Thr Cys Ala Phe Phe Gly Val Gly Val Asn Leu Val Val Phe Leu Arg	
50 55 60	
cgg gtg ctc cac cag gac aac gca gag gca gcc aac agc atc agc aag	240
Arg Val Leu His Gln Asp Asn Ala Glu Ala Ala Asn Ser Ile Ser Lys	

PF59082SeqList_PF59082.txt

65	70	75	80	
tgg acc ggc acg gtc tac atc ttc tcc ctc atc ggc gcc ttc atg agc	Trp Thr Gly Thr Val Tyr Ile Phe Ser Leu Ile Gly Ala Phe Met Ser	288		
gac tcc tac tgg ggc cga tac atc acg tgt gca atc ttc cag atg atc	Asp Ser Tyr Trp Gly Arg Tyr Ile Thr Cys Ala Ile Phe Gln Met Ile	336		
tat gtc acg ggc ctg gtg ata ctg tca ctc gcg tcg tgg ttc ttg ctg	Tyr Val Thr Gly Leu Val Ile Leu Ser Leu Ala Ser Trp Phe Leu Leu	384		
gtg aag ccc acc ggc tgc ggc gcc gcg ggg gag cac tgc gac gcg ccg	Val Lys Pro Thr Gly Cys Gly Ala Ala Gly Glu His Cys Asp Ala Pro	432		
tcg agc gcc ggc gtc gcg ctc ttc tac ctg tcg acc tac atg atc gcg	Ser Ser Ala Gly Val Ala Leu Phe Tyr Leu Ser Thr Tyr Met Ile Ala	480		
ttc ggc aac gga ggg tac cag ccg tcc atc gcc acg ttc ggc tcc gac	Phe Gly Asn Gly Gly Tyr Gln Pro Ser Ile Ala Thr Phe Gly Ser Asp	528		
cag ttc gac gag acg gac ccc agg gag gcc cgc tcc aag gtg gcc ttc	Gln Phe Asp Glu Thr Asp Pro Arg Glu Ala Arg Ser Lys Val Ala Phe	576		
ttc agc tac ttc tac ctg gcg ctc aac gtg ggc tcc ctc ttc tcc aac	Phe Ser Tyr Phe Tyr Leu Ala Leu Asn Val Gly Ser Leu Phe Ser Asn	624		
acg gtg ctg gtg tac tac gag gac gag ggg agg tgg gtc atg ggg ttc	Thr Val Leu Val Tyr Tyr Glu Asp Glu Gly Arg Trp Val Met Gly Phe	672		
tgg gtc tcg gcc gcg gcg gcc atg gcg ctc gtg ctc ttc ttg ctc	Trp Val Ser Ala Ala Ala Met Ala Leu Val Leu Phe Leu Leu	720		
ggc acc ccc aac tac cgc cac ttc aag ccg acc ggc aac ccg ttg acc	Gly Thr Pro Asn Tyr Arg His Phe Lys Pro Thr Gly Asn Pro Leu Thr	768		
cgc atc gcg cag gtg ttc gtc gcc gcg ttc cgc aag tgg cgc gcc gag	Arg Ile Ala Gln Val Phe Val Ala Ala Phe Arg Lys Trp Arg Ala Glu	816		
gtg cca cgc agc gag ctc ctg cac gag gtt gac ggc gac gag tcc cag	Val Pro Arg Ser Glu Leu Leu His Glu Val Asp Gly Asp Glu Ser Gln	864		
att gct ggc atc cga aag atc ctc cac agc gac cag atc agg ttc ctt	Ile Ala Gly Ile Arg Lys Ile Leu His Ser Asp Gln Ile Arg Phe Leu	912		
gac aag gcg gcg acg gtc acc gag gag gac tac tgc acg ccg gag aac	Asp Lys Ala Ala Thr Val Thr Glu Glu Asp Tyr Cys Thr Pro Glu Asn	960		
atg cag gat ccg tgg agg ctg tgc acg gtg acc cag gtg gag gaa gtg	Met Gln Asp Pro Trp Arg Leu Cys Thr Val Thr Gln Val Glu Glu Val	1008		
aag tgc atc ctg aag atg ctg ccc atc tgg ctg tgc acg atc gta tac	Lys Cys Ile Leu Lys Met Leu Pro Ile Trp Leu Cys Thr Ile Val Tyr	1056		
tcg gtg gtg ttc acc cag atg gcg tcg ctg ttc gtg gag cag gga acc	Ser Val Val Phe Thr Gln Met Ala Ser Leu Phe Val Glu Gln Gly Thr	1104		
acc atg aac acc aac atc ggg tcg ttc cac gtg ccc gcg gcg agc atg	Thr Met Asn Thr Asn Ile Gly Ser Phe His Val Pro Ala Ala Ser Met	1152		
tcg gtg ttc gac atc ctc agc gtg ctg gcg ttc atc gcc atc tac cgg	Ser Val Phe Asp Ile Ser Val Leu Ala Phe Ile Ala Ile Tyr Arg	1200		
cgc gtg ctc gtg ccg gtc atg tcg cgc ctg tcc ggc aac ccg cag ggg	Arg Val Leu Val Pro Val Met Ser Arg Leu Ser Gly Asn Pro Gln Gly	1248		
ctg acc gag ctg cag ccg atg ggc gtg ggg ctc gtg gtc ggc atg gcg	Leu Thr Glu Leu Gln Arg Met Gly Val Gly Leu Val Val Gly Met Ala	1296		
gcc atg gtg gtc gcc ggc gtg gtg gag gtg gag cgg ctg aag ccg gtg	Ala Met Val Val Ala Gly Val Val Glu Val Glu Arg Leu Lys Arg Val	1344		

PF59082SeqList_PF59082.txt

435	440	445	
ggc gcg ccg gac cag ccg agc tcc ctg agc gtg ctg tgg cag gtg ccg			1392
Gly Ala Pro Asp Gln Pro Ser Ser Leu Ser Val Leu Trp Gln Val Pro			
450	455	460	
cag tac gcg ctg atc ggg gcg tcg gag gtg ttc atg tac gtg ggg cag			1440
Gln Tyr Ala Leu Ile Gly Ala Ser Glu Val Phe Met Tyr Val Gly Gln			
465	470	475	
ctg gag ttc ttc aac ggg cag gcc ccc gac ggc gtg aag agc ttc ggg			1488
Leu Glu Phe Phe Asn Gly Gln Ala Pro Asp Gly Val Lys Ser Phe Gly			
485	490	495	
agc tcg ctg tgc atg gcg tcc atc tcg ctg ggg aac tac gtg agc atc			1536
Ser Ser Leu Cys Met Ala Ser Ile Ser Leu Gly Asn Tyr Val Ser Ile			
500	505	510	
atg ctg gtg agc gtg gtc acc agc ctc acc gcc ggc gac agg cgg ccc			1584
Met Leu Val Ser Val Val Thr Ser Leu Thr Ala Gly Asp Arg Arg Pro			
515	520	525	
ggg tgg atc ccc ggg aac ctc aac tcc ggc cac ctc gac agg ttc tac			1632
Gly Trp Ile Pro Gly Asn Leu Asn Ser Gly His Leu Asp Arg Phe Tyr			
530	535	540	
ttc ctc ctc gcc gcg ctc tcg ctg gtc gac ctc gtg tac gtc gcg			1680
Phe Leu Leu Ala Ala Leu Ser Leu Val Asp Leu Ala Val Tyr Val Ala			
545	550	555	
tgc gcc gtg tgg tac aag ggc atc aag ctc gac agc aac gag gag aag			1728
Cys Ala Val Trp Tyr Lys Gly Ile Lys Leu Asp Ser Asn Glu Glu Lys			
565	570	575	
gcg aac aag atc acc gtg cac gtt tag			1755
Ala Asn Lys Ile Thr Val His Val			
580			

<210> 279

<211> 584

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<400> 279

Met Ala Pro Thr Ala Val Asp Ser Lys Arg Ile Ser Asp Ile Thr Glu	
1 5 10 15	
Asp Gly Ser Met Asp Arg Arg Gly Asn Pro Ala Val Lys Ala Lys Thr	
20 25 30	
Gly Asn Trp Arg Ser Ser Ile Leu Leu Val Asn Tyr Gly Leu Val	
35 40 45	
Thr Cys Ala Phe Phe Gly Val Gly Val Asn Leu Val Val Phe Leu Arg	
50 55 60	
Arg Val Leu His Gln Asp Asn Ala Glu Ala Ala Asn Ser Ile Ser Lys	
65 70 75 80	
Trp Thr Gly Thr Val Tyr Ile Phe Ser Leu Ile Gly Ala Phe Met Ser	
85 90 95	
Asp Ser Tyr Trp Gly Arg Tyr Ile Thr Cys Ala Ile Phe Gln Met Ile	
100 105 110	
Tyr Val Thr Gly Leu Val Ile Leu Ser Leu Ala Ser Trp Phe Leu Leu	
115 120 125	
Val Lys Pro Thr Gly Cys Gly Ala Ala Gly Glu His Cys Asp Ala Pro	
130 135 140	
Ser Ser Ala Gly Val Ala Leu Phe Tyr Leu Ser Thr Tyr Met Ile Ala	
145 150 155 160	
Phe Gly Asn Gly Gly Tyr Gln Pro Ser Ile Ala Thr Phe Gly Ser Asp	
165 170 175	
Gln Phe Asp Glu Thr Asp Pro Arg Glu Ala Arg Ser Lys Val Ala Phe	
180 185 190	
Phe Ser Tyr Phe Tyr Leu Ala Leu Asn Val Gly Ser Leu Phe Ser Asn	
195 200 205	
Thr Val Leu Val Tyr Tyr Glu Asp Glu Gly Arg Trp Val Met Gly Phe	
210 215 220	
Trp Val Ser Ala Ala Ala Ala Met Ala Leu Val Leu Phe Leu Leu	
225 230 235 240	
Gly Thr Pro Asn Tyr Arg His Phe Lys Pro Thr Gly Asn Pro Leu Thr	
245 250 255	
Arg Ile Ala Gln Val Phe Val Ala Ala Phe Arg Lys Trp Arg Ala Glu	
260 265 270	

PF59082SeqList_PF59082.txt

Val Pro Arg Ser Glu Leu Leu His Glu Val Asp Gly Asp Glu Ser Gln
 275 280 285
 Ile Ala Gly Ile Arg Lys Ile Leu His Ser Asp Gln Ile Arg Phe Leu
 290 295 300
 Asp Lys Ala Ala Thr Val Thr Glu Glu Asp Tyr Cys Thr Pro Glu Asn
 305 310 315 320
 Met Gln Asp Pro Trp Arg Leu Cys Thr Val Thr Gln Val Glu Glu Val
 325 330 335
 Lys Cys Ile Leu Lys Met Leu Pro Ile Trp Leu Cys Thr Ile Val Tyr
 340 345 350
 Ser Val Val Phe Thr Gln Met Ala Ser Leu Phe Val Glu Gln Gly Thr
 355 360 365
 Thr Met Asn Thr Asn Ile Gly Ser Phe His Val Pro Ala Ala Ser Met
 370 375 380
 Ser Val Phe Asp Ile Leu Ser Val Leu Ala Phe Ile Ala Ile Tyr Arg
 385 390 395 400
 Arg Val Leu Val Pro Val Met Ser Arg Leu Ser Gly Asn Pro Gln Gly
 405 410 415
 Leu Thr Glu Leu Gln Arg Met Gly Val Gly Leu Val Val Gly Met Ala
 420 425 430
 Ala Met Val Val Ala Gly Val Val Glu Val Glu Arg Leu Lys Arg Val
 435 440 445
 Gly Ala Pro Asp Gln Pro Ser Ser Leu Ser Val Leu Trp Gln Val Pro
 450 455 460
 Gln Tyr Ala Leu Ile Gly Ala Ser Glu Val Phe Met Tyr Val Gly Gln
 465 470 475 480
 Leu Glu Phe Phe Asn Gly Gln Ala Pro Asp Gly Val Lys Ser Phe Gly
 485 490 495
 Ser Ser Leu Cys Met Ala Ser Ile Ser Leu Gly Asn Tyr Val Ser Ile
 500 505 510
 Met Leu Val Ser Val Val Thr Ser Leu Thr Ala Gly Asp Arg Arg Pro
 515 520 525
 Gly Trp Ile Pro Gly Asn Leu Asn Ser Gly His Leu Asp Arg Phe Tyr
 530 535 540
 Phe Leu Leu Ala Ala Leu Ser Leu Val Asp Leu Ala Val Tyr Val Ala
 545 550 555 560
 Cys Ala Val Trp Tyr Lys Gly Ile Lys Leu Asp Ser Asn Glu Glu Lys
 565 570 575
 Ala Asn Lys Ile Thr Val His Val
 580

<210> 280

<211> 1725

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<221> CDS

<222> (1)..(1725)

<400> 280

atg	gcg	ttg	aac	gcg	ttc	gcc	cag	ccc	gtc	acc	aac	tac	ctc	atc	aaa	48
Met	Ala	Leu	Asn	Ala	Phe	Ala	Gln	Pro	Val	Thr	Asn	Tyr	Leu	Ile	Lys	
1				5					10					15		
cgt	tac	aac	atg	aag	ccg	aat	gcc	gca	aca	aac	gtg	gcc	aac	gtc	ttc	96
Arg	Tyr	Asn	Met	Lys	Pro	Asn	Ala	Ala	Thr	Asn	Val	Ala	Asn	Val	Phe	
			20					25					30			
agt	ggc	acc	tac	agc	ttc	tcg	ccg	gtg	gtc	gga	gcc	ttc	gtc	gcc	gat	144
Ser	Gly	Thr	Tyr	Ser	Phe	Ser	Pro	Val	Val	Gly	Ala	Phe	Val	Ala	Asp	
			35				40					45				
gcg	ttc	tgc	ggc	agg	ttc	tgg	acc	ctc	ttg	ttc	gga	gcc	gtc	gcc	gcc	192
Ala	Phe	Cys	Gly	Arg	Phe	Trp	Thr	Leu	Leu	Phe	Gly	Ala	Val	Ala	Ala	
	50				55					60						
ttt	gtt	gca	atg	gtg	gtc	atc	acg	cta	tcg	gcg	acg	atc	cgt	cag	ctc	240
Phe	Val	Ala	Met	Val	Val	Ile	Thr	Leu	Ser	Ala	Thr	Ile	Arg	Gln	Leu	
	65				70				75						80	
aag	cca	ccg	tcg	tgc	agc	gac	gtg	gca	cgg	caa	gcc	ggc	acg	tgc	gcg	288
Lys	Pro	Pro	Ser	Cys	Ser	Asp	Val	Ala	Arg	Gln	Ala	Gly	Thr	Cys	Ala	
				85					90					95		

PF59082SeqList_PF59082.txt

ggg	ccg	tcg	ggc	ctc	cac	cgc	gcc	gtg	ctc	tac	atc	ggc	atg	gcg	ctg	336
Gly	Pro	Ser	Gly	Leu	His	Arg	Ala	Val	Leu	Tyr	Ile	Gly	Met	Ala	Leu	
			100					105					110			
ctc	gtc	gtg	gcc	acg	ggc	ggc	gcg	aac	ccg	acc	agc	ctg	ccg	ttc	ggc	384
Leu	Val	Val	Ala	Thr	Gly	Gly	Ala	Asn	Pro	Thr	Ser	Leu	Pro	Phe	Gly	
			115					120					125			
gcg	gac	cag	ttc	gac	cac	gac	gac	gcg	agc	agc	ggc	agc	agc	agc	aac	432
Ala	Asp	Gln	Phe	Asp	His	Asp	Asp	Ala	Ser	Ser	Gly	Ser	Ser	Ser	Asn	
			130					135					140			
gaa	gcc	gac	gag	cga	cga	cgg	gcg	gcc	gag	gag	ccc	gcg	ggg	ctc	aag	480
Glu	Ala	Asp	Glu	Arg	Arg	Arg	Arg	Ala	Glu	Glu	Pro	Ala	Gly	Leu	Lys	
															160	
145																
cgc	ttc	tac	aac	tgg	tac	tac	gtg	gtc	acc	atg	atg	gcc	tcg	ttc	atg	528
Arg	Phe	Tyr	Asn	Trp	Tyr	Tyr	Val	Val	Thr	Met	Met	Ala	Ser	Phe	Met	
				165					170							
gcg	ctc	acc	ttc	atc	gcg	tac	atc	cag	gac	aag	gtg	agc	tgg	ggc	ctc	576
Ala	Leu	Thr	Phe	Ile	Ala	Tyr	Ile	Gln	Asp	Lys	Val	Ser	Trp	Gly	Leu	
			180					185					190			
ggc	ttc	ggc	atc	ccc	acg	gcg	ctc	gtg	gcc	gcc	acc	ttc	ggc	gtg	ttc	624
Gly	Phe	Gly	Ile	Pro	Thr	Ala	Leu	Val	Ala	Ala	Thr	Phe	Ala	Val	Phe	
			195					200					205			
ctc	gcc	ggc	acg	ccg	ctg	tac	gtc	gcg	gtg	ccg	gcc	gag	ggc	agc	atc	672
Leu	Ala	Gly	Thr	Pro	Leu	Tyr	Val	Arg	Val	Pro	Ala	Glu	Gly	Ser	Ile	
			210					215					220			
ttc	tcg	agc	gtc	gcg	cgg	gtg	gtc	gtc	gcg	tcg	tcg	cgg	aag	cgg	agg	720
Phe	Ser	Ser	Val	Ala	Arg	Val	Val	Val	Ala	Ser	Cys	Arg	Lys	Arg	Arg	
															240	
225																
ctc	acg	ctg	cct	cac	ccg	cgc	gac	gcg	cgg	cag	cag	gag	gcc	gtt	ctg	768
Leu	Thr	Leu	Pro	His	Pro	Arg	Asp	Ala	Arg	Gln	Gln	Glu	Ala	Val	Leu	
			245											255		
tac	aat	cct	ccc	gtc	gtc	gtc	gca	gct	gga	acg	gga	acc	agc	cgc	gtc	816
Tyr	Asn	Pro	Pro	Val	Val	Val	Ala	Ala	Gly	Thr	Gly	Thr	Ser	Arg	Val	
			260					265					270			
ttc	aag	ctc	cca	ctc	acg	ttg	cag	ctg	agc	ttt	ctg	aac	aag	gcg	gcc	864
Phe	Lys	Leu	Pro	Leu	Thr	Leu	Gln	Leu	Ser	Phe	Leu	Asn	Lys	Ala	Ala	
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Ile	Val	Thr	Ala	Asp	Ala	Asp	Glu	Ile	Arg	Pro	Asp	Gly	Ser	Pro	Ala	
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agg	ccg	tgg	agc	ctg	tgc	gtg	cag	cag	gtg	gag	gag	gtg	aag	tgc		960
Arg	Pro	Trp	Ser	Leu	Cys	Ser	Val	Gln	Gln	Val	Glu	Glu	Val	Lys	Cys	
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305																
ctc	gtc	aag	atc	gtc	ccc	gtg	tgg	atc	tcc	ggc	gtg	atg	tgg	ttc	atc	1008
Leu	Val	Lys	Ile	Val	Pro	Val	Trp	Ile	Ser	Gly	Val	Met	Trp	Phe	Ile	
			325											335		
tcg	gtg	gcg	gag	ctg	acc	aac	tac	acg	ttc	ctg	cag	gcc	ctg	acc	atg	1056
Ser	Val	Ala	Glu	Leu	Thr	Asn	Tyr	Thr	Phe	Leu	Gln	Ala	Leu	Thr	Met	
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gac	ctc	cac	atg	ggc	agg	agc	ttc	acc	atc	ccg	ccc	gtg	tcg	atc	gcc	1104
Asp	Leu	His	Met	Gly	Arg	Ser	Phe	Thr	Ile	Pro	Pro	Val	Ser	Ile	Ala	
			355					360					365			
gcc	ata	ttc	aac	ctc	gcc	atc	gtg	ctc	ttc	gtg	ccg	gtc	tac	gat	ctg	1152
Ala	Ile	Phe	Asn	Leu	Ala	Ile	Val	Leu	Phe	Val	Pro	Val	Tyr	Asp	Leu	
			370					375					380			
ctc	gtc	gcc	cgc	gca	gcg	cag	gtc	acc	ggg	gtg	gag	ggc	ggc	atc		1200
Leu	Val	Ala	Arg	Ala	Ala	Gln	Arg	Val	Thr	Gly	Val	Glu	Gly	Gly	Ile	
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385																
acg	gtg	ctg	cag	agg	cag	ggc	gtc	ggc	gtg	gcg	atc	agc	ggc	ctg	gcg	1248
Thr	Val	Leu	Gln	Arg	Gln	Gly	Val	Gly	Val	Ala	Ile	Ser	Gly	Leu	Ala	
			405					410						415		
ctc	gtg	gtc	gcg	gcc	gtc	gtc	gag	cgc	agg	cgc	cgg	gcc	tcc	gcc	ttg	1296
Leu	Val	Val	Ala	Ala	Val	Val	Glu	Arg	Arg	Arg	Arg	Ala	Ser	Ala	Leu	
			420					425					430			
gac	aac	ggc	ggg	acg	tcg	ccg	atg	tcg	gtg	ttc	gtg	ctc	gcg	ccg	cag	1344
Asp	Asn	Gly	Gly	Thr	Ser	Pro	Met	Ser	Val	Phe	Val	Leu	Ala	Pro	Gln	
			435					440					445			
ctc	gcc	gtg	atg	ggc	gtc	tcg	gcg	gcg	ttc	aac	atg	atc	ggg	cag	atg	1392
Leu	Ala	Val	Met	Gly	Val	Ser	Ala	Ala	Phe	Asn	Met	Ile	Gly	Gln	Met	
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gcg	gcg	ttc	tac	tcg	gcg	cag	ggg	gcg	agc	agc	tac	ctg	gcc	acg	gcg	1488
Ala	Ala	Phe	Tyr	Cys	Ala	Gln	Gly	Ala	Ser	Ser	Tyr	Leu	Ala	Thr	Ala	
				485					490						495	
gtt	gtg	aac	gtc	gtg	aac	gcg	agg	acg	agg	cgg	cgc	ggc	ggc	ggg	cag	1536
Val	Val	Asn	Val	Val	Asn	Ala	Arg	Thr	Arg	Arg	Arg	Gly	Gly	Gly	Gln	
				500					505							
ggc	tgg	gtc	gcc	gag	gac	atc	aac	gcc	ggg	aag	ctg	gac	cac	ttc	tac	1584
Gly	Trp	Val	Ala	Glu	Asp	Ile	Asn	Ala	Gly	Lys	Leu	Asp	His	Phe	Tyr	
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tac	gcc	atg	gcc	gtg	ttc	gcg	gcg	atc	aac	ttc	gtc	tac	ttc	ctc	gtc	1632
Tyr	Ala	Met	Ala	Val	Phe	Ala	Ala	Ile	Asn	Phe	Val	Tyr	Phe	Leu	Val	
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tgc	tcc	tac	ttc	tac	cgc	tac	aag	ggc	gag	cca	gag	gtg	gcg	gcc	gag	1680
Cys	Ser	Tyr	Phe	Tyr	Arg	Tyr	Lys	Gly	Glu	Pro	Glu	Val	Ala	Ala	Glu	
545					550					555					560	
gac	tcg	cca	ccg	gcc	act	cca	gag	gcc	gtc	ctc	ctg	aag	cac	tag		1725
Asp	Ser	Pro	Pro	Ala	Thr	Pro	Glu	Ala	Val	Leu	Leu	Lys	His			
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<210> 281

<211> 574

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<400> 281

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			20					25					30			
Ser	Gly	Thr	Tyr	Ser	Phe	Ser	Pro	Val	Val	Gly	Ala	Phe	Val	Ala	Asp	
		35					40					45				
Ala	Phe	Cys	Gly	Arg	Phe	Trp	Thr	Leu	Leu	Phe	Gly	Ala	Val	Ala	Ala	
	50					55					60					
Phe	Val	Ala	Met	Val	Val	Ile	Thr	Leu	Ser	Ala	Thr	Ile	Arg	Gln	Leu	
65					70					75					80	
Lys	Pro	Pro	Ser	Cys	Ser	Asp	Val	Ala	Arg	Gln	Ala	Gly	Thr	Cys	Ala	
				85					90					95		
Gly	Pro	Ser	Gly	Leu	His	Arg	Ala	Val	Leu	Tyr	Ile	Gly	Met	Ala	Leu	
			100					105					110			
Leu	Val	Val	Ala	Thr	Gly	Gly	Ala	Asn	Pro	Thr	Ser	Leu	Pro	Phe	Gly	
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Ala	Asp	Gln	Phe	Asp	His	Asp	Ala	Ser	Ser	Gly	Ser	Ser	Ser	Ser	Asn	
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Glu	Ala	Asp	Glu	Arg	Arg	Arg	Ala	Glu	Glu	Pro	Ala	Gly	Leu	Lys		
145					150				155					160		
Arg	Phe	Tyr	Asn	Trp	Tyr	Tyr	Val	Val	Thr	Met	Met	Ala	Ser	Phe	Met	
				165					170					175		
Ala	Leu	Thr	Phe	Ile	Ala	Tyr	Ile	Gln	Asp	Lys	Val	Ser	Trp	Gly	Leu	
			180					185						190		
Gly	Phe	Gly	Ile	Pro	Thr	Ala	Leu	Val	Ala	Ala	Thr	Phe	Ala	Val	Phe	
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Leu	Ala	Gly	Thr	Pro	Leu	Tyr	Val	Arg	Val	Pro	Ala	Glu	Gly	Ser	Ile	
	210					215					220					
Phe	Ser	Ser	Val	Ala	Arg	Val	Val	Val	Ala	Ser	Cys	Arg	Lys	Arg	Arg	
225					230					235					240	
Leu	Thr	Leu	Pro	His	Pro	Arg	Asp	Ala	Arg	Gln	Gln	Glu	Ala	Val	Leu	
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Tyr	Asn	Pro	Pro	Val	Val	Val	Ala	Ala	Gly	Thr	Gly	Thr	Ser	Arg	Val	
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Phe	Lys	Leu	Pro	Leu	Thr	Leu	Gln	Leu	Ser	Phe	Leu	Asn	Lys	Ala	Ala	
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Ile	Val	Thr	Ala	Asp	Ala	Asp	Glu	Ile	Arg	Pro	Asp	Gly	Ser	Pro	Ala	
	290					295					300					
Arg	Pro	Trp	Ser	Leu	Cys	Ser	Val	Gln	Gln	Val	Glu	Glu	Val	Lys	Cys	
305					310					315					320	
Leu	Val	Lys	Ile	Val	Pro	Val	Trp	Ile	Ser	Gly	Val	Met	Trp	Phe	Ile	

PF59082SeqList_PF59082.txt

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          325          330          335
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          340          345          350
Asp Leu His Met Gly Arg Ser Phe Thr Ile Pro Pro Val Ser Ile Ala
          355          360          365
Ala Ile Phe Asn Leu Ala Ile Val Leu Phe Val Pro Val Tyr Asp Leu
          370          375          380
Leu Val Ala Arg Ala Ala Gln Arg Val Thr Gly Val Glu Gly Gly Ile
          385          390          400
Thr Val Leu Gln Arg Gln Gly Val Gly Val Ala Ile Ser Gly Leu Ala
          405          410          415
Leu Val Val Ala Ala Val Val Glu Arg Arg Arg Arg Ala Ser Ala Leu
          420          425          430
Asp Asn Gly Gly Thr Ser Pro Met Ser Val Phe Val Leu Ala Pro Gln
          435          440          445
Leu Ala Val Met Gly Val Ser Ala Ala Phe Asn Met Ile Gly Gln Met
          450          455          460
Glu Phe Tyr Asn Thr Glu Phe Pro Asp Gln Met Arg Thr Leu Ala Asn
          465          470          475
Ala Ala Phe Tyr Cys Ala Gln Gly Ala Ser Tyr Leu Ala Thr Ala
          485          490          495
Val Val Asn Val Val Asn Ala Arg Thr Arg Arg Arg Gly Gly Gly Gln
          500          505          510
Gly Trp Val Ala Glu Asp Ile Asn Ala Gly Lys Leu Asp His Phe Tyr
          515          520          525
Tyr Ala Met Ala Val Phe Ala Ile Asn Phe Val Tyr Phe Leu Val
          530          535          540
Cys Ser Tyr Phe Tyr Arg Tyr Lys Gly Glu Pro Glu Val Ala Ala Glu
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Asp Ser Pro Pro Ala Thr Pro Glu Ala Val Leu Leu Lys His
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<210> 282

<211> 1857

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<221> CDS

<222> (1)..(1857)

<400> 282

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gag gcc cac ctc gac ggc gac gtg gga aac ggc aat gcc aga tca gac      96
Glu Ala His Leu Asp Gly Asp Val Gly Asn Gly Asn Ala Arg Ser Asp
          20          25          30
tcc gcg gcg gcg gcg gcg gcg ccg gag ctc cgg tac cgg ggg tgg aag      144
Ser Ala Ala Ala Ala Ala Ala Pro Glu Leu Arg Tyr Arg Gly Trp Lys
          35          40          45
gcg atg ccg ttc gtg atc ggc aac gag acg ttc gag aag ctg ggc agc      192
Ala Met Pro Phe Val Ile Gly Asn Glu Thr Phe Glu Lys Leu Gly Ser
          50          55          60
atc ggc acg gcg gcg aac ctc atg gtg tac ctc acc acc gtc ttc cac      240
Ile Gly Thr Ala Ala Asn Leu Met Val Tyr Leu Thr Thr Val Phe His
          65          70          75
atg tcc agc ctc gac gcc gcc gtc gcg ctc aac gtg ttc gct ggc acc      288
Met Ser Ser Leu Asp Ala Ala Val Ala Leu Asn Val Phe Ala Gly Thr
          85          90          95
acc aac ctc gcc acc gtc gtc ggc gcc ttc gcc tcc gac ctc tac ctc      336
Thr Asn Leu Ala Thr Val Val Gly Ala Phe Ala Ser Asp Leu Tyr Leu
          100          105          110
ggc cgc tac gcc acc gtc gcc gcc ggc tgc gtc tcc acc ttc atc ggg      384
Gly Arg Tyr Ala Thr Val Ala Ala Gly Cys Val Ser Thr Phe Ile Gly
          115          120          125
atg gtc atc ttg acg atg acg gcc ggc gtg ccg gcg ctg cac ccg ccg      432
Met Val Ile Leu Thr Met Thr Ala Gly Val Pro Ala Leu His Pro Pro
          130          135          140

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PF59082SeqList_PF59082.txt

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Val	Leu	Gly	Leu	Ala	Phe	Ala	Phe	Ile	Val	Ala	Gly	Ala	Gly	Gly	Ile	
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cgg	ccg	tgc	agc	ctg	ccg	ttc	ggc	gcc	gac	cag	ttc	gac	ccg	cgc	acg	576
Arg	Pro	Cys	Ser	Leu	Pro	Phe	Gly	Ala	Asp	Gln	Phe	Asp	Pro	Arg	Thr	
			180					185					190			
gag	tcc	ggc	cgc	cgc	ggc	atc	aac	agc	ttc	ttc	aac	tgg	tac	tac	ttc	624
Glu	Ser	Gly	Arg	Arg	Gly	Ile	Asn	Ser	Phe	Phe	Asn	Trp	Tyr	Tyr	Phe	
		195					200					205				
acg	ctc	acc	atc	gcc	gtc	tgc	gcc	tcg	tcg	acg	gcg	atc	gtc	tac	gtg	672
Thr	Leu	Thr	Ile	Ala	Val	Cys	Ala	Ser	Ser	Thr	Ala	Ile	Val	Tyr	Val	
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cag	agc	agc	gtg	agc	tgg	gtc	ggg	ctc	gcc	atc	ccg	gcg	gcg	ctc		720
Gln	Ser	Ser	Val	Ser	Trp	Trp	Val	Gly	Leu	Ala	Ile	Pro	Ala	Ala	Leu	
225					230					235					240	
atg	ctc	gcc	tcc	tgc	gcc	ctc	ttc	ttc	gcc	ggc	gcg	ggg	ctc	tac	gtc	768
Met	Leu	Ala	Ser	Cys	Ala	Leu	Phe	Phe	Ala	Gly	Ala	Gly	Leu	Tyr	Val	
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cgc	gtg	cgc	ccc	gag	ggg	agc	ccc	ttc	gcc	ggc	gtc	gcg	cgc	gtc	gcc	816
Arg	Val	Arg	Pro	Glu	Gly	Ser	Pro	Phe	Ala	Gly	Val	Ala	Arg	Val	Ala	
			260					265					270			
gtc	gcc	gcg	ttc	cgg	aag	cgg	tcg	gcc	gcc	gcg	ccc	tcc	gac	gcc	gac	864
Val	Ala	Ala	Phe	Arg	Lys	Arg	Ser	Ala	Ala	Ala	Pro	Ser	Asp	Ala	Asp	
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gag	tcc	ctc	ttc	cgg	acg	cgc	cac	gcc	agc	ggc	gtc	gtg	tcg	agg	ctc	912
Glu	Ser	Leu	Phe	Arg	Thr	Arg	His	Ala	Ser	Gly	Val	Val	Ser	Arg	Leu	
		290				295					300					
ccc	tac	acc	gac	cag	ttc	agg	ttc	ctc	gac	aag	gcc	gcc	gtc	gtg	gtc	960
Pro	Tyr	Thr	Asp	Gln	Phe	Arg	Phe	Leu	Asp	Lys	Ala	Ala	Val	Val	Val	
305					310					315					320	
gac	gcc	aag	agc	gag	gtg	ggc	ggc	gac	ggg	cac	ccc	aag	aat	cca	tgg	1008
Asp	Ala	Lys	Ser	Glu	Val	Gly	Gly	Asp	Gly	His	Pro	Lys	Asn	Pro	Trp	
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Arg	Leu	Cys	Ser	Leu	Gln	Gln	Val	Glu	Glu	Ala	Lys	Cys	Ile	Leu	Arg	
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gtc	gtc	ccc	gtg	tgg	ctc	acc	tgc	atc	gtc	tac	tac	gtc	gcg	ttc	gcg	1104
Val	Val	Pro	Val	Trp	Leu	Thr	Cys	Ile	Val	Tyr	Tyr	Val	Ala	Phe	Ala	
		355					360					365				
cag	acg	aac	acc	tac	gtc	atc	ctc	cag	gcg	gcg	cag	tcc	gac	cgc	cac	1152
Gln	Thr	Asn	Thr	Tyr	Val	Ile	Leu	Gln	Ala	Ala	Gln	Ser	Asp	Arg	His	
		370				375					380					
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Leu	Gly	Gly	Gly	Gly	Gly	Ala	Gly	Ser	Phe	Glu	Val	Pro	Pro	Gly	Ser	
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ttc	acc	gtc	ttc	ccc	atg	ctg	gcg	ctc	gcc	gtc	tgg	atc	ccg	ctc	tac	1248
Phe	Thr	Val	Phe	Pro	Met	Leu	Ala	Leu	Ala	Val	Trp	Ile	Pro	Leu	Tyr	
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gac	cgc	ctc	gtc	gtg	cca	tgg	gcg	cgc	cgc	ctc	acg	ggg	cgc	gag	ggc	1296
Asp	Arg	Leu	Val	Val	Pro	Trp	Ala	Arg	Arg	Leu	Thr	Gly	Arg	Glu	Gly	
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ggc	atc	acg	ccg	ctc	cag	cgg	atg	ggc	gtc	ggc	atg	gcg	ctg	tcc	gtc	1344
Gly	Ile	Thr	Pro	Leu	Gln	Arg	Met	Gly	Val	Gly	Met	Ala	Leu	Ser	Val	
		435					440					445				
ctc	gcc	atg	ctc	gtc	gcc	gcc	atg	gcc	gag	aag	cgg	cgg	cgc	gac	ctc	1392
Leu	Ala	Met	Leu	Val	Ala	Ala	Met	Ala	Glu	Lys	Arg	Arg	Arg	Asp	Leu	
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gcc	gcc	ggc	tcg	ccg	tcg	aac	acc	ggc	cgg	gtg	tcg	cgg	cag	tcg	gcg	1440
Ala	Ala	Gly	Ser	Pro	Ser	Asn	Thr	Gly	Arg	Val	Ser	Arg	Gln	Ser	Ala	
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Phe	Trp	Leu	Val	Pro	Gln	Leu	Ala	Ala	Leu	Gly	Leu	Ser	Glu	Ala	Phe	
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aac	cag	gtg	agc	cag	acg	gag	ttc	tac	tac	agg	gag	ttc	ccg	gag	agc	1536
Asn	Gln	Val	Ser	Gln	Thr	Glu	Phe	Tyr	Tyr	Arg	Glu	Phe	Pro	Glu	Ser	
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agc	tac	ctg	agc	ggg	gtg	ctg	gtc	gcc	gcc	gtg	gag	cgc	gcc	acg	agg	1632
Ser	Tyr	Leu	Ser	Gly	Val	Leu	Val	Ala	Ala	Val	Glu	Arg	Ala	Thr	Arg	
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Gly	Ala	Ser	Ala	Gly	Asp	Asp	Gly	Gly	Trp	Leu	Ala	Glu	Asp	Leu	Asn	
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Lys	Gly	Arg	Leu	Asp	Trp	Phe	Tyr	Leu	Leu	Ile	Ala	Ala	Ile	Gly	Ala	
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gcc	aac	ttc	ttg	gcg	ttc	gtc	gcg	tgc	gcc	aag	tgg	tac	agg	tac	aag	1776
Ala	Asn	Phe	Leu	Ala	Phe	Val	Ala	Cys	Ala	Lys	Trp	Tyr	Arg	Tyr	Lys	
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Gly	Ser	Asp	Asp	Asp	Asp	Asp	Asp	Asp	His	Glu	His	Glu	Gln	Val	Asn	
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gtt	gca	gat	agg	att	agt	gct	gct	gct	gct	taa						1857
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<210> 283

<211> 618

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<400> 283

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			20					25					30			
Ser	Ala	Ala	Ala	Ala	Ala	Ala	Pro	Glu	Leu	Arg	Tyr	Arg	Gly	Trp	Lys	
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Met	Ser	Ser	Leu	Asp	Ala	Ala	Val	Ala	Leu	Asn	Val	Phe	Ala	Gly	Thr	
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Thr	Asn	Leu	Ala	Thr	Val	Val	Gly	Ala	Phe	Ala	Ser	Asp	Leu	Tyr	Leu	
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Glu	Ser	Gly	Arg	Arg	Gly	Ile	Asn	Ser	Phe	Phe	Asn	Trp	Tyr	Tyr	Phe	
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Glu	Ser	Leu	Phe	Arg	Thr	Arg	His	Ala	Ser	Gly	Val	Val	Ser	Arg	Leu	
	290					295					300					
Pro	Tyr	Thr	Asp	Gln	Phe	Arg	Phe	Leu	Asp	Lys	Ala	Ala	Val	Val	Val	
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Asp	Ala	Lys	Ser	Glu	Val	Gly	Gly	Asp	Gly	His	Pro	Lys	Asn	Pro	Trp	

PF59082SeqList_PF59082.txt

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 Val Val Pro Val Trp Leu Thr Cys Ile Val Tyr Tyr Val Ala Phe Ala
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 355 360 365
 Gln Thr Asn Thr Tyr Val Ile Leu Gln Ala Ala Gln Ser Asp Arg His
 370 375 380
 Leu Gly Gly Gly Gly Gly Ala Gly Ser Phe Glu Val Pro Pro Gly Ser
 385 390 400
 Phe Thr Val Phe Pro Met Leu Ala Leu Ala Val Trp Ile Pro Leu Tyr
 405 415
 Asp Arg Leu Val Val Pro Trp Ala Arg Arg Leu Thr Gly Arg Glu Gly
 420 425 430
 Gly Ile Thr Pro Leu Gln Arg Met Gly Val Gly Met Ala Leu Ser Val
 435 440 445
 Leu Ala Met Leu Val Ala Ala Met Ala Glu Lys Arg Arg Arg Asp Leu
 450 455 460
 Ala Ala Gly Ser Pro Ser Asn Thr Gly Arg Val Ser Arg Gln Ser Ala
 465 470 475 480
 Phe Trp Leu Val Pro Gln Leu Ala Ala Leu Gly Leu Ser Glu Ala Phe
 485 490 495
 Asn Gln Val Ser Gln Thr Glu Phe Tyr Tyr Arg Glu Phe Pro Glu Ser
 500 505 510
 Met Arg Ser Val Ala Gly Ser Val Leu Phe Ser Gly Leu Ala Leu Ser
 515 520 525
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 530 535 540
 Gly Ala Ser Ala Gly Asp Asp Gly Gly Trp Leu Ala Glu Asp Leu Asn
 545 550 555 560
 Lys Gly Arg Leu Asp Trp Phe Tyr Leu Ile Ala Ala Ile Gly Ala
 565 570 575
 Ala Asn Phe Leu Ala Phe Val Ala Cys Ala Lys Trp Tyr Arg Tyr Lys
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 Val Ala Asp Arg Ile Ser Ala Ala Ala
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Ile Lys Gly Asn Pro Ala Leu Lys Lys Asp Thr Gly Asn Trp Arg Ala	
20 25 30	
tgc ccc tac atc ctc gcg aac gag tgc tgc gag cgg ctg gcc tac tac	144
Cys Pro Tyr Ile Leu Ala Asn Glu Cys Cys Glu Arg Leu Ala Tyr Tyr	
35 40 45	
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Gly Met Ser Thr Asn Leu Val Asn Phe Met Lys Asp Arg Met Gly Met	
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gcc aac gcg gcg gct gcc aac aac gtc acc aac tgg ggc ggc acc tgc	240
Ala Asn Ala Ala Ala Ala Asn Asn Val Thr Asn Trp Gly Gly Thr Cys	
65 70 75 80	
tac atc acc ccg ctc atc ggc gcc ttc ctc gcc gac gcc tac ctc ggc	288
Tyr Ile Thr Pro Leu Ile Gly Ala Phe Leu Ala Asp Ala Tyr Leu Gly	
85 90 95	
cgc ttc tgg acc atc gcc tcc ttc atg atc atc tac atc ttc ggc ctg	336
Arg Phe Trp Thr Ile Ala Ser Phe Met Ile Ile Tyr Ile Phe Gly Leu	
100 105 110	

PF59082SeqList_PF59082.txt

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Ala	Ser	Lys	Gly	Val	Cys	Asp	Pro	Thr	Pro	Gly	Gln	Ser	Ala	Ala	Val	
	130					135					140					
ttc	atc	gcg	ctc	tac	ctc	atc	gcg	ctc	ggc	acc	ggc	ggg	atc	aag	ccc	480
Phe	Ile	Ala	Leu	Tyr	Leu	Ile	Ala	Leu	Gly	Thr	Gly	Gly	Ile	Lys	Pro	
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tgc	gtc	tca	tcc	ttc	ggg	gcc	gac	cag	ttc	gac	gag	cac	gac	gac	gtg	528
Cys	Val	Ser	Ser	Phe	Gly	Ala	Asp	Gln	Phe	Asp	Glu	His	Asp	Asp	Val	
				165					170					175		
gag	cgc	aag	agc	aag	agc	tcc	ttc	ttc	aac	tgg	ttc	tac	ttc	tcc	atc	576
Glu	Arg	Lys	Ser	Lys	Ser	Ser	Phe	Phe	Asn	Trp	Phe	Tyr	Phe	Ser	Ile	
			180					185					190			
aac	atc	ggc	gcg	ctg	gtg	gcc	tcg	gtg	gtg	ctg	gtg	tac	gtg	cag	aca	624
Asn	Ile	Gly	Ala	Leu	Val	Ala	Ser	Ser	Val	Leu	Val	Tyr	Val	Gln	Thr	
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His	Val	Gly	Trp	Ser	Trp	Gly	Phe	Gly	Ile	Pro	Ala	Val	Val	Met	Ala	
	210					215					220					
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Ile	Ala	Val	Gly	Ser	Phe	Phe	Val	Gly	Thr	Ser	Leu	Tyr	Arg	His	Gln	
225					230				235						240	
cgc	ccc	ggc	ggc	agc	ccg	ctc	acc	cgc	atc	gca	cag	gtg	ctc	gtc	gcc	768
Arg	Pro	Gly	Gly	Ser	Pro	Leu	Thr	Arg	Ile	Ala	Gln	Val	Leu	Val	Ala	
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gcc	acg	cgc	aag	ctg	ggc	gtc	gcc	gtc	gac	ggg	tcg	gcg	ctg	tac	gag	816
Ala	Thr	Arg	Lys	Leu	Gly	Val	Ala	Val	Asp	Gly	Ser	Ala	Leu	Tyr	Glu	
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acc	gcg	gac	aag	gag	tcc	ggc	atc	gag	ggg	agc	cgc	aag	ctg	gag	cac	864
Thr	Ala	Asp	Lys	Glu	Ser	Gly	Ile	Glu	Gly	Ser	Arg	Lys	Leu	Glu	His	
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acg	cgg	cag	ttc	agg	ttc	ctc	gac	aag	gcg	gcg	gtg	gag	acg	cat	gcc	912
Thr	Arg	Gln	Phe	Arg	Phe	Leu	Asp	Lys	Ala	Ala	Val	Glu	Thr	His	Ala	
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Asp	Arg	Thr	Ala	Ala	Ala	Pro	Ser	Pro	Trp	Arg	Leu	Cys	Thr	Val	Thr	
305					310				315						320	
cag	gtg	gag	gag	ctc	aag	agc	gtg	gtg	cgc	ctg	ctg	ccc	atc	tgg	gca	1008
Gln	Val	Glu	Glu	Leu	Lys	Ser	Val	Val	Arg	Leu	Leu	Pro	Ile	Trp	Ala	
				325					330					335		
agc	ggc	atc	gtg	ttc	gcc	acg	gtg	tac	ggg	cag	atg	agc	acc	atg	ttc	1056
Ser	Gly	Ile	Val	Phe	Ala	Thr	Val	Tyr	Gly	Gln	Met	Ser	Thr	Met	Phe	
			340					345					350			
gtg	ctc	caa	ggc	aac	acc	ctg	gac	gcc	tcc	atg	ggg	ccc	aag	ttc	aag	1104
Val	Leu	Gln	Gly	Asn	Thr	Leu	Asp	Ala	Ser	Met	Gly	Pro	Lys	Phe	Lys	
		355					360					365				
atc	ccc	tcc	gcc	tcc	ctc	tcc	atc	ttc	gac	acc	ctc	agc	gtc	atc	gcc	1152
Ile	Pro	Ser	Ala	Ser	Leu	Ser	Ile	Phe	Asp	Thr	Leu	Ser	Val	Ile	Ala	
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Trp	Val	Pro	Val	Tyr	Asp	Arg	Ile	Leu	Val	Pro	Ala	Val	Arg	Ser	Val	
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Thr	Gly	Arg	Pro	Arg	Gly	Phe	Thr	Gln	Leu	Gln	Arg	Met	Gly	Ile	Gly	
				405					410					415		
ctc	gtg	gtc	tcc	atg	ttc	gcc	atg	ctc	gcc	gcc	ggc	gtg	ctc	gag	ctc	1296
Leu	Val	Val	Ser	Met	Phe	Ala	Met	Leu	Ala	Ala	Gly	Val	Leu	Glu	Leu	
			420					425					430			
gtc	cgc	ctc	cgc	acc	atc	gcg	cag	cac	ggg	ctg	tac	ggg	gag	aag	gac	1344
Val	Arg	Leu	Arg	Thr	Ile	Ala	Gln	His	Gly	Leu	Tyr	Gly	Glu	Lys	Asp	
		435					440					445				
gtg	gtg	ccc	atc	tcc	atc	ttc	tgg	cag	gtg	ccg	cag	tac	ttc	atc	atc	1392
Val	Val	Pro	Ile	Ser	Ile	Phe	Trp	Gln	Val	Pro	Gln	Tyr	Phe	Ile	Ile	
		450				455					460					
ggc	tgc	gcc	gag	gtg	ttc	acc	ttc	gtg	ggg	cag	ctc	gag	ttc	ttc	tac	1440
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Asp	Gln	Ala	Pro	Asp	Ala	Met	Arg	Ser	Met	Cys	Ser	Ala	Leu	Ser	Leu	
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acc	acc	gtg	gcg	ctc	ggg	aac	tac	ctc	agc	acg	ctg	ctc	gtc	acg	gtg	1536
Thr	Thr	Val	Ala	Leu	Gly	Asn	Tyr	Leu	Ser	Thr	Leu	Leu	Val	Thr	Val	
			500					505					510			
gtg	gcc	aag	gtg	acc	acc	agg	gga	ggc	aag	caa	ggg	tgg	atc	ccg	gac	1584
Val	Ala	Lys	Val	Thr	Thr	Arg	Gly	Gly	Lys	Gln	Gly	Trp	Ile	Pro	Asp	
		515					520				525					
aac	ctc	aac	gtc	ggc	cac	ctc	gac	tac	ttc	ttc	tgg	ctg	ctc	gcc	gcg	1632
Asn	Leu	Asn	Val	Gly	His	Leu	Asp	Tyr	Phe	Phe	Trp	Leu	Leu	Ala	Ala	
	530					535					540					
ctc	agc	ctc	gtc	aac	ttc	gcc	gtc	tac	ctg	ctc	atc	gcc	agc	tgg	tac	1680
Leu	Ser	Leu	Val	Asn	Phe	Ala	Val	Tyr	Leu	Leu	Ile	Ala	Ser	Trp	Tyr	
	545				550				555						560	
acc	tac	aag	aag	acc	ggc	gat	tct	ccg	gac	gcc	aaa	gga	gga	gct		1728
Thr	Tyr	Lys	Lys	Thr	Ala	Gly	Asp	Ser	Pro	Asp	Ala	Lys	Gly	Gly	Ala	
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cat	gat	cag	tga													1740
His	Asp	Gln														

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<211> 579

<212> PRT

<213> Hordeum vulgare

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			20					25					30			
Cys	Pro	Tyr	Ile	Leu	Ala	Asn	Glu	Cys	Cys	Glu	Arg	Leu	Ala	Tyr	Tyr	
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Tyr	Ile	Thr	Pro	Leu	Ile	Gly	Ala	Phe	Leu	Ala	Asp	Ala	Tyr	Leu	Gly	
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Ala	Ser	Lys	Gly	Val	Cys	Asp	Pro	Thr	Pro	Gly	Gln	Ser	Ala	Ala	Val	
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Phe	Ile	Ala	Leu	Tyr	Leu	Ile	Ala	Leu	Gly	Thr	Gly	Gly	Ile	Lys	Pro	
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Cys	Val	Ser	Ser	Phe	Gly	Ala	Asp	Gln	Phe	Asp	Glu	His	Asp	Asp	Val	
			165					170					175			
Glu	Arg	Lys	Ser	Lys	Ser	Ser	Phe	Phe	Asn	Trp	Phe	Tyr	Phe	Ser	Ile	
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Asn	Ile	Gly	Ala	Leu	Val	Ala	Ser	Ser	Val	Leu	Val	Tyr	Val	Gln	Thr	
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Arg	Pro	Gly	Gly	Ser	Pro	Leu	Thr	Arg	Ile	Ala	Gln	Val	Leu	Val	Ala	
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Ala	Thr	Arg	Lys	Leu	Gly	Val	Ala	Val	Asp	Gly	Ser	Ala	Leu	Tyr	Glu	
			260				265						270			
Thr	Ala	Asp	Lys	Glu	Ser	Gly	Ile	Glu	Gly	Ser	Arg	Lys	Leu	Glu	His	
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Asp	Arg	Thr	Ala	Ala	Ala	Pro	Ser	Pro	Trp	Arg	Leu	Cys	Thr	Val	Thr	
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PF59082SeqList_PF59082.txt

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370 Trp Val Pro Val Tyr Asp Arg Ile Leu Val Pro Ala Val Arg Ser Val
385 Thr Gly Arg Pro Arg Gly Phe Thr Gln Leu Gln Arg Met Gly Ile Gly
          405          410          415
Leu Val Val Ser Met Phe Ala Met Leu Ala Ala Gly Val Leu Glu Leu
          420          425          430
Val Arg Leu Arg Thr Ile Ala Gln His Gly Leu Tyr Gly Glu Lys Asp
          435          440          445
Val Val Pro Ile Ser Ile Phe Trp Gln Val Pro Gln Tyr Phe Ile Ile
450 Gly Cys Ala Glu Val Phe Thr Phe Val Gly Gln Leu Glu Phe Phe Tyr
465 Asp Gln Ala Pro Asp Ala Met Arg Ser Met Cys Ser Ala Leu Ser Leu
          485          490          495
Thr Thr Val Ala Leu Gly Asn Tyr Leu Ser Thr Leu Leu Val Thr Val
          500          505          510
Val Ala Lys Val Thr Thr Arg Gly Gly Lys Gln Gly Trp Ile Pro Asp
          515          520          525
Asn Leu Asn Val Gly His Leu Asp Tyr Phe Phe Trp Leu Leu Ala Ala
530 Leu Ser Leu Val Asn Phe Ala Val Tyr Leu Leu Ile Ala Ser Trp Tyr
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tct gta ccg ttc atg cga ttc ttt ctt cct cta tat ata gtg aat act      96
Ser Val Pro Phe Met Arg Phe Phe Leu Pro Leu Tyr Ile Val Asn Thr
          20          25          30
tcc aca cac tct gtt tca tca tta aat ctc ctt gtc ttc ggc ttt cat      144
Ser Thr His Ser Val Ser Ser Leu Asn Leu Leu Val Phe Gly Phe His
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cca aat caa caa caa tct tcc tct gct tca tca ttt ttc tca ctc ttt      192
Pro Asn Gln Gln Gln Ser Ser Ser Ala Ser Ser Phe Phe Ser Leu Phe
          50          55          60
ttc ttc ctt ttt gtc ttt gaa act ttg tca tca cca atg gct tgc tta      240
Phe Phe Leu Phe Val Phe Glu Thr Leu Ser Ser Pro Met Ala Cys Leu
          65          70          75          80
gag gtc tgc aaa gag ggg aag ttc aaa gaa gaa aca gaa gag tta act      288
Glu Val Cys Lys Glu Gly Lys Phe Lys Glu Glu Thr Glu Glu Leu Thr
          85          90          95
ctt gat ggg agt gtt gat tgg cat ggt cgc cca tca atc aga gcc aca      336
Leu Asp Gly Ser Val Asp Trp His Gly Arg Pro Ser Ile Arg Ala Thr
          100          105          110
tcc ggg aga tgg ttt gcc gga act att ata ctc ttg aac caa ggt cta      384
Ser Gly Arg Trp Phe Ala Gly Thr Ile Ile Leu Leu Asn Gln Gly Leu
          115          120          125
gca acc tta gca ttc ttt gga gtt gga gtg aac cta gtt ctg ttc ttg      432

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PF59082SeqList_PF59082.txt

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Thr	Arg	Val	Leu	Gly	Gln	Asp	Asn	Ala	Ala	Ala	Ala	Asn	Asn	Val	Ser	
145					150					155					160	
aag	tgg	act	ggc	aca	gtt	tac	atc	ttc	tct	ctt	gtt	ggg	gct	ttc	ctt	528
Lys	Trp	Thr	Gly	Thr	Val	Tyr	Ile	Phe	Ser	Leu	Val	Gly	Ala	Phe	Leu	
				165					170					175		
agt	gat	tct	tat	tgg	gga	aga	tac	aaa	aca	tgt	gct	atc	ttt	caa	ggc	576
Ser	Asp	Ser	Tyr	Trp	Gly	Arg	Tyr	Lys	Thr	Cys	Ala	Ile	Phe	Gln	Gly	
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Ile	Phe	Val	Thr	Gly	Leu	Val	Ser	Leu	Ser	Val	Thr	Thr	Tyr	Leu	Ala	
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Leu	Leu	Arg	Pro	Lys	Gly	Cys	Gly	Asn	Gly	Lys	Leu	Glu	Cys	Gly	Glu	
		210				215					220					
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His	Ser	Ser	Leu	Glu	Met	Gly	Met	Phe	Tyr	Leu	Ser	Ile	Tyr	Leu	Ile	
225					230					235					240	
gcc	tta	gga	aat	gga	ggg	tat	caa	cca	aac	att	gca	aca	ttt	ggt	gct	768
Ala	Leu	Gly	Asn	Gly	Gly	Tyr	Gln	Pro	Asn	Ile	Ala	Thr	Phe	Gly	Ala	
				245					250					255		
gac	caa	ttt	gat	gaa	gat	cac	tca	aag	gag	agt	tat	tca	aaa	gtg	gca	816
Asp	Gln	Phe	Asp	Glu	Asp	His	Ser	Lys	Glu	Ser	Tyr	Ser	Lys	Val	Ala	
			260					265					270			
ttt	ttt	agc	tac	ttt	tac	ttg	gca	ttg	aac	ctt	ggg	tca	ctt	ttc	tca	864
Phe	Phe	Ser	Tyr	Phe	Tyr	Leu	Ala	Leu	Asn	Leu	Gly	Ser	Leu	Phe	Ser	
		275					280					285				
aac	act	att	ttg	ggc	tat	ttt	gaa	gat	gaa	gga	tta	tgg	gct	ctt	ggg	912
Asn	Thr	Ile	Leu	Gly	Tyr	Phe	Glu	Asp	Glu	Gly	Leu	Trp	Ala	Leu	Gly	
		290				295					300					
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Phe	Trp	Ala	Ser	Ala	Gly	Ser	Ala	Phe	Leu	Ala	Leu	Val	Leu	Phe	Leu	
305					310					315					320	
gtt	ggc	acc	cca	aaa	tat	aga	cac	ttt	aaa	cct	tgt	ggc	aat	cct	ctt	1008
Val	Gly	Thr	Pro	Lys	Tyr	Arg	His	Phe	Lys	Pro	Cys	Gly	Asn	Pro	Leu	
				325					330					335		
tct	aga	ttc	tgc	caa	gtg	ttt	ttc	gct	gct	tca	agg	aaa	ttg	gga	gtt	1056
Ser	Arg	Phe	Cys	Gln	Val	Phe	Phe	Ala	Ala	Ser	Arg	Lys	Leu	Gly	Val	
			340					345					350			
caa	atg	act	tca	aat	gga	gat	gac	ttg	tat	gtc	ata	gat	gaa	aag	gag	1104
Gln	Met	Thr	Ser	Asn	Gly	Asp	Asp	Leu	Tyr	Val	Ile	Asp	Glu	Lys	Glu	
		355				360						365				
tct	tct	aac	aac	tcc	aac	aga	aag	att	ctc	cac	aca	cat	ggc	ttc	aag	1152
Ser	Ser	Asn	Asn	Ser	Asn	Arg	Lys	Ile	Leu	His	Thr	His	Gly	Phe	Lys	
		370				375					380					
ttt	ttg	gat	agg	gca	gct	tat	ata	act	tca	aga	gat	tta	gag	gtc	caa	1200
Phe	Leu	Asp	Arg	Ala	Ala	Tyr	Ile	Thr	Ser	Arg	Asp	Leu	Glu	Val	Gln	
385					390					395					400	
aaa	gga	ggc	caa	cat	aac	cca	tgg	tat	ctg	tgt	cct	att	act	caa	gtt	1248
Lys	Gly	Gly	Gln	His	Asn	Pro	Trp	Tyr	Leu	Cys	Pro	Ile	Thr	Gln	Val	
				405					410					415		
gaa	gaa	gta	aaa	tgc	ata	cta	aga	ctt	ctt	cca	att	tgg	ctt	tgc	aca	1296
Glu	Glu	Val	Lys	Cys	Ile	Leu	Arg	Leu	Leu	Pro	Ile	Trp	Leu	Cys	Thr	
			420					425					430			
ata	atc	tac	tca	gta	gtt	ttc	act	cag	atg	gct	tcc	ctt	ttt	gtg	gag	1344
Ile	Ile	Tyr	Ser	Val	Val	Phe	Thr	Gln	Met	Ala	Ser	Leu	Phe	Val	Glu	
		435					440					445				
caa	ggt	gct	gca	atg	aaa	acc	aca	att	tcc	agt	ttc	aaa	ata	cca	cca	1392
Gln	Gly	Ala	Ala	Met	Lys	Thr	Thr	Ile	Ser	Ser	Phe	Lys	Ile	Pro	Pro	
		450				455					460					
gca	agc	atg	tct	agc	ttc	gat	atc	ctc	agc	gta	gcc	atc	ttc	att	ttc	1440
Ala	Ser	Met	Ser	Ser	Phe	Asp	Ile	Leu	Ser	Val	Ala	Ile	Phe	Ile	Phe	
465					470					475					480	
ttc	tac	cgt	cga	gta	ctt	gat	cca	ctc	gtc	gga	aaa	ctc	aaa	aaa	tca	1488
Phe	Tyr	Arg	Arg	Val	Leu	Asp	Pro	Leu	Val	Gly	Lys	Leu	Lys	Lys	Ser	
				485					490					495		
agt	tcc	aag	gga	ctc	act	gaa	ctt	caa	aga	atg	gga	atc	ggg	ctc	gtt	1536

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Ser	Ser	Lys	Gly	Leu	Thr	Glu	Leu	Gln	Arg	Met	Gly	Ile	Gly	Leu	Val		
500			500					505					510				
ata	gct	ata	atc	gca	atg	gtt	aca	gct	gga	ata	gtt	gaa	tgt	tac	agg	1584	
Ile	Ala	Ile	Ile	Ala	Met	Val	Thr	Ala	Gly	Ile	Val	Glu	Cys	Tyr	Arg		
515							520					525					
ctt	aag	tat	gca	aaa	caa	ggt	gac	aca	agc	tct	cta	agt	atc	ttc	tgg	1632	
Leu	Lys	Tyr	Ala	Lys	Gln	Gly	Asp	Thr	Ser	Ser	Leu	Ser	Ile	Phe	Trp		
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Gln	Ile	Pro	Gln	Tyr	Ala	Leu	Ile	Gly	Ala	Ser	Glu	Val	Phe	Met	Tyr		
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Val	Gly	Gln	Leu	Glu	Phe	Phe	Asn	Ala	Gln	Thr	Pro	Asp	Gly	Leu	Lys		
			565					570						575			
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Ser	Phe	Gly	Ser	Ala	Leu	Cys	Met	Thr	Ser	Ile	Ser	Leu	Gly	Asn	Tyr		
			580					585						590			
gtg	agt	agc	tta	att	gtt	agt	att	gtt	atg	aag	att	tca	act	gaa	gat	1824	
Val	Ser	Ser	Leu	Ile	Val	Ser	Ile	Val	Met	Lys	Ile	Ser	Thr	Glu	Asp		
			595			600						605					
cac	atg	cca	gga	tgg	atc	cct	gga	aac	ttg	aat	aga	ggg	cac	ttg	gat	1872	
His	Met	Pro	Gly	Trp	Ile	Pro	Gly	Asn	Leu	Asn	Arg	Gly	His	Leu	Asp		
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Arg	Phe	Phe	Phe	Leu	Leu	Ala	Val	Leu	Thr	Ser	Leu	Asp	Leu	Ile	Ala		
625					630					635					640		
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Tyr	Ile	Ala	Cys	Ala	Lys	Trp	Phe	Gln	Asn	Ile	Gln	Met	Ala	Cys	Lys		
			645					650						655			
tat	gat	aac	aat	gac	gag	cct	agt	agc	aaa	gtt	taa					2007	
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<210> 287

<211> 668

<212> PRT

<213> Medicago truncatula

<400> 287

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			20					25					30				
Ser	Thr	His	Ser	Val	Ser	Ser	Leu	Asn	Leu	Leu	Val	Phe	Gly	Phe	His		
			35				40					45					
Pro	Asn	Gln	Gln	Gln	Ser	Ser	Ser	Ala	Ser	Ser	Phe	Phe	Ser	Leu	Phe		
			50			55					60						
Phe	Phe	Leu	Phe	Val	Phe	Glu	Thr	Leu	Ser	Ser	Pro	Met	Ala	Cys	Leu		
65					70				75					80			
Glu	Val	Cys	Lys	Glu	Gly	Lys	Phe	Lys	Glu	Glu	Thr	Glu	Glu	Leu	Thr		
			85					90						95			
Leu	Asp	Gly	Ser	Val	Asp	Trp	His	Gly	Arg	Pro	Ser	Ile	Arg	Ala	Thr		
			100					105					110				
Ser	Gly	Arg	Trp	Phe	Ala	Gly	Thr	Ile	Ile	Leu	Leu	Asn	Gln	Gly	Leu		
			115				120					125					
Ala	Thr	Leu	Ala	Phe	Phe	Gly	Val	Gly	Val	Asn	Leu	Val	Leu	Phe	Leu		
			130			135					140						
Thr	Arg	Val	Leu	Gly	Gln	Asp	Asn	Ala	Ala	Ala	Ala	Asn	Asn	Val	Ser		
145					150				155						160		
Lys	Trp	Thr	Gly	Thr	Val	Tyr	Ile	Phe	Ser	Leu	Val	Gly	Ala	Phe	Leu		
			165					170						175			
Ser	Asp	Ser	Tyr	Trp	Gly	Arg	Tyr	Lys	Thr	Cys	Ala	Ile	Phe	Gln	Gly		
			180					185						190			
Ile	Phe	Val	Thr	Gly	Leu	Val	Ser	Leu	Ser	Val	Thr	Thr	Tyr	Leu	Ala		
			195				200					205					
Leu	Leu	Arg	Pro	Lys	Gly	Cys	Gly	Asn	Gly	Lys	Leu	Glu	Cys	Gly	Glu		
			210			215					220						
His	Ser	Ser	Leu	Glu	Met	Gly	Met	Phe	Tyr	Leu	Ser	Ile	Tyr	Leu	Ile		
225					230				235						240		

PF59082SeqList_PF59082.txt

Ala Leu Gly Asn Gly Gly Tyr Gln Pro Asn Ile Ala Thr Phe Gly Ala
 245 250 255
 Asp Gln Phe Asp Glu Asp His Ser Lys Glu Ser Tyr Ser Lys Val Ala
 260 265 270
 Phe Phe Ser Tyr Phe Tyr Leu Ala Leu Asn Leu Gly Ser Leu Phe Ser
 275 280 285
 Asn Thr Ile Leu Gly Tyr Phe Glu Asp Glu Gly Leu Trp Ala Leu Gly
 290 295 300
 Phe Trp Ala Ser Ala Gly Ser Ala Phe Leu Ala Leu Val Leu Phe Leu
 305 310 315 320
 Val Gly Thr Pro Lys Tyr Arg His Phe Lys Pro Cys Gly Asn Pro
 325 330 335
 Ser Arg Phe Cys Gln Val Phe Phe Ala Ala Ser Arg Lys Leu Gly Val
 340 345 350
 Gln Met Thr Ser Asn Gly Asp Asp Leu Tyr Val Ile Asp Glu Lys Glu
 355 360 365
 Ser Ser Asn Asn Ser Asn Arg Lys Ile Leu His Thr His Gly Phe Lys
 370 375 380
 Phe Leu Asp Arg Ala Ala Tyr Ile Thr Ser Arg Asp Leu Glu Val Gln
 385 390 395 400
 Lys Gly Gly Gln His Asn Pro Trp Tyr Leu Cys Pro Ile Thr Gln Val
 405 410 415
 Glu Glu Val Lys Cys Ile Leu Arg Leu Leu Pro Ile Trp Leu Cys Thr
 420 425 430
 Ile Ile Tyr Ser Val Val Phe Thr Thr Ile Ser Ser Phe Lys Ile Pro Pro
 435 440 445
 Gln Gly Ala Ala Met Lys Thr Thr Ile Ser Ser Phe Lys Ile Pro Pro
 450 455 460
 Ala Ser Met Ser Ser Phe Asp Ile Leu Ser Val Ala Ile Phe Ile Phe
 465 470 475 480
 Phe Tyr Arg Arg Val Leu Asp Pro Leu Val Gly Lys Leu Lys Lys Ser
 485 490 495
 Ser Ser Lys Gly Leu Thr Glu Leu Gln Arg Met Gly Ile Gly Leu Val
 500 505 510
 Ile Ala Ile Ile Ala Met Val Thr Ala Gly Ile Val Glu Cys Tyr Arg
 515 520 525
 Leu Lys Tyr Ala Lys Gln Gly Asp Thr Ser Ser Leu Ser Ile Phe Trp
 530 535 540
 Gln Ile Pro Gln Tyr Ala Leu Ile Gly Ala Ser Glu Val Phe Met Tyr
 545 550 555 560
 Val Gly Gln Leu Glu Phe Phe Asn Ala Gln Thr Pro Asp Gly Leu Lys
 565 570 575
 Ser Phe Gly Ser Ala Leu Cys Met Thr Ser Ile Ser Leu Gly Asn Tyr
 580 585 590
 Val Ser Ser Leu Ile Val Ser Ile Val Met Lys Ile Ser Thr Glu Asp
 595 600 605
 His Met Pro Gly Trp Ile Pro Gly Asn Leu Asn Arg Gly His Leu Asp
 610 615 620
 Arg Phe Phe Phe Leu Leu Ala Val Leu Thr Ser Leu Asp Leu Ile Ala
 625 630 635 640
 Tyr Ile Ala Cys Ala Lys Trp Phe Gln Asn Ile Gln Met Ala Cys Lys
 645 650 655
 Tyr Asp Asn Asn Asp Glu Pro Ser Ser Cys Lys Val
 660 665

<210> 288
 <211> 1767
 <212> DNA
 <213> Hordeum vulgare

<220>
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 <222> (1)..(1767)

<400> 288
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 Met Val Met Gly Ser Thr Asp Arg Phe Asp Lys Ser Pro Leu Leu Asp
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 gga ggc agc tca tca cag gag agt acc aca gaa tat aca ggt gat gga 96
 Seite 406

PF59082SeqList_PF59082.txt

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Ser	Val	Cys	Thr	Ser	Gly	His	Pro	Ala	Ser	Lys	Lys	His	Thr	Gly	Asn		
		35					40					45					
tgg	aag	gcc	tcc	tcc	tta	acc	ata	gtc	tgt	tca	ttc	tgc	tgt	tat	ttg	192	
Trp	Lys	Ala	Ser	Ser	Leu	Thr	Ile	Val	Cys	Ser	Phe	Cys	Cys	Tyr	Leu		
	50					55					60						
gcc	tat	tcc	tca	att	gga	aaa	aac	cta	gtc	agt	tat	ctc	aca	aaa	gtc	240	
Ala	Tyr	Ser	Ser	Ile	Gly	Lys	Asn	Leu	Val	Ser	Tyr	Leu	Thr	Lys	Val		
	65				70					75					80		
ttg	cat	gaa	aca	aat	ttg	gat	gct	gca	aga	cac	ggt	gca	act	ttg	cga	288	
Leu	His	Glu	Thr	Asn	Leu	Asp	Ala	Ala	Arg	His	Val	Ala	Thr	Trp	Arg		
				85					90					95			
ggg	act	agc	tat	ctc	gct	cct	ctg	ggt	gga	gcc	ttt	ggt	gct	gat	tca	336	
Gly	Thr	Ser	Tyr	Leu	Ala	Pro	Leu	Val	Gly	Ala	Phe	Val	Ala	Asp	Ser		
			100					105					110				
tat	ctg	ggg	aag	tac	cgg	aca	gct	ttg	atc	gcc	tgc	aca	att	ttc	att	384	
Tyr	Leu	Gly	Lys	Tyr	Arg	Thr	Ala	Leu	Ile	Ala	Cys	Thr	Ile	Phe	Ile		
		115					120					125					
atg	gga	atg	atg	atg	ttg	ctt	cta	tca	gca	gca	ctt	cca	tta	atc	tca	432	
Met	Gly	Met	Met	Met	Leu	Leu	Leu	Ser	Ala	Ala	Leu	Pro	Leu	Ile	Ser		
	130					135					140						
gcc	ggt	cct	cac	gct	ttg	act	ctt	ttg	gca	gat	cct	gtc	tct	tct	cgg	480	
Ala	Gly	Pro	His	Ala	Trp	Thr	Leu	Trp	Ala	Asp	Pro	Val	Ser	Ser	Arg		
					150					155					160		
tac	att	atg	ttc	ttg	gtc	agg	ttg	tac	atg	ggt	ggg	tta	ggg	tac	ggg	528	
Tyr	Ile	Met	Phe	Leu	Val	Arg	Leu	Tyr	Met	Val	Gly	Leu	Gly	Tyr	Gly		
				165					170					175			
gca	cag	agc	cct	tgc	gtc	acg	tct	ttt	gga	gcc	gat	caa	ttt	gat	gac	576	
Ala	Gln	Ser	Pro	Cys	Val	Thr	Ser	Phe	Gly	Ala	Asp	Gln	Phe	Asp	Asp		
			180					185					190				
act	gat	gaa	gtg	gag	aag	acc	aga	aag	agc	tct	ttc	ttt	aat	ttg	cac	624	
Thr	Asp	Glu	Val	Glu	Lys	Thr	Arg	Lys	Ser	Ser	Phe	Phe	Asn	Trp	His		
		195					200					205					
tat	ttc	tca	atc	aat	gct	ggt	tca	ttg	atc	gct	ggg	act	ggt	att	gtc	672	
Tyr	Phe	Ser	Ile	Asn	Ala	Gly	Ser	Leu	Ile	Ala	Gly	Thr	Val	Ile	Val		
	210					215					220						
tgg	ggt	caa	gaa	cat	gaa	ggc	ttg	ctc	ttg	ggt	ttt	aca	att	tct	aca	720	
Trp	Val	Gln	Glu	His	Glu	Gly	Trp	Leu	Trp	Gly	Phe	Thr	Ile	Ser	Thr		
	225				230					235					240		
cta	ttt	gtg	act	tta	gga	ata	agt	ggt	ttt	tcc	ttg	ggc	tcc	att	gtg	768	
Leu	Phe	Val	Thr	Leu	Gly	Ile	Ser	Val	Phe	Ser	Leu	Gly	Ser	Ile	Val		
				245										255			
tat	aga	ttt	cag	aaa	cct	gga	gga	agc	cct	cta	gca	aga	ata	ttg	cag	816	
Tyr	Arg	Phe	Gln	Lys	Pro	Gly	Gly	Ser	Pro	Leu	Ala	Arg	Ile	Trp	Gln		
			260					265					270				
ggt	gtc	ggt	gca	gct	tct	cgg	aac	ttc	gat	aaa	ggt	tta	cca	tgt	gat	864	
Val	Val	Val	Ala	Ala	Ser	Arg	Asn	Phe	Asp	Lys	Val	Leu	Pro	Cys	Asp		
		275					280					285					
tcc	tcg	gct	ctt	tat	gag	ttt	tcg	ggg	caa	ggt	tcg	gca	att	gaa	ggc	912	
Ser	Ser	Ala	Leu	Tyr	Glu	Phe	Ser	Gly	Gln	Gly	Ser	Ala	Ile	Glu	Gly		
		290				295					300						
agc	cgg	aaa	ttg	gta	cat	aca	agt	gga	ctt	gag	ttc	ttt	gat	aaa	gct	960	
Ser	Arg	Lys	Leu	Val	His	Thr	Ser	Gly	Leu	Glu	Phe	Phe	Asp	Lys	Ala		
					310					315					320		
gcg	att	gtg	aca	cta	cct	gac	tgt	gaa	tct	cct	ggc	caa	ctt	aat	gaa	1008	
Ala	Ile	Val	Thr	Leu	Pro	Asp	Cys	Glu	Ser	Pro	Gly	Gln	Leu	Asn	Glu		
				325					330					335			
tgg	aag	att	tgt	act	gtc	act	cag	gta	gag	gag	tta	aag	att	ctg	atc	1056	
Trp	Lys	Ile	Cys	Thr	Val	Thr	Gln	Val	Glu	Glu	Leu	Lys	Ile	Leu	Ile		
			340					345					350				
aga	atg	ttc	cca	att	ttg	tca	gca	atg	gta	ttg	ttt	gct	gca	gtt	cag	1104	
Arg	Met	Phe	Pro	Ile	Trp	Ser	Ala	Met	Val	Leu	Phe	Ala	Ala	Val	Gln		
		355					360					365					
gaa	caa	atg	ttt	tca	aca	ttt	gta	gag	caa	ggg	atg	aca	atg	gag	aaa	1152	
Glu	Gln	Met	Phe	Ser	Thr	Phe	Val	Glu	Gln	Gly	Met	Thr	Met	Glu	Lys		
		370				375					380						
cac	atc	ggg	tct	ttc	gaa	ata	ccc	gct	gca	tca	ttt	caa	tct	ata	gat	1200	

PF59082SeqList_PF59082.txt

His 385	Ile	Gly	Ser	Phe	Glu 390	Ile	Pro	Ala	Ala	Ser 395	Phe	Gln	Ser	Ile	Asp 400	
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Thr	Ile	Thr	Val	Ile	Met	Leu	Val	Pro	Ile	Tyr	Glu	Lys	Val	Leu	Val	
				405					410					415		
cca	gta	ata	aga	aaa	ttc	acc	ggc	aga	gcg	aat	ggc	att	aca	tca	cca	1296
Pro	Val	Ile	Arg	Lys	Phe	Thr	Gly	Arg	Ala	Asn	Gly	Ile	Thr	Ser	Pro	
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cag	aga	ata	ggg	att	ggt	tta	tgt	ttc	tcc	atg	ttc	tca	atg	ctg	ttg	1344
Gln	Arg	Ile	Gly	Ile	Gly	Leu	Cys	Phe	Ser	Met	Phe	Ser	Met	Leu	Leu	
				435										445		
gca	gca	ttg	gtg	gag	agt	aac	cgg	tta	cag	att	gca	cag	gcc	gaa	ggt	1392
Ala	Ala	Leu	Val	Glu	Ser	Asn	Arg	Leu	Gln	Ile	Ala	Gln	Ala	Glu	Gly	
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ttg	gtg	cac	agc	aag	gtg	gtt	ggt	ccg	atg	agc	atc	ctg	tgg	caa	gga	1440
Leu	Val	His	Ser	Lys	Val	Val	Val	Pro	Met	Ser	Ile	Leu	Trp	Gln	Gly	
					470									480		
ccc	cag	tac	ttc	ctg	cta	ggc	gtc	gcg	gag	gtg	ttc	tcc	aac	att	ggg	1488
Pro	Gln	Tyr	Phe	Leu	Leu	Gly	Val	Ala	Glu	Val	Phe	Ser	Asn	Ile	Gly	
				485										495		
cta	act	gaa	ttt	ttc	tac	gac	gaa	tct	cca	gac	gcc	atg	aga	agc	tta	1536
Leu	Thr	Glu	Phe	Phe	Tyr	Asp	Glu	Ser	Pro	Asp	Ala	Met	Arg	Ser	Leu	
				500					505					510		
ggc	atg	gca	ttc	tcg	ctc	ctt	aac	atc	tcg	gtt	gga	aat	tac	ctt	agt	1584
Gly	Met	Ala	Phe	Ser	Leu	Leu	Asn	Ile	Ser	Val	Gly	Asn	Tyr	Leu	Ser	
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tcg	ttt	atc	ctt	tcc	ctt	gtg	cct	gta	ttc	aca	gcc	aga	gga	ggc	agc	1632
Ser	Phe	Ile	Leu	Ser	Leu	Val	Pro	Val	Phe	Thr	Ala	Arg	Gly	Gly	Ser	
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Pro	Gly	Trp	Ile	Pro	Asp	Asn	Leu	Asn	Glu	Gly	His	Leu	Asp	Arg	Phe	
					550										560	
tac	ctg	atg	atg	gct	ggg	ctg	agt	tta	ctg	aat	ata	ttt	gtg	ttt	gca	1728
Tyr	Leu	Met	Met	Ala	Gly	Leu	Ser	Leu	Leu	Asn	Ile	Phe	Val	Phe	Ala	
				565										575		
ttc	tat	gct	agg	agg	tac	aaa	tgt	aag	aag	gct	tcc	tga				1767
Phe	Tyr	Ala	Arg	Arg	Tyr	Lys	Cys	Lys	Lys	Ala	Ser					
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<210> 289

<211> 588

<212> PRT

<213> Hordeum vulgare

<400> 289

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Ser	Val	Cys	Thr	Ser	Gly	His	Pro	Ala	Ser	Lys	Lys	His	Thr	Gly	Asn	
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Trp	Lys	Ala	Ser	Ser	Leu	Thr	Ile	Val	Cys	Ser	Phe	Cys	Cys	Tyr	Leu	
				50				55				60				
Ala	Tyr	Ser	Ser	Ile	Gly	Lys	Asn	Leu	Val	Ser	Tyr	Leu	Thr	Lys	Val	
65					70					75				80		
Leu	His	Glu	Thr	Asn	Leu	Asp	Ala	Ala	Arg	His	Val	Ala	Thr	Trp	Arg	
				85					90					95		
Gly	Thr	Ser	Tyr	Leu	Ala	Pro	Leu	Val	Gly	Ala	Phe	Val	Ala	Asp	Ser	
				100				105					110			
Tyr	Leu	Gly	Lys	Tyr	Arg	Thr	Ala	Leu	Ile	Ala	Cys	Thr	Ile	Phe	Ile	
				115				120					125			
Met	Gly	Met	Met	Met	Leu	Leu	Leu	Ser	Ala	Ala	Leu	Pro	Leu	Ile	Ser	
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Ala	Gly	Pro	His	Ala	Trp	Thr	Leu	Trp	Ala	Asp	Pro	Val	Ser	Ser	Arg	
145					150					155					160	
Tyr	Ile	Met	Phe	Leu	Val	Arg	Leu	Tyr	Met	Val	Gly	Leu	Gly	Tyr	Gly	
				165					170					175		
Ala	Gln	Ser	Pro	Cys	Val	Thr	Ser	Phe	Gly	Ala	Asp	Gln	Phe	Asp	Asp	
				180				185					190			

PF59082SeqList_PF59082.txt

Thr Asp Glu Val Glu Lys Thr Arg Lys Ser Ser Phe Phe Asn Trp His
 195 200 205
 Tyr Phe Ser Ile Asn Ala Gly Ser Leu Ile Ala Gly Thr Val Ile Val
 210 215 220
 Trp Val Gln Glu His Glu Gly Trp Leu Trp Gly Phe Thr Ile Ser Thr
 225 230 235 240
 Leu Phe Val Thr Leu Gly Ile Ser Val Phe Ser Leu Gly Ser Ile Val
 245 250 255
 Tyr Arg Phe Gln Lys Pro Gly Gly Ser Pro Leu Ala Arg Ile Trp Gln
 260 265 270
 Val Val Val Ala Ala Ser Arg Asn Phe Asp Lys Val Leu Pro Cys Asp
 275 280 285
 Ser Ser Ala Leu Tyr Glu Phe Ser Gly Gln Gly Ser Ala Ile Glu Gly
 290 295 300
 Ser Arg Lys Leu Val His Thr Ser Gly Leu Glu Phe Phe Asp Lys Ala
 305 310 315 320
 Ala Ile Val Thr Leu Pro Asp Cys Glu Ser Pro Gly Gln Leu Asn Glu
 325 330 335
 Trp Lys Ile Cys Thr Val Thr Gln Val Glu Glu Leu Lys Ile Leu Ile
 340 345 350
 Arg Met Phe Pro Ile Trp Ser Ala Met Val Leu Phe Ala Val Gln
 355 360 365
 Glu Gln Met Phe Ser Thr Phe Val Glu Gln Gly Met Thr Met Glu Lys
 370 375 380
 His Ile Gly Ser Phe Glu Ile Pro Ala Ala Ser Phe Gln Ser Ile Asp
 385 390 395 400
 Thr Ile Thr Val Ile Met Leu Val Pro Ile Tyr Glu Lys Val Leu Val
 405 410 415
 Pro Val Ile Arg Lys Phe Thr Gly Arg Ala Asn Gly Ile Thr Ser Pro
 420 425 430
 Gln Arg Ile Gly Ile Gly Leu Cys Phe Ser Met Phe Ser Met Leu Leu
 435 440 445
 Ala Ala Leu Val Glu Ser Asn Arg Leu Gln Ile Ala Gln Ala Glu Gly
 450 455 460
 Leu Val His Ser Lys Val Val Val Pro Met Ser Ile Leu Trp Gln Gly
 465 470 475 480
 Pro Gln Tyr Phe Leu Leu Gly Val Ala Glu Val Phe Ser Asn Ile Gly
 485 490 495
 Leu Thr Glu Phe Tyr Asp Glu Ser Pro Asp Ala Met Arg Ser Leu
 500 505 510
 Gly Met Ala Phe Ser Leu Leu Asn Ile Ser Val Gly Asn Tyr Leu Ser
 515 520 525
 Ser Phe Ile Leu Ser Leu Val Pro Val Phe Thr Ala Arg Gly Gly Ser
 530 535 540
 Pro Gly Trp Ile Pro Asp Asn Leu Asn Glu Gly His Leu Asp Arg Phe
 545 550 555 560
 Tyr Leu Met Met Ala Gly Leu Ser Leu Leu Asn Ile Phe Val Phe Ala
 565 570 575
 Phe Tyr Ala Arg Tyr Lys Cys Lys Lys Ala Ser
 580 585

<210> 290

<211> 1758

<212> DNA

<213> Medicago truncatula

<220>

<221> CDS

<222> (1)..(1758)

<400> 290

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aag aga aag aaa ggt gga ttt agg gct tct atg ttt att ttt gta ttg 96

Lys Arg Lys Lys Gly Gly Phe Arg Ala Ser Met Phe Ile Phe Val Leu
 20 25 30

tca gca ttg gac aac atg ggt ttt gtg gca aac atg gtt agc tta gtt 144

Ser Ala Leu Asp Asn Met Gly Phe Val Ala Asn Met Val Ser Leu Val

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gaa Glu	gtg Val	aaa Lys	aga Arg 420	aga Arg	gac Asp	caa Gln	agt Ser	aga Arg 425	aaa Lys	aac Asn	cca Pro	tct Ser	aac Asn 430	cca Pro	ata Ile	
agc Ser	cta Leu	ttt Phe 435	tgg Trp	ctt Leu	tca Ser	ttc Phe	caa Gln 440	tat Tyr	ggg Gly	att Ile	ttt Phe	ggg Gly 445	att Ile	gct Ala	gat Asp	1344
atg Met	ttc Phe 450	aca Thr	ctt Leu	gtg Val	gga Gly	ctc Leu 455	ttg Leu	gaa Glu	ttt Phe	ttt Phe	tat Tyr 460	agg Arg	gaa Glu	tca Ser	cct Pro	1392
tca Ser 465	agt Ser	atg Met	aaa Lys	tca Ser	ttg Leu 470	tca Ser	aca Thr	tct Ser	ttc Phe	aca Thr 475	tgg Trp	tta Leu	tca Ser	atg Met	tct Ser 480	1440
att Ile	ggg Gly	tac Tyr	ttc Phe	ctg Leu 485	agc Ser	act Thr	gtt Val	ttt Phe	gtc Val 490	aat Asn	ttg Leu	att Ile	aat Asn	gtt Val 495	gtt Val	1488
acc Thr	aaa Lys	agg Arg	att Ile 500	act Thr	cct Pro	agt Ser	aaa Lys	caa Gln 505	ggg Gly	tgg Trp	tta Leu	cat His	ggg Gly 510	ttt Phe	gat Asp	1536
ttg Leu	aat Asn	caa Gln 515	agt Ser	aat Asn	ttg Leu	aac Asn	ctg Leu 520	ttc Phe	tat Tyr	tgg Trp	ttc Phe	cta Leu 525	gct Ala	ata Ile	ctt Leu	1584
agt Ser	tgt Cys 530	ctt Leu	aat Asn	ttt Phe	ttc Phe	aac Asn 535	tac Tyr	ctt Leu	tat Tyr	tgg Trp	gcc Ala 540	tca Ser	cgc Arg	tat Tyr	aag Lys	1632
tac Tyr 545	aaa Lys	tct Ser	gaa Glu	gac Asp	caa Gln 550	aat Asn	tca Ser	agc Ser	cca Pro	ata Ile 555	ggg Gly	ttg Leu	aag Lys	agt Ser	ttg Leu 560	1680
cat His	gaa Glu	atg Met	cct Pro	ctc Leu 565	aaa Lys	atg Met	att Ile	ggg Gly 570	ggg Gly 570	aca Thr	aaa Lys	caa Gln	aat Asn	tgg Trp 575	gaa Glu	1728
ggg Gly	agc Ser	att Ile	ggg Gly 580	gga Gly	cac His	aca Thr	caa Gln	gat Asp 585	tga							1758

<210> 291

<211> 585

<212> PRT

<213> Medicago truncatula

<400> 291

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			20					25					30		
Ser	Ala	Leu	Asp	Asn	Met	Gly	Phe	Val	Ala	Asn	Met	Val	Ser	Leu	Val
		35					40					45			
Leu	Tyr	Phe	Tyr	Gly	Val	Met	His	Phe	Asp	Ile	Pro	Ser	Ser	Ala	Asn
	50					55					60				
Thr	Leu	Thr	Asn	Phe	Met	Gly	Ser	Thr	Phe	Leu	Leu	Ser	Leu	Val	Gly
65					70					75					80
Gly	Phe	Ile	Ser	Asp	Thr	Tyr	Leu	Asn	Arg	Phe	Thr	Thr	Cys	Leu	Leu
				85					90					95	
Phe	Gly	Ser	Leu	Glu	Val	Leu	Ala	Leu	Ala	Leu	Val	Thr	Phe	Gln	Ala
			100					105					110		
Ala	Ser	Asp	His	Leu	His	Pro	Asn	Ala	Cys	Gly	Lys	Ser	Ser	Cys	Val
		115					120					125			
Lys	Gly	Gly	Ile	Glu	Phe	Met	Phe	Tyr	Thr	Ser	Leu	Ser	Leu	Leu	Ala
		130				135					140				
Leu	Gly	Ile	Gly	Gly	Val	Arg	Gly	Ser	Met	Thr	Ala	Phe	Gly	Ala	Asp
145					150					155					160
Gln	Phe	Glu	Glu	Lys	Asp	Ser	Asn	Glu	Ala	Lys	Ala	Leu	Ala	Ser	Phe
				165					170					175	
Phe	Asn	Trp	Leu	Leu	Leu	Ser	Ser	Thr	Leu	Gly	Ala	Ile	Thr	Gly	Val
			180					185					190		
Thr	Gly	Val	Val	Trp	Val	Ser	Thr	Gln	Arg	Ala	Trp	His	Trp	Gly	Phe
		195					200					205			
Phe	Ile	Ile	Thr	Ile	Ala	Ser	Ser	Ile	Gly	Phe	Val	Thr	Leu	Ala	Leu
	210					215					220				

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Gly 225 Lys Pro Phe Tyr Arg 230 Ile Lys Thr Pro Gly 235 Asp Ser Pro Thr Ile 240
 Arg 245 Ile Ala Gln Val Ile Val Val Ala Phe 250 Lys Asn Arg Lys Leu Ser 255
 Leu 260 Pro Glu Ser His Glu Glu Leu Tyr 265 Glu Ile Ser Asp Lys Asp Gly 270
 Thr 275 Val Glu Lys Ile Val His Thr 280 Lys Gln Met Arg Phe Leu Asp Lys 285
 Ala 290 Ala Ile Pro Gln Glu Tyr 295 Ile Lys Pro Gln Pro Trp Lys Val Cys 300
 Thr 305 Val Thr Gln Val Glu 310 Glu Val Lys Ile Leu Thr Arg Met Leu Pro 320
 Ile 325 Val Ala Ser Thr Ile Ile Met Asn Thr Cys Leu Ala Gln Leu Gln 335
 Thr 340 Phe Ser Val Gln Gln Gly Asn Val Met Asn Leu Lys Leu Gly Ser 350
 Phe 355 Thr Val Pro Ala Ser Ser Ile Pro Val Ile Pro Leu Ile Phe Ile 365
 Ser 370 Ile Leu Val Pro Ile Tyr 375 Glu Leu Phe Phe Val Pro Phe Ala Arg 380
 Lys 385 Ile Thr Asn His Pro 390 Ser Gly Ile Thr Gln 395 Leu Gln Arg Val Gly 400
 Val 405 Glu Leu Val Leu Ser Val Ile Ser Met Thr Val Ala Gly Ile Val 415
 Glu 420 Val Lys Arg Asp Gln Ser Arg Lys Asn Pro Ser Asn Pro Ile 430
 Ser 435 Leu Phe Trp Leu Ser Phe Gln Tyr Gly Ile Phe Gly Ile Ala Asp 445
 Met 450 Phe Thr Leu Val Gly Leu Leu Glu Phe Phe Tyr Arg Glu Ser Pro 460
 Ser 465 Ser Met Lys Ser Leu 470 Ser Thr Ser Phe Thr Trp Leu Ser Met Ser 480
 Ile 485 Gly Tyr Phe Leu Ser Thr Val Phe Val Asn Leu Ile Asn Val Val 495
 Thr 500 Lys Arg Ile Thr Pro Ser Lys Gln Gly Trp Leu His Gly Phe Asp 510
 Leu 515 Asn Gln Ser Asn Leu Asn Leu Phe Tyr Trp Phe Leu Ala Ile Leu 525
 Ser 530 Cys Leu Asn Phe Phe Asn Tyr Leu Tyr Trp Ala Ser Arg Tyr Lys 540
 Tyr 545 Lys Ser Glu Asp Gln Asn Ser Ser Pro Ile Gly Leu Lys Ser Leu 555
 His 565 Glu Met Pro Leu Lys Met Ile Gly Gly Thr Lys Gln Asn Trp Glu 575
 Gly 580 Ser Ile Gly His Thr Gln Asp 585

<210> 292

<211> 1914

<212> DNA

<213> Medicago truncatula

<220>

<221> CDS

<222> (1)..(1914)

<400> 292

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 Glu Met Val Ser Gln Gln Pro Gln Arg Arg Lys Gly Gly Leu Ile Thr 20 25 30

atg cct ttt ata att ggg aat gag gca ctt gct agg atg gca agt ttg 144
 Met Pro Phe Ile Ile Gly Asn Glu Ala Leu Ala Arg Met Ala Ser Leu 35 40 45

gga cta tta cca aac atg ata ttg tat ttg atg gga tca tac aga ctt 192
 Gly Leu Leu Pro Asn Met Ile Leu Tyr Leu Met Gly Ser Tyr Arg Leu 50 55 60

PF59082SeqList_PF59082.txt

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aat	ttc	aca	cct	gtg	att	ggt	gct	ttt	att	gca	gat	tct	ttt	ctg	ggt	288
Asn	Phe	Thr	Pro	Val	Ile	Gly	Ala	Phe	Ile	Ala	Asp	Ser	Phe	Leu	Gly	
				85					90					95		
cga	ttc	cta	ggt	ggt	gga	ata	ggt	tct	tct	atc	agt	ttc	ctg	gga	atg	336
Arg	Phe	Leu	Gly	Val	Gly	Ile	Gly	Ser	Ser	Ile	Ser	Phe	Leu	Gly	Met	
			100					105					110			
tca	ctg	ctg	tgg	tta	aca	gcc	atg	atc	ccg	tcg	gca	cgg	cct	cct	gct	384
Ser	Leu	Leu	Trp	Leu	Thr	Ala	Met	Ile	Pro	Ser	Ala	Arg	Pro	Pro	Ala	
			115				120					125				
tgc	aac	cat	cca	tct	gaa	ggt	tgt	gaa	tca	gca	aca	cca	ggt	caa	ttg	432
Cys	Asn	His	Pro	Ser	Glu	Gly	Cys	Glu	Ser	Ala	Thr	Pro	Gly	Gln	Leu	
	130					135					140					
gca	atg	tta	ttc	tct	gcc	cta	att	ctg	ata	gca	att	gga	aat	ggt	ggt	480
Ala	Met	Leu	Phe	Ser	Ala	Leu	Ile	Leu	Ile	Ala	Ile	Gly	Asn	Gly	Gly	
145					150					155					160	
att	tca	tgt	tct	tta	gca	ttt	ggt	gca	gac	caa	ggt	aat	aga	aaa	gat	528
Ile	Ser	Cys	Ser	Leu	Ala	Phe	Gly	Ala	Asp	Gln	Val	Asn	Arg	Lys	Asp	
				165				170						175		
aac	cct	aat	aac	cgc	agg	gtt	ttg	gaa	ata	ttc	ttc	agt	tgg	tat	tat	576
Asn	Pro	Asn	Asn	Arg	Arg	Val	Leu	Glu	Ile	Phe	Phe	Ser	Trp	Tyr	Tyr	
				180				185					190			
gct	ttc	aca	act	ata	gct	gtc	ata	ata	gct	ctc	act	gga	ata	gta	tat	624
Ala	Phe	Thr	Thr	Ile	Ala	Val	Ile	Ile	Ala	Leu	Thr	Gly	Ile	Val	Tyr	
			195				200					205				
atc	caa	gat	cat	ctt	ggt	tgg	aaa	gtt	ggt	ttt	ggt	ggt	cca	gca	ata	672
Ile	Gln	Asp	His	Leu	Gly	Trp	Lys	Val	Gly	Phe	Gly	Val	Pro	Ala	Ile	
	210				215						220					
ctc	atg	ctt	ata	tcc	act	gtc	tta	ttc	ttt	ctt	gct	tct	cct	ctt	tat	720
Leu	Met	Leu	Ile	Ser	Thr	Val	Leu	Phe	Phe	Leu	Ala	Ser	Pro	Leu	Tyr	
225					230					235					240	
gtg	aaa	att	aaa	caa	aaa	acc	agc	tta	ttc	act	ggt	ttt	gca	caa	gta	768
Val	Lys	Ile	Lys	Gln	Lys	Thr	Ser	Leu	Phe	Thr	Gly	Phe	Ala	Gln	Val	
				245				250						255		
tct	gtt	gct	gcc	tac	aag	aac	aga	aaa	ctt	cca	ttg	cca	cct	aaa	acc	816
Ser	Val	Ala	Ala	Tyr	Lys	Asn	Arg	Lys	Leu	Pro	Leu	Pro	Pro	Lys	Thr	
			260				265						270			
tct	cct	gaa	ttt	tac	cat	caa	caa	aaa	gac	tca	gaa	ctc	gtt	gtt	cca	864
Ser	Pro	Glu	Phe	Tyr	His	Gln	Gln	Lys	Asp	Ser	Glu	Leu	Val	Val	Pro	
			275				280					285				
act	gat	aaa	cta	agg	ttt	cta	aat	aaa	gct	tgt	gtt	att	aag	gat	cat	912
Thr	Asp	Lys	Leu	Arg	Phe	Leu	Asn	Lys	Ala	Cys	Val	Ile	Lys	Asp	His	
	290					295					300					
gaa	caa	gat	ata	gcc	tca	gat	ggt	tca	gcg	ata	aat	cgt	tgg	agt	cta	960
Glu	Gln	Asp	Ile	Ala	Ser	Asp	Gly	Ser	Ala	Ile	Asn	Arg	Trp	Ser	Leu	
305					310					315					320	
tgc	aca	gta	gat	caa	gtt	gaa	gaa	cta	aaa	gcc	att	att	aaa	gtt	att	1008
Cys	Thr	Val	Asp	Gln	Val	Glu	Glu	Leu	Lys	Ala	Ile	Ile	Lys	Val	Ile	
				325				330						335		
cca	ttg	tgg	tca	aca	gcg	atc	aca	atg	tct	att	aac	att	gga	ggc	tca	1056
Pro	Leu	Trp	Ser	Thr	Ala	Ile	Thr	Met	Ser	Ile	Asn	Ile	Gly	Gly	Ser	
			340				345						350			
ttt	gga	ttg	ctg	caa	gct	aaa	tcc	tta	gac	aga	cat	atc	att	tca	agt	1104
Phe	Gly	Leu	Leu	Gln	Ala	Lys	Ser	Leu	Asp	Arg	His	Ile	Ile	Ser	Ser	
			355				360					365				
tca	aac	ttt	gaa	gta	cca	gca	gga	tct	ttt	tct	gtt	atc	ttg	ata	gtt	1152
Ser	Asn	Phe	Glu	Val	Pro	Ala	Gly	Ser	Phe	Ser	Val	Ile	Leu	Ile	Val	
			370				375					380				
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Ala	Ile	Leu	Ile	Trp	Ile	Ile	Ile	Tyr	Asp	Arg	Val	Leu	Ile	Pro	Leu	
385					390					395					400	
gca	tca	aag	ata	aga	ggg	aag	ccc	gta	att	atc	agc	cca	aag	aaa	aga	1248
Ala	Ser	Lys	Ile	Arg	Gly	Lys	Pro	Val	Ile	Ile	Ser	Pro	Lys	Lys	Arg	
				405				410						415		
atg	gga	att	ggg	ttg	ttt	ttt	aat	ttt	ctt	cac	ttg	ata	act	gca	gca	1296
Met	Gly	Ile	Gly	Leu	Phe	Phe	Asn	Phe	Leu	His	Leu	Ile	Thr	Ala	Ala	
			420					425					430			

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		435					440					445				
aat	gat	act	cat	gga	gtg	ttg	aaa	atg	tct	gca	atg	tgg	ctt	gca	cct	1392
Asn	Asp	Thr	His	Gly	Val	Leu	Lys	Met	Ser	Ala	Met	Trp	Leu	Ala	Pro	
	450					455					460					
caa	ctt	tgt	ttg	gct	ggc	ata	gca	gaa	atg	ttc	aat	ggt	att	ggc	cag	1440
Gln	Leu	Cys	Leu	Ala	Gly	Ile	Ala	Glu	Met	Phe	Asn	Val	Ile	Gly	Gln	
465				470						475					480	
aat	gag	ttt	tat	tac	aaa	gag	ttt	cca	aag	agt	atg	tct	agt	ggt	gct	1488
Asn	Glu	Phe	Tyr	Tyr	Lys	Glu	Phe	Pro	Lys	Ser	Met	Ser	Ser	Val	Ala	
			485					490						495		
gct	tcc	ctt	tct	gga	ttg	gca	atg	ggc	gta	gga	aac	ttg	gta	tcc	tct	1536
Ala	Ser	Leu	Ser	Gly	Leu	Ala	Met	Gly	Val	Gly	Asn	Leu	Val	Ser	Ser	
			500					505					510			
tta	gta	ttg	agc	att	ata	gaa	agc	act	act	cca	agt	gga	gga	aat	gaa	1584
Leu	Val	Leu	Ser	Ile	Ile	Glu	Ser	Thr	Thr	Pro	Ser	Gly	Gly	Asn	Glu	
		515					520					525				
ggg	tgg	ggt	tct	gat	aat	att	aac	aaa	ggc	cat	ttc	gac	aag	tat	tat	1632
Gly	Trp	Val	Ser	Asp	Asn	Ile	Asn	Lys	Gly	His	Phe	Asp	Lys	Tyr	Tyr	
	530				535						540					
tgg	ggt	ata	ggt	gga	att	aat	gct	cta	aat	cta	ttg	tat	tac	tta	gta	1680
Trp	Val	Ile	Val	Gly	Ile	Asn	Ala	Leu	Asn	Leu	Leu	Tyr	Tyr	Leu	Val	
545				550					555						560	
tgc	agt	tgg	gct	tat	gga	cct	aca	ggt	gat	gaa	gta	tcc	aat	gtg	agt	1728
Cys	Ser	Trp	Ala	Tyr	Gly	Pro	Thr	Val	Asp	Glu	Val	Ser	Asn	Val	Ser	
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Lys	Glu	Asn	Gly	Ser	Lys	Val	Glu	Glu	Ser	Thr	Glu	Phe	Lys	His	Met	
			580					585					590			
aat	cca	cac	ttt	gat	gac	aag	ggt	agt	ggc	gaa	act	agt	tca	aag	gag	1824
Asn	Pro	His	Phe	Asp	Asp	Lys	Val	Ser	Gly	Glu	Thr	Ser	Ser	Lys	Glu	
		595				600						605				
aaa	gag	tta	act	gaa	ttc	aag	aat	ggg	gcc	cag	ggt	gag	aaa	gta	ttc	1872
Lys	Glu	Leu	Thr	Glu	Phe	Lys	Asn	Gly	Ala	Gln	Val	Glu	Lys	Val	Phe	
	610				615						620					
aag	aat	agt	gaa	caa	agg	gac	ttg	aag	gag	gaa	gat	ttg	tga			1914
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<210> 293

<211> 637

<212> PRT

<213> Medicago truncatula

<400> 293

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Glu	Met	Val	Ser	Gln	Gln	Pro	Gln	Arg	Lys	Gly	Gly	Gly	Leu	Ile	Thr
			20					25					30		
Met	Pro	Phe	Ile	Ile	Gly	Asn	Glu	Ala	Leu	Ala	Arg	Met	Ala	Ser	Leu
		35				40						45			
Gly	Leu	Leu	Pro	Asn	Met	Ile	Leu	Tyr	Leu	Met	Gly	Ser	Tyr	Arg	Leu
	50				55					60					
His	Leu	Gly	Ile	Ser	Thr	Gln	Ile	Leu	Leu	Leu	Ser	Ser	Ala	Ala	Ser
65				70					75						80
Asn	Phe	Thr	Pro	Val	Ile	Gly	Ala	Phe	Ile	Ala	Asp	Ser	Phe	Leu	Gly
			85					90						95	
Arg	Phe	Leu	Gly	Val	Gly	Ile	Gly	Ser	Ile	Ser	Phe	Leu	Gly	Met	
		100					105					110			
Ser	Leu	Leu	Trp	Leu	Thr	Ala	Met	Ile	Pro	Ser	Ala	Arg	Pro	Pro	Ala
		115				120						125			
Cys	Asn	His	Pro	Ser	Glu	Gly	Cys	Glu	Ser	Ala	Thr	Pro	Gly	Gln	Leu
	130					135					140				
Ala	Met	Leu	Phe	Ser	Ala	Leu	Ile	Leu	Ile	Ala	Ile	Gly	Asn	Gly	Gly
145				150						155					160
Ile	Ser	Cys	Ser	Leu	Ala	Phe	Gly	Ala	Asp	Gln	Val	Asn	Arg	Lys	Asp
			165					170						175	
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Tyr Gln Pro Thr Ile Ala Thr Phe Gly Ala Asp Gln Phe Asp Glu Ser
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tct gct gcc cta gca ttg gtt ttg ttt ctt tgt ggc aca tca aaa tat     720
Ser Ala Ala Leu Ala Leu Val Leu Phe Leu Cys Gly Thr Ser Lys Tyr
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aga tac ttt aaa cct gtt gga aac cct ctt cct agg ttt tgt caa gtt     768
Arg Tyr Phe Lys Pro Val Gly Asn Pro Leu Pro Arg Phe Cys Gln Val
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Phe Val Ala Ala Ile Arg Lys Trp Lys Val Gln Met Phe Asp Gly Glu
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gat aaa ctt cat gag gtt gaa gat tgt tta tcc aat gga ggg aga aaa     864
Asp Lys Leu His Glu Val Glu Asp Cys Leu Ser Asn Gly Gly Arg Lys
          265          270          275
atg tac cac aca caa ggc ttt agg ttt tta gat aaa gca gca ttt att     912
Met Tyr His Thr Gln Gly Phe Arg Phe Leu Asp Lys Ala Ala Phe Ile
          280          285          290
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Thr Pro Lys Asp Leu Lys Gln Met Glu Glu Asn Lys Cys Ser Pro Trp

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PF59082SeqList_PF59082.txt

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Leu	Leu	Pro	Ile	Trp	Leu	Cys	Thr	Ile	Leu	Phe	Ser	Val	Val	Phe	Ser	
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Gln	Met	Ala	Ser	Leu	Phe	Val	Glu	Gln	Gly	Ala	Ala	Met	Glu	Thr	Lys	
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Gly	Met	Leu	Gly	Trp	Ile	Pro	Gly	Asn	Leu	Asn	Met	Gly	His	Leu	Asp	
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Tyr	Ile	Ala	Met	Ala	Arg	Trp	Tyr	Lys	Tyr	Val	Lys	Phe	His	Gly	Asn	
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 Cys Gly Ser Lys Glu Leu Pro Cys Gly Thr His Ser Ser Tyr Glu Thr
 Thr Leu Phe Tyr Val Ser Ile Tyr Leu Val Ala Leu Gly Asn Gly Gly
 Tyr Gln Pro Thr Ile Ala Thr Phe Gly Ala Asp Gln Phe Asp Glu Ser
 Asp Pro Ser Glu Gln His Ser Lys Ile Ala Phe Phe Ser Tyr Phe Tyr
 Leu Ala Leu Asn Ile Gly Ser Leu Phe Ser Asn Thr Ile Leu Asp Tyr
 Phe Glu Asp Asp Gly Leu Trp Thr Leu Gly Phe Cys Val Ser Ala Gly
 Ser Ala Ala Leu Ala Leu Val Leu Phe Leu Cys Gly Thr Ser Lys Tyr
 Arg Tyr Phe Lys Pro Val Gly Asn Pro Leu Pro Arg Phe Cys Gln Val
 Phe Val Ala Ala Ile Arg Lys Trp Lys Val Gln Met Phe Asp Gly Glu
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 Met Tyr His Thr Gln Gly Phe Arg Phe Leu Asp Lys Ala Ala Phe Ile
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 Gln Met Ala Ser Leu Phe Val Glu Gln Gly Ala Ala Met Glu Thr Lys
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 Leu Ser Val Val Ser Phe Ile Phe Ile Tyr Arg Arg Ile Leu Asp Pro
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 Arg Met Gly Ile Gly Leu Val Leu Ala Ile Ile Ala Met Val Ser Ala
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 Ser Ser Leu Leu Val Ala Ile Val Met Lys Ile Ser Thr Arg Asn Glu
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 Arg Phe Tyr Phe Leu Leu Ala Ala Leu Thr Ala Ala Asp Leu Leu Val
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caggccaaat ctttcttcat ttttgaatt aatactgcac ctgaactttt tttggataaa      300

aaagaaagtg tatcagcttt gaatgaagcc tactagttct ttatgagtag tgtgtggtca      360

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gatatgctag tggcctaatt tcaactgaatt ttcagaagac caagacagca caaatgggtg      900

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aattaattgc aagtagctta gagtcgtcgg ttttcttcca acaaaattgc tgaagaagcc     1080

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Leu Pro Pro Gln Glu Gln Cys Ser Lys Tyr Thr Cys Asp Gly Thr Val
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Tyr	Gly	Val	Ser	Lys	Asn	Leu	Val	Thr	Tyr	Leu	Thr	Ser	Val	Leu	His	
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Met	Ile	Val	Leu	Thr	Val	Ser	Ala	Ser	Pro	Leu	Phe	Leu	Asn	Ala	Ser	
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Phe	Tyr	Asn	Gly	Gly	Ile	Ser	Arg	Leu	Thr	Val	Tyr	Leu	Gly	Leu	Tyr	
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Val	Thr	Glu	Gly	Asp	Tyr	Arg	Thr	Gln	His	Thr	Tyr	Gln	Phe	Arg	Phe	
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Trp	Ile	Pro	Asp	Lys	Leu	Asp	Glu	Gly	His	Leu	Asp	Tyr	Phe	Phe	Trp	
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PF59082SeqList_PF59082.txt

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ctg	tgg	atc	ccc	atc	tac	gac	cgc	ctc	ctc	gtg	ccg	cgc	ctc	cgc	agg	1248
Leu	Trp	Ile	Pro	Ile	Tyr	Asp	Arg	Leu	Leu	Val	Pro	Arg	Leu	Arg	Arg	
			405					410						415		
gtc	acg	ggc	aag	gac	gag	ggc	ctc	acc	ctc	ctg	cag	cgg	cag	ggg	atc	1296

PF59082SeqList_PF59082.txt

Val	Thr	Gly	Lys	Asp	Glu	Gly	Leu	Thr	Leu	Leu	Gln	Arg	Gln	Gly	Ile	
			420					425					430			
ggg	atc	gcg	ctg	tcg	acg	gtg	gcg	atg	gtg	atg	tcg	gcc	gtg	gtg	gag	1344
Gly	Ile	Ala	Leu	Ser	Thr	Val	Ala	Met	Val	Met	Ser	Ala	Val	Val	Glu	
		435					440					445				
gac	cgg	agg	cgg	cac	atc	gcg	ctg	acg	cag	ccg	acg	ctg	ggg	acg	acc	1392
Asp	Arg	Arg	Arg	His	Ile	Ala	Leu	Thr	Gln	Pro	Thr	Leu	Gly	Thr	Thr	
	450					455					460					
atc	acc	ggg	ggc	gcc	atc	tcg	gcc	atg	tcc	agc	ctg	tgg	atg	gtg	ccg	1440
Ile	Thr	Gly	Gly	Ala	Ile	Ser	Ala	Met	Ser	Ser	Leu	Trp	Met	Val	Pro	
	465				470					475					480	
cag	ctc	atg	gtg	ctg	ggg	ctc	tcg	gag	gcg	ttc	aac	ctc	atc	agc	cag	1488
Gln	Leu	Met	Val	Leu	Gly	Leu	Ser	Glu	Ala	Phe	Asn	Leu	Ile	Ser	Gln	
			485					490						495		
atc	gag	ttc	tac	tac	aag	gag	atc	ccg	gag	cac	atg	cgg	agc	gtg	gcc	1536
Ile	Glu	Phe	Tyr	Tyr	Lys	Glu	Ile	Pro	Glu	His	Met	Arg	Ser	Val	Ala	
			500					505					510			
ggc	gcg	ctc	gcc	ttc	tgc	aac	ctg	gcg	ctg	ggg	aac	tac	ctc	agt	ggg	1584
Gly	Ala	Leu	Ala	Phe	Cys	Asn	Leu	Ala	Leu	Gly	Asn	Tyr	Leu	Ser	Gly	
		515				520						525				
ttc	ctc	gtc	acc	atc	gtg	cac	cgg	acc	acc	ggc	gcc	ggg	agc	aac	tgg	1632
Phe	Leu	Val	Thr	Ile	Val	His	Arg	Thr	Thr	Gly	Ala	Gly	Ser	Asn	Trp	
		530				535					540					
ctg	gcg	cag	gac	ctc	aac	aag	ggg	agg	ctc	gac	ctc	ttc	tac	tgg	atg	1680
Leu	Ala	Gln	Asp	Leu	Asn	Lys	Gly	Arg	Leu	Asp	Leu	Phe	Tyr	Trp	Met	
					550					555					560	
atc	gcc	ggc	atc	ggc	atc	ttc	aac	atc	atc	tac	ttc	atg	atc	tgc	gcc	1728
Ile	Ala	Gly	Ile	Gly	Ile	Phe	Asn	Ile	Ile	Tyr	Phe	Met	Ile	Cys	Ala	
			565					570						575		
aag	tgg	tac	agg	ttc	aag	ggg	gca	gcc	gcc	aac	tga					1764
Lys	Trp	Tyr	Arg	Phe	Lys	Gly	Ala	Ala	Ala	Asn						
			580					585								

<210> 303

<211> 587

<212> PRT

<213> Oryza sativa

<400> 303

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Gln	Lys	Leu	Lys	Ser	Met	Asp	Val	Asp	Lys	Leu	Glu	Asn	Gly	Gly	Asp	
			20					25					30			
Lys	Pro	Ala	Leu	Lys	Tyr	His	Gly	Trp	Arg	Ala	Met	Pro	Phe	Ile	Ile	
		35					40					45				
Gly	Asn	Glu	Thr	Phe	Glu	Lys	Leu	Gly	Thr	Leu	Gly	Thr	Ser	Ala	Asn	
	50					55					60					
Leu	Leu	Val	Tyr	Leu	Thr	Gln	Val	Phe	His	Met	Arg	Ser	Val	Asp	Ala	
65					70					75					80	
Ala	Thr	Leu	Leu	Asn	Gly	Leu	Asn	Gly	Thr	Ser	Leu	Ala	Pro	Ile		
				85				90					95			
Ile	Gly	Ala	Phe	Leu	Ser	Asp	Ala	Tyr	Leu	Gly	Arg	Tyr	Leu	Ala	Leu	
		100						105					110			
Ala	Ile	Ala	Ser	Val	Ala	Ser	Leu	Ile	Gly	Met	Phe	Leu	Thr	Met		
		115					120					125				
Thr	Ala	Ala	Ala	Asp	Gly	Leu	His	Pro	Ala	Glu	Cys	Gly	Val	Gly	Glu	
	130					135					140					
Thr	Cys	Ser	Lys	Ala	Thr	Ser	Gly	Gln	Phe	Ala	Val	Leu	Phe	Met	Ser	
145					150					155					160	
Phe	Ala	Phe	Leu	Val	Leu	Gly	Ser	Ala	Gly	Ile	Arg	Pro	Cys	Ser	Met	
			165					170						175		
Pro	Phe	Gly	Ala	Asp	Gln	Phe	Asp	Pro	His	Thr	Glu	Ser	Gly	Lys	Arg	
			180					185					190			
Gly	Ile	Asn	Ser	Phe	Phe	Asn	Trp	Tyr	Tyr	Phe	Thr	Phe	Thr	Ser	Ala	
		195					200					205				
Met	Leu	Val	Ser	Ala	Thr	Val	Ile	Ile	Tyr	Val	Gln	Ser	Asn	Val	Ser	
	210					215					220					
Trp	Pro	Ile	Gly	Leu	Gly	Ile	Pro	Thr	Ala	Leu	Met	Leu	Leu	Ala	Cys	
225					230					235					240	

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Val Leu Phe Phe Met Gly Thr Arg Leu Tyr Val Arg Val Thr Pro Glu
 245 250 255
 Gly Ser Pro Phe Thr Ser Ile Val Gln Val Phe Ala Ala Ala Ala Arg
 260 265 270
 Lys Arg Ser Leu Lys Gln Pro Lys Asp Pro Lys Gln Asp Leu Phe Asp
 275 280 285
 Pro Pro His Thr Ser Ala Ile Val Thr Lys Leu Ala His Thr Asp Gln
 290 295 300
 Phe Arg Cys Leu Asp Lys Ala Ala Ile Val Ser Gly Pro Asp Asp Val
 305 310 315 320
 Arg Ala Gly Gly Ala Pro Ser Asn Pro Trp Arg Leu Cys Ser Val
 325 330 335
 Gln Gln Val Glu Glu Val Lys Cys Leu Ile Arg Ile Val Pro Val Trp
 340 345 350
 Ser Thr Gly Ile Ile Tyr Tyr Val Ala Val Val Gln Gln Ser Thr Tyr
 355 360 365
 Val Val Leu Ser Ala Leu Gln Ser Asp Arg His Leu Gly Arg Ser Phe
 370 375 380
 Gln Ile Pro Ala Ala Ser Phe Thr Val Phe Ala Met Leu Ala Gln Thr
 385 390 395 400
 Leu Trp Ile Pro Ile Tyr Asp Arg Leu Leu Val Pro Arg Leu Arg Arg
 405 410 415
 Val Thr Gly Lys Asp Glu Gly Leu Thr Leu Leu Gln Arg Gln Gly Ile
 420 425 430
 Gly Ile Ala Leu Ser Thr Val Ala Met Val Met Ser Ala Val Val Glu
 435 440 445
 Asp Arg Arg Arg His Ile Ala Leu Thr Gln Pro Thr Leu Gly Thr Thr
 450 455 460
 Ile Thr Gly Gly Ala Ile Ser Ala Met Ser Ser Leu Trp Met Val Pro
 465 470 475 480
 Gln Leu Met Val Leu Gly Leu Ser Glu Ala Phe Asn Leu Ile Ser Gln
 485 490 495
 Ile Glu Phe Tyr Tyr Lys Glu Ile Pro Glu His Met Arg Ser Val Ala
 500 505 510
 Gly Ala Leu Ala Phe Cys Asn Leu Ala Leu Gly Asn Tyr Leu Ser Gly
 515 520 525
 Phe Leu Val Thr Ile Val His Arg Thr Thr Gly Ala Gly Ser Asn Trp
 530 535 540
 Leu Ala Gln Asp Leu Asn Lys Gly Arg Leu Asp Leu Phe Tyr Trp Met
 545 550 555 560
 Ile Ala Gly Ile Gly Ile Phe Asn Ile Ile Tyr Phe Met Ile Cys Ala
 565 570 575
 Lys Trp Tyr Arg Phe Lys Gly Ala Ala Ala Asn
 580 585

<210> 304

<211> 1761

<212> DNA

<213> Triticum aestivum

<220>

<221> CDS

<222> (1)..(1761)

<400> 304

atg gac tcc acg gat cag ttt gac aac agc cct ctg cta gac gga gac	48
Met Asp Ser Thr Asp 5 Gln Phe Asp Asn Ser 10 Pro Leu Leu Asp Gly 15 Asp	
ggc tca tca caa gag aat aca aca gaa tat aca ggt gat ggg tct gtt	96
Gly Ser Ser Gln Glu Asn Thr Thr Gln Tyr Thr Gly Asp Gly Ser Val	
tgc atc agt ggg cat cct gct tcc aga aaa cat aca ggg aat tgg aag	144
Cys Ile Ser 35 Gly His Pro Ala Ser 40 Arg Lys His Thr Gly 45 Asn Trp Lys	
gcc tcc ttc tta atc ata gtc tgt tca ttc tgt tgt tat ctt gcg tat	192
Ala Ser Phe Leu Ile Ile Val Cys Ser Phe Cys Cys Tyr Leu Ala Tyr	
tct tcc att gga aaa aac cta gtc agt tat ctc aca aaa gtc cta cat	240
Ser Ser Ile Gly Lys Asn Leu Val Ser Tyr Leu Thr Lys Val Leu His	

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65											70											75											80	
gaa	aca	aat	ttg	gat	gct	gca	aga	cat	gtt	gca	act	tgg	caa	ggg	act	288	Glu	Thr	Asn	Leu	Asp	Ala	Ala	Arg	His	Val	Ala	Thr	Trp	Gln	Gly	Thr		
agc	tat	ctc	gcg	cct	ctg	ggt	gga	gcc	ttc	gtt	gcc	gat	tca	tat	ctg	336	Ser	Tyr	Leu	Ala	Pro	Leu	Val	Gly	Ala	Phe	Val	Ala	Asp	Ser	Tyr	Leu		
ggg	aag	tac	cgg	aca	gct	ttg	atc	gcc	tgc	aag	att	ttc	att	att	gga	384	Gly	Lys	Tyr	Arg	Thr	Ala	Leu	Ile	Ala	Cys	Lys	Ile	Phe	Ile	Ile	Gly		
atg	atg	atg	ttg	ctt	cta	tca	gca	ctt	caa	tta	atc	tca	gcc	ggg	432	Met	Met	Met	Leu	Leu	Leu	Ser	Ala	Ala	Leu	Gln	Leu	Ile	Ser	Ala	Gly			
cct	cac	gct	tgg	act	gtt	tgg	gta	cat	cta	gtc	tct	tct	cag	tac	acc	480	Pro	His	Ala	Trp	Thr	Val	Trp	Val	His	Leu	Val	Ser	Ser	Gln	Tyr	Thr		
ata	ttc	ttg	att	ggg	ttg	tac	atg	gtg	ggg	cta	ggg	tat	ggg	gca	cag	528	Ile	Phe	Leu	Ile	Gly	Leu	Tyr	Met	Val	Gly	Leu	Gly	Tyr	Gly	Ala	Gln		
cgc	cct	tgc	gtc	acg	tct	ttt	gga	gcc	gat	caa	ttc	gat	gac	acc	gat	576	Arg	Pro	Cys	Val	Thr	Ser	Phe	Gly	Ala	Asp	Gln	Phe	Asp	Asp	Thr	Asp		
tat	gtg	gag	aaa	acc	aga	aag	agc	tcc	ttc	ttc	aat	tgg	cac	tat	ttc	624	Tyr	Val	Glu	Lys	Thr	Arg	Lys	Ser	Ser	Phe	Phe	Asn	Trp	His	Tyr	Phe		
gca	atc	aat	gct	ggg	tca	ttg	att	gct	ggg	act	gtt	att	gtc	tgg	gtt	672	Ala	Ile	Asn	Ala	Gly	Ser	Leu	Ile	Ala	Gly	Thr	Val	Ile	Val	Trp	Val		
caa	gaa	cat	gaa	ggc	tgg	ctc	tgg	ggg	ttt	aca	att	tct	aca	ttg	ttt	720	Gln	Glu	His	Glu	Gly	Trp	Leu	Trp	Gly	Phe	Ile	Ser	Thr	Leu	Phe			
gtg	act	tta	ggg	gta	tgt	att	ttt	ttc	ttg	ggc	tcc	atc	gtg	tat	aga	768	Val	Thr	Leu	Gly	Val	Cys	Ile	Phe	Phe	Leu	Gly	Ser	Ile	Val	Tyr	Arg		
ttt	cag	aag	cct	aga	gga	agc	cct	ctg	aca	aga	cta	tgc	cag	gtt	gtc	816	Phe	Gln	Lys	Pro	Arg	Gly	Ser	Pro	Leu	Thr	Arg	Leu	Cys	Gln	Val	Val		
att	gca	gct	act	cgg	aac	ttt	gat	aag	gtt	ttg	cca	tgt	gat	tcc	tca	864	Ile	Ala	Ala	Thr	Arg	Asn	Phe	Asp	Lys	Val	Leu	Pro	Cys	Asp	Ser	Ser		
gct	ctt	tat	gag	ttt	atg	ggg	caa	ggc	tcg	gca	atc	gaa	ggc	aga	cgg	912	Ala	Leu	Tyr	Glu	Phe	Met	Gly	Gln	Gly	Ser	Ala	Ile	Glu	Gly	Arg	Arg		
aaa	ttg	gag	cat	aca	act	gga	ctc	ggg	ttc	ttt	gat	aaa	gct	gca	att	960	Lys	Leu	Glu	His	Thr	Thr	Gly	Leu	Gly	Phe	Asp	Lys	Ala	Ala	Ile			
gtg	aca	tta	cct	gac	tgt	gaa	tct	cct	ggc	caa	cat	aat	aaa	tgg	aag	1008	Val	Thr	Leu	Pro	Asp	Cys	Glu	Ser	Pro	Gly	Gln	His	Asn	Lys	Trp	Lys		
att	tgc	act	gtc	cag	gtt	gag	gag	gag	tta	aag	att	ctg	atc	agg	atg	1056	Ile	Cys	Thr	Val	Thr	Gln	Val	Glu	Glu	Leu	Lys	Ile	Leu	Ile	Arg	Met		
ttt	cca	att	tgg	tcg	gca	atg	att	ttg	ttt	gct	gca	gtt	cag	gaa	caa	1104	Phe	Pro	Ile	Trp	Ser	Ala	Met	Ile	Leu	Phe	Ala	Ala	Val	Gln	Glu	Gln		
atg	tcc	tca	aca	ttt	gta	gag	caa	ggg	atg	gca	atg	gat	aaa	cac	atc	1152	Met	Ser	Ser	Thr	Phe	Val	Glu	Gln	Gly	Met	Ala	Met	Asp	Lys	His	Ile		
ggg	tct	ttc	gaa	ata	cct	tct	gca	tcc	ttc	cag	tgt	gta	gat	aca	att	1200	Gly	Ser	Phe	Glu	Ile	Pro	Ser	Ala	Ser	Phe	Gln	Cys	Val	Asp	Thr	Ile		
act	gtc	att	gta	ctg	gtt	cca	att	tat	gag	aga	ctc	att	gtt	cca	gta	1248	Thr	Val	Ile	Val	Leu	Val	Pro	Ile	Tyr	Glu	Arg	Leu	Ile	Val	Pro	Val		
att	aga	aaa	ttt	act	ggc	aga	gag	aat	ggc	att	aca	tca	cca	cag	cga	1296	Ile	Arg	Lys	Phe	Thr	Gly	Arg	Ala	Asn	Gly	Ile	Thr	Ser	Pro	Gln	Arg		
ata	ggg	att	ggg	tta	tgt	ttc	tcg	atg	ttc	tca	atg	gtg	tca	gca	gca	1344	Ile	Gly	Ile	Gly	Leu	Cys	Phe	Ser	Met	Phe	Ser	Met	Val	Ser	Ala	Ala		

PF59082SeqList_PF59082.txt

435	440	445	
ttg gtg gag ggt aac cgg cta cag att gca cag gcc gaa ggt ttg gtg			1392
Leu Val Glu Gly Asn Arg Leu Gln Ile Ala Gln Ala Glu Gly Leu Val			
450	455	460	
cac cgc aag gtg gct gtt ccg atg agc atc atg tgg caa gga ccc cag			1440
His Arg Lys Val Ala Val Pro Met Ser Ile Met Trp Gln Gly Pro Gln			
465	470	475	
tac ttc ctg cta ggc gtc gcc gag gtg ttc tcc aat att ggg cta act			1488
Tyr Phe Leu Leu Gly Val Ala Glu Val Phe Ser Asn Ile Gly Leu Thr			
485	490	495	
gag gct ttc tat gat gaa tct cca gat ggc atg cga agc tta tgt atg			1536
Glu Ala Phe Tyr Asp Glu Ser Pro Asp Gly Met Arg Ser Leu Cys Met			
500	505	510	
gca ttc tcg ctt gtt aac atg tcg gct gga aat tac ctt agt tca ctt			1584
Ala Phe Ser Leu Val Asn Met Ser Ala Gly Asn Tyr Leu Ser Ser Leu			
515	520	525	
atc ctt tcc ctt gtg cca gta ttc aca gcc aga gga ggc agc cca ggg			1632
Ile Leu Ser Leu Val Pro Val Phe Thr Ala Arg Gly Gly Ser Pro Gly			
530	535	540	
tgg ata cct gat aac ttg aat gaa ggg cat ttg gat aga ttc tac ctg			1680
Trp Ile Pro Asp Asn Leu Asn Glu Gly His Leu Asp Arg Phe Tyr Leu			
545	550	555	
atg atg gct ggg ctg agt ttt ttt aat ata gta gtc ttt gta ttc tgt			1728
Met Met Ala Gly Leu Ser Phe Phe Asn Ile Val Val Phe Val Phe Cys			
565	570	575	
gct atg agg tac aaa tgt aag aag gct tca tga			1761
Ala Met Arg Tyr Lys Cys Lys Lys Ala Ser			
580	585		

<210> 305

<211> 586

<212> PRT

<213> Triticum aestivum

<400> 305

Met Asp Ser Thr Asp Gln Phe Asp Asn Ser Pro Leu Leu Asp Gly Asp	
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20 25 30	
Cys Ile Ser Gly His Pro Ala Ser Arg Lys His Thr Gly Asn Trp Lys	
35 40 45	
Ala Ser Phe Leu Ile Ile Val Cys Ser Phe Cys Cys Tyr Leu Ala Tyr	
50 55 60	
Ser Ser Ile Gly Lys Asn Leu Val Ser Tyr Leu Thr Lys Val Leu His	
65 70 75 80	
Glu Thr Asn Leu Asp Ala Ala Arg His Val Ala Thr Trp Gln Gly Thr	
85 90 95	
Ser Tyr Leu Ala Pro Leu Val Gly Ala Phe Val Ala Asp Ser Tyr Leu	
100 105 110	
Gly Lys Tyr Arg Thr Ala Leu Ile Ala Cys Lys Ile Phe Ile Ile Gly	
115 120 125	
Met Met Met Leu Leu Leu Ser Ala Ala Leu Gln Leu Ile Ser Ala Gly	
130 135 140	
Pro His Ala Trp Thr Val Trp Val His Leu Val Ser Ser Gln Tyr Thr	
145 150 155 160	
Ile Phe Leu Ile Gly Leu Tyr Met Val Gly Leu Gly Tyr Gly Ala Gln	
165 170 175	
Arg Pro Cys Val Thr Ser Phe Gly Ala Asp Gln Phe Asp Asp Thr Asp	
180 185 190	
Tyr Val Glu Lys Thr Arg Lys Ser Phe Phe Asn Trp His Tyr Phe	
195 200 205	
Ala Ile Asn Ala Gly Ser Leu Ile Ala Gly Thr Val Ile Val Trp Val	
210 215 220	
Gln Glu His Glu Gly Trp Leu Trp Gly Phe Thr Ile Ser Thr Leu Phe	
225 230 235 240	
Val Thr Leu Gly Val Cys Ile Phe Phe Leu Gly Ser Ile Val Tyr Arg	
245 250 255	
Phe Gln Lys Pro Arg Gly Ser Pro Leu Thr Arg Leu Cys Gln Val Val	
260 265 270	

PF59082SeqList_PF59082.txt

Ile Ala Ala Thr Arg Asn Phe Asp Lys Val Leu Pro Cys Asp Ser Ser
 275 280 285
 Ala Leu Tyr Glu Phe Met Gly Gln Gly Ser Ala Ile Glu Gly Arg Arg
 290 295 300
 Lys Leu Glu His Thr Thr Gly Leu Gly Phe Phe Asp Lys Ala Ala Ile
 305 310 315 320
 Val Thr Leu Pro Asp Cys Glu Ser Pro Gly Gln His Asn Lys Trp Lys
 325 330 335
 Ile Cys Thr Val Thr Gln Val Glu Glu Leu Lys Ile Leu Ile Arg Met
 340 345 350
 Phe Pro Ile Trp Ser Ala Met Ile Leu Phe Ala Ala Val Gln Glu Gln
 355 360 365
 Met Ser Ser Thr Phe Val Glu Gln Gly Met Ala Met Asp Lys His Ile
 370 375 380
 Gly Ser Phe Glu Ile Pro Ser Ala Ser Phe Gln Cys Val Asp Thr Ile
 385 390 395 400
 Thr Val Ile Val Leu Val Pro Ile Tyr Glu Arg Leu Ile Val Pro Val
 405 410 415
 Ile Arg Lys Phe Thr Gly Arg Ala Asn Gly Ile Thr Ser Pro Gln Arg
 420 425 430
 Ile Gly Ile Gly Leu Cys Phe Ser Met Phe Ser Met Val Ser Ala Ala
 435 440 445
 Leu Val Glu Gly Asn Arg Leu Gln Ile Ala Gln Ala Glu Gly Leu Val
 450 455 460
 His Arg Lys Val Ala Val Pro Met Ser Ile Met Trp Gln Gly Pro Gln
 465 470 475 480
 Tyr Phe Leu Leu Gly Val Ala Glu Val Phe Ser Asn Ile Gly Leu Thr
 485 490 495
 Glu Ala Phe Tyr Asp Glu Ser Pro Asp Gly Met Arg Ser Leu Cys Met
 500 505 510
 Ala Phe Ser Leu Val Asn Met Ser Ala Gly Asn Tyr Leu Ser Ser Leu
 515 520 525
 Ile Leu Ser Leu Val Pro Val Phe Thr Ala Arg Gly Gly Ser Pro Gly
 530 535 540
 Trp Ile Pro Asp Asn Leu Asn Glu Gly His Leu Asp Arg Phe Tyr Leu
 545 550 555 560
 Met Met Ala Gly Leu Ser Phe Phe Asn Ile Val Val Phe Val Phe Cys
 565 570 575
 Ala Met Arg Tyr Lys Cys Lys Lys Ala Ser
 580 585

<210> 306

<211> 1761

<212> DNA

<213> Triticum aestivum

<220>

<221> CDS

<222> (1)..(1761)

<400> 306

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agc tca tca cag gag aat tcc acg gaa tat aca ggt gat gga tct gtt	96
Ser Ser Ser Gln Glu Asn Ser Thr Glu Tyr Thr Gly Asp Gly Ser Val	
20 25 30	
tgt acc agt ggt cat cct gct tcc aga aaa cat aca ggg aac tgg aag	144
Cys Thr Ser Gly His Pro Ala Ser Arg Lys His Thr Gly Asn Trp Lys	
35 40 45	
gtc tcc tcc tta acc ata gtc tgt tca ttc tgc tgc tat ctg gcc tat	192
Val Ser Ser Leu Thr Ile Val Cys Ser Phe Cys Cys Tyr Leu Ala Tyr	
50 55 60	
tct tca att gga aaa aac cta gtc agt tat ctc aca aaa gtc cta gat	240
Ser Ser Ile Gly Lys Asn Leu Val Ser Tyr Leu Thr Lys Val Leu Asp	
65 70 75 80	
gaa aca aat ctg gat gct gca aga cat gtt gca act tgg caa ggt act	288
Glu Thr Asn Leu Asp Ala Ala Arg His Val Ala Thr Trp Gln Gly Thr	
85 90 95	

PF59082SeqList_PF59082.txt

agc	tat	ctc	gcg	cct	ctg	gtt	gga	gcc	ttc	gtt	gct	gat	tca	tac	ctg	336
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			100					105					110			
ggg	aag	tac	cgg	aca	gct	ttg	atc	agc	tgc	aca	att	ttc	att	atg	gga	384
Gly	Lys	Tyr	Arg	Thr	Ala	Leu	Ile	Ser	Cys	Thr	Ile	Phe	Ile	Met	Gly	
			115				120						125			
atg	atg	atg	ctg	ctt	cta	tca	gca	gca	ctt	cca	tta	atc	tca	gcc	ggt	432
Met	Met	Met	Leu	Leu	Leu	Ser	Ala	Ala	Leu	Pro	Leu	Ile	Ser	Ala	Gly	
			130			135					140					
cct	cat	gct	tgg	act	ctt	tgg	gca	gat	cct	atc	tct	tct	cgg	tac	att	480
Pro	His	Ala	Trp	Thr	Leu	Trp	Ala	Asp	Pro	Ile	Ser	Ser	Arg	Tyr	Ile	
145					150				155						160	
ata	ttc	ttg	gtt	ggg	ttg	tac	atg	gtt	ggt	tta	ggg	tac	ggt	gca	cag	528
Ile	Phe	Leu	Val	Gly	Leu	Tyr	Met	Val	Gly	Leu	Gly	Tyr	Gly	Ala	Gln	
			165						170					175		
tgc	cct	tgc	gtc	tct	ttt	gga	gcc	gat	caa	ttt	gat	gac	acc	aat		576
Cys	Pro	Cys	Val	Thr	Ser	Phe	Gly	Ala	Asp	Gln	Phe	Asp	Asp	Thr	Asn	
			180				185					190				
gag	atg	gag	aag	acc	aga	aag	agc	tct	ttc	ttt	aat	tgg	cac	tat	ttc	624
Glu	Met	Glu	Lys	Thr	Arg	Lys	Ser	Ser	Phe	Phe	Asn	Trp	His	Tyr	Phe	
			195				200					205				
tca	atc	aat	gct	ggt	tca	ttg	atc	gct	ggg	act	gtt	att	gtc	tgg	gtt	672
Ser	Ile	Asn	Ala	Gly	Ser	Leu	Ile	Ala	Gly	Thr	Val	Ile	Val	Trp	Val	
			210			215					220					
caa	gaa	cat	gaa	ggc	tgg	ctc	tgg	ggc	ttt	aca	att	tct	aca	cta	ttt	720
Gln	Glu	His	Glu	Gly	Trp	Leu	Trp	Gly	Phe	Thr	Ile	Ser	Thr	Leu	Phe	
225					230				235						240	
gtg	act	tta	ggt	ata	agt	gtg	ttt	ttc	ttg	ggc	tcc	att	gtg	tat	aga	768
Val	Thr	Leu	Gly	Ile	Ser	Val	Phe	Phe	Leu	Gly	Ser	Ile	Val	Tyr	Arg	
			245						250					255		
ttt	cag	aaa	cct	gga	gga	agc	cct	cta	gca	aga	ata	tgg	cag	gtt	gtt	816
Phe	Gln	Lys	Pro	Gly	Gly	Ser	Pro	Leu	Ala	Arg	Ile	Trp	Gln	Val	Val	
			260				265					270				
gtt	gca	gct	tct	cgg	aac	ttc	gat	aaa	gtt	ttg	cca	tgt	gat	tcc	tca	864
Val	Ala	Ala	Ser	Arg	Asn	Phe	Asp	Lys	Val	Leu	Pro	Cys	Asp	Ser	Ser	
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gct	ctt	tat	gag	ttt	tcg	ggg	caa	gga	tcg	gca	atc	gaa	ggc	agc	cgg	912
Ala	Leu	Tyr	Glu	Phe	Ser	Gly	Gln	Gly	Ser	Ala	Ile	Glu	Gly	Ser	Arg	
			290			295					300					
aaa	tcg	gaa	cat	aca	agt	gga	ctt	gag	ttc	ttt	gat	aaa	gct	gca	att	960
Lys	Ser	Glu	His	Thr	Ser	Gly	Leu	Glu	Phe	Phe	Asp	Lys	Ala	Ala	Ile	
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ctg	aca	cta	cct	gac	tgt	gaa	tct	cct	ggc	caa	ctt	aat	aag	tgg	aag	1008
Leu	Thr	Leu	Pro	Asp	Cys	Glu	Ser	Pro	Gly	Gln	Leu	Asn	Lys	Trp	Lys	
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att	tgt	acc	gtc	act	cag	gta	gag	gag	tta	aag	att	ctg	atc	aga	atg	1056
Ile	Cys	Thr	Val	Thr	Gln	Val	Glu	Glu	Leu	Lys	Ile	Leu	Ile	Arg	Met	
			340				345					350				
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Phe	Pro	Ile	Trp	Ser	Ala	Met	Val	Leu	Phe	Ala	Ala	Val	Gln	Glu	Gln	
			355			360						365				
atg	ttt	tca	aca	ttt	gta	gag	caa	ggg	atg	aca	atg	gag	aaa	cac	gtc	1152
Met	Phe	Ser	Thr	Phe	Val	Glu	Gln	Gly	Met	Thr	Met	Glu	Lys	His	Val	
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ggg	tct	ttc	gaa	ata	ccc	act	gca	tcc	ttt	caa	tcc	ata	gat	aca	ctt	1200
Gly	Ser	Phe	Glu	Ile	Pro	Thr	Ala	Ser	Phe	Gln	Ser	Ile	Asp	Thr	Leu	
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act	gtc	att	atg	ctg	gtt	cca	att	tat	gag	aga	gtc	ctt	gtt	cca	gta	1248
Thr	Val	Ile	Met	Leu	Val	Pro	Ile	Tyr	Glu	Arg	Val	Leu	Val	Pro	Val	
			405						410					415		
ata	aga	aaa	ttc	acc	ggc	aga	gcg	aat	ggc	ata	tcg	tcg	cca	cag	cga	1296
Ile	Arg	Lys	Phe	Thr	Gly	Arg	Ala	Asn	Gly	Ile	Ser	Ser	Pro	Gln	Arg	
			420				425						430			
ata	ggg	att	ggt	tta	tgt	ttc	tcc	atg	ctc	tca	atg	gtg	tta	gca	gca	1344
Ile	Gly	Ile	Gly	Leu	Cys	Phe	Ser	Met	Leu	Ser	Met	Val	Leu	Ala	Ala	
			435			440						445				
ttg	gtg	gag	agt	aac	cgg	tta	cag	att	gca	cag	tcc	gaa	ggt	ttg	gtg	1392
Leu	Val	Glu	Ser	Asn	Arg	Leu	Gln	Ile	Ala	Gln	Ser	Glu	Gly	Leu	Val	
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Tyr	Phe	Leu	Leu	Gly	Val	Ala	Glu	Val	Phe	Ser	Asn	Ile	Gly	Leu	Thr	
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gaa	ttt	ttc	tgt	gat	gag	tct	cca	gac	gcc	atg	aga	agt	tta	ggc	atg	1536
Glu	Phe	Phe	Cys	Asp	Glu	Ser	Pro	Asp	Ala	Met	Arg	Ser	Leu	Gly	Met	
			500					505					510			
gca	ttc	tcg	ctt	ctt	aac	atc	tcg	gct	gga	aat	tac	ctt	agt	tcg	ttt	1584
Ala	Phe	Ser	Leu	Leu	Asn	Ile	Ser	Ala	Gly	Asn	Tyr	Leu	Ser	Ser	Phe	
		515					520					525				
atc	ctt	tcc	ctt	gtg	ccg	gta	ttc	aca	gcc	aga	gga	ggc	agc	cca	ggg	1632
Ile	Leu	Ser	Leu	Val	Pro	Val	Phe	Thr	Ala	Arg	Gly	Gly	Ser	Pro	Gly	
	530					535					540					
tgg	ata	cct	gat	aac	ttg	aat	gaa	ggg	cat	ctg	gac	aga	ttc	tac	ctg	1680
Trp	Ile	Pro	Asp	Asn	Leu	Asn	Glu	Gly	His	Leu	Asp	Arg	Phe	Tyr	Leu	
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atg	atg	gct	ggg	ctg	agt	tta	ctg	aat	ata	ttt	gtc	ttt	gta	ttc	tat	1728
Met	Met	Ala	Gly	Leu	Ser	Leu	Leu	Asn	Ile	Phe	Val	Phe	Val	Phe	Tyr	
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gct	agg	agg	tac	aaa	tgt	aag	aag	gct	tcc	tga						1761
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<210> 307

<211> 586

<212> PRT

<213> Triticum aestivum

<400> 307

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Cys	Thr	Ser	Gly	His	Pro	Ala	Ser	Arg	Lys	His	Thr	Gly	Asn	Trp	Lys	
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Val	Ser	Ser	Leu	Thr	Ile	Val	Cys	Ser	Phe	Cys	Cys	Tyr	Leu	Ala	Tyr	
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Ser	Ser	Ile	Gly	Lys	Asn	Leu	Val	Ser	Tyr	Leu	Thr	Lys	Val	Leu	Asp	
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Glu	Thr	Asn	Leu	Asp	Ala	Ala	Arg	His	Val	Ala	Thr	Trp	Gln	Gly	Thr	
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Ser	Tyr	Leu	Ala	Pro	Leu	Val	Gly	Ala	Phe	Val	Ala	Asp	Ser	Tyr	Leu	
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Gly	Lys	Tyr	Arg	Thr	Ala	Leu	Ile	Ser	Cys	Thr	Ile	Phe	Ile	Met	Gly	
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	130					135				140						
Pro	His	Ala	Trp	Thr	Leu	Trp	Ala	Asp	Pro	Ile	Ser	Ser	Arg	Tyr	Ile	
145				150					155						160	
Ile	Phe	Leu	Val	Gly	Leu	Tyr	Met	Val	Gly	Leu	Gly	Tyr	Gly	Ala	Gln	
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Cys	Pro	Cys	Val	Thr	Ser	Phe	Gly	Ala	Asp	Gln	Phe	Asp	Asp	Thr	Asn	
		180					185					190				
Glu	Met	Glu	Lys	Thr	Arg	Lys	Ser	Ser	Phe	Phe	Asn	Trp	His	Tyr	Phe	
		195					200				205					
Ser	Ile	Asn	Ala	Gly	Ser	Leu	Ile	Ala	Gly	Thr	Val	Ile	Val	Trp	Val	
	210					215					220					
Gln	Glu	His	Glu	Gly	Trp	Leu	Trp	Gly	Phe	Thr	Ile	Ser	Thr	Leu	Phe	
225				230					235						240	
Val	Thr	Leu	Gly	Ile	Ser	Val	Phe	Phe	Leu	Gly	Ser	Ile	Val	Tyr	Arg	
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Phe	Gln	Lys	Pro	Gly	Gly	Ser	Pro	Leu	Ala	Arg	Ile	Trp	Gln	Val	Val	
		260					265						270			
Val	Ala	Ala	Ser	Arg	Asn	Phe	Asp	Lys	Val	Leu	Pro	Cys	Asp	Ser	Ser	
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Ala	Leu	Tyr	Glu	Phe	Ser	Gly	Gln	Gly	Ser	Ala	Ile	Glu	Gly	Ser	Arg	
	290					295					300					

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Lys Ser Glu His Thr Ser Gly Leu Glu Phe Phe Asp Lys Ala Ala Ile
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 Leu Thr Leu Pro Asp Cys Glu Ser Pro Gly Gln Leu Asn Lys Trp Lys
 325 330 335
 Ile Cys Thr Val Thr Gln Val Glu Glu Leu Lys Ile Leu Ile Arg Met
 340 345 350
 Phe Pro Ile Trp Ser Ala Met Val Leu Phe Ala Ala Val Gln Glu Gln
 355 360 365
 Met Phe Ser Thr Phe Val Glu Gln Gly Met Thr Met Glu Lys His Val
 370 375 380
 Gly Ser Phe Glu Ile Pro Thr Ala Ser Phe Gln Ser Ile Asp Thr Leu
 385 390 395 400
 Thr Val Ile Met Leu Val Pro Ile Tyr Glu Arg Val Leu Val Pro Val
 405 410 415
 Ile Arg Lys Phe Thr Gly Arg Ala Asn Gly Ile Ser Ser Pro Gln Arg
 420 425 430
 Ile Gly Ile Gly Leu Cys Phe Ser Met Leu Ser Met Val Leu Ala Ala
 435 440 445
 Leu Val Glu Ser Asn Arg Leu Gln Ile Ala Gln Ser Glu Gly Leu Val
 450 455 460
 His Ser Lys Val Thr Val Pro Met Ser Ile Leu Trp Gln Gly Pro Gln
 465 470 475 480
 Tyr Phe Leu Leu Gly Val Ala Glu Val Phe Ser Asn Ile Gly Leu Thr
 485 490 495
 Glu Phe Phe Cys Asp Glu Ser Pro Asp Ala Met Arg Ser Leu Gly Met
 500 505 510
 Ala Phe Ser Leu Leu Asn Ile Ser Ala Gly Asn Tyr Leu Ser Ser Phe
 515 520 525
 Ile Leu Ser Leu Val Pro Val Phe Thr Ala Arg Gly Gly Ser Pro Gly
 530 535 540
 Trp Ile Pro Asp Asn Leu Asn Glu Gly His Leu Asp Arg Phe Tyr Leu
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 Ala Arg Arg Tyr Lys Cys Lys Lys Ala Ser
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<210> 308

<211> 1704

<212> DNA

<213> Solanum demissum

<220>

<221> CDS

<222> (1)..(1704)

<400> 308

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tct acg cgt cga aag aat ggc gga tgg ata acc ttc ccc ttc att ata	96
Ser Thr Arg Arg Lys Asn Gly Gly Trp Ile Thr Phe Pro Phe Ile Ile	
20 25 30	
gtg tca gca act atg gcg ggc tta tcg ctt gca tct gga ggg tgg acg	144
Val Ser Ala Thr Met Ala Gly Leu Ser Leu Ala Ser Gly Gly Trp Thr	
35 40 45	
agc aac ctg att gtt tat ttg ata gat gaa ttc aac atg aag agc atc	192
Ser Asn Leu Ile Val Tyr Leu Ile Asp Glu Phe Asn Met Lys Ser Ile	
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aaa aca gct aaa gtt tac aat gtg atc aat gga tgc acc aca ctt ttc	240
Lys Thr Ala Lys Val Tyr Asn Val Ile Asn Gly Cys Thr Thr Leu Phe	
65 70 75 80	
ccc att gtt ggt gga atc cta gct gac tct tat ctt ggc agt ttt tct	288
Pro Ile Val Gly Gly Ile Leu Ala Asp Ser Tyr Leu Gly Ser Phe Ser	
85 90 95	
gtc att tgg ttt tca tct ctt atc tct gct ttg ggt ata ttg ctt cta	336
Val Ile Trp Phe Ser Ser Leu Ile Ser Ala Leu Gly Ile Leu Leu Leu	
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PF59082SeqList_PF59082.txt

Leu	Phe	Thr	Ser	Ala	Ile	Asp	Val	Leu	Arg	Pro	Pro	Cys	Asp	Asp	
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Gly	Ser	Ser	Leu	Cys	Thr	Ser	Pro	Ser	Thr	His	Gln	Tyr	Ala	Val	Leu
tat	gtg	gct	ctg	gca	tta	gca	tca	cta	ggg	gtc	gcg	ggt	aca	cgt	480
Tyr	Val	Ala	Leu	Ala	Leu	Ala	Ser	Leu	Gly	Val	Ala	Gly	Thr	Arg	Phe
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ata	ata	gca	ccc	atg	gga	gct	aat	caa	ttt	gat	aaa	cca	aaa	cat	caa
Ile	Ile	Ala	Pro	Met	Gly	Ala	Asn	Gln	Phe	Asp	Lys	Pro	Lys	His	Gln
				165					170					175	
gca	att	ttc	ttc	aat	tgg	tac	ata	ttc	gcc	ttt	tac	atg	tcc	ttt	gcc
Ala	Ile	Phe	Phe	Asn	Trp	Tyr	Ile	Phe	Ala	Phe	Tyr	Met	Ser	Phe	Ala
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Ile	Ser	Thr	Thr	Val	Ile	Val	Tyr	Val	Glu	Asp	Asn	Val	Ser	Trp	Ser
				195			200					205			
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Trp	Gly	Tyr	Gly	Ile	Ser	Met	Ala	Phe	Asn	Ile	Leu	Gly	Leu	Ala	Met
	210					215					220				
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Phe	Leu	Ile	Gly	Lys	Arg	Phe	Tyr	Cys	Asp	Val	Lys	Glu	Gln	Gly	Gly
225					230					235					240
agc	cct	ttc	gtc	aac	tta	gct	cgt	gtt	ata	gtc	gtt	gcc	att	cag	aaa
Ser	Pro	Phe	Val	Asn	Leu	Ala	Arg	Val	Ile	Val	Val	Ala	Ile	Gln	Lys
				245					250					255	
tgg	aga	gtc	cct	ctt	tca	gaa	caa	act	caa	cac	tac	tat	cat	gat	cca
Trp	Arg	Val	Pro	Leu	Ser	Glu	Gln	Thr	Gln	His	Tyr	Tyr	His	Asp	Pro
				260					265				270		
agt	gac	act	act	acc	aca	cta	aca	ata	act	caa	att	cct	acg	aaa	tcc
Ser	Asp	Thr	Thr	Thr	Thr	Leu	Thr	Ile	Thr	Gln	Ile	Pro	Thr	Lys	Ser
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Phe	Lys	Phe	Leu	Asn	Cys	Ala	Ala	Phe	Ile	Thr	Glu	Gly	Asp	Thr	Lys
	290					295					300				
cca	gac	ggc	tcg	att	agt	aac	ccc	tgg	aga	cta	tgc	aca	gtg	cag	caa
Pro	Asp	Gly	Ser	Ile	Ser	Asn	Pro	Trp	Arg	Leu	Cys	Thr	Val	Gln	Gln
305					310					315					320
gta	gaa	gat	ttg	aaa	agc	ttg	atc	aag	ctt	ttc	cct	cta	tgg	gct	agt
Val	Glu	Asp	Leu	Lys	Ser	Leu	Ile	Lys	Leu	Phe	Pro	Leu	Trp	Ala	Ser
				325					330					335	
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Gly	Phe	Leu	Ile	Ser	Thr	Gln	Leu	Val	Ile	Gln	Ala	Ser	Leu	Leu	Ile
				340					345					350	
ctt	cag	gct	ctc	aaa	atg	gat	cgc	cat	atg	gga	cct	cat	ttc	gag	atc
Leu	Gln	Ala	Leu	Lys	Met	Asp	Arg	His	Met	Gly	Pro	His	Phe	Glu	Ile
				355			360					365			
cca	gct	ggg	tct	atg	ttg	gtc	ttc	att	ttg	cta	ttc	aca	tgt	ata	gcc
Pro	Ala	Gly	Ser	Met	Leu	Val	Phe	Ile	Leu	Leu	Phe	Thr	Cys	Ile	Ala
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Ile	Phe	Ile	Ile	Asp	Arg	Phe	Leu	Tyr	Pro	Phe	Leu	Ala	Lys	Tyr	Thr
385					390					395					400
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Thr	Phe	Ser	Leu	Thr	Pro	Leu	Gln	Arg	Ile	Gly	Ile	Gly	His	Val	Ile
				405					410					415	
act	att	att	agc	atg	gct	gtt	tcc	gcc	ctg	gtt	gag	tct	aga	cga	ttg
Thr	Ile	Ile	Ser	Met	Ala	Val	Ser	Ala	Leu	Val	Glu	Ser	Arg	Arg	Leu
				420				425				430			
agg	atc	gtt	agg	act	cac	aaa	ctc	caa	ggc	caa	aac	aat	gac	att	gtt
Arg	Ile	Val	Arg	Thr	His	Lys	Leu	Gln	Gly	Gln	Asn	Asn	Asp	Ile	Val
				435			440					445			
cca	atg	tcc	gtg	ttt	tgg	cta	gtg	cca	caa	cta	gct	ctt	aat	gga	att
Pro	Met	Ser	Val	Phe	Trp	Leu	Val	Pro	Gln	Leu	Ala	Leu	Asn	Gly	Ile
						455					460				
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Gly	Glu	Gly	Phe	His	Phe	Pro	Gly	His	Ile	Ala	Phe	Tyr	Tyr	Gln	Glu
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PF59082SeqList_PF59082.txt

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Ile	Gly	Ile	Ala	His	Tyr	Leu	Gly	Asn	Thr	Leu	Ile	Asp	Leu	Val	Gln	
			500					505					510			
cga	tta	tca	gga	tgg	tta	cca	gac	aat	atc	aac	aag	ggg	aga	act	gat	1584
Arg	Leu	Ser	Gly	Trp	Leu	Pro	Asp	Asn	Ile	Asn	Lys	Gly	Arg	Thr	Asp	
		515					520					525				
aat	gtc	ttc	tgg	ctt	tgt	tgc	atc	ctg	gga	tca	gct	aac	ttc	atg	tat	1632
Asn	Val	Phe	Trp	Leu	Cys	Cys	Ile	Leu	Gly	Ser	Ala	Asn	Phe	Met	Tyr	
	530					535					540					
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Tyr	Val	Val	Cys	Ala	Ser	Leu	Tyr	Lys	Tyr	Lys	Asn	Val	Asp	Asn	Lys	
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Ser	Asn	Ile	Ala	Pro	Ser	Lys										
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<210> 309

<211> 567

<212> PRT

<213> Solanum demissum

<400> 309

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Val	Ser	Ala	Thr	Met	Ala	Gly	Leu	Ser	Leu	Ala	Ser	Gly	Gly	Trp	Thr	
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Ser	Asn	Leu	Ile	Val	Tyr	Leu	Ile	Asp	Glu	Phe	Asn	Met	Lys	Ser	Ile	
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Pro	Ile	Val	Gly	Gly	Ile	Leu	Ala	Asp	Ser	Tyr	Leu	Gly	Ser	Phe	Ser	
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Val	Ile	Trp	Phe	Ser	Ser	Leu	Ile	Ser	Ala	Leu	Gly	Ile	Leu	Leu	Leu	
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Leu	Phe	Thr	Ser	Ala	Ile	Asp	Val	Leu	Arg	Pro	Pro	Pro	Cys	Asp	Asp	
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Ile	Ile	Ala	Pro	Met	Gly	Ala	Asn	Gln	Phe	Asp	Lys	Pro	Lys	His	Gln	
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Ala	Ile	Phe	Phe	Asn	Trp	Tyr	Ile	Phe	Ala	Phe	Tyr	Met	Ser	Phe	Ala	
		180						185					190			
Ile	Ser	Thr	Thr	Val	Ile	Val	Tyr	Val	Glu	Asp	Asn	Val	Ser	Trp	Ser	
		195					200					205				
Trp	Gly	Tyr	Gly	Ile	Ser	Met	Ala	Phe	Asn	Ile	Leu	Gly	Leu	Ala	Met	
	210					215					220					
Phe	Leu	Ile	Gly	Lys	Arg	Phe	Tyr	Cys	Asp	Val	Lys	Glu	Gln	Gly	Gly	
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Ser	Pro	Phe	Val	Asn	Leu	Ala	Arg	Val	Ile	Val	Val	Ala	Ile	Gln	Lys	
			245					250					255			
Trp	Arg	Val	Pro	Leu	Ser	Glu	Gln	Thr	Gln	His	Tyr	Tyr	His	Asp	Pro	
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Ser	Asp	Thr	Thr	Thr	Leu	Thr	Ile	Thr	Gln	Ile	Pro	Thr	Lys	Ser		
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Phe	Lys	Phe	Leu	Asn	Cys	Ala	Ala	Phe	Ile	Thr	Glu	Gly	Asp	Thr	Lys	
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Pro	Asp	Gly	Ser	Ile	Ser	Asn	Pro	Trp	Arg	Leu	Cys	Thr	Val	Gln	Gln	
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Val	Glu	Asp	Leu	Lys	Ser	Leu	Ile	Lys	Leu	Phe	Pro	Leu	Trp	Ala	Ser	
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Gly	Phe	Leu	Ile	Ser	Thr	Gln	Leu	Val	Ile	Gln	Ala	Ser	Leu	Leu	Ile	
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Leu	Gln	Ala	Leu	Lys	Met	Asp	Arg	His	Met	Gly	Pro	His	Phe	Glu	Ile	

PF59082SeqList_PF59082.txt

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 385      390      395
Thr Phe Ser Leu Thr Pro Leu Gln Arg Ile Gly Ile Gly His Val Ile
      405      410      415
Thr Ile Ile Ser Met Ala Val Ser Ala Leu Val Glu Ser Arg Arg Leu
      420      425      430
Arg Ile Val Arg Thr His Lys Leu Gln Gly Gln Asn Asn Asp Ile Val
      435      440      445
Pro Met Ser Val Phe Trp Leu Val Pro Gln Leu Ala Leu Asn Gly Ile
      450      455      460
Gly Glu Gly Phe His Phe Pro Gly His Ile Ala Phe Tyr Tyr Gln Glu
 465      470      475
Phe Pro Thr Ser Leu Lys Ser Thr Ser Thr Ala Met Val Ala Leu Phe
      485      490      495
Ile Gly Ile Ala His Tyr Leu Gly Asn Thr Leu Ile Asp Leu Val Gln
      500      505      510
Arg Leu Ser Gly Trp Leu Pro Asp Asn Ile Asn Lys Gly Arg Thr Asp
      515      520      525
Asn Val Phe Trp Leu Cys Cys Ile Leu Gly Ser Ala Asn Phe Met Tyr
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Tyr Val Val Cys Ala Ser Leu Tyr Lys Tyr Lys Asn Val Asp Asn Lys
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cag gat gaa gaa agt aag cta tac aca gga gat ggc tcg gtc gac ttt	96
Gln Asp Glu Glu Ser Lys Leu Tyr Thr Gly Asp Gly Ser Val 30 Asp Phe	
aaa ggg agg cct gtg ctt aag aag aat act ggc aat tgg aaa gct tgc	144
Lys Gly Arg Pro Val Leu Lys Lys Asn Thr Gly Asn Trp Lys Ala Cys	
cca ttt atc cta ggc aat gag tgc tgt gaa cgt ttg gca tac tat ggc	192
Pro Phe Ile Leu Gly Asn Glu Cys Cys Glu Arg 60 Ala Tyr Tyr Gly	
att gca aca aat ctt gtt aaa cct atc tta ctc gcc aag cta cat gaa	240
Ile Ala Thr Asn Leu Val Lys Pro Ile Leu Leu Ala Lys Leu His Glu	
gga aat gtc tct gcg gca aga aac gtc acc act tgg caa ggc act tgt	288
Gly Asn Val Ser Ala 85 Arg Asn Val Thr Trp Gln Gly Thr Cys	
tac ctt gca cct ctc att gga gca gtt cta gca gat tct tac tgg gga	336
Tyr Leu Ala Pro Leu Ile Gly Ala Val 105 Leu Ala Asp Ser Tyr Trp Gly	
cga tac tgg aca att gcc att ttc tcc atg att tat ttc att gga atg	384
Arg Tyr Trp Thr Ile Ala Ile Phe Ser Met Ile Tyr Phe Ile Gly Met	
ggt acg ttg aca ctt tct gct tct att cca gca ttg aag cct gct gaa	432
Gly Thr Leu Thr Leu Ser Ala Ser Ile Pro Ala Leu Lys Pro Ala Glu	

PF59082SeqList_PF59082.txt

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Cys Leu Gly Ala Val Cys Pro Pro Ala Thr Pro Ala Gln Tyr Ala Val				
145	150	155		
ttc ttc att ggt ctc tat ctg att gcg ctt ggg act ggt ggt att aaa				528
Phe Phe Ile Gly Leu Tyr Leu Ile Ala Leu Gly Thr Gly Gly Ile Lys				
165	170	175		
cca tgt gtg tct tct ttt ggg gca gac cag ttt gat gat act gat tcg				576
Pro Cys Val Ser Ser Phe Gly Ala Asp Gln Phe Asp Asp Thr Asp Ser				
180	185	190		
cgg gaa agg gtt aag aag gga tcg ttt ttc aac tgg ttt tac ttt tct				624
Arg Glu Arg Val Lys Lys Gly Ser Phe Phe Asn Trp Phe Tyr Phe Ser				
195	200	205		
atc aac ata gga gcc ctc ata tca agc agt ttt att gtg tgg att caa				672
Ile Asn Ile Gly Ala Leu Ile Ser Ser Ser Phe Ile Val Trp Ile Gln				
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gaa aat gca ggc tgg ggt ctt gga ttt gga att cct gct tta ttt atg				720
Glu Asn Ala Gly Trp Gly Leu Gly Phe Gly Ile Pro Ala Leu Phe Met				
225	230	235		
gga tta gct atc gga agc ttc ttt tta ggc aca ccc cta tat agg ttt				768
Gly Leu Ala Ile Gly Ser Phe Phe Leu Gly Thr Pro Leu Tyr Arg Phe				
245	250	255		
caa aaa cca gga gga agc cct ctt aca aga atg tgc cag gtt gtg gct				816
Gln Lys Pro Gly Gly Ser Pro Leu Thr Arg Met Cys Gln Val Val Ala				
260	265	270		
gca tct ttt cgg aaa cgg aat ctt act gtt cct gaa gat agt agt ctc				864
Ala Ser Phe Arg Lys Arg Asn Leu Thr Val Pro Glu Asp Ser Ser Leu				
275	280	285		
ctc tat gag aca cca gac aag agc tct gca att gaa gga agt cgg aaa				912
Leu Tyr Glu Thr Pro Asp Lys Ser Ser Ala Ile Glu Gly Ser Arg Lys				
290	295	300		
cta cag cat agc gat gaa tta agg tgt ctt gac aga gca gct gta atc				960
Leu Gln His Ser Asp Glu Leu Arg Cys Leu Asp Arg Ala Ala Val Ile				
305	310	315		
tct gat gat gaa agg aaa aga ggt gac tat tct aat ttg tgg aga ctt				1008
Ser Asp Asp Glu Arg Lys Arg Gly Asp Tyr Ser Asn Leu Trp Arg Leu				
325	330	335		
tgc act gtg aca cag gtg gag gaa tta aaa atc ttg atc cgc atg ttt				1056
Cys Thr Val Gln Val Glu Glu Leu Lys Ile Leu Ile Arg Met Phe				
340	345	350		
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Ser Thr Met Phe Val Glu Gly Thr Met Met Asp Thr Ser Val Gly				
370	375	380		
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Ser Phe Lys Ile Pro Ala Ala Ser Leu Ser Thr Phe Asp Val Ile Ser				
385	390	395		
ggt att ttc tgg gtc cct gtc tat gac agg ttt ata gtt ccc att gca				1248
Val Ile Phe Trp Val Pro Val Tyr Asp Arg Phe Ile Val Pro Ile Ala				
405	410	415		
agg aaa ttt act ggc aaa gaa agg gga ttt tca gag ttg caa aga atg				1296
Arg Lys Phe Thr Gly Lys Glu Arg Gly Phe Ser Glu Leu Gln Arg Met				
420	425	430		
gga att ggt ctt ttt att tca gtc ytg tgc atg tca gct gct gct att				1344
Gly Ile Gly Leu Phe Ile Ser Val Leu Cys Met Ser Ala Ala Ala Ile				
435	440	445		
gtc gag att aag cgt ctg cag ctt gcc aaa gag ctt gac ctt gtt gat				1392
Val Glu Ile Lys Arg Leu Gln Leu Ala Lys Glu Leu Asp Leu Val Asp				
450	455	460		
aaa gct gtc ccc gta cca ctt act ata ttt ttg caa atc ccc cag tat				1440
Lys Ala Val Pro Val Pro Leu Thr Ile Phe Leu Gln Ile Pro Gln Tyr				
465	470	475		
ttc tta ttg gga gca gca gaa gta ttc aca ttt gtg ggg cag ctt gag				1488
Phe Leu Leu Gly Ala Ala Glu Val Phe Thr Phe Val Gly Gln Leu Glu				
485	490	495		
ttc ttc tat gac caa tct cca gat gct atg cga agt tta tgc agt gct				1536
Phe Phe Tyr Asp Gln Ser Pro Asp Ala Met Arg Ser Leu Cys Ser Ala				

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Leu	Thr	Val	Val	Leu	Tyr	Phe	Thr	Thr	Arg	Gly	Gly	Asn	Pro	Gly	Trp	
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Ile	Pro	Asp	Asn	Leu	Asn	Lys	Gly	His	Leu	Asp	Tyr	Phe	Ser	Gly	Leu	
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gct	gga	ctc	agc	ttc	tta	aat	atg	ttt	ctg	tac	ata	gtt	gct	gcc	aaa	1728
Ala	Gly	Leu	Ser	Phe	Leu	Asn	Met	Phe	Leu	Tyr	Ile	Val	Ala	Ala	Lys	
				565					570					575		
aga	tac	aag	tca	aag	aag	gct	tcg	taa								1755
Arg	Tyr	Lys	Ser	Lys	Lys	Ala	Ser									
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<400> 311

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Lys	Gly	Arg	Pro	Val	Leu	Lys	Lys	Asn	Thr	Gly	Asn	Trp	Lys	Ala	Cys	
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Pro	Phe	Ile	Leu	Gly	Asn	Glu	Cys	Cys	Glu	Arg	Leu	Ala	Tyr	Tyr	Gly	
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Ile	Ala	Thr	Asn	Leu	Val	Lys	Pro	Ile	Leu	Leu	Ala	Lys	Leu	His	Glu	
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Gly	Asn	Val	Ser	Ala	Arg	Asn	Val	Thr	Thr	Trp	Gln	Gly	Thr	Cys		
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Tyr	Leu	Ala	Pro	Leu	Ile	Gly	Ala	Val	Leu	Ala	Asp	Ser	Tyr	Trp	Gly	
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Arg	Tyr	Trp	Thr	Ile	Ala	Ile	Phe	Ser	Met	Ile	Tyr	Phe	Ile	Gly	Met	
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Phe	Phe	Ile	Gly	Leu	Tyr	Leu	Ile	Ala	Leu	Gly	Thr	Gly	Gly	Ile	Lys	
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Pro	Cys	Val	Ser	Ser	Phe	Gly	Ala	Asp	Gln	Phe	Asp	Asp	Thr	Asp	Ser	
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Arg	Glu	Arg	Val	Lys	Lys	Gly	Ser	Phe	Phe	Asn	Trp	Phe	Tyr	Phe	Ser	
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Ile	Asn	Ile	Gly	Ala	Leu	Ile	Ser	Ser	Ser	Phe	Ile	Val	Trp	Ile	Gln	
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Glu	Asn	Ala	Gly	Trp	Gly	Leu	Gly	Phe	Gly	Ile	Pro	Ala	Leu	Phe	Met	
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Gly	Leu	Ala	Ile	Gly	Ser	Phe	Phe	Leu	Gly	Thr	Pro	Leu	Tyr	Arg	Phe	
			245					250					255			
Gln	Lys	Pro	Gly	Gly	Ser	Pro	Leu	Thr	Arg	Met	Cys	Gln	Val	Val	Ala	
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Ala	Ser	Phe	Arg	Lys	Arg	Asn	Leu	Thr	Val	Pro	Glu	Asp	Ser	Ser	Leu	
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Leu	Tyr	Glu	Thr	Pro	Asp	Lys	Ser	Ser	Ala	Ile	Glu	Gly	Ser	Arg	Lys	
	290					295					300					
Leu	Gln	His	Ser	Asp	Glu	Leu	Arg	Cys	Leu	Asp	Arg	Ala	Ala	Val	Ile	
305					310					315					320	
Ser	Asp	Asp	Glu	Arg	Lys	Arg	Gly	Asp	Tyr	Ser	Asn	Leu	Trp	Arg	Leu	
			325					330						335		
Cys	Thr	Val	Thr	Gln	Val	Glu	Glu	Leu	Lys	Ile	Leu	Ile	Arg	Met	Phe	
			340					345					350			
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PF59082SeqList_PF59082.txt

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 385 390 395 400
 Val Ile Phe Trp Val Pro Val Tyr Asp Arg Phe Ile Val Pro Ile Ala
 405 410 415
 Arg Lys Phe Thr Gly Lys Glu Arg Gly Phe Ser Glu Leu Gln Arg Met
 420 425 430
 Gly Ile Gly Leu Phe Ile Ser Val Leu Cys Met Ser Ala Ala Ala Ile
 435 440 445
 Val Glu Ile Lys Arg Leu Gln Leu Ala Lys Glu Leu Asp Leu Val Asp
 450 455 460
 Lys Ala Val Pro Val Pro Leu Thr Ile Phe Leu Gln Ile Pro Gln Tyr
 465 470 475 480
 Phe Leu Leu Gly Ala Ala Glu Val Phe Thr Phe Val Gly Gln Leu Glu
 485 490 495
 Phe Phe Tyr Asp Gln Ser Pro Asp Ala Met Arg Ser Leu Cys Ser Ala
 500 505 510
 Leu Ser Leu Leu Thr Thr Ser Leu Gly Asn Tyr Leu Ser Ser Phe Ile
 515 520 525
 Leu Thr Val Val Leu Tyr Phe Thr Thr Arg Gly Gly Asn Pro Gly Trp
 530 535 540
 Ile Pro Asp Asn Leu Asn Lys Gly His Leu Asp Tyr Phe Ser Gly Leu
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 Arg Tyr Lys Ser Lys Lys Ala Ser
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 Asp Ala Trp Asp Phe Lys Gly Arg Pro Ala Glu Arg Ser Lys Thr Gly
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 ggc tgg acg gcg gcc gcc atg att cta ggt gga gag gct tgt gag agg 144
 Gly Trp Thr Ala Ala Ala Met Ile Leu Gly Gly Glu Ala Cys Glu Arg
 35 40 45
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 Leu Thr Thr Leu Gly Ile Ala Val Asn Leu Val Thr Tyr Leu Thr Gly
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 acc atg cac ttg ggc aat gct acc tct gct aat acc gtc acc aat ttt 240
 Thr Met His Leu Gly Asn Ala Thr Ser Ala Asn Thr Val Thr Asn Phe
 65 70 75 80
 ctt ggt act tcc ttc atg ctc tgc ttg ctc ggc ggt ttt gtg gcc gat 288
 Leu Gly Thr Ser Phe Met Leu Cys Leu Leu Gly Gly Phe Val Ala Asp
 85 90 95
 acc ttt ctt ggc aga tac cta acc atc gct ata ttt gcc acc ttc caa 336
 Thr Phe Leu Gly Arg Tyr Leu Thr Ile Ala Ile Phe Ala Thr Phe Gln
 100 105 110
 gca atg ggt gtg aca ata ttg aca atc tca acc aca atc ccc agc ctc 384
 Ala Met Gly Val Thr Ile Leu Thr Ile Ser Thr Thr Ile Pro Ser Leu
 115 120 125
 cga ccc cca aaa tgc acc tcc gac acc agc aca cct tgc atc ccg gca 432
 Arg Pro Pro Lys Cys Thr Ser Asp Thr Ser Thr Pro Cys Ile Pro Ala
 130 135 140
 agc ggc aag caa ctc atg gtt ctc tac ata gcc ctc tac ctg aca gcc 480
 Ser Gly Lys Gln Leu Met Val Leu Tyr Ile Ala Leu Tyr Leu Thr Ala
 145 150 155 160

PF59082SeqList_PF59082.txt

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			165						170					175		
caa	ttt	gat	gag	tca	gac	aaa	caa	gaa	aga	aga	caa	atg	aca	aac	ttc	576
Gln	Phe	Asp	Glu	Ser	Asp	Lys	Gln	Glu	Arg	Arg	Gln	Met	Thr	Asn	Phe	
			180					185					190			
ttc	aac	tgg	ttc	ttc	ttc	ttc	ata	agc	ata	ggc	tca	ctt	gcc	gca	gtc	624
Phe	Asn	Trp	Phe	Phe	Phe	Phe	Ile	Ser	Ile	Gly	Ser	Leu	Ala	Ala	Val	
		195					200					205				
acc	ggt	ctt	gtc	tac	ata	caa	gac	aac	ttg	ggg	agg	caa	tgg	ggc	tat	672
Thr	Val	Leu	Val	Tyr	Ile	Gln	Asp	Asn	Leu	Gly	Arg	Gln	Trp	Gly	Tyr	
	210					215					220					
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Gly	Ile	Cys	Val	Cys	Ala	Ile	Val	Leu	Gly	Leu	Ile	Val	Phe	Leu	Ser	
225					230				235						240	
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Gly	Thr	Arg	Arg	Tyr	Arg	Phe	Lys	Lys	Leu	Val	Gly	Ser	Pro	Leu	Thr	
			245						250					255		
cag	ata	tcg	ggg	gtg	tgt	gtg	gcg	gcg	tgg	agg	aag	agg	aac	atg	gag	816
Gln	Ile	Ser	Gly	Val	Cys	Val	Ala	Ala	Trp	Arg	Lys	Arg	Asn	Met	Glu	
			260				265						270			
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Leu	Pro	Ser	Asp	Met	Ser	Phe	Leu	Tyr	Asn	Val	Asp	Asp	Ile	Asp	Asp	
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gga	ctc	aag	aag	aag	aag	aag	cag	aag	ttg	cct	cat	agc	aag	cag	ttc	912
Gly	Leu	Lys	Lys	Lys	Lys	Lys	Gln	Lys	Leu	Pro	His	Ser	Lys	Gln	Phe	
	290					295					300					
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Arg	Phe	Leu	Asp	Lys	Ala	Ala	Ile	Lys	Glu	Pro	Lys	Thr	Thr	Ser	Gly	
305					310					315					320	
aca	gcc	atg	atc	ata	aac	aag	tgg	agc	tta	tca	acc	cta	acc	gat	ggt	1008
Thr	Ala	Met	Ile	Ile	Asn	Lys	Trp	Ser	Leu	Ser	Thr	Leu	Thr	Asp	Val	
			325						330					335		
gag	gaa	gta	aaa	ttg	att	atc	aga	atg	ttg	cca	att	tgg	gcc	acc	aca	1056
Glu	Glu	Val	Lys	Leu	Ile	Ile	Arg	Met	Leu	Pro	Ile	Trp	Ala	Thr	Thr	
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Ile	Met	Phe	Trp	Thr	Val	Tyr	Ala	Gln	Met	Thr	Thr	Phe	Ser	Val	Ser	
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Gln	Ala	Thr	Ser	Met	Asp	Arg	His	Ile	Gly	Lys	Ser	Phe	Gln	Ile	Pro	
	370					375					380					
cct	gcc	tct	ctc	aca	gct	ttc	ttt	gta	ggc	agc	att	ctc	ttg	aca	gtc	1200
Pro	Ala	Ser	Leu	Thr	Ala	Phe	Phe	Val	Gly	Ser	Ile	Leu	Leu	Thr	Val	
385					390					395					400	
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Pro	Val	Tyr	Asp	Arg	Leu	Ile	Val	Pro	Met	Ala	Arg	Lys	Ala	Leu	Glu	
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aac	cca	caa	ggt	cta	acc	cca	ttg	caa	cgc	atg	ggg	ggt	ggc	cta	ggt	1296
Asn	Pro	Gln	Gly	Leu	Thr	Pro	Leu	Gln	Arg	Met	Gly	Val	Gly	Leu	Val	
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ttc	tca	atc	ttt	gca	atg	gta	gca	gca	gct	ctc	aca	gaa	gtc	aag	cgc	1344
Phe	Ser	Ile	Phe	Ala	Met	Val	Ala	Ala	Ala	Leu	Thr	Glu	Val	Lys	Arg	
		435				440						445				
ttg	aac	atc	gca	cga	tca	cat	ggc	ttg	acc	gac	aat	cca	acg	gct	gag	1392
Leu	Asn	Ile	Ala	Arg	Ser	His	Gly	Leu	Thr	Asp	Asn	Pro	Thr	Ala	Glu	
	450					455					460					
atc	cca	ctg	agt	ggt	ttc	tgg	ctg	gtc	cca	cag	ttt	ttc	ttt	gtg	ggg	1440
Ile	Pro	Leu	Ser	Val	Phe	Trp	Leu	Val	Pro	Gln	Phe	Phe	Phe	Val	Gly	
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tcc	ggg	gag	gcc	ttc	aca	tat	att	ggg	cag	ctt	gac	ttc	ttc	ctc	agg	1488
Ser	Gly	Glu	Ala	Phe	Thr	Tyr	Ile	Gly	Gln	Leu	Asp	Phe	Phe	Leu	Arg	
			485					490						495		
gag	tgc	cct	aag	ggg	atg	aag	acc	atg	agc	aca	ggc	ttg	ttc	ttg	agc	1536
Glu	Cys	Pro	Lys	Gly	Met	Lys	Thr	Met	Ser	Thr	Gly	Leu	Phe	Leu	Ser	
			500					505					510			
act	ctt	tca	ttg	ggg	ttc	ttc	ttt	agc	tct	cta	ttg	gtc	act	att	gtg	1584
Thr	Leu	Ser	Leu	Gly	Phe	Phe	Phe	Ser	Ser	Leu	Leu	Val	Thr	Ile	Val	
		515					520					525				

PF59082SeqList_PF59082.txt

cat	aag	act	aca	ggg	cac	aat	aag	cca	tgg	ctg	gca	gac	aat	ctc	aac	1632
His	Lys	Thr	Thr	Gly	His	Asn	Lys	Pro	Trp	Leu	Ala	Asp	Asn	Leu	Asn	
	530					535					540					
caa	ggg	aag	ctt	tat	gat	ttc	tat	tgg	ctt	ttg	gca	ctt	ctg	agt	gct	1680
Gln	Gly	Lys	Leu	Tyr	Asp	Phe	Tyr	Trp	Leu	Leu	Ala	Leu	Leu	Ser	Ala	
	545				550					555					560	
ttg	aat	ttg	gtg	atc	tat	ttg	ttt	tgt	gcc	aat	tgg	tat	gtt	tac	aag	1728
Leu	Asn	Leu	Val	Ile	Tyr	Leu	Phe	Cys	Ala	Asn	Trp	Tyr	Val	Tyr	Lys	
				565					570					575		
gac	aag	agg	ctt	gct	gag	gag	ggc	ata	gaa	ttg	gag	gaa	cca	gag	att	1776
Asp	Lys	Arg	Leu	Ala	Glu	Glu	Gly	Ile	Glu	Leu	Glu	Glu	Pro	Glu	Ile	
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tgt	gcc	cat	gca	taa												1791
Cys	Ala	His	Ala													
		595														

<210> 313

<211> 596

<212> PRT

<213> Prunus persica

<400> 313

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			20					25					30			
Gly	Trp	Thr	Ala	Ala	Ala	Met	Ile	Leu	Gly	Gly	Glu	Ala	Cys	Glu	Arg	
		35					40					45				
Leu	Thr	Thr	Leu	Gly	Ile	Ala	Val	Asn	Leu	Val	Thr	Tyr	Leu	Thr	Gly	
		50				55					60					
Thr	Met	His	Leu	Gly	Asn	Ala	Thr	Ser	Ala	Asn	Thr	Val	Thr	Asn	Phe	
65					70					75					80	
Leu	Gly	Thr	Ser	Phe	Met	Leu	Cys	Leu	Leu	Gly	Gly	Phe	Val	Ala	Asp	
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Thr	Phe	Leu	Gly	Arg	Tyr	Leu	Thr	Ile	Ala	Ile	Phe	Ala	Thr	Phe	Gln	
			100					105					110			
Ala	Met	Gly	Val	Thr	Ile	Leu	Thr	Ile	Ser	Thr	Thr	Ile	Pro	Ser	Leu	
		115					120					125				
Arg	Pro	Pro	Lys	Cys	Thr	Ser	Asp	Thr	Ser	Thr	Pro	Cys	Ile	Pro	Ala	
		130				135					140					
Ser	Gly	Lys	Gln	Leu	Met	Val	Leu	Tyr	Ile	Ala	Leu	Tyr	Leu	Thr	Ala	
145					150					155					160	
Leu	Gly	Thr	Gly	Gly	Leu	Lys	Ser	Ser	Val	Ser	Gly	Phe	Gly	Ser	Asp	
				165					170					175		
Gln	Phe	Asp	Glu	Ser	Asp	Lys	Gln	Glu	Arg	Arg	Gln	Met	Thr	Asn	Phe	
			180					185					190			
Phe	Asn	Trp	Phe	Phe	Phe	Phe	Ile	Ser	Ile	Gly	Ser	Leu	Ala	Ala	Val	
		195					200					205				
Thr	Val	Leu	Val	Tyr	Ile	Gln	Asp	Asn	Leu	Gly	Arg	Gln	Trp	Gly	Tyr	
		210				215					220					
Gly	Ile	Cys	Val	Cys	Ala	Ile	Val	Leu	Gly	Leu	Ile	Val	Phe	Leu	Ser	
225					230					235					240	
Gly	Thr	Arg	Arg	Tyr	Arg	Phe	Lys	Lys	Leu	Val	Gly	Ser	Pro	Leu	Thr	
				245					250					255		
Gln	Ile	Ser	Gly	Val	Cys	Val	Ala	Ala	Trp	Arg	Lys	Arg	Asn	Met	Glu	
			260					265					270			
Leu	Pro	Ser	Asp	Met	Ser	Phe	Leu	Tyr	Asn	Val	Asp	Asp	Ile	Asp	Asp	
		275					280					285				
Gly	Leu	Lys	Lys	Lys	Lys	Lys	Gln	Lys	Leu	Pro	His	Ser	Lys	Gln	Phe	
		290				295					300					
Arg	Phe	Leu	Asp	Lys	Ala	Ala	Ile	Lys	Glu	Pro	Lys	Thr	Thr	Ser	Gly	
305					310					315					320	
Thr	Ala	Met	Ile	Ile	Asn	Lys	Trp	Ser	Leu	Ser	Thr	Leu	Thr	Asp	Val	
				325					330					335		
Glu	Glu	Val	Lys	Leu	Ile	Ile	Arg	Met	Leu	Pro	Ile	Trp	Ala	Thr	Thr	
			340					345					350			
Ile	Met	Phe	Trp	Thr	Val	Tyr	Ala	Gln	Met	Thr	Thr	Phe	Ser	Val	Ser	
		355					360					365				
Gln	Ala	Thr	Ser	Met	Asp	Arg	His	Ile	Gly	Lys	Ser	Phe	Gln	Ile	Pro	

PF59082SeqList_PF59082.txt

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370          375          380
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385          390          400
Pro Val Tyr Asp Arg Leu Ile Val Pro Met Ala Arg Lys Ala Leu Glu
          405          410
Asn Pro Gln Gly Leu Thr Pro Leu Gln Arg Met Gly Val Gly Leu Val
          420          425          430
Phe Ser Ile Phe Ala Met Val Ala Ala Ala Leu Thr Glu Val Lys Arg
          435          440          445
Leu Asn Ile Ala Arg Ser His Gly Leu Thr Asp Asn Pro Thr Ala Glu
          450          455          460
Ile Pro Leu Ser Val Phe Trp Leu Val Pro Gln Phe Phe Phe Val Gly
465          470          475          480
Ser Gly Glu Ala Phe Thr Tyr Ile Gly Gln Leu Asp Phe Phe Leu Arg
          485          490          495
Glu Cys Pro Lys Gly Met Lys Thr Met Ser Thr Gly Leu Phe Leu Ser
          500          505          510
Thr Leu Ser Leu Gly Phe Phe Phe Ser Ser Leu Leu Val Thr Ile Val
          515          520          525
His Lys Thr Thr Gly His Asn Lys Pro Trp Leu Ala Asp Asn Leu Asn
          530          535          540
Gln Gly Lys Leu Tyr Asp Phe Tyr Trp Leu Leu Ala Leu Leu Ser Ala
545          550          555          560
Leu Asn Leu Val Ile Tyr Leu Phe Cys Ala Asn Trp Tyr Val Tyr Lys
          565          570          575
Asp Lys Arg Leu Ala Glu Glu Gly Ile Glu Leu Glu Glu Pro Glu Ile
          580          585          590
Cys Ala His Ala
          595

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<210> 314
 <211> 1752
 <212> DNA
 <213> Alnus glutinosa

<220>
 <221> CDS
 <222> (1)..(1752)

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<400> 314
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aag ggt gac cct gcc gat agg aac aca acg ggt ggt tgg gtg ccg gcg      96
Lys Gly Asp Pro Ala Asp Arg Asn Thr Gly Gly Trp Val Pro Ala
          20          25          30
gct cta atc gta ggt att gaa gta agc gag aga ctg tca aca atg gga      144
Ala Leu Ile Val Gly Ile Glu Val Ser Glu Arg Leu Ser Thr Met Gly
          35          40          45
ata att gtg aac ctt gtg acg tat cta aaa ggc aca atg cat cag tct      192
Ile Ile Val Asn Leu Val Thr Tyr Leu Lys Gly Thr Met His Gln Ser
          50          55          60
agt aca acc tcc tca aac agc aca tca aat gta gca ggc aca tca ttt      240
Ser Thr Thr Ser Ser Asn Ser Thr Ser Asn Val Ala Gly Thr Ser Phe
          65          70          75          80
ctt ctg tgt ttg ctt gga ggg att ctc gcc gat tct ttc ctt ggc cga      288
Leu Leu Cys Leu Leu Gly Gly Ile Leu Ala Asp Ser Phe Leu Gly Arg
          85          90          95
tat tgg aca atc gcc att ttc tct gta att cat gca ctg ggg aca tgc      336
Tyr Trp Thr Ile Ala Ile Phe Ser Val Ile His Ala Leu Gly Thr Cys
          100          105          110
atg ctg gct ata tcg gca gca ctg cca gaa cta cgc cct tct gaa tgc      384
Met Leu Ala Ile Ser Ala Ala Leu Pro Glu Leu Arg Pro Ser Glu Cys
          115          120          125
aac ctg cat cat gat ttt cct ctc aaa tgt gaa gag ccc agc agc ttc      432
Asn Leu His His Asp Phe Pro Leu Lys Cys Glu Glu Pro Ser Ser Phe
          130          135          140
caa atg ggc att ttg tat act gct ctc tac tca atg gct cta gga gtc      480
Gln Met Gly Ile Leu Tyr Thr Ala Leu Tyr Ser Met Ala Leu Gly Val

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PF59082SeqList_PF59082.txt

145	ggc	ggg	ata	aag	tct	agt	gtt	tca	ggg	ttt	gga	aca	gag	cag	ttt	gat	528
	Gly	Gly	Ile	Lys	Ser	Ser	Val	Ser	Gly	Phe	Gly	Thr	Glu	Gln	Phe	Asp	
					165					170					175		
	caa	aac	gat	gag	aaa	gaa	atg	tct	gaa	atg	gcc	cat	ttc	ttc	aac	agg	576
	Gln	Asn	Asp	Glu	Lys	Glu	Met	Ser	Glu	Met	Ala	His	Phe	Phe	Asn	Arg	
				180					185					190			
	ttt	tac	ctc	atc	atc	agc	ttc	gga	acc	cta	cta	gcc	gtt	acc	gtg	ctt	624
	Phe	Tyr	Leu	Ile	Ile	Ser	Phe	Gly	Thr	Leu	Leu	Ala	Val	Thr	Val	Leu	
			195					200					205				
	gtt	tat	gta	caa	gac	caa	gtg	gga	cgg	agc	tgg	gga	tat	ggg	att	tgc	672
	Val	Tyr	Val	Gln	Asp	Gln	Val	Gly	Arg	Ser	Trp	Gly	Tyr	Gly	Ile	Cys	
		210					215					220					
	tcg	gcc	tcc	atg	ttt	ctt	tca	ata	gtt	gcc	ttc	ctt	gtc	ggg	act	aaa	720
	Ser	Ala	Ser	Met	Phe	Leu	Ser	Ile	Val	Ala	Phe	Leu	Val	Gly	Thr	Lys	
	225					230					235					240	
	aga	tat	agg	tac	agg	gag	tgt	acc	gga	agc	cct	atc	att	caa	att	cta	768
	Arg	Tyr	Arg	Tyr	Arg	Glu	Cys	Thr	Gly	Ser	Pro	Ile	Ile	Gln	Ile	Leu	
				245					250					255			
	cag	gtt	ata	gtg	gct	gct	ata	agg	aaa	agg	aag	gcc	gag	ctt	cca	act	816
	Gln	Val	Ile	Val	Ala	Ala	Ile	Arg	Lys	Arg	Lys	Ala	Glu	Leu	Pro	Thr	
				260					265					270			
	gat	ctt	agc	ttc	tta	tac	gac	aaa	gct	tct	gat	aag	gaa	tca	acg	atc	864
	Asp	Leu	Ser	Phe	Leu	Tyr	Asp	Lys	Ala	Ser	Asp	Lys	Glu	Ser	Thr	Ile	
			275					280					285				
	tct	cat	aca	gat	aaa	tat	agt	tgt	ttg	gac	aag	ggg	gca	atc	ata	acc	912
	Ser	His	Thr	Asp	Lys	Tyr	Ser	Cys	Leu	Asp	Lys	Gly	Ala	Ile	Ile	Thr	
		290					295					300					
	gga	atg	gac	cgt	gga	gct	gat	ggg	tta	acg	att	tcc	aat	cca	tgg	gga	960
	Gly	Met	Asp	Arg	Gly	Ala	Asp	Gly	Leu	Thr	Ile	Ser	Asn	Pro	Trp	Gly	
	305					310					315					320	
	ctt	tgt	aca	gtc	acc	gag	gtg	gaa	gaa	gta	aaa	atg	ttg	atc	aga	ata	1008
	Leu	Cys	Thr	Val	Thr	Glu	Val	Glu	Glu	Val	Lys	Met	Leu	Ile	Arg	Ile	
				325					330						335		
	ttg	cca	ata	atg	gct	tca	acg	ata	atc	ttt	tgg	aca	ata	cgt	gca	cag	1056
	Leu	Pro	Ile	Met	Ala	Ser	Thr	Ile	Ile	Phe	Trp	Thr	Ile	Arg	Ala	Gln	
				340					345					350			
	ctg	cta	agc	ttc	tca	gtg	caa	caa	gct	gcc	acc	atg	gag	aga	aca	atc	1104
	Leu	Leu	Ser	Phe	Ser	Val	Gln	Gln	Ala	Ala	Thr	Met	Glu	Arg	Thr	Ile	
			355				360						365				
	gaa	aat	ttc	cca	atc	cca	cca	gct	tca	ttc	aac	ggc	ttc	ttc	gtg	gga	1152
	Glu	Asn	Phe	Pro	Ile	Pro	Pro	Ala	Ser	Phe	Asn	Gly	Phe	Phe	Val	Gly	
		370				375						380					
	tcc	aca	att	atc	act	ctc	atc	atg	tat	gac	cgc	cta	ctg	cct	ttc	ttg	1200
	Ser	Thr	Ile	Ile	Thr	Leu	Ile	Met	Tyr	Asp	Arg	Leu	Leu	Pro	Phe	Leu	
	385					390				395						400	
	aga	caa	tca	tcc	aat	ggg	gtt	caa	ggg	ttc	aca	aat	ttg	caa	aaa	ata	1248
	Arg	Gln	Ser	Ser	Asn	Gly	Val	Gln	Gly	Phe	Thr	Asn	Leu	Gln	Lys	Ile	
				405					410						415		
	ggg	ata	gca	ata	ttc	tta	agc	att	tta	gga	atg	gca	gct	gca	tca	ttt	1296
	Gly	Ile	Ala	Ile	Phe	Leu	Ser	Ile	Leu	Gly	Met	Ala	Ala	Ala	Ser	Phe	
				420					425					430			
	gcg	gaa	atg	aaa	cga	tta	gaa	gtt	gtt	aga	gcc	aat	aga	ggg	agc	aca	1344
	Ala	Glu	Met	Lys	Arg	Leu	Glu	Val	Val	Arg	Ala	Asn	Arg	Gly	Ser	Thr	
			435				440						445				
	agc	acc	tca	agt	act	cta	cca	ata	act	gcc	ttc	tac	ttg	ctt	cca	caa	1392
	Ser	Thr	Ser	Ser	Thr	Leu	Pro	Ile	Thr	Ala	Phe	Tyr	Leu	Leu	Pro	Gln	
		450				455						460					
	ttc	gtc	ttg	gtc	ggg	atc	ggg	gac	ggg	ttt	atg	tat	act	ggg	cag	ctt	1440
	Phe	Val	Leu	Val	Gly	Ile	Gly	Asp	Gly	Phe	Met	Tyr	Thr	Gly	Gln	Leu	
	465				470					475						480	
	gat	ttc	ttc	ata	acc	gag	tca	ccc	aaa	ggg	atg	aaa	gca	att	agc	acc	1488
	Asp	Phe	Phe	Ile	Thr	Glu	Ser	Pro	Lys	Gly	Met	Lys	Ala	Ile	Ser	Thr	
				485						490					495		
	ggc	ctg	ttc	ctc	aca	acc	aac	gcc	ctt	ggg	ttc	ttt	gga	agt	agt	att	1536
	Gly	Leu	Phe	Leu	Thr	Thr	Asn	Ala	Leu	Gly	Phe	Phe	Gly	Ser	Ser	Ile	
				500					505					510			
	ttg	gtc	aca	atc	ata	acg	aaa	gtc	aca	ggg	gaa	gag	gtt	ggg	cat	ggt	1584
	Leu	Val	Thr	Ile	Ile	Thr	Lys	Val	Thr	Gly	Glu	Glu	Val	Gly	His	Gly	

PF59082SeqList_PF59082.txt

515	520	525	
ttg cta ctg tcc agg ata aat gat agc aga ttg gat ttt ttc tat gct			1632
Trp Leu Leu Ser Arg Ile Asn Asp Ser Arg Leu Asp Phe Phe Tyr Ala			
530	535	540	
ttg ctg gct gtg cta ggg ttt atc aat ttg gta ttt tat ctg gtc ttg			1680
Leu Leu Ala Val Leu Gly Phe Ile Asn Leu Val Phe Tyr Leu Val Leu			
545	550	555	560
gca tca tgg tat aag cca agt cct gtt gaa gat gct cat cag aag ata			1728
Ala Ser Trp Tyr Lys Pro Ser Pro Val Glu Asp Ala His Gln Lys Ile			
565	570	575	
aat ggt aaa gaa gaa aaa gtg tga			1752
Asn Gly Lys Glu Glu Lys Val			
580			

<210> 315

<211> 583

<212> PRT

<213> Alnus glutinosa

<400> 315

Met Glu Glu Ser Lys Lys Ser Cys Phe Ile Ser Asp Arg Val Asp Tyr	
1 Lys Gly Asp Pro Ala Asp Arg Asn Thr Thr Gly Gly Trp Val Pro Ala	
20 Ala Leu Ile Val Gly Ile Glu Val Ser Glu Arg Leu Ser Thr Met Gly	
35 Ile Ile Val Asn Leu Val Thr Tyr Leu Lys Gly Thr Met His Gln Ser	
50 Ser Thr Thr Ser Ser Asn Ser Thr Ser Asn Val Ala Gly Thr Ser Phe	
65 Leu Leu Cys Leu Leu Gly Gly Ile Leu Ala Asp Ser Phe Leu Gly Arg	
85 Tyr Trp Thr Ile Ala Ile Phe Ser Val Ile His Ala Leu Gly Thr Cys	
100 Met Leu Ala Ile Ser Ala Ala Leu Pro Glu Leu Arg Pro Ser Glu Cys	
115 Asn Leu His His Asp Phe Pro Leu Lys Cys Glu Glu Pro Ser Ser Phe	
130 Gln Met Gly Ile Leu Tyr Thr Ala Leu Tyr Ser Met Ala Leu Gly Val	
145 Gly Gly Ile Lys Ser Ser Val Ser Gly Phe Gly Thr Glu Gln Phe Asp	
165 Gln Asn Asp Glu Lys Glu Met Ser Glu Met Ala His Phe Phe Asn Arg	
180 Phe Tyr Leu Ile Ile Ser Phe Gly Thr Leu Leu Ala Val Thr Val Leu	
195 Val Tyr Val Gln Asp Gln Val Gly Arg Ser Trp Gly Tyr Gly Ile Cys	
210 Ser Ala Ser Met Phe Leu Ser Ile Val Ala Phe Leu Val Gly Thr Lys	
225 Arg Tyr Arg Tyr Arg Glu Cys Thr Gly Ser Pro Ile Ile Gln Ile Leu	
245 Gln Val Ile Val Ala Ala Ile Arg Lys Arg Lys Ala Glu Leu Pro Thr	
260 Asp Leu Ser Phe Leu Tyr Asp Lys Ala Ser Asp Lys Glu Ser Thr Ile	
275 Ser His Thr Asp Lys Tyr Ser Cys Leu Asp Lys Gly Ala Ile Ile Thr	
290 Gly Met Asp Arg Gly Ala Asp Gly Leu Thr Ile Ser Asn Pro Trp Gly	
305 Leu Cys Thr Val Thr Glu Val Glu Glu Val Lys Met Leu Ile Arg Ile	
325 Leu Pro Ile Met Ala Ser Thr Ile Ile Phe Trp Thr Ile Arg Ala Gln	
340 Leu Leu Ser Phe Ser Val Gln Gln Ala Ala Thr Met Glu Arg Thr Ile	
355 Glu Asn Phe Pro Ile Pro Pro Ala Ser Phe Asn Gly Phe Phe Val Gly	
370 Ser Thr Ile Ile Thr Leu Ile Met Tyr Asp Arg Leu Leu Pro Phe Leu	

PF59082SeqList_PF59082.txt

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385          390          395          400
Arg Gln Ser Ser Asn Gly Val Gln Gly Phe Thr Asn Leu Gln Lys Ile
      405
Gly Ile Ala Ile Phe Leu Ser Ile Leu Gly Met Ala Ala Ala Ser Phe
      420
Ala Glu Met Lys Arg Leu Glu Val Val Arg Ala Asn Arg Gly Ser Thr
      435
Ser Thr Ser Ser Thr Leu Pro Ile Thr Ala Phe Tyr Leu Leu Pro Gln
      450
Phe Val Leu Val Gly Ile Gly Asp Gly Phe Met Tyr Thr Gly Gln Leu
      465
Asp Phe Phe Ile Thr Glu Ser Pro Lys Gly Met Lys Ala Ile Ser Thr
      485
Gly Leu Phe Leu Thr Thr Asn Ala Leu Gly Phe Phe Gly Ser Ser Ile
      500
Leu Val Thr Ile Ile Thr Lys Val Thr Gly Glu Glu Val Gly His Gly
      515
Trp Leu Leu Ser Arg Ile Asn Asp Ser Arg Leu Asp Phe Phe Tyr Ala
      530
Leu Leu Ala Val Leu Gly Phe Ile Asn Leu Val Phe Tyr Leu Val Leu
      545
Ala Ser Trp Tyr Lys Pro Ser Pro Val Glu Asp Ala His Gln Lys Ile
      565
Asn Gly Lys Glu Glu Lys Val
      580

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<210> 316

<211> 1785

<212> DNA

<213> Nicotiana tabacum

<220>

<221> CDS

<222> (1)..(1785)

<400> 316

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1      5      10      15
tgg gat tac aaa ggc aga cca gcc ctt aga tcc tcc tct ggt ggt tgg      96
Trp Asp Tyr Lys Gly Arg Pro Ala Leu Arg Ser Ser Ser Gly Gly Trp
20      25      30
gct agt ggt gca atg att tta ggt gtt gaa gct gtg gag agg cta aca      144
Ala Ser Gly Ala Met Ile Leu Gly Val Glu Ala Val Glu Arg Leu Thr
35      40      45
aca cta ggg att gct gta aac tta gtg aca tat ttg act gga act atg      192
Thr Leu Gly Ile Ala Val Asn Leu Val Thr Tyr Leu Thr Gly Thr Met
50      55      60
cat tta ggg aat gct tct tca gcc aac aat gtt acc aat ttt ctt gga      240
His Leu Gly Asn Ala Ser Ala Asn Asn Val Thr Asn Phe Leu Gly
65      70      75      80
act tct ttc atg ctc act tta ctt ggt ggt ttt gtc gcc gac act ttc      288
Thr Ser Phe Met Leu Thr Leu Leu Gly Gly Phe Val Ala Asp Thr Phe
85      90      95
ctc gga agg tat ctt aca att ggt atc ttt gcc act gtt caa gca atg      336
Leu Gly Arg Tyr Leu Thr Ile Gly Ile Phe Ala Thr Val Gln Ala Met
100      105      110
ggg ggt aca atc ttg acc atc tca act ata atc cca agc cta cga cca      384
Gly Val Thr Ile Leu Thr Ile Ser Thr Ile Ile Pro Ser Leu Arg Pro
115      120      125
cca aaa tgt gaa caa gtt ggt agc tca tca tgc atc ccc gca aat agc      432
Pro Lys Cys Glu Gln Val Gly Ser Ser Ser Cys Ile Pro Ala Asn Ser
130      135      140
aaa caa ctc atg gtc cta tat att gcc cta tac atg acg gcc ctc ggc      480
Lys Gln Leu Met Val Tyr Ile Ala Leu Tyr Met Thr Ala Leu Gly
145      150      155      160
acc ggc ggc cta aaa tcg agc gtc tcc ggc ttt ggc acc gac caa ttc      528
Thr Gly Gly Leu Lys Ser Ser Val Ser Gly Phe Gly Thr Asp Gln Phe
165      170      175

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PF59082SeqList_PF59082.txt

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			180					185					190			
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Trp	Phe	Phe	Phe	Phe	Ile	Asn	Val	Gly	Ser	Leu	Gly	Ala	Val	Thr	Val	
		195					200					205				
ttg	ggt	tat	att	caa	gat	aat	ttg	gga	aga	gag	ttg	ggg	tat	gga	ata	672
Leu	Val	Tyr	Ile	Gln	Asp	Asn	Leu	Gly	Arg	Glu	Trp	Gly	Tyr	Gly	Ile	
	210					215					220					
tgt	gca	tgt	gct	att	gtg	att	gca	ctt	ggt	gtg	ttc	tta	ttt	ggg	aca	720
Cys	Ala	Cys	Ala	Ile	Val	Ile	Ala	Leu	Val	Val	Phe	Leu	Phe	Gly	Thr	
225					230				235						240	
agg	aaa	tat	agg	ttc	aag	aaa	ctt	ggg	ggg	agt	cca	ttg	aca	caa	att	768
Arg	Lys	Tyr	Arg	Phe	Lys	Lys	Leu	Gly	Gly	Ser	Pro	Leu	Thr	Gln	Ile	
				245				250						255		
gct	tca	ggt	att	gtg	gct	gct	tgg	aag	aaa	agg	cat	ttg	gaa	tta	ccc	816
Ala	Ser	Val	Ile	Val	Ala	Ala	Trp	Lys	Lys	Arg	His	Leu	Glu	Leu	Pro	
			260				265					270				
tca	gat	tct	tca	ctt	ctc	ttt	gaa	att	gat	gat	att	ttt	ggg	gaa	gga	864
Ser	Asp	Ser	Ser	Leu	Leu	Phe	Glu	Ile	Asp	Asp	Ile	Phe	Gly	Glu	Gly	
		275					280					285				
aat	aaa	aaa	agc	aaa	caa	aag	ttg	ccc	cat	agc	aag	gag	tac	cga	ttc	912
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Thr	Asn	Val	Val	Ile	Asn	Lys	Trp	Lys	Leu	Ala	Thr	Leu	Thr	Asp	Val	
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gaa	gaa	gta	aaa	ata	tta	atc	aga	atg	ttg	cca	act	tgg	gcc	aca	act	1056
Glu	Glu	Val	Lys	Ile	Leu	Ile	Arg	Met	Leu	Pro	Thr	Trp	Ala	Thr	Thr	
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att	atg	ttc	tgg	act	gtc	tat	gca	caa	atg	acc	aca	ttt	tct	gtg	tca	1104
Ile	Met	Phe	Trp	Thr	Val	Tyr	Ala	Gln	Met	Thr	Thr	Phe	Ser	Val	Ser	
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Gln	Ala	Thr	Thr	Met	Asp	Arg	His	Ile	Gly	Thr	Phe	Glu	Ile	Pro	Pro	
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Ala	Thr	Leu	Thr	Val	Phe	Val	Gly	Ser	Ile	Leu	Leu	Thr	Val	Ile	400	
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Phe	Tyr	Asp	Arg	Ile	Ile	Val	Pro	Ile	Cys	Arg	Arg	Phe	Met	Asn	Lys	
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cct	cat	gga	ctt	acc	cca	tta	caa	aga	att	ttc	aca	ggc	cta	ggt	ctt	1296
Pro	His	Gly	Leu	Thr	Pro	Leu	Gln	Arg	Ile	Phe	Thr	Gly	Leu	Val	Leu	
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Ser	Ile	Leu	Ala	Met	Ile	Ala	Ala	Ala	Leu	Thr	Glu	Val	Lys	Arg	Leu	
		435				440					445					
aaa	ggt	gca	cat	ttg	cat	gga	ttg	acc	aat	gat	gca	aat	gcc	acg	att	1392
Lys	Val	Ala	His	Leu	His	Gly	Leu	Thr	Asn	Asp	Ala	Asn	Ala	Thr	Ile	
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cca	ttg	act	gta	ttt	tgg	ttt	ccg	caa	ttc	ttg	cta	gtg	ggc	gca	1440	
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Gly	Glu	Ala	Phe	Thr	Tyr	Ile	Gly	Gln	Leu	Asp	Phe	Phe	Leu	Arg	Glu	
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Cys	Pro	Lys	Gly	Met	Lys	Thr	Met	Ser	Thr	Gly	Leu	Phe	Leu	Ser	Thr	
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Leu	Ala	Leu	Gly	Phe	Phe	Phe	Ser	Ser	Ile	Leu	Val	Thr	Ile	Val	His	
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ggt	gtg	act	ggg	aca	aca	aat	cca	tgg	cta	gct	gat	aat	ttg	aac	caa	1632
Val	Val	Thr	Gly	Thr	Thr	Asn	Pro	Trp	Leu	Ala	Asp	Asn	Leu	Asn	Gln	
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PF59082SeqList_PF59082.txt

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Asn	Leu	Met	Phe	Phe	Leu	Tyr	Ser	Ser	Arg	Lys	Tyr	Val	Tyr	Lys	Glu	
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Lys	Arg	Leu	Ala	Glu	Met	Gly	Ile	Glu	Leu	Glu	Asp	Asp	Gly	Pro	Val	
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Cys	His															

<210> 317
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 <212> PRT
 <213> Nicotiana tabacum

<400> 317

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Ala	Ser	Gly	Ala	Met	Ile	Leu	Gly	Val	Glu	Ala	Val	Glu	Arg	Leu	Thr	
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Thr	Leu	Gly	Ile	Ala	Val	Asn	Leu	Val	Thr	Tyr	Leu	Thr	Gly	Thr	Met	
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Thr	Ser	Phe	Met	Leu	Thr	Leu	Leu	Gly	Gly	Phe	Val	Ala	Asp	Thr	Phe	
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Leu	Gly	Arg	Tyr	Leu	Thr	Ile	Gly	Ile	Phe	Ala	Thr	Val	Gln	Ala	Met	
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Gly	Val	Thr	Ile	Leu	Thr	Ile	Ser	Thr	Ile	Ile	Pro	Ser	Leu	Arg	Pro	
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Cys	Ala	Cys	Ala	Ile	Val	Ile	Ala	Leu	Val	Val	Phe	Leu	Phe	Gly	Thr	
225				230					235					240		
Arg	Lys	Tyr	Arg	Phe	Lys	Lys	Leu	Gly	Gly	Ser	Pro	Leu	Thr	Gln	Ile	
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Ala	Ser	Val	Ile	Val	Ala	Ala	Trp	Lys	Lys	Arg	His	Leu	Glu	Leu	Pro	
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Ser	Asp	Ser	Ser	Leu	Leu	Phe	Glu	Ile	Asp	Asp	Ile	Phe	Gly	Glu	Gly	
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Leu	Asp	Lys	Ala	Ala	Ile	Lys	Glu	Asp	Asp	Asp	Leu	Glu	Ser	Asn	Gly	
305				310					315					320		
Thr	Asn	Val	Val	Ile	Asn	Lys	Trp	Lys	Leu	Ala	Thr	Leu	Thr	Asp	Val	
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Glu	Glu	Val	Lys	Ile	Leu	Ile	Arg	Met	Leu	Pro	Thr	Trp	Ala	Thr	Thr	
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Ile	Met	Phe	Trp	Thr	Val	Tyr	Ala	Gln	Met	Thr	Thr	Phe	Ser	Val	Ser	
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Gln	Ala	Thr	Thr	Met	Asp	Arg	His	Ile	Gly	Thr	Phe	Glu	Ile	Pro	Pro	
	370				375						380					
Ala	Thr	Leu	Thr	Val	Phe	Phe	Val	Gly	Ser	Ile	Leu	Leu	Thr	Val	Ile	
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PF59082SeqList_PF59082.txt

Phe Tyr Asp Arg Ile Ile Val Pro Ile Cys Arg Arg Phe Met Asn Lys
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 Pro His Gly Leu Thr Pro Leu Gln Arg Ile Phe Thr Gly Leu Val Leu
 420 425 430
 Ser Ile Leu Ala Met Ile Ala Ala Leu Thr Glu Val Lys Arg Leu
 435 440 445
 Lys Val Ala His Leu His Gly Leu Thr Asn Asp Ala Asn Ala Thr Ile
 450 455 460
 Pro Leu Thr Val Phe Trp Leu Val Pro Gln Phe Leu Leu Val Gly Ala
 465 470 475 480
 Gly Glu Ala Phe Thr Tyr Ile Gly Gln Leu Asp Phe Phe Leu Arg Glu
 485 490 495
 Cys Pro Lys Gly Met Lys Thr Met Ser Thr Gly Leu Phe Leu Ser Thr
 500 505 510
 Leu Ala Leu Gly Phe Phe Phe Ser Ile Leu Val Thr Ile Val His
 515 520 525
 Val Val Thr Gly Thr Thr Asn Pro Trp Leu Ala Asp Asn Leu Asn Gln
 530 535 540
 Gly Arg Leu Tyr Asp Phe Tyr Trp Leu Leu Ala Ile Leu Ser Val Phe
 545 550 555 560
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 Trp Asp Tyr Lys Gly Arg Pro Ala Leu Arg Ser Ser Ser Gly Gly Trp 20 25 30
 gct agt ggt gca atg att tta ggt gtt gaa gct gtg gag agg cta aca 144
 Ala Ser Gly Ala Met Ile Leu Val Glu Ala Val Glu Arg Leu Thr 35 40 45
 aca cta ggg att gct gta aat ttg gtg aca tat ttg act gga act atg 192
 Thr Leu Gly Ile Ala Val Asn Leu Val Thr Tyr Leu Thr Gly Thr Met 50 55 60
 cat tta ggg aat gct act gca gcc aac aat gtt acc aat ttt ctt gga 240
 His Leu Gly Asn Ala Thr Ala Ala Asn Asn Val Thr Asn Phe Leu Gly 65 70 75 80
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 Thr Ser Phe Met Leu Thr Leu Phe Gly Gly Phe Val Ala Asp Thr Phe 85 90 95
 ctc gga agg tat ctt aca att ggt atc ttt gcc act gtt caa gca atg 336
 Leu Gly Arg Tyr Leu Thr Ile Gly Ile Phe Ala Thr Val Gln Ala Met 100 105 110
 ggt gtt aca atc ttg acc att tcc acc ata atc cca agc cta cgg cca 384
 Gly Val Thr Ile Leu Thr Ile Ser Thr Ile Ile Pro Ser Leu Arg Pro 115 120 125
 cca aaa tgc gaa caa gtt ggt agc tca tca tgc atc ccc gca aat agc 432
 Pro Lys Cys Glu Gln Val Gly Ser Ser Ser Cys Ile Pro Ala Asn Ser 130 135 140
 aaa caa ctt atg gtc cta tac att gcc cta tac atg acg gcg ctc ggc 480
 Lys Gln Leu Met Val Leu Tyr Ile Ala Leu Tyr Met Thr Ala Leu Gly 145 150 155 160
 acc ggc ggc cta aaa tcg agc gtc tcc ggc ttt ggc acc gac caa ttc 528
 Thr Gly Gly Leu Lys Ser Ser Val Ser Gly Phe Gly Thr Asp Gln Phe

PF59082SeqList_PF59082.txt

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tgg Trp	ttc Phe	ttt Phe 195	ttc Phe	ttt Phe	att Ile	aat Asn	gta Val 200	ggc Gly	tcg Ser	ctc Leu	ggt Gly	gct Ala 205	ggt Val	aca Thr	gta Val	624																																																		
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aat Asn	aaa Lys 290	aaa Lys	aac Asn	aag Lys	caa Gln	aag Lys 295	ttg Leu	cct Pro	cat His	agc Ser	aag Lys 300	gaa Glu	tac Tyr	cga Arg	ttc Phe	912																																																		
ttg Leu 305	gac Asp	aag Lys	gca Ala	gca Ala	att Ile 310	aag Lys	gaa Glu	gat Asp	cat His	gat Asp 315	ctt Leu	gaa Glu	tct Ser	aat Asn	ggc Gly 320	960																																																		
act Thr	aac Asn	gtt Val	gta Val	atc Ile 325	aac Asn	aag Lys	ttg Trp	aaa Lys	tta Leu 330	gca Ala	acc Thr	tta Leu	acc Thr	gat Asp 335	gtt Val	1008																																																		
gaa Glu	gaa Glu	gta Val	aaa Lys 340	tta Leu	tta Leu	atc Ile	aga Arg	atg Met 345	tta Leu	cca Pro	act Thr	ttg Trp	gcc Ala 350	aca Thr	act Thr	1056																																																		
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caa Gln	gct Ala 370	aca Thr	aca Thr	atg Met	gat Asp	cgt Arg 375	cac His	att Ile	gga Gly	acc Thr	ttt Phe 380	gaa Glu	att Ile	cca Pro	ccg Pro	1152																																																		
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PF59082SeqList_PF59082.txt

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	Asn Leu Met Phe Phe Leu Tyr Phe Ser Arg Lys Tyr Val Tyr Lys Glu	
565	aag aga ctt gct gaa atg ggg att gaa ttg gaa gat gat gga ccg gtt	1776
	Lys Arg Leu Ala Glu Met Gly Ile Glu Leu Glu Asp Asp Gly Pro Val	
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<210> 319

<211> 594

<212> PRT

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<400> 319

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			20					25					30		
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Thr	Leu	Gly	Ile	Ala	Val	Asn	Leu	Val	Thr	Tyr	Leu	Thr	Gly	Thr	Met
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Pro	Lys	Cys	Glu	Gln	Val	Gly	Ser	Ser	Ser	Cys	Ile	Pro	Ala	Asn	Ser
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Lys	Gln	Leu	Met	Val	Leu	Tyr	Ile	Ala	Leu	Tyr	Met	Thr	Ala	Leu	Gly
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Thr	Gly	Gly	Leu	Lys	Ser	Ser	Val	Ser	Gly	Phe	Gly	Thr	Asp	Gln	Phe
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Arg	Lys	Tyr	Arg	Phe	Lys	Lys	Leu	Val	Gly	Ser	Pro	Leu	Thr	Gln	Ile
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Ser	Asp	Ser	Ser	Leu	Leu	Phe	Glu	Ile	Asp	Asp	Ile	Phe	Gly	Glu	Gly
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Asn	Lys	Lys	Asn	Lys	Gln	Lys	Leu	Pro	His	Ser	Lys	Glu	Tyr	Arg	Phe
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Thr	Asn	Val	Val	Ile	Asn	Lys	Trp	Lys	Leu	Ala	Thr	Leu	Thr	Asp	Val
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Glu	Glu	Val	Lys	Leu	Leu	Ile	Arg	Met	Leu	Pro	Thr	Trp	Ala	Thr	Thr
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Gln	Ala	Thr	Thr	Met	Asp	Arg	His	Ile	Gly	Thr	Phe	Glu	Ile	Pro	Pro
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Ser Ile Leu Ala Met Ile Ala Ala Leu Thr Glu Val Lys Arg Leu
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Lys Val Ala His Leu His Gly Leu Thr Asn Asp Ala Asn Ala Thr Ile
                               450                               455                               460
Pro Leu Ser Val Phe Trp Leu Val Pro Gln Phe Leu Leu Val Gly Ala
465                               470                               475                               480
Gly Glu Ala Phe Thr Tyr Ile Gly Gln Leu Asp Phe Phe Leu Arg Glu
                               485                               490                               495
Cys Pro Lys Gly Met Lys Thr Met Ser Thr Gly Leu Phe Leu Ser Thr
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Val Val Thr Gly Thr Thr Asn Pro Trp Leu Ala Asp Asn Leu Asn Gln
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Gly Arg Leu Tyr Asp Phe Tyr Trp Leu Leu Ala Ile Leu Ser Val Leu
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Asp Glu Glu Lys Asn 20 Glu Lys Glu Glu Met Lys Met Lys Met Lys Met
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aag aga aag ctt ggt ggt gtc aag aca atg cct ttc att ctt gga aat      144
Lys Arg Lys Leu Gly Gly Val Lys Thr Met Pro Phe Ile Leu Gly Asn
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gaa gtg tgc gat aga ttt gca agc tca ggg ttt cat tcc aac att ata      192
Glu Val 50 Cys Asp Arg Phe Ala 55 Ser Ser Gly Phe His 60 Ser Asn Ile Ile
aca tat ttg aca caa gat ctt aac atg cct ctt gtt cct gcc tcc aac      240
Thr Tyr Leu Thr Gln Asp 70 Leu Asn Met Pro Leu Val Pro Ala Ser Asn
65
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Ile Leu Thr Asn Phe 85 Ala Ala Thr Ser 90 Phe Thr Ser Leu Ile Gly
85
gct ctc att gcc gat tcc ttt gct ggt cgc ttc tgg acc atc acc atc      336
Ala Leu Ile 100 Ala Asp Ser Phe Ala Gly Arg Phe Trp Thr Ile Thr Ile
100
gcc tcc atc atc tat gag ctc gga atg gtt acc atc acc att tca gct      384
Ala Ser Ile Ile Tyr Glu Leu Gly Met Val Thr Ile Thr Ile Ser Ala
115
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Ile Leu Pro Ser Leu His 130 Pro Pro Cys Pro 140 Gln Ile Asn Cys
130
acg caa gca tcc ggc acg caa cta atg atc ctt tat ctc gcc cta ctc      480
Thr Gln Ala Ser Gly Thr 150 Gln Leu Met Ile Leu Tyr Leu Ala Leu Leu
145
ctc aca tct ctt ggc gca ggc ggt att cga ccc tgt gtt gtt gca ttt      528
155

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PF59082SeqList_PF59082.txt

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Trp	Asn	Phe	Phe	Asn	Trp	Tyr	Tyr	Phe	Cys	Met	Gly	Met	Ala	Thr	Leu		
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Leu	Tyr	Asp	Arg	Leu	Leu	Val	Pro	Phe	Ala	Lys	Lys	Leu	Thr	His	Asn		
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Asn	Ile	Leu	Ala	Thr	Leu	Val	Ser	Ser	Ile	Val	Glu	Ile	Lys	Arg	Lys		
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Ala	Glu	Val	Phe	Met	Ser	Val	Gly	His	Leu	Glu	Phe	Met	Tyr	Asp	Gln		
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Arg	Gly	Arg	Leu	Glu	Tyr	Tyr	Tyr	Trp	Leu	Val	Ser	Gly	Ile	Gln	Val	
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Met	Asn	Leu	Val	Tyr	Tyr	Val	Ile	Cys	Ala	Trp	Phe	Tyr	Thr	Tyr	Lys	
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<211> 604

<212> PRT

<213> Cucumis sativus

<400> 321

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 420 425 430
 Asn Ile Leu Ala Thr Leu Val Ser Ser Ile Val Glu Ile Lys Arg Lys
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 Lys Val Ala Ala Asn His Gly Leu Leu Asp Asn Pro Thr Ala Thr Ile
 450 455 460
 Pro Phe Ser Val Phe Trp Leu Val Pro Gln Phe Trp Leu His Gly Ile
 465 470 475
 Ala Glu Val Phe Met Ser Val Gly His Leu Glu Phe Met Tyr Asp Gln
 485 490 495
 Ser Pro Glu Ser Leu Arg Ser Thr Ala Thr Ala Leu Tyr Trp Leu Ala
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 Ile Ser Val Gly Asn Tyr Ile Gly Thr Leu Met Val Tyr Leu Val His
 515 520 525
 Lys Tyr Thr Gly Glu Glu His Asn Trp Leu Pro Asp Arg Asn Leu Asn
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 545 550 555
 Met Asn Leu Val Tyr Tyr Val Ile Cys Ala Trp Phe Tyr Thr Tyr Lys
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 Lys Asn Glu Lys Ser Val Ile Asp Glu Glu Pro Lys Ile Asn Tyr Arg
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 Gly Trp Lys Val Met Pro Phe Ile Ile Gly Asn Glu Thr Phe Glu Lys
 35 40 45
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 Leu Gly Thr Ile Gly Thr Leu Ala Asn Leu Leu Val Tyr Leu Thr Thr
 50 55 60
 gtc ttc aac ttg agc agt ctt aca gct aca aat att att aac atc ttc 240
 Val Phe Asn Leu Ser Ser Leu Thr Ala Thr Asn Ile Ile Asn Ile Phe
 65 70 75 80
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 Thr Gly Ser Ala Ser Leu Ser Thr Leu Leu Gly Ala Phe Leu Cys Asp
 85 90 95
 act tat ttt ggc cgc tac aag aca ctg gga ttc tgc aca att gct tct 336
 Thr Tyr Phe Gly Arg Tyr Lys Thr Leu Gly Phe Cys Thr Ile Ala Ser
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 Phe Leu Gly Leu Leu Val Ile Gln Leu Thr Ala Trp Ile Lys Lys Met
 115 120 125
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 His Pro Pro His Cys Gly Ser Glu Ser Ile Thr Cys Thr Gly Pro Thr
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Ile	Pro	Ala	Ala	Leu	Met	Leu	Ile	Ser	Cys	Thr	Leu	Tyr	Tyr	Thr	Gly	
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Ser	Asn	Tyr	Tyr	Val	Lys	Val	Lys	Ala	Thr	Gly	Pro	Ala	Pro	Leu	Thr	
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Gln	Ser	Ile	Asn	Ser	Lys	Leu	Leu	His	Thr	Ser	Gln	Phe	Arg	Phe	Leu	
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Phe	Tyr	Ile	Ala	Ile	Val	Gln	Gln	Asn	Thr	Met	Leu	Val	Phe	Gln	Ala	
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Ile	Tyr	Asp	Arg	Ile	Leu	Val	Pro	Ser	Leu	Gln	Arg	Val	Thr	Lys	Lys	
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gag	ggt	ggc	atc	aca	ggt	ctt	caa	aga	ata	ggc	ttt	ggc	atg	ttc	ctc	1296
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Thr	Leu	Ala	Leu	Thr	Asn	Pro	Ile	Gly	Leu	Glu	Pro	Arg	Lys	Gly	Ala	
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465					470					475					480	
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Lys	Gln	Phe	Pro	Glu	Asn	Met	Lys	Ser	Leu	Ala	Ala	Ser	Leu	Phe	Phe	
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tgt	ggc	ctc	gcg	gga	tca	agt	tat	ttg	agt	agt	ttg	ctg	att	tct	att	1584
Cys	Gly	Leu	Ala	Gly	Ser	Ser	Tyr	Leu	Ser	Ser	Leu	Leu	Ile	Ser	Ile	
		515					520					525				

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atc	cat	agg	gcg	aca	gct	aaa	tct	tca	act	ggg	aat	tgg	tta	cct	cag	1632
Ile	His	Arg	Ala	Thr	Ala	Lys	Ser	Ser	Thr	Gly	Asn	Trp	Leu	Pro	Gln	
	530					535					540					
gat	ctc	aat	aag	ggg	aga	ttg	gat	tat	ttt	tat	tac	att	ata	act	gct	1680
Asp	Leu	Asn	Lys	Gly	Arg	Leu	Asp	Tyr	Phe	Tyr	Tyr	Ile	Ile	Thr	Ala	
545					550					555					560	
cta	gca	gtc	gtt	aat	ttc	ggg	tac	ttt	ata	ttg	tgt	gcc	aag	tgg	tat	1728
Leu	Ala	Val	Val	Asn	Phe	Gly	Tyr	Phe	Ile	Leu	Cys	Ala	Lys	Trp	Tyr	
				565					570					575		
aaa	tac	aaa	ggg	act	ggg	tct	agc	agc	agt	ggg	gac	ctt	caa	ctc	gat	1776
Lys	Tyr	Lys	Gly	Thr	Gly	Ser	Ser	Ser	Ser	Gly	Asp	Leu	Gln	Leu	Asp	
			580					585					590			
caa	gta	tcc	aaa	cca	tcc	gaa	aga	act	gtt	aac	act	gtc	tag			1818
Gln	Val	Ser	Lys	Pro	Ser	Glu	Arg	Thr	Val	Asn	Thr	Val				
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 <211> 605
 <212> PRT
 <213> Glycine max

<400> 323

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Lys	Asn	Glu	Lys	Ser	Val	Ile	Asp	Glu	Glu	Pro	Lys	Ile	Asn	Tyr	Arg	
			20					25					30			
Gly	Trp	Lys	Val	Met	Pro	Phe	Ile	Ile	Gly	Asn	Glu	Thr	Phe	Glu	Lys	
		35				40						45				
Leu	Gly	Thr	Ile	Gly	Thr	Leu	Ala	Asn	Leu	Leu	Val	Tyr	Leu	Thr	Thr	
		50				55					60					
Val	Phe	Asn	Leu	Ser	Ser	Leu	Thr	Ala	Thr	Asn	Ile	Ile	Asn	Ile	Phe	
65					70					75					80	
Thr	Gly	Ser	Ala	Ser	Leu	Ser	Thr	Leu	Leu	Gly	Ala	Phe	Leu	Cys	Asp	
				85					90					95		
Thr	Tyr	Phe	Gly	Arg	Tyr	Lys	Thr	Leu	Gly	Phe	Cys	Thr	Ile	Ala	Ser	
			100					105					110			
Phe	Leu	Gly	Leu	Leu	Val	Ile	Gln	Leu	Thr	Ala	Trp	Ile	Lys	Lys	Met	
		115				120						125				
His	Pro	Pro	His	Cys	Gly	Ser	Glu	Ser	Ile	Thr	Cys	Thr	Gly	Pro	Thr	
	130					135					140					
Thr	Gly	Gln	Met	Thr	Phe	Leu	Leu	Ala	Gly	Phe	Gly	Leu	Leu	Ile	Val	
145					150					155					160	
Gly	Ala	Ala	Gly	Ile	Arg	Pro	Cys	Asn	Leu	Ala	Phe	Gly	Val	Asp	Gln	
				165					170					175		
Phe	Asn	Pro	Asn	Thr	Glu	Ser	Gly	Lys	Lys	Gly	Ile	Asn	Ser	Phe	Phe	
			180					185					190			
Asn	Trp	Tyr	Phe	Phe	Thr	Tyr	Thr	Phe	Ala	Gln	Met	Val	Ser	Leu	Ser	
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Leu	Ile	Val	Tyr	Ile	Gln	Ser	Asn	Val	Ser	Trp	Ala	Ile	Gly	Leu	Gly	
	210					215					220					
Ile	Pro	Ala	Ala	Leu	Met	Leu	Ile	Ser	Cys	Thr	Leu	Tyr	Tyr	Thr	Gly	
225					230					235					240	
Ser	Asn	Tyr	Tyr	Val	Lys	Val	Lys	Ala	Thr	Gly	Pro	Ala	Pro	Leu	Thr	
				245					250					255		
Ser	Leu	Ala	Gln	Ala	Val	Val	Val	Ala	Ile	Lys	Lys	Arg	Arg	Leu	Asn	
			260					265					270			
Leu	Ser	Glu	Tyr	Pro	Leu	Asp	Ser	Ser	Leu	Phe	Ala	Tyr	Val	Ser	Pro	
		275					280					285				
Gln	Ser	Ile	Asn	Ser	Lys	Leu	Leu	His	Thr	Ser	Gln	Phe	Arg	Phe	Leu	
	290					295					300					
Asp	Lys	Ala	Ala	Ile	Ile	Thr	Pro	Gln	Asp	Gly	Ile	Asn	Pro	Asp	Gly	
305					310					315					320	
Ser	Ala	Ser	Asp	Pro	Trp	Ser	Leu	Cys	Ser	Met	Gln	Gln	Val	Glu	Glu	
				325					330					335		
Leu	Lys	Cys	Leu	Leu	Arg	Val	Ile	Pro	Ile	Trp	Phe	Ala	Gly	Ile	Phe	
			340					345					350			
Phe	Tyr	Ile	Ala	Ile	Val	Gln	Gln	Asn	Thr	Met	Leu	Val	Phe	Gln	Ala	
		355					360					365				
Leu	Gln	Ser	Asp	Arg	Arg	Ile	Leu	Ser	Thr	Asn	Phe	Lys	Ile	Leu	Ala	

PF59082SeqList_PF59082.txt

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370          375          380
Ala Ser Tyr Thr Ile Phe Gln Met Leu Ser Leu Thr Ile Trp Leu Pro
385 385 Ile Tyr Asp Arg Ile 390 Leu Val Pro Ser Leu 395 Gln Arg Val Thr Lys 400
Ile Tyr Asp Arg Ile 405 Val Leu Gln Arg 410 Ile Gly Phe Gly Met 415 Phe Leu
Glu Gly Gly Ile 420 Thr Val Leu Gln Arg 425 Ile Gly Phe Gly Met 430 Phe Leu
Ser Ile Leu Cys Thr Met Val Ser Gly Val Val Glu Glu Arg Arg Arg
435 440 445
Thr Leu Ala Leu Thr Asn Pro Ile Gly Leu Glu Pro Arg Lys Gly Ala
450 455 460
Ile Ser Ser Met Ser Gly Leu Trp Leu Val Pro Gln Leu Thr Leu Ala
465 470 475
Gly Leu Ser Asp Ala Phe Ala Ile Val Gly Gln Val Glu Phe Phe Tyr
485 490
Lys Gln Phe Pro Glu Asn Met Lys Ser Leu Ala Ala Ser Leu Phe Phe
500 505 510
Cys Gly Leu Ala Gly Ser Ser Tyr Leu Ser Ser Leu Leu Ile Ser Ile
515 520 525
Ile His Arg Ala Thr Ala Lys Ser Ser Thr Gly Asn Trp Leu Pro Gln
530 535 540
Asp Leu Asn Lys Gly Arg Leu Asp Tyr Phe Tyr Tyr Ile Ile Thr Ala
545 550 555
Leu Ala Val Val Asn Phe Gly Tyr Phe Ile Leu Cys Ala Lys Trp Tyr
565 570 575
Lys Tyr Lys Gly Thr Gly Ser Ser Ser Gly Asp Leu Gln Leu Asp
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Gln Val Ser Lys Pro Ser Glu Arg Thr Val Asn Thr Val
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gag gag cca aag att aac tac aga gga tgg aaa gtc atg ccc ttt atc      96
Glu Glu Pro Lys Ile Asn Tyr Arg Gly Trp Lys Val Met Pro Phe Ile
20      25      30
att ggg aat gaa act ttt gag aag cta gga acc att gga acc ttg gcc      144
Ile Gly Asn Glu Thr Phe Glu Lys Leu Gly Thr Ile Gly Thr Leu Ala
35      40      45
aac ctc tta gtc tat ctt aca acc gtc ttc aac ttg agc agt ctt gca      192
Asn Leu Leu Val Tyr Leu Thr Thr Val Phe Asn Leu Ser Ser Leu Ala
50      55      60
gct aca aat att gtc aac atc ttt aat ggc agc gcc agt tta tct acc      240
Ala Thr Asn Ile Val Asn Ile Phe Asn Gly Ser Ala Ser Leu Ser Thr
65      70      75
ttg ctc ggg gct ttt ctt tgt gac act tat ttt ggc cgc tac aag aca      288
Leu Leu Gly Ala Phe Leu Cys Asp Thr Tyr Phe Gly Arg Tyr Lys Thr
85      90      95
ctg gga ttc tcc aca atg gct tct ttt ctg ggg ttg ctt gtt ata caa      336
Leu Gly Phe Ser Thr Met Ala Ser Phe Leu Gly Leu Leu Val Ile Gln
100      105      110
cta aca gca tgg att aag aaa atg cat cca cct cac tgt gga aga gac      384
Leu Thr Ala Trp Ile Lys Lys Met His Pro Pro His Cys Gly Arg Asp
115      120      125
agc atc aca tgc ata ggc cca acc aca ggg caa atg gga ttt cta ctt      432
Ser Ile Thr Cys Ile Gly Pro Thr Thr Gly Gln Met Gly Phe Leu Leu
130      135      140
gct gga ttt gga ctt cta att gtg ggg gct gca ggg att aga cct tgt      480
Ala Gly Phe Gly Leu Leu Ile Val Gly Ala Ala Gly Ile Arg Pro Cys

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PF59082SeqList_PF59082.txt

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Asn Leu Ala Phe Gly Val Asp Gln Phe Asn Pro Asn Thr Glu Ser Gly					
aag aag gga atc aat agc ttc ttc aat tgg tac ttc ttt acc ttc aca	165	170			576
Lys Lys Gly Ile Asn Ser Phe Phe Asn Trp Tyr Phe Phe Thr Phe Thr	180	185			
ttt gct cag atg gtg tct ttg tca cta att gtc tac ata cag tca aac	195	200			624
Phe Ala Gln Met Val Ser Leu Ser Leu Ile Val Tyr Ile Gln Ser Asn	210	215			
gtg agc tgg gca ata ggg ttg gga att cct gcg gct ttg atg cta atc	220	225			672
Val Ser Trp Ala Ile Gly Leu Gly Ile Pro Ala Ala Leu Met Leu Ile	230	235			
tct tgc aca ctc tac tac acg gga agc aat tat tac gtg aaa gtt aaa	245	250			720
Ser Cys Thr Leu Tyr Tyr Thr Gly Ser Asn Tyr Tyr Val Lys Val Lys	255	260			
gca act ggt cca gct cca cta aca agt tta gct caa gct gta gtt gtg	265	270			768
Ala Thr Gly Pro Ala Pro Leu Thr Ser Leu Ala Gln Ala Val Val Val	275	280			
gct ata aag aaa aga aga ctg aat cta tca gaa tat cca ctg gat tct	285	290			816
Ala Ile Lys Lys Arg Arg Leu Asn Leu Ser Glu Tyr Pro Leu Asp Ser	295	300			
tcg ctc ttt gcc tat gtt tct ccc cag tct att aac tcc aag ctt ctt	305	310			864
Ser Leu Phe Ala Tyr Val Ser Pro Gln Ser Ile Asn Ser Lys Leu Leu	315	320			
cac acg tct cag ttc agg ttc cta gac aaa gct gca att ata acc cca	325	330			912
His Thr Ser Gln Phe Arg Phe Leu Asp Lys Ala Ala Ile Ile Thr Pro	335	340			
caa gac ggc ata aac cca gac ggg tct gca tca gat cct tgg agt ctt	345	350			960
Gln Asp Gly Ile Asn Pro Asp Gly Ser Ala Ser Asp Pro Trp Ser Leu	355	360			
tgc agc atg caa caa gtg gaa gag cta aaa tgc ttg ctg aga gtg atc	365	370			1008
Cys Ser Met Gln Gln Val Glu Glu Leu Lys Cys Leu Leu Arg Val Ile	375	380			
ccc att tgg ttc gca gga att ttc ttc tta att gca ata gtc caa cag	385	390			1056
Pro Ile Trp Phe Ala Gly Ile Phe Phe Tyr Ile Ala Ile Val Gln Gln	395	400			
aac aca atg ctg gtc ttc caa gcc ctt caa tcc gac aga cgc att ctc	405	410			1104
Asn Thr Met Leu Val Phe Gln Ala Leu Gln Ser Asp Arg Arg Ile Leu	415	420			
agc acc aac ttc aag atc cta gca gcc tcc tac acc atc ttc cag atg	425	430			1152
Ser Thr Asn Phe Lys Ile Leu Ala Ala Ser Tyr Thr Ile Phe Gln Met	435	440			
ctg agc cta acc ata tgg cta ccc atc tac gac cga atc ctc gtg ccg	445	450			1200
Leu Ser Leu Thr Ile Trp Leu Pro Ile Tyr Asp Arg Ile Leu Val Pro	455	460			
tcg ctc caa agg gtc acc aaa aaa gag ggt ggc atc aca gtt ctt caa	465	470			1248
Ser Leu Gln Arg Val Thr Lys Lys Glu Gly Gly Ile Thr Val Leu Gln	475	480			
aga ata ggc ttt ggc atg ttc ctc tct ata cta tgc aca atg gtg tct	485	490			1296
Arg Ile Gly Phe Gly Met Phe Leu Ser Ile Leu Cys Thr Met Val Ser	495	500			
ggg gta gtg gaa gaa aga aga agg aca ttg gct ttg acc aat cct att	505	510			1344
Gly Val Val Glu Glu Arg Arg Arg Thr Leu Ala Leu Thr Asn Pro Ile	515	520			
gga tta gag cca aga aaa ggt gcc att tct tca atg tca ggt cta tgg	525	530			1392
Gly Leu Glu Pro Arg Lys Gly Ala Ile Ser Ser Met Ser Gly Leu Trp	535	540			
ttg gtt cct cag cta aca ctg gca ggg tta tct gat gca ttc gcg att	545	550			1440
Leu Val Pro Gln Leu Thr Leu Ala Gly Leu Ser Asp Ala Phe Ala Ile	555	560			
gtg gga caa gtt gag ttt ttc tac aaa cag ttt cca gag aac atg aaa	565	570			1488
Val Gly Gln Val Glu Phe Phe Tyr Lys Gln Phe Pro Glu Asn Met Lys	575	580			
agc ctt gca gcg tct cta ttt ttc tgt ggc ctc gcg gga tca agt tat	585	590			1536
Ser Leu Ala Ala Ser Leu Phe Phe Cys Gly Leu Ala Gly Ser Ser Tyr	595	600			
ttg agt agt ttg ctg att tct att atc cat agg gcg aca gct aaa tct	605	610			1584
Leu Ser Ser Leu Leu Ile Ser Ile Ile His Arg Ala Thr Ala Lys Ser	615	620			

PF59082SeqList_PF59082.txt

515	520	525		
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Ser Thr Gly Asn Trp Leu Pro Gln Asp Leu Asn Lys Gly Arg Leu Asp				
530	535	540		
aga tta tat tac att ata act gct cta gaa gtc gtt aat ttc ggt tac				1680
Arg Leu Tyr Tyr Ile Ile Thr Ala Leu Glu Val Val Asn Phe Gly Tyr				
545	550	555		560
ttt ata ttg tgt gcc aag tgg tat aaa tac aaa ggg act ggt tct agc				1728
Phe Ile Leu Cys Ala Lys Trp Tyr Lys Tyr Lys Gly Thr Gly Ser Ser				
565	570			
agc agt ggt gac ctt caa ctc gat caa gta tcc aaa cca tcc gaa aga				1776
Ser Ser Gly Asp Leu Gln Leu Asp Gln Val Ser Lys Pro Ser Glu Arg				
580	585	590		
act gtt aac act gtc tag				1794
Thr Val Asn Thr Val				
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35 40 45	
Asn Leu Val Tyr Leu Thr Val Phe Asn Leu Ser Ser Leu Ala	
50 55 60	
Ala Thr Asn Ile Val Asn Ile Phe Asn Gly Ser Ala Ser Leu Ser Thr	
65 70 75 80	
Leu Leu Gly Ala Phe Leu Cys Asp Thr Tyr Phe Gly Arg Tyr Lys Thr	
85 90 95	
Leu Gly Phe Ser Thr Met Ala Ser Phe Leu Gly Leu Leu Val Ile Gln	
100 105 110	
Leu Thr Ala Trp Ile Lys Lys Met His Pro Pro His Cys Gly Arg Asp	
115 120 125	
Ser Ile Thr Cys Ile Gly Pro Thr Thr Gly Gln Met Gly Phe Leu Leu	
130 135 140	
Ala Gly Phe Gly Leu Leu Ile Val Gly Ala Ala Gly Ile Arg Pro Cys	
145 150 155 160	
Asn Leu Ala Phe Gly Val Asp Gln Phe Asn Pro Asn Thr Glu Ser Gly	
165 170 175	
Lys Lys Gly Ile Asn Ser Phe Phe Asn Trp Tyr Phe Phe Thr Phe Thr	
180 185 190	
Phe Ala Gln Met Val Ser Leu Ser Leu Ile Val Tyr Ile Gln Ser Asn	
195 200 205	
Val Ser Trp Ala Ile Gly Leu Gly Ile Pro Ala Ala Leu Met Leu Ile	
210 215 220	
Ser Cys Thr Leu Tyr Tyr Thr Gly Ser Asn Tyr Tyr Val Lys Val Lys	
225 230 235 240	
Ala Thr Gly Pro Ala Pro Leu Thr Ser Leu Ala Gln Ala Val Val Val	
245 250 255	
Ala Ile Lys Lys Arg Arg Leu Asn Leu Ser Glu Tyr Pro Leu Asp Ser	
260 265 270	
Ser Leu Phe Ala Tyr Val Ser Pro Gln Ser Ile Asn Ser Lys Leu Leu	
275 280 285	
His Thr Ser Gln Phe Arg Phe Leu Asp Lys Ala Ala Ile Ile Thr Pro	
290 295 300	
Gln Asp Gly Ile Asn Pro Asp Gly Ser Ala Ser Asp Pro Trp Ser Leu	
305 310 315 320	
Cys Ser Met Gln Gln Val Glu Glu Leu Lys Cys Leu Leu Arg Val Ile	
325 330 335	
Pro Ile Trp Phe Ala Gly Ile Phe Phe Tyr Ile Ala Ile Val Gln Gln	
340 345 350	
Asn Thr Met Leu Val Phe Gln Ala Leu Gln Ser Asp Arg Arg Ile Leu	
355 360 365	

PF59082SeqList_PF59082.txt

Ser Thr Asn Phe Lys Ile Leu Ala Ala Ser Tyr Thr Ile Phe Gln Met
 370 375 380
 Leu Ser Leu Thr Ile Trp Leu Pro Ile Tyr Asp Arg Ile Leu Val Pro
 385 390 400
 Ser Leu Gln Arg Val Thr Lys Lys Glu Gly Ile Thr Val Leu Gln
 405 410 415
 Arg Ile Gly Phe Gly Met Phe Leu Ser Ile Leu Cys Thr Met Val Ser
 420 425 430
 Gly Val Val Glu Glu Arg Arg Arg Thr Leu Ala Leu Thr Asn Pro Ile
 435 440 445
 Gly Leu Glu Pro Arg Lys Gly Ala Ile Ser Ser Met Ser Gly Leu Trp
 450 455 460
 Leu Val Pro Gln Leu Thr Leu Ala Gly Leu Ser Asp Ala Phe Ala Ile
 465 470 480
 Val Gly Gln Val Glu Phe Phe Tyr Lys Gln Phe Pro Glu Asn Met Lys
 485 490 495
 Ser Leu Ala Ala Ser Leu Phe Phe Cys Gly Leu Ala Gly Ser Ser Tyr
 500 505 510
 Leu Ser Ser Leu Leu Ile Ser Ile Ile His Arg Ala Thr Ala Lys Ser
 515 520 525
 Ser Thr Gly Asn Trp Leu Pro Gln Asp Leu Asn Lys Gly Arg Leu Asp
 530 535 540
 Arg Leu Tyr Tyr Ile Ile Thr Ala Leu Glu Val Val Asn Phe Gly Tyr
 545 550 560
 Phe Ile Leu Cys Ala Lys Trp Tyr Lys Tyr Lys Gly Thr Gly Ser Ser
 565 570 575
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 580 585 590
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 595

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 <212> DNA
 <213> Brassica napus

<220>
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 Phe Gln Gly Arg Pro Ala Asp Arg Ser Lys Thr Gly Gly Trp Ala Ser
 20 25 30
 gcc gcg atg att ctc tgt att gag gcg gta gag agg ctg aca act tta 144
 Ala Ala Met Ile Leu Cys Ile Glu Ala Val Glu Arg Leu Thr Thr Leu
 35 40 45
 ggt atc ggc gtt aat tta gtg act tat ttg acg gga act atg cat tta 192
 Gly Ile Gly Val Asn Leu Val Thr Tyr Leu Thr Gly Thr Met His Leu
 50 55 60
 ggc aat gca aca gcg gct aac acc gtt acc aac ttc ctc gga act tca 240
 Gly Asn Ala Thr Ala Ala Asn Thr Val Thr Asn Phe Leu Gly Thr Ser
 65 70 75 80
 ttc atg ctc tgt ctc ctc ggt ggc ttc ata gct cac acc ttt ctt gga 288
 Phe Met Leu Cys Leu Leu Gly Gly Phe Ile Ala His Thr Phe Leu Gly
 85 90 95
 agg tac tta acg att gct ata ttc gcc gca atc caa gcc acg ggt gtt 336
 Arg Tyr Leu Thr Ile Ala Ile Phe Ala Ala Ile Gln Ala Thr Gly Val
 100 105 110
 tcg att tta acc ctc tca act att ata ccg gga ttt caa cca cca aga 384
 Ser Ile Leu Thr Leu Ser Thr Ile Ile Pro Gly Phe Gln Pro Pro Arg
 115 120 125
 tgt cca acg acg tcg tct cac tgc gta caa cca agt gga ata caa ctg 432
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 130 135 140
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PF59082SeqList_PF59082.txt

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Val	Lys	Ala	Ser	Val 165	Ser	Gly	Phe	Gly	Ser 170	Asp	Gln	Phe	Asp	Glu 175	
gaa	ccg	aaa	gaa	cag	tca	caa	atg	aca	tat	ttc	ttc	aac	cgc	ttc	576
Glu	Pro	Lys	Glu 180	Gln	Ser	Gln	Met	Thr	Tyr	Phe	Phe	Asn	Arg	Phe 190	
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Phe	Cys	Ile 195	Asn	Val	Gly	Ser	Leu 200	Leu	Ala	Val	Thr	Val 205	Leu	Val	
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Met	Gln	Asp	Asp	Val	Gly	Arg	Lys	Trp	Gly	Tyr	Gly	Leu	Cys	Ala 210	
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Ala 225	Ile	Val	Leu	Ser	Leu 230	Ser	Ile	Phe	Leu	Ala 235	Gly	Thr	Asn	Arg	
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Arg	Phe	Lys	Lys	Leu 245	Ile	Gly	Ser	Pro	Met 250	Thr	Gln	Val	Ala 255	Val	
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Ile	Val	Ala 260	Ala	Trp	Trp	Asn	Arg	Arg	Leu 265	Glu	Leu	Pro	Ser 270	Pro	
tcg	ttt	cta	tat	gac	ttg	gac	gat	ggt	att	gcg	gct	gaa	ggt	tcg	864
Ser	Phe	Leu 275	Tyr	Asp	Leu	Asp	Val 280	Val	Ile	Ala	Ala	Glu 285	Gly	Ser	
aag	agt	aaa	caa	aag	ttg	ccg	cat	acc	aat	cag	ttc	cgg	tca	ttg	912
Lys	Ser 290	Lys	Gln	Lys	Leu	Pro 295	His	Thr	Asn	Gln	Phe	Arg	Ser	Leu	
aaa	gca	gcg	ata	aag	gac	caa	gaa	atg	gca	atg	acc	caa	aac	gta	960
Lys 305	Ala	Ala	Ile	Lys	Asp 310	Gln	Glu	Met	Ala	Met 315	Thr	Gln	Asn	Val	
aac	aaa	tgg	aca	cta	tca	aca	gta	act	gat	att	gag	gaa	gtg	aaa	1008
Asn	Lys	Trp	Thr	Leu 325	Ser	Thr	Val	Thr	Asp 330	Ile	Glu	Glu	Val	Lys 335	
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Ile	Val	Arg 340	Met	Leu	Pro	Ile	Trp	Ala 345	Thr	Cys	Ile	Leu	Phe 350	Trp	
gtc	cat	gct	caa	cta	acg	aca	tta	tcg	gtc	gcg	cag	tcc	gag	acc	1104
Val	His	Ala 355	Gln	Leu	Thr	Thr	Leu 360	Ser	Val	Ala	Gln	Ser	Glu 365	Thr	
gac	cgt	cac	att	ggg	agc	ttt	gag	atc	cct	cca	gcc	gca	atg	gcc	1152
Asp	Arg 370	His	Ile	Gly	Ser	Phe 375	Glu	Ile	Pro	Pro	Ala 380	Ala	Met	Ala	
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Phe 385	Tyr	Ile	Gly	Gly	Leu 390	Leu	Leu	Thr	Thr	Ala 395	Val	Tyr	Asp	Arg	
gcg	att	ccc	tta	tgc	aaa	aag	cta	ttc	aac	tac	ccc	cac	ggt	ctg	1248
Ala	Ile	Pro	Leu 405	Cys	Lys	Lys	Leu	Phe	Asn 410	Tyr	Pro	His	Gly	Arg 415	
cct	ctt	caa	cgc	att	ggt	ttg	ggt	ctc	tta	ctt	gca	gcc	atg	ggt	1296
Pro	Leu	Gln 420	Arg	Ile	Gly	Leu	Gly	Leu	Leu	Leu	Ala	Ala	Met 430	Gly	
gcc	gta	gct	gct	ttg	gtc	gag	atc	aaa	cgt	ctt	aga	aca	gca	cat	1344
Ala	Val	Ala 435	Ala	Leu	Val	Glu	Ile 440	Lys	Arg	Leu	Arg	Thr	Ala 445	His	
cac	ggt	cca	aca	gtc	aaa	acc	ctt	cct	cta	ggg	ttt	tct	cta	ctc	1392
His	Gly 450	Pro	Thr	Val	Lys	Thr 455	Leu	Pro	Leu	Gly	Phe 460	Ser	Leu	Leu	
cca	caa	tac	ctt	att	gtg	ggt	atc	ggc	gag	gcg	ttg	atc	tac	aca	1440
Pro 465	Gln	Tyr	Leu	Ile	Val 470	Gly	Ile	Gly	Glu	Ala 475	Leu	Ile	Tyr	Thr	
cag	cta	gat	ttt	ttc	ttg	aga	gag	tgt	cct	aaa	ggt	atg	aaa	aca	1488
Gln	Leu	Asp	Phe 485	Leu	Arg	Glu	Cys	Pro	Pro 490	Lys	Gly	Met	Lys	Met 495	
agc	acg	ggt	tta	ttg	ttg	agc	aca	ttg	gct	tta	ggg	ttt	ttc	ttc	1536
Ser	Thr	Gly 500	Leu	Leu	Leu	Ser	Thr	Leu 505	Ala	Leu	Gly	Phe	Phe 510	Ser	
tcg	gtt	ctc	gta	acc	atc	gtt	gag	aaa	gtc	act	gat	aaa	gct	cat	1584

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Ser	Val	Leu	Val	Thr	Ile	Val	Glu	Lys	Val	Thr	Asp	Lys	Ala	His	Pro	
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Trp	Ile	Ala	Asp	Asp	Leu	Asn	Lys	Gly	Arg	Leu	Tyr	Asn	Phe	Tyr	Trp	
	530					535					540					
ctt	gtg	gca	gta	att	gtt	gct	ttg	aac	ttc	ctc	gtt	ttc	ctt	gtt	ttc	1680
Leu	Val	Ala	Val	Ile	Val	Ala	Leu	Asn	Phe	Leu	Val	Phe	Leu	Val	Phe	
	545				550					555					560	
tcc	aag	tgg	tac	gtc	tac	aag	gag	aag	aga	cta	gct	gac	ctt	ggg	att	1728
Ser	Lys	Trp	Tyr	Val	Tyr	Lys	Glu	Lys	Arg	Leu	Ala	Asp	Leu	Gly	Ile	
				565					570					575		
gag	ttg	gaa	gac	gag	cca	gac	att	ccc	atg	ggg	cat	tga				1767
Glu	Leu	Glu	Asp	Glu	Pro	Asp	Ile	Pro	Met	Gly	His					
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<211> 588

<212> PRT

<213> Brassica napus

<400> 327

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Ala	Ala	Met	Ile	Leu	Cys	Ile	Glu	Ala	Val	Glu	Arg	Leu	Thr	Thr	Leu	
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Gly	Ile	Gly	Val	Asn	Leu	Val	Thr	Tyr	Leu	Thr	Gly	Thr	Met	His	Leu	
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Gly	Asn	Ala	Thr	Ala	Ala	Asn	Thr	Val	Thr	Asn	Phe	Leu	Gly	Thr	Ser	
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Phe	Met	Leu	Cys	Leu	Leu	Gly	Gly	Phe	Ile	Ala	His	Thr	Phe	Leu	Gly	
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Arg	Tyr	Leu	Thr	Ile	Ala	Ile	Phe	Ala	Ala	Ile	Gln	Ala	Thr	Gly	Val	
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Ser	Ile	Leu	Thr	Leu	Ser	Thr	Ile	Ile	Pro	Gly	Phe	Gln	Pro	Pro	Arg	
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Cys	Pro	Thr	Thr	Ser	Ser	His	Cys	Val	Gln	Pro	Ser	Gly	Ile	Gln	Leu	
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Val	Lys	Ala	Ser	Val	Ser	Gly	Phe	Gly	Ser	Asp	Gln	Phe	Asp	Glu	Thr	
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Glu	Pro	Lys	Glu	Gln	Ser	Gln	Met	Thr	Tyr	Phe	Phe	Asn	Arg	Phe	Phe	
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Phe	Cys	Ile	Asn	Val	Gly	Ser	Leu	Leu	Ala	Val	Thr	Val	Leu	Val	Tyr	
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Met	Gln	Asp	Asp	Val	Gly	Arg	Lys	Trp	Gly	Tyr	Gly	Leu	Cys	Ala	Leu	
	210					215					220					
Ala	Ile	Val	Leu	Ser	Leu	Ser	Ile	Phe	Leu	Ala	Gly	Thr	Asn	Arg	Tyr	
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Arg	Phe	Lys	Lys	Leu	Ile	Gly	Ser	Pro	Met	Thr	Gln	Val	Ala	Ala	Val	
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Ile	Val	Ala	Ala	Trp	Trp	Asn	Arg	Arg	Leu	Glu	Leu	Pro	Ser	Asp	Pro	
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Ser	Phe	Leu	Tyr	Asp	Leu	Asp	Asp	Val	Ile	Ala	Ala	Glu	Gly	Ser	Met	
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Lys	Ser	Lys	Gln	Lys	Leu	Pro	His	Thr	Asn	Gln	Phe	Arg	Ser	Leu	Asp	
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Lys	Ala	Ala	Ile	Lys	Asp	Gln	Glu	Met	Ala	Met	Thr	Gln	Asn	Val	Tyr	
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Asn	Lys	Trp	Thr	Leu	Ser	Thr	Val	Thr	Asp	Ile	Glu	Glu	Val	Lys	Gln	
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Ile	Val	Arg	Met	Leu	Pro	Ile	Trp	Ala	Thr	Cys	Ile	Leu	Phe	Trp	Thr	
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Val	His	Ala	Gln	Leu	Thr	Thr	Leu	Ser	Val	Ala	Gln	Ser	Glu	Thr	Met	
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 405 410 415
 Pro Leu Gln Arg Ile Gly Leu Gly Leu Leu Ala Ala Met Gly Met
 420 425 430
 Ala Val Ala Ala Leu Val Glu Ile Lys Arg Leu Arg Thr Ala His Ala
 435 440 445
 His Gly Pro Thr Val Lys Thr Leu Pro Leu Gly Phe Ser Leu Leu Ile
 450 455 460
 Pro Gln Tyr Leu Ile Val Gly Ile Gly Glu Ala Ile Tyr Thr Gly
 465 470 475 480
 Gln Leu Asp Phe Phe Leu Arg Glu Cys Pro Lys Gly Met Lys Thr Met
 485 490 495
 Ser Thr Gly Leu Leu Ser Thr Leu Ala Leu Gly Phe Phe Phe Ser
 500 505 510
 Ser Val Leu Val Thr Ile Val Glu Lys Val Thr Asp Lys Ala His Pro
 515 520 525
 Trp Ile Ala Asp Asp Leu Asn Lys Gly Arg Leu Tyr Asn Phe Tyr Trp
 530 535 540
 Leu Val Ala Val Ile Val Ala Leu Asn Phe Leu Val Phe Leu Val Phe
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<210> 328

<211> 1785

<212> DNA

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<222> (1)..(1785)

<400> 328

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tgg gat tat aaa ggc aga cca gct ctt aga tcc tcc tct ggt ggt tgg	96
Trp Asp Tyr Lys Gly Arg Pro Ala Leu Arg Ser Ser Ser Gly Gly Trp	
20 25 30	
gct agt ggt gca atg att tta ggt gtt gaa gct gtg gag agg cta aca	144
Ala Ser Gly Ala Met Ile Leu Val Glu Ala Val Glu Arg Leu Thr	
35 40 45	
aca cta ggg att gct gta aat ttg gtg aca tat ttg act gga act atg	192
Thr Leu Gly Ile Ala Val Asn Leu Val Thr Tyr Leu Thr Gly Thr Met	
50 55 60	
cat tta ggg aat gct act gca gcc aac aat gtt acc aat ttt ctt gga	240
His Leu Gly Asn Ala Thr Ala Ala Asn Asn Val Thr Asn Phe Leu Gly	
65 70 75 80	
act tct ttc atg ctc act tta ctt ggt ggt ttt gtt gct gac act ttc	288
Thr Ser Phe Met Leu Thr Leu Leu Gly Gly Phe Val Ala Asp Thr Phe	
85 90 95	
ctc gga agg tat ctt aca att ggt atc ttt gcc act gtt caa gca atg	336
Leu Gly Arg Tyr Leu Thr Ile Gly Ile Phe Ala Thr Val Gln Ala Met	
100 105 110	
ggg gtt aca atc ttg acc att tcc acc ata atc cca agc cta cgt cca	384
Gly Val Thr Ile Leu Thr Ile Thr Thr Ile Ile Pro Ser Leu Arg Pro	
115 120 125	
cca aaa tgt gaa caa gtt ggt agc tca tca tgc att ccc gca aat agc	432
Pro Lys Cys Glu Gln Val Gly Ser Ser Ser Cys Ile Pro Ala Asn Ser	
130 135 140	
aaa caa ctt atg gtc cta tac att gcc cta tac acg gcg ctc ggc	480
Lys Gln Leu Met Val Leu Tyr Ile Ala Leu Tyr Met Thr Ala Leu Gly	
145 150 155 160	
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tgg Trp	ttc Phe	ttt Phe 195	ttc Phe	ttt Phe	att Ile	aat Asn	gta Val 200	ggc Gly	tcg Ser	ctc Leu	ggc Gly	gca Ala 205	ggt Val	aca Thr	gta Val	624																																
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tgt Cys 225	gca Ala	tgt Cys	gct Ala	att Ile	gtt Val 230	att Ile	gga Gly	ctt Leu	gtt Val	gtg Val 235	ttc Phe	tta Leu	tct Ser	ggg Gly	aca Thr 240	720																																
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ttg Leu 305	gac Asp	aag Lys	gca Ala	gcc Ala	att Ile 310	aag Lys	gaa Glu	gat Asp	aat Asn	gac Asp 315	ctt Leu	gaa Glu	tct Ser	aat Asn	ggc Gly 320																																	
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gaa Glu	gaa Glu	gta Val	aaa Lys 340	tta Leu	tta Leu	atc Ile	aga Arg	atg Met 345	tta Leu	cca Pro	act Thr	tgg Trp	gcc Ala 350	aca Thr	act Thr																																	
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aaa Lys	gct Ala 370	aca Thr	aca Thr	atg Met	gat Asp	cgt Arg 375	cac His	att Ile	gga Gly	acc Thr	ttt Phe 380	gaa Glu	att Ile	cca Pro	ccg Pro																																	
gct Ala 385	tca Ser	ctc Leu	acc Thr	gta Val	ttt Phe 390	ttc Phe	gtc Val	gga Gly	agt Ser	ata Ile 395	ctc Leu	ttg Leu	acc Thr	gta Val	att Ile 400	1200																																
ttc Phe	tac Tyr	gat Asp	aga Arg	att Ile 405	atc Ile	gtt Val	cct Pro	att Ile	tgt Cys 410	cgt Arg	cgt Arg	ttc Phe	atg Met	aat Asn 415	aaa Lys																																	
cct Pro	cat His	gga Gly	ctt Leu 420	acc Thr	cca Pro	tta Leu	cat His	aga Arg 425	att Ile	ttc Phe	aca Thr	ggg Gly	cta Leu 430	gtt Val	ctt Leu	1296																																
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530	ggg agg tta tat gat ttc tat tgg ctt ttg gca ata ttg agt gtg ttt	1680
	Gly Arg Leu Tyr Asp Phe Tyr Trp Leu Leu Ala Ile Leu Ser Val Phe	
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555	aat ttg atg ttt ttc ttg tat tcg tcg aga aaa tat gtg tac aag gag	1728
	Asn Leu Met Phe Leu Tyr Ser Ser Arg Lys Tyr Val Tyr Lys Glu	
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	aag agg ctt gct gaa atg ggg att gaa ttg gaa gat gat gga ccg gtt	1776
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		585
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	Cys His	

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 <211> 594
 <212> PRT
 <213> Nicotiana plumbaginifolia

<400> 329

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Ala	Ser	Gly	Ala	Met	Ile	Leu	Gly	Val	Glu	Ala	Val	Glu	Arg	Leu	Thr
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Thr	Ser	Phe	Met	Leu	Thr	Leu	Leu	Gly	Gly	Phe	Val	Ala	Asp	Thr	Phe
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Lys	Gln	Leu	Met	Val	Leu	Tyr	Ile	Ala	Leu	Tyr	Met	Thr	Ala	Leu	Gly
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Thr	Gly	Gly	Leu	Lys	Ser	Ser	Val	Ser	Gly	Phe	Gly	Thr	Asp	Gln	Phe
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		210				215					220				
Cys	Ala	Cys	Ala	Ile	Val	Ile	Gly	Leu	Val	Val	Phe	Leu	Ser	Gly	Thr
225					230					235					240
Arg	Lys	Tyr	Arg	Phe	Lys	Lys	Leu	Val	Gly	Ser	Pro	Leu	Thr	Gln	Ile
			245						250					255	
Ala	Ser	Val	Ile	Val	Ala	Ala	Trp	Lys	Lys	Thr	His	Leu	Glu	Leu	Pro
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Ser	Asn	Ser	Ser	Leu	Leu	Phe	Glu	Ile	Asp	Asn	Ile	Phe	Gly	Glu	Gly
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Asn	Lys	Lys	Ser	Lys	Gln	Lys	Leu	Pro	His	Ser	Lys	Glu	Tyr	Arg	Phe
	290					295					300				
Leu	Asp	Lys	Ala	Ala	Ile	Lys	Glu	Asp	Asn	Asp	Leu	Glu	Ser	Asn	Gly
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Thr	Lys	Val	Val	Ile	Asn	Lys	Trp	Lys	Leu	Ala	Thr	Leu	Thr	Asp	Val
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Glu	Glu	Val	Lys	Leu	Leu	Ile	Arg	Met	Leu	Pro	Thr	Trp	Ala	Thr	Thr
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Ile	Met	Phe	Trp	Thr	Val	Tyr	Ala	Gln	Met	Thr	Thr	Phe	Ser	Val	Ser
		355					360					365			
Lys	Ala	Thr	Thr	Met	Asp	Arg	His	Ile	Gly	Thr	Phe	Glu	Ile	Pro	Pro
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Ala	Ser	Leu	Thr	Val	Phe	Phe	Val	Gly	Ser	Ile	Leu	Leu	Thr	Val	Ile

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Ser Ile Leu Ala Met Ile Ala Ala Leu Thr Glu Val Lys Arg Leu
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Lys Val Ala His Leu His Gly Leu Thr Asn Asp Ala Asn Ala Thr Ile
                               450                               455                               460
Pro Leu Thr Val Phe Trp Leu Val Pro Gln Phe Leu Leu Val Gly Ala
465                               470                               475                               480
Gly Glu Ala Phe Thr Tyr Ile Gly Gln Leu Asp Phe Phe Leu Arg Glu
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Cys Pro Lys Gly Met Lys Thr Met Ser Thr Gly Leu Phe Leu Ser Thr
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Leu Ala Leu Gly Phe Phe Val Ser Ile Leu Val Thr Ile Val His
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Val Val Thr Gly Thr Lys Asn Pro Trp Leu Ala Asp Asn Leu Asn Gln
                               530                               535                               540
Gly Arg Leu Tyr Asp Phe Tyr Trp Leu Leu Ala Ile Leu Ser Val Phe
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Asn Leu Met Phe Phe Leu Tyr Ser Ser Arg Lys Tyr Val Tyr Lys Glu
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<210> 330
 <211> 1773
 <212> DNA
 <213> Nicotiana plumbaginifolia

<220>
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tgg gat tac aaa ggt cga cca gct gtt cgt tcc tcg tca ggc ggt tgg      96
Trp Asp Tyr Lys Gly Arg Pro Ala Val Arg Ser Ser Ser Gly Gly Trp
                               20                               25                               30
tcc agc gcc gcc atg att tta ggg att gag gca gtg gag agg ctg acg      144
Ser Ser Ala Ala Met Ile Leu Gly Ile Glu Ala Val Glu Arg Leu Thr
                               35                               40                               45
acg tta ggt att gct gta aat ttg gtg aca tat ttg act gga acc atg      192
Thr Leu Gly Ile Ala Val Asn Leu Val Thr Tyr Leu Thr Gly Thr Met
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cat tta gga aat gct agt tcg gcc aac aat gtt act aat ttt ctt gga      240
His Leu Gly Asn Ala Ser Ser Ala Asn Asn Val Thr Asn Phe Leu Gly
                               65                               70                               75                               80
act tca ttt atg ctc act ttg ctt ggt ggt ttc gta gcc gac act ttt      288
Thr Ser Phe Met Leu Thr Leu Leu Gly Gly Phe Val Ala Asp Thr Phe
                               85                               90                               95
ctt gga cgg tat ctt aca att ggt atc ttt acc act att caa gcc atg      336
Leu Gly Arg Tyr Leu Thr Ile Gly Ile Phe Thr Thr Ile Gln Ala Met
                               100                               105                               110
ggg gtt acc ata ttg acc atc tcc acc ata atc cca agc cta cga cca      384
Gly Val Thr Ile Leu Thr Ile Ser Thr Ile Ile Pro Ser Leu Arg Pro
                               115                               120                               125
cca aag tgt tcc cca ggt agc tca aca tgc att cca gca agt tcc aaa      432
Pro Lys Cys Ser Pro Gly Ser Ser Thr Cys Ile Pro Ala Ser Ser Lys
                               130                               135                               140
caa ctc atg gtt tta tac ata gca tta tac atg acg gcg ctc ggc act      480
Gln Leu Met Val Leu Tyr Ile Ala Leu Tyr Met Thr Ala Leu Gly Thr
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ggc ggc ctg aaa tcc agc gtc tcc ggc ttc ggt tcc gat cag ttc gac      528

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PF59082SeqList_PF59082.txt																
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gaa	acc	gac	aag	aaa	gaa	aga	gga	cag	atg	ata	aaa	ttc	ttc	aac	tgg	576
Glu	Thr	Asp	Lys	Lys	Glu	Arg	Gly	Gln	Met	Ile	Lys	Phe	Phe	Asn	Trp	
ttc	ttt	ttc	ttc	att	aat	gtg	gga	tca	ctt	ggt	gca	gtg	aca	gta	tta	624
Phe	Phe	Phe	Phe	Ile	Asn	Val	Gly	Ser	Leu	Gly	Ala	Val	Thr	Val	Leu	
gtg	tat	att	caa	gat	aat	ttg	gga	aga	gaa	tat	ggt	tat	gga	ata	tgt	672
Val	Tyr	Ile	Gln	Asp	Asn	Leu	Gly	Arg	Glu	Tyr	Gly	Tyr	Gly	Ile	Cys	
gct	tgt	gct	att	gtt	att	ggt	ttg	gtc	ata	ttc	tta	tcg	ggg	aca	aga	720
Ala	Cys	Ala	Ile	Val	Ile	Gly	Leu	Val	Ile	Phe	Leu	Ser	Gly	Thr	Arg	
225	aaa	tat	cgt	ttc	aag	aaa	ctt	gtg	gga	agt	cca	ttg	aca	caa	att	768
Lys	Tyr	Arg	Phe	Lys	Lys	Leu	Val	Gly	Ser	Pro	Leu	Thr	Gln	Ile	Ala	
tca	gtt	ttt	gtg	gct	gct	tgg	aac	aaa	aga	cat	atg	gat	ttg	cct	tct	816
Ser	Val	Phe	Val	Ala	Ala	Trp	Asn	Lys	Arg	His	Met	Asp	Leu	Pro	Ser	
gat	tct	act	ctt	tta	tat	aat	att	gat	gat	att	cct	ggg	gat	gga	aat	864
Asp	Ser	Thr	Leu	Leu	Tyr	Asn	Ile	Asp	Asp	Ile	Pro	Gly	Asp	Gly	Asn	
aaa	aaa	gct	aag	cag	aga	ttg	cct	cac	agc	aaa	gaa	ttc	cgt	ttc	ttg	912
Lys	Lys	Ala	Lys	Gln	Arg	Leu	Pro	His	Ser	Lys	Glu	Phe	Arg	Phe	Leu	
290	gac	aag	gca	gct	att	aaa	gta	cag	gac	act	gaa	tcc	gct	gga	att	960
Asp	Lys	Ala	Ala	Ile	Lys	Val	Gln	Asp	Thr	Glu	Ser	Ala	Gly	Ile	Thr	
305	gtg	gta	aat	aaa	tgg	aat	tta	tca	act	tta	acc	gat	ggt	gaa	gta	1008
Val	Val	Asn	Lys	Trp	Asn	Leu	Ser	Thr	Leu	Thr	Asp	Val	Glu	Glu	Val	
aaa	tta	gta	gtc	cga	atg	tta	cca	aca	tgg	gcc	acg	acc	att	atg	ttt	1056
Lys	Leu	Val	Val	Arg	Met	Leu	Pro	Thr	Trp	Ala	Thr	Thr	Ile	Met	Phe	
tggt	act	gtc	tat	gct	caa	atg	aca	aca	ttt	tcc	gtg	tca	caa	gct	aca	1104
Trp	Thr	Val	Tyr	Ala	Gln	Met	Thr	Thr	Phe	Ser	Val	Ser	Gln	Ala	Thr	
acc	atg	gac	cgt	cac	ata	gga	aat	ttc	gaa	att	cct	ccg	gca	tca	ttg	1152
Thr	Met	Asp	Arg	His	Ile	Gly	Asn	Phe	Glu	Ile	Pro	Pro	Ala	Ser	Leu	
370	acg	ctc	ttc	ttc	gtc	gga	agt	atc	ctc	tta	acg	tgc	ata	ttc	tac	1200
Thr	Leu	Phe	Phe	Val	Gly	Ser	Ile	Leu	Leu	Thr	Thr	Cys	Ile	Phe	Tyr	
385	cgt	gcc	gtc	gtg	ccg	ggt	tgt	cga	cgt	gtc	ctc	aac	aat	cct	cac	1248
Arg	Ala	Val	Val	Pro	Val	Cys	Arg	Arg	Arg	Val	Leu	Asn	Asn	Pro	His	
aca	acc	ccg	ttg	caa	cgt	att	gca	gtt	ggt	tta	att	ctt	tca	att	ata	1296
Thr	Thr	Pro	Leu	Gln	Arg	Ile	Ala	Val	Gly	Leu	Ile	Leu	Ser	Ile	Ile	
gcc	atg	gtt	gct	gct	gct	tta	act	gaa	gtg	aag	aga	ttg	aac	gtt	gca	1344
Ala	Met	Val	Ala	Ala	Ala	Leu	Thr	Glu	Val	Lys	Arg	Leu	Asn	Val	Ala	
cat	ttg	cat	gga	ttg	acc	aat	gat	gct	aat	gcc	aaa	ggt	cct	ttg	agt	1392
His	Leu	His	Gly	Leu	Thr	Asn	Asp	Ala	Asn	Ala	Lys	Val	Pro	Leu	Ser	
gtt	ttt	tgg	tta	gtt	ccg	caa	ttc	ttg	cta	gta	ggg	gca	ggt	gag	gca	1440
Val	Phe	Trp	Leu	Val	Pro	Gln	Phe	Leu	Leu	Val	Gly	Ala	Gly	Glu	Ala	
465	ttt	act	tat	att	gga	caa	ctt	gat	ttc	ttt	cta	agg	gaa	tgt	cct	1488
Phe	Thr	Tyr	Ile	Gly	Gln	Leu	Asp	Phe	Phe	Leu	Arg	Glu	Cys	Pro	Lys	
gga	atg	aag	aca	atg	agt	aca	ggg	tta	ttc	ttg	agt	aca	ctt	tca	tta	1536
Gly	Met	Lys	Thr	Met	Ser	Thr	Gly	Leu	Phe	Leu	Ser	Thr	Leu	Ser	Leu	
ggg	ttt	ttc	gtt	agt	tct	att	ttg	gtg	act	ata	gtg	cat	aag	gtg	aca	1584
Gly	Phe	Phe	Val	Ser	Ser	Ile	Leu	Val	Thr	Ile	Val	His	Lys	Val	Thr	
gtg	aaa	aac	cca	tgg	tta	gct	gat	aat	tta	aac	caa	ggg	agg	ctc	tat	1632

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Val	Lys	Asn	Pro	Trp	Leu	Ala	Asp	Asn	Leu	Asn	Gln	Gly	Arg	Leu	Tyr	
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Asp	Phe	Tyr	Trp	Leu	Leu	Ala	Thr	Leu	Ser	Val	Leu	Asn	Leu	Met	Val	
545					550					555					560	
ttc	ttg	ttt	ata	tca	aga	cgg	tat	gtg	tac	aag	gaa	aag	aga	ctt	gct	1728
Phe	Leu	Phe	Ile	Ser	Arg	Arg	Tyr	Val	Tyr	Lys	Glu	Lys	Arg	Leu	Ala	
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gag	tgt	ggg	att	gaa	atg	gag	gat	tca	gaa	cca	gct	tgc	cac	taa		1773
Glu	Cys	Gly	Ile	Glu	Met	Glu	Asp	Ser	Glu	Pro	Ala	Cys	His		590	
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<210> 331

<211> 590

<212> PRT

<213> Nicotiana plumbaginifolia

<400> 331

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Ser	Ser	Ala	Ala	Met	Ile	Leu	Gly	Ile	Glu	Ala	Val	Glu	Arg	Leu	Thr	
		35					40					45				
Thr	Leu	Gly	Ile	Ala	Val	Asn	Leu	Val	Thr	Tyr	Leu	Thr	Gly	Thr	Met	
	50					55					60					
His	Leu	Gly	Asn	Ala	Ser	Ser	Ala	Asn	Asn	Val	Thr	Asn	Phe	Leu	Gly	
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Thr	Ser	Phe	Met	Leu	Thr	Leu	Leu	Gly	Gly	Phe	Val	Ala	Asp	Thr	Phe	
			85					90					95			
Leu	Gly	Arg	Tyr	Leu	Thr	Ile	Gly	Ile	Phe	Thr	Thr	Ile	Gln	Ala	Met	
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Gly	Val	Thr	Ile	Leu	Thr	Ile	Ser	Thr	Ile	Ile	Pro	Ser	Leu	Arg	Pro	
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Pro	Lys	Cys	Ser	Pro	Gly	Ser	Ser	Thr	Cys	Ile	Pro	Ala	Ser	Ser	Lys	
	130					135					140					
Gln	Leu	Met	Val	Leu	Tyr	Ile	Ala	Leu	Tyr	Met	Thr	Ala	Leu	Gly	Thr	
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Gly	Gly	Leu	Lys	Ser	Val	Ser	Gly	Phe	Gly	Ser	Asp	Gln	Phe	Asp		
			165					170					175			
Glu	Thr	Asp	Lys	Lys	Glu	Arg	Gly	Gln	Met	Ile	Lys	Phe	Phe	Asn	Trp	
			180					185					190			
Phe	Phe	Phe	Phe	Ile	Asn	Val	Gly	Ser	Leu	Gly	Ala	Val	Thr	Val	Leu	
		195					200					205				
Val	Tyr	Ile	Gln	Asp	Asn	Leu	Gly	Arg	Glu	Tyr	Gly	Tyr	Gly	Ile	Cys	
	210					215					220					
Ala	Cys	Ala	Ile	Val	Ile	Gly	Leu	Val	Ile	Phe	Leu	Ser	Gly	Thr	Arg	
225					230					235					240	
Lys	Tyr	Arg	Phe	Lys	Lys	Leu	Val	Gly	Ser	Pro	Leu	Thr	Gln	Ile	Ala	
			245					250					255			
Ser	Val	Phe	Val	Ala	Ala	Trp	Asn	Lys	Arg	His	Met	Asp	Leu	Pro	Ser	
			260					265					270			
Asp	Ser	Thr	Leu	Leu	Tyr	Asn	Ile	Asp	Asp	Ile	Pro	Gly	Asp	Gly	Asn	
		275					280					285				
Lys	Lys	Ala	Lys	Gln	Arg	Leu	Pro	His	Ser	Lys	Glu	Phe	Arg	Phe	Leu	
	290					295					300					
Asp	Lys	Ala	Ala	Ile	Lys	Val	Gln	Asp	Thr	Glu	Ser	Ala	Gly	Ile	Thr	
305					310					315					320	
Val	Val	Asn	Lys	Trp	Asn	Leu	Ser	Thr	Leu	Thr	Asp	Val	Glu	Glu	Val	
			325						330				335			
Lys	Leu	Val	Val	Arg	Met	Leu	Pro	Thr	Trp	Ala	Thr	Thr	Ile	Met	Phe	
			340						345				350			
Trp	Thr	Val	Tyr	Ala	Gln	Met	Thr	Thr	Phe	Ser	Val	Ser	Gln	Ala	Thr	
		355					360					365				
Thr	Met	Asp	Arg	His	Ile	Gly	Asn	Phe	Glu	Ile	Pro	Pro	Ala	Ser	Leu	
	370					375					380					
Thr	Leu	Phe	Phe	Val	Gly	Ser	Ile	Leu	Leu	Thr	Cys	Ile	Phe	Tyr	Asp	
385					390					395					400	
Arg	Ala	Val	Val	Pro	Val	Cys	Arg	Arg	Val	Leu	Asn	Asn	Pro	His	Gly	

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      405      410      415
Thr Thr Pro Leu Gln Arg Ile Ala Val Gly Leu Ile Leu Ser Ile Ile
      420      425      430
Ala Met Val Ala Ala Ala Leu Thr Glu Val Lys Arg Leu Asn Val Ala
      435      440      445
His Leu His Gly Leu Thr Asn Asp Ala Asn Ala Lys Val Pro Leu Ser
      450      455      460
Val Phe Trp Leu Val Pro Gln Phe Leu Leu Val Gly Ala Gly Glu Ala
      465      470      475
Phe Thr Tyr Ile Gly Gln Leu Asp Phe Phe Leu Arg Glu Cys Pro Lys
      485      490      495
Gly Met Lys Thr Met Ser Thr Gly Leu Phe Leu Ser Thr Leu Ser Leu
      500      505      510
Gly Phe Phe Val Ser Ser Ile Leu Val Thr Ile Val His Lys Val Thr
      515      520      525
Val Lys Asn Pro Trp Leu Ala Asp Asn Leu Asn Gln Gly Arg Leu Tyr
      530      535      540
Asp Phe Tyr Trp Leu Leu Ala Thr Leu Ser Val Leu Asn Leu Met Val
      545      550      555
Phe Leu Phe Ile Ser Arg Arg Tyr Val Tyr Lys Glu Lys Arg Leu Ala
      565      570      575
Glu Cys Gly Ile Glu Met Glu Asp Ser Glu Pro Ala Cys His
      580      585      590

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<210> 332
 <211> 1680
 <212> DNA
 <213> Prunus dulcis

<220>
 <221> CDS
 <222> (1)..(1680)

<220>
 <221> misc_feature
 <222> (136)..(136)
 <223> n is a, g, c or t

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cag gat gaa acc aat gga ctg tac act gga gac ggt tca gtt gac att      96
Gln Asp Glu Thr Asn Gly Leu Tyr Thr Gly Asp Gly Ser Val Asp Ile
      20      25      30
acc ggg aag cct gtt ctt aag caa agt act ggg aat tgg nga gcg tgc      144
Thr Gly Lys Pro Val Leu Lys Gln Ser Thr Gly Asn Trp Xaa Ala Cys
      35      40      45
ccc ttc att cta ggt act gaa tgt tgt gaa cgt ttg gcc ttc tat ggg      192
Pro Phe Ile Leu Gly Thr Glu Cys Cys Glu Arg Leu Ala Phe Tyr Gly
      50      55      60
att tcc act aac ctg gtt aca tat ctc aca cac aaa ttg cac gaa gga      240
Ile Ser Thr Asn Leu Val Thr Tyr Leu Thr His Lys Leu His Glu Gly
      65      70      75      80
aat gtg tct gca gca aga aat gtt acc act tgg tcg ggc act tgc tat      288
Asn Val Ser Ala Ala Arg Asn Val Thr Thr Trp Ser Gly Thr Cys Tyr
      85      90      95
ctc aca cct cta att gga gct gtc cta gca gat gct tac tgg ggg aga      336
Leu Thr Pro Leu Ile Gly Ala Val Leu Ala Asp Ala Tyr Trp Gly Arg
      100      105      110
tat tgg act att gct att ttc tcc acc att tat ttc att ggg atg tgt      384
Tyr Trp Thr Ile Ala Ile Phe Ser Thr Ile Tyr Phe Ile Gly Met Cys
      115      120      125
act ttg act atc tcg gca tca gtt cct gca ctg aag cct ccc caa tgt      432
Thr Leu Thr Ile Ser Ala Ser Val Pro Ala Leu Lys Pro Pro Gln Cys
      130      135      140
gtg gat tca gta tgt cct tca gct agt ccg gca cag tat gga gta ttc      480
Val Asp Ser Val Cys Pro Ser Ala Ser Pro Ala Gln Tyr Gly Val Phe
      145      150      155      160

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PF59082SeqList_PF59082.txt

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Phe	Phe	Gly	Leu	Tyr	Leu	Ile	Ala	Leu	Arg	Thr	Gly	Gly	Ile	Lys	Pro	
			165						170					175		
tgt	gtt	tca	tcc	ttt	ggg	gct	gat	cag	ttt	gat	gat	act	gat	tct	agg	576
Cys	Val	Ser	Ser	Phe	Gly	Ala	Asp	Gln	Phe	Asp	Asp	Thr	Asp	Ser	Arg	
			180					185						190		
gaa	aga	gta	aag	aag	gga	tcc	ttc	ttc	aac	tgg	ttt	tac	ttt	tca	atc	624
Glu	Arg	Val	Lys	Lys	Gly	Ser	Phe	Phe	Asn	Trp	Phe	Tyr	Phe	Ser	Ile	
		195					200					205				
aac	att	ggt	gct	cta	gta	tcg	agt	act	cta	ata	gtc	tgg	ggt	caa	gac	672
Asn	Ile	Gly	Ala	Leu	Val	Ser	Ser	Thr	Leu	Ile	Val	Trp	Val	Gln	Asp	
	210					215					220					
aat	gct	ggg	tgg	gga	tta	ggt	ttt	ggt	att	cct	gca	ttg	ttt	atg	ggc	720
Asn	Ala	Gly	Trp	Gly	Leu	Gly	Phe	Gly	Ile	Pro	Ala	Leu	Phe	Met	Gly	
	225				230					235					240	
atc	gct	att	gtt	agt	ttc	ttt	tct	ggc	aca	ccc	cta	tat	aga	ttt	cag	768
Ile	Ala	Ile	Val	Ser	Phe	Phe	Ser	Gly	Thr	Pro	Leu	Tyr	Arg	Phe	Gln	
			245					250						255		
aaa	ccg	ggg	gga	agc	cct	ctt	aca	aga	atg	tgc	cag	ggt	ttg	ggt	gca	816
Lys	Pro	Gly	Ser	Pro	Leu	Thr	Arg	Met	Cys	Gln	Val	Leu	Val	Val	Ala	
		260					265						270			
tca	ttt	cgt	aag	tgg	aat	ttg	gac	gtc	cct	aga	gac	agc	agt	ctc	ctg	864
Ser	Phe	Arg	Lys	Trp	Asn	Leu	Asp	Val	Pro	Arg	Asp	Ser	Ser	Leu	Leu	
		275					280					285				
tat	gaa	aca	caa	gat	aaa	ggc	tct	gcc	att	aaa	gga	agt	cgt	aag	ctg	912
Tyr	Glu	Thr	Gln	Asp	Lys	Gly	Ser	Ala	Ile	Lys	Gly	Ser	Arg	Lys	Leu	
	290					295					300					
gag	cac	agt	gat	gaa	ctg	aat	tgc	ctt	gat	aaa	gct	gct	gtg	ata	tca	960
Glu	His	Ser	Asp	Glu	Leu	Asn	Cys	Leu	Asp	Lys	Ala	Ala	Val	Ile	Ser	
	305				310					315					320	
gaa	act	gag	acc	aaa	act	ggg	gac	ttc	tcc	aat	cca	tgg	agg	att	tgc	1008
Glu	Thr	Glu	Thr	Lys	Thr	Gly	Asp	Phe	Ser	Asn	Pro	Trp	Arg	Ile	Cys	
			325					330						335		
act	gta	aca	caa	gtg	gag	gag	ttg	aag	att	tta	ata	cga	atg	ttt	cca	1056
Thr	Val	Thr	Gln	Val	Glu	Glu	Leu	Lys	Ile	Leu	Ile	Arg	Met	Phe	Pro	
			340					345					350			
atc	tgg	gct	act	gga	att	gtc	ttt	tct	gct	ggt	tat	gcc	caa	atg	gcg	1104
Ile	Trp	Ala	Thr	Gly	Ile	Val	Phe	Ser	Ala	Val	Tyr	Ala	Gln	Met	Ala	
		355					360					365				
act	atg	ttt	gtg	gaa	caa	ggg	atg	atg	atg	gac	aca	tct	ggt	ggg	tct	1152
Thr	Met	Phe	Val	Glu	Gln	Gly	Met	Met	Met	Asp	Thr	Ser	Val	Gly	Ser	
	370					375					380					
ttc	acc	att	ccc	ccg	gcc	tcc	ctc	tca	tct	ttt	gat	gtc	atc	agt	ggt	1200
Phe	Thr	Ile	Pro	Pro	Ala	Ser	Leu	Ser	Ser	Phe	Asp	Val	Ile	Ser	Val	
					390					395					400	
att	ttc	tgg	gtc	ccc	att	tat	gac	agg	ttt	att	gtc	ccg	att	gct	agg	1248
Ile	Phe	Trp	Val	Pro	Ile	Tyr	Asp	Arg	Phe	Ile	Val	Pro	Ile	Ala	Arg	
			405					410						415		
aaa	ttt	acc	ggt	aaa	gaa	agg	ggt	ttc	tca	gag	ttg	cag	cgg	atg	ggt	1296
Lys	Phe	Thr	Gly	Lys	Glu	Arg	Gly	Phe	Ser	Glu	Leu	Gln	Arg	Met	Gly	
			420				425						430			
att	ggt	ctc	ttt	ctg	tca	gtg	cta	tgc	atg	tcg	gct	gct	gcc	gtg	gta	1344
Ile	Gly	Leu	Phe	Leu	Ser	Val	Leu	Cys	Met	Ser	Ala	Ala	Ala	Val	Val	
		435					440					445				
gag	atg	aaa	cga	ttg	cag	ctt	gca	aca	gaa	ctt	ggt	ttg	ggt	gac	aaa	1392
Glu	Met	Lys	Arg	Leu	Gln	Leu	Ala	Thr	Glu	Leu	Gly	Leu	Val	Asp	Lys	
	450					455					460					
gag	gta	gct	gta	ccg	ctc	agt	atc	ttt	tgg	caa	ata	cct	caa	tat	ttc	1440
Glu	Val	Ala	Val	Pro	Leu	Ser	Ile	Phe	Trp	Gln	Ile	Pro	Gln	Tyr	Phe	
	465				470					475					480	
ttg	ttg	ggt	gct	gcc	gag	ata	ttc	aca	ttc	att	ggg	cag	ctg	gag	ttc	1488
Leu	Leu	Gly	Ala	Ala	Glu	Ile	Phe	Thr	Phe	Ile	Gly	Gln	Leu	Glu	Phe	
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ttc	tat	gac	caa	tct	tca	gat	gct	atg	cgg	agt	ttg	tgc	agt	gca	ttg	1536
Phe	Tyr	Asp	Gln	Ser	Ser	Asp	Ala	Met	Arg	Ser	Leu	Cys	Ser	Ala	Leu	
			500					505					510			
tcc	gct	tct	gac	gac	ttc	att	ggg	aaa	cta	tct	gag	ctc	ttt	gat	tct	1584
Ser	Ala	Ser	Asp	Asp	Phe	Ile	Gly	Lys	Leu	Ser	Glu	Leu	Phe	Asp	Ser	
		515					520					525				

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gac	atc	gtg	act	tac	ttc	aca	aca	cag	ggc	ggt	aag	gcc	gga	tgg	ata		1632
Asp	Ile	Val	Thr	Tyr	Phe	Thr	Thr	Gln	Gly	Gly	Lys	Ala	Gly	Trp	Ile		
	530					535					540						
cca	gac	aat	ttg	aat	gat	ggc	cat	ttg	gat	tat	ttt	tct	ggc	tct			1677
Pro	Asp	Asn	Leu	Asn	Asp	Gly	His	Leu	Asp	Tyr	Phe	Ser	Gly	Ser			
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tag																	1680

<210> 333
 <211> 559
 <212> PRT
 <213> Prunus dulcis

 <220>
 <221> misc_feature
 <222> (46)..(46)
 <223> The Xaa at location 46 stands for Stop, Arg, or Gly.

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 35 40 45
 Pro Phe Ile Leu Gly Thr Glu Cys Cys Glu Arg Leu Ala Phe Tyr Gly
 50 55 60
 Ile Ser Thr Asn Leu Val Thr Tyr Leu Thr His Lys Leu His Glu Gly
 65 70 75 80
 Asn Val Ser Ala Ala Arg Asn Val Thr Thr Trp Ser Gly Thr Cys Tyr
 85 90 95
 Leu Thr Pro Leu Ile Gly Ala Val Leu Ala Asp Ala Tyr Trp Gly Arg
 100 105 110
 Tyr Trp Thr Ile Ala Ile Phe Ser Thr Ile Tyr Phe Ile Gly Met Cys
 115 120 125
 Thr Leu Thr Ile Ser Ala Ser Val Pro Ala Leu Lys Pro Pro Gln Cys
 130 135 140
 Val Asp Ser Val Cys Pro Ser Ala Ser Pro Ala Gln Tyr Gly Val Phe
 145 150 155 160
 Phe Phe Gly Leu Tyr Leu Ile Ala Leu Arg Thr Gly Gly Ile Lys Pro
 165 170 175
 Cys Val Ser Ser Phe Gly Ala Asp Gln Phe Asp Asp Thr Asp Ser Arg
 180 185 190
 Glu Arg Val Lys Lys Gly Ser Phe Phe Asn Trp Phe Tyr Phe Ser Ile
 195 200 205
 Asn Ile Gly Ala Leu Val Ser Ser Thr Leu Ile Val Trp Val Gln Asp
 210 215 220
 Asn Ala Gly Trp Gly Leu Gly Phe Gly Ile Pro Ala Leu Phe Met Gly
 225 230 235 240
 Ile Ala Ile Val Ser Phe Phe Ser Gly Thr Pro Leu Tyr Arg Phe Gln
 245 250 255
 Lys Pro Gly Gly Ser Pro Leu Thr Arg Met Cys Gln Val Leu Val Ala
 260 265 270
 Ser Phe Arg Lys Trp Asn Leu Asp Val Pro Arg Asp Ser Ser Leu Leu
 275 280 285
 Tyr Glu Thr Gln Asp Lys Gly Ser Ala Ile Lys Gly Ser Arg Lys Leu
 290 295 300
 Glu His Ser Asp Glu Leu Asn Cys Leu Asp Lys Ala Ala Val Ile Ser
 305 310 315 320
 Glu Thr Glu Thr Lys Thr Gly Asp Phe Ser Asn Pro Trp Arg Ile Cys
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 Thr Val Thr Gln Val Glu Glu Leu Lys Ile Leu Ile Arg Met Phe Pro
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 Thr Met Phe Val Glu Gln Gly Met Met Met Asp Thr Ser Val Gly Ser
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PF59082SeqList_PF59082.txt

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 Lys Phe Thr Gly Lys Glu Arg Gly Phe Ser Glu Leu Gln Arg Met Gly
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 Ile Gly Leu Phe Leu Ser Val Leu Cys Met Ser Ala Ala Ala Val Val
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 Glu Met Lys Arg Leu Gln Leu Ala Thr Glu Leu Gly Leu Val Asp Lys
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 Glu Val Ala Val Pro Leu Ser Ile Phe Trp Gln Ile Pro Gln Tyr Phe
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 Leu Leu Gly Ala Ala Glu Ile Phe Thr Phe Ile Gly Gln Leu Glu Phe
 485 490 495
 Phe Tyr Asp Gln Ser Ser Asp Ala Met Arg Ser Leu Cys Ser Ala Leu
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 Ser Ala Ser Asp Asp Phe Ile Gly Lys Leu Ser Glu Leu Phe Asp Ser
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 Ser Gly Leu Tyr Thr Arg Asp Gly Ser Val Asp Ile Lys Gly Asn Pro 20
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 gtc tta aaa agt gag aca ggg aac tgg aga gct tgc cca ttt att ctt 144
 Val Leu Lys Ser Glu Thr Gly Asn Trp Arg Ala Cys Pro Phe Ile Leu 35
 40 45
 ggt aat gaa tgt tgt gaa cgt ttg gca tac tat ggc att gct gct aat 192
 Gly Asn Glu Cys Cys Glu Arg Leu Ala Tyr Tyr Gly Ile Ala Ala Asn 50
 55 60
 ctt gtt act tat ctt act aaa aag tta cat gag gga aac gtt tca gct 240
 Leu Val Thr Tyr Leu Thr Lys Lys Leu His Glu Gly Asn Val Ser Ala 65
 70 75 80
 gct aga aat gtc act act tgg caa ggc act tgt tac ata acg ccc cta 288
 Ala Arg Asn Val Thr Trp Gln Gly Thr Cys Tyr Ile Thr Pro Leu 85
 90 95
 att ggg gct gta ctg gca gat gca tac tgg gga aga tat tgg acg att 336
 Ile Gly Ala Val Leu Ala Asp Ala Tyr Trp Gly Arg Tyr Trp Thr Ile 100
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 gct acc ttc tca act atc tac ttc atc ggc atg tgc acg ttg aca cta 384
 Ala Thr Phe Ser Thr Ile Tyr Phe Ile Gly Met Cys Thr Leu Thr Leu 115
 120 125
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 Ser Ala Ser Val Pro Ala Lys Pro Pro Gln Cys Val Gly Ser Val 130
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 Cys Pro Ser Ala Ser Pro Ala Gln Tyr Ala Ile Phe Phe Phe Gly Leu 145
 150 155 160
 tat ctg att gct ctt ggt act ggt ggg atc aaa cca tgt gtt tcg tca 528
 Tyr Leu Ile Ala Leu Gly Thr Gly Gly Ile Lys Pro Cys Val Ser Ser 165
 170 175
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 Phe Gly Ala Asp Gln Phe Asp Asp Thr Asp Pro Lys Glu Arg Val Lys 180
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Ser	Pro	Leu	Thr	Arg	Met	Cys	Gln	Val	Leu	Val	Ala	Val	Phe	His	Lys	
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Trp	Asn	Leu	Ser	Val	Pro	Asp	Asp	Ser	Thr	Leu	Leu	Tyr	Glu	Thr	Pro	
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Gly	Ile	Val	Phe	Ser	Ala	Val	Tyr	Ala	Gln	Met	Ser	Thr	Met	Phe	Val	
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cca	gtc	tat	gat	aag	atc	ctt	gtt	cca	att	gca	agg	agg	ttt	act	gga	1248
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Phe	Gly	Ala	Asp	Gln	Phe	Asp	Asp	Thr	Asp	Pro	Lys	Glu	Arg	Val	Lys	
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Lys	Gly	Ser	Phe	Phe	Asn	Trp	Phe	Tyr	Phe	Ser	Ile	Asn	Ile	Gly	Ala	
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PF59082SeqList_PF59082.txt

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 485 490 495
 Ser Pro Asp Ala Met Arg Ser Leu Cys Ser Ala Leu Ser Leu Leu Thr
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 530 535 540
 Asn Gly Gly His Leu Asp Tyr Phe Phe Trp Leu Leu Ala Ala Leu Ser
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 Lys Lys Ala Ser
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 Pro Phe Ser Trp Lys Ala Pro Ala Ile Ile Leu Ala Phe Glu Phe Leu
 35 40 45
 gag agc att gct tac tct ggt ata gca ctc aac ctg gtc gtg tac ctt 192
 Glu Ser Ile Ala Tyr Ser Gly Ile Ala Leu Asn Leu Val Val Tyr Leu
 50 55 60
 gga acc gtc ctc cat gga acc acc gcc tcc aat gca gcg aac gtc gat 240
 Gly Thr Val Leu His Gly Thr Thr Ala Ser Asn Ala Ala Asn Val Asp
 65 70 75 80
 gcg tgg aac ggc gcc acg ttt ctt acg ccg gtc ctt gga gcc ttt ctt 288
 Ala Trp Asn Gly Ala Thr Phe Leu Thr Pro Val Leu Gly Ala Phe Leu
 85 90 95
 gct gat aca tac tgg ggg aag tac aag acc gca gct atc tcc ata ata 336
 Ala Asp Thr Trp Gly Lys Tyr Lys Thr Ala Ala Ile Ser Ile Ile
 100 105 110
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 Phe Tyr Val Val Gly Leu Leu Ile Ile Thr Thr Ser Ala Val Ile Pro
 115 120 125
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 Ser Leu Arg Pro Ala Ser Cys Glu Gly Gly Ser Cys Pro Pro Ala Thr
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 Gly Phe Gln Tyr Phe Val Leu Phe Gly Ser Leu Tyr Leu Ile Ser Ile
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 Gly Thr Gly Gly Val Lys Ser Ala Leu Leu Pro Leu Gly Ala Asp Gln
 165 170 175
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 Tyr Asn Asp Ala Asn Ala Glu Glu Ser Lys Ser Lys Gln Leu Phe Phe
 180 185 190
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 Ser Trp Phe Phe Met Ala Val Asn Leu Gly Val Phe Ile Ser Gly Thr
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Thr	Pro	Leu	Tyr	Arg	Val	Gln	Leu	Pro	Thr	Gly	Ser	Pro	Leu	Lys	Ser	
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Val	Pro	Asn	Lys	Ile	Glu	His	Thr	Asp	Glu	Phe	Arg	Cys	Leu	Asp	Lys	
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Ala	Ala	Val	Val	Val	Glu	Asp	Gln	Glu	Met	Lys	Asp	Ser	His	Arg	Pro	
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Trp	Leu	Leu	Cys	Thr	Val	Thr	Gln	Val	Glu	Glu	Val	Lys	Ile	Leu	Ile	
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Ser	Gln	Thr	Ala	Thr	Thr	Phe	Val	Gln	Gln	Gly	Asn	Ala	Met	Asn	Thr	
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Lys	Ile	Gly	Ser	Phe	Ser	Val	Pro	Ala	Ala	Ser	Met	Asn	Ser	Ala	Glu	
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Pro	Ile	Ala	Arg	Arg	Tyr	Thr	Gly	Asn	Pro	Met	Gly	Leu	Thr	Leu	Leu	
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Ala	Ala	Leu	Val	Glu	Thr	Trp	Arg	Leu	Arg	Ser	Val	Lys	Ala	Gly	His	
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Ser	Asp	Val	Phe	Cys	Gly	Ile	Ala	Gln	Leu	Glu	Phe	Phe	Tyr	Ala	Glu	
465					470					475					480	
gcg	cct	gcg	tcc	atg	cgc	agc	ctg	tgc	tcg	gca	ttc	cag	ttc	ctg	gcc	1488
Ala	Pro	Ala	Ser	Met	Arg	Ser	Leu	Cys	Ser	Ala	Phe	Gln	Phe	Leu	Ala	
			485					490						495		
atg	tcg	ctg	gcg	tac	tac	gtg	aac	acg	ctg	gtg	gtc	gca	ttg	gtg	gcg	1536
Met	Ser	Leu	Ala	Tyr	Tyr	Val	Asn	Thr	Leu	Val	Val	Ala	Leu	Val	Ala	
			500					505					510			
tcc	gtg	acc	acg	gcc	tgg	ggc	ggc	aag	ggc	tgg	ctc	ccc	gct	gac	ctc	1584
Ser	Val	Thr	Thr	Ala	Trp	Gly	Gly	Lys	Gly	Trp	Leu	Pro	Ala	Asp	Leu	
		515				520						525				
aac	gac	ggc	cac	ctg	gac	tac	tac	ttc	tgg	ctg	tgg	acg	ggg	atc	agt	1632
Asn	Asp	Gly	His	Leu	Asp	Tyr	Tyr	Phe	Trp	Leu	Trp	Thr	Gly	Ile	Ser	
	530					535					540					
gtg	gtg	aac	tac	gtc	gtg	tac	acg	gca	ttt	gca	agg	cggt	tat	acg	gtc	1680
Val	Val	Asn	Tyr	Val	Val	Tyr	Thr	Ala	Phe	Ala	Arg	Arg	Tyr	Thr	Val	
545					550					555					560	
aag	aag	gtt	gtc	ggt	cag	taa										1701
Lys	Lys	Val	Val	Gly	Gln											
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PF59082SeqList_PF59082.txt

<210> 337
 <211> 566
 <212> PRT
 <213> Zea mays

<400> 337

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Pro Phe Ser Trp Lys Ala Pro Ala Ile Ile Leu Ala Phe Glu Phe Leu
35      40      45
Glu Ser Ile Ala Tyr Ser Gly Ile Ala Leu Asn Leu Val Val Tyr Leu
50      55      60
Gly Thr Val Leu His Gly Thr Thr Ala Ser Asn Ala Ala Asn Val Asp
65      70      75
Ala Trp Asn Gly Ala Thr Phe Leu Thr Pro Val Leu Gly Ala Phe Leu
85      90      95
Ala Asp Thr Tyr Trp Gly Lys Tyr Lys Thr Ala Ala Ile Ser Ile Ile
100     105     110
Phe Tyr Val Val Gly Leu Leu Ile Ile Thr Thr Ser Ala Val Ile Pro
115     120     125
Ser Leu Arg Pro Ala Ser Cys Glu Gly Gly Ser Cys Pro Pro Ala Thr
130     135     140
Gly Phe Gln Tyr Phe Val Leu Phe Gly Ser Leu Tyr Leu Ile Ser Ile
145     150     155
Gly Thr Gly Gly Val Lys Ser Ala Leu Leu Pro Leu Gly Ala Asp Gln
165     170     175
Tyr Asn Asp Ala Asn Ala Glu Glu Ser Lys Ser Lys Gln Leu Phe Phe
180     185     190
Ser Trp Phe Phe Met Ala Val Asn Leu Gly Val Phe Ile Ser Gly Thr
195     200     205
Val Leu Val Trp Ile Gln Gln Asn Val Ala Trp Ser Leu Gly Phe Gly
210     215     220
Ile Ser Ser Ile Cys Leu Val Ile Ala Ala Val Ala Phe Leu Val Gly
225     230     235
Thr Pro Leu Tyr Arg Val Gln Leu Pro Thr Gly Ser Pro Leu Lys Ser
245     250     255
Ile Val Met Val Phe Val Ala Ser Tyr Lys Lys Arg Gly Val Ala Val
260     265     270
Pro Ala Asp Ser Thr Leu Leu Phe Glu Gly Asn Glu Ser Ser Ser Ile
275     280     285
Val Pro Asn Lys Ile Glu His Thr Asp Glu Phe Arg Cys Leu Asp Lys
290     295     300
Ala Ala Val Val Val Glu Asp Gln Glu Met Lys Asp Ser His Arg Pro
305     310     315
Trp Leu Leu Cys Thr Val Thr Gln Val Glu Glu Val Lys Ile Leu Ile
325     330     335
Arg Met Leu Pro Ile Trp Phe Thr Cys Val Phe Tyr Ser Ala Ala Met
340     345     350
Ser Gln Thr Ala Thr Thr Phe Val Gln Gln Gly Asn Ala Met Asn Thr
355     360     365
Lys Ile Gly Ser Phe Ser Val Pro Ala Ala Ser Met Asn Ser Ala Glu
370     375     380
Val Ile Phe Met Leu Val Trp Val Val Phe Gln Asp Ser Val Val Ile
385     390     395
Pro Ile Ala Arg Arg Tyr Thr Gly Asn Pro Met Gly Leu Thr Leu Leu
405     410     415
Gln Arg Met Gly Val Gly Arg Leu Leu Ala Ile Pro Ser Leu Ala Ala
420     425     430
Ala Ala Leu Val Glu Thr Trp Arg Leu Arg Ser Val Lys Ala Gly His
435     440     445
Asn Leu Ser Ile Gly Trp Gln Leu Pro Gln Phe Val Ile Leu Ala Cys
450     455     460
Ser Asp Val Phe Cys Gly Ile Ala Gln Leu Glu Phe Phe Tyr Ala Glu
465     470     475
Ala Pro Ala Ser Met Arg Ser Leu Cys Ser Ala Phe Gln Phe Leu Ala
485     490     495
Met Ser Leu Ala Tyr Tyr Val Asn Thr Leu Val Val Ala Leu Val Ala

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PF59082SeqList_PF59082.txt

500
 Ser Val Thr Thr Ala Trp Gly Gly Lys Gly Trp Leu Pro Ala Asp Leu
 515
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 Lys Lys Val Val Gly Gln
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 cca cta ctc cag gat gaa agt act tcc gaa ttc act agc gac ggg acg 96
 Pro Leu Leu Gln Asp Glu Ser Thr Ser Glu Phe Thr Ser Asp Gly Thr
 20 25 30
 gtt gat ctt cgc aat cag cct gct cgg aag cag aga act ggg aag tgg 144
 Val Asp Leu Arg Asn Gln Pro Ala Arg Lys Gln Arg Thr Gly Lys Trp
 35 40 45
 aaa gca tgc ttc ttc atc tta ggt gcc gag ttt gct gaa tgt gtg gcc 192
 Lys Ala Cys Phe Phe Ile Leu Gly Ala Glu Phe Ala Glu Cys Val Ala
 50 55 60
 ttc ttc gcg atc tcg aag aac ctg gtg acg tac ctc acg ggc gtt ctg 240
 Phe Phe Ala Ile Ser Lys Asn Leu Val Thr Tyr Leu Thr Gly Val Leu
 65 70 75 80
 cac gag agc aac gtg gac gcc gcg acg act gtg tcc acc tgg atc ggg 288
 His Glu Ser Asn Val Asp Ala Ala Thr Thr Val Ser Thr Trp Ile Gly
 85 90 95
 acc tcg ttc ttc acg ccg ctc gtc ggc gcg ttc ttg gcc gac aca ttc 336
 Thr Ser Phe Phe Thr Pro Leu Val Gly Ala Phe Leu Ala Asp Thr Phe
 100 105 110
 tgg ggg cga tac tgg acg ata ctg gcc ttc ctc tcc gtg tac gtc acg 384
 Trp Gly Arg Tyr Trp Thr Ile Leu Ala Phe Leu Ser Val Tyr Val Thr
 115 120 125
 ggg atg acg gtc ctg act gct tca gct ctt ctc ccg ctg ctc atg ggc 432
 Gly Met Thr Val Leu Thr Ala Ser Ala Leu Leu Pro Leu Leu Met Gly
 130 135 140
 gcg tcc tac agc cgt agc gcc cac cgc ctc ttc gcg tac ctg ggc ctc 480
 Ala Ser Tyr Ser Arg Ser Ala His Arg Leu Phe Ala Tyr Leu Gly Leu
 145 150 155 160
 tac ctc gcc gct ctc ggc acc ggc gga atc aag ccg tgc gtc tgc gcg 528
 Tyr Leu Ala Ala Leu Gly Thr Gly Gly Ile Lys Pro Cys Val Cys Ala
 165 170 175
 ctc ggt gcc gac cag ttc gac gcg tct gac ccc gtg gag cgg cgg gcc 576
 Leu Gly Ala Asp Gln Phe Asp Ala Ser Asp Pro Val Glu Arg Arg Ala
 180 185 190
 aag ggc tcc ttc ttc aac tgg tac tac ttc tcc atc aac atc ggc tcc 624
 Lys Gly Ser Phe Phe Asn Trp Tyr Tyr Phe Ser Ile Asn Ile Gly Ser
 195 200 205
 ctg ctg tcc gcg acg gtg gtc gtc tgg gtg cag gac aac gtt ggg tgg 672
 Leu Leu Ser Ala Thr Val Val Val Trp Val Gln Asp Asn Val Gly Trp
 210 215 220
 gga gtc ggg ttc gcg atc ccg acc ctg ctc atg ctg tcg gga ctc gtg 720
 Gly Val Gly Phe Ala Ile Pro Thr Leu Leu Met Leu Ser Gly Leu Val
 225 230 235 240
 ctg ttc gtc gcc ggt agg aag gtt tac agg tac cag aga gtg gga ggg 768
 Leu Phe Val Ala Gly Arg Lys Val Tyr Arg Tyr Gln Arg Val Gly Gly
 245 250 255
 agc cct ctg aca aga gcc tcg cag gtg gtg gtt gct gct gtc agg aac 816

PF59082SeqList_PF59082.txt

Ser	Pro	Leu	Thr	Arg	Ala	Ser	Gln	Val	Val	Val	Ala	Ala	Val	Arg	Asn	
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Tyr	Arg	Leu	Val	Leu	Pro	Glu	Pro	Asp	Asp	Ser	Ser	Ala	Leu	Leu	His	
		275					280					285				
cag	gcg	cct	ccc	gga	acg	acg	gaa	gga	aat	gat	tcc	acg	atg	cag	cat	912
Gln	Ala	Pro	Pro	Gly	Thr	Thr	Glu	Gly	Asn	Asp	Ser	Thr	Met	Gln	His	
	290					295					300					
acg	agt	caa	ttc	agg	ttc	ctt	gac	aag	gct	gcc	att	gta	gcg	cca	tcc	960
Thr	Ser	Gln	Phe	Arg	Phe	Leu	Asp	Lys	Ala	Ala	Ile	Val	Ala	Pro	Ser	
	305				310					315					320	
tcc	ggc	gag	aaa	gga	gcg	acg	gca	agc	cca	tgg	cgg	ctc	tgc	acg	gtc	1008
Ser	Gly	Glu	Lys	Gly	Ala	Thr	Ala	Ser	Pro	Trp	Arg	Leu	Cys	Thr	Val	
			325						330					335		
tcc	cag	gtc	gag	gag	ctg	aag	acg	gtg	ctg	cgg	atg	ttc	ccc	gtg	tgg	1056
Ser	Gln	Val	Glu	Glu	Leu	Lys	Thr	Val	Leu	Arg	Met	Phe	Pro	Val	Trp	
			340					345					350			
gtg	tcg	atg	gtg	ctc	ttc	ttc	gcg	gcc	acc	gcg	cag	atg	tcg	tcc	acc	1104
Val	Ser	Met	Val	Leu	Phe	Phe	Ala	Ala	Thr	Ala	Gln	Met	Ser	Ser	Thr	
		355				360						365				
ttc	atc	gag	caa	ggc	gag	acc	atg	gac	aac	cgc	gtg	ggg	ccg	ttc	acc	1152
Phe	Ile	Glu	Gln	Gly	Glu	Thr	Met	Asp	Asn	Arg	Val	Gly	Pro	Phe	Thr	
	370					375					380					
gtg	ccg	ccg	gcg	tcc	ctc	tcc	acc	ttc	gac	gtc	atc	agc	gtc	atg	gtc	1200
Val	Pro	Pro	Ala	Ser	Leu	Ser	Thr	Phe	Asp	Val	Ile	Ser	Val	Met	Val	
	385				390					395					400	
tgc	ata	ccc	atc	tac	gac	aaa	gcg	ctg	gtg	ccg	ctg	gcc	cgg	cgc	gcc	1248
Cys	Ile	Pro	Ile	Tyr	Asp	Lys	Ala	Leu	Val	Pro	Leu	Ala	Arg	Arg	Ala	
			405					410						415		
acg	ggc	aag	gag	cgg	ggc	ctg	tcg	cag	ctg	cag	cgg	ctg	ggc	gtc	ggc	1296
Thr	Gly	Lys	Glu	Arg	Gly	Leu	Ser	Gln	Leu	Gln	Arg	Leu	Gly	Val	Gly	
			420					425					430			
ctc	gcg	ctg	tcc	gtg	gcc	ggc	atg	gtg	tac	gcg	gcg	ctg	ctc	gag	gcc	1344
Leu	Ala	Leu	Ser	Val	Ala	Gly	Met	Val	Tyr	Ala	Ala	Leu	Leu	Glu	Ala	
		435				440						445				
agg	cgg	ctg	tcg	ctc	gcc	cgc	gca	gcg	gcg	gac	ggg	cgg	ccg	ccg	atg	1392
Arg	Arg	Leu	Ser	Leu	Ala	Arg	Ala	Ala	Ala	Asp	Gly	Arg	Pro	Pro	Met	
	450					455					460					
tcc	atc	atg	tgg	cag	gcg	ccg	gcg	ttc	gcg	gtg	ctc	ggc	gcg	ggg	gag	1440
Ser	Ile	Met	Trp	Gln	Ala	Pro	Ala	Phe	Ala	Val	Leu	Gly	Ala	Gly	Glu	
	465			470						475					480	
gtg	ttc	gcg	acc	atc	ggc	atc	ctc	gag	ttc	ttc	tac	gac	cag	tcg	ccc	1488
Val	Phe	Ala	Thr	Ile	Gly	Ile	Leu	Glu	Phe	Phe	Tyr	Asp	Gln	Ser	Pro	
			485					490						495		
gac	ggc	atg	aag	agc	ctc	ggc	acg	gcc	ctt	gcg	cag	ctc	gcc	gtc	gcg	1536
Asp	Gly	Met	Lys	Ser	Leu	Gly	Thr	Ala	Leu	Ala	Gln	Leu	Ala	Val	Ala	
		500						505					510			
gca	ggc	aac	tac	ttc	aac	tct	gcc	gtg	ctc	gcc	gcc	gtc	gcc	gcc	gtc	1584
Ala	Gly	Asn	Tyr	Phe	Asn	Ser	Ala	Val	Leu	Ala	Ala	Val	Ala	Ala	Val	
		515					520					525				
acc	acg	cgc	aac	ggg	gag	gca	gga	tgg	atc	ccc	gac	gac	ctg	gac	aag	1632
Thr	Thr	Arg	Asn	Gly	Glu	Ala	Gly	Trp	Ile	Pro	Asp	Asp	Leu	Asp	Lys	
	530					535					540					
ggc	cac	ctc	gac	tat	ttc	tgg	ttc	atg	gct	ggt	ctc	ggc	gtg	gtg	gtg	1680
Gly	His	Leu	Asp	Tyr	Phe	Phe	Trp	Phe	Met	Ala	Val	Leu	Gly	Val	Val	
	545				550				555						560	
aac	ctg	ctg	cac	ttc	ctg	cat	tgc	tcc	gtc	agg	tac	aga	ggc	agc	agc	1728
Asn	Leu	Leu	His	Phe	Leu	His	Cys	Ser	Val	Arg	Tyr	Arg	Gly	Ser	Ser	
			565						570					575		
aac	aac	agc	aca	tac	tct	tct	tga									1752
Asn	Asn	Ser	Thr	Tyr	Ser	Ser										
			580													

<210> 339
 <211> 583
 <212> PRT
 <213> Zea mays

<400> 339

PF59082SeqList_PF59082.txt

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Pro	Leu	Leu	Gln	Asp	Glu	Ser	Thr	Ser	Glu	Phe	Thr	Ser	Asp	Gly	Thr
			20					25					30		
Val	Asp	Leu	Arg	Asn	Gln	Pro	Ala	Arg	Lys	Gln	Arg	Thr	Gly	Lys	Trp
		35					40					45			
Lys	Ala	Cys	Phe	Phe	Ile	Leu	Gly	Ala	Glu	Phe	Ala	Glu	Cys	Val	Ala
	50					55					60				
Phe	Phe	Ala	Ile	Ser	Lys	Asn	Leu	Val	Thr	Tyr	Leu	Thr	Gly	Val	Leu
65					70					75					80
His	Glu	Ser	Asn	Val	Asp	Ala	Ala	Thr	Thr	Val	Ser	Thr	Trp	Ile	Gly
				85					90					95	
Thr	Ser	Phe	Phe	Thr	Pro	Leu	Val	Gly	Ala	Phe	Leu	Ala	Asp	Thr	Phe
			100					105					110		
Trp	Gly	Arg	Tyr	Trp	Thr	Ile	Leu	Ala	Phe	Leu	Ser	Val	Tyr	Val	Thr
		115					120					125			
Gly	Met	Thr	Val	Leu	Thr	Ala	Ser	Ala	Leu	Leu	Pro	Leu	Leu	Met	Gly
	130					135					140				
Ala	Ser	Tyr	Ser	Arg	Ser	Ala	His	Arg	Leu	Phe	Ala	Tyr	Leu	Gly	Leu
145					150					155					160
Tyr	Leu	Ala	Ala	Leu	Gly	Thr	Gly	Gly	Ile	Lys	Pro	Cys	Val	Cys	Ala
				165					170					175	
Leu	Gly	Ala	Asp	Gln	Phe	Asp	Ala	Ser	Asp	Pro	Val	Glu	Arg	Arg	Ala
			180					185					190		
Lys	Gly	Ser	Phe	Phe	Asn	Trp	Tyr	Tyr	Phe	Ser	Ile	Asn	Ile	Gly	Ser
		195					200					205			
Leu	Leu	Ser	Ala	Thr	Val	Val	Val	Trp	Val	Gln	Asp	Asn	Val	Gly	Trp
	210					215					220				
Gly	Val	Gly	Phe	Ala	Ile	Pro	Thr	Leu	Leu	Met	Leu	Ser	Gly	Leu	Val
225					230					235					240
Leu	Phe	Val	Ala	Gly	Arg	Lys	Val	Tyr	Arg	Tyr	Gln	Arg	Val	Gly	Gly
				245					250					255	
Ser	Pro	Leu	Thr	Arg	Ala	Ser	Gln	Val	Val	Val	Ala	Ala	Val	Arg	Asn
			260					265					270		
Tyr	Arg	Leu	Val	Leu	Pro	Glu	Pro	Asp	Asp	Ser	Ser	Ala	Leu	Leu	His
		275					280					285			
Gln	Ala	Pro	Pro	Gly	Thr	Thr	Glu	Gly	Asn	Asp	Ser	Thr	Met	Gln	His
	290					295					300				
Thr	Ser	Gln	Phe	Arg	Phe	Leu	Asp	Lys	Ala	Ala	Ile	Val	Ala	Pro	Ser
305					310					315					320
Ser	Gly	Glu	Lys	Gly	Ala	Thr	Ala	Ser	Pro	Trp	Arg	Leu	Cys	Thr	Val
				325					330					335	
Ser	Gln	Val	Glu	Glu	Leu	Lys	Thr	Val	Leu	Arg	Met	Phe	Pro	Val	Trp
			340					345					350		
Val	Ser	Met	Val	Leu	Phe	Phe	Ala	Ala	Thr	Ala	Gln	Met	Ser	Ser	Thr
		355					360					365			
Phe	Ile	Glu	Gln	Gly	Glu	Thr	Met	Asp	Asn	Arg	Val	Gly	Pro	Phe	Thr
	370					375					380				
Val	Pro	Pro	Ala	Ser	Leu	Ser	Thr	Phe	Asp	Val	Ile	Ser	Val	Met	Val
385					390					395					400
Cys	Ile	Pro	Ile	Tyr	Asp	Lys	Ala	Leu	Val	Pro	Leu	Ala	Arg	Arg	Ala
				405					410					415	
Thr	Gly	Lys	Glu	Arg	Gly	Leu	Ser	Gln	Leu	Gln	Arg	Leu	Gly	Val	Gly
			420					425					430		
Leu	Ala	Leu	Ser	Val	Ala	Gly	Met	Val	Tyr	Ala	Ala	Leu	Leu	Glu	Ala
		435					440					445			
Arg	Arg	Leu	Ser	Leu	Ala	Arg	Ala	Ala	Ala	Asp	Gly	Arg	Pro	Pro	Met
	450					455					460				
Ser	Ile	Met	Trp	Gln	Ala	Pro	Ala	Phe	Ala	Val	Leu	Gly	Ala	Gly	Glu
465					470					475					480
Val	Phe	Ala	Thr	Ile	Gly	Ile	Leu	Glu	Phe	Phe	Tyr	Asp	Gln	Ser	Pro
				485					490					495	
Asp	Gly	Met	Lys	Ser	Leu	Gly	Thr	Ala	Leu	Ala	Gln	Leu	Ala	Val	Ala
			500					505					510		
Ala	Gly	Asn	Tyr	Phe	Asn	Ser	Ala	Val	Leu	Ala	Ala	Val	Ala	Ala	Val
		515					520					525			
Thr	Thr	Arg	Asn	Gly	Glu	Ala	Gly	Trp	Ile	Pro	Asp	Asp	Leu	Asp	Lys
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Gly	His	Leu	Asp	Tyr	Phe	Phe	Trp	Phe	Met	Ala	Val	Leu	Gly	Val	Val

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PF59082SeqList_PF59082.txt

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35      40      45
Glu Arg Leu Thr Thr Leu Gly Ile Ala Val Asn Leu Val Thr Tyr Leu
50      55      60
Thr Gly Thr Met His Leu Gly Asn Ala Glu Ser Ala Asn Val Val Thr
65      70      75      80
Asn Phe Met Gly Thr Ser Phe Met Leu Cys Leu Leu Gly Gly Phe Val
85      90      95
Ala Asp Ser Phe Leu Gly Arg Tyr Leu Thr Ile Ala Ile Phe Thr Ala
100     105     110
Val Gln Ala Ser Gly Val Thr Ile Leu Thr Ile Ser Thr Ala Ala Pro
115     120     125
Gly Leu Arg Pro Ala Ser Cys Ser Ala Thr Gly Asp Gly Gly Gly Val
130     135     140
Val Gly Glu Cys Ala Arg Ala Ser Gly Ala Gln Leu Gly Val Leu Tyr
145     150     155     160
Leu Ala Leu Tyr Leu Thr Ala Leu Gly Thr Gly Gly Leu Lys Ser Ser
165     170     175
Val Ser Gly Phe Gly Ser Asp Gln Phe Asp Glu Ser Asp Gly Gly Glu
180     185     190
Lys Arg Gln Met Met Arg Phe Phe Asn Trp Phe Phe Phe Phe Ile Ser
195     200     205
Leu Gly Ser Leu Leu Ala Val Thr Val Leu Val Tyr Val Gln Asp Asn
210     215     220
Leu Gly Arg Arg Trp Gly Tyr Gly Ala Cys Ala Cys Ala Ile Ala Ala
225     230     235     240
Gly Leu Leu Val Phe Leu Ala Gly Thr Arg Arg Tyr Arg Phe Lys Lys
245     250     255
Leu Ala Gly Ser Pro Leu Thr Gln Ile Ala Ala Val Val Val Ala Ala
260     265     270
Trp Arg Lys Arg Arg Leu Pro Leu Pro Ala Asp Pro Ala Met Leu Tyr
275     280     285
Asp Val Asp Val Gly Lys Ala Ala Ala Val Glu Asp Gly Ser Ser Ser
290     295     300
Lys Lys Ser Lys Arg Lys Glu Arg Leu Pro His Thr Asp Gln Phe Arg
305     310     315     320
Phe Leu Asp His Ala Ala Ile Asn Glu Asp Pro Ala Ala Gly Ala Ser
325     330     335
Ser Ser Ser Lys Trp Arg Leu Ala Thr Leu Thr Asp Val Glu Glu Val
340     345     350
Lys Thr Val Ala Arg Met Leu Pro Ile Trp Ala Thr Thr Ile Met Phe
355     360     365
Trp Thr Val Tyr Ala Gln Met Thr Thr Phe Ser Val Ser Gln Ala Thr
370     375     380
Thr Met Asp Arg Arg Val Gly Gly Ser Phe Gln Ile Pro Ala Gly Ser
385     390     395     400
Leu Thr Val Phe Phe Val Gly Ser Ile Leu Leu Thr Val Pro Val Tyr
405     410     415
Asp Arg Leu Val Val Pro Val Ala Arg Arg Val Ser Gly Asn Pro His
420     425     430
Gly Leu Thr Pro Leu Gln Arg Ile Ala Val Gly Leu Ala Leu Ser Val
435     440     445
Val Ala Met Ala Gly Ala Ala Leu Thr Glu Val Arg Arg Leu Arg Val
450     455     460
Ala Arg Glu Ser Ser Glu Ser Ala Ser Gly Gly Val Val Pro Met Ser
465     470     475     480
Val Phe Trp Leu Ile Pro Gln Phe Phe Leu Val Gly Ala Gly Glu Ala
485     490     495
Phe Thr Tyr Ile Gly Gln Leu Asp Phe Phe Leu Arg Glu Cys Pro Lys
500     505     510
Gly Met Lys Thr Met Ser Thr Gly Leu Phe Leu Ser Thr Leu Ser Leu
515     520     525
Gly Phe Phe Val Ser Ser Ala Leu Val Ala Ala Val His Arg Val Thr

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PF59082SeqList_PF59082.txt

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 Asp Asn Phe Tyr Trp Leu Leu Ala Ala Val Cys Leu Ala Asn Leu Leu
 565 570 575
 Val Tyr Leu Val Ala Ala Arg Trp Tyr Lys Tyr Lys Ala Gly Arg Pro
 580 585 590
 Gly Ala Asp Gly Ser Val Asn Gly Val Glu Met Ala Asp Glu Pro Thr
 595 600 605
 Leu His
 610

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 Leu Lys Ser Met Asp Val Asp Lys Leu Glu Asn Gly Gly Gly Gly Gly
 20 25 30
 gac gag gag agc ccg cgc ccc gcc gtc aag tac cac ggc tgg aag gcc 144
 Asp Glu Ser Pro Arg Pro Ala Val Lys Tyr His Gly Trp Lys Ala
 35 40 45
 atg ccc ttc atc atc ggc aac gag acg ttc gag aag ctg ggc acg ctg 192
 Met Pro Phe Ile Ile Gly Asn Glu Thr Phe Glu Lys Leu Gly Thr Leu
 50 55 60
 ggc acg tcg gcc aac ctg ctg gtg tac ctg acg cag gtg ttc cac atg 240
 Gly Thr Ser Ala Asn Leu Leu Val Tyr Leu Thr Gln Val Phe His Met
 65 70 75 80
 cgg agc gtg gac gcg gcc acg ctg ctc aac ggc ctc aac ggc acc acc 288
 Arg Ser Val Asp Ala Ala Thr Leu Leu Asn Gly Leu Asn Gly Thr Thr
 85 90 95
 agc ctc gcc ccc atc atc ggc gcc ttc ctc tcc gac gcc tac ctc ggc 336
 Ser Leu Ala Pro Ile Ile Gly Ala Phe Leu Ser Asp Ala Tyr Leu Gly
 100 105 110
 cgc tac ctc gcg ctc gcc atc gcc tcc ata gcc tcc ctc atc ggc atg 384
 Arg Tyr Leu Ala Leu Ala Ile Ala Ser Ile Ala Ser Ile Gly Met
 115 120 125
 ttc ctg ctg acg atg acg gcc ggc gcg aac agc ctg cac ccg ccg gag 432
 Phe Leu Leu Thr Met Thr Ala Gly Ala Asn Ser Leu His Pro Pro Glu
 130 135 140
 tgc acc gtg ggc gag acc tgc gag aag gca acg tcg tac cag ttc gcg 480
 Cys Thr Val Gly Glu Thr Cys Glu Lys Ala Thr Ser Tyr Gln Phe Ala
 145 150 155 160
 gtg ctc ttc gtc gcc ttc gcg ttc ctg gtg ctg ggc tcg gcg ggc atc 528
 Val Leu Phe Val Ala Phe Ala Phe Leu Val Leu Gly Ser Ala Gly Ile
 165 170 175
 cgc ccc tgc agc atg ccc ttc ggc gcc gac cag ttc gac ccc aac acg 576
 Arg Pro Cys Ser Met Pro Phe Gly Ala Asp Gln Phe Asp Pro Asn Thr
 180 185 190
 gag tct ggc aag cgc ggc atc aac agc ttc ttc aac tgg tac tac ttc 624
 Glu Ser Gly Lys Arg Gly Ile Asn Ser Phe Phe Asn Trp Tyr Tyr Phe
 195 200 205
 acc ttc acg gcc gcc atg atg atc tcc gcc acc gtc atc atc tac gtg 672
 Thr Phe Thr Ala Ala Met Met Ile Ser Ala Thr Val Ile Ile Tyr Val
 210 215 220
 cag agc aac gtg agc tgg ccc atc ggc ctg ggc atc ccc acg gca ctc 720
 Gln Ser Asn Val Ser Trp Pro Ile Gly Leu Gly Ile Pro Thr Ala Leu
 225 230 235 240
 atg ttc ctg gca tgc gtg ctc ttc ttc atg ggc acg cgc cta tac gtg 768
 Met Phe Leu Ala Cys Val Leu Phe Phe Met Gly Thr Arg Leu Tyr Val

PF59082SeqList_PF59082.txt

PT550625cgt13t_PT550627.txt																
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Arg	Val	Thr	Pro	Glu	Gly	Ser	Pro	Phe	Thr	Ser	Val	Val	Gln	Val	Leu	
				260					265					270		
tca	gcc	gcg	ctc	aag	aag	cgg	tcg	ctg	aag	cag	ccc	aag	gac	ccg	aag	864
Ser	Ala	Ala	Leu	Lys	Lys	Arg	Ser	Leu	Lys	Gln	Pro	Lys	Asp	Pro	Lys	
				275					280					285		
cag	gac	ctc	ttc	gac	ccg	ccg	cac	acc	agc	gcc	atc	gtc	acc	aag	ttg	912
Gln	Asp	Leu	Phe	Asp	Pro	Pro	His	Thr	Ser	Ala	Ile	Val	Thr	Lys	Leu	
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gcg	cac	acg	gac	cag	ttc	cgc	tgc	cta	gac	aag	gcg	gcc	atc	gtg	gca	960
Ala	His	Thr	Asp	Gln	Phe	Arg	Cys	Leu	Asp	Lys	Ala	Ala	Ile	Val	Ala	
				305					310					315		
tcc	ccg	gac	gag	gtg	cgt	tcc	ggc	ggc	ggc	gcg	ccc	gcg	gac	ccc	tgg	1008
Ser	Pro	Asp	Glu	Val	Arg	Ser	Gly	Gly	Gly	Ala	Pro	Ala	Asp	Pro	Trp	
				325					330					335		
agg	ctc	tgc	agc	gtg	cag	cag	gtg	gag	gag	gtc	aag	cac	acc	aac	cac	1056
Arg	Leu	Cys	Ser	Val	Gln	Gln	Val	Glu	Glu	Val	Lys	His	Thr	Asn	His	
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atc	ctg	ccc	gtc	ggg	tcc	acg	ggg	atc	atc	tac	tac	gtc	gcc	gtg	gtg	1104
Ile	Leu	Pro	Val	Gly	Ser	Thr	Gly	Ile	Ile	Tyr	Tyr	Val	Ala	Val	Val	
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cag	cag	tcc	acg	tac	gtg	gtg	ctc	tcg	gcg	ctg	cag	tcc	gac	cgc	cac	1152
Gln	Gln	Ser	Thr	Tyr	Val	Val	Leu	Ser	Ala	Leu	Gln	Ser	Asp	Arg	His	
				370					375					380		
ctc	ggc	cgc	gcc	ggc	ttc	cag	atc	ccc	gcc	gcg	tcc	ttc	acc	gtc	ttc	1200
Leu	Gly	Arg	Ala	Gly	Phe	Gln	Ile	Pro	Ala	Ala	Ser	Phe	Thr	Val	Phe	
				385					390					395		
gcc	atg	ctc	gcg	cag	acg	ctg	tgg	atc	ccc	ttc	tac	gac	cgc	ctc	ctg	1248
Ala	Met	Leu	Ala	Gln	Thr	Leu	Trp	Ile	Pro	Phe	Tyr	Asp	Arg	Leu	Leu	
				405					410					415		
ctg	ccc	aag	ctc	cgg	aag	ata	acc	ggc	aag	gag	gag	ggg	ttc	acg	ctg	1296
Leu	Pro	Lys	Leu	Arg	Lys	Ile	Thr	Gly	Lys	Glu	Glu	Gly	Phe	Thr	Leu	
				420					425					430		
ctc	cag	cgc	cag	ggc	atc	ggc	atc	ctc	ctc	tcc	act	gtc	gcc	atg	gtc	1344
Leu	Gln	Arg	Gln	Gly	Ile	Gly	Ile	Ala	Leu	Ser	Thr	Val	Ala	Met	Val	
				435					440					445		
atc	tcg	gcc	atc	gtc	gag	gac	cgg	cgc	cg	gcc	atc	gcg	ctc	agc	cag	1392
Ile	Ser	Ala	Ile	Val	Glu	Asp	Arg	Arg	Arg	Ala	Ile	Ala	Leu	Ser	Gln	
				450					455					460		
ccg	acg	ctc	ggc	acc	acc	atc	act	ggc	ggg	gcg	atc	tcg	gcc	atg	tcc	1440
Pro	Thr	Leu	Gly	Thr	Thr	Ile	Thr	Gly	Gly	Ala	Ile	Ser	Ala	Met	Ser	
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agc	ctg	tgg	atg	gtg	cca	cag										

PF59082SeqList_PF59082.txt

<211> 592

<212> PRT

<213> Zea mays

<400> 343

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20      25      30
Asp Glu Glu Ser Pro Arg Pro Ala Val Lys Tyr His Gly Trp Lys Ala
35      40      45
Met Pro Phe Ile Ile Gly Asn Glu Thr Phe Glu Lys Leu Gly Thr Leu
50      55      60
Gly Thr Ser Ala Asn Leu Leu Val Tyr Leu Thr Gln Val Phe His Met
65      70      75
Arg Ser Val Asp Ala Thr Leu Leu Asn Gly Leu Asn Gly Thr Thr
85      90      95
Ser Leu Ala Pro Ile Ile Gly Ala Phe Leu Ser Asp Ala Tyr Leu Gly
100     105
Arg Tyr Leu Ala Leu Ala Ile Ala Ser Ile Ala Ser Leu Ile Gly Met
115     120     125
Phe Leu Leu Thr Met Thr Ala Gly Ala Asn Ser Leu His Pro Pro Glu
130     135     140
Cys Thr Val Gly Glu Thr Cys Glu Lys Ala Thr Ser Tyr Gln Phe Ala
145     150     155
Val Leu Phe Val Ala Phe Ala Phe Leu Val Leu Gly Ser Ala Gly Ile
165     170     175
Arg Pro Cys Ser Met Pro Phe Gly Ala Asp Gln Phe Asp Pro Asn Thr
180     185     190
Glu Ser Gly Lys Arg Gly Ile Asn Ser Phe Phe Asn Trp Tyr Tyr Phe
195     200     205
Thr Phe Thr Ala Ala Met Met Ile Ser Ala Thr Val Ile Ile Tyr Val
210     215     220
Gln Ser Asn Val Ser Trp Pro Ile Gly Leu Gly Ile Pro Thr Ala Leu
225     230     235
Met Phe Leu Ala Cys Val Leu Phe Phe Met Gly Thr Arg Leu Tyr Val
245     250     255
Arg Val Thr Pro Glu Gly Ser Pro Phe Thr Ser Val Val Gln Val Leu
260     265     270
Ser Ala Ala Leu Lys Lys Arg Ser Leu Lys Gln Pro Lys Asp Pro Lys
275     280     285
Gln Asp Leu Phe Asp Pro Pro His Thr Ser Ala Ile Val Thr Lys Leu
290     295     300
Ala His Thr Asp Gln Phe Arg Cys Leu Asp Lys Ala Ala Ile Val Ala
305     310     315
Ser Pro Asp Glu Val Arg Ser Gly Gly Gly Ala Pro Ala Asp Pro Trp
325     330     335
Arg Leu Cys Ser Val Gln Gln Val Glu Glu Val Lys His Thr Asn His
340     345     350
Ile Leu Pro Val Gly Ser Thr Gly Ile Ile Tyr Tyr Val Ala Val Val
355     360     365
Gln Gln Ser Thr Tyr Val Val Leu Ser Ala Leu Gln Ser Asp Arg His
370     375     380
Leu Gly Arg Ala Gly Phe Gln Ile Pro Ala Ala Ser Phe Thr Val Phe
385     390     395
Ala Met Leu Ala Gln Thr Leu Trp Ile Pro Phe Tyr Asp Arg Leu Leu
405     410     415
Leu Pro Lys Leu Arg Lys Ile Thr Gly Lys Glu Glu Gly Phe Thr Leu
420     425     430
Leu Gln Arg Gln Gly Ile Gly Ile Ala Leu Ser Thr Val Ala Met Val
435     440     445
Ile Ser Ala Ile Val Glu Asp Arg Arg Arg Ala Ile Ala Leu Ser Gln
450     455     460
Pro Thr Leu Gly Thr Thr Ile Thr Gly Gly Ala Ile Ser Ala Met Ser
465     470     475
Ser Leu Trp Met Val Pro Gln Leu Met Ile Leu Gly Leu Ser Glu Ala
485     490     495
Phe Asn Leu Ile Ser Gln Ile Glu Phe Tyr Tyr Lys Glu Ile Pro Glu
500     505     510

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PF59082SeqList_PF59082.txt

His Met Arg Ser Val Ala Gly Ala Leu Ala Phe Cys Asn Leu Ala Leu
 515 520 525
 Gly Asn Tyr Leu Ser Gly Phe Leu Val Thr Ile Val His Arg Thr Thr
 530 535 540
 Gly Ser Gly Gln Asn Trp Leu Ala Gln Asp Leu Asn Lys Gly Arg Leu
 545 550 555 560
 Asp Leu Phe Tyr Trp Thr Ile Ala Gly Ile Gly Val Phe Asn Phe Ile
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 Tyr Phe Val Ile Cys Ala Arg Trp Tyr Arg Phe Lys Gly Ala Ser Asn
 580 585 590

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<220>
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 act ccg cag gtc gta gct tcg gag tac gca agt gat ggt tca gtt gat 96
 Thr Pro Gln Val Val Ala Ser Glu Tyr Ala Ser Asp Gly Ser Val Asp
 20 25 30
 atc aac aaa caa cct gct ctc aag cac aga acg ggt aac tgg agg gca 144
 Ile Asn Lys Gln Pro Ala Leu Lys His Arg Thr Gly Asn Trp Arg Ala
 35 40 45
 tgc tac ccc gtc tta ggt gta gga ttc agt gaa ggc atg gtg ttc tct 192
 Cys Tyr Pro Val Leu Gly Val Gly Phe Ser Glu Gly Met Val Phe Ser
 50 55 60
 gca atc gcg acg aat tta gtg acg tat ctc acc act gtg ctc cac gag 240
 Ala Ile Ala Thr Asn Leu Val Thr Tyr Leu Thr Val Leu His Glu
 65 70 75 80
 agc aag gtg gat gca gcg aaa aat atc tcc gcc tgg tcc gga gtg tgc 288
 Ser Lys Val Asp Ala Ala Lys Asn Ile Ser Ala Trp Ser Gly Val Cys
 85 90 95
 ttc ctc acg cca ctt ctt ggg gct ttc gtt gcg gac agt tac ttg gga 336
 Phe Leu Thr Pro Leu Leu Gly Ala Phe Val Ala Asp Ser Tyr Leu Gly
 100 105 110
 aga tac tgg acc att gtt gtg gtc ctc ccg gtc tac atc gtg gca atg 384
 Arg Tyr Trp Thr Ile Val Val Val Leu Pro Val Tyr Ile Val Ala Met
 115 120 125
 ctc gtc ctg ata gct tca gca tca ctc ccg gta ttg ttc cag agc gac 432
 Leu Val Leu Ile Ala Ser Ala Ser Leu Pro Val Leu Phe Gln Ser Asp
 130 135 140
 gtg cac cct gca gtg gtt tac ctt ggt atc tac ctt gcc gcc att gcc 480
 Val His Pro Ala Val Val Tyr Leu Gly Ile Tyr Leu Ala Ala Ile Ala
 145 150 155 160
 agc ggt ggc gtg aag ccc tgc att tct gcc ttc ggg gct gat caa ttt 528
 Ser Gly Gly Val Lys Pro Cys Ile Ser Ala Phe Gly Ala Asp Gln Phe
 165 170 175
 gac agc aat gac ccg gcg gag ctg gtg aag ggc tcc ttc ttc aac 576
 Asp Ser Asn Asp Pro Ala Glu Leu Val Lys Lys Gly Ser Phe Phe Asn
 180 185 190
 tgg tac ttc ttc ctg acg acc acc agc tcc ctg ctg tct ggc acc gtg 624
 Trp Tyr Phe Phe Leu Thr Thr Ser Ser Leu Leu Ser Gly Thr Val
 195 200 205
 att gtt tgg ctg cag gac aat gtt agg tgg gca gtc agc tac gtg atc 672
 Ile Val Trp Leu Gln Asp Asn Val Arg Trp Ala Val Ser Tyr Val Ile
 210 215 220
 ccg acc gtg ctc atg ctc atc tgt ttc ccc gca ttt tta gct ggc tcc 720
 Pro Thr Val Leu Met Leu Ile Cys Phe Pro Ala Phe Leu Ala Gly Ser
 225 230 235 240
 agg gtg tac agg ttt agg gaa atg gga gta agc ccc att acg agc tta 768
 Arg Val Tyr Arg Phe Arg Glu Met Gly Val Ser Pro Ile Thr Ser Leu
 245 250 255

PF59082SeqList_PF59082.txt

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Leu	Gln	Val	Val	Val	Ala	Ala	Val	Arg	Lys	Trp	Asn	Ala	Lys	Leu	Pro	
			260					265					270			
gac	gat	agc	tcg	ctg	cta	tat	gag	cag	gcc	agt	tca	cct	tgt	acg	act	864
Asp	Asp	Ser	Ser	Leu	Leu	Tyr	Glu	Gln	Ala	Ser	Ser	Pro	Cys	Thr	Thr	
		275					280					285				
gaa	gca	agt	cat	aag	aac	aag	cat	acc	aat	cag	ttc	agg	ttc	ttt	gac	912
Glu	Ala	Ser	His	Lys	Asn	Lys	His	Thr	Asn	Gln	Phe	Arg	Phe	Phe	Asp	
	290					295					300					
aag	gcc	gcc	att	gtc	cca	ggc	aac	gaa	tcc	acg	gtg	cag	acg	agt		960
Lys	Ala	Ala	Ile	Val	Pro	Gly	Asn	Glu	Ser	Thr	Val	Gln	Thr	Ser		
	305				310				315					320		
cca	tgg	agg	ctc	tgc	aca	gtg	aca	cag	gtc	gag	gag	cta	aag	atg	ctg	1008
Pro	Trp	Arg	Leu	Cys	Thr	Val	Thr	Gln	Val	Glu	Glu	Leu	Lys	Met	Leu	
			325					330						335		
ctc	tcg	acg	ctg	cct	acc	tgg	gcg	tcg	ttc	gtg	att	ttc	tac	gca	gtc	1056
Leu	Ser	Thr	Leu	Pro	Thr	Trp	Ala	Ser	Phe	Val	Ile	Phe	Tyr	Ala	Val	
			340					345					350			
acg	tct	cag	atg	cag	tcg	acg	atg	att	gag	caa	ggc	atg	ctc	atg	gac	1104
Thr	Ser	Gln	Met	Gln	Ser	Thr	Met	Ile	Glu	Gln	Gly	Met	Leu	Met	Asp	
		355					360					365				
aac	cac	ggt	ggc	tcg	ttt	gcc	atc	ccg	ccg	gca	tcc	atg	ccg	atc	att	1152
Asn	His	Val	Gly	Ser	Phe	Ala	Ile	Pro	Pro	Ala	Ser	Met	Pro	Ile	Ile	
	370					375					380					
ggt	gtg	ctc	agc	ttc	ctc	atc	tgg	gtc	gcc	gcc	tat	gaa	acc	gtc	cta	1200
Gly	Val	Leu	Ser	Phe	Leu	Ile	Trp	Val	Ala	Ala	Tyr	Glu	Thr	Val	Leu	
	385				390				395						400	
gcg	cca	ttg	gcg	cgg	cgc	ttc	acc	ggg	aac	gag	aag	ggc	ttc	tcc	cag	1248
Ala	Pro	Leu	Ala	Arg	Arg	Phe	Thr	Gly	Asn	Glu	Lys	Gly	Phe	Ser	Gln	
				405				410						415		
tgg	cag	cgc	ctc	gcg	atc	ggc	caa	gcc	ctg	tcc	att	ctg	aca	atg	gcg	1296
Trp	Gln	Arg	Leu	Ala	Ile	Gly	Gln	Ala	Leu	Ser	Ile	Leu	Thr	Met	Ala	
			420					425					430			
ctt	gct	gcg	ctg	gtg	gag	aca	agg	agg	ctg	gcg	atc	gcg	gaa	gcc	agc	1344
Leu	Ala	Ala	Leu	Val	Glu	Thr	Arg	Arg	Leu	Ala	Ile	Ala	Glu	Ala	Ser	
		435					440					445				
ggg	ctg	agg	cat	cgg	gag	gtg	ccg	gtg	ccc	atg	agc	atc	ctg	tgg	cag	1392
Gly	Leu	Arg	His	Arg	Glu	Val	Pro	Val	Pro	Met	Ser	Ile	Leu	Trp	Gln	
	450					455					460					
ggc	cca	ggt	ttc	ttt	gtg	cat	ggc	gcg	gcc	gag	gtc	ttc	ggc	gcc	atc	1440
Gly	Pro	Val	Phe	Phe	Val	His	Gly	Ala	Ala	Glu	Val	Phe	Gly	Ala	Ile	
	465				470					475					480	
ggc	atg	aca	gag	ttc	ttc	tac	gac	caa	gcc	ccg	gcg	acc	atg	aag	agc	1488
Gly	Met	Thr	Glu	Phe	Phe	Tyr	Asp	Gln	Ala	Pro	Ala	Thr	Met	Lys	Ser	
				485				490						495		
ctg	tgc	gcc	gcg	ttc	ggg	cag	ctc	gcg	gtg	gct	tcc	ggg	tcg	tac	ctc	1536
Leu	Cys	Ala	Ala	Phe	Gly	Gln	Leu	Ala	Val	Ala	Ser	Gly	Ser	Tyr	Leu	
			500					505					510			
aac	acg	gtc	gtg	ctc	agc	gtc	ggt	gcg	ttg	gcc	aca	acg	cgc	ggc	ggc	1584
Asn	Thr	Val	Val	Leu	Ser	Val	Val	Ala	Leu	Ala	Thr	Thr	Arg	Gly	Gly	
		515					520						525			
gca	acc	gga	tgg	att	tcg	gac	aac	ctc	aat	gaa	ggc	cat	ctt	gac	tat	1632
Ala	Thr	Gly	Trp	Ile	Ser	Asp	Asn	Leu	Asn	Glu	Gly	His	Leu	Asp	Tyr	
		530				535					540					
ttc	ttc	tgg	atg	atg	gcc	gct	ctt	agc	ttg	ctg	aac	cta	gct	ctg	ttt	1680
Phe	Phe	Trp	Met	Met	Ala	Ala	Leu	Ser	Leu	Leu	Asn	Leu	Ala	Leu	Phe	
	545				550					555					560	
gtg	cgc	tac	tca	atg	cgg	cat	aca	gac	agg	caa	cgt	aag	caa	gac	ctt	1728
Val	Arg	Tyr	Ser	Met	Arg	His	Thr	Asp	Arg	Gln	Arg	Lys	Gln	Asp	Leu	
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ggt	tta	tca	taa													1740
Gly	Leu	Ser														

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 <212> PRT
 <213> Zea mays

PF59082SeqList_PF59082.txt

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Ile Asn Lys Gln Pro Ala Leu Lys His Arg Thr Gly Asn Trp Arg Ala
      35      40      45
Cys Tyr Pro Val Leu Gly Val Gly Phe Ser Glu Gly Met Val Phe Ser
      50      55      60
Ala Ile Ala Thr Asn Leu Val Thr Tyr Leu Thr Val Leu His Glu
65      70      75      80
Ser Lys Val Asp Ala Ala Lys Asn Ile Ser Ala Trp Ser Gly Val Cys
      85      90      95
Phe Leu Thr Pro Leu Leu Gly Ala Phe Val Ala Asp Ser Tyr Leu Gly
      100      105      110
Arg Tyr Trp Thr Ile Val Val Val Leu Pro Val Tyr Ile Val Ala Met
      115      120      125
Leu Val Leu Ile Ala Ser Ala Ser Leu Pro Val Leu Phe Gln Ser Asp
      130      135      140
Val His Pro Ala Val Val Tyr Leu Gly Ile Tyr Leu Ala Ala Ile Ala
145      150      155      160
Ser Gly Gly Val Lys Pro Cys Ile Ser Ala Phe Gly Ala Asp Gln Phe
      165      170      175
Asp Ser Asn Asp Pro Ala Glu Leu Val Lys Lys Gly Ser Phe Phe Asn
      180      185      190
Trp Tyr Phe Phe Leu Thr Thr Thr Ser Ser Leu Leu Ser Gly Thr Val
      195      200      205
Ile Val Trp Leu Gln Asp Asn Val Arg Trp Ala Val Ser Tyr Val Ile
      210      215      220
Pro Thr Val Leu Met Leu Ile Cys Phe Pro Ala Phe Leu Ala Gly Ser
225      230      235      240
Arg Val Tyr Arg Phe Arg Glu Met Gly Val Ser Pro Ile Thr Ser Leu
      245      250      255
Leu Gln Val Val Val Ala Ala Val Arg Lys Trp Asn Ala Lys Leu Pro
      260      265      270
Asp Asp Ser Ser Leu Leu Tyr Glu Gln Ala Ser Ser Pro Cys Thr Thr
      275      280      285
Glu Ala Ser His Lys Asn Lys His Thr Asn Gln Phe Arg Phe Phe Asp
      290      295      300
Lys Ala Ala Ile Val Pro Pro Gly Asn Glu Ser Thr Val Gln Thr Ser
305      310      315      320
Pro Trp Arg Leu Cys Thr Val Thr Gln Val Glu Glu Leu Lys Met Leu
      325      330      335
Leu Ser Thr Leu Pro Thr Trp Ala Ser Phe Val Ile Phe Tyr Ala Val
      340      345      350
Thr Ser Gln Met Gln Ser Thr Met Ile Glu Gln Gly Met Leu Met Asp
      355      360      365
Asn His Val Gly Ser Phe Ala Ile Pro Pro Ala Ser Met Pro Ile Ile
      370      375      380
Gly Val Leu Ser Phe Leu Ile Trp Val Ala Ala Tyr Glu Thr Val Leu
385      390      395      400
Ala Pro Leu Ala Arg Arg Phe Thr Gly Asn Glu Lys Gly Phe Ser Gln
      405      410      415
Trp Gln Arg Leu Ala Ile Gly Gln Ala Leu Ser Ile Leu Thr Met Ala
      420      425      430
Leu Ala Ala Leu Val Glu Thr Arg Arg Leu Ala Ile Ala Glu Ala Ser
      435      440      445
Gly Leu Arg His Arg Glu Val Pro Val Pro Met Ser Ile Leu Trp Gln
450      455      460
Gly Pro Val Phe Phe Val His Gly Ala Ala Glu Val Phe Gly Ala Ile
465      470      475      480
Gly Met Thr Glu Phe Phe Tyr Asp Gln Ala Pro Ala Thr Met Lys Ser
      485      490      495
Leu Cys Ala Ala Phe Gly Gln Leu Ala Val Ala Ser Gly Ser Tyr Leu
      500      505      510
Asn Thr Val Val Leu Ser Val Val Ala Leu Ala Thr Thr Arg Gly Gly
      515      520      525
Ala Thr Gly Trp Ile Ser Asp Asn Leu Asn Glu Gly His Leu Asp Tyr
530      535      540

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PF59082SeqList_PF59082.txt

Phe Phe Trp Met Met Ala Ala Leu Ser Leu Leu Asn Leu Ala Leu Phe
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 Val Arg Tyr Ser Met Arg His Thr Asp Arg Gln Arg Lys Gln Asp Leu
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 Gly Leu Ser

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<220>
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 gac caa gaa gct ctc ctc ctt cca ctt cca cag gat gtt ggc ctt tac 96
 Asp Gln Glu Ala Leu Leu Leu Pro Leu Pro Gln Asp Val Gly Leu Tyr
 20 25 30
 aca ggt gat gga tct gtt gat gtc aaa ggg cgc cct gcg tta aag ggc 144
 Thr Gly Asp Gly Ser Val Asp Val Lys Gly Arg Pro Ala Leu Lys Gly
 35 40 45
 act aca ggc aat tgg aaa gca tgc ttt ttc atc cta ggg aat gaa tgt 192
 Thr Thr Gly Asn Trp Lys Ala Cys Phe Phe Ile Leu Gly Asn Glu Cys
 50 55 60
 tgt gaa agg ctg gcc tac tac gga att gca aaa aac cta gtt act tat 240
 Cys Glu Arg Leu Ala Tyr Tyr Gly Ile Ala Lys Asn Leu Val Thr Tyr
 65 70 75 80
 ttg aaa gtg aag ctt cat cta ggc aac ctc gag gct gca aga cat gtt 288
 Leu Lys Val Lys Leu His Leu Gly Asn Leu Glu Ala Ala Arg His Val
 85 90 95
 acc act tgg caa ggg aca tgc tat ctc act ccc ctt gtt gga ggc atc 336
 Thr Thr Trp Gln Gly Thr Cys Tyr Leu Thr Pro Leu Val Gly Gly Ile
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 Leu Ala Asp Ser Arg Trp Gly Lys Tyr Trp Thr Ile Ala Val Phe Ser
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 Ser Val Tyr Phe Ile Gly Leu Ala Ile Leu Thr Leu Ser Ala Ser Val
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 Pro Ala Leu Gln Pro Pro Ser Cys Leu Arg Thr Val Cys Pro Glu Ala
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 Ser Leu Leu Gln Tyr Gly Ile Phe Phe Gly Gly Leu Tyr Met Ile Ala
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 Leu Gly Thr Gly Gly Ile Lys Pro Cys Val Ser Ser Phe Gly Ala Asp
 180 185 190
 caa ttt gat gac act gac caa gca gag aga gct aag aag ggt tca ttc 624
 Gln Phe Asp Asp Thr Asp Gln Ala Glu Arg Ala Lys Lys Gly Ser Phe
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 ttc aat tgg ttc tac ttc tgt ata aat ata ggt tca ttc ata tca ggc 672
 Phe Asn Trp Phe Tyr Phe Cys Ile Asn Ile Gly Ser Phe Ile Ser Gly
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 Thr Met Ile Val Trp Ile Gln Asp Asn Thr Gly Trp Gly Ile Gly Phe
 225 230 235 240
 gcg att cct act ata ttc atg gca tta gct att tca ttc ttc ttc tca 768
 Ala Ile Pro Thr Ile Phe Met Ala Leu Ala Ile Ser Phe Phe Phe Ser
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 gct tca aat aag tac aga ttc caa aaa cct ggt ggg agt cca ctc aca 816
 Ala Ser Asn Lys Tyr Arg Phe Gln Lys Pro Gly Gly Ser Pro Leu Thr
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PF59082SeqList_PF59082.txt

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Val	Pro	His	Asp	Thr	Ser	Leu	Leu	Tyr	Glu	Val	Asp	Gly	Gln	Thr	Ser	
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Ala	Ile	Glu	Gly	Ser	Arg	Lys	Leu	Glu	His	Thr	Asn	Glu	Leu	Glu	Phe	
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Leu	Asp	Arg	Ala	Ala	Val	Ile	Ser	Ser	Ala	Asp	Leu	Lys	Ser	Glu	Ser	
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Phe	Thr	Asp	Pro	Trp	Lys	Leu	Cys	Thr	Val	Thr	Gln	Val	Glu	Glu	Leu	
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Lys	Ile	Leu	Ile	Arg	Met	Phe	Pro	Ile	Trp	Ala	Thr	Thr	Ile	Ile	Phe	
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Ser	Ala	Val	Tyr	Ala	Gln	Asn	Ser	Ser	Met	Phe	Ile	Glu	Gln	Gly	Met	
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Ser	Thr	Phe	Asp	Val	Ile	Ser	Val	Ile	Met	Trp	Val	Pro	Leu	Tyr	Asp	
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Phe	Ser	Glu	Leu	Gln	Arg	Met	Gly	Ile	Gly	Leu	Val	Leu	Ser	Ile	Leu	
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Thr	Cys	Ile	Gly	Gln	Val	Glu	Phe	Phe	Tyr	Asp	Gln	Ala	Pro	Asp	Ala	
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Asn	Tyr	Ile	Ser	Ser	Ile	Ile	Leu	Thr	Leu	Val	Ser	Tyr	Ile	Thr	Thr	
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cag	gga	gga	gat	cct	gga	tgg	atc	cct	gac	aat	ctg	aat	gaa	ggc	cat	1680
Gln	Gly	Gly	Asp	Pro	Gly	Trp	Ile	Pro	Asp	Asn	Leu	Asn	Glu	Gly	His	
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Leu	Asp	Arg	Phe	Phe	Trp	Leu	Ile	Ala	Gly	Ile	Ser	Phe	Val	Asn	Leu	
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      35      40      45
Thr Thr Gly Asn Trp Lys Ala Cys Phe Phe Ile Leu Gly Asn Glu Cys
      50      55      60
Cys Glu Arg Leu Ala Tyr Tyr Gly Ile Ala Lys Asn Leu Val Thr Tyr
65      70      75      80
Leu Lys Val Lys Leu His Leu Gly Asn Leu Glu Ala Ala Arg His Val
      85      90      95
Thr Thr Trp Gln Gly Thr Cys Tyr Leu Thr Pro Leu Val Gly Gly Ile
      100      105      110
Leu Ala Asp Ser Arg Trp Gly Lys Tyr Trp Thr Ile Ala Val Phe Ser
      115      120      125
Ser Val Tyr Phe Ile Gly Leu Ala Ile Leu Thr Leu Ser Ala Ser Val
      130      135      140
Pro Ala Leu Gln Pro Pro Ser Cys Leu Arg Thr Val Cys Pro Glu Ala
145      150      155      160
Ser Leu Leu Gln Tyr Gly Ile Phe Phe Gly Gly Leu Tyr Met Ile Ala
      165      170      175
Leu Gly Thr Gly Gly Ile Lys Pro Cys Val Ser Ser Phe Gly Ala Asp
      180      185      190
Gln Phe Asp Thr Asp Gln Ala Glu Arg Ala Lys Lys Gly Ser Phe
      195      200      205
Phe Asn Trp Phe Tyr Phe Cys Ile Asn Ile Gly Ser Phe Ile Ser Gly
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Thr Met Ile Val Trp Ile Gln Asp Asn Thr Gly Trp Gly Ile Gly Phe
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Val Pro His Asp Thr Ser Leu Leu Tyr Glu Val Asp Gly Gln Thr Ser
      290      295      300
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305      310      315      320
Leu Asp Arg Ala Ala Val Ile Ser Ser Ala Asp Leu Lys Ser Glu Ser
      325      330      335
Phe Thr Asp Pro Trp Lys Leu Cys Thr Val Thr Gln Val Glu Glu Leu
      340      345      350
Lys Ile Leu Ile Arg Met Phe Pro Ile Trp Ala Thr Thr Ile Ile Phe
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      515      520      525
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PF59082SeqList_PF59082.txt

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Leu	Leu	Asp	Ala	Pro	Lys	Ala	Thr	Leu	Pro	Met	Ser	Val	Phe	Trp	Leu	
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Val	Pro	Gln	Tyr	Ala	Ile	His	Gly	Ile	Ala	Asn	Ala	Phe	Met	Asp	Val	
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Glu	Val	Glu	Leu	Tyr	His	His	Gly	Asn	Gly	Thr	Asp	Asp	Ala	Lys	Lys	
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PF59082SeqList_PF59082.txt

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PF59082SeqList_PF59082.txt

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 Ile Thr Pro Leu Ile Gly Ala Phe Phe Ala Asp Ala Tyr Met Gly Arg
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 Phe Trp Thr Ile Ala Ile Phe Met Ile Ile Tyr Ile Phe Gly Leu Ala
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 Leu Leu Thr Met Ala Ser Ser Val Lys Gly Leu Val Pro Thr Ser Cys
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 Glu Lys Lys Ser Lys Ser Ser Phe Phe Asn Trp Phe Tyr Phe Ser Ile
 180 185 190
 aac atc ggc gcg ctg gtg gcg tcc acg gtg ctg gtg tac gtg cag acg 624
 Asn Ile Gly Ala Leu Val Ala Ser Thr Val Leu Val Tyr Val Gln Thr
 195 200 205
 cac gtg ggc tgg ggc tgg ggc ttc ggc atc ccc gcc gtg gtc atg gcc 672
 His Val Gly Trp Gly Trp Gly Phe Gly Ile Pro Ala Val Val Met Ala
 210 215 220
 atc gcc gtc ggc agc ttc gtg ggc acg ccg ctg tac agg cac cag 720
 Ile Ala Val Gly Ser Phe Phe Val Gly Thr Pro Leu Tyr Arg His Gln
 225 230 235 240
 aag ccc ggg ggc agc ccg ctg acg cgc atc gcg cag gtg ctc gtc gcg 768
 Lys Pro Gly Gly Ser Pro Leu Thr Arg Ile Ala Gln Val Leu Val Ala
 245 250 255
 tgc gcg cgc aag tgg aac gtg gcc gtg ccc gcg gac aag tcg cgg ctg 816
 Cys Ala Arg Lys Trp Asn Val Ala Val Pro Ala Asp Lys Ser Arg Leu
 260 265 270
 cac gag acg gtg gac ggg gag tcc ggc atc gag ggg agc cgc aag ctg 864

PF59082SeqList_PF59082.txt

His	Glu	Thr	Val	Asp	Gly	Glu	Ser	Gly	Ile	Glu	Gly	Ser	Arg	Lys	Leu	
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Glu	His	Ser	Glu	Gln	Leu	Ala	Cys	Leu	Asp	Arg	Ala	Ala	Val	Val	Thr	
	290					295					300					
gcc	gag	gac	ggc	gcg	gag	acg	agc	ccg	tgg	cg	ctg	tgc	tcg	gtg	acg	960
Ala	Glu	Asp	Gly	Ala	Glu	Thr	Ser	Pro	Trp	Arg	Leu	Cys	Ser	Val	Thr	
305					310					315					320	
cag	gtg	gag	gag	ctc	aag	agc	gtg	atc	cg	ctg	ctg	ccc	atc	tgg	gcc	1008
Gln	Val	Glu	Glu	Leu	Lys	Ser	Val	Ile	Arg	Leu	Leu	Pro	Ile	Trp	Ala	
				325					330					335		
agc	ggg	atc	gtg	ttc	gcg	gcg	gtg	tac	tcg	cag	atg	agc	acc	atg	ttc	1056
Ser	Gly	Ile	Val	Phe	Ala	Ala	Val	Tyr	Ser	Gln	Met	Ser	Thr	Met	Phe	
		340						345					350			
gtg	ctg	cag	ggc	aac	acg	ctg	gac	cag	agc	atg	ggg	ccc	cgg	ttc	aag	1104
Val	Leu	Gln	Gly	Asn	Thr	Leu	Asp	Gln	Ser	Met	Gly	Pro	Arg	Phe	Lys	
		355					360					365				
atc	ccc	tcg	gcg	acg	ctg	tcc	atg	gtg	gac	acc	atc	agc	gtc	atc	gtc	1152
Ile	Pro	Ser	Ala	Thr	Leu	Ser	Met	Val	Asp	Thr	Ile	Ser	Val	Ile	Val	
	370					375					380					
tgg	gtc	ccc	gtg	tac	gac	gcg	gcc	atc	gtg	ccc	ctg	gtg	cgc	tcc	tac	1200
Trp	Val	Pro	Val	Tyr	Asp	Arg	Ala	Ile	Val	Pro	Leu	Val	Arg	Ser	Tyr	
385					390					395					400	
acc	ggg	agg	ccg	cg	ggg	ttc	acg	cag	ctg	cag	cgc	atg	ggc	atc	ggc	1248
Thr	Gly	Arg	Pro	Arg	Gly	Phe	Thr	Gln	Leu	Gln	Arg	Met	Gly	Ile	Gly	
				405					410					415		
ctc	gtc	gtc	tcc	atc	ttc	tcc	atg	gtg	gcg	gcg	ggc	gtg	ctg	gac	atc	1296
Leu	Val	Val	Ser	Ile	Phe	Ser	Met	Val	Ala	Ala	Gly	Val	Leu	Asp	Ile	
			420					425					430			
gtg	cgg	ctg	cgc	gcc	atc	gcg	cgg	cac	ggc	ctg	tac	ggc	gag	aac	gac	1344
Val	Arg	Leu	Arg	Ala	Ile	Ala	Arg	His	Gly	Leu	Tyr	Gly	Glu	Asn	Asp	
		435					440					445				
atc	gtg	ccc	atc	tcc	atc	ttc	tgg	cag	ata	ccg	cag	tac	ttc	atc	atc	1392
Ile	Val	Pro	Ile	Ser	Ile	Phe	Trp	Gln	Ile	Pro	Gln	Tyr	Phe	Ile	Ile	
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gga	tgc	gcg	gag	gtg	ttc	acc	ttc	gtg	ggg	cag	ctg	gag	ttc	ttc	tac	1440
Gly	Cys	Ala	Glu	Val	Phe	Thr	Phe	Val	Gly	Gln	Leu	Glu	Phe	Phe	Tyr	
465					470				475						480	
gac	cag	gcg	ccc	gac	gcc	atg	agg	agc	atg	tgc	tcc	gcg	ctg	tcg	ctc	1488
Asp	Gln	Ala	Pro	Asp	Ala	Met	Arg	Ser	Met	Cys	Ser	Ala	Leu	Ser	Leu	
				485					490					495		
acc	acc	gtc	gcg	ctc	ggc	aac	tac	ctc	agc	acg	gtc	ctg	gtg	acc	atc	1536
Thr	Thr	Val	Ala	Leu	Gly	Asn	Tyr	Leu	Ser	Thr	Val	Leu	Val	Thr	Ile	
			500					505					510			
gtc	acc	cac	atc	acc	acc	agg	cac	ggc	atc	ggg	tgg	atc	ccg	gag		1584
Val	Thr	His	Ile	Thr	Thr	Arg	His	Gly	Arg	Ile	Gly	Trp	Ile	Pro	Glu	
		515					520					525				
aac	ctc	aac	cgc	ggc	cac	ctc	gac	tac	ttc	ttc	tgg	ctg	ctc	gca	gtg	1632
Asn	Leu	Asn	Arg	Gly	His	Leu	Asp	Tyr	Phe	Phe	Trp	Leu	Leu	Ala	Val	
	530					535					540					
ctc	agc	ctc	ctc	aac	ttc	ctt	gcc	tac	ctc	gtc	atc	gcc	agc	tgg	tac	1680
Leu	Ser	Leu	Leu	Asn	Phe	Leu	Ala	Tyr	Leu	Val	Ile	Ala	Ser	Trp	Tyr	
545					550					555					560	
aag	tac	aag	aag	acg	gcc	gat	gat	tac	cct	ggc	gcc	aaa	ggg	gag	cac	1728
Lys	Tyr	Lys	Lys	Thr	Ala	Asp	Asp	Tyr	Pro	Gly	Ala	Lys	Gly	Glu	His	
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ggt	aca	gag	cac	tga												1743
Gly	Thr	Glu	His													
			580													

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<212> PRT

<213> Zea mays

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Lys Gly Asn Pro Ala Val Lys Lys Gly Thr Gly Asn Trp Arg Ala Cys
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Pro	Tyr	Ile	20	Leu	Ala	Asn	Glu	Cys	25	Glu	Arg	Leu	Ala	Tyr	Tyr	Gly																																																																																												
			35						40								45	50	55	60	65	70	75	80	85	90	95	100	105	110	115	120	125	130	135	140	145	150	155	160	165	170	175	180	185	190	195	200	205	210	215	220	225	230	235	240	245	250	255	260	265	270	275	280	285	290	295	300	305	310	315	320	325	330	335	340	345	350	355	360	365	370	375	380	385	390	395	400	405	410	415	420	425	430	435	440	445	450	455	460	465	470	475	480	485	490	495	500
Met	Ser	Thr	Asn	Leu	Val	Asn	Tyr	Met	Lys	Thr	Arg	Leu	Gly	Gln	Val	Val																																																																																												
Asn	Ser	Val	Ala	Ser	Asn	Asn	Val	Thr	Asn	Trp	Gln	Gly	Thr	Cys	Tyr	Arg																																																																																												
Ile	Thr	Pro	Leu	Ile	Gly	Ala	Phe	Phe	Ala	Asp	Ala	Tyr	Met	Gly	Arg	Val																																																																																												
Phe	Trp	Thr	Ile	Ala	Ile	Phe	Met	Ile	Ile	Tyr	Ile	Phe	Gly	Leu	Ala	Val																																																																																												
Leu	Leu	Thr	Met	Ala	Ser	Ser	Val	Lys	Gly	Leu	Val	Pro	Thr	Ser	Cys	Val																																																																																												
Gly	Asp	Lys	Asp	Val	Cys	His	Pro	Thr	Asp	Ala	Gln	Ala	Ala	Val	Val	Val																																																																																												
Phe	Val	Ala	Leu	Tyr	Leu	Ile	Ala	Leu	Gly	Thr	Gly	Gly	Ile	Lys	Pro	Arg																																																																																												
Cys	Val	Ser	Ser	Phe	Gly	Ala	Asp	Gln	Phe	Asp	Glu	Asn	Asp	Glu	Arg	Val																																																																																												
Glu	Lys	Lys	Ser	Lys	Ser	Ser	Phe	Phe	Asn	Trp	Phe	Tyr	Phe	Ser	Ile	Val																																																																																												
Asn	Ile	Gly	Ala	Leu	Val	Ala	Ser	Thr	Val	Leu	Val	Tyr	Val	Gln	Thr	Val																																																																																												
His	Val	Gly	Trp	Gly	Trp	Gly	Phe	Gly	Ile	Pro	Ala	Val	Val	Met	Ala	Val																																																																																												
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His	Glu	Thr	Val	Asp	Gly	Glu	Ser	Gly	Ile	Glu	Gly	Ser	Arg	Lys	Leu	Val																																																																																												
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Gln	Val	Glu	Glu	Leu	Lys	Ser	Val	Ile	Arg	Leu	Leu	Pro	Ile	Trp	Ala	Val																																																																																												
Ser	Gly	Ile	Val	Phe	Ala	Ala	Val	Tyr	Ser	Gln	Met	Ser	Thr	Met	Phe	Val																																																																																												
Val	Leu	Gln	Gly	Asn	Thr	Leu	Asp	Gln	Ser	Met	Gly	Pro	Arg	Phe	Lys	Val																																																																																												
Ile	Pro	Ser	Ala	Thr	Leu	Ser	Met	Val	Asp	Thr	Ile	Ser	Val	Ile	Val	Val																																																																																												
Trp	Val	Pro	Val	Tyr	Asp	Arg	Ala	Ile	Val	Pro	Leu	Val	Arg	Ser	Tyr	Val																																																																																												
Thr	Gly	Arg	Pro	Arg	Gly	Phe	Thr	Gln	Leu	Gln	Arg	Met	Gly	Ile	Gly	Val																																																																																												
Leu	Val	Val	Ser	Ile	Phe	Ser	Met	Val	Ala	Ala	Gly	Val	Leu	Asp	Ile	Val																																																																																												
Val	Arg	Leu	Arg	Ala	Ile	Ala	Arg	His	Gly	Leu	Tyr	Gly	Glu	Asn	Asp	Val																																																																																												
Ile	Val	Pro	Ile	Ser	Ile	Phe	Trp	Gln	Ile	Pro	Gln	Tyr	Phe	Ile	Ile	Val																																																																																												
Gly	Cys	Ala	Glu	Val	Phe	Thr	Phe	Val	Gly	Gln	Leu	Glu	Phe	Phe	Tyr	Val																																																																																												
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PF59082SeqList_PF59082.txt

Gly Thr Glu His
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cag cgg cag gag gcg gtt tcg tcc atg gaa tcc ggc ggc ggc gcg tcg      96
Gln Arg Gln Glu Ala Val Ser Ser Met Glu Ser Gly Gly Gly Ala Ser
          20          25          30
ggg gcg gcg acc aag cgc ttc acc tgg aag ggc ccg gta atc gtc cta     144
Gly Ala Ala Thr Lys Arg Phe Thr Trp Lys Gly Pro Val Ile Val Leu
          35          40          45
gtc ttc gag ctg ctg gag agc atc gcg ttc tcg ggc gtg gct ctc aac     192
Val Phe Glu Leu Leu Glu Ser Ile Ala Phe Ser Gly Val Ala Leu Asn
          50          55          60
ctg gtg gtg tac ctg gcc acg gtg ctg cac ggc agc acc gcc ttc aac     240
Leu Val Val Tyr Leu Ala Thr Val Leu His Gly Ser Thr Ala Phe Asn
          65          70          75          80
gcc gcc cac gtc gac acc tgg aac ggc acc acc ttc atc gtc ccc gtc     288
Ala Ala His Val Asp Thr Trp Asn Gly Thr Phe Ile Val Pro Val
          85          90          95
atc ggc gcc ttc ctc gcc gac agc tac tgg ggc aag tac agg acc atc     336
Ile Gly Ala Phe Leu Ala Asp Ser Tyr Trp Gly Lys Tyr Arg Thr Ile
          100          105          110
ctc gcc tcc atc gtc ttc tac ctc gtg ggc ctg gtg ctc ctc acc gtg     384
Leu Ala Ser Ile Val Phe Tyr Leu Val Gly Leu Val Leu Leu Thr Val
          115          120          125
tcc gcc gcg atc ccg tcg ctg cgg cct gcc acg gcg tgc cag atg ggc     432
Ser Ala Ala Ile Pro Ser Leu Arg Pro Ala Thr Ala Cys Gln Met Gly
          130          135          140
gag tcg tgc gcg ccg gcg acc aag acg cag ttc tct gtc ttc ttc gcc     480
Glu Ser Cys Ala Pro Ala Thr Lys Thr Gln Phe Ser Val Phe Phe Ala
          145          150          155          160
gcg ctc tac ctc acc tcc atc ggc acg gga ggc gtc aag tcc gcg ctg     528
Ala Leu Tyr Leu Thr Ser Ile Gly Thr Gly Val Lys Ser Ala Leu
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ctc ccc ttc ggc gcc gag cag tac gtc gac gac gcg ggc ccg ccg gag     576
Leu Pro Phe Gly Ala Glu Gln Tyr Val Asp Asp Ala Gly Arg Pro Glu
          180          185          190
cgg aag cag gcc ttt ttc agc tgg ttc ttc gcc gcc atc aac ctg ggc     624
Arg Lys Gln Ala Phe Phe Ser Trp Phe Phe Ala Ala Ile Asn Leu Gly
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Ile Phe Val Ala Gly Thr Leu Val Ser Trp Leu Glu Gln Asn Val Ser
          210          215          220
tgg gcg ctc ggc ttc ggc atc ggc acg gcc tgc ctg ttc gtg gcc gcg     720
Trp Ala Leu Gly Phe Gly Ile Gly Thr Ala Cys Leu Phe Val Ala Ala
          225          230          235          240
ctc gcc ttc gcg gcg ggc acg ccc tgc tac agg gtg cag atg ccg acg     768
Leu Ala Phe Ala Ala Gly Thr Pro Cys Tyr Arg Val Gln Met Pro Thr
          245          250          255
ggc agc ccg ctc aag gac atc atc agg gtg ttc gtc gcc gcc ttc agg     816
Gly Ser Pro Leu Lys Asp Ile Ile Arg Val Phe Val Ala Ala Phe Arg
          260          265          270
aag cgc gac gtc agg atg gaa cgg gac gag ggc gcg gcg gtg ctg ctg     864
Lys Arg Asp Val Arg Met Glu Arg Asp Glu Gly Ala Ala Val Leu Leu
          275          280          285
cac gaa gac gaa gcc gaa gac gaa gac gaa gac ggc gat agc gct gga     912
His Glu Asp Glu Ala Glu Asp Glu Asp Glu Asp Gly Asp Ser Ala Gly

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PF59082SeqList_PF59082.txt

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305	310	315	320
gcc gcg gcg atc atc gtc atg gac gga gac aag gag cgg gag agc gaa			1008
Ala Ala Ala Ile Ile Val Met Asp Gly Asp Lys Glu Arg Glu Ser Glu			
	325	330	335
tgg tct ctg tgc acg gtg agc gag gtg gag ggc gtg aag atc ctg gtg			1056
Trp Ser Leu Cys Thr Val Ser Glu Val Glu Gly Val Lys Ile Leu Val			
	340	345	350
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Arg Met Leu Pro Ile Trp Met Thr Cys Val Leu Tyr Ala Ala Ser Leu			
	355	360	365
ggg cag atg acc acc acc ttc atc cag cag ggg atg gcc atg gac acg			1152
Gly Gln Met Thr Thr Thr Phe Ile Gln Gln Gly Met Ala Met Asp Thr			
	370	375	380
cgg ctg ggc ggc cgg ttc aag gtg ccc gtg gcg tcg ttg gtg tcc gtg			1200
Arg Leu Gly Gly Arg Phe Lys Val Pro Val Ala Ser Leu Val Ser Val			
	385	390	400
gag gtg gtg ttc atg ttc ctg tgg gtg gcg ctg cac gac gcc gcc atc			1248
Glu Val Val Phe Met Leu Leu Trp Val Ala Leu His Asp Ala Ala Ile			
	405	410	415
atc ccg gcg gcc cgg cgg ctg acg ggg cgc ccc ggt ggg ctg acg cat			1296
Ile Pro Ala Ala Arg Arg Leu Thr Gly Arg Pro Gly Gly Leu Thr His			
	420	425	430
gtg cag cgc atg ggc gtg ggg cgg ttc ctg gtg gtg ctg gcc gtg ggg			1344
Val Gln Arg Met Gly Val Gly Arg Phe Leu Val Val Leu Ala Val Gly			
	435	440	445
acg gtc gcg ctt gtc gag agg cgc ctg ctc cgc tcc atc cac ggc ggt			1392
Thr Val Ala Leu Val Glu Arg Arg Leu Leu Arg Ser Ile His Gly Gly			
	450	455	460
agc tgc ccg atg agc atc gtg tgg cag gtg ccg cag ttc gtg ctg gtg			1440
Ser Cys Pro Met Ser Ile Val Trp Gln Val Pro Gln Phe Val Leu Val			
	465	470	480
gcg ggc tcc gac gtt ttc tgc ggc atc gcg cag ctg gag ttc ttc tac			1488
Ala Gly Ser Asp Val Phe Cys Gly Ile Ala Gln Leu Glu Phe Phe Tyr			
	485	490	495
ggg gag gcc ccc gcc gcg atg cgc agc atc tgc tcg gcc ttc tcc ttc			1536
Gly Glu Ala Pro Ala Ala Met Arg Ser Ile Cys Ser Ala Phe Ser Phe			
	500	505	510
ctg gcg ctg tcg ctg ggg ttc tac gtc aac tcg ctg gtg gtg acg ctg			1584
Leu Ala Leu Ser Leu Gly Phe Tyr Val Asn Ser Leu Val Val Thr Leu			
	515	520	525
gtg gcg gcc gtg acg aag cgg ccc ggg tgg ctg gcg acg gac ctc gac			1632
Val Ala Ala Val Thr Lys Arg Pro Gly Trp Leu Ala Thr Asp Leu Asp			
	530	535	540
acc ggc cac ctg gac tac tac ttc tgg ctc tgg acc atc atc agc gtc			1680
Thr Gly His Leu Asp Tyr Tyr Phe Trp Leu Trp Thr Ile Ile Ser Val			
	545	550	560
gcc aac ctg ctg ctc tac atg gtg ctc gcc cgg tac acg ccc aag			1728
Ala Asn Leu Leu Leu Tyr Met Val Leu Ala Arg Tyr Thr Pro Lys			
	565	570	575
cag gtc gcc gct gcc gtg gtg gag ccg atg cgt ccc agc aac agt ggc			1776
Gln Val Ala Ala Val Val Glu Pro Met Arg Pro Ser Asn Ser Gly			
	580	585	590
ggc agc gac gaa tga			1791
Gly Ser Asp Glu			
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PF59082SeqList_PF59082.txt

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Ala	Ala	His	Val	Asp	Thr	Trp	Asn	Gly	Thr	Thr	Phe	Ile	Val	Pro	Val
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Ile	Gly	Ala	Phe	Leu	Ala	Asp	Ser	Tyr	Trp	Gly	Lys	Tyr	Arg	Thr	Ile
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Leu	Ala	Ser	Ile	Val	Phe	Tyr	Leu	Val	Gly	Leu	Val	Leu	Leu	Thr	Val
		115					120					125			
Ser	Ala	Ala	Ile	Pro	Ser	Leu	Arg	Pro	Ala	Thr	Ala	Cys	Gln	Met	Gly
	130					135					140				
Glu	Ser	Cys	Ala	Pro	Ala	Thr	Lys	Thr	Gln	Phe	Ser	Val	Phe	Phe	Ala
145					150					155					160
Ala	Leu	Tyr	Leu	Thr	Ser	Ile	Gly	Thr	Gly	Gly	Val	Lys	Ser	Ala	Leu
				165					170					175	
Leu	Pro	Phe	Gly	Ala	Glu	Gln	Tyr	Val	Asp	Asp	Ala	Gly	Arg	Pro	Glu
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Arg	Lys	Gln	Ala	Phe	Phe	Ser	Trp	Phe	Phe	Ala	Ala	Ile	Asn	Leu	Gly
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Ile	Phe	Val	Ala	Gly	Thr	Leu	Val	Ser	Trp	Leu	Glu	Gln	Asn	Val	Ser
	210					215					220				
Trp	Ala	Leu	Gly	Phe	Gly	Ile	Gly	Thr	Ala	Cys	Leu	Phe	Val	Ala	Ala
225					230					235					240
Leu	Ala	Phe	Ala	Ala	Gly	Thr	Pro	Cys	Tyr	Arg	Val	Gln	Met	Pro	Thr
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Gly	Ser	Pro	Leu	Lys	Asp	Ile	Ile	Arg	Val	Phe	Val	Ala	Ala	Phe	Arg
			260					265					270		
Lys	Arg	Asp	Val	Arg	Met	Glu	Arg	Asp	Glu	Gly	Ala	Ala	Val	Leu	Leu
		275					280					285			
His	Glu	Asp	Glu	Ala	Glu	Asp	Glu	Asp	Glu	Asp	Gly	Asp	Ser	Ala	Gly
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Gln	Gln	Gln	Arg	Leu	Ala	Arg	Thr	Lys	Gly	Leu	Arg	Cys	Leu	Asp	Lys
305					310					315					320
Ala	Ala	Ala	Ile	Ile	Val	Met	Asp	Gly	Asp	Lys	Glu	Arg	Glu	Ser	Glu
				325					330					335	
Trp	Ser	Leu	Cys	Thr	Val	Ser	Glu	Val	Glu	Gly	Val	Lys	Ile	Leu	Val
			340					345					350		
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		355					360					365			
Gly	Gln	Met	Thr	Thr	Thr	Phe	Ile	Gln	Gln	Gly	Met	Ala	Met	Asp	Thr
	370					375					380				
Arg	Leu	Gly	Gly	Arg	Phe	Lys	Val	Pro	Val	Ala	Ser	Leu	Val	Ser	Val
385					390					395					400
Glu	Val	Val	Phe	Met	Leu	Leu	Trp	Val	Ala	Leu	His	Asp	Ala	Ala	Ile
				405					410					415	
Ile	Pro	Ala	Ala	Arg	Arg	Leu	Thr	Gly	Arg	Pro	Gly	Gly	Leu	Thr	His
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Val	Gln	Arg	Met	Gly	Val	Gly	Arg	Phe	Leu	Val	Val	Leu	Ala	Val	Gly
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Thr	Val	Ala	Leu	Val	Glu	Arg	Arg	Leu	Leu	Arg	Ser	Ile	His	Gly	Gly
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Ser	Cys	Pro	Met	Ser	Ile	Val	Trp	Gln	Val	Pro	Gln	Phe	Val	Leu	Val
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Ala	Gly	Ser	Asp	Val	Phe	Cys	Gly	Ile	Ala	Gln	Leu	Glu	Phe	Phe	Tyr
				485					490					495	
Gly	Glu	Ala	Pro	Ala	Ala	Met	Arg	Ser	Ile	Cys	Ser	Ala	Phe	Ser	Phe
				500				505					510		
Leu	Ala	Leu	Ser	Leu	Gly	Phe	Tyr	Val	Asn	Ser	Leu	Val	Val	Thr	Leu
		515					520					525			
Val	Ala	Ala	Val	Thr	Lys	Arg	Pro	Gly	Trp	Leu	Ala	Thr	Asp	Leu	Asp
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Ala	Asn	Leu	Leu	Leu	Tyr	Met	Val	Leu	Ala	Ala	Arg	Tyr	Thr	Pro	Lys
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cca gag gat gat gaa gct tcc tca cga tac act agc gac gga acg ctc 96
Pro Glu Asp Asp Glu Ala Ser Ser Arg Tyr Thr Ser Asp Gly Thr Leu
20 25 30
gat atc aac aag cag cgt gct ctg aag aag agc acc ggg aac tgg aga 144
Asp Ile Asn Lys Gln Arg Ala Leu Lys Lys Ser Thr Gly Asn Trp Arg
35 40 45
gca tgc ttc atg att ctg ggt acc gag ttc gcc gaa tgc ctg gca ttt 192
Ala Cys Phe Met Ile Leu Gly Thr Glu Phe Ala Glu Cys Leu Ala Phe
50 55 60
tac gcg acc gca aag aac ctg gtc acc tac ctg acg gct gag ctt ggt 240
Tyr Ala Thr Ala Lys Asn Leu Val Thr Tyr Leu Thr Ala Glu Leu Gly
65 70 75 80
gag acc aac atc gat gcc gcg acg aac gtg acc tgg att ggc agc 288
Glu Thr Asn Ile Asp Ala Ala Thr Asn Val Ser Thr Trp Ile Gly Ser
85 90 95
tgc tac ctg acg ccg ctc atc ggc gcc ttc ttg gcc gac acg tac tgg 336
Cys Tyr Leu Thr Pro Leu Ile Gly Ala Phe Leu Ala Asp Thr Tyr Trp
100 105 110
gga aga tac aag acg atg ata gtc ttc ctc ttg ctc tac atc gtt ggg 384
Gly Arg Tyr Lys Thr Met Ile Val Phe Leu Leu Leu Tyr Ile Val Gly
115 120 125
atg ctt act ctg aca gcg tcg gcg tgg ctc ccc ttg gcc atg gag gac 432
Met Leu Thr Leu Thr Ala Ser Ala Trp Leu Pro Leu Ala Met Glu Asp
130 135 140
gac tca cct gac aac agc gga ctt cgg cgt gcc aca gcg tac ctg ggg 480
Asp Ser Pro Asp Asn Ser Gly Leu Arg Arg Ala Thr Ala Tyr Leu Gly
145 150 155 160
ctc tac ctg gtt tcc cta ggc aca gga ggc atc aag ccc tgc acg gcg 528
Leu Tyr Leu Val Ser Leu Gly Thr Gly Gly Ile Lys Pro Cys Thr Ala
165 170 175
gcc ctc ggg gcc gac cag ttc gac ggc ggc gac gcg gcg gag ccg gtc 576
Ala Leu Gly Ala Asp Gln Phe Asp Gly Gly Asp Ala Ala Glu Arg Val
180 185 190
acc aag gcc tcc ttc ttc aac tgg tac tac ttc tgc acc aac atc ggc 624
Thr Lys Ala Ser Phe Phe Asn Trp Tyr Tyr Phe Cys Thr Asn Ile Gly
195 200 205
tcc ctg ctg tcg ggg acc gtg ctc gtc tgg gtg cag gaa aat att gga 672
Ser Leu Leu Ser Gly Thr Val Leu Val Trp Val Gln Glu Asn Ile Gly
210 215 220
tgg gga gtc ggg ttt acg gtg cag acg gtg ttc atg ctg ttc ggc ctc 720
Trp Gly Val Gly Phe Thr Val Gln Thr Val Phe Met Leu Phe Gly Leu
225 230 235 240
gcc gtg ttc gtc gcc ggt cgc aag gtg tat agg tac aag aag ctg ggc 768
Ala Val Phe Val Ala Gly Arg Lys Val Tyr Arg Tyr Lys Lys Leu Gly
245 250 255
ggg agc cct ctg aca agg gta gcc cag gtg gtt gtc gca gct gtg agg 816
Gly Ser Pro Leu Thr Arg Val Ala Gln Val Val Val Ala Ala Val Arg
260 265 270
aac tgc cat ctg gtg ctg cct gat gat acg tca gcc ctg tac cac gat 864
Asn Cys His Leu Val Leu Pro Asp Asp Thr Ser Ala Leu Tyr His Asp
275 280 285
aag ctt cta cca act gaa cca aat ttc agg att gag tct gcc aga caa 912

PF59082SeqList_PF59082.txt

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Phe	Arg	Phe	Phe	Asp	Lys	Ala	Ala	Ile	Ile	Thr	Gly	Glu	Lys	Gly	Ala	
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gca	gcg	ccg	acg	agc	ccg	tgg	aga	ctg	tgc	acg	gtg	tcc	cag	gtg	gag	1008
Ala	Ala	Pro	Thr	Ser	Pro	Trp	Arg	Leu	Cys	Thr	Val	Ser	Gln	Val	Glu	
				325					330					335		
gag	ctg	aag	atg	ctg	ctc	cgg	ttg	ctg	ccg	gtc	tgg	gca	tcc	atg	gtg	1056
Glu	Leu	Lys	Met	Leu	Leu	Arg	Leu	Leu	Pro	Val	Trp	Ala	Ser	Met	Val	
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ctc	ttc	ttc	gcc	gtc	agt	gcg	cag	acg	gta	acc	acg	ttc	att	gag	cag	1104
Leu	Phe	Phe	Ala	Val	Ser	Ala	Gln	Thr	Val	Thr	Thr	Phe	Ile	Glu	Gln	
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gct	agg	gtg	atg	gac	aac	cgc	atc	ggc	ccg	ttc	acc	att	cct	ccg	gcg	1152
Ala	Arg	Val	Met	Asp	Asn	Arg	Ile	Gly	Pro	Phe	Thr	Ile	Pro	Pro	Ala	
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tcg	ata	gcg	acc	ttc	gac	gtg	atc	agc	gtc	atg	gtc	tgc	gtc	ccc	gtc	1200
Ser	Ile	Ala	Thr	Phe	Asp	Val	Ile	Ser	Val	Met	Val	Cys	Val	Pro	Val	
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tac	gac	gcc	gtg	ctg	gtg	cct	ctg	gcc	cgg	cgt	gcc	act	ggc	aac	gac	1248
Tyr	Asp	Ala	Val	Leu	Val	Pro	Leu	Ala	Arg	Arg	Ala	Thr	Gly	Asn	Asp	
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cgc	ggc	ctg	tcg	cag	ctg	cac	cgg	ctc	tcc	atc	ggg	atc	gcg	ctg	tcc	1296
Arg	Gly	Leu	Ser	Gln	Leu	His	Arg	Leu	Ser	Ile	Gly	Ile	Ala	Leu	Ser	
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Val	Val	Val	Met	Val	Tyr	Ala	Ala	Leu	Leu	Glu	Gly	Arg	Arg	Leu	Ala	
		435				440					445					
ctc	gcg	cgg	gcc	aac	atg	ccc	gcc	atg	aac	atc	gcg	tgg	cag	gca	ccc	1392
Leu	Ala	Arg	Ala	Asn	Met	Pro	Ala	Met	Asn	Ile	Ala	Trp	Gln	Ala	Pro	
	450				455						460					
atg	ttc	gcc	gtg	cac	ggc	gcg	gcg	gcg	gtc	ttc	gcc	acc	gtc	ggc	gtg	1440
Met	Phe	Ala	Val	His	Gly	Ala	Ala	Ala	Val	Phe	Ala	Thr	Val	Gly	Val	
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ctc	gag	ttc	ttc	tac	gac	cag	tcg	ccg	gac	ggg	atg	aag	agc	ctc	ggc	1488
Leu	Glu	Phe	Phe	Tyr	Asp	Gln	Ser	Pro	Asp	Gly	Met	Lys	Ser	Leu	Gly	
			485				490						495			
aac	gcg	ctc	gcg	ctg	ctc	tcc	atg	gcg	gcc	ggg	agc	tat	ttc	aac	tcg	1536
Asn	Ala	Leu	Ala	Leu	Leu	Ser	Met	Ala	Ala	Gly	Ser	Tyr	Phe	Asn	Ser	
		500					505					510				
ctt	gcg	ctc	agc	gct	gtc	ggg	tcg	atc	acg	gcg	cgc	ggc	ggg	gaa	cgc	1584
Leu	Ala	Leu	Ser	Ala	Val	Gly	Ser	Ile	Thr	Ala	Arg	Gly	Gly	Glu	Arg	
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ggg	tgg	ctc	ccg	gac	gac	ctg	aac	aag	ggt	cat	atg	gac	tat	ttc	ttc	1632
Gly	Trp	Leu	Pro	Asp	Asp	Leu	Asn	Lys	Gly	His	Met	Asp	Tyr	Phe	Phe	
	530				535						540					
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Trp	Met	Met	Ala	Ala	Leu	Gly	Thr	Leu	Asn	Leu	Leu	His	Phe	Leu	His	
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 35 40 45
 Ala Cys Phe Met Ile Leu Gly Thr Glu Phe Ala Glu Cys Leu Ala Phe
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 Tyr Ala Thr Ala Lys Asn Leu Val Thr Tyr Leu Thr Ala Glu Leu Gly
 Seite 507

PF59082SeqList_PF59082.txt

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Gly	Arg	Tyr	Lys	Thr	Met	Ile	Val	Phe	Leu	Leu	Leu	Tyr	Ile	Val
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Met	Leu	Thr	Leu	Thr	Ala	Ser	Ala	Trp	Leu	Pro	Leu	Ala	Met	Glu
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Asp	Ser	Pro	Asp	Asn	Ser	Gly	Leu	Arg	Arg	Ala	Thr	Ala	Tyr	Leu
					150					155				160
Leu	Tyr	Leu	Val	Ser	Leu	Gly	Thr	Gly	Gly	Ile	Lys	Pro	Cys	Thr
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Ala	Leu	Gly	Ala	Asp	Gln	Phe	Asp	Gly	Gly	Asp	Ala	Ala	Glu	Arg
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Thr	Lys	Ala	Ser	Phe	Phe	Asn	Trp	Tyr	Tyr	Phe	Cys	Thr	Asn	Ile
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Ser	Leu	Leu	Ser	Gly	Thr	Val	Leu	Val	Trp	Val	Gln	Glu	Asn	Ile
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Trp	Gly	Val	Gly	Phe	Thr	Val	Gln	Thr	Val	Phe	Met	Leu	Phe	Gly
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Ala	Val	Phe	Val	Ala	Gly	Arg	Lys	Val	Tyr	Arg	Tyr	Lys	Lys	Leu
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Gly	Ser	Pro	Leu	Thr	Arg	Val	Ala	Gln	Val	Val	Val	Ala	Ala	Val
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Asn	Cys	His	Leu	Val	Leu	Pro	Asp	Asp	Thr	Ser	Ala	Leu	Tyr	His
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Phe	Arg	Phe	Phe	Asp	Lys	Ala	Ala	Ile	Ile	Thr	Gly	Glu	Lys	Gly
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Ala	Ala	Pro	Thr	Ser	Pro	Trp	Arg	Leu	Cys	Thr	Val	Ser	Gln	Val
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Glu	Leu	Lys	Met	Leu	Leu	Arg	Leu	Leu	Pro	Val	Trp	Ala	Ser	Met
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Leu	Phe	Phe	Ala	Val	Ser	Ala	Gln	Thr	Val	Thr	Thr	Phe	Ile	Glu
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Ala	Arg	Val	Met	Asp	Asn	Arg	Ile	Gly	Pro	Phe	Thr	Ile	Pro	Pro
					375						380			
Ser	Ile	Ala	Thr	Phe	Asp	Val	Ile	Ser	Val	Met	Val	Cys	Val	Pro
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Tyr	Asp	Ala	Val	Leu	Val	Pro	Leu	Ala	Arg	Arg	Ala	Thr	Gly	Asn
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Arg	Gly	Leu	Ser	Gln	Leu	His	Arg	Leu	Ser	Ile	Gly	Ile	Ala	Leu
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Val	Val	Val	Met	Val	Tyr	Ala	Ala	Leu	Leu	Glu	Gly	Arg	Arg	Leu
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Leu	Glu	Phe	Phe	Tyr	Asp	Gln	Ser	Pro	Asp	Gly	Met	Lys	Ser	Leu
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Asn	Ala	Leu	Ala	Leu	Leu	Ser	Met	Ala	Ala	Gly	Ser	Tyr	Phe	Asn
				500				505					510	
Leu	Ala	Leu	Ser	Ala	Val	Gly	Ser	Ile	Thr	Ala	Arg	Gly	Gly	Glu
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Trp	Met	Met	Ala	Ala	Leu	Gly	Thr	Leu	Asn	Leu	Leu	His	Phe	Leu
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Met Asn Thr Ile Gly 5

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Leu Leu Lys Asn Glu Asn Ser Gly Thr Asp Asp Asp Ser Lys Ile Asn 25 30 35

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Tyr Arg Gly Trp Lys Val Met Pro Phe Ile Ile Gly Asn Glu Ile Phe 40 45 50

gag aag cta gga gcc att ggc act tta tcc aat ctc ttg gtc tat ctc 306
Glu Lys Leu Gly Ala Ile Gly Thr Leu Ser Asn Leu Leu Val Tyr Leu 55 60 65

act acg gta ttc aac ttg gaa aac atc atg gct aca aat att atc aac 354
Thr Thr Val Phe Asn Leu Glu Asn Ile Met Ala Thr Asn Ile Ile Asn 70 75 80 85

atc ttt aat ggc agc acc aac ttt gct aca ttg cta gga gct ttt ctc 402
Ile Phe Asn Gly Ser Thr Asn Phe Ala Thr Leu Leu Gly Ala Phe Leu 90 95 100

tct gat gcc ttt ttg ggt cgc tac aag ata ctg gca ttc tgc aca atg 450
Ser Asp Ala Phe Phe Gly Arg Tyr Lys Ile Leu Ala Phe Cys Thr Met 105 110 115

gct tcc ttt gtg ggt ttg ttt gca ata caa ctg aca gca gca gtt gag 498
Ala Ser Phe Val Gly Leu Phe Ala Ile Gln Leu Thr Ala Ala Val Glu 120 125 130

aag ctg cat cca cct cac tgt gaa gag tcc acc ata tgc cag ggg cca 546
Lys Leu His Pro Pro His Cys Glu Glu Ser Thr Ile Cys Gln Gly Pro 135 140 145

aca gag ggg cag atg aca ttt cta aag aca ggt tta ggt tta ttg atg 594
Thr Glu Gly Gln Met Thr Phe Leu Lys Thr Gly Leu Gly Leu Leu Met 150 155 160 165

gta gga gct gca ggg atc cga cca tgt aac tta gca ttt ggt gct gat 642
Val Gly Ala Ala Gly Ile Arg Pro Cys Asn Leu Ala Phe Gly Ala Asp 170 175 180

caa ttt aat cct aac aca gat tcg gga aag ggg atc gct agc ttc 690
Gln Phe Asn Pro Asn Thr Asp Ser Gly Lys Lys Gly Ile Ala Ser Phe 185 190 195

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Phe Asn Trp Tyr Phe Phe Thr Phe Thr Val Ala Gln Met Ile Ser Leu 200 205 210

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Thr Ile Ile Val Tyr Ile Gln Ser Asn Val Ser Trp Ala Val Gly Leu 215 220 225

gga att cct tct gct ttg atg ttt gta tct tct ata atc ttc ttc atg 834
Gly Ile Pro Ser Ala Leu Met Phe Val Ser Ser Ile Ile Phe Phe Met 230 235 240 245

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Gly Ser Lys Leu Tyr Val Lys Val Lys Pro Ser Gly Ser Pro Ile Thr 250 255 260

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Ser Ile Val Gln Val Ile Val Val Ala Thr Lys Lys Arg Arg Leu Lys 265 270 275

ctt cct gaa tat caa tat cct tcc ctc ttc aac tat gtg gct ccc aag 978
Leu Pro Glu Tyr Gln Tyr Pro Ser Leu Phe Asn Tyr Val Ala Pro Lys 280 285 290

tca gtg aat tct aaa ctt ccc tat aca tat caa ttc agg ttc ctt gac 1026
Ser Val Asn Ser Lys Leu Pro Tyr Thr Tyr Gln Phe Arg Phe Leu Asp 295 300 305

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PF59082SeqList_PF59082.txt

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Ala	Thr	Asp	Pro	Trp 330	Asn	Leu	Cys	Ser	Met 335	Gln	Gln	Val	Glu	Glu	Val	
aaa	tgc	ttg	ttg	aga	gtg	tta	ccc	ata	tgg	gtt	tca	ggc	att	ttg	tac	1170
Lys	Cys	Leu	Leu	Arg	Val	Leu	Pro	Ile	Trp	Val	Ser	Gly	Ile	Leu	Tyr	
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Phe	Val	Val	Ile	Val	Gln	Gln	His	Thr	Ile	Leu	Val	Phe	Gln	Ala	Leu	
cta	tct	gac	agg	cgt	att	ggg	caa	agc	ggg	ttc	ttg	atc	cca	gga	gca	1266
Leu	Ser	Asp	Arg	Arg	Ile	Gly	Gln	Ser	Gly	Phe	Leu	Ile	Pro	Gly	Ala	
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Ser	Tyr	Tyr	Val	Phe	Leu	Met	Ile	Ser	Val	Ala	Ile	Trp	Leu	Pro	Val	
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Tyr	Asp	Arg	Lys	Val	Val	Pro	Leu	Leu	Gln	Lys	Leu	Thr	Arg	Lys	Glu	
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Ile	Leu	Ser	Met	Leu	Val	Ser	Ala	Arg	Val	Glu	Gln	His	Arg	Arg	Thr	
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Ser	Ser	Met	Ser	Gly	Leu	Trp	Leu	Ile	Pro	Gln	Leu	Ser	Leu	Ala	Gly	
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Leu	Ala	Glu	Ala	Phe	Met	Ser	Val	Ala	Gln	Val	Glu	Phe	Tyr	Tyr	Lys	
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Gln	Phe	Pro	Glu	Asn	Met	Arg	Ser	Ile	Ala	Gly	Ser	Leu	Tyr	Tyr	Cys	
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Gly	His	Ala	Gly	Ser	Ser	Tyr	Leu	Ser	Ser	Val	Leu	Ile	Ala	Val	Ile	
cac	caa	atc	act	gcc	aaa	tct	gaa	act	ggg	aat	tgg	tta	ccg	gag	gat	1746
His	Gln	Ile	Thr	Ala	Lys	Ser	Glu	Thr	Gly	Asn	Trp	Leu	Pro	Glu	Asp	
ctg	aac	aag	ggg	aga	ttg	gat	aac	ttc	tat	tcg	ctc	att	gct	gct	cta	1794
Leu	Asn	Lys	Gly	Arg	Leu	Asp	Asn	Phe	Tyr	Ser	Leu	Ile	Ala	Ala	Leu	
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Glu	Ile	Ile	Asn	Leu	Gly	Tyr	Phe	Val	Leu	Cys	Ala	Arg	Trp	Phe	Arg	
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Tyr	Lys	Gly	Thr	Gly	Ser	Ser	Ser	Ile	Glu	Leu	Glu	Lys	Ala	Thr	Lys	
caa	tcg	gaa	aga	agt	gct	aat	ggg	gtt	aat	gat	tcg	aat	cta	tag		1935
Gln	Ser	Glu	Arg	Ser	Ala	Asn	Gly	Val	Asn	Asp	Ser	Asn	Leu			
ctattgcata	gaaatgggct	actacaatttt	ttcatcaagt	ggagccacaa	ctagcaaagg											1995
ttaaaaatca	aattgagtat	agcaacaaaa	gcacagtctc	tgcccttttca	attagataga											2055
tacttcatgt	gtagatgtat	gatgagatga	agtgacattat	tcttaggata	ggatgcctgc											2115
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PF59082SeqList_PF59082.txt

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 <213> Glycine max

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 20 25 30
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 35 40 45
 Gly Asn Glu Ile Phe Glu Lys Leu Gly Ala Ile Gly Thr Leu Ser Asn
 50 55 60
 Leu Leu Val Tyr Leu Thr Thr Val Phe Asn Leu Glu Asn Ile Met Ala
 65 70 75 80
 Thr Asn Ile Ile Asn Ile Phe Asn Gly Ser Thr Asn Phe Ala Thr Leu
 85 90 95
 Leu Gly Ala Phe Leu Ser Asp Ala Phe Phe Gly Arg Tyr Lys Ile Leu
 100 105 110
 Ala Phe Cys Thr Met Ala Ser Phe Val Gly Leu Phe Ala Ile Gln Leu
 115 120 125
 Thr Ala Ala Val Glu Lys Leu His Pro Pro His Cys Glu Ser Thr
 130 135 140
 Ile Cys Gln Gly Pro Thr Glu Gly Gln Met Thr Phe Leu Lys Thr Gly
 145 150 155 160
 Leu Gly Leu Leu Met Val Gly Ala Ala Gly Ile Arg Pro Cys Asn Leu
 165 170 175
 Ala Phe Gly Ala Asp Gln Phe Asn Pro Asn Thr Asp Ser Gly Lys Lys
 180 185 190
 Gly Ile Ala Ser Phe Phe Asn Trp Tyr Phe Phe Thr Phe Thr Val Ala
 195 200 205
 Gln Met Ile Ser Leu Thr Ile Ile Val Tyr Ile Gln Ser Asn Val Ser
 210 215 220
 Trp Ala Val Gly Leu Gly Ile Pro Ser Ala Leu Met Phe Val Ser Ser
 225 230 235 240
 Ile Ile Phe Phe Met Gly Ser Lys Leu Tyr Val Lys Val Lys Pro Ser
 245 250 255
 Gly Ser Pro Ile Thr Ser Ile Val Gln Val Ile Val Val Ala Thr Lys
 260 265 270
 Lys Arg Arg Leu Lys Leu Pro Glu Tyr Gln Tyr Pro Ser Leu Phe Asn
 275 280 285
 Tyr Val Ala Pro Lys Ser Val Asn Ser Lys Leu Pro Tyr Thr Tyr Gln
 290 295 300
 Phe Arg Phe Leu Asp Lys Ala Ala Ile Met Thr Pro Gln Asp Gln Ile
 305 310 315 320
 Asn Pro Asn Gly Ser Ala Thr Asp Pro Trp Asn Leu Cys Ser Met Gln
 325 330 335
 Gln Val Glu Glu Val Lys Cys Leu Leu Arg Val Leu Pro Ile Trp Val
 340 345 350
 Ser Gly Ile Leu Tyr Phe Val Val Ile Val Gln Gln His Thr Ile Leu
 355 360 365
 Val Phe Gln Ala Leu Leu Ser Asp Arg Arg Ile Gly Gln Ser Gly Phe
 370 375 380
 Leu Ile Pro Gly Ala Ser Tyr Tyr Val Phe Leu Met Ile Ser Val Ala
 385 390 395 400
 Ile Trp Leu Pro Val Tyr Asp Arg Lys Val Val Pro Leu Leu Gln Lys
 405 410 415
 Leu Thr Arg Lys Glu Gly Gly Ile Thr Leu Leu Gln Arg Met Gly Ile
 420 425 430
 Gly Ile Phe Ser Ile Leu Ser Met Leu Val Ser Ala Arg Val Glu
 435 440 445
 Gln His Arg Arg Thr Leu Ala Leu Ile Asn Pro Leu Gly Val Glu Thr
 450 455 460
 Arg Lys Gly Ala Ile Ser Ser Met Ser Gly Leu Trp Leu Ile Pro Gln
 465 470 475 480

PF59082SeqList_PF59082.txt

Leu Ser Leu Ala Gly Leu Ala Glu Ala Phe Met Ser Val Ala Gln Val
 485 490 495
 Glu Phe Tyr Tyr Lys Gln Phe Pro Glu Asn Met Arg Ser Ile Ala Gly
 500 505 510
 Ser Leu Tyr Tyr Cys Gly His Ala Gly Ser Ser Tyr Leu Ser Ser Val
 515 520 525
 Leu Ile Ala Val Ile His Gln Ile Thr Ala Lys Ser Glu Thr Gly Asn
 530 535 540
 Trp Leu Pro Glu Asp Leu Asn Lys Gly Arg Leu Asp Asn Phe Tyr Ser
 545 550 555 560
 Leu Ile Ala Ala Leu Glu Ile Ile Asn Leu Gly Tyr Phe Val Leu Cys
 565 570 575
 Ala Arg Trp Phe Arg Tyr Lys Gly Thr Gly Ser Ser Ser Ile Glu Leu
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 595 600 605
 Ser Asn Leu
 610

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 <212> DNA
 <213> Zea mays

<220>
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 <222> (1)..(1707)

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 Pro Pro Ser Gln Thr Gln Val Ser Ser Ala Asn Gln His Tyr Asn Lys
 20 25 30
 ccc ttc agc tgg aag ggc cca gcc att att ttg gcc ttc gaa ttc ttg 144
 Pro Phe Ser Trp Lys Gly Pro Ala Ile Ile Leu Ala Phe Glu Phe Leu
 35 40 45
 gag agc att gct tac tct ggt ata gca ctc aac ctg gtc gtg tac ctt 192
 Glu Ser Ile Ala Tyr Ser Gly Ile Ala Leu Asn Leu Val Val Tyr Leu
 50 55 60
 gga acc gtc ctc cat gga acc acc gcc tcc aat gca gcg aac gtc gat 240
 Gly Thr Val Leu His Gly Thr Thr Ala Ser Asn Ala Ala Asn Val Asp
 65 70 75 80
 gcg tgg aac ggc gcc acg ttt ctt acg ccg gtc ctt gga gcc ttt ctt 288
 Ala Trp Asn Gly Ala Thr Phe Leu Thr Pro Val Leu Gly Ala Phe Leu
 85 90 95
 gct gat aca tac tgg ggg aag tac aag acc gca gct atc tcc ata ata 336
 Ala Asp Thr Tyr Trp Gly Lys Tyr Lys Thr Ala Ala Ile Ser Ile Ile
 100 105 110
 ttc tac gtt gtt ggc ctg ctc ata att acc acc tct gcc gtc ata ccg 384
 Phe Tyr Val Val Gly Leu Leu Ile Ile Thr Thr Ser Ala Val Ile Pro
 115 120 125
 tcc cta cgg cct gcc tcg tgt gaa ggc ggt tca tgc cca cct gca aca 432
 Ser Leu Arg Pro Ala Ser Cys Glu Gly Gly Ser Cys Pro Pro Ala Thr
 130 135 140
 ggg ttt cag tat ttt gtg ctc ttt ggt tca ttg tac ctc atc tcc att 480
 Gly Phe Gln Tyr Phe Val Leu Phe Gly Ser Leu Tyr Leu Ile Ser Ile
 145 150 155 160
 ggt acg ggg ggc gtc aag tca gct tta ctt cca ttg gga gca gat cag 528
 Gly Thr Gly Gly Val Lys Ser Ala Leu Leu Pro Leu Gly Ala Asp Gln
 165 170 175
 tac aat gat gcg aac gcc gaa gag agc aaa agc aag caa ctg ttc ttc 576
 Tyr Asn Asp Ala Asn Ala Glu Glu Ser Lys Ser Lys Gln Leu Phe Phe
 180 185 190
 agt tgg ttc ttc atg gct gtc aac ctt gga gtg ttc atc tct ggc act 624
 Ser Trp Phe Phe Met Ala Val Asn Leu Gly Val Phe Ile Ser Gly Thr
 195 200 205
 gtt ctt gtc tgg ata cag caa aat gtc gct tgg tct ctt gga ttc ggc 672

PF59082SeqList_PF59082.txt

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Ile	Ser	Ser	Ile	Cys	Leu	Val	Ile	Ala	Ala	Val	Ala	Phe	Leu	Val	Gly	
225					230					235					240	
aca	ccg	ctt	tac	agg	gtt	caa	ctt	cca	act	ggg	agt	cca	ctc	aag	agt	768
Thr	Pro	Leu	Tyr	Arg	Val	Gln	Leu	Pro	Thr	Gly	Ser	Pro	Leu	Lys	Ser	
			245					250						255		
ata	gtc	atg	gtg	ttt	gtt	gcc	tct	tat	aag	aag	aga	gga	gtg	gcg	gtt	816
Ile	Val	Met	Val	Phe	Val	Ala	Ser	Tyr	Lys	Lys	Arg	Gly	Val	Ala	Val	
			260					265					270			
cct	gct	gat	agc	aca	ctg	ttg	ttt	gaa	ggg	aat	gac	gct	gaa	tca	agc	864
Pro	Ala	Asp	Ser	Thr	Leu	Leu	Phe	Glu	Gly	Asn	Asp	Ala	Glu	Ser	Ser	
		275					280					285				
agc	ata	gtg	ccg	aac	aaa	att	gaa	cac	act	gat	gaa	ttc	agg	tgc	tta	912
Ser	Ile	Val	Pro	Asn	Lys	Ile	Glu	His	Thr	Asp	Glu	Phe	Arg	Cys	Leu	
	290					295					300					
gat	aag	gct	gct	gtc	gtt	gta	gag	gac	caa	gag	atg	aag	gac	agc	cat	960
Asp	Lys	Ala	Ala	Val	Val	Val	Glu	Asp	Gln	Glu	Met	Lys	Asp	Ser	His	
305					310				315						320	
cgc	cca	tgg	cta	cta	tgt	acg	gta	acc	cag	gtg	gag	gaa	gtg	aag	att	1008
Arg	Pro	Trp	Leu	Leu	Cys	Thr	Val	Thr	Gln	Val	Glu	Glu	Val	Lys	Ile	
			325					330						335		
ctg	atc	cgg	atg	ctt	ccg	ata	tgg	ttc	acc	tgt	gtc	ttc	tat	tcg	gct	1056
Leu	Ile	Arg	Met	Leu	Pro	Ile	Trp	Phe	Thr	Cys	Val	Phe	Tyr	Ser	Ala	
			340				345						350			
gca	atg	agc	cag	act	gct	acc	act	ttc	gtc	cag	cag	ggg	aac	gcg	atg	1104
Ala	Met	Ser	Gln	Thr	Ala	Thr	Thr	Phe	Val	Gln	Gln	Gly	Asn	Ala	Met	
		355				360						365				
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Asn	Thr	Lys	Ile	Gly	Ser	Phe	Ser	Val	Pro	Ala	Ala	Ser	Met	Asn	Ser	
	370					375					380					
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Ala	Glu	Val	Ile	Phe	Met	Leu	Val	Trp	Val	Val	Phe	Gln	Asp	Ser	Val	
385					390					395					400	
gtc	atc	ccg	ata	gcc	agg	agg	tac	acg	ggg	aac	ccg	atg	ggg	ctg	acg	1248
Val	Ile	Pro	Ile	Ala	Arg	Arg	Tyr	Thr	Gly	Asn	Pro	Met	Gly	Leu	Thr	
			405					410						415		
ctg	ctg	cag	cgg	atg	ggc	gtc	ggg	cgg	ttg	ctg	gcg	atc	cca	tct	ctg	1296
Leu	Leu	Gln	Arg	Met	Gly	Val	Gly	Arg	Leu	Leu	Ala	Ile	Pro	Ser	Leu	
			420				425						430			
gcg	gcc	gcc	gca	ctg	gtg	gag	acg	tgg	agg	ctg	cgc	agc	gtg	aag	gcc	1344
Ala	Ala	Ala	Ala	Leu	Val	Glu	Thr	Trp	Arg	Leu	Arg	Ser	Val	Lys	Ala	
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ggg	cat	aac	ctg	agc	atc	ggg	tgg	cag	ctc	ccg	cag	ttc	gtg	atc	ctg	1392
Gly	His	Asn	Leu	Ser	Ile	Gly	Trp	Gln	Leu	Pro	Gln	Phe	Val	Ile	Leu	
	450					455					460					
gcc	tgc	tcc	gac	gtg	ttc	tgc	ggc	atc	gcg	cag	ctg	gag	ttc	ttc	tac	1440
Ala	Cys	Ser	Asp	Val	Phe	Cys	Gly	Ile	Ala	Gln	Leu	Glu	Phe	Phe	Tyr	
465					470					475					480	
gcg	gag	gcg	cct	gcg	tcc	atg	cgc	agc	ctg	tgc	tcg	gcg	ttc	cag	ttt	1488
Ala	Glu	Ala	Pro	Ala	Ser	Met	Arg	Ser	Leu	Cys	Ser	Ala	Phe	Gln	Phe	
			485					490						495		
ctg	gcc	atg	tcg	ctg	gcg	tac	tac	gtg	aac	acg	ctg	gtg	gtc	gca	ttg	1536
Leu	Ala	Met	Ser	Leu	Ala	Tyr	Tyr	Val	Asn	Thr	Leu	Val	Val	Ala	Leu	
			500				505						510			
gtg	gcg	tcc	gtg	acc	acg	gcc	tgg	ggc	ggc	aag	ggc	tgg	ctc	ccc	gct	1584
Val	Ala	Ser	Val	Thr	Thr	Ala	Trp	Gly	Gly	Lys	Gly	Trp	Leu	Pro	Ala	
		515					520					525				
gac	ctc	aac	gac	ggc	cac	ctg	gac	tac	tac	ttc	tgg	ctg	tgg	acg	ggg	1632
Asp	Leu	Asn	Asp	Gly	His	Leu	Asp	Tyr	Tyr	Phe	Trp	Leu	Trp	Thr	Gly	
	530					535					540					
atc	agt	gtg	gtg	aac	tac	gtc	gtg	tac	acg	gca	ttt	gca	agg	cgt	tat	1680
Ile	Ser	Val	Val	Asn	Tyr	Val	Val	Tyr	Thr	Ala	Phe	Ala	Arg	Arg	Tyr	
545					550					555					560	
acg	gtc	aag	aag	gtt	gtc	ggt	cag	taa								1707
Thr	Val	Lys	Lys	Val	Val	Gly	Gln									
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PF59082SeqList_PF59082.txt

<210> 359
 <211> 568
 <212> PRT
 <213> Zea mays

<400> 359

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20      25      30
Pro Phe Ser Trp Lys Gly Pro Ala Ile Ile Leu Ala Phe Glu Phe Leu
35      40      45
Glu Ser Ile Ala Tyr Ser Gly Ile Ala Leu Asn Leu Val Val Tyr Leu
50      55      60
Gly Thr Val Leu His Gly Thr Thr Ala Ser Asn Ala Ala Asn Val Asp
65      70      75
Ala Trp Asn Gly Ala Thr Phe Leu Thr Pro Val Leu Gly Ala Phe Leu
85      90      95
Ala Asp Thr Tyr Trp Gly Lys Tyr Lys Thr Ala Ala Ile Ser Ile Ile
100     105     110
Phe Tyr Val Val Gly Leu Leu Ile Ile Thr Thr Ser Ala Val Ile Pro
115     120     125
Ser Leu Arg Pro Ala Ser Cys Glu Gly Gly Ser Cys Pro Pro Ala Thr
130     135     140
Gly Phe Gln Tyr Phe Val Leu Phe Gly Ser Leu Tyr Leu Ile Ser Ile
145     150     155
Gly Thr Gly Gly Val Lys Ser Ala Leu Leu Pro Leu Gly Ala Asp Gln
165     170     175
Tyr Asn Asp Ala Asn Ala Glu Glu Ser Lys Ser Lys Gln Leu Phe Phe
180     185     190
Ser Trp Phe Phe Met Ala Val Asn Leu Gly Val Phe Ile Ser Gly Thr
195     200     205
Val Leu Val Trp Ile Gln Gln Asn Val Ala Trp Ser Leu Gly Phe Gly
210     215     220
Ile Ser Ser Ile Cys Leu Val Ile Ala Ala Val Ala Phe Leu Val Gly
225     230     235
Thr Pro Leu Tyr Arg Val Gln Leu Pro Thr Gly Ser Pro Leu Lys Ser
245     250     255
Ile Val Met Val Phe Val Ala Ser Tyr Lys Lys Arg Gly Val Ala Val
260     265     270
Pro Ala Asp Ser Thr Leu Leu Phe Glu Gly Asn Asp Ala Glu Ser Ser
275     280     285
Ser Ile Val Pro Asn Lys Ile Glu His Thr Asp Glu Phe Arg Cys Leu
290     295     300
Asp Lys Ala Ala Val Val Glu Asp Gln Glu Met Lys Asp Ser His
305     310     315
Arg Pro Trp Leu Leu Cys Thr Val Thr Gln Val Glu Glu Val Lys Ile
325     330     335
Leu Ile Arg Met Leu Pro Ile Trp Phe Thr Cys Val Phe Tyr Ser Ala
340     345     350
Ala Met Ser Gln Thr Ala Thr Thr Phe Val Gln Gln Gly Asn Ala Met
355     360     365
Asn Thr Lys Ile Gly Ser Phe Ser Val Pro Ala Ala Ser Met Asn Ser
370     375     380
Ala Glu Val Ile Phe Met Leu Val Trp Val Val Phe Gln Asp Ser Val
385     390     395
Val Ile Pro Ile Ala Arg Arg Tyr Thr Gly Asn Pro Met Gly Leu Thr
405     410     415
Leu Leu Gln Arg Met Gly Val Gly Arg Leu Leu Ala Ile Pro Ser Leu
420     425     430
Ala Ala Ala Ala Leu Val Glu Thr Trp Arg Leu Arg Ser Val Lys Ala
435     440     445
Gly His Asn Leu Ser Ile Gly Trp Gln Leu Pro Gln Phe Val Ile Leu
450     455     460
Ala Cys Ser Asp Val Phe Cys Gly Ile Ala Gln Leu Glu Phe Phe Tyr
465     470     475
Ala Glu Ala Pro Ala Ser Met Arg Ser Leu Cys Ser Ala Phe Gln Phe
485     490     495
Leu Ala Met Ser Leu Ala Tyr Tyr Val Asn Thr Leu Val Val Ala Leu

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PF59082SeqList_PF59082.txt

Val Ala Ser Val Thr Thr Ala Trp Gly Gly Lys Gly Trp Leu Pro Ala
 500 505 510
 515 520 525
 Asp Leu Asn Asp Gly His Leu Asp Tyr Tyr Phe Trp Leu Trp Thr Gly
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 Ile Ser Val Val Asn Tyr Val Val Tyr Thr Ala Phe Ala Arg Arg Tyr
 545 550 555 560
 Thr Val Lys Lys Val Val Gly Gln
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 <213> Glycine max

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 <222> (1)..(1731)

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 aca atg ccc ttc atc ttt ggt aat gag gtt tgt gag aag ctg gct gtg 96
 Thr Met Pro Phe Ile Phe Gly Asn Glu Val Cys Glu Lys Leu Ala Val
 20 25 30
 gta ggt ttc aac aca aac atg att agc tac ttg aca aca cag ctt cac 144
 Val Gly Phe Asn Thr Asn Met Ile Ser Tyr Leu Thr Thr Gln Leu His
 35 40 45
 atg cca ttg acc aaa gca gct aac acc ctc act aac ttt ggt gga act 192
 Met Pro Leu Thr Lys Ala Ala Asn Thr Leu Thr Asn Phe Gly Gly Thr
 50 55 60
 gca agc ttg aca cca ttg ctt ggt gct ttc att gct gat tct tat gcc 240
 Ala Ser Leu Thr Pro Leu Leu Gly Ala Phe Ile Ala Asp Ser Tyr Ala
 65 70 75 80
 gga aag ttc tgg act gtc acc ctt gct tcc att ata tac cag ata ggg 288
 Gly Lys Phe Trp Thr Val Thr Leu Ala Ser Ile Ile Tyr Gln Ile Gly
 85 90 95
 atg att agt ttg acc cta tcg gca gtg cta cca cag ttt agg cca cct 336
 Met Ile Ser Leu Thr Leu Ser Ala Val Leu Pro Gln Phe Arg Pro Pro
 100 105 110
 ccc tgc aag ggt gaa gag gtg tgc cag caa gca agt gca gga cag ctg 384
 Pro Cys Lys Gly Glu Glu Val Cys Gln Gln Ala Ser Ala Gly Gln Leu
 115 120 125
 gca atc ctc tac atc tca ctc ctc ggg gca ctc ggg tcg ggt ggg 432
 Ala Ile Leu Tyr Ile Ser Leu Leu Leu Gly Ala Leu Gly Ser Gly Gly
 130 135 140
 atc cga ccc tgc atc gtg gcg ttc ggg gcg gat cag ttc gac gag tct 480
 Ile Arg Pro Cys Ile Val Ala Phe Gly Ala Asp Gln Phe Asp Glu Ser
 145 150 155 160
 gat ccc aag cag aca aca agg aca tgg acc tac ttc aac tgg tac tac 528
 Asp Pro Lys Gln Thr Thr Arg Thr Trp Thr Tyr Phe Asn Trp Tyr Tyr
 165 170 175
 ttt gtc atg ggt gta gca att ctt gtg gct gtg act gtt ttg gtg tat 576
 Phe Val Met Gly Val Ala Ile Leu Val Ala Val Thr Val Leu Val Tyr
 180 185 190
 att cag gac aat att ggt tgg gga att ggc ctt gga atc cct acc att 624
 Ile Gln Asp Asn Ile Gly Trp Gly Ile Gly Leu Gly Ile Pro Thr Ile
 195 200 205
 gca atg ttc ctc tca att att gca ttc att gtc gga tac ccg ctt tac 672
 Ala Met Phe Leu Ser Ile Ile Ala Phe Ile Val Gly Tyr Pro Leu Tyr
 210 215 220
 cgt aac ttg aac ccg tcc ggg agc ccg ttt acc cgg tta gtg caa gtg 720
 Arg Asn Leu Asn Pro Ser Gly Ser Pro Phe Thr Arg Leu Val Gln Val
 225 230 235 240
 gct gtg gct gca ttt cgt aag aga aag gtc cca aat gtg tca cac cct 768
 Ala Val Ala Ala Phe Arg Lys Arg Lys Val Pro Asn Val Ser His Pro
 245 250 255
 agt tta ctc tac caa aat gat gaa cta gat gcc tct att tct atg gga 816

PF59082SeqList_PF59082.txt

Ser	Leu	Leu	Tyr	Gln	Asn	Asp	Glu	Leu	Asp	Ala	Ser	Ile	Ser	Met	Gly	
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Gly	Lys	Leu	Leu	His	Ser	Gly	Gln	Met	Lys	Phe	Leu	Asp	Lys	Ala	Ala	
275							280						285			
ata	gtt	aca	gaa	gaa	gat	gac	aac	aaa	aca	cct	aac	tta	tgg	aga	tta	912
Ile	Val	Thr	Glu	Glu	Asp	Asp	Asn	Lys	Thr	Pro	Asn	Leu	Trp	Arg	Leu	
290						295					300					
aac	aca	att	cat	aga	gtg	gag	gaa	ttg	aag	tcc	ata	atc	aga	atg	ggt	960
Asn	Thr	Ile	His	Arg	Val	Glu	Glu	Leu	Lys	Ser	Ile	Ile	Arg	Met	Gly	
305					310					315					320	
cca	ata	tgg	gca	tca	gga	att	ctc	ctc	atc	aca	gct	tat	gcc	caa	caa	1008
Pro	Ile	Trp	Ala	Ser	Gly	Ile	Leu	Leu	Ile	Thr	Ala	Tyr	Ala	Gln	Gln	
				325					330					335		
aac	aca	ttc	tcc	ctc	caa	caa	gcc	aag	acc	atg	gac	aga	cac	cta	acc	1056
Asn	Thr	Phe	Ser	Leu	Gln	Gln	Ala	Lys	Thr	Met	Asp	Arg	His	Leu	Thr	
			340					345					350			
aaa	acc	ttt	caa	atc	cca	gct	ggg	tcc	atg	tct	gtc	ttc	acc	atc	ctt	1104
Lys	Thr	Phe	Gln	Ile	Pro	Ala	Gly	Ser	Met	Ser	Val	Phe	Thr	Ile	Leu	
		355					360					365				
acc	atg	ctc	acc	acc	act	gcc	ttc	tat	gac	cga	gtc	ttc	atc	aaa	gtg	1152
Thr	Met	Leu	Thr	Thr	Thr	Ala	Phe	Tyr	Asp	Arg	Val	Phe	Ile	Lys	Val	
	370					375					380					
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Ala	Arg	Arg	Phe	Thr	Gly	Leu	Asp	Arg	Gly	Ile	Ser	Phe	Leu	His	Arg	
385					390				395						400	
atg	ggc	att	ggg	ttt	gtg	atc	tca	acc	tta	gcc	aca	ttg	gtt	gct	ggg	1248
Met	Gly	Ile	Gly	Phe	Val	Ile	Ser	Thr	Leu	Ala	Thr	Leu	Val	Ala	Gly	
			405					410						415		
ttt	gtt	gaa	atg	aaa	aga	aag	aag	gca	gct	ttg	gcc	cat	ggg	ctt	ttt	1296
Phe	Val	Glu	Met	Lys	Arg	Lys	Lys	Ala	Ala	Leu	Ala	His	Gly	Leu	Phe	
		420						425					430			
gac	cac	cca	cat	gcc	ata	atc	cca	atc	tca	gtg	ttc	tgg	ctt	gtc	cct	1344
Asp	His	Pro	His	Ala	Ile	Ile	Pro	Ile	Ser	Val	Phe	Trp	Leu	Val	Pro	
		435					440					445				
caa	tac	agc	ctt	cat	gga	atg	gct	gag	gcc	ttt	atg	tca	att	gga	cac	1392
Gln	Tyr	Ser	Leu	His	Gly	Met	Ala	Glu	Ala	Phe	Met	Ser	Ile	Gly	His	
	450				455				460							
ttg	gag	ttt	ttc	tat	gac	cag	gcc	cct	gag	agt	atg	agg	agc	act	gcc	1440
Leu	Glu	Phe	Phe	Tyr	Asp	Gln	Ala	Pro	Glu	Ser	Met	Arg	Ser	Thr	Ala	
465					470				475						480	
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Met	Ala	Leu	Phe	Trp	Thr	Ala	Ile	Ala	Ala	Gly	Asn	Tyr	Val	Ser	Thr	
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Ile	Met	Val	Thr	Leu	Val	His	Lys	Phe	Ser	Ala	Gly	Ser	Asn	Gly	Ser	
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aat	tgg	ctc	cct	gac	aac	aac	ctc	aac	aaa	ggg	aag	ttg	gag	tac	ttt	1584
Asn	Trp	Leu	Pro	Asp	Asn	Asn	Leu	Asn	Lys	Gly	Lys	Leu	Glu	Tyr	Phe	
		515					520					525				
tac	tgg	ctt	atc	acc	ata	ttg	cag	ttt	ctc	aat	ctt	att	tac	tac	ttg	1632
Tyr	Trp	Leu	Ile	Thr	Ile	Leu	Gln	Phe	Leu	Asn	Leu	Ile	Tyr	Tyr	Leu	
	530					535					540					
gtt	tgt	gcc	aaa	ttg	tac	acc	tac	aag	cca	att	cag	gtc	cat	gac	aaa	1680
Val	Cys	Ala	Lys	Leu	Tyr	Thr	Tyr	Lys	Pro	Ile	Gln	Val	His	Asp	Lys	
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ggg	gat	agc	aat	tca	gaa	ggg	aac	caa	att	gag	ctc	tct	acc	acg	gtt	1728
Gly	Asp	Ser	Asn	Ser	Glu	Gly	Asn	Gln	Ile	Glu	Leu	Ser	Thr	Thr	Val	
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 <212> PRT
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PF59082SeqList_PF59082.txt

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Val Gly Phe Asn Thr Asn Met Ile Ser Tyr Leu Thr Thr Gln Leu His
35 40 45
Met Pro Leu Thr Lys Ala Ala Asn Thr Leu Thr Asn Phe Gly Gly Thr
50 55 60
Ala Ser Leu Thr Pro Leu Leu Gly Ala Phe Ile Ala Asp Ser Tyr Ala
65 70 75 80
Gly Lys Phe Trp Thr Val Thr Leu Ala Ser Ile Ile Tyr Gln Ile Gly
85 90 95
Met Ile Ser Leu Thr Leu Ser Ala Val Leu Pro Gln Phe Arg Pro Pro
100 105 110
Pro Cys Lys Gly Glu Glu Val Cys Gln Gln Ala Ser Ala Gly Gln Leu
115 120 125
Ala Ile Leu Tyr Ile Ser Leu Leu Leu Gly Ala Leu Gly Ser Gly Gly
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Ile Arg Pro Cys Ile Val Ala Phe Gly Ala Asp Gln Phe Asp Glu Ser
145 150 155 160
Asp Pro Lys Gln Thr Thr Arg Thr Trp Thr Tyr Phe Asn Trp Tyr Tyr
165 170 175
Phe Val Met Gly Val Ala Ile Leu Val Ala Val Thr Val Leu Val Tyr
180 185 190
Ile Gln Asp Asn Ile Gly Trp Gly Ile Gly Leu Gly Ile Pro Thr Ile
195 200 205
Ala Met Phe Leu Ser Ile Ile Ala Phe Ile Val Gly Tyr Pro Leu Tyr
210 215 220
Arg Asn Leu Asn Pro Ser Gly Ser Pro Phe Thr Arg Leu Val Gln Val
225 230 235 240
Ala Val Ala Ala Phe Arg Lys Arg Lys Val Pro Asn Val Ser His Pro
245 250 255
Ser Leu Leu Tyr Gln Asn Asp Glu Leu Asp Ala Ser Ile Ser Met Gly
260 265 270
Gly Lys Leu Leu His Ser Gly Gln Met Lys Phe Leu Asp Lys Ala Ala
275 280 285
Ile Val Thr Glu Glu Asp Asp Asn Lys Thr Pro Asn Leu Trp Arg Leu
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Asn Thr Ile His Arg Val Glu Glu Leu Lys Ser Ile Ile Arg Met Gly
305 310 315 320
Pro Ile Trp Ala Ser Gly Ile Leu Leu Ile Thr Ala Tyr Ala Gln Gln
325 330 335
Asn Thr Phe Ser Leu Gln Gln Ala Lys Thr Met Asp Arg His Leu Thr
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Lys Thr Phe Gln Ile Pro Ala Gly Ser Met Ser Val Phe Thr Ile Leu
355 360 365
Thr Met Leu Thr Thr Thr Ala Phe Tyr Asp Arg Val Phe Ile Lys Val
370 375 380
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385 390 395 400
Met Gly Ile Gly Phe Val Ile Ser Thr Leu Ala Thr Leu Val Ala Gly
405 410 415
Phe Val Glu Met Lys Arg Lys Lys Ala Ala Leu Ala His Gly Leu Phe
420 425 430
Asp His Pro His Ala Ile Ile Pro Ile Ser Val Phe Trp Leu Val Pro
435 440 445
Gln Tyr Ser Leu His Gly Met Ala Glu Ala Phe Met Ser Ile Gly His
450 455 460
Leu Glu Phe Phe Tyr Asp Gln Ala Pro Glu Ser Met Arg Ser Thr Ala
465 470 475 480
Met Ala Leu Phe Trp Thr Ala Ile Ala Ala Gly Asn Tyr Val Ser Thr
485 490 495
Ile Met Val Thr Leu Val His Lys Phe Ser Ala Gly Ser Asn Gly Ser
500 505 510
Asn Trp Leu Pro Asp Asn Asn Leu Asn Lys Gly Lys Leu Glu Tyr Phe
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Tyr Trp Leu Ile Thr Ile Leu Gln Phe Leu Asn Leu Ile Tyr Tyr Leu
530 535 540
Val Cys Ala Lys Leu Tyr Thr Tyr Lys Pro Ile Gln Val His Asp Lys

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PF59082SeqList_PF59082.txt

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Asp Glu Glu Lys Trp Val His Asp Ala Ser Val Asp Tyr Lys Glu Arg
20 25 30
atc cct ctc cgt gct tcc acg ggt gta tgg aaa gct tca ctt ttt gcc 144
Ile Pro Leu Arg Ala Ser Thr Gly Val Trp Lys Ala Ser Leu Phe Ala
35 40 45
ctt gca att gaa ttt agg gaa agg ata gcc cac ttt ggg ata gcc act 192
Leu Ala Ile Glu Phe Arg Glu Arg Ile Ala His Phe Gly Ile Ala Thr
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aat ctt atc atg tac ctg act aaa gta atg cat gaa gat ctc aaa aca 240
Asn Leu Ile Met Tyr Leu Thr Lys Val Met His Glu Asp Leu Lys Thr
65 70 75 80
gcg acc aag aat gta aac tac tgg gta gga gca aca act ttg atg cct 288
Ala Thr Lys Asn Val Asn Tyr Trp Val Gly Ala Thr Thr Leu Met Pro
85 90 95
cta att gga gga ttt gtt gct gat gcc tac act ggt cga ttt cgt atg 336
Leu Ile Gly Gly Phe Val Ala Asp Ala Tyr Thr Gly Arg Phe Arg Met
100 105 110
gtc ctc ttt tct tcc ctc tta tac ctc aag gga tta agc ctc ttg acc 384
Val Leu Phe Ser Ser Leu Leu Tyr Leu Lys Gly Leu Ser Leu Leu Thr
115 120 125
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Met Ser Gln Phe Ile Pro Ser 135 Leu Lys Pro Cys Asn Asn Glu Ile Cys
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cat tgg cca agg aag gtt cat gaa gtg gtt tta ttc ctt gcc ctt tac 480
His Trp Pro Arg Lys Val His Glu Val Val Leu Phe Leu Ala Leu Tyr
145 150 155 160
tgt gtc gcc ttg gga act gga gga ttc aaa ccg tgc tta caa agc ttt 528
Cys Val Ala Leu Gly Thr Gly Gly Phe Lys Pro Cys Leu Gln Ser Phe
165 170 175
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Gly Ala Asp Gln Phe Asp Asp Asp His Leu Glu Glu Arg Lys Lys Lys
180 185 190
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Met Ser Phe Phe Asn Trp Trp Asn Phe Thr Leu Cys Thr Ala Met Leu
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ctt ggg gca aca gtg att gtt tat gtt caa gac ttt gtc agc tgg gga 672
Leu Gly Ala Thr Val Ile Val Tyr Val Gln Asp Phe Val Ser Trp Gly
210 215 220
gta tct tat ctc atc ctc agc atg ttc atg gct ctc act atc att gct 720
Val Ser Tyr Leu Ile Leu Ser Met Phe Met Ala Leu Thr Ile Ile Ala
225 230 235 240
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Phe Tyr Glu Gly Lys Arg Phe Tyr Arg Tyr Arg Ser Thr Glu Gly Asn
245 250 255
cct ttc atg cta att cta caa gta cta att gca gca ata agg aaa agc 816
Pro Phe Met Leu Ile Leu Gln Val Ile Ala Ala Ile Arg Lys Ser
260 265 270
aac ttg tcc tgt cct tca aat ccc gat tca ttg tat gaa ttc cca aag 864
Asn Leu Ser Cys Pro Ser Asn Pro Asp Ser Leu Tyr Glu Phe Pro Lys
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PF59082SeqList_PF59082.txt

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Phe	Leu	Asp	Lys	Ala	Ala	Ile	Val	Glu	Gly	Lys	Tyr	Thr	Glu	His	Arg	
305					310					315					320	
gac	cag	aat	cca	tgg	aga	tta	gca	aca	gtg	aca	aga	gtg	gag	gag	aca	1008
Asp	Gln	Asn	Pro	Trp	Arg	Leu	Ala	Thr	Val	Thr	Arg	Val	Glu	Glu	Thr	
				325					330						335	
aag	ctt	att	ctg	aat	ggt	att	ccc	ata	tgg	cta	act	tca	tta	ata	att	1056
Lys	Leu	Ile	Asn	Val	Ile	Pro	Ile	Trp	Leu	Thr	Ser	Leu	Ile	Ile		
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Gly	Ile	Cys	Ile	Ala	Gln	Gly	Ser	Thr	Leu	Phe	Val	Asn	Gln	Ala	Ala	
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Ser	Met	Asn	Leu	Lys	Ile	Ile	Asn	Ser	Phe	Lys	Ile	Pro	Pro	Ala	Ser	
		370				375					380					
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Met	Thr	Ser	Val	Ser	Ala	Ile	Ser	Pro	Ile	Ile	Ala	Ile	Pro	Ile	Tyr	
385					390					395					400	
gat	aag	att	ata	ggt	cca	att	atg	agg	aaa	gtc	aaa	ggg	aac	gaa	agg	1248
Asp	Lys	Ile	Ile	Val	Pro	Ile	Met	Arg	Lys	Val	Lys	Gly	Asn	Glu	Arg	
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ggc	atc	agc	gtc	ctt	tgg	agg	ggt	ggc	att	ggc	tta	gca	ttc	tta	gtc	1296
Gly	Ile	Ser	Val	Leu	Trp	Arg	Val	Gly	Ile	Gly	Leu	Ala	Phe	Leu	Val	
			420					425					430			
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Ile	Ala	Met	Val	Val	Ala	Ala	Leu	Val	Glu	Thr	Lys	Arg	Leu	Arg	Met	
		435				440					445					
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Val	Glu	His	Asp	Glu	Thr	Met	Ser	Val	Leu	Trp	Leu	Ile	Pro	Gln	Tyr	
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Leu	Ile	Leu	Gly	Ile	Gly	Ala	Asp	Ser	Leu	Ser	Leu	Ile	Gly	Leu	Gln	
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gag	tat	ttc	tat	gac	gaa	ggt	cct	gac	tca	atg	aga	agc	ata	gga	atg	1488
Glu	Tyr	Phe	Tyr	Asp	Glu	Val	Pro	Asp	Ser	Met	Arg	Ser	Ile	Gly	Met	
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gcc	ttg	tat	ctt	agt	gta	ctt	gga	gta	gga	ttt	ttc	tta	agt	agc	ttt	1536
Ala	Leu	Tyr	Leu	Ser	Val	Leu	Gly	Val	Gly	Phe	Phe	Leu	Ser	Ser	Phe	
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Leu	Ile	Ile	Ile	Val	Glu	His	Val	Thr	Gly	Lys	Thr	Gly	Lys	Ser	Trp	
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Ile	Gly	Lys	Asp	Ile	Asn	Ser	Ser	Arg	Leu	Asp	Lys	Phe	Tyr	Trp	Met	
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Leu	Ala	Val	Ile	Asn	Ala	Phe	Val	Leu	Cys	Val	Phe	Leu	Leu	Val	Ser	
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aaa	agg	tac	acc	tat	aag	act	gta	cag	aga	aga	gct	atg	gaa	act	gat	1728
Lys	Arg	Tyr	Thr	Tyr	Lys	Thr	Val	Gln	Arg	Arg	Ala	Met	Glu	Thr	Asp	
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tct	tgt	aag	agt	gat	ggg	ggt	gag	atg	gtg	gct	tga					1764
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PF59082SeqList_PF59082.txt

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Leu	Ile	Gly	Gly	Phe	Val	Ala	Asp	Ala	Tyr	Thr	Gly	Arg	Phe	Arg	Met
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Val	Leu	Phe	Ser	Ser	Leu	Leu	Tyr	Leu	Lys	Gly	Leu	Ser	Leu	Leu	Thr
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Cys	Val	Ala	Leu	Gly	Thr	Gly	Gly	Phe	Lys	Pro	Cys	Leu	Gln	Ser	Phe
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Gly	Ala	Asp	Gln	Phe	Asp	Asp	Asp	His	Leu	Glu	Glu	Arg	Lys	Lys	Lys
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Met	Ser	Phe	Phe	Asn	Trp	Trp	Asn	Phe	Thr	Leu	Cys	Thr	Ala	Met	Leu
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Val	Ser	Tyr	Leu	Ile	Leu	Ser	Met	Phe	Met	Ala	Leu	Thr	Ile	Ile	Ala
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Phe	Tyr	Glu	Gly	Lys	Arg	Phe	Tyr	Arg	Tyr	Arg	Ser	Thr	Glu	Gly	Asn
				245					250					255	
Pro	Phe	Met	Leu	Ile	Leu	Gln	Val	Leu	Ile	Ala	Ala	Ile	Arg	Lys	Ser
			260					265					270		
Asn	Leu	Ser	Cys	Pro	Ser	Asn	Pro	Asp	Ser	Leu	Tyr	Glu	Phe	Pro	Lys
		275					280						285		
Ser	Glu	Lys	Ser	Gln	Gly	Arg	Leu	Leu	Ser	His	Thr	Cys	Arg	Leu	Arg
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Phe	Leu	Asp	Lys	Ala	Ala	Ile	Val	Glu	Gly	Lys	Tyr	Thr	Glu	His	Arg
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Asp	Gln	Asn	Pro	Trp	Arg	Leu	Ala	Thr	Val	Thr	Arg	Val	Glu	Glu	Thr
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Lys	Leu	Ile	Leu	Asn	Val	Ile	Pro	Ile	Trp	Leu	Thr	Ser	Leu	Ile	Ile
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Gly	Ile	Cys	Ile	Ala	Gln	Gly	Ser	Thr	Leu	Phe	Val	Asn	Gln	Ala	Ala
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Ser	Met	Asn	Leu	Lys	Ile	Ile	Asn	Ser	Phe	Lys	Ile	Pro	Pro	Ala	Ser
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Asp	Lys	Ile	Ile	Val	Pro	Ile	Met	Arg	Lys	Val	Lys	Gly	Asn	Glu	Arg
				405					410					415	
Gly	Ile	Ser	Val	Leu	Trp	Arg	Val	Gly	Ile	Gly	Leu	Ala	Phe	Leu	Val
			420					425					430		
Ile	Ala	Met	Val	Val	Ala	Ala	Leu	Val	Glu	Thr	Lys	Arg	Leu	Arg	Met
		435					440					445			
Val	Glu	His	Asp	Glu	Thr	Met	Ser	Val	Leu	Trp	Leu	Ile	Pro	Gln	Tyr
	450					455					460				
Leu	Ile	Leu	Gly	Ile	Gly	Ala	Asp	Ser	Leu	Ser	Leu	Ile	Gly	Leu	Gln
465					470					475					480
Glu	Tyr	Phe	Tyr	Asp	Glu	Val	Pro	Asp	Ser	Met	Arg	Ser	Ile	Gly	Met
				485					490					495	
Ala	Leu	Tyr	Leu	Ser	Val	Leu	Gly	Val	Gly	Phe	Phe	Leu	Ser	Ser	Phe
			500					505					510		
Leu	Ile	Ile	Ile	Val	Glu	His	Val	Thr	Gly	Lys	Thr	Gly	Lys	Ser	Trp
		515					520					525			
Ile	Gly	Lys	Asp	Ile	Asn	Ser	Ser	Arg	Leu	Asp	Lys	Phe	Tyr	Trp	Met
	530					535					540				
Leu	Ala	Val	Ile	Asn	Ala	Phe	Val	Leu	Cys	Val	Phe	Leu	Leu	Val	Ser
545					550					555					560
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PF59082SeqList_PF59082.txt

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Lys Trp Val His Asp Ala Ser Val Asp Tyr Lys Gly Arg Leu Pro Leu
      20      25
cgt gct tcc aca ggc gta tgg aaa gcg tcg ctt ttt gtc ctt gca att      144
Arg Ala Ser Thr Gly Val Trp Lys Ala Ser Leu Phe Val Leu Ala Ile
      35      40      45
gaa ttt agt gaa agg ata tgc cac ttt ggg ata gcc act aat ctt atc      192
Glu Phe Ser Glu Arg Ile Cys His Phe Gly Ile Ala Thr Asn Leu Ile
      50      55      60
atg tac ctg act aaa gta atg cat gaa gat ctc aaa aca gcg acc aag      240
Met Tyr Leu Thr Lys Val Met His Glu Asp Leu Lys Thr Ala Thr Lys
      65      70      75      80
aat gta aac tac tgg gta gga gca aca act ttg atg cct cta att gga      288
Asn Val Asn Tyr Trp Val Gly Ala Thr Thr Leu Met Pro Leu Ile Gly
      85      90      95
gga ttt gtt gct gat gcc tac act ggt cga ttt cgt atg gtc ctc ttt      336
Gly Phe Val Ala Asp Ala Tyr Thr Gly Arg Phe Arg Met Val Leu Phe
      100      105
tct tcc ctc tta tac ctc aag gga tta agc ctc ttg acc atg tct caa      384
Ser Ser Leu Leu Tyr Leu Lys Gly Leu Ser Leu Leu Thr Met Ser Gln
      115      120      125
ttc att cca agt cta aaa cca tgc aac aat gag ata tgc cat tgg cca      432
Phe Ile Pro Ser Leu Lys Pro Cys Asn Asn Glu Ile Cys His Trp Pro
      130      135      140
agg aag gtt cat gaa gtg gtt tta ttc ctt gcc ctt tac tgt gtc gcc      480
Arg Lys Val His Glu Val Val Leu Phe Leu Ala Leu Tyr Cys Val Ala
      145      150      155      160
ttg gga act gga gga ttc aaa ccg tgc tta caa agc ttt gga gca gat      528
Leu Gly Thr Gly Gly Phe Lys Pro Cys Leu Gln Ser Phe Gly Ala Asp
      165      170      175
caa ttt gat gat gac cac ctt gaa gaa agg aag aag aag atg tca ttc      576
Gln Phe Asp Asp His Leu Glu Glu Arg Lys Lys Lys Met Ser Phe
      180      185      190
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Phe Asn Trp Trp Asn Phe Thr Leu Cys Thr Ala Met Leu Leu Gly Ala
      195      200      205
aca gtg att gtt tat gtt caa gac ttt gtc agc tgg gga gta tct tat      672
Thr Val Ile Val Tyr Val Gln Asp Phe Val Ser Trp Gly Val Ser Tyr
      210      215      220
ctc atc ctc agc atg ttc atg gct ctc act atc att gct ttc tat gag      720
Leu Ile Leu Ser Met Phe Met Ala Leu Thr Ile Ile Ala Phe Tyr Glu
      225      230      235      240
ggg aag cgt ttt tac agg tac agg agc aca gaa ggt aac cct ttc atg      768
Gly Lys Arg Phe Tyr Arg Tyr Arg Ser Thr Glu Gly Asn Pro Phe Met
      245      250      255
cta att cta caa gta cta att gca gca ata agg aaa agc aac ttg tcc      816
Leu Ile Leu Gln Val Leu Ile Ala Ala Ile Arg Lys Ser Asn Leu Ser
      260      265      270      275
tgt cct tca aat ccc gat tca ttg tat gaa ttc cca aag tca gag aag      864
Cys Pro Ser Asn Pro Asp Ser Leu Tyr Glu Phe Pro Lys Ser Glu Lys
      280      285      290      295
tca caa gga agg ctt cta agc cat act tgc agg ctc agg ttt ctt gac      912
Ser Gln Gly Arg Leu Leu Ser His Thr Cys Arg Leu Arg Phe Leu Asp
      300
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Lys Ala Ala Ile Val Glu Gly Lys Tyr Thr Glu His Arg Asp Gln Asn

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PF59082SeqList_PF59082.txt

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Leu Asn Val Ile Pro Ile Trp Leu Thr Ser Leu Ile Ile Gly Ile Cys							
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Ile Ala Gln Gly Ser Thr Leu Phe Val Asn Gln Ala Ala Ser Met Asn							
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tta aag ata atc aac agc ttc aaa atc cca cca gct tcc atg aca tct							1152
Leu Lys Ile Ile Asn Ser Phe Lys Ile Pro Pro Ala Ser Met Thr Ser							
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gtt tca gct att agc cca ata ata gct atc cca ata tat gat aag att							1200
Val Ser Ala Ile Ser Pro Ile Ile Ala Ile Pro Ile Tyr Asp Lys Ile							
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Ile Val Pro Ile Met Arg Lys Val Lys Gly Asn Glu Arg Gly Ile Ser							
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Val Leu Trp Arg Val Gly Ile Gly Leu Ala Phe Leu Val Ile Ala Met							
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Val Val Ala Ala Leu Val Glu Thr Lys Arg Leu Arg Met Val Glu His							
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Asp Glu Val Ile Thr Val Gly Gly Thr Arg His Glu Thr Met Ser Val							
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Gly Phe Phe Leu Ser Ser Phe Leu Ile Ile Thr Val Asp His Val Thr							
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Gly Lys Asn Gly Lys Ser Trp Ile Ala Lys Asp Ile Asn Ser Ser Arg							
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Leu Asp Lys Phe Tyr Trp Met Leu Ala Val Ile Asn Ala Phe Asn Leu							
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Cys Phe Phe Leu Phe Leu Ala Lys Gly Tyr Thr Tyr Lys Thr Val Gln							
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Asp Tyr Lys Gly Arg Pro Ala Glu Arg Ser Lys Thr Gly Gly Trp Thr	
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Ala Ser Ala Met Ile Leu Gly Gly Glu Val Met Glu Arg Leu Thr Thr	
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Ala 225	Gly	Ala	Ile	Val	Val 230	Ala	Leu	Leu	Val	Phe 235	Leu	Ser	Gly	Thr	Arg 240
Lys	Tyr	Arg	Phe	Lys 245	Lys	Leu	Val	Gly	Ser 250	Pro	Leu	Thr	Gln	Phe 255	Ala
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Ala Val Asn Leu Val Thr Tyr Met Ile Ser Ile Met His Leu Pro Ser	
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Ser Thr Ala Ala Asn Thr Val Thr Asp Phe Met Gly Thr Ser Phe Leu	
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Leu Cys Leu Leu Gly Gly Phe Leu Ala Asp Ser Phe Leu Gly Arg Tyr	
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Lys Thr Ile Gly Ile Phe Ala Ser Ile Gln Thr Leu Gly Thr Ala Thr	
100 105 110	
tta gca atc tca aca aaa ttg cca ggg cta cgt cca cca cct tgc cat	384
Leu Ala Ile Ser Thr Lys Leu Pro Gly Leu Arg Pro Pro Pro Cys His	
115 120 125	
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Ala Asn Ser Asp Ser Cys Lys Gln Ala Asn Gly Phe Gln Met Gly Ile	
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Leu Tyr Leu Ser Leu Tyr Leu Ile Ala Leu Gly Thr Gly Gly Leu Lys	
145 150 155 160	
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Ser Ser Val Ser Gly Phe Gly Ser Asp Gln Phe Asp Glu Lys Asp Glu	
165 170 175	
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Lys Glu Lys Ser Gln Met Ala Tyr Phe Phe Asn Arg Phe Phe Phe Phe	
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atc agt ttt gga act ctg gca gct gtc aca gta ctt gtc tat ctg caa	624
Ile Ser Phe Gly Thr Leu Ala Ala Val Thr Val Leu Val Tyr Leu Gln	
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gat gaa gtg agt cgc agc ttg gcg tat gga ata tgt tct gtc tct atg	672
Asp Glu Val Ser Arg Ser Leu Tyr Gly Ile Cys Ser Val Ser Met	
210 215 220	
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Ile Ile Ala Ile Ile Val Phe Leu Ser Gly Thr Lys Arg Tyr Arg Tyr	
225 230 235 240	
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Lys Arg Ser Leu Gly Ser Pro Ile Val His Ile Phe Gln Val Ile Ala	
245 250 255	
gca tca ata aag aaa aga aag agg caa ctc cca tac aat gtt ggt tct	816
Ala Ser Ile Lys Lys Arg Lys Arg Gln Leu Pro Tyr Asn Val Gly Ser	
260 265 270	
ttg tat gag gac act ccc gag gct tca aga ata gag cac acc gaa cag	864
Leu Tyr Glu Asp Thr Pro Glu Ala Ser Arg Ile Glu His Thr Glu Gln	
275 280 285	
ttc cgt ttc ttg gag aaa gca gcc att gtg gca gaa gat gat ttt gag	912
Phe Arg Phe Leu Glu Lys Ala Ala Ile Val Ala Glu Asp Asp Phe Glu	
290 295 300	
aca aat tta tgt ggt tct gga cca aac cca tgg aaa tta tgc tca cta	960
Thr Asn Leu Cys Gly Ser Gly Pro Asn Pro Trp Lys Leu Cys Ser Leu	
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aca agg gta gag gag gtg aaa atg atg gtg aga ctt ctg cca gtg tgg	1008
Thr Arg Val Glu Glu Val Lys Met Met Val Arg Leu Leu Pro Val Trp	
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PF59082SeqList_PF59082.txt

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Ser	Val	Glu	Gln	Ala	Ser	Thr	Met	Glu	Arg	Asn	Ile	Gly	Ser	Phe	Gln		
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atc	cct	gca	ggc	tct	gtc	aca	gtc	ttt	ttt	gtg	gct	gca	ata	cta	atc		1152
Ile	Pro	Ala	Gly	Ser	Val	Thr	Val	Phe	Phe	Val	Ala	Ala	Ile	Leu	Ile		
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Thr	Leu	Ala	Val	Tyr	Asp	Arg	Leu	Ile	Met	Pro	Leu	Trp	Lys	Lys	Trp		
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Asn	Gly	Lys	Pro	Gly	Phe	Thr	Asp	Leu	Gln	Arg	Ile	Ala	Ile	Gly	Leu		
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gta	ttt	tcc	att	ttt	gga	atg	gcg	gct	gct	tct	gta	tgc	gag	agg	aaa		1296
Val	Phe	Ser	Ile	Phe	Gly	Met	Ala	Ala	Ala	Ser	Val	Cys	Glu	Arg	Lys		
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cgg	tta	tcc	ggt	gca	aaa	agt	ggt	agt	ggc	ggc	aac	caa	gca	aca	aca		1344
Arg	Leu	Ser	Val	Ala	Lys	Ser	Val	Ser	Gly	Gly	Asn	Gln	Ala	Thr	Thr		
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Thr	Leu	Pro	Ile	Ser	Val	Phe	Leu	Leu	Ile	Pro	Gln	Phe	Phe	Leu	Val		
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Gly	Ser	Gly	Glu	Ala	Phe	Ile	Tyr	Thr	Gly	Gln	Leu	Asp	Phe	Phe	Ile		
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aca	cgg	tca	cca	aaa	gga	atg	aaa	acc	atg	agc	act	ggt	ctc	ttt	ctc		1488
Thr	Arg	Ser	Pro	Lys	Gly	Met	Lys	Thr	Met	Ser	Thr	Gly	Leu	Phe	Leu		
			485					490						495			
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Thr	Thr	Leu	Ser	Leu	Gly	Phe	Phe	Phe	Ser	Ser	Phe	Leu	Val	Ser	Val		
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Val	Lys	Lys	Val	Thr	Gly	Thr	Arg	Asp	Gly	Gln	Gly	Trp	Leu	Ala	Asp		
		515				520					525						
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Ser	Ile	Asn	Lys	Gly	Arg	Leu	Asp	Leu	Phe	Tyr	Ala	Leu	Leu	Thr	Ile		
	530				535						540						
ctt	agt	ttc	ggt	aac	ttt	gca	gca	ttt	gcg	gta	tgt	gca	ggt	tgg	ttc		1680
Leu	Ser	Phe	Val	Asn	Phe	Ala	Ala	Phe	Ala	Val	Cys	Ala	Val	Trp	Phe		
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Lys	Pro	Lys	Lys	Pro	Lys	Gln	Pro	Ala	Ala	Met	Gln	Met	Gly	Pro	Val		
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<212> PRT

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Leu	Ile	Leu	Gly	Ile	Glu	Ile	Val	Glu	Arg	Leu	Ser	Thr	Met	Gly	Ile	
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Ala	Val	Asn	Leu	Val	Thr	Tyr	Met	Ile	Ser	Ile	Met	His	Leu	Pro	Ser	
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Ser	Thr	Ala	Ala	Asn	Thr	Val	Thr	Asp	Phe	Met	Gly	Thr	Ser	Phe	Leu	
	65				70				75						80	
Leu	Cys	Leu	Leu	Gly	Gly	Phe	Leu	Ala	Asp	Ser	Phe	Leu	Gly	Arg	Tyr	
			85					90						95		
Lys	Thr	Ile	Gly	Ile	Phe	Ala	Ser	Ile	Gln	Thr	Leu	Gly	Thr	Ala	Thr	
		100						105					110			
Leu	Ala	Ile	Ser	Thr	Lys	Leu	Pro	Gly	Leu	Arg	Pro	Pro	Pro	Cys	His	

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Ser	Ser	Val	Ser	Gly	Phe	Gly	Ser	Asp	Gln	Phe	Asp	Glu	Lys	Asp	Glu
				165					170					175	
Lys	Glu	Lys	Ser	Gln	Met	Ala	Tyr	Phe	Phe	Asn	Arg	Phe	Phe	Phe	Phe
			180					185					190		
Ile	Ser	Phe	Gly	Thr	Leu	Ala	Ala	Val	Thr	Val	Leu	Val	Tyr	Leu	Gln
		195					200					205			
Asp	Glu	Val	Ser	Arg	Ser	Leu	Ala	Tyr	Gly	Ile	Cys	Ser	Val	Ser	Met
	210					215					220				
Ile	Ile	Ala	Ile	Ile	Val	Phe	Leu	Ser	Gly	Thr	Lys	Arg	Tyr	Arg	Tyr
225					230					235					240
Lys	Arg	Ser	Leu	Gly	Ser	Pro	Ile	Val	His	Ile	Phe	Gln	Val	Ile	Ala
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Ala	Ser	Ile	Lys	Lys	Arg	Lys	Arg	Gln	Leu	Pro	Tyr	Asn	Val	Gly	Ser
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Leu	Tyr	Glu	Asp	Thr	Pro	Glu	Ala	Ser	Arg	Ile	Glu	His	Thr	Glu	Gln
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	290					295					300				
Thr	Asn	Leu	Cys	Gly	Ser	Gly	Pro	Asn	Pro	Trp	Lys	Leu	Cys	Ser	Leu
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Thr	Arg	Val	Glu	Glu	Val	Lys	Met	Met	Val	Arg	Leu	Leu	Pro	Val	Trp
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Ala	Thr	Thr	Ile	Ile	Phe	Trp	Thr	Ile	Tyr	Ala	Gln	Leu	Ile	Thr	Phe
			340					345					350		
Ser	Val	Glu	Gln	Ala	Ser	Thr	Met	Glu	Arg	Asn	Ile	Gly	Ser	Phe	Gln
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Ile	Pro	Ala	Gly	Ser	Val	Thr	Val	Phe	Phe	Val	Ala	Ala	Ile	Leu	Ile
	370					375					380				
Thr	Leu	Ala	Val	Tyr	Asp	Arg	Leu	Ile	Met	Pro	Leu	Trp	Lys	Lys	Trp
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Asn	Gly	Lys	Pro	Gly	Phe	Thr	Asp	Leu	Gln	Arg	Ile	Ala	Ile	Gly	Leu
				405					410					415	
Val	Phe	Ser	Ile	Phe	Gly	Met	Ala	Ala	Ala	Ser	Val	Cys	Glu	Arg	Lys
			420					425					430		
Arg	Leu	Ser	Val	Ala	Lys	Ser	Val	Ser	Gly	Gly	Asn	Gln	Ala	Thr	Thr
		435					440					445			
Thr	Leu	Pro	Ile	Ser	Val	Phe	Leu	Leu	Ile	Pro	Gln	Phe	Phe	Leu	Val
	450					455					460				
Gly	Ser	Gly	Glu	Ala	Phe	Ile	Tyr	Thr	Gly	Gln	Leu	Asp	Phe	Phe	Ile
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Thr	Arg	Ser	Pro	Lys	Gly	Met	Lys	Thr	Met	Ser	Thr	Gly	Leu	Phe	Leu
				485					490					495	
Thr	Thr	Leu	Ser	Leu	Gly	Phe	Phe	Phe	Ser	Ser	Phe	Leu	Val	Ser	Val
			500					505					510		
Val	Lys	Lys	Val	Thr	Gly	Thr	Arg	Asp	Gly	Gln	Gly	Trp	Leu	Ala	Asp
		515					520					525			
Ser	Ile	Asn	Lys	Gly	Arg	Leu	Asp	Leu	Phe	Tyr	Ala	Leu	Leu	Thr	Ile
	530					535					540				
Leu	Ser	Phe	Val	Asn	Phe	Ala	Ala	Phe	Ala	Val	Cys	Ala	Val	Trp	Phe
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Lys	Pro	Lys	Lys	Pro	Lys	Gln	Pro	Ala	Ala	Met	Gln	Met	Gly	Pro	Val
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PF59082SeqList_PF59082.txt

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tat atc tta gga aac gaa tgt tgt gag aga ttg gct tat tat ggg atg      144
Tyr Ile Leu Gly Asn Glu Cys Cys Glu Arg Leu Ala Tyr Tyr Gly Met
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agc aca aac ctg gtg ctt tat ttc aag aac cgg cta aat cag cat agt      192
Ser Thr Asn Leu Val Leu Tyr Phe Lys Asn Arg Leu Asn Gln His Ser
50      55      60
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Ala Thr Ala Ser Lys Asn Val Ser Asn Trp Ser Gly Thr Cys Tyr Ile
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Thr Pro Leu Ile Gly Ala Tyr Leu Ala Asp Ser Tyr Leu Gly Arg Tyr
85      90      95
tgg aca att gct gtt ttt tca ata att tat gct att gga atg aca ctc      336
Trp Thr Ile Ala Val Phe Ser Ile Ile Tyr Ala Ile Gly Met Thr Leu
100      105      110
ttg aca ttg tct gca tca gtt cct ggc ata aaa cca aca tgt cat gga      384
Leu Thr Leu Ser Ala Ser Val Pro Gly Ile Lys Pro Thr Cys His Gly
115      120      125
cat gga gat gaa aat tgt cgt gct act act cta gag agt gca gtg tgc      432
His Gly Asp Glu Asn Cys Arg Ala Thr Thr Leu Glu Ser Ala Val Cys
130      135      140
ttc cta gct ctt tac ctt att gct ctt ggc acc ggt ggc att aag cct      480
Phe Leu Ala Leu Tyr Leu Ile Ala Leu Gly Thr Gly Ile Lys Pro
145      150      155
tgt gtc tca tcc tat gga gca gat cag ttt gat gac act gac tcg gct      528
Cys Val Ser Ser Tyr Gly Ala Asp Gln Phe Asp Asp Thr Asp Ser Ala
165      170      175
gag aag gaa cgc agt tct ttc ttc aat tgg ttc tat ttt tca atc aac      576
Glu Lys Glu Arg Ser Ser Phe Phe Asn Trp Phe Tyr Phe Ser Ile Asn
180      185      190
att ggc gct ctt att gca tct tct cta ttg gtt tgg ata caa gat aat      624
Ile Gly Ala Leu Ile Ala Ser Ser Leu Leu Val Trp Ile Gln Asp Asn
195      200      205
gtg ggt tgg gga tgg ggc ttt ggt att cct gct gta gcc atg gca att      672
Val Gly Trp Gly Trp Gly Phe Gly Ile Pro Ala Val Ala Met Ala Ile
210      215      220
gct gtg gtg agt ttc ttt tca ggc act agg ttg tat agg aat cag aag      720
Ala Val Val Ser Phe Phe Ser Gly Thr Arg Leu Tyr Arg Asn Gln Lys
225      230      235
cct gga ggc agt gcc atc act aga atc tgt cag gtg gta atg gca tcc      768
Pro Gly Gly Ser Ala Ile Thr Arg Ile Cys Gln Val Val Met Ala Ser
245      250      255
ata aga aaa tac aat gtt gaa gta cct gct gac gag tca ctt tta tat      816
Ile Arg Lys Tyr Asn Val Glu Val Pro Ala Asp Glu Ser Leu Leu Tyr
260      265      270
gag act gct gaa act gaa tct gct ata aaa gga agc cga aag ctt gac      864
Glu Thr Ala Glu Thr Glu Ser Ala Ile Lys Gly Ser Arg Lys Leu Asp
275      280      285
cac aca aat gag cta aga ttt ttt gac aaa gca aca gtg cta gca cag      912
His Thr Asn Glu Leu Arg Phe Phe Asp Lys Ala Thr Val Leu Ala Gln
290      295      300
tca gat aaa gtg aag gaa tca aca aac cct tgg aga ctt tgc act gta      960
Ser Asp Lys Val Lys Glu Ser Thr Asn Pro Trp Arg Leu Cys Thr Val
305      310      315
act caa gtg gaa gag ctg aaa tcc att tta aga ata ctt cct gta tgg      1008
Thr Gln Val Glu Glu Leu Lys Ser Ile Leu Arg Ile Leu Pro Val Trp
325      330      335
gca acc ggc atc ata ttt tcc act gtc tat ggt caa atg agc acc tta      1056
Ala Thr Gly Ile Ile Phe Ser Thr Val Tyr Gly Gln Met Ser Thr Leu
340      345      350
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PF59082SeqList_PF59082.txt

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Lys Phe Thr Gly Asn Lys Asn Gly Leu Thr Gln Leu Gln Arg Met Gly			
405	410	415	
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Glu Glu Ile Pro Met Thr Ile Phe Trp Gln Val Pro Gln Tyr Phe Ile			
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Tyr Glu Gln Ala Pro Asp Ala Met Arg Ser Phe Cys Ser Ala Leu Ser			
485	490	495	
ctt acc act gtt gcg ctt gga cag tac ttg agc tct ctg ctt gtg aca			1536
Leu Thr Thr Val Ala Leu Gly Gln Tyr Leu Ser Ser Leu Leu Val Thr			
500	505	510	
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Ile Val Thr Lys Ile Ser Thr Arg Asn Gly Ser Pro Gly Trp Ile Pro			
515	520	525	
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Asp Asn Leu Asn Phe Gly His Ile Asp Tyr Phe Phe Trp Leu Leu Ala			
530	535	540	
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Leu Leu Ser Val Val Asn Leu Ile Ala Phe Leu Val Val Ser Met Leu			
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 Ala Thr Ala Ser Lys Asn Val Ser Asn Trp Ser Gly Thr Cys Tyr Ile
 65 70 75 80
 Thr Pro Leu Ile Gly Ala Tyr Leu Ala Asp Ser Tyr Leu Gly Arg Tyr
 85 90 95
 Trp Thr Ile Ala Val Phe Ser Ile Ile Tyr Ala Ile Gly Met Thr Leu
 100 105 110
 Leu Thr Leu Ser Ala Ser Val Pro Gly Ile Lys Pro Thr Cys His Gly
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 His Gly Asp Glu Asn Cys Arg Ala Thr Thr Leu Glu Ser Ala Val Cys
 130 135 140
 Phe Leu Ala Leu Tyr Leu Ile Ala Leu Gly Thr Gly Gly Ile Lys Pro
 145 150 155 160
 Cys Val Ser Ser Tyr Gly Ala Asp Gln Phe Asp Asp Thr Asp Ser Ala
 165 170 175

PF59082SeqList_PF59082.txt

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Val Gly Trp Gly Trp Gly Phe Gly Ile Pro Ala Val Ala Met Ala Ile
210 215 220
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225 230 235 240
Pro Gly Gly Ser Ala Ile Thr Arg Ile Cys Gln Val Val Met Ala Ser
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260 265 270
Glu Thr Ala Glu Thr Glu Ser Ala Ile Lys Gly Ser Arg Lys Leu Asp
275 280 285
His Thr Asn Glu Leu Arg Phe Phe Asp Lys Ala Thr Val Leu Ala Gln
290 295 300
Ser Asp Lys Val Lys Glu Ser Thr Asn Pro Trp Arg Leu Cys Thr Val
305 310 315 320
Thr Gln Val Glu Glu Leu Lys Ser Ile Leu Arg Ile Leu Pro Val Trp
325 330 335
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340 345 350
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355 360 365
Phe Lys Ile Pro Pro Ala Ser Leu Ser Ile Phe Asp Thr Leu Ser Val
370 375 380
Ile Phe Trp Val Pro Val Tyr Asp Arg Ile Ile Val Pro Ile Ala Thr
385 390 395 400
Lys Phe Thr Gly Asn Lys Asn Gly Leu Thr Gln Leu Gln Arg Met Gly
405 410 415
Ile Gly Leu Phe Ile Ser Ile Phe Ser Met Val Ala Ala Ala Ile Leu
420 425 430
Glu Leu Ile Arg Leu Arg Met Val Arg Arg His Asn Tyr Tyr Gln Leu
435 440 445
Glu Glu Ile Pro Met Thr Ile Phe Trp Gln Val Pro Gln Tyr Phe Ile
450 455 460
Ile Gly Cys Ala Glu Val Phe Tyr Phe Ile Gly Gln Leu Glu Phe Phe
465 470 475 480
Tyr Glu Gln Ala Pro Asp Ala Met Arg Ser Phe Cys Ser Ala Leu Ser
485 490 495
Leu Thr Thr Val Ala Leu Gly Gln Tyr Leu Ser Ser Leu Leu Val Thr
500 505 510
Ile Val Thr Lys Ile Ser Thr Arg Asn Gly Ser Pro Gly Trp Ile Pro
515 520 525
Asp Asn Leu Asn Phe Gly His Ile Asp Tyr Phe Phe Trp Leu Leu Ala
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Asp Tyr Lys Gly Arg Pro Ala Glu Arg Ser Lys Thr Gly Gly Trp Thr	
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Ala Ser Ala Met Ile Leu Gly Gly Glu Val Met Glu Arg Leu Thr Thr	

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Ser	Phe	Met	Leu	Cys	Leu	Leu	Gly	Gly	Phe	Leu	Ala	Asp	Thr	Phe	Leu	
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gtg	aca	atc	ttg	aca	ata	tca	acc	ata	att	ccg	agc	ctt	cac	cct	cca	384
Val	Thr	Ile	Leu	Thr	Ile	Ser	Thr	Ile	Ile	Pro	Ser	Leu	His	Pro	Pro	
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Lys	Cys	Asn	Gly	Asp	Thr	Val	Pro	Pro	Cys	Val	Arg	Ala	Asn	Glu	Lys	
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Lys	Tyr	Arg	Phe	Lys	Lys	Leu	Val	Gly	Ser	Pro	Leu	Thr	Gln	Phe	Ala	
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Trp	Ala	Thr	Thr	Ile	Met	Phe	Trp	Thr	Ile	His	Ala	Gln	Met	Thr	Thr	
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 Pro His Ser Lys Gln Phe Arg Phe Leu Asp Lys Ala Ala Ile Met Asp
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 Lys Val Leu Lys Asn Pro His Gly Phe Thr Pro Leu Gln Arg Ile Gly
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 Leu Arg Ser Thr Ser Gly Gly Trp Lys Ala Ala Ala Phe Ile Ile Thr
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Leu	Ala		Leu	Ile	Tyr	Val	Leu	Gly	Leu	Ser	Leu	Leu	Thr	Phe	Ser	
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Lys	Ala	Val	Leu	Arg	Leu	Val	Pro	Ile	Trp	Ala	Thr	Cys	Leu	Ile	Phe	
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Gly	Ile	Thr	Met	Leu	Gln	Arg	Ile	Gly	Thr	Gly	Met	Leu	Leu	Ser	Ala	
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Gln	Glu	Leu	Arg	Ser	Val	Gly	Leu	Ser	Leu	Tyr	Leu	Ser	Ile	Phe	Gly	
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Thr	Gly	Lys	Asp	Asn	Arg	His	Ser	Trp	Phe	Ser	Ser	Asn	Leu	Asn	Arg	
		515					520					525				
gcg	cat	ctt	gat	tat	ttc	tat	gcc	ctt	cta	gct	gct	ctc	agt	gca	gtg	1632
Ala	His	Leu	Asp	Tyr	Phe	Tyr	Ala	Leu	Leu	Ala	Ala	Leu	Ser	Ala	Val	
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 Ile Asn Tyr Leu Thr Gly Pro Leu Gly Gln Ser Thr Val Thr Ala Ala
 65 70 75 80
 Glu Asn Val Asn Leu Trp Ser Gly Thr Ala Ser Leu Leu Pro Leu Leu
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 Gly Ala Phe Leu Ala Asp Ser Phe Leu Gly Arg Tyr Arg Thr Ile Val
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 Leu Ala Ser Leu Ile Tyr Val Leu Gly Leu Ser Leu Leu Thr Phe Ser
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 Thr Ile Leu Pro Val Thr Thr Ser Asp Gly Glu Val Ala Arg Pro Gln
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 Leu Ile Phe Phe Phe Phe Ser Leu Tyr Leu Val Ala Leu Ala Gln Gly
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 Gly His Lys Pro Cys Val Gln Ala Phe Gly Ala Asp Gln Phe Asp Val
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 Asn Asp Pro Glu Glu Cys Lys Ala Arg Ser Ser Phe Phe Asn Trp Trp
 180 185 190
 Tyr Phe Ala Phe Ser Ala Gly Leu Phe Val Thr Leu Phe Ile Leu Asn
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 Tyr Val Gln Asp Asn Val Gly Trp Val Leu Gly Phe Gly Ile Pro Cys
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 Ile Ala Met Leu Thr Ala Leu Val Ile Phe Leu Ile Gly Thr Trp Thr
 225 230 235 240
 Tyr Arg Phe Ser Ile Arg Arg Glu Glu Arg Gly Pro Phe Leu Arg Ile
 245 250 255
 Gly Arg Val Phe Ile Val Ala Val Asn Asn Trp Arg Ile Thr Pro Ser
 260 265 270
 Ala Val Thr Ser Glu Glu Glu Ala Cys Gly Thr Leu Pro Cys His Gly
 Seite 537

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Thr Met Asp Arg Glu Ile Leu Pro Gly Phe Tyr Val Pro Ala Ser
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Ile Ser Met Val Ile Ala Ala Phe Val Glu Met Lys Arg Leu Lys Val
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Thr Gly Lys Asp Asn Arg His Ser Trp Phe Ser Ser Asn Leu Asn Arg
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Asn Lys Pro Ala Leu Ser Gly Cys Asn Gly Gly Met Leu Ala Ala Ser	
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Phe Val Leu Val Val Glu Ile Leu Glu Asn Leu Ala Phe Leu Ala Asn	
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gca agc aat ttg gtg ctg tat ctg agg cag tac atg cac atg tcc cct	192
Ala Ser Asn Leu Val Leu Tyr Ser Leu Arg Gln Tyr Met His Met Ser Pro	
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Ser Lys Ser Ala Asn Asn Val Thr Asn Phe Met Gly Thr Ala Phe Leu	
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Leu Ala Leu Leu Gly Gly Phe Leu Ser Asp Ala Phe Phe Thr Thr Tyr	
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cac atc tac ctg ata agt gca gtc att gaa ttc ctg gga ttg att gtt	336
His Ile Tyr Leu Ile Ser Ala Val Ile Glu Phe Leu Gly Leu Ile Val	
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PF59082SeqList_PF59082.txt

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Ala	Ala	Thr	Pro	Cys	Asn	Glu	Val	Ser	Gly	Gly	Lys	Ala	Ala	Met	Leu	
	130					135					140					
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Phe	Ala	Gly	Leu	Tyr	Leu	Val	Ala	Leu	Gly	Val	Gly	Gly	Val	Lys	Gly	
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Gly	Arg	Arg	Gln	Arg	Ser	Thr	Phe	Phe	Asn	Tyr	Phe	Val	Phe	Cys	Leu	
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Ser	Cys	Gly	Ala	Leu	Ile	Ala	Val	Thr	Phe	Val	Val	Trp	Val	Glu	Asp	
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Asn	Lys	Gly	Trp	Glu	Trp	Gly	Phe	Gly	Ile	Ser	Thr	Ile	Ala	Ile	Phe	
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225					230					235					240	
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Ile	Pro	Ser	Gly	Ser	Pro	Leu	Thr	Thr	Ile	Leu	Lys	Val	Leu	Val	Ala	
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Ala	Ser	Leu	Asn	Ser	Cys	Phe	Asn	Ser	Arg	Asn	Ser	Ser	Ser	Ala	Val	
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Val	Asn	Met	Thr	Ser	Ser	Pro	Ser	Asn	Pro	His	Ser	Gly	Ser	Arg	Lys	
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Gln	Gln	Ala	Gly	Lys	Glu	Glu	Ser	Asn	Thr	Thr	Asn	Lys	Glu	Pro	Glu	
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Ile	Met	Leu	Asn	Cys	Cys	Leu	Ala	Gln	Leu	Ser	Thr	Phe	Ser	Val	Glu	
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Gln	Ala	Ala	Thr	Met	Asp	Thr	Lys	Leu	Gly	Ser	Leu	Lys	Val	Pro	Pro	
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Glu	Met	Gly	Ile	Thr	His	Leu	Gln	Arg	Ile	Gly	Ile	Gly	Leu	Val	Leu	
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Ser	Ile	Val	Ala	Met	Ala	Val	Ala	Ala	Val	Val	Glu	Val	Lys	Arg	Lys	
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Arg	Val	Ala	Met	Glu	Thr	His	Thr	Asn	Asn	Asn	Asn	Ser	Leu	Leu	Gly	
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cca	tg	ctc	tct	ggg	gca	aac	ctt	aac	cac	tac	cac	cta	gag	agg	ttt	1680
Pro	Trp	Leu	Ser	Gly	Ala	Asn	Leu	Asn	His	Tyr	His	Leu	Glu	Arg	Phe	
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tac	tg	ctc	atg	tgt	gtg	ctg	agt	gcg	ttg	aat	ttc	ttg	cat	tac	ttg	1728
Tyr	Trp	Leu	Met	Cys	Val	Leu	Ser	Ala	Leu	Asn	Phe	Leu	His	Tyr	Leu	
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Asn																

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Phe	Val	Leu	Val	Val	Glu	Ile	Leu	Glu	Asn	Leu	Ala	Phe	Leu	Ala	Asn
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Leu	Ala	Leu	Leu	Gly	Gly	Phe	Leu	Ser	Asp	Ala	Phe	Phe	Thr	Thr	Tyr
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His	Ile	Tyr	Leu	Ile	Ser	Ala	Val	Ile	Glu	Phe	Leu	Gly	Leu	Ile	Val
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Leu	Thr	Ala	Gln	Ala	Arg	Val	Pro	Ser	Leu	Lys	Pro	Pro	Ala	Cys	Asp
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Ser	Leu	Pro	Ser	His	Gly	Ala	Glu	Gln	Phe	Asp	Asp	Asn	Thr	Pro	Ser
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Ser	Cys	Gly	Ala	Leu	Ile	Ala	Val	Thr	Phe	Val	Val	Trp	Val	Glu	Asp
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Ile	Pro	Ser	Gly	Ser	Pro	Leu	Thr	Thr	Ile	Leu	Lys	Val	Leu	Val	Ala
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Ala	Ser	Leu	Asn	Ser	Cys	Phe	Asn	Ser	Arg	Asn	Ser	Ser	Ser	Ala	Val
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PF59082SeqList_PF59082.txt

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 355 360 365
 Gln Ala Ala Thr Met Asp Thr Lys Leu Gly Ser Leu Lys Val Pro Pro
 370 375 380
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 385 390 395 400
 Ile Tyr Asp His Ile Ile Thr Pro Phe Ala Arg Arg Val Thr Lys Thr
 405 410 415
 Glu Met Gly Ile Thr His Leu Gln Arg Ile Gly Ile Gly Leu Val Leu
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 Ser Ile Val Ala Met Ala Val Ala Ala Val Val Glu Val Lys Arg Lys
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 Arg Val Ala Met Glu Thr His Thr Asn Asn Asn Asn Ser Leu Leu Gly
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 His Asp Ala Thr Lys Pro Leu Pro Ile Thr Phe Leu Trp Ile Ala Phe
 465 470 475 480
 Gln Tyr Leu Phe Leu Gly Ser Ala Asp Leu Phe Thr Leu Ala Gly Leu
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 Leu Glu Phe Phe Thr Glu Ala Pro Ser Ser Met Arg Ser Leu Ala
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 Thr Ser Leu Ser Trp Ala Ser Leu Ala Val Gly Tyr Tyr Leu Ser Ser
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 530 535 540
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 545 550 555 560
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 Gly Phe Pro Ala Asp Arg Ser Lys Thr Gly Gly Trp Val Pro Ala Ala
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 Leu Ile Leu Gly Ile Glu Ile Val Glu Arg Leu Ser Thr Met Gly Ile
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 Ala Val Asn Leu Val Thr Tyr Met Ile Ser Ile Met His Leu Pro Ser
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 Ser Thr Ala Ala Asn Thr Val Thr Asp Phe Met Gly Thr Ser Phe Leu
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 Leu Cys Leu Leu Gly Gly Phe Leu Ala Asp Ser Phe Leu Gly Arg Tyr
 85 90 95
 aag aca att gga atc ttt gct tca ata caa aca ctg ggt act gct aca 336
 Lys Thr Ile Gly Ile Phe Ala Ser Ile Gln Thr Leu Gly Thr Ala Thr

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gct	aac	agt	gac	agc	tgc	aaa	caa	gcc	aac	gga	ttc	caa	atg	gga	atc		432
Ala	Asn	Ser	Asp	Ser	Cys	Lys	Gln	Ala	Asn	Gly	Phe	Gln	Met	Gly	Ile		
	130					135					140						
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Leu	Tyr	Leu	Ser	Leu	Tyr	Leu	Ile	Ala	Leu	Gly	Thr	Gly	Gly	Leu	Lys		
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tcc	agt	gtt	tca	gga	ttt	ggg	tct	gac	caa	ttc	gat	gag	aaa	gat	gag		528
Ser	Ser	Val	Ser	Gly	Phe	Gly	Ser	Asp	Gln	Phe	Asp	Glu	Lys	Asp	Glu		
				165				170						175			
aag	gag	aaa	tgc	caa	atg	gcc	tat	ttt	ttc	aac	agg	ttt	ttc	ttc	ttc		576
Lys	Glu	Lys	Ser	Gln	Met	Ala	Tyr	Phe	Phe	Asn	Arg	Phe	Phe	Phe	Phe		
			180					185					190				
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Ile	Ser	Phe	Gly	Thr	Leu	Ala	Ala	Val	Thr	Val	Leu	Val	Tyr	Leu	Gln		
		195				200						205					
gat	gaa	gtg	agt	cgc	agc	ttg	gcg	tat	gga	ata	tgt	tct	gtc	tct	atg		672
Asp	Glu	Val	Ser	Arg	Ser	Leu	Ala	Tyr	Gly	Ile	Cys	Ser	Val	Ser	Met		
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Lys	Arg	Ser	Leu	Gly	Ser	Pro	Ile	Val	His	Ile	Phe	Gln	Val	Ile	Ala		
			245					250					255				
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Ala	Ser	Ile	Lys	Lys	Arg	Lys	Met	Gln	Leu	Pro	Tyr	Asn	Val	Gly	Ser		
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Leu	Tyr	Glu	Asp	Thr	Pro	Glu	Ala	Ser	Arg	Ile	Glu	His	Thr	Glu	Gln		
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Phe	Arg	Phe	Leu	Glu	Lys	Ala	Ala	Ile	Val	Ala	Glu	Asp	Asp	Phe	Glu		
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Thr	Asn	Leu	Cys	Gly	Ser	Gly	Pro	Asn	Pro	Trp	Lys	Leu	Cys	Ser	Leu		
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aca	agg	gta	gag	gag	gtg	aaa	atg	atg	gtg	aga	ctt	ctg	cca	gtg	tg		1008
Thr	Arg	Val	Glu	Glu	Val	Lys	Met	Met	Val	Arg	Leu	Leu	Pro	Val	Trp		
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Ala	Thr	Thr	Ile	Ile	Phe	Trp	Thr	Ile	Tyr	Ala	Gln	Leu	Ile	Thr	Phe		
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Ser	Val	Glu	Gln	Ala	Ser	Thr	Met	Glu	Arg	Asn	Ile	Gly	Ser	Phe	Gln		
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atc	cct	gca	ggc	tct	gtc	aca	gtc	ttt	ttt	gtg	gct	gca	ata	cta	atc		1152
Ile	Pro	Ala	Gly	Ser	Val	Thr	Val	Phe	Phe	Val	Ala	Ala	Ile	Leu	Ile		
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Thr	Leu	Ala	Val	Tyr	Asp	Arg	Leu	Ile	Met	Pro	Leu	Trp	Lys	Lys	Trp		
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aac	ggc	aaa	cca	ggg	ttc	act	gac	cta	caa	agg	ata	gca	att	ggg	ctt		1248
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Val	Phe	Ser	Ile	Phe	Gly	Met	Ala	Ala	Ala	Ser	Val	Cys	Glu	Arg	Lys		
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Arg	Leu	Ser	Val	Ala	Lys	Ser	Val	Ser	Gly	Gly	Asn	Gln	Ala	Thr	Thr		
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Thr	Leu	Pro	Ile	Ser	Val	Phe	Leu	Leu	Ile	Pro	Gln	Phe	Phe	Leu	Val		
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Thr	Thr	Leu	Ser	Leu	Gly	Phe	Phe	Phe	Ser	Ser	Phe	Leu	Val	Ser	Val	
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Ser	Thr	Ala	Ala	Asn	Thr	Val	Thr	Asp	Phe	Met	Gly	Thr	Ser	Phe	Leu	
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Lys	Glu	Lys	Ser	Gln	Met	Ala	Tyr	Phe	Phe	Asn	Arg	Phe	Phe	Phe	Phe	
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 Ser Val Glu Gln Ala Ser Thr Met Glu Arg Asn Ile Gly Ser Phe Gln
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 Ile Pro Ala Gly Ser Val Thr Val Phe Phe Val Ala Ala Ile Leu Ile
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 385 390 395 400
 Asn Gly Lys Pro Gly Phe Thr Asp Leu Gln Arg Ile Ala Ile Gly Leu
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 Val Phe Ser Ile Phe Gly Met Ala Ala Ala Ser Val Cys Glu Arg Lys
 420 425 430
 Arg Leu Ser Val Ala Lys Ser Val Ser Gly Gly Asn Gln Ala Thr Thr
 435 440 445
 Thr Leu Pro Ile Ser Val Phe Leu Leu Ile Pro Gln Phe Phe Leu Val
 450 455 460
 Gly Ser Gly Glu Ala Phe Ile Tyr Thr Gly Gln Leu Asp Phe Phe Ile
 465 470 475 480
 Thr Arg Ser Pro Lys Gly Met Lys Thr Met Ser Thr Gly Leu Phe Leu
 485 490 495
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 Val Lys Lys Val Thr Gly Thr Arg Asp Gly Gln Gly Trp Leu Ala Asp
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 Ser Ile Asn Lys Gly Arg Leu Asp Leu Phe Tyr Ala Leu Leu Thr Ile
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 Leu Ser Phe Val Asn Phe Ala Ala Phe Ala Val Cys Ala Val Trp Phe
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<400> 380
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 Glu Ser Glu Val Thr Leu Asp Gly Ser Val Asp Phe His Gly Arg
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 cct gca atc aga gcc aaa tct ggc aga tgg gtg gct gca att atc atc 144
 Pro Ala Ile Arg Ala Lys Ser Gly Arg Trp Val Ala Ala Ile Ile Ile
 35 40 45
 ctc ttg aac caa gct ctg gca act ctt gca ttt ttt ggg att gga gtg 192
 Leu Leu Asn Gln Ala Leu Ala Thr Leu Ala Phe Phe Gly Ile Gly Val
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 aac cta gtg ttg ttt ctg aca agg gtg gta gga caa aac aat gct gat 240
 Asn Leu Val Leu Phe Leu Thr Arg Val Val Gly Gln Asn Asn Ala Asp
 65 70 75 80
 gca gcc aac aat gtg agc aag tgg acc gga act gtt tac atc ttc tct 288
 Ala Ala Asn Asn Val Ser Lys Trp Thr Gly Thr Val Tyr Ile Phe Ser
 85 90 95
 cta gtg ggt gct ttc ctc agt gat tct tat tgg gga aga tat aaa act 336
 Leu Val Gly Ala Phe Leu Ser Asp Ser Tyr Trp Gly Arg Tyr Lys Thr
 100 105 110
 tgt gct gtc ttt cag gtc ata ttt gtt ata ggt cta atg tcc tta tcc 384
 Cys Ala Val Phe Gln Val Ile Phe Val Ile Gly Leu Met Ser Leu Ser
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Leu	Ser	Ile	Tyr	Leu	Val	Ala	Leu	Gly	Asn	Gly	Gly	Tyr	Gln	Pro	Asn	
				165					170					175		
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Ala	Leu	Val	Leu	Phe	Leu	Val	Cys	Thr	Pro	Arg	Tyr	Arg	His	Phe	Lys	
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Asn	Met	Asp	Ala	Lys	Glu	Ala	Ser	Asn	Asn	Ala	Asn	Arg	Lys	Ile	Leu	
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Cys	Pro	Val	Ser	Gln	Val	Glu	Glu	Val	Lys	Cys	Ile	Leu	Arg	Leu	Leu	
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Gly	His	Asn	Lys	Val	Ala	Phe	Phe	Ser	Tyr	Phe	Tyr	Leu	Ala	Phe	Asn	
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Ala	Leu	Val	Leu	Phe	Leu	Val	Cys	Thr	Pro	Arg	Tyr	Arg	His	Phe	Lys	
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			260					265						270		
Ser	Arg	Lys	Ser	Lys	Val	Gln	Met	Ser	Ser	Asn	Gly	Glu	Asp	Leu	Phe	
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Asn	Met	Asp	Ala	Lys	Glu	Ala	Ser	Asn	Asn	Ala	Asn	Arg	Lys	Ile	Leu	
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His	Thr	His	Gly	Phe	Lys	Phe	Leu	Asp	Arg	Ala	Ala	Phe	Ile	Ser	Ser	
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Arg	Asp	Leu	Gly	Asp	Gln	Lys	Gly	Leu	Gly	Tyr	Asn	Pro	Trp	His	Leu	

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 Pro Ile Trp Leu Cys Thr Ile Ile Tyr Ser Val Val Phe Thr Gln Met
 355 360 365
 Ala Ser Leu Phe Val Glu Gln Gly Ala Ala Met Lys Thr Lys Val Ser
 370 375 380
 Asn Phe Arg Ile Pro Pro Ala Ser Met Ser Ser Phe Asp Ile Leu Ser
 385 390 400
 Val Ala Val Phe Ile Phe Phe Tyr Arg Arg Val Leu Asp Pro Phe Val
 405 410 415
 Gly Lys Leu Lys Lys Thr Asp Ser Lys Gly Leu Thr Glu Leu Gln Arg
 420 425 430
 Met Gly Val Gly Leu Val Ile Ala Val Leu Ala Met Val Ser Ala Gly
 435 440 445
 Leu Val Glu Cys Tyr Arg Leu Lys Tyr Ala Lys Gln Gly Cys Ile His
 450 455 460
 Cys Asn Asp Ser Ser Thr Leu Ser Ile Phe Trp Gln Ile Pro Gln Tyr
 465 470 475 480
 Ala Phe Ile Gly Ala Ser Glu Val Phe Met Tyr Val Gly Gln Leu Glu
 485 490 495
 Phe Phe Asn Ala Gln Thr Pro Asp Gly Leu Lys Ser Phe Gly Ser Ala
 500 505 510
 Leu Cys Met Thr Ser Ile Ser Leu Gly Asn Tyr Val Ser Ser Leu Leu
 515 520 525
 Val Ser Val Val Met Lys Ile Ser Thr Glu Asp His Met Pro Gly Trp
 530 535 540
 Ile Pro Gly Asn Leu Asn Lys Gly His Leu Asp Arg Phe Tyr Phe Leu
 545 550 555 560
 Leu Ala Ala Leu Thr Ser Ile Asp Leu Ile Ala Tyr Ile Ala Cys Ala
 565 570 575
 Lys Trp Tyr Lys Ser Ile Gln Leu Glu Ala Asn Thr Gly Glu Ile Asp
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 Glu Pro Glu Val
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 Glu Glu Lys Lys Lys Lys Gln His Arg Arg Gly Gly Ile Arg Thr Leu
 20 25 30
 cct ttc att ctt gca aat gaa gtg tgt gac aga ttt gca agt gct ggt 144
 Pro Phe Ile Leu Ala Asn Glu Val Cys Asp Arg Phe Ala Ser Ala Gly
 35 40 45
 ttt cat ggt aac ttg ata agt tac ttg acc caa gag ctg aac atg cca 192
 Phe His Gly Asn Leu Ile Ser Tyr Leu Thr Gln Glu Leu Asn Met Pro
 50 55 60
 ttg gta gct gcc tca aac aca ctg aca aac ttt gga gga aca tct agc 240
 Leu Val Ala Ala Ser Asn Thr Leu Thr Asn Phe Gly Gly Thr Ser Ser
 65 70 75 80
 ttc acc cct ctc att ggg gct att ata gca gat tcc ttt gct gga cgt 288
 Phe Thr Pro Leu Ile Gly Ala Ile Ile Ala Asp Ser Phe Ala Gly Arg
 85 90 95
 ttt tgg acc att acc gtt gct tct ctc att tat gaa ctg gga ttg att 336
 Phe Trp Thr Ile Thr Val Ala Ser Leu Ile Tyr Glu Leu Gly Leu Ile
 100 105 110
 agc atc act gta tca gct ata ctg cca caa ttt cgt ccc cca cca tgc 384
 Ser Ile Thr Val Ser Ala Ile Leu Pro Gln Phe Arg Pro Pro Pro Cys

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Pro	Thr	Gln	Ala	Asn	Cys	Gln	Glu	Ala	Thr	Ser	Ser	Gln	Leu	Trp	Ile	
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Leu	Tyr	Ile	Ser	Leu	Leu	Leu	Thr	Ser	Val	Gly	Ser	Gly	Gly	Ile	Arg	
	145				150					155					160	
cca	tgt	ggt	gtg	ccc	ttt	tca	gca	gac	caa	att	gac	atg	acc	aaa	agt	528
Pro	Cys	Val	Val	Pro	Phe	Ser	Ala	Asp	Gln	Ile	Asp	Met	Thr	Lys	Ser	
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ggt	gtg	gca	tca	aga	aag	tgg	aac	atc	ttc	aat	tgg	tac	ttt	ttc	agc	576
Gly	Val	Ala	Ser	Arg	Lys	Trp	Asn	Ile	Phe	Asn	Trp	Tyr	Phe	Phe	Ser	
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Met	Gly	Phe	Ala	Ser	Leu	Ser	Ala	Leu	Thr	Ile	Val	Val	Tyr	Ile	Gln	
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Leu	Ile	Ser	Ile	Val	Ala	Phe	Val	Leu	Gly	Ser	Pro	Leu	Tyr	Lys	Thr	
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Val	Lys	Pro	Glu	Gly	Ser	Pro	Leu	Val	Arg	Leu	Ala	Gln	Val	Thr	Val	
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Ala	Ala	Ile	Lys	Lys	Arg	Lys	Glu	Ala	Leu	Pro	Glu	Asp	Pro	Lys	Leu	
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Leu	Tyr	His	Asn	Trp	Glu	Leu	Asp	Ala	Ser	Ile	Ser	Leu	Glu	Gly	Arg	
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ctt	cta	cac	tct	gat	caa	tat	aaa	tgg	ttg	gac	aaa	gct	gca	att	gtc	912
Leu	Leu	His	Ser	Asp	Gln	Tyr	Lys	Trp	Leu	Asp	Lys	Ala	Ala	Ile	Val	
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Thr	Glu	Glu	Glu	Ala	Lys	Asp	Pro	Thr	Thr	Thr	Pro	Lys	Leu	Trp	Lys	
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Leu	Ala	Thr	Val	His	Arg	Val	Glu	Glu	Leu	Lys	Ser	Ile	Ile	Arg	Met	
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Leu	His	Ser	Phe	Val	Ile	Gln	Gln	Ala	Arg	Thr	Met	Asp	Arg	His	Leu	
		355					360					365				
tct	ccc	tcg	ttc	caa	att	tcc	cca	gcc	agc	atg	tcc	att	ttc	agc	gtg	1152
Ser	Pro	Ser	Phe	Gln	Ile	Ser	Pro	Ala	Ser	Met	Ser	Ile	Phe	Ser	Val	
	370				375						380					
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Leu	Thr	Met	Met	Ser	Gly	Val	Val	Leu	Tyr	Glu	Arg	Leu	Phe	Val	Pro	
	385				390				395					400		
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Phe	Ala	Arg	Arg	Phe	Thr	Gly	Asn	Pro	Ser	Gly	Ile	Thr	Cys	Leu	Gln	
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aga	atg	gga	ata	ggc	ttc	ata	atc	aat	atc	ata	gcc	act	gtg	att	gct	1296
Arg	Met	Gly	Ile	Gly	Phe	Ile	Ile	Asn	Ile	Ile	Ala	Thr	Val	Ile	Ala	
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Gly	Leu	Met	Glu	Met	Lys	Arg	Lys	Ser	Val	Ala	Ala	Lys	Tyr	His	Leu	
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Leu	Asp	Asp	Pro	Lys	Ala	Thr	Ile	Pro	Ile	Ser	Val	Phe	Trp	Leu	Val	
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Pro	Gln	Tyr	Cys	Leu	His	Gly	Val	Ala	Glu	Ile	Phe	Met	Ser	Val	Gly	
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cat	ttg	gaa	ttt	ctc	ttt	gag	caa	tca	cct	gaa	agc	atg	aga	agc	agt	1488
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<213> Glycine max

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Pro	Phe	Ile ₃₅	Leu	Ala	Asn	Glu	Val ₄₀	Cys	Asp	Arg	Phe	Ala ₄₅	Ser	Ala	Gly
Phe	His ₅₀	Gly	Asn	Leu	Ile	Ser ₅₅	Tyr	Leu	Thr	Gln	Glu ₆₀	Leu	Asn	Met	Pro
Leu	Val	Ala	Ala	Ser	Asn ₇₀	Thr	Leu	Thr	Asn	Phe ₇₅	Gly	Gly	Thr	Ser	Ser ₈₀
65	Phe	Thr	Pro	Leu	Ile ₈₅	Gly	Ala	Ile	Ile	Ala ₉₀	Asp	Ser	Phe	Ala	Gly ₉₅
Phe	Trp	Thr	Ile ₁₀₀	Thr	Val	Ala	Ser	Leu ₁₀₅	Ile	Tyr	Glu	Leu	Gly ₁₁₀	Leu	Ile
Ser	Ile	Thr ₁₁₅	Val	Ser	Ala	Ile	Leu ₁₂₀	Pro	Gln	Phe	Arg	Pro ₁₂₅	Pro	Pro	Cys
Pro	Thr	Gln	Ala	Asn	Cys	Gln ₁₃₅	Glu	Ala	Thr	Ser	Ser ₁₄₀	Gln	Leu	Trp	Ile
Leu	Tyr	Ile	Ser	Leu	Leu ₁₅₀	Leu	Thr	Ser	Val	Gly ₁₅₅	Ser	Gly	Gly	Ile	Arg ₁₆₀
145	Pro	Cys	Val	Val	Pro ₁₆₅	Phe	Ser	Ala	Asp	Gln ₁₇₀	Ile	Asp	Met	Thr	Lys ₁₇₅
Gly	Val	Ala	Ser ₁₈₀	Arg	Lys	Trp	Asn	Ile ₁₈₅	Phe	Asn	Trp	Tyr	Phe ₁₉₀	Phe	Ser
Met	Gly	Phe ₁₉₅	Ala	Ser	Leu	Ser	Ala ₂₀₀	Leu	Thr	Ile	Val	Val ₂₀₅	Tyr	Ile	Gln
Asp	Asn	Met	Gly	Trp	Gly	Trp ₂₁₅	Gly	Leu	Gly	Ile	Pro ₂₂₀	Cys	Ile	Ala	Met
Leu	Ile	Ser	Ile	Val	Ala ₂₃₀	Phe	Val	Leu	Gly	Ser ₂₃₅	Pro	Leu	Tyr	Lys	Thr ₂₄₀
Val	Lys	Pro	Glu	Gly ₂₄₅	Ser	Pro	Leu	Val	Arg ₂₅₀	Leu	Ala	Gln	Val	Thr ₂₅₅	Val
Ala	Ala	Ile	Lys ₂₆₀	Lys	Arg	Lys	Glu	Ala ₂₆₅	Leu	Pro	Glu	Asp	Pro ₂₇₀	Lys	Leu
Leu	Tyr	His ₂₇₅	Asn	Trp	Glu	Leu	Asp ₂₈₀	Ala	Ser	Ile	Ser	Leu ₂₈₅	Glu	Gly	Arg
Leu	Leu	His	Ser	Asp	Gln	Tyr	Lys	Trp	Leu	Asp	Lys	Ala	Ala	Ile	Val

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 305 310 315 320
 Leu Ala Thr Val His Arg Val Glu Glu Leu Lys Ser Ile Ile Arg Met
 325 330 335
 Leu Pro Ile Trp Ala Ser Gly Ile Leu Leu Ile Thr Ser Ser Ser His
 340 345 350
 Leu His Ser Phe Val Ile Gln Gln Ala Arg Thr Met Asp Arg His Leu
 355 360 365
 Ser Pro Ser Phe Gln Ile Ser Pro Ala Ser Met Ser Ile Phe Ser Val
 370 375 380
 Leu Thr Met Met Ser Gly Val Val Leu Tyr Glu Arg Leu Phe Val Pro
 385 390 395 400
 Phe Ala Arg Arg Phe Thr Gly Asn Pro Ser Gly Ile Thr Cys Leu Gln
 405 410 415
 Arg Met Gly Ile Gly Phe Ile Ile Asn Ile Ile Ala Thr Val Ile Ala
 420 425 430
 Gly Leu Met Glu Met Lys Arg Lys Ser Val Ala Ala Lys Tyr His Leu
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 Leu Asp Asp Pro Lys Ala Thr Ile Pro Ile Ser Val Phe Trp Leu Val
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 Pro Gln Tyr Cys Leu His Gly Val Ala Glu Ile Phe Met Ser Val Gly
 465 470 475 480
 His Leu Glu Phe Leu Phe Glu Gln Ser Pro Glu Ser Met Arg Ser Ser
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 Trp Leu Pro Asp Arg Asn Leu Asn Arg Gly Gly Leu Asp Tyr Tyr Tyr
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Lys Ser Met Asp Val Asp Lys Leu Glu Asn Gly Gly Gly Gly Gly Asp	
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gcg gag agc ccg cgc ccc gtc gtc aag tac cac ggc tgg aag gcc atg	144
Ala Glu Ser Pro Arg Pro Val Lys Tyr His Gly Trp Lys Ala Met	
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ccc ttc atc atc ggc aac gag acg ttc gag aag ctg ggc acg ctg ggc	192
Pro Phe Ile Ile Gly Asn Glu Thr Phe Glu Lys Leu Gly Thr Leu Gly	
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Thr Ser Ala Asn Leu Leu Val Tyr Leu Thr Gln Val Phe His Met Arg	
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agc gtg gac gcg gcc acg ctg ctc aac ggg ctc aac ggc acc acc agc	288
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PF59082SeqList_PF59082.txt

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tac	ctc	gcg	ctc	ggc	atc	ggc	tcc	atc	ggc	tcc	ctc	atc	ggc	atg	ttc	384
Tyr	Leu	Ala	Leu	Ala	Ile	Ala	Ser	Ile	Ala	Ser	Leu	Ile	Gly	Met	Phe	
			115					120					125			
ctg	ctg	acg	ctt	acg	ggc	ggc	gag	gac	agc	ctg	cac	ccg	ccg	gaa	tgc	432
Leu	Leu	Thr	Leu	Thr	Ala	Gly	Ala	Asp	Ser	Leu	His	Pro	Pro	Glu	Cys	
			130													
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Gly	Val	Gly	Glu	Ala	Cys	Glu	Lys	Ala	Thr	Ser	Tyr	Gln	Phe	Ala	Val	
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Pro	Cys	Ser	Met	Pro	Phe	Gly	Ala	Asp	Gln	Phe	Asp	Pro	His	Thr	Glu	
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Ser	Gly	Lys	Arg	Gly	Ile	Asn	Ser	Phe	Phe	Asn	Trp	Tyr	Tyr	Phe	Thr	
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Phe	Thr	Ala	Ala	Met	Met	Ile	Ser	Ala	Thr	Val	Ile	Ile	Tyr	Val	Gln	
						215					220					
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Ser	Asn	Val	Ser	Trp	Pro	Ile	Gly	Leu	Gly	Ile	Pro	Thr	Ala	Leu	Met	
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Phe	Leu	Ala	Cys	Val	Leu	Phe	Phe	Met	Gly	Thr	Arg	Leu	Tyr	Val	Arg	
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gtg	acg	ccc	gag	ggg	agc	ccc	ttc	acc	agc	gtc	gtg	cag	gtg	ctg	tcg	816
Val	Thr	Pro	Glu	Gly	Ser	Pro	Phe	Thr	Ser	Val	Val	Gln	Val	Leu	Ser	
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gcc	gag	ctc	aag	aag	cag	tcg	ctg	aag	cag	ccc	aag	gac	ccg	aag	cag	864
Ala	Ala	Leu	Lys	Lys	Arg	Ser	Leu	Lys	Gln	Pro	Lys	Asp	Pro	Lys	Gln	
			275				280					285				
gac	ctc	ttc	gac	ccg	ccg	cac	acc	agc	ggc	atc	gtc	acc	cag	ctc	gag	912
Asp	Leu	Phe	Asp	Pro	Pro	His	Thr	Ser	Ala	Ile	Val	Thr	Gln	Leu	Ala	
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His	Thr	Asp	Gln	Phe	Arg	Cys	Leu	Asp	Lys	Ala	Ala	Ile	Val	Ala	Ser	
305					310					315					320	
cag	gac	gag	ttg	cgc	ccc	ggc	ggc	ggc	gag	ccc	gag	gac	ccc	tgg	agg	1008
Gln	Asp	Glu	Leu	Arg	Pro	Gly	Gly	Ala	Ala	Pro	Ala	Asp	Pro	Trp	Arg	
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ctc	tgc	agc	gtg	cag	cag	gtg	gag	gag	gtc	aag	tgc	ctc	atc	cgc	atc	1056
Leu	Cys	Ser	Val	Gln	Gln	Val	Glu	Glu	Val	Lys	Cys	Leu	Ile	Arg	Ile	
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gtg	ccc	gtc	tgg	tcc	acg	ggg	atc	atc	tac	tac	gtc	ggc	gtg	gtg	cag	1104
Val	Pro	Val	Trp	Ser	Thr	Gly	Ile	Ile	Tyr	Tyr	Val	Ala	Val	Val	Gln	
			355				360					365				
cag	tcc	acg	tac	gtg	gtg	ctc	tcg	gag	ctg	cag	tcc	gac	cgc	cac	ctc	1152
Gln	Ser	Thr	Tyr	Val	Val	Leu	Ser	Ala	Leu	Gln	Ser	Asp	Arg	His	Leu	
						375					380					
ggc	ggc	ggc	ggc	ttc	cag	atc	ccc	ggc	gag	tcc	ttc	acc	gtc	ttc	ggc	1200
Gly	Gly	Ala	Gly	Phe	Gln	Ile	Pro	Ala	Ala	Ser	Phe	Thr	Val	Phe	Ala	
385					390					395					400	
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Met	Leu	Ala	Gln	Thr	Leu	Trp	Ile	Pro	Phe	Tyr	Asp	Arg	Leu	Leu	Leu	
				405					410					415		
ccc	aag	ctc	cgg	aag	ata	acc	ggc	aag	gaa	gag	ggg	ttc	acg	ctg	ctc	1296
Pro	Lys	Leu	Arg	Lys	Ile	Thr	Gly	Lys	Glu	Glu	Gly	Phe	Thr	Leu	Leu	
			420					425				430				
cag	cgc	cag	ggc	atc	ggc	atc	gag	ctc	tcc	acc	gtc	ggc	atg	gtc	atc	1344
Gln	Arg	Gln	Gly	Ile	Gly	Ile	Ala	Leu	Ser	Thr	Val	Ala	Met	Val	Ile	
			435				440					445				
tct	gcc	atc	gtc	gag	gac	cgg	cgc	cgt	ggc	atc	gag	ctc	agc	cag	ccg	1392
Ser	Ala	Ile	Val	Glu	Asp	Arg	Arg	Arg	Ala	Ile	Ala	Leu	Ser	Gln	Pro	

PF59082SeqList_PF59082.txt

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Thr Leu Gly Thr Thr Ile Thr Gly Gly Ala Ile Ser Ala Met Ser Ser		
465	ctg tgg atg gtg ccg cag ctc atg atc ctg ggc cta tcg gag gca ttc	1488
Leu Trp Met Val Pro Gln Leu Met Ile Leu Gly Leu Ser Glu Ala Phe		
485	aac ctc atc agc cag att gag ttc tac tac aag gag atc ccg gag cac	1536
Asn Leu Ile Ser Gln Ile Glu Phe Tyr Tyr Lys Glu Ile Pro Glu His		
500	atg cgg agc gtg gcg ggg gcg ctc gca ttc tgc aac ctg gca ctc ggc	1584
Met Arg Ser Val Ala Gly Ala Leu Ala Phe Cys Asn Leu Ala Leu Gly		
515	aac tac ctc agt ggc ttc ctg gtg acc atc gtg cac cgg acc acg ggg	1632
Asn Tyr Leu Ser Gly Phe Leu Val Thr Ile Val His Arg Thr Thr Gly		
530	tcc ggg cag aac tgg ctg gcg cag gac ctc aac aag ggc cgc ctc gac	1680
Ser Gly Gln Asn Trp Leu Ala Gln Asp Leu Asn Lys Gly Arg Leu Asp		
545	ctc ttc tac tgg acc atc gca ggc atc ggc ttt aat ctc atc tac	1728
Leu Phe Tyr Trp Thr Ile Ala Gly Ile Gly Val Phe Asn Leu Ile Tyr		
565	ttc gtc atc tgc gcc agg tgg tac agg ttc aag gga acc agc aac	1773
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580	tga	1776

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 <211> 591
 <212> PRT
 <213> Zea mays

<400> 385

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Ala Glu Ser Pro Arg Pro Val Val Lys Tyr His Gly Trp Lys Ala Met	
35 40 45	
Pro Phe Ile Ile Gly Asn Glu Thr Phe Glu Lys Leu Gly Thr Leu Gly	
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Thr Ser Ala Asn Leu Leu Val Tyr Leu Thr Gln Val Phe His Met Arg	
65 70 75 80	
Ser Val Asp Ala Ala Thr Leu Leu Asn Gly Leu Asn Gly Thr Thr Ser	
85 90 95	
Leu Ala Pro Ile Val Gly Ala Phe Leu Ser Asp Ala Tyr Leu Gly Arg	
100 105 110	
Tyr Leu Ala Leu Ala Ile Ala Ser Ile Ala Ser Leu Ile Gly Met Phe	
115 120 125	
Leu Leu Thr Leu Thr Ala Gly Ala Asp Ser Leu His Pro Pro Glu Cys	
130 135 140	
Gly Val Gly Glu Ala Cys Glu Lys Ala Thr Ser Tyr Gln Phe Ala Val	
145 150 155 160	
Leu Phe Val Ala Phe Ala Phe Leu Val Leu Gly Ser Ala Gly Ile Arg	
165 170 175	
Pro Cys Ser Met Pro Phe Gly Ala Asp Gln Phe Asp Pro His Thr Glu	
180 185 190	
Ser Gly Lys Arg Gly Ile Asn Ser Phe Phe Asn Trp Tyr Tyr Phe Thr	
195 200 205	
Phe Thr Ala Ala Met Met Ile Ser Ala Thr Val Ile Ile Tyr Val Gln	
210 215 220	
Ser Asn Val Ser Trp Pro Ile Gly Leu Gly Ile Pro Thr Ala Leu Met	
225 230 235 240	
Phe Leu Ala Cys Val Leu Phe Phe Met Gly Thr Arg Leu Tyr Val Arg	
245 250 255	
Val Thr Pro Glu Gly Ser Pro Phe Thr Ser Val Val Gln Val Leu Ser	
260 265 270	

PF59082SeqList_PF59082.txt

Ala Ala Leu Lys Lys Arg Ser Leu Lys Gln Pro Lys Asp Pro Lys Gln
 275 280 285
 Asp Leu Phe Asp Pro Pro His Thr Ser Ala Ile Val Thr Gln Leu Ala
 290 295 300
 His Thr Asp Gln Phe Arg Cys Leu Asp Lys Ala Ala Ile Val Ala Ser
 305 310 315 320
 Gln Asp Glu Leu Arg Pro Gly Gly Ala Ala Pro Ala Asp Pro Trp Arg
 325 330 335
 Leu Cys Ser Val Gln Gln Val Glu Glu Val Lys Cys Leu Ile Arg Ile
 340 345 350
 Val Pro Val Trp Ser Thr Gly Ile Tyr Tyr Val Ala Val Val Gln
 355 360 365
 Gln Ser Thr Tyr Val Val Leu Ser Ala Leu Gln Ser Asp Arg His Leu
 370 375 380
 Gly Gly Ala Gly Phe Gln Ile Pro Ala Ala Ser Phe Thr Val Phe Ala
 385 390 395 400
 Met Leu Ala Gln Thr Leu Trp Ile Pro Phe Tyr Asp Arg Leu Leu Leu
 405 410 415
 Pro Lys Leu Arg Lys Ile Thr Gly Lys Glu Glu Gly Phe Thr Leu Leu
 420 425 430
 Gln Arg Gln Gly Ile Gly Ile Ala Leu Ser Thr Val Ala Met Val Ile
 435 440 445
 Ser Ala Ile Val Glu Asp Arg Arg Arg Ala Ile Ala Leu Ser Gln Pro
 450 455 460
 Thr Leu Gly Thr Thr Ile Thr Gly Gly Ala Ile Ser Ala Met Ser Ser
 465 470 475 480
 Leu Trp Met Val Pro Gln Leu Met Ile Leu Gly Leu Ser Glu Ala Phe
 485 490 495
 Asn Leu Ile Ser Gln Ile Glu Phe Tyr Lys Glu Ile Pro Glu His
 500 505 510
 Met Arg Ser Val Ala Gly Ala Leu Ala Phe Cys Asn Leu Ala Leu Gly
 515 520 525
 Asn Tyr Leu Ser Gly Phe Leu Val Thr Ile Val His Arg Thr Thr Gly
 530 535 540
 Ser Gly Gln Asn Trp Leu Ala Gln Asp Leu Asn Lys Gly Arg Leu Asp
 545 550 555 560
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 565 570 575
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 ccc ctc tcg cag tcc agc aag cag cag gat cct ctc gcc ggc gtc 96
 Pro Leu Ser Gln Ser Ser Lys Gln Gln Gln Asp Pro Leu Ala Gly Val
 20 25 30
 tcc gac tac ctt ggg cgg tcc gtg cac cgc gga agc tcc ggg gga tgg 144
 Ser Asp Tyr Leu Gly Arg Ser Val His Arg Gly Ser Ser Gly Gly Trp
 35 40 45
 aga tcc gcg ctc ttc gtc gtg ggc gtc gag atc gcc ggt agc ttc gcc 192
 Arg Ser Ala Leu Phe Val Val Gly Val Glu Ile Ala Gly Ser Phe Ala
 50 55 60
 tac ttc ggc atc tct gcc aac cta atc acg tac ctg act ggt ccg ctg 240
 Tyr Phe Gly Ile Ser Ala Asn Leu Ile Thr Tyr Leu Thr Gly Pro Leu
 65 70 75 80
 gga cag tcc aac gcc tcc gct gcc gcc tcc gtc aac gcc tgg tcc ggc 288
 Gly Gln Ser Asn Ala Ser Ala Ala Ala Ser Val Asn Ala Trp Ser Gly
 85 90 95

PF59082SeqList_PF59082.txt

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ctg Leu	ggc Gly	cgc Arg	tac Tyr	cga Arg	tcc Ser	gtc Val	atc Ile	atc Ile	gcc Ala	tgc Cys	acc Thr	ctc Leu	tac Tyr	gtc Val	ctg Leu	384
ggg Gly	tat Tyr	ggt Gly	atg Met	ctg Leu	acg Thr	ctg Leu	tcg Ser	gcg Ala	acg Thr	gtg Val	ccg Pro	gcg Ala	ctg Leu	cag Gln	ccg Pro	432
tcg Ser	cac His	atg Met	ccc Pro	tgc Cys	agg Arg	gag Glu	gat Asp	ggc Gly	gtc Val	tcg Ser	tcg Ser	tca Ser	tgc Cys	caa Gln	160	480
ccc Pro	ggg Gly	tgg Trp	ccg Pro	cag Gln	gtg Val	gcc Ala	ttc Phe	ttc Phe	tac Tyr	gtg Val	ccc Pro	ctg Leu	tac Tyr	ctg Leu	atc Ile	528
gcc Ala	atc Ile	gcg Ala	cag Gln	ggc Gly	gcc Ala	gac Asp	aag Lys	ccg Pro	tgc Cys	ggg Gly	ctg Leu	gcg Ala	ttc Phe	gcg Ala	gcg Ala	576
gac Asp	cag Gln	ttc Phe	gac Asp	gcg Ala	gag Glu	cac His	cag Gln	ggg Gly	gag Glu	cgc Arg	gcc Ala	tcc Ser	cgc Arg	ggg Gly	tcc Ser	624
cta Leu	ttc Phe	aac Asn	tgg Trp	tgg Trp	ttc Phe	ttc Phe	tgc Cys	atg Met	gcc Ala	atc Ile	ggc Gly	atc Ile	tcc Ser	gtg Val	tca Ser	672
gtc Val	tcc Ser	gtg Val	gtg Val	ggc Gly	tac Tyr	atc Ile	cag Gln	gag Glu	tac Tyr	gtc Val	ggg Gly	tgg Trp	ggg Gly	ctc Leu	ggc Gly	720
ttc Phe	ggc Gly	gtc Val	ccc Pro	tgc Cys	gcc Ala	atc Ile	gtg Val	ctc Leu	tgc Cys	gcc Ala	ttc Phe	ctc Leu	gtc Val	ttc Phe	ctg Leu	768
ttg Leu	ggc Gly	acc Thr	ccg Pro	acg Thr	tac Tyr	cgc Arg	ctg Leu	tac Tyr	gca Ala	ccc Pro	acg Thr	ccg Pro	gaa Glu	gcc Ala	aag Lys	816
tcc Ser	ccg Pro	ttc Phe	cgc Arg	cgc Arg	ctg Leu	gca Ala	cgc Arg	ggc Gly	ctg Leu	gcc Ala	gcc Ala	aac Asn	gcc Ala	aac Asn	aaa Lys	864
aca Thr	gga Gly	ggc Gly	ctc Leu	tcc Ser	gcc Ala	tcg Ser	cat His	tcg Ser	gag Glu	gag Glu	gag Glu	gaa Glu	gcg Ala	gca Ala	gca Ala	912
gac Asp	gcg Ala	cgg Arg	tgc Cys	gtg Val	ctg Leu	cgc Arg	ctg Leu	ccc Pro	atc Ile	tcg Trp	ggc Ala	gcg Ala	gcg Ala	agc Ser	ctg Leu	960
gcg Ala	tac Tyr	ggc Gly	gtg Val	gtg Val	tac Tyr	gcg Ala	cag Gln	att Ile	atg Met	acg Thr	ctg Leu	ttc Phe	aac Asn	aag Lys	cag Gln	1008
ggg Gly	cgc Arg	acc Thr	ctg Leu	gac Asp	cgc Arg	cac His	atc Ile	ggg Gly	gac Asp	ggc Gly	ctt Leu	gag Glu	ctg Leu	cct Pro	ccg Pro	1056
gcg Ala	gcg Ala	ctg Leu	cag Gln	acg Thr	ctg Leu	ggc Gly	ccc Pro	gcg Ala	agc Ser	atc Ile	ctg Leu	ctg Leu	ttc Phe	gtg Val	cct Pro	1104
gtt Val	tac Tyr	gac Asp	cgc Arg	gcg Ala	gtg Val	gtg Val	ccg Pro	gcg Ala	ctg Leu	cgg Arg	tgg Trp	gcg Ala	acg Thr	ggc Gly	aac Asn	1152
ccg Pro	tcg Ser	ggg Gly	ctg Leu	agc Ser	atg Met	ctg Leu	cag Gln	cgc Arg	gtg Val	ggc Gly	ggc Ala	atg Met	gcg Ala	gtg Val	1200	
tcg Ser	ctg Leu	gcg Ala	ggc Gly	gtg Val	gcg Ala	gtg Val	gcc Ala	gcg Ala	ctg Leu	gtg Val	gag Glu	gcg Ala	cgg Arg	cgg Arg	ctg Leu	1248
gcg Ala	atg Met	gcg Ala	cgg Arg	gag Glu	cac His	ggg Gly	ttg Leu	gtg Val	gac Asp	gac Asp	ccg Pro	tcg Ser	gcg Ala	acg Thr	gtg Val	1296
ccc Pro	atg Met	agc Ser	tgg Trp	gcg Ala	tgg Trp	atc Ile	gtg Val	ccg Pro	cag Gln	tac Tyr	gcc Ala	atg Met	atg Met	ggg Gly	gtg Val	1344
gcg Ala	gac Asp	gtg Val	ctg Leu	gcc Ala	gtg Val	gtg Val	ggc Gly	ctg Leu	cag Gln	gag Glu	ctc Leu	ttc Phe	tac Tyr	gac Asp	cag Gln	1392

PF59082SeqList_PF59082.txt

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atg	ggc	atc	ggg	gga	ttc	atc	agc	agt	ctg	ctc	atc	tcc	ctc	atc	gac	1488
Met	Gly	Ile	Gly	Gly	Phe	Ile	Ser	Ser	Leu	Leu	Ile	Ser	Leu	Ile	Asp	
				485					490						495	
ggc	gtc	acc	ggc	agc	ggt	ggc	ggg	gac	agc	tgg	ttc	gcc	gac	aac	ctc	1536
Gly	Val	Thr	Gly	Ser	Gly	Gly	Gly	Asp	Ser	Trp	Phe	Ala	Asp	Asn	Leu	
			500					505					510			
aac	cgc	gcg	cac	gtc	gac	tac	ttc	tac	tgg	ctg	ctg	gcg	ggg	ctc	agc	1584
Asn	Arg	Ala	His	Val	Asp	Tyr	Phe	Tyr	Trp	Leu	Leu	Ala	Gly	Leu	Ser	
		515					520					525				
gcc	gtc	gaa	ctc	gcg	ctc	ttc	ctc	tac	ttt	gcg	cgc	tcc	tac	gtc	tac	1632
Ala	Val	Glu	Leu	Ala	Leu	Phe	Leu	Tyr	Phe	Ala	Arg	Ser	Tyr	Val	Tyr	
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Lys	His	Lys	Pro	Asn												
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<211> 549

<212> PRT

<213> Zea mays

<400> 387

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Ser	Asp	Tyr	Leu	Gly	Arg	Ser	Val	His	Arg	Gly	Ser	Ser	Gly	Gly	Trp	
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Tyr	Phe	Gly	Ile	Ser	Ala	Asn	Leu	Ile	Thr	Tyr	Leu	Thr	Gly	Pro	Leu	
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Thr	Ala	Cys	Ile	Met	Pro	Leu	Leu	Gly	Ala	Phe	Leu	Ala	Asp	Ala	Tyr	
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Leu	Gly	Arg	Tyr	Arg	Ser	Val	Ile	Ile	Ala	Cys	Thr	Leu	Tyr	Val	Leu	
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Gly	Tyr	Gly	Met	Leu	Thr	Leu	Ser	Ala	Thr	Val	Pro	Ala	Leu	Gln	Pro	
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Ser	His	Met	Pro	Cys	Arg	Glu	Asp	Gly	Val	Ser	Ser	Ser	Ser	Cys	Gln	
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Pro	Gly	Trp	Pro	Gln	Val	Ala	Phe	Phe	Tyr	Val	Pro	Leu	Tyr	Leu	Ile	
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Ala	Ile	Ala	Gln	Gly	Ala	Asp	Lys	Pro	Cys	Gly	Leu	Ala	Phe	Ala	Ala	
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Asp	Gln	Phe	Asp	Ala	Glu	His	Gln	Gly	Glu	Arg	Ala	Ser	Arg	Gly	Ser	
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Val	Ser	Val	Val	Gly	Tyr	Ile	Gln	Glu	Tyr	Val	Gly	Trp	Gly	Leu	Gly	
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Phe	Gly	Val	Pro	Cys	Ala	Ile	Val	Leu	Cys	Ala	Phe	Leu	Val	Phe	Leu	
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Asp	Ala	Arg	Cys	Val	Leu	Arg	Leu	Leu	Pro	Ile	Trp	Ala	Ala	Ser	Leu	
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Ala	Tyr	Gly	Val	Val	Tyr	Ala	Gln	Ile	Met	Thr	Leu	Phe	Asn	Lys	Gln	
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Gly	Arg	Thr	Leu	Asp	Arg	His	Ile	Gly	Asp	Gly	Leu	Glu	Leu	Pro	Pro	
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PF59082SeqList_PF59082.txt

Ala Ala Leu Gln Thr Leu Gly Pro Ala Ser Ile Leu Leu Phe Val Pro
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 Val Tyr Asp Arg Ala Val Val Pro Ala Leu Arg Trp Ala Thr Gly Asn
 370 375 380
 Pro Ser Gly Leu Ser Met Leu Gln Arg Val Gly Ala Gly Met Ala Val
 385 390 395 400
 Ser Leu Ala Gly Val Ala Val Ala Ala Leu Val Glu Ala Arg Arg Leu
 405 410 415
 Ala Met Ala Arg Glu His Gly Leu Val Asp Asp Pro Ser Ala Thr Val
 420 425 430
 Pro Met Ser Trp Ala Trp Ile Val Pro Gln Tyr Ala Met Met Gly Val
 435 440 445
 Ala Asp Val Leu Ala Val Val Gly Leu Gln Glu Leu Phe Tyr Asp Gln
 450 455 460
 Met Pro Asp Gly Leu Arg Ser Leu Gly Leu Ala Leu Tyr Leu Ser Val
 465 470 475 480
 Met Gly Ile Gly Gly Phe Ile Ser Ser Leu Leu Ile Ser Leu Ile Asp
 485 490 495
 Gly Val Thr Gly Ser Gly Gly Gly Asp Ser Trp Phe Ala Asp Asn Leu
 500 505 510
 Asn Arg Ala His Val Asp Tyr Phe Tyr Trp Leu Leu Ala Gly Leu Ser
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<211> 1758

<212> DNA

<213> Triticum aestivum

<220>

<221> CDS

<222> (1)..(1758)

<400> 388

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Pro Glu Glu Ser Asn Gln Leu Thr Tyr Thr Gly Asp Gly Ser Val Asp	
20 25 30	
ttt tcg gga aac cct gtc gtg aag gag aaa act ggc aga tgg aag gca	144
Phe Ser Gly 35 Asn Pro Val Val 40 Glu Lys Thr Gly Arg Trp Lys Ala	
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tgc cca ttc atc tta ggt aat gaa tgc tgt gag cgg ttg gcc tat tat	192
Cys Pro Phe Ile Leu Gly Asn 55 Glu Cys Cys Glu Arg 60 Leu Ala Tyr Tyr	
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Gly Ile Ser Thr Asn Leu Val Thr Tyr Leu Thr Lys Lys Leu His Asp	
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Gly Asn Ser Ser Ala Arg Asn Val Thr Trp Gln Gly Thr Cys	
85 90 95	
tat ttg act ccc ctt att gga gct atc ctg gct gat gca tac tgg ggg	336
Tyr Leu Thr Pro Leu Ile Gly Ala Ile Leu Ala Asp Ala Tyr Trp Gly	
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agg tat tgg acg atc gca acg ttc tcc aca ata tac ttc att ggg atg	384
Arg Tyr Trp Thr Ile Ala Thr Phe Ser Thr Ile Tyr Phe Ile Gly Met	
115 120 125	
tca gta ctg act ctt tca gca tca gtt cct atg ctc atg cct cca tct	432
Ser Val Leu Thr Leu Ser Ala Ser Val Pro Met Leu Met Pro Pro Ser	
130 135 140	
tgt gaa gga gcc att tgc cca gaa gcc agt cct ttg cag tat acc gta	480
Cys Glu Gly Ala Ile Cys Pro Glu Ala Ser Pro Leu Gln Tyr Thr Val	
145 150 155 160	
ttt ttt ctt ggt ctt tac cta att gcg ctc ggc act ggt gga atc aag	528
Phe Phe Leu Gly Leu Tyr Leu Ile Ala Leu Gly Thr Gly Gly Ile Lys	

PF59082SeqList_PF59082.txt

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			180					185					190				
gct	gag	cga	atc	cag	aag	ggg	tct	ttc	ttc	aat	tgg	ttc	tat	ttt	tca		624
Ala	Glu	Arg	Ile	Gln	Lys	Gly	Ser	Phe	Phe	Asn	Trp	Phe	Tyr	Phe	Ser		
		195					200					205					
ata	aac	att	ggt	gcc	ctt	ata	tca	agc	agt	ttt	ctg	ggt	tgg	gtg	caa		672
Ile	Asn	Ile	Gly	Ala	Leu	Ile	Ser	Ser	Ser	Phe	Leu	Val	Trp	Val	Gln		
	210					215					220						
gac	aat	tta	gga	tgg	gga	tta	ggc	ttt	ggc	att	ccg	acc	gta	ttc	atg		720
Asp	Asn	Leu	Gly	Trp	Gly	Leu	Gly	Phe	Gly	Ile	Pro	Thr	Val	Phe	Met		
225			230			235				235					240		
ggt	ctt	gcc	atc	ata	agc	ttc	ttt	gcc	ggc	acc	tca	ctt	tat	aga	ttc		768
Gly	Leu	Ala	Ile	Ile	Ser	Phe	Phe	Ala	Gly	Thr	Ser	Leu	Tyr	Arg	Phe		
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caa	aag	cca	ggt	ggc	agt	cct	atc	aca	cga	gta	tgc	cag	gta	ggt	gct		816
Gln	Lys	Pro	Gly	Gly	Ser	Pro	Ile	Thr	Arg	Val	Cys	Gln	Val	Val	Ala		
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gcc	act	ttg	cgc	aag	tgg	aac	gca	cat	gtt	cca	gag	gac	agc	tct	ctc		864
Ala	Thr	Leu	Arg	Lys	Trp	Asn	Ala	His	Val	Pro	Glu	Asp	Ser	Ser	Leu		
		275				280						285					
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Leu	Tyr	Glu	Leu	Pro	Asp	Gly	Val	Ser	Ala	Ile	Glu	Gly	Ser	Arg	Gln		
	290					295					300						
ttg	gag	cac	act	gat	gaa	ctc	aga	tgt	ctg	gac	aag	gcg	gct	aca	att		960
Leu	Glu	His	Thr	Asp	Glu	Leu	Arg	Cys	Leu	Asp	Lys	Ala	Ala	Thr	Ile		
305					310				315						320		
act	gat	ctt	gat	gtg	aaa	gaa	gat	agc	ttc	aac	aac	cca	tgg	cgg	gtg		1008
Thr	Asp	Leu	Asp	Val	Lys	Glu	Asp	Ser	Phe	Asn	Asn	Pro	Trp	Arg	Val		
			325					330					335				
tgc	acc	gtc	acc	cag	gtg	gag	gaa	ctg	aag	att	ttg	gta	agg	atg	ttc		1056
Cys	Thr	Val	Thr	Gln	Val	Glu	Glu	Leu	Lys	Ile	Leu	Val	Arg	Met	Phe		
		340						345				350					
cct	gtc	tgg	gca	acg	aca	att	gtg	ttt	tca	gct	gtc	tat	gct	cag	atg		1104
Pro	Val	Trp	Ala	Thr	Thr	Ile	Val	Phe	Ser	Ala	Val	Tyr	Ala	Gln	Met		
		355					360					365					
tcc	acc	atg	ttt	gtg	gaa	caa	ggg	atg	gtg	ctt	gat	cca	aca	atc	ggc		1152
Ser	Thr	Met	Phe	Val	Glu	Gln	Gly	Met	Val	Leu	Asp	Pro	Thr	Ile	Gly		
		370				375					380						
tca	ttc	aag	atc	cct	cca	gca	tct	cta	tcc	acc	ttt	gac	gtg	gtt	agt		1200
Ser	Phe	Lys	Ile	Pro	Pro	Ala	Ser	Leu	Ser	Thr	Phe	Asp	Val	Val	Ser		
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gtc	att	ata	tgg	gtt	cct	atc	tac	gac	agc	atc	ctg	gtc	ccg	ata	gcc		1248
Val	Ile	Ile	Trp	Val	Pro	Ile	Tyr	Asp	Ser	Ile	Leu	Val	Pro	Ile	Ala		
			405					410						415			
agg	agg	ttc	acc	ggc	aag	gag	agg	ggc	ttt	tca	gag	ctg	cag	cgg	atg		1296
Arg	Arg	Phe	Thr	Gly	Lys	Glu	Arg	Gly	Phe	Ser	Glu	Leu	Gln	Arg	Met		
		420						425				430					
ggc	atc	ggc	ctg	gta	atc	tcc	atc	ctc	gca	atg	tca	gca	gcc	gcg	gtc		1344
Gly	Ile	Gly	Leu	Val	Ile	Ser	Ile	Leu	Ala	Met	Ser	Ala	Ala	Ala	Val		
		435				440					445						
ctc	gag	ata	aag	agg	ctg	gcc	atc	gcc	agg	gag	gcg	cac	ctg	gtg	gac		1392
Leu	Glu	Ile	Lys	Arg	Leu	Ala	Ile	Ala	Arg	Glu	Ala	His	Leu	Val	Asp		
	450					455					460						
cag	aac	gtc	ccg	gtt	ccg	ctg	agc	atc	ctg	tgg	caa	atc	cct	cag	tac		1440
Gln	Asn	Val	Pro	Val	Pro	Leu	Ser	Ile	Leu	Trp	Gln	Ile	Pro	Gln	Tyr		
465				470					475					480			
ttc	ctg	gtc	ggc	gcc	tcg	gag	gtg	ttc	acc	ttc	atc	ggg	gcg	ctc	gag		1488
Phe	Leu	Val	Gly	Ala	Ser	Glu	Val	Phe	Thr	Phe	Ile	Gly	Ala	Leu	Glu		
			485					490						495			
ttc	ttc	tac	gac	cag	tcg	ccg	gac	gcc	atg	cgg	agc	ctc	tgc	agt	gcg		1536
Phe	Phe	Tyr	Asp	Gln	Ser	Pro	Asp	Ala	Met	Arg	Ser	Leu	Cys	Ser	Ala		
		500						505				510					
ctg	cag	ctc	atc	acc	acc	gcg	ctc	ggg	aac	tac	ctc	agc	gcc	ttc	atc		1584
Leu	Gln	Leu	Ile	Thr	Thr	Ala	Leu	Gly	Asn	Tyr	Leu	Ser	Ala	Phe	Ile		
		515				520					525						
ctc	acg	atg	gtc	gcc	tac	ttc	acg	acc	agg	gga	ggg	agg	ccc	ggg	tgg		1632
Leu	Thr	Met	Val	Ala	Tyr	Phe	Thr	Thr	Arg	Gly	Gly	Arg	Pro	Gly	Trp		

PF59082SeqList_PF59082.txt

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Ile Pro Asp Asn Leu Asn	Glu Gly Arg Leu Asp	Tyr Phe Phe Trp Leu				
545	ctc gcg ggg ctc agc ttt	550	ctc aac ttt ttg gtg	555	tac gtg ctg tgc gcc	1728
Leu Ala Gly Leu Ser Phe	Leu Asn Phe Leu Val	Tyr Val Leu Cys Ala				
	565	570		575		
aac agg ttc aag agc aag	aaa gcg gct tga				1758	
Asn Arg Phe Lys Ser Lys	Lys Ala Ala					
	580	585				

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<212> PRT

<213> Triticum aestivum

<400> 389

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Phe Ser Gly Asn Pro Val	Val Lys Glu Lys Thr Gly Arg Trp Lys Ala	
	35	40
Cys Pro Phe Ile Leu Gly	Asn Glu Cys Cys Glu Arg Leu Ala Tyr Tyr	
	50	55
Gly Ile Ser Thr Asn Leu	Val Thr Tyr Leu Thr Lys Lys Leu His Asp	
65	70	75
Gly Asn Ser Ser Ala Ala	Arg Asn Val Thr Thr Trp Gln Gly Thr Cys	
	85	90
Tyr Leu Thr Pro Leu Ile	Gly Ala Ile Leu Ala Asp Ala Tyr Trp Gly	
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Arg Tyr Trp Thr Ile Ala	Thr Phe Ser Thr Ile Tyr Phe Ile Gly Met	
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Ser Val Leu Thr Leu Ser	Ala Ser Val Pro Met Leu Met Pro Pro Ser	
	130	135
Cys Glu Gly Ala Ile Cys	Pro Glu Ala Ser Pro Leu Gln Tyr Thr Val	
145	150	155
Phe Phe Leu Gly Leu Tyr	Leu Ile Ala Leu Gly Thr Gly Gly Ile Lys	
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Pro Cys Val Ser Phe Gly	Ala Asp Gln Phe Asp Asp Thr Asp Pro	
	180	185
Ala Glu Arg Ile Gln Lys	Gly Ser Phe Phe Asn Trp Phe Tyr Phe Ser	
	195	200
Ile Asn Ile Gly Ala Leu	Ile Ser Ser Ser Phe Leu Val Trp Val Gln	
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Asp Asn Leu Gly Trp Gly	Leu Gly Phe Gly Ile Pro Thr Val Phe Met	
225	230	235
Gly Leu Ala Ile Ile Ser	Phe Phe Ala Gly Thr Ser Leu Tyr Arg Phe	
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Gln Lys Pro Gly Gly Ser	Pro Ile Thr Arg Val Cys Gln Val Val Ala	
	260	265
Ala Thr Leu Arg Lys Trp	Asn Ala His Val Pro Glu Asp Ser Ser Leu	
	275	280
Leu Tyr Glu Leu Pro Asp	Gly Val Ser Ala Ile Glu Gly Ser Arg Gln	
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Leu Glu His Thr Asp Glu	Leu Arg Cys Leu Asp Lys Ala Ala Thr Ile	
305	310	315
Thr Asp Leu Asp Val Lys	Glu Asp Ser Phe Asn Asn Pro Trp Arg Val	
	325	330
Cys Thr Val Thr Gln Val	Glu Glu Leu Lys Ile Leu Val Arg Met Phe	
	340	345
Pro Val Trp Ala Thr Thr	Ile Val Phe Ser Ala Val Tyr Ala Gln Met	
	355	360
Ser Thr Met Phe Val Glu	Gln Gly Met Val Leu Asp Pro Thr Ile Gly	
	370	375
Ser Phe Lys Ile Pro Pro	Ala Ser Leu Ser Thr Phe Asp Val Val Ser	
385	390	395
Val Ile Ile Trp Val Pro	Ile Tyr Asp Ser Ile Leu Val Pro Ile Ala	
	405	410
		415

PF59082SeqList_PF59082.txt

Arg Arg Phe Thr Gly Lys Glu Arg Gly Phe Ser Glu Leu Gln Arg Met
 420 425 430
 Gly Ile Gly Leu Val Ile Ser Ile Leu Ala Met Ser Ala Ala Ala Val
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 450 455 460
 Gln Asn Val Pro Val Pro Leu Ser Ile Leu Trp Gln Ile Pro Gln Tyr
 465 470 475
 Phe Leu Val Gly Ala Ser Glu Val Phe Thr Phe Ile Gly Ala Leu Glu
 485 490 495
 Phe Phe Tyr Asp Gln Ser Pro Asp Ala Met Arg Ser Leu Cys Ser Ala
 500 505 510
 Leu Gln Leu Ile Thr Thr Ala Leu Gly Asn Tyr Leu Ser Ala Phe Ile
 515 520 525
 Leu Thr Met Val Ala Tyr Phe Thr Thr Arg Gly Gly Arg Pro Gly Trp
 530 535 540
 Ile Pro Asp Asn Leu Asn Glu Gly Arg Leu Asp Tyr Phe Phe Trp Leu
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 Asn Arg Phe Lys Ser Lys Lys Ala Ala
 580 585

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 Asp Glu Glu Lys Trp Val His Asp Ala Ser Val Asp Tyr Lys Gly Arg
 20 25 30
 atc cct ctc cgt gct tcc acg ggt gta tgg aaa gct tcg ctt ttt gtc 144
 Ile Pro Leu Arg Ala Ser Thr Gly Val Trp Lys Ala Ser Leu Phe Val
 35 40 45
 ctt gca att gaa ttt agt gaa agg ata gcc cac ttt ggg ata tcc agt 192
 Leu Ala Ile Glu Phe Ser Glu Arg Ile Ala His Phe Gly Ile Ser Ser
 50 55 60
 aat ctt atc atg tat ctg act gaa gtg atg cat gaa gac cta aag aca 240
 Asn Leu Ile Met Tyr Leu Thr Glu Val Met His Glu Asp Leu Lys Thr
 65 70 75 80
 gca acc aat aat gca aac ttg tgg aaa gga gca aca acc ttg ttg cct 288
 Ala Thr Asn Asn Ala Asn Leu Trp Lys Gly Ala Thr Thr Leu Leu Pro
 85 90 95
 atg att ggg gga ttt ctt ggt gat gcc tac acc ggt cga ttt cgt atg 336
 Met Ile Gly Gly Phe Leu Gly Asp Ala Tyr Thr Gly Arg Phe Arg Met
 100 105 110
 gta gtc ttt tct tcc ctc gta tac ttc aag gga tta agc ctc ttg acc 384
 Val Val Phe Ser Ser Leu Val Tyr Phe Lys Gly Leu Ser Leu Leu Thr
 115 120 125
 atg tct caa ttc att cca aat cta aaa cca tgc aac aat gat ata tgt 432
 Met Ser Gln Phe Ile Pro Asn Leu Lys Pro Cys Asn Asn Asp Ile Cys
 130 135 140
 cat cag cca aga aag gtt cat gaa gtg gtt ttc ttc ctt gct ctt tac 480
 His Gln Pro Arg Lys Val His Glu Val Val Phe Phe Leu Ala Leu Tyr
 145 150 155 160
 tgt atc gcc ttg gga act gga gga ttc aaa cca tgc tta gaa agt ttt 528
 Cys Ile Ala Leu Gly Thr Gly Gly Phe Lys Pro Cys Leu Glu Ser Phe
 165 170 175
 gga ggt gat caa ttt gat ggt gac aac ctt gaa gaa cga aag aag aag 576
 Gly Gly Asp Gln Phe Asp Gly Asp Asn Leu Glu Glu Arg Lys Lys Lys
 180 185 190

PF59082SeqList_PF59082.txt																
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		195					200					205				
cta	gcg	aca	acg	gtg	gtt	gtt	tat	gtt	cag	gac	ttc	gtt	agc	ttg	gga	672
Leu	Ala	Thr	Thr	Val	Val	Val	Tyr	Val	Gln	Asp	Phe	Val	Ser	Trp	Gly	
	210					215					220					
gtt	gct	tat	ctc	atc	ctc	gct	atg	ttc	atg	gct	ctc	act	atc	att	gct	720
Val	Ala	Tyr	Leu	Ile	Leu	Ala	Met	Phe	Met	Ala	Leu	Thr	Ile	Ile	Ala	
225					230					235					240	
ttc	tat	gtg	ggg	ata	cct	ttt	tac	agg	tac	aga	atg	agg	cca	aac	gca	768
Phe	Tyr	Val	Gly	Ile	Pro	Phe	Tyr	Arg	Tyr	Arg	Met	Arg	Pro	Asn	Ala	
				245				250						255		
aat	cct	ttc	ata	cca	att	cta	caa	gtc	cta	att	gca	tcc	ata	agg	aaa	816
Asn	Pro	Phe	Ile	Pro	Ile	Leu	Gln	Val	Leu	Ile	Ala	Ser	Ile	Arg	Lys	
		260						265				270				
agg	aat	ttg	tct	tgt	cct	tca	aat	cct	gct	tta	tta	tgt	gaa	gtc	cca	864
Arg	Asn	Leu	Ser	Cys	Pro	Ser	Asn	Pro	Ala	Leu	Leu	Cys	Glu	Val	Pro	
		275					280					285				
atg	tca	gag	aat	tcc	caa	gga	agg	ctt	cta	aac	cat	act	agc	agg	ctc	912
Met	Ser	Glu	Asn	Ser	Gln	Gly	Arg	Leu	Leu	Asn	His	Thr	Ser	Arg	Leu	
	290					295					300					
agg	ttt	ctt	gac	aag	gct	gca	ata	gtt	gaa	gaa	aag	tat	att	gag	aag	960
Arg	Phe	Leu	Asp	Lys	Ala	Ala	Ile	Val	Glu	Glu	Lys	Tyr	Ile	Glu	Lys	
305					310				315						320	
aaa	gct	ggc	cca	ttg	aga	tta	gca	aca	gtg	aca	aga	gtg	gag	gag	aca	1008
Lys	Ala	Gly	Pro	Trp	Arg	Leu	Ala	Thr	Val	Thr	Arg	Val	Glu	Glu	Thr	
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aag	ctt	att	cta	aat	gtt	gtt	ccg	ata	tgg	cta	act	tca	tta	atg	att	1056
Lys	Leu	Ile	Leu	Asn	Val	Val	Pro	Ile	Trp	Leu	Thr	Ser	Leu	Met	Ile	
			340					345					350			
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Gly	Val	Cys	Ile	Ala	Gln	Gly	Ser	Thr	Leu	Phe	Val	Lys	Gln	Ala	Ala	
		355					360					365				
gct	atg	aac	tta	aag	ata	agc	gac	aac	ttc	aaa	att	cca	cca	gct	tcc	1152
Ala	Met	Asn	Leu	Lys	Ile	Ser	Asp	Asn	Phe	Lys	Ile	Pro	Pro	Ala	Ser	
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Met	Ala	Ser	Leu	Ser	Ala	Phe	Ser	Thr	Ile	Ile	Ser	Val	Pro	Ile	Tyr	
385					390				395						400	
gat	aga	att	att	gtt	cca	att	cta	agg	aaa	gtc	aga	ggg	aac	gaa	aga	1248
Asp	Arg	Ile	Ile	Val	Pro	Ile	Leu	Arg	Lys	Val	Arg	Gly	Asn	Glu	Arg	
				405				410					415			
ggc	atc	agc	atc	ctt	ggg	agg	att	ggc	att	ggc	tta	ata	ttc	tta	gtc	1296
Gly	Ile	Ser	Ile	Leu	Gly	Arg	Ile	Gly	Ile	Gly	Leu	Ile	Phe	Leu	Val	
			420					425					430			
ata	ctc	atg	gtt	gtt	gct	gcc	tta	gta	gaa	aat	atg	aga	tta	aga	atg	1344
Ile	Leu	Met	Val	Val	Ala	Ala	Leu	Val	Glu	Asn	Met	Arg	Leu	Arg	Met	
		435				440					445					
cct	ggg	cat	gag	aca	atg	agt	gtg	atg	tgg	ttg	ata	ccc	caa	tac	ttg	1392
Pro	Gly	His	Glu	Thr	Met	Ser	Val	Met	Trp	Leu	Ile	Pro	Gln	Tyr	Leu	
	450					455					460					
atc	ctt	ggc	att	gga	aat	tca	ttt	tat	cta	att	gct	ttg	caa	gag	tat	1440
Ile	Leu	Gly	Ile	Gly	Asn	Ser	Phe	Tyr	Leu	Ile	Ala	Leu	Gln	Glu	Tyr	
465					470				475						480	
ttc	tat	gat	gaa	gtt	cct	gac	tca	atg	aga	agc	gta	gga	atg	gct	ttg	1488
Phe	Tyr	Asp	Glu	Val	Pro	Asp	Ser	Met	Arg	Ser	Val	Gly	Met	Ala	Leu	
				485				490					495			
tat	ctt	agt	gtg	att	gga	ata	gga	ttc	ttc	tta	agc	agc	ttt	cta	ata	1536
Tyr	Leu	Ser	Val	Ile	Gly	Ile	Gly	Phe	Phe	Leu	Ser	Ser	Phe	Leu	Ile	
			500				505						510			
ata	att	gtg	gac	cat	gtc	aca	ggg	aag	aat	ggc	aaa	ggg	ttg	att	gcc	1584
Ile	Ile	Val	Asp	His	Val	Thr	Gly	Lys	Asn	Gly	Lys	Gly	Trp	Ile	Ala	
		515				520						525				
aag	gat	gta	aac	tca	agt	cgt	cta	gat	aag	ttt	tat	ttg	atg	ttg	gct	1632
Lys	Asp	Val	Asn	Ser	Ser	Arg	Leu	Asp	Lys	Phe	Tyr	Trp	Met	Leu	Ala	
		530				535					540					
gtc	ata	agt	gct	tta	aat	ttg	tgt	ctc	ttc	cta	ttc	ttg	gca	aag	agg	1680
Val	Ile	Ser	Ala	Leu	Asn	Leu	Cys	Leu	Phe	Leu	Phe	Leu	Ala	Lys	Arg	
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PF59082SeqList_PF59082.txt

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35 40 45
Leu Ala Ile Glu Phe Ser Glu Arg Ile Ala His Phe Gly Ile Ser Ser
50 55 60
Asn Leu Ile Met Tyr Leu Thr Glu Val Met His Glu Asp Leu Lys Thr
65 70 75 80
Ala Thr Asn Asn Ala Asn Leu Trp Lys Gly Ala Thr Thr Leu Leu Pro
85 90 95
Met Ile Gly Gly Phe Leu Gly Asp Ala Tyr Thr Gly Arg Phe Arg Met
100 105 110
Val Val Phe Ser Ser Leu Val Tyr Phe Lys Gly Leu Ser Leu Leu Thr
115 120 125
Met Ser Gln Phe Ile Pro Asn Lys Pro Cys Asn Asn Asp Ile Cys
130 135 140
His Gln Pro Arg Lys Val His Glu Val Val Phe Phe Leu Ala Leu Tyr
145 150 155 160
Cys Ile Ala Leu Gly Thr Gly Gly Phe Lys Pro Cys Leu Glu Ser Phe
165 170 175
Gly Gly Asp Gln Phe Asp Gly Asp Asn Leu Glu Glu Arg Lys Lys Lys
180 185 190
Met Ser Phe Phe Asn Trp Trp Thr Phe Thr Phe Ser Ile Ala Leu Leu
195 200 205
Leu Ala Thr Thr Val Val Val Tyr Val Gln Asp Phe Val Ser Trp Gly
210 215 220
Val Ala Tyr Leu Ile Leu Ala Met Phe Met Ala Leu Thr Ile Ile Ala
225 230 235 240
Phe Tyr Val Gly Ile Pro Phe Tyr Arg Tyr Arg Met Arg Pro Asn Ala
245 250 255
Asn Pro Phe Ile Pro Ile Leu Gln Val Leu Ile Ala Ser Ile Arg Lys
260 265 270
Arg Asn Leu Ser Cys Pro Ser Asn Pro Ala Leu Leu Cys Glu Val Pro
275 280 285
Met Ser Glu Asn Ser Gln Gly Arg Leu Leu Asn His Thr Ser Arg Leu
290 295 300
Arg Phe Leu Asp Lys Ala Ala Ile Val Glu Glu Lys Tyr Ile Glu Lys
305 310 315 320
Lys Ala Gly Pro Trp Arg Leu Ala Thr Val Thr Arg Val Glu Glu Thr
325 330 335
Lys Leu Ile Leu Asn Val Val Pro Ile Trp Leu Thr Ser Leu Met Ile
340 345 350
Gly Val Cys Ile Ala Gln Gly Ser Thr Leu Phe Val Lys Gln Ala Ala
355 360 365
Ala Met Asn Leu Lys Ile Ser Asp Asn Phe Lys Ile Pro Pro Ala Ser
370 375 380
Met Ala Ser Leu Ser Ala Phe Ser Thr Ile Ile Ser Val Pro Ile Tyr
385 390 395 400
Asp Arg Ile Ile Val Pro Ile Leu Arg Lys Val Arg Gly Asn Glu Arg
405 410 415
Gly Ile Ser Ile Leu Gly Arg Ile Gly Ile Gly Leu Ile Phe Leu Val
420 425 430
Ile Leu Met Val Val Ala Ala Leu Val Glu Asn Met Arg Leu Arg Met
435 440 445

PF59082SeqList_PF59082.txt

Pro Gly His Glu Thr Met Ser Val Met Trp Leu Ile Pro Gln Tyr Leu
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 Ile Leu Gly Ile Gly Asn Ser Phe Tyr Leu Ile Ala Leu Gln Glu Tyr
 465 470 475 480
 Phe Tyr Asp Glu Val Pro Asp Ser Met Arg Ser Val Gly Met Ala Leu
 485 490 495
 Tyr Leu Ser Val Ile Gly Ile Gly Phe Phe Leu Ser Ser Phe Leu Ile
 500 505 510
 Ile Ile Val Asp His Val Thr Gly Lys Asn Gly Lys Gly Trp Ile Ala
 515 520 525
 Lys Asp Val Asn Ser Ser Arg Leu Asp Lys Phe Tyr Trp Met Leu Ala
 530 535 540
 Val Ile Ser Ala Leu Asn Leu Cys Leu Phe Leu Phe Leu Ala Lys Arg
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 Pro Leu Leu Asp Asp Lys Asn Cys Ala Gly Ser Lys Ala Pro Leu Val
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 gtt ctt ggg ttc gag tgc ttg gag agc aca gct ttc aat ggc atc tcg 144
 Val Leu Gly Phe Glu Cys Leu Glu Ser Thr Ala Phe Asn Gly Ile Ser
 35 40 45
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 Thr Asn Leu Val Met Tyr 55 Glu Thr Val Leu His Gly Ser Asn Val
 50 60
 gcc agc gcc tcc aac gtc acg ctg tgg ttc ggc acc agc tac ctg aca 240
 Ala Ser Ala Ser Asn Val Thr Leu Trp Phe Gly Thr Ser Tyr Leu Thr
 65 70 75 80
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 Pro Val Phe Gly Ala Ile Ile Ala Asp Ala Phe Trp Gly Asn Tyr Asn
 85 90 95
 acc atc ctc gtc tcc ctc gcc atc tac ctt ctt ggg atg att ctg gtg 336
 Thr Ile Leu Val Ser Leu Ala Ile Tyr 105 Leu Leu Gly Met Ile Leu Val
 100 110
 acc tta tcg gcg ttc ctg ccg acg gac acg gtg ctc ggc ggc tcc tcg 384
 Thr Leu Ser Ala Phe Leu Pro Thr Asp Thr Val Leu Gly Gly Ser Ser
 115 120 125
 gtg ttc ggc gcg cac acg gta gcg ttc gtg ggc ctt tac ctc gtc gcg 432
 Val Phe Gly Ala His Thr Val Ala Phe Val Gly Leu Tyr Leu Val Ala
 130 135 140
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 Ile Gly Ser Gly Gly Val Arg Ser Ser Leu Leu Thr Phe Gly Ala Glu
 145 150 155 160
 cag ttc gat gac gac aat gcg gcg gat cgc gag aac aag ctg tcc ttc 528
 Gln Phe Asp Asp Asn Ala Ala Asp Arg Glu Asn Lys Leu Ser Phe
 165 170 175
 ttc agc tgg ttt tac cta tgc gtc gac ttt ggc ccg atc gtc tcc ggc 576
 Phe Ser Trp Phe Tyr Leu Cys Val 185 Phe Gly Pro Ile Val Ser Gly
 180 190
 ctg ttc atc gtg tgg atc cag gag aac atc agc tgg ggc ctc ggc ttt 624
 Leu Phe Ile Val Trp Ile Gln Glu Asn Ile Ser Trp Gly Leu Gly Phe
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PF59082SeqList_PF59082.txt

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Ala	Thr	Pro	Met	Tyr	Lys	Arg	Ser	Thr	Pro	Thr	Ala	Gly	Lys	Ala	Ser	
225					230					235					240	
gtc	atc	tcc	gac	tcc	gag	acg	ggc	ttg	gaa	gcg	ata	tcg	gag	gag	gcg	768
Val	Ile	Ser	Asp	Ser	Glu	Thr	Gly	Leu	Glu	Ala	Ile	Ser	Glu	Glu	Ala	
				245					250						255	
ggc	tcg	tcg	cag	aag	ctc	cgc	gcc	gcg	acg	aag	gca	gag	gag	ttc	aag	816
Gly	Ser	Ser	Gln	Lys	Leu	Arg	Ala	Ala	Thr	Lys	Ala	Glu	Glu	Phe	Lys	
			260						265					270		
acc	ctg	ctg	gga	ctt	ctg	ccc	atc	tgg	gcg	acc	agc	atc	atc	gtc	tcc	864
Thr	Leu	Leu	Gly	Leu	Leu	Pro	Ile	Trp	Ala	Thr	Ser	Ile	Ile	Val	Ser	
			275				280							285		
tcg	gcg	tac	acg	cag	atg	aac	acc	acc	ttc	atc	cag	caa	ggc	agc	gcc	912
Ser	Ala	Tyr	Thr	Gln	Met	Asn	Thr	Thr	Phe	Ile	Gln	Gln	Gly	Ser	Ala	
						295					300					
atg	aac	gtg	tcc	gtc	ctg	tcg	gtg	cag	gtg	cca	ccg	gcg	tcg	atg	ggc	960
Met	Asn	Val	Ser	Val	Leu	Ser	Val	Gln	Val	Pro	Pro	Ala	Ser	Met	Gly	
305					310					315					320	
tcg	ttc	gag	gtg	gtc	tgc	gtc	ctc	ata	tgg	gtg	ctg	ctg	tac	ggc	cac	1008
Ser	Phe	Glu	Val	Val	Cys	Val	Leu	Ile	Trp	Val	Leu	Leu	Tyr	Gly	His	
				325					330					335		
gtg	atc	gtg	ccg	gcg	ctg	agg	gga	tgc	ggg	ttc	tcg	ttc	ggc	ggc	gac	1056
Val	Ile	Val	Pro	Ala	Leu	Arg	Gly	Cys	Gly	Phe	Ser	Phe	Gly	Gly	Asp	
				340				345						350		
ggc	gaa	ccg	tct	cag	ctg	cag	cgc	atg	ggc	gcc	ggc	cgg	ctc	ctc	atg	1104
Gly	Glu	Pro	Ser	Gln	Leu	Gln	Arg	Met	Gly	Ala	Gly	Arg	Leu	Leu	Met	
		355					360					365				
gcc	ctg	gcg	atg	gcg	gtc	gcg	ctc	gtg	gag	atg	atg	aag	cgg	ctc	ggc	1152
Ala	Leu	Ala	Met	Ala	Val	Ala	Ala	Leu	Val	Glu	Met	Lys	Arg	Leu	Gly	
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Ser	Ala	Ala	Arg	Gly	Glu	Glu	Ile	Thr	Ile	Ala	Trp	Gln	Ile	Pro	Gln	
385					390					395					400	
tac	ttc	ttc	ctg	gcc	ggc	gcg	gag	gtg	ttg	tgc	tac	atc	gcg	cag	ctg	1248
Tyr	Phe	Phe	Leu	Ala	Gly	Ala	Glu	Val	Leu	Cys	Tyr	Ile	Ala	Gln	Leu	
				405					410					415		
gag	ttc	ttc	tac	gaa	gag	gcg	ccg	gaa	acc	atg	aag	agc	acg	tgc	acg	1296
Glu	Phe	Phe	Tyr	Glu	Glu	Ala	Pro	Glu	Thr	Met	Lys	Ser	Thr	Cys	Thr	
				420				425						430		
tcg	ctc	gcg	ctg	ctc	acc	atc	gcc	ctg	ggc	agc	tac	ctc	agc	tcc	ttc	1344
Ser	Leu	Ala	Leu	Leu	Thr	Ile	Ala	Leu	Gly	Ser	Tyr	Leu	Ser	Ser	Phe	
				435			440					445				
atc	tac	gct	atc	gtg	gca	gca	ttc	acg	gcc	acg	gcg	gac	agt	ccc	gga	1392
Ile	Tyr	Ala	Ile	Val	Ala	Ala	Phe	Thr	Ala	Thr	Ala	Asp	Ser	Pro	Gly	
					455						460					
tgg	atc	tcc	gac	aac	cta	aac	cag	ggc	cat	ctc	gac	tac	ttc	ttc	tgg	1440
Trp	Ile	Ser	Asp	Asn	Leu	Asn	Gln	Gly	His	Leu	Asp	Tyr	Phe	Phe	Trp	
465					470					475					480	
acc	atg	gcc	gcc	att	tca	acg	ctc	aac	ttc	gtc	gtg	tac	agc	gtg	ttc	1488
Thr	Met	Ala	Ala	Ile	Ser	Thr	Leu	Asn	Phe	Val	Val	Tyr	Ser	Val	Phe	
				485					490					495		
gcc	agg	aac	tac	aag	ccc	aag	agt	caa	gac	tat	gct	ctc	atg	acg		1533
Ala	Arg	Asn	Tyr	Lys	Pro	Lys	Ser	Gln	Asp	Tyr	Ala	Leu	Met	Thr		
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tga																1536

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 <213> Zea mays

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 Seite 563

PF59082SeqList_PF59082.txt

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Thr	Asn ⁵⁰	Leu	Val	Met	Tyr	Leu ⁵⁵	Glu	Thr	Val	Leu	His ⁶⁰	Gly	Ser	Asn	Val
Ala ⁶⁵	Ser	Ala	Ser	Asn	Val ⁷⁰	Thr	Leu	Trp	Phe	Gly ⁷⁵	Thr	Ser	Tyr	Leu	Thr ⁸⁰
Pro	Val	Phe	Gly	Ala ⁸⁵	Ile	Ile	Ala	Asp	Ala ⁹⁰	Phe	Trp	Gly	Asn	Tyr ⁹⁵	Asn
Thr	Ile	Leu	Val ¹⁰⁰	Ser	Leu	Ala	Ile	Tyr ¹⁰⁵	Leu	Leu	Gly	Met	Ile ¹¹⁰	Leu	Val
Thr	Leu	Ser ¹¹⁵	Ala	Phe	Leu	Pro	Thr ¹²⁰	Asp	Thr	Val	Leu	Gly ¹²⁵	Gly	Ser	Ser
Val	Phe ¹³⁰	Gly	Ala	His	Thr	Val ¹³⁵	Ala	Phe	Val	Gly	Leu ¹⁴⁰	Tyr	Leu	Val	Ala
Ile ¹⁴⁵	Gly	Ser	Gly	Gly	Val ¹⁵⁰	Arg	Ser	Ser	Leu	Leu ¹⁵⁵	Thr	Phe	Gly	Ala	Glu ¹⁶⁰
Gln	Phe	Asp	Asp	Asp ¹⁶⁵	Asn	Ala	Ala	Asp	Arg ¹⁷⁰	Glu	Asn	Lys	Leu	Ser ¹⁷⁵	Phe
Phe	Ser	Trp	Phe ¹⁸⁰	Tyr	Leu	Cys	Val	Asp ¹⁸⁵	Phe	Gly	Pro	Ile	Val ¹⁹⁰	Ser	Gly
Leu	Phe	Ile ¹⁹⁵	Val	Trp	Ile	Gln	Glu ²⁰⁰	Asn	Ile	Ser	Trp	Gly ²⁰⁵	Leu	Gly	Phe
Gly	Ile ²¹⁰	Ser	Thr	Ala	Cys	Ile ²¹⁵	Ala	Leu	Ala	Leu	Gly ²²⁰	Ala	Phe	Val	Leu
Ala ²²⁵	Thr	Pro	Met	Tyr	Lys ²³⁰	Arg	Ser	Thr	Pro	Thr ²³⁵	Ala	Gly	Lys	Ala	Ser ²⁴⁰
Val	Ile	Ser	Asp	Ser ²⁴⁵	Glu	Thr	Gly	Leu	Glu ²⁵⁰	Ala	Ile	Ser	Glu	Glu ²⁵⁵	Ala
Gly	Ser	Ser	Gln ²⁶⁰	Lys	Leu	Arg	Ala	Ala ²⁶⁵	Thr	Lys	Ala	Glu	Glu ²⁷⁰	Phe	Lys
Thr	Leu	Leu ²⁷⁵	Gly	Leu	Leu	Pro	Ile ²⁸⁰	Trp	Ala	Thr	Ser	Ile ²⁸⁵	Ile	Val	Ser
Ser	Ala ²⁹⁰	Tyr	Thr	Gln	Met	Asn ²⁹⁵	Thr	Thr	Phe	Ile	Gln ³⁰⁰	Gln	Gly	Ser	Ala
Met ³⁰⁵	Asn	Val	Ser	Val	Leu ³¹⁰	Ser	Val	Gln	Val	Pro ³¹⁵	Pro	Ala	Ser	Met	Gly ³²⁰
Ser	Phe	Glu	Val	Val ³²⁵	Cys	Val	Leu	Ile	Trp ³³⁰	Val	Leu	Leu	Tyr	Gly ³³⁵	His
Val	Ile	Val	Pro ³⁴⁰	Ala	Leu	Arg	Gly	Cys ³⁴⁵	Gly	Phe	Ser	Phe	Gly ³⁵⁰	Gly	Asp
Gly	Glu	Pro ³⁵⁵	Ser	Gln	Leu	Gln	Arg ³⁶⁰	Met	Gly	Ala	Gly	Arg ³⁶⁵	Leu	Leu	Met
Ala	Leu ³⁷⁰	Ala	Met	Ala	Val	Ala ³⁷⁵	Ala	Leu	Val	Glu	Met ³⁸⁰	Lys	Arg	Leu	Gly
Ser ³⁸⁵	Ala	Ala	Arg	Gly	Glu ³⁹⁰	Glu	Ile	Thr	Ile	Ala ³⁹⁵	Trp	Gln	Ile	Pro	Gln ⁴⁰⁰
Tyr	Phe	Phe	Leu	Ala ⁴⁰⁵	Gly	Ala	Glu	Val	Leu ⁴¹⁰	Cys	Tyr	Ile	Ala	Gln ⁴¹⁵	Leu
Glu	Phe	Phe	Tyr ⁴²⁰	Glu	Glu	Ala	Pro	Glu ⁴²⁵	Thr	Met	Lys	Ser	Thr ⁴³⁰	Cys	Thr
Ser	Leu	Ala ⁴³⁵	Leu	Leu	Thr	Ile	Ala ⁴⁴⁰	Leu	Gly	Ser	Tyr	Leu ⁴⁴⁵	Ser	Ser	Phe
Ile	Tyr ⁴⁵⁰	Ala	Ile	Val	Ala	Ala ⁴⁵⁵	Phe	Thr	Ala	Thr	Ala ⁴⁶⁰	Asp	Ser	Pro	Gly
Trp ⁴⁶⁵	Ile	Ser	Asp	Asn	Leu ⁴⁷⁰	Asn	Gln	Gly	His	Leu ⁴⁷⁵	Asp	Tyr	Phe	Phe	Trp ⁴⁸⁰
Thr	Met	Ala	Ala	Ile ⁴⁸⁵	Ser	Thr	Leu	Asn	Phe ⁴⁹⁰	Val	Val	Tyr	Ser	Val ⁴⁹⁵	Phe
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<212> DNA
<213> Zea mays

<220>
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<400> 394

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tca	tgt	cat	gac	gag	gaa	aca	cag	agt	cta	ttg	gaa	gca	aat	cta	ggg	96
Ser	Cys	His	Asp	Glu	Glu	Thr	Gln	Ser	Leu	Leu	Glu	Ala	Asn	Leu	Gly	
			20					25					30			
cca	cag	ctg	aaa	agt	aaa	tgc	tct	gat	tgg	aga	gca	ccg	gca	ctc	atc	144
Pro	Gln		Lys	Ser	Lys	Cys	Ser	Asp	Trp	Arg	Ala	Pro	Ala	Leu	Ile	
			35				40					45				
ctg	gga	ttg	gaa	tgc	ttg	gag	agc	atg	gct	ttc	aat	ggc	att	gcc	aca	192
Leu	Gly	Leu	Glu	Cys	Leu	Glu	Ser	Met	Ala	Phe	Asn	Gly	Ile	Ala	Thr	
	50					55					60					
aac	cta	gtt	gtg	tat	ctc	cgt	tca	gtt	ctc	cat	ggg	ggg	att	gct	tcc	240
Asn	Leu	Val	Val	Tyr	Leu	Arg	Ser	Val	Leu	His	Gly	Gly	Ile	Ala	Ser	
65					70				75						80	
agt	gca	gca	act	gta	tct	ctt	tgg	tac	ggg	aca	agc	ttc	ttt	gtg	cca	288
Ser	Ala	Ala	Thr	Val	Ser	Leu	Trp	Tyr	Gly	Thr	Ser	Phe	Phe	Val	Pro	
				85					90					95		
att	ctt	gga	gcc	gcc	ata	gca	gat	act	tgc	ttg	gga	aat	tat	aag	acc	336
Ile	Leu	Gly	Ala	Ala	Ile	Ala	Asp	Thr	Cys	Leu	Gly	Asn	Tyr	Lys	Thr	
			100				105						110			
atc	ttg	atc	tcc	ctt	atc	atg	tac	cta	ttt	gga	atg	gta	cta	att	aca	384
Ile	Leu	Ile	Ser	Leu	Ile	Met	Tyr	Leu	Phe	Gly	Met	Val	Leu	Ile	Thr	
		115					120					125				
gtt	gca	aca	ttc	atg	cct	tct	act	tca	gtc	ttg	tgc	gac	gtc	agt	tca	432
Val	Ala	Thr	Phe	Met	Pro	Ser	Thr	Ser	Val	Leu	Cys	Asp	Val	Ser	Ser	
	130					135					140					
tgc	ttg	tca	tca	aat	gga	act	caa	acc	atg	att	ttc	ttt	gct	ggg	ttg	480
Cys	Leu	Ser	Ser	Asn	Gly	Thr	Gln	Thr	Met	Ile	Phe	Phe	Ala	Gly	Leu	
145				150					155					160		
tat	ctc	act	gct	gtt	gga	tgt	gga	gga	gta	aga	tct	gca	ttg	ctt	ccg	528
Tyr	Leu	Thr	Ala	Val	Gly	Cys	Gly	Gly	Val	Arg	Ser	Ala	Leu	Leu	Pro	
				165					170					175		
ttt	ggg	gct	aac	cag	ttc	aac	aac	gag	aac	agt	cta	gac	ata	aaa	aag	576
Phe	Gly	Ala	Asn	Gln	Phe	Asn	Asn	Glu	Asn	Ser	Leu	Asp	Ile	Lys	Lys	
			180					185					190			
aga	aga	aat	ttc	ttc	agc	ttg	ttc	tat	ata	tgt	gtc	atc	ttt	ggg	gtg	624
Arg	Arg	Asn	Phe	Phe	Ser	Leu	Phe	Tyr	Ile	Cys	Val	Ile	Phe	Gly	Val	
		195					200					205				
att	act	tct	ggg	aca	atc	ata	gtt	tgg	gtt	cag	gaa	aat	gtt	agc	tgg	672
Ile	Thr	Ser	Gly	Thr	Ile	Ile	Val	Trp	Val	Gln	Glu	Asn	Val	Ser	Trp	
	210					215					220					
gct	att	gga	tat	gga	gtc	gcc	act	aca	tgc	ata	ggg	ctt	gct	ttg	ata	720
Ala	Ile	Gly	Tyr	Gly	Val	Ala	Thr	Thr	Cys	Ile	Gly	Leu	Ala	Leu	Ile	
225				230					235					240		
gga	ttt	ctg	ggg	gga	aca	cca	ata	ttc	caa	gaa	gat	gag	cct	tgt	ggg	768
Gly	Phe	Leu	Gly	Gly	Thr	Pro	Ile	Phe	Gln	Glu	Asp	Glu	Pro	Cys	Gly	
				245				250						255		
tct	cca	gtg	aag	agt	att	ttc	cag	gtt	att	gtt	gcc	tct	ttt	agg	aac	816
Ser	Pro	Val	Lys	Ser	Ile	Phe	Gln	Val	Ile	Val	Ala	Ser	Phe	Arg	Asn	
			260					265					270			
atg	agc	ttg	gaa	gta	cct	gct	gat	agc	tgt	ctt	ctg	tat	gag	gtc	ggg	864
Met	Ser	Leu	Glu	Val	Pro	Ala	Asp	Ser	Cys	Leu	Leu	Tyr	Glu	Val	Gly	
		275					280					285				
agc	aac	cac	ata	caa	agg	aca	aaa	ctt	gct	cac	tct	gat	gat	ttt	agg	912
Ser	Asn	His	Ile	Gln	Arg	Thr	Lys	Leu	Ala	His	Ser	Asp	Asp	Phe	Arg	
	290					295					300					
ttc	tta	gat	aag	gcg	gca	gtt	att	tct	gat	cca	agc	ctg	gtg	tat	gga	960
Phe	Leu	Asp	Lys	Ala	Ala	Val	Ile	Ser	Asp	Pro	Ser	Leu	Val	Tyr	Gly	
305				310					315					320		
ggc	tgt	cga	agc	tca	tgg	agc	ata	tgt	aca	gtt	act	gaa	gtt	gag	gaa	1008
Gly	Cys	Arg	Ser	Trp	Ser	Ser	Ile	Cys	Thr	Val	Thr	Glu	Val	Glu	Glu	
				325				330						335		
ctg	aaa	ata	ctt	atc	cgc	ttg	ctc	cca	ata	tgg	gtg	act	gga	ata	ttc	1056
Leu	Lys	Ile	Leu	Ile	Arg	Leu	Leu	Pro	Ile	Trp	Val	Thr	Gly	Ile	Phe	
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PF59082SeqList_PF59082.txt

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Thr Val Met Asp Thr Lys Ile Gly Ser Leu Ser Ile Pro Pro Ala Ser	
tta tac tca ttt gaa gtg ata tgt gtc acg ctt tgg gta ctt gct gtc	1200
Leu Tyr Ser Phe Glu Val Ile Cys Val Thr Leu Trp Val Leu Ala Val	
aac aaa gtg ctt gtg ccg gca atc cga acg tat ttt gca aat ggg gta	1248
Asn Lys Val Leu Val Pro Ala Ile Arg Thr Tyr Phe Ala Asn Gly Val	
gag ctc aca cag tta cag agg att ggg atc ggt cgt ttc ctg atg atc	1296
Glu Leu Thr Gln Leu Gln Arg Ile Gly Ile Gly Arg Phe Leu Met Ile	
ttt gcc ata gca atg gca gca ctt cta gaa acc aag agg ctg cat att	1344
Phe Ala Ile Ala Met Ala Ala Leu Leu Glu Thr Lys Arg Leu His Ile	
gtt cag gag ggg gaa ctg cta agc att gta tgg cag ctt cca cag tac	1392
Val Gln Glu Gly Glu Leu Ser Ile Val Trp Gln Leu Pro Gln Tyr	
ttc gtc att gct ggg gct gag tgc ttc ggt atc atc act cag ctg gag	1440
Phe Val Ile Ala Gly Ala Glu Cys Phe Gly Ile Ile Thr Gln Leu Glu	
ttc ttt cat ggc cag gcg cca gac tcc atg aag agc att tta acg gca	1488
Phe Phe His Gly Gln Ala Pro Asp Ser Met Lys Ser Ile Leu Thr Ala	
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Phe Ala Leu Leu Thr Thr Ala Leu Gly Asn Tyr Leu Ser Ser Ala Ile	
atc acc ctc atc gca ggg gtg acc agg gta tgg cat agc cct ggt tgg	1584
Ile Thr Leu Ile Ala Gly Val Thr Arg Val Trp His Ser Pro Gly Trp	
ata cca gat gat ctg aac aaa gga cac ctt gac tac tac tac tgg tgt	1632
Ile Pro Asp Asp Leu Asn Lys Gly His Leu Asp Tyr Tyr Tyr Trp Cys	
ctt act acc ctc tca ttg gtg aat ttt gtt gtg tat ctg tat ttt gct	1680
Leu Thr Thr Leu Ser Leu Val Asn Phe Val Val Tyr Leu Tyr Phe Ala	
agt aaa tac aaa ttg aag aaa gtt gtt tgt taa	1713
Ser Lys Tyr Lys Leu Lys Lys Val Val Cys	

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 <213> Zea mays

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 35 Leu Gly Leu Glu Cys Leu Glu Ser Met Ala Phe Asn Gly Ile Ala Thr
 50 Asn Leu Val Val Tyr Leu Arg Ser Val Leu His Gly Gly Ile Ala Ser
 65 Ser Ala Ala Thr Val Ser Leu Trp Tyr Gly Thr Ser Phe Phe Val Pro
 85 Ile Leu Gly Ala Ala Ile Ala Asp Thr Cys Leu Gly Asn Tyr Lys Thr
 100 Ile Leu Ile Ser Leu Ile Met Tyr Leu Phe Gly Met Val Leu Ile Thr
 115 Val Ala Thr Phe Met Pro Ser Thr Ser Val Leu Cys Asp Val Ser Ser
 130 Cys Leu Ser Ser Asn Gly Thr Gln Thr Met Ile Phe Phe Ala Gly Leu
 145 150 155 160

PF59082SeqList_PF59082.txt

Tyr Leu Thr Ala Val Gly Cys Gly Gly Val Arg Ser Ala Leu Pro
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Phe Gly Ala Asn Gln Phe Asn Asn Glu Asn Ser Leu Asp Ile Lys Lys
180 185
Arg Arg Asn Phe Phe Ser Leu Phe Tyr Ile Cys Val Ile Phe Gly Val
195 200
Ile Thr Ser Gly Thr Ile Ile Val Trp Val Gln Glu Asn Val Ser Trp
210 215
Ala Ile Gly Tyr Gly Val Ala Thr Thr Cys Ile Gly Leu Ala Leu Ile
225 230
Gly Phe Leu Gly Gly Thr Pro Ile Phe Gln Glu Asp Glu Pro Cys Gly
245 250
Ser Pro Val Lys Ser Ile Phe Gln Val Ile Val Ala Ser Phe Arg Asn
260 265
Met Ser Leu Glu Val Pro Ala Asp Ser Cys Leu Leu Tyr Glu Val Gly
275 280
Ser Asn His Ile Gln Arg Thr Lys Leu Ala His Ser Asp Asp Phe Arg
290 295
Phe Leu Asp Lys Ala Ala Val Ile Ser Asp Pro Ser Leu Val Tyr Gly
305 310
Gly Cys Arg Ser Ser Trp Ser Ile Cys Thr Val Thr Glu Val Glu Glu
325 330
Leu Lys Ile Leu Ile Arg Leu Leu Pro Ile Trp Val Thr Gly Ile Phe
340 345
Phe Ala Ala Ala Ile Ser Gln Met His Thr Thr Phe Ile Gln Gln Gly
355 360
Thr Val Met Asp Thr Lys Ile Gly Ser Leu Ser Ile Pro Pro Ala Ser
370 375
Leu Tyr Ser Phe Glu Val Ile Cys Val Thr Leu Trp Val Leu Ala Val
385 390
Asn Lys Val Leu Val Pro Ala Ile Arg Thr Tyr Phe Ala Asn Gly Val
405 410
Glu Leu Thr Gln Leu Gln Arg Ile Gly Ile Gly Arg Phe Leu Met Ile
420 425
Phe Ala Ile Ala Met Ala Ala Leu Glu Thr Lys Arg Leu His Ile
435 440
Val Gln Glu Gly Glu Leu Leu Ser Ile Val Trp Gln Leu Pro Gln Tyr
450 455
Phe Val Ile Ala Gly Ala Glu Cys Phe Gly Ile Ile Thr Gln Leu Glu
465 470
Phe Phe His Gly Gln Ala Pro Asp Ser Met Lys Ser Ile Leu Thr Ala
485 490
Phe Ala Leu Leu Thr Thr Ala Leu Gly Asn Tyr Leu Ser Ser Ala Ile
500 505
Ile Thr Leu Ile Ala Gly Val Thr Arg Val Trp His Ser Pro Gly Trp
515 520
Ile Pro Asp Asp Leu Asn Lys Gly His Leu Asp Tyr Tyr Tyr Trp Cys
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545 550
Ser Lys Tyr Lys Leu Lys Lys Val Val Cys
565 570

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ccc ctc tcg cag tcc agc aag cag cag cag gat cct ctc gcc ggc gtc 96
Pro Leu Ser Gln Ser Ser Lys Gln Gln Gln Asp Pro Leu Ala Gly Val
20 25 30

PF59082SeqList_PF59082.txt																
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aga	tcc	gcg	ctc	ttc	gtc	gtg	ggc	gtc	gag	atc	gcc	ggg	agc	ttc	gcc	192
Arg	Ser	Ala	Leu	Phe	Val	Val	Gly	Val	Glu	Ile	Ala	Gly	Ser	Phe	Ala	
	50					55					60					
tac	ttc	ggc	atc	tct	gcc	aac	cta	atc	acg	tac	ctg	act	ggg	ccg	cta	240
Tyr	Phe	Gly	Ile	Ser	Ala	Asn	Leu	Ile	Thr	Tyr	Leu	Thr	Gly	Pro	Leu	
65					70					75					80	
cga	cag	tcc	aac	gcc	tcc	gcc	gcc	gcc	tcc	gtc	aac	gcc	tgg	tcc	ggc	288
Arg	Gln	Ser	Asn	Ala	Ser	Ala	Ala	Ala	Ser	Val	Asn	Ala	Trp	Ser	Gly	
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<223> Xaa in position 587 is any amino acid

<220>
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<222> (589)..(589)
<223> Xaa in position 589 is any amino acid

<220>
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<222> (592)..(592)
<223> Xaa in position 592 is any amino acid

<220>
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<222> (594)..(596)
<223> Xaa in position 594 to 596 is any amino acid

<220>
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<222> (597)..(603)
<223> Xaa in position 597 to 603 is any or no amino acid

<220>
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<222> (605)..(613)
<223> Xaa in position 605 to 613 is any amino acid

<220>
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<222> (614)..(614)
<223> Xaa in position 614 is any or no amino acid

<220>
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<222> (616)..(617)
<223> Xaa in position 616 to 617 is any amino acid

<400> 406
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20      25      30
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35      40      45
Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa
50      55      60
Xaa Asp Xaa Xaa Xaa Gly Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65      70      75      80
Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
85      90      95
Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
100     105     110
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
115     120     125
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Gly Gly Xaa Xaa Xaa Xaa
130     135     140
Xaa Xaa Xaa Phe Gly Xaa Asp Gln Phe Asp Xaa Xaa Xaa Xaa Xaa Xaa
145     150     155     160
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
165     170     175
Xaa Xaa Xaa Xaa Xaa Xaa Phe Phe Asn Trp Xaa Xaa Xaa Xaa Xaa Xaa
180     185     190
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Xaa Val Xaa Xaa Gln Xaa Xaa
195     200     205
Xaa Xaa Trp Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
210     215     220
Xaa Xaa Xaa Xaa Phe Xaa Xaa Gly Xaa Xaa Xaa Tyr Xaa Xaa Xaa Xaa

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PF59082SeqList_PF59082.txt

225					230					235					240
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ser	Pro	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Val	Xaa
				245					250					255	
Xaa	Ala	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			260					265					270		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			275					280					285		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			290					295					300		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Leu	Asp	Xaa	Ala	Ala	Xaa
305						310				315					320
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				325					330					335	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Trp	Xaa	Leu	Xaa	Xaa	Xaa	Xaa
			340					345					350		
Xaa	Val	Glu	Glu	Xaa	Lys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Pro	Xaa	Trp	Xaa
		355					360					365			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Gln	Xaa	Xaa	Xaa	Xaa	Xaa
		370					375				380				
Xaa	Xaa	Gln	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
385						390				395					400
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Pro	Xaa	Xaa	Ser	Xaa	Xaa	Xaa	Xaa
				405					410					415	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Tyr	Asp	Xaa	Xaa	Xaa
			420					425					430		
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		435					440					445			
Xaa	Xaa	Xaa	Leu	Gln	Arg	Xaa	Gly	Xaa	Gly	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		450				455					460				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Glu	Xaa	Xaa	Arg	Xaa	Xaa	Xaa	Xaa
465						470				475					480
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				485					490					495	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ser	Xaa	Xaa	Trp	Xaa	Xaa	Pro	Gln	Xaa	Xaa
			500					505					510		
Xaa	Xaa	Gly	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Xaa	Xaa	Xaa	Gly	Xaa	Xaa	Glu
		515					520					525			
Phe	Xaa	Xaa	Xaa	Xaa	Xaa	Pro	Xaa	Xaa	Met	Xaa	Ser	Xaa	Xaa	Xaa	Xaa
	530					535					540				
Leu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ser	Xaa	Xaa	Xaa
545						550					555				560
Xaa	Xaa	Xaa	Val	Xaa	Xaa	Xaa	Thr	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			565					570						575	
Xaa	Xaa	Trp	Xaa	Xaa	Xaa	Xaa	Xaa	Asn	Xaa	Gly	Xaa	Leu	Asp	Xaa	Xaa
			580					585				590			
Phe	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asn	Xaa	Xaa	Xaa	Xaa
		595					600					605			
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<210> 407
 <211> 18
 <212> PRT
 <213> Artificial sequence

<220>
 <223> protein pattern

<220>
 <221> Variant
 <222> (4)..(4)
 <223> Xaa in position 4 is any amino acid

<220>
 <221> Variant
 <222> (6)..(6)
 <223> Xaa in position 6 is any amino acid

PF59082SeqList_PF59082.txt

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<220>
<221> Variant
<222> (7)..(7)
<223> Xaa in position 7 is Ile, Leu, Met or Val

<220>
<221> Variant
<222> (8)..(8)
<223> Xaa in position 8 is Ala, Ile, Leu or Val

<220>
<221> Variant
<222> (9)..(11)
<223> Xaa in position 9 to 11 is any amino acid

<220>
<221> Variant
<222> (13)..(13)
<223> Xaa in position 13 is any amino acid

<220>
<221> Variant
<222> (15)..(17)
<223> Xaa in position 15 to 17 is any amino acid

<220>
<221> Variant
<222> (18)..(18)
<223> Xaa in position 18 is Ala, Ile, Leu or Val

<400> 407
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1          5          10          15
Xaa Xaa

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<210> 408
<211> 24
<212> PRT
<213> Artificial sequence

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<220>
<223> protein pattern

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<220>
<221> Variant
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<223> Xaa in position 2 to 4 is any amino acid

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<220>
<221> Variant
<222> (5)..(5)
<223> Xaa in position 5 is Ala, Gly or Ser

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<220>
<221> Variant
<222> (6)..(7)
<223> Xaa in position 6 to 7 is any amino acid

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<220>
<221> Variant
<222> (8)..(8)
<223> Xaa in position 8 is Ala, Asp or Glu

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<220>
<221> Variant
<222> (10)..(12)
<223> Xaa in position 10 to 12 is any amino acid

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PF59082SeqList_PF59082.txt

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<220>
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<222> (13)..(13)
<223> Xaa in position 13 is Glu, Gln or Arg

<220>
<221> Variant
<222> (14)..(14)
<223> Xaa in position 14 is any amino acid

<220>
<221> Variant
<222> (15)..(15)
<223> Xaa in position 15 is Pro or Ser

<220>
<221> Variant
<222> (16)..(17)
<223> Xaa in position 16 to 17 is any amino acid

<220>
<221> Variant
<222> (18)..(18)
<223> Xaa in position 18 is Leu, Met or Val

<220>
<221> Variant
<222> (19)..(19)
<223> Xaa in position 19 is any amino acid

<220>
<221> Variant
<222> (20)..(20)
<223> Xaa in position 20 is Ala, Ser or Thr

<220>
<221> Variant
<222> (21)..(21)
<223> Xaa in position 21 is any amino acid

<220>
<221> Variant
<222> (22)..(22)
<223> Xaa in position 22 is Ala, Cys, Gly or Ser

<220>
<221> Variant
<222> (23)..(23)
<223> Xaa in position 23 is any amino acid

<220>
<221> Variant
<222> (24)..(24)
<223> Xaa in position 24 is Ala, Gly or Ser

<400> 408
Phe Xaa Xaa Xaa Xaa Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1      5      10      15
Xaa Xaa Xaa Xaa Xaa Xaa Xaa
      20

<210> 409
<211> 18
<212> PRT
<213> Artificial sequence

<220>

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<223> protein pattern

<220>

<221> Variant

<222> (2)..(3)

<223> Xaa in position 2 to 3 is any or no amino acid

<220>

<221> Variant

<222> (5)..(6)

<223> Xaa in position 5 to 6 is any amino acid

<220>

<221> Variant

<222> (7)..(7)

<223> Xaa in position 7 is Ala, Pro or Ser

<220>

<221> Variant

<222> (8)..(8)

<223> Xaa in position 8 is Ala, Cys, Asn, Ser or Thr

<220>

<221> Variant

<222> (9)..(10)

<223> Xaa in position 9 to 10 is any amino acid

<220>

<221> Variant

<222> (11)..(11)

<223> Xaa in position 11 is Ala, Gly, Pro, Ser or Thr

<220>

<221> Variant

<222> (12)..(12)

<223> Xaa in position 12 is any amino acid

<220>

<221> Variant

<222> (14)..(14)

<223> Xaa in position 14 is Ala, Gly, Ser, Thr or Val

<220>

<221> Variant

<222> (17)..(17)

<223> Xaa in position 17 is any amino acid

<220>

<221> Variant

<222> (18)..(18)

<223> Xaa in position 18 is Asp or Asn

<400> 409

Gly Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Asp Gln
 1 5 10 15
 Xaa Xaa

<210> 410

<211> 555

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(555)

<400> 410

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PF59082SeqList_PF59082.txt

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Gln	Leu	Ser	Tyr	Arg	Gly	Ile	Arg	Arg	Arg	Lys	Trp	Gly	Lys	Trp	Val	
			20					25					30			
tcg	gag	atc	cga	gaa	ccc	ggt	aag	aaa	aca	agg	att	tgg	ctt	gga	agc	144
Ser	Glu	Ile	Arg	Glu	Pro	Gly	Lys	Lys	Thr	Arg	Ile	Trp	Leu	Gly	Ser	
		35					40					45				
tac	gag	acg	gcc	gag	atg	gct	gca	gcg	gcc	tac	gat	gct	gcg	gct	ctt	192
Tyr	Glu	Thr	Ala	Glu	Met	Ala	Ala	Ala	Ala	Tyr	Asp	Ala	Ala	Ala	Leu	
		50				55					60					
cac	ctc	cga	gga	cgt	ggg	acc	aat	ctc	aac	ttt	ccg	gaa	ctc	gtc	gac	240
His	Leu	Arg	Gly	Arg	Gly	Thr	Asn	Leu	Asn	Phe	Pro	Glu	Leu	Val	Asp	
65				70				75						80		
agt	ttt	cct	cgg	ccg	gaa	agc	tct	agt	tcg	gag	cac	att	caa	gcg	gct	288
Ser	Phe	Pro	Arg	Pro	Glu	Ser	Ser	Ser	Ser	Glu	His	Ile	Gln	Ala	Ala	
				85				90					95			
gca	caa	gat	gca	gca	ctt	atg	ttt	aaa	cca	ggt	agg	ttg	agt	gaa	cca	336
Ala	Gln	Asp	Ala	Ala	Leu	Met	Phe	Lys	Pro	Gly	Arg	Leu	Ser	Glu	Pro	
			100					105					110			
gct	ctc	gag	tct	ggt	caa	gga	ctt	tct	cga	gta	gga	ttg	tct	ccg	gat	384
Ala	Leu	Glu	Ser	Gly	Gln	Gly	Leu	Ser	Arg	Val	Gly	Leu	Ser	Pro	Asp	
		115				120						125				
cag	att	caa	gcg	att	aat	gag	tct	cca	tta	gac	tcg	ccg	agg	atg	ggg	432
Gln	Ile	Gln	Ala	Ile	Asn	Glu	Ser	Pro	Leu	Asp	Ser	Pro	Arg	Met	Gly	
		130				135					140					
tgg	atg	cag	gat	ttg	gaa	gtt	gct	gac	tac	gaa	gaa	tta	tac	gga	caa	480
Trp	Met	Gln	Asp	Leu	Glu	Val	Ala	Asp	Tyr	Glu	Glu	Leu	Tyr	Gly	Gln	
145				150				155						160		
ttt	ttt	ggt	cag	cac	gat	agg	gat	gag	ttt	ttt	gaa	atg	cag	caa	ttt	528
Phe	Phe	Gly	Gln	His	Asp	Arg	Asp	Glu	Phe	Phe	Glu	Met	Gln	Gln	Phe	
				165				170						175		
cag	tcc	ata	tgg	aat	tct	aat	aat	tga								555
Gln	Ser	Ile	Trp	Asn	Ser	Asn	Asn									
			180													

<210> 411
 <211> 184
 <212> PRT
 <213> Arabidopsis thaliana

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			20					25					30			
Ser	Glu	Ile	Arg	Glu	Pro	Gly	Lys	Lys	Thr	Arg	Ile	Trp	Leu	Gly	Ser	
		35					40					45				
Tyr	Glu	Thr	Ala	Glu	Met	Ala	Ala	Ala	Ala	Tyr	Asp	Ala	Ala	Ala	Leu	
		50				55					60					
His	Leu	Arg	Gly	Arg	Gly	Thr	Asn	Leu	Asn	Phe	Pro	Glu	Leu	Val	Asp	
65				70				75						80		
Ser	Phe	Pro	Arg	Pro	Glu	Ser	Ser	Ser	Ser	Glu	His	Ile	Gln	Ala	Ala	
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Ala	Gln	Asp	Ala	Ala	Leu	Met	Phe	Lys	Pro	Gly	Arg	Leu	Ser	Glu	Pro	
			100					105					110			
Ala	Leu	Glu	Ser	Gly	Gln	Gly	Leu	Ser	Arg	Val	Gly	Leu	Ser	Pro	Asp	
		115				120						125				
Gln	Ile	Gln	Ala	Ile	Asn	Glu	Ser	Pro	Leu	Asp	Ser	Pro	Arg	Met	Gly	
		130				135					140					
Trp	Met	Gln	Asp	Leu	Glu	Val	Ala	Asp	Tyr	Glu	Glu	Leu	Tyr	Gly	Gln	
145				150				155						160		
Phe	Phe	Gly	Gln	His	Asp	Arg	Asp	Glu	Phe	Phe	Glu	Met	Gln	Gln	Phe	
				165				170						175		
Gln	Ser	Ile	Trp	Asn	Ser	Asn	Asn									
			180													

<210> 412
 <211> 552

PF59082SeqList_PF59082.txt

<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (1)..(552)

<400> 412

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 1      5      10      15
caa gtg tct tat aga ggc gtt cgc cag agg aag tgg gga aaa tgg gtg      96
Gln Val Ser Tyr Arg Gly Val Arg Gln Arg Lys Trp Gly Lys Trp Val
      20      25      30
tcg gaa atc cga gaa ccc ggt aag aaa acc cgt att tgg ctc gga agc      144
Ser Glu Ile Arg Glu Pro Gly Lys Thr Arg Ile Trp Leu Gly Ser
      35      40      45
tac gag acg gcc gaa atg gcc gca gct gct tac gac gtt gcg gct att      192
Tyr Glu Thr Ala Glu Met Ala Ala Ala Tyr Asp Val Ala Ala Ile
      50      55      60
cac ctc cga gga cgt ggg aca cat gtc aac ttt ccg gag ctt gct gac      240
His Leu Arg Gly Arg Gly Thr His Val Asn Phe Pro Glu Leu Ala Asp
      65      70      75      80
agt ttt cct cag ccg caa agc tca agt tcc gag cac att caa gct gct      288
Ser Phe Pro Gln Pro Gln Ser Ser Ser Ser Glu His Ile Gln Ala Ala
      85      90      95
gct cag gag gca gca ctg ctg ttt aaa ccg ggc gtg tcg tct act gaa      336
Ala Gln Glu Ala Ala Leu Leu Phe Lys Pro Gly Val Ser Ser Thr Glu
      100      105      110
gca gat ctc ggg tcg ggt cag gga cat tct cgg gtc gga ttg tct ccg      384
Ala Asp Leu Gly Ser Gly Gln Gly His Ser Arg Val Gly Leu Ser Pro
      115      120      125
gat cag att cag gcg att aat gaa ttt cca ttg gac tcg ccg agg agg      432
Asp Gln Ile Gln Ala Ile Asn Glu Phe Pro Leu Asp Ser Pro Arg Arg
      130      135      140
ggg tgg atg cag gat ttg gaa gtg gat gat tat gaa gag ttg tac gga      480
Gly Trp Met Gln Asp Leu Glu Val Asp Asp Tyr Glu Glu Leu Tyr Gly
      145      150      155      160
cga att ttt ggt caa tgc gat aga gat gag tat ttt gaa atg cag cag      528
Arg Ile Phe Gly Gln Cys Asp Arg Asp Glu Tyr Phe Glu Met Gln Gln
      165      170      175
ttt cga tcc ata ttg gga tct taa
Phe Arg Ser Ile Leu Gly Ser
      180

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<210> 413

<211> 183

<212> PRT

<213> Brassica napus

<400> 413

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Met Glu Asn Lys Asn Val Gly Gln Leu Glu Gln Arg Phe Ser Val Asp
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      20      25      30
Ser Glu Ile Arg Glu Pro Gly Lys Lys Thr Arg Ile Trp Leu Gly Ser
      35      40      45
Tyr Glu Thr Ala Glu Met Ala Ala Ala Tyr Asp Val Ala Ala Ile
      50      55      60
His Leu Arg Gly Arg Gly Thr His Val Asn Phe Pro Glu Leu Ala Asp
      65      70      75      80
Ser Phe Pro Gln Pro Gln Ser Ser Ser Ser Glu His Ile Gln Ala Ala
      85      90      95
Ala Gln Glu Ala Leu Leu Phe Lys Pro Gly Val Ser Ser Thr Glu
      100      105      110
Ala Asp Leu Gly Ser Gly Gln Gly His Ser Arg Val Gly Leu Ser Pro
      115      120      125
Asp Gln Ile Gln Ala Ile Asn Glu Phe Pro Leu Asp Ser Pro Arg Arg
      130      135      140

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PF59082SeqList_PF59082.txt

Gly Trp Met Gln Asp Leu Glu Val Asp Asp Tyr Glu Glu Leu Tyr Gly
 145 150 155 160
 Arg Ile Phe Gly Gln Cys Asp Arg Asp Glu Tyr Phe Glu Met Gln Gln
 165 170 175
 Phe Arg Ser Ile Leu Gly Ser
 180

<210> 414
 <211> 1158
 <212> DNA
 <213> glycine max

<220>
 <221> CDS
 <222> (59)..(757)

<400> 414
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atg gtc atg gaa gaa tct aac cct tta gac aat gaa gtt caa cca acc 106
 Met Val Met Glu Glu Ser Asn Pro Leu Asp Asn Glu Val Gln Pro Thr
 1 5 10 15
 act tca tca tcc tct ttc acc att act act ccc tct acc tcc tct tcc 154
 Thr Ser Ser Ser Phe Thr Ile Thr Pro Ser Thr Ser Ser
 20 25 30
 tcc tcc ata gaa gaa gcc act aac act act act aag gag aaa aag aag 202
 Ser Ser Ile Glu Glu Ala Thr Asn Thr Thr Thr Lys Glu Lys Lys Lys
 35 40 45
 aag aga gcc att agt aat att gaa ggg aag cac cct acg tat aga gga 250
 Lys Arg Ala Ile Ser Asn Ile Glu Gly Lys His Pro Thr Tyr Arg Gly
 50 55 60
 gta cgt atg cgt caa tgg ggc aaa tgg gta tcc gaa att aga gag cca 298
 Val Arg Met Arg Gln Trp Gly Lys Trp Val Ser Glu Ile Arg Glu Pro
 65 70 75 80
 agg aag aaa tca aga att tgg ctt gga act ttt ccc act ccc gat atg 346
 Arg Lys Lys Ser Arg Ile Trp Leu Gly Thr Phe Pro Thr Pro Asp Met
 85 90 95
 gcg gct cga gcc cat gat gtg gcg gct ctc acg atc aaa ggc agc tcg 394
 Ala Ala Arg Ala His Asp Val Ala Ala Leu Thr Ile Lys Gly Ser Ser
 100 105 110
 gct tac ctc aat ttc ccc gaa tta gcc gcc aag ctg ccc cgc ccc gcc 442
 Ala Tyr Leu Asn Phe Pro Glu Leu Ala Ala Lys Leu Pro Arg Pro Ala
 115 120 125
 agc acc tcc ccc aag gac atc caa gct gcg gcg gct aaa gcc tcc gcc 490
 Ser Thr Ser Pro Lys Asp Ile Gln Ala Ala Ala Lys Lys Ala Ser Ala
 130 135 140
 ttg gat ttc ggt cac caa agc cat gaa gcc gaa tcc gag ctg agc caa 538
 Leu Asp Phe Gly His Gln Ser His Glu Ala Glu Ser Glu Leu Ser Gln
 145 150 155 160
 gcc gtt tcc tcc tca atc caa aca caa tca tca tca tca tcc aat 586
 Ala Val Ser Ser Ser Ile Gln Thr Gln Ser Ser Ser Ser Ser Ser Asn
 165 170 175
 tca tcg ttg aag ggt gtg gat gac aca ttc ttg gac ctt cct gat ctc 634
 Ser Ser Leu Lys Gly Val Asp Asp Thr Phe Leu Asp Leu Pro Asp Leu
 180 185 190
 tct ctt gac ttg agc cat gga gcc gat gag ttt cat tat tca tcg gct 682
 Ser Leu Asp Leu Ser His Gly Ala Asp Glu Phe His Tyr Ser Ser Ala
 195 200 205
 tgg ctt gta gcc gga gcc gaa cat ata gag ctg ggt ttc cgg ctt gag 730
 Trp Leu Val Ala Gly Ala Glu His Ile Glu Leu Gly Phe Arg Leu Glu
 210 215 220
 gaa cct ttt ctt tgg gaa tca tat taagttacct tcctcaagta ggccaatttc 784
 Glu Pro Phe Leu Trp Glu Ser Tyr
 225 230
 cctttttttg atgtttgtgc tgcctctctt ttttctttgt tcctttcact tttgagctac 844

ttgcaagaac cttgaagaat ccaatatgct ctatggcagc atgacgtggg ggtgtcaaac 904

PF59082SeqList_PF59082.txt

ttcagtgtcc atgacaaata aagaagtttt actaaacca ctccatagct ttttttattc 964
aagaatttat gtaaatatta aaatatcatc tgtcattttc agataaggta attaattaag 1024
ttgccttgca tcatattcct caatttggtg taaatttcct cgcttggtcat ctgtatatcc 1084
tcccctttgt caaaattcag ttttaatttgt gtatgggtga atgtggaata aagttcagct 1144
gggtaaattt gatt 1158

<210> 415
<211> 232
<212> PRT
<213> glycine max

<400> 415
Met Val Met Glu Glu Ser Asn Pro Leu Asp Asn Glu Val Gln Pro Thr
1 5 10 15
Thr Ser Ser Ser Ser Phe Thr Ile Thr Thr Pro Ser Thr Ser Ser
20 25 30
Ser Ser Ile Glu Glu Ala Thr Asn Thr Thr Thr Lys Glu Lys Lys Lys
35 40 45
Lys Arg Ala Ile Ser Asn Ile Glu Gly Lys His Pro Thr Tyr Arg Gly
50 55 60
Val Arg Met Arg Gln Trp Gly Lys Trp Val Ser Glu Ile Arg Glu Pro
65 70 75 80
Arg Lys Lys Ser Arg Ile Trp Leu Gly Thr Phe Pro Thr Pro Asp Met
85 90 95
Ala Ala Arg Ala His Asp Val Ala Ala Leu Thr Ile Lys Gly Ser Ser
100 105 110
Ala Tyr Leu Asn Phe Pro Glu Leu Ala Ala Lys Leu Pro Arg Pro Ala
115 120 125
Ser Thr Ser Pro Lys Asp Ile Gln Ala Ala Ala Lys Ala Ser Ala
130 135 140
Leu Asp Phe Gly His Gln Ser His Glu Ala Glu Ser Glu Leu Ser Gln
145 150 155 160
Ala Val Ser Ser Ser Ile Gln Thr Gln Ser Ser Ser Ser Ser Asn
165 170 175
Ser Ser Leu Lys Gly Val Asp Asp Thr Phe Leu Asp Leu Pro Asp Leu
180 185 190
Ser Leu Asp Leu Ser His Gly Ala Asp Glu Phe His Tyr Ser Ser Ala
195 200 205
Trp Leu Val Ala Gly Ala Glu His Ile Glu Leu Gly Phe Arg Leu Glu
210 215 220
Glu Pro Phe Leu Trp Glu Ser Tyr
225 230

<210> 416
<211> 1207
<212> DNA
<213> zea mays

<220>
<221> CDS
<222> (203)..(853)

<400> 416
aagcaccacc aacagctctt ccattctact gcaacatcgc atcgacagtc tacagcattt 60

gtcgatcaaa cactgctcat caagcttagt tgtagtctgt cactactgta acttggtcag 120
Seite 586

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ctctcatcgt ccagaaaaca agaggtggcg gaacggaagg aacacataca caagatagaa 180

gcttttggtc gctgcaacaa ta atg gag atg gtg ctc gac aac agc gct ccg 232
Met Glu Met Val Leu Asp Asn Ser Ala Pro 10

ggc gtc gtc gcg gcc ggg cag tcg tac cgc ggc gtg agg aag agg aag 280
Gly Val Val Ala Ala Gly Gln Ser Tyr Arg Gly Val Arg Lys Arg Lys 25

tgg gga aag tgg gtg tcg gag ata aga gag ccg ggc aag aag acg cgc 328
Trp Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Gly Lys Lys Thr Arg 40

atc tgg ctg ggc agc ttc gag tct ccg gag atg gcc gcg gtg gcg cac 376
Ile Trp Leu Gly Ser Phe Glu Ser Pro Glu Met Ala Ala Val Ala His 55

gac gtg gcg gcg ctg cgc ctg cgc ggc cgc gag gcg cgg ctc aac ttc 424
Asp Val Ala Ala Leu Arg Leu Arg Gly Arg Glu Ala Arg Leu Asn Phe 70

ccg ggc ctg gtc cac cgc ttc cgc cgc ccg gcc acc gcc gag ccc gac 472
Pro Gly Leu Val His Arg Phe Arg Arg Pro Ala Thr Ala Glu Pro Asp 85 90

gac gtc cgc gcc gcc gcg ctg gag gcc gcg gcc cag gtc cgg ttc agg 520
Asp Val Arg Ala Ala Leu Glu Ala Ala Gln Val Arg Phe Arg 105

ccc gac ctc gtc gca atg cag gcc tcc ggc ggc gag ggc ggc tgc cgc 568
Pro Asp Leu Val Ala Met Gln Ala Ser Gly Gly Glu Gly Gly Cys Arg 110 115 120

ttc ggc ggc gcc ggc ggc agc gac gcc acc ggc agc ccg gag ccg ctg 616
Phe Gly Gly Ala Gly Gly Ser Asp Thr Gly Ser Pro Glu Pro Leu 125 130 135

gct gca ggc gag gac gat gtg gcg tgg gac gtc ttg ctc ggg acc gac 664
Ala Ala Gly Glu Asp Asp Val Ala Trp Asp Val Leu Leu Gly Thr Asp 140 145 150

gtg gag gtg gtg gag tcg ccc aag atg tgg gat gag ctg gcc gag gcc 712
Val Glu Val Val Glu Ser Pro Lys Met Trp Asp Glu Leu Ala Glu Ala 155 160 165 170

atg ctc gtg gcc ccg ccg cca gtg tgg gag ggc gat atg gag gac act 760
Met Leu Val Ala Pro Pro Val Trp Glu Gly Asp Met Glu Asp Thr 175 180 185

gac gac tgg gcc cag ggc ggt aat ctc tgg gac cta cct gtc tgg gcc 808
Asp Asp Trp Ala Gln Gly Gly Asn Leu Trp Asp Leu Pro Val Trp Ala 190 195 200

ctg ggc ccc acc ggc aga tgc agc ttc aca tcc ttt ggt ttt tagaggtgtg 860
Leu Gly Pro Thr Gly Arg Cys Ser Phe Thr Ser Phe Gly Phe 205 210 215

aactgaaaac ccatcagttt aatcaatctt cttcttaaaa gttaaaacca tatatatagg 920

ccaatgagca catgaggtat tctattctag agagcataat tgatcatcgt taagaatgtt 980

ctaattgatcc tttgattttc tttggtttct aaacgtctat ggggtcccgtc tgtcagtggtg 1040

tgcagacttg gtagctagca aagaaggtct agctagctag ctagcacgtg caattcacgt 1100

gggtaaaaaa aacaacaagc aggatgtaat tctttctgtt tccctctcat ctcatggatg 1160

agaagttgaa atgcaactgc tgctctaaaa taaaaaaaaa aaaaaaa 1207

<210> 417
<211> 216
<212> PRT

<213> zea mays

<400> 417

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Met Glu Met Val Leu Asp Asn Ser Ala Pro Gly Val Val Ala Ala Gly
1      5      10      15
Gln Ser Tyr Arg Gly Val Arg Lys Arg Lys Trp Gly Lys Trp Val Ser
20      25      30
Glu Ile Arg Glu Pro Gly Lys Lys Thr Arg Ile Trp Leu Gly Ser Phe
35      40      45
Glu Ser Pro Glu Met Ala Ala Val Ala His Asp Val Ala Ala Leu Arg
50      55      60
Leu Arg Gly Arg Glu Ala Arg Leu Asn Phe Pro Gly Leu Val His Arg
65      70      75      80
Phe Arg Arg Pro Ala Thr Ala Glu Pro Asp Asp Val Arg Ala Ala Ala
85      90      95
Leu Glu Ala Ala Ala Gln Val Arg Phe Arg Pro Asp Leu Val Ala Met
100     105     110
Gln Ala Ser Gly Gly Glu Gly Gly Cys Arg Phe Gly Gly Ala Gly Gly
115     120     125
Ser Asp Thr Gly Ser Pro Glu Pro Leu Ala Ala Gly Glu Asp Asp
130     135     140
Val Ala Trp Asp Val Leu Leu Gly Thr Asp Val Glu Val Val Glu Ser
145     150     155     160
Pro Lys Met Trp Asp Glu Leu Ala Glu Ala Met Leu Val Ala Pro Pro
165     170     175
Pro Val Trp Glu Gly Asp Met Glu Asp Thr Asp Asp Trp Ala Gln Gly
180     185     190
Gly Asn Leu Trp Asp Leu Pro Val Trp Ala Leu Gly Pro Thr Gly Arg
195     200     205
Cys Ser Phe Thr Ser Phe Gly Phe
210     215

```

<210> 418

<211> 730

<212> DNA

<213> glycine max

<220>

<221> CDS

<222> (6)..(500)

<400> 418

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tattg atg tgc agc atc agt gag aaa gcc aaa agg aag cgc caa tct gca      50
      Met Cys Ser Ile Ser Glu Lys Ala Lys Lys Arg Lys Ser Ala
1      5      10      15
ttc cgc gga gtg cgc aaa cgc agc tgg gga cgc tac gtc tct gag ata      98
Phe Arg Gly Val Arg Lys Arg Ser Trp Gly Arg Tyr Val Ser Glu Ile
20      25      30
agg ctc ccg ggc cag aaa aca cgc ata tgg ctc ggc tcc ttc ggc tcg      146
Arg Leu Pro Gly Gln Lys Thr Arg Ile Trp Leu Gly Ser Phe Gly Ser
35      40      45
cct gag atg gcg gct cgc gct tat gac tcc gct gct ttc ttc ctc aaa      194
Pro Glu Met Ala Ala Arg Ala Tyr Asp Ser Ala Ala Phe Phe Leu Lys
50      55      60
gga aca tct gcc act ctt aat ttc ccc gac ctc gta cac tcc ctg cct      242
Gly Thr Ser Ala Thr Leu Asn Phe Pro Asp Leu Val His Ser Leu Pro
65      70      75
cga cct ctc tca tct tcc cgg agg gac ata cag tcc gcc gca gct gaa      290
Arg Pro Leu Ser Ser Ser Arg Arg Asp Ile Gln Ser Ala Ala Ala Glu
80      85      90      95
gcc gct ctc cac tct ccg cct ccc aaa gaa gaa caa gaa tct att ttc      338
Ala Ala Leu His Ser Pro Pro Pro Lys Glu Glu Gln Glu Ser Ile Phe
100     105     110
act tcc acc acc acc tcg tcc ttt cac gat gtc atg gaa gct cct ctt      386
Thr Ser Thr Thr Ser Ser Phe His Asp Val Met Glu Ala Pro Leu
115     120     125
atg agt ccc ctt agg gtg gac tcc act ttc gga gat ttc tca tgg gac      434
Met Ser Pro Leu Arg Val Asp Ser Thr Phe Gly Asp Phe Ser Trp Asp
130     135     140

```

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caa ctc ttc gat ttc aac gat gac att ctc atc gtg gga tca act tct      482
Gln Leu Phe Asp Phe Asn Asp Asp Ile Leu Ile Val Gly Ser Thr Ser
    145          150          155
gcc act ctt gtc cct taacgctgct ttgcaattc gccacccact gcttctagaa      537
Ala Thr Leu Val Pro
160
actagctgga ttttctttca ctttctgtta ataactcttc tctgcttttc taagacttgc      597

ttctgaactc ttgtacaaag gagctctcca agacaaatat atatatatat atatatatat      657

atatatatat atatatatat atatatatat atatatgttt actgagagac tgatttcact      717

aagcacctta att                                                         730

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<210> 419
 <211> 164
 <212> PRT
 <213> glycine max

<400> 419

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Met Cys Ser Ile Ser Glu Lys Ala Lys Arg Lys Arg Gln Ser Ala Phe
1          5          10          15
Arg Gly Val Arg Lys Arg Ser Trp Gly Arg Tyr Val Ser Glu Ile Arg
    20          25          30
Leu Pro Gly Gln Lys Thr Arg Ile Trp Leu Gly Ser Phe Gly Ser Pro
    35          40          45
Glu Met Ala Ala Arg Ala Tyr Asp Ser Ala Ala Phe Phe Leu Lys Gly
    50          55          60
Thr Ser Ala Thr Leu Asn Phe Pro Asp Leu Val His Ser Leu Pro Arg
65          70          75          80
Pro Leu Ser Ser Ser Arg Arg Asp Ile Gln Ser Ala Ala Ala Glu Ala
    85          90          95
Ala Leu His Ser Pro Pro Pro Lys Glu Glu Gln Glu Ser Ile Phe Thr
    100          105          110
Ser Thr Thr Thr Ser Ser Phe His Asp Val Met Glu Ala Pro Leu Met
    115          120          125
Ser Pro Leu Arg Val Asp Ser Thr Phe Gly Asp Phe Ser Trp Asp Gln
    130          135          140
Leu Phe Asp Phe Asn Asp Asp Ile Leu Ile Val Gly Ser Thr Ser Ala
145          150          155          160
Thr Leu Val Pro

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<210> 420
 <211> 876
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (40)..(681)

<400> 420

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cgaaagcacg ggggtgcggct cgagcttcat tcattcttt atg gat caa gaa aca      54
                                Met Asp Gln Glu Thr
                                1          5
aca aga aga aac acc atg caa gaa tgt cat gtg ata gcc cca aca aca      102
Thr Arg Arg Asn Thr Met Gln Glu Cys His Val Ile Ala Pro Thr Thr
    10          15          20
aca acg gca aca tca tgc tat cgt gga gtt cgt cag cga aaa tgg ggc      150
Thr Thr Ala Thr Ser Ser Tyr Arg Gly Val Arg Gln Arg Lys Trp Gly
    25          30          35
aaa tgg gtg tcc gaa atc cgt gag cct gga aag aag agc aga ata tgg      198
Lys Trp Val Ser Glu Ile Arg Glu Pro Gly Lys Lys Ser Arg Ile Trp

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PF59082SeqList_PF59082.txt

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      40      45      50
tta ggg agc tat gag tca cca gag atg gct gca gca gca tat gac gtg      246
Leu Gly Ser Tyr Glu Ser Pro Glu Met Ala Ala Ala Tyr Asp Val
      55      60      65
gca gcg tta cac ctt cgg gga cga gct gca aga ctc aat ttc ccc gaa      294
Ala Ala Leu His Leu Arg Gly Arg Ala Ala Arg Leu Asn Phe Pro Glu
      70      75      80      85
tta gtt gag acg ctg cca cgt cca acg agt tcg aaa ccc gaa gat gtc      342
Leu Val Glu Thr Leu Pro Arg Pro Thr Ser Ser Lys Pro Glu Asp Val
      90      95      100
caa gtg gca gca caa cca gcg gcg gtg atg ttc aga ata tca cca aca      390
Gln Val Ala Ala Gln Gln Ala Ala Val Met Phe Arg Ile Ser Pro Thr
      105      110      115
atg tca cct att aac aat cat caa gga tgt gtc aat gac aat aac att      438
Met Ser Pro Ile Asn Asn His Gln Gly Cys Val Asn Asp Asn Asn Ile
      120      125      130
att aag ggt agt gtg gtt cct gtg aga gtg gga ctc tca ccc aca caa      486
Ile Lys Gly Ser Val Val Pro Val Arg Val Gly Leu Ser Pro Thr Gln
      135      140      145
att cag gcc atc aat gag tcc cca ttg gac tca cca aag atg tgg atg      534
Ile Gln Ala Ile Asn Glu Ser Pro Leu Asp Ser Pro Lys Met Trp Met
      150      155      160      165
gtg caa atg gca gag gca ctc agg ttt ggt ttc gat gat cac tct atg      582
Val Gln Met Ala Glu Ala Leu Arg Phe Gly Phe Asp Asp His Ser Met
      170      175      180
atg atg ctg cct tct gat gat gat gat tat gct ttg gag ttg agt gga      630
Met Met Leu Pro Ser Asp Asp Asp Asp Tyr Ala Leu Glu Leu Ser Gly
      185      190      195
tg gaa gaa ata cag cat gaa tct tta tgg gac tct cca gaa tat atg      678
Trp Glu Glu Ile Gln His Glu Ser Leu Trp Asp Ser Pro Glu Tyr Met
      200      205      210
taattaatta cgtaactatt aattaataat caatgtaccc ttgatttagg gcattatata      738

ttacatatga ttaaagaatc atgtgggtttt agtgagactg attcaatgaa gcaaaaggat      798

taataaatta tatatttgta aattgcgtac agtatttcat gaccatttg tttctccaat      858

tgatttggtg atgtgtct      876

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<210> 421
 <211> 213
 <212> PRT
 <213> Glycine max

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<400> 421
Met Asp Gln Glu Thr Thr Arg Arg Asn Thr Met Gln Glu Cys His Val
1      5      10      15
Ile Ala Pro Thr Thr Thr Ala Thr Ser Ser Tyr Arg Gly Val Arg
20      25      30
Gln Arg Lys Trp Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Gly Lys
35      40      45
Lys Ser Arg Ile Trp Leu Gly Ser Tyr Glu Ser Pro Glu Met Ala Ala
50      55      60
Ala Ala Tyr Asp Val Ala Ala Leu His Leu Arg Gly Arg Ala Ala Arg
65      70      75      80
Leu Asn Phe Pro Glu Leu Val Glu Thr Leu Pro Arg Pro Thr Ser Ser
85      90      95
Lys Pro Glu Asp Val Gln Val Ala Ala Gln Gln Ala Ala Val Met Phe
100      105      110
Arg Ile Ser Pro Thr Met Ser Pro Ile Asn Asn His Gln Gly Cys Val
115      120      125
Asn Asp Asn Asn Ile Ile Lys Gly Ser Val Val Pro Val Arg Val Gly
130      135      140
Leu Ser Pro Thr Gln Ile Gln Ala Ile Asn Glu Ser Pro Leu Asp Ser

```

PF59082SeqList_PF59082.txt

```

145                               150                               155                               160
Pro Lys Met Trp Met Val Gln Met Ala Glu Ala Leu Arg Phe Gly Phe
Asp Asp His Ser Met Met Met Leu Pro Ser Asp Asp Asp Tyr Ala
Leu Glu Leu Ser Gly Trp Glu Glu Ile Gln His Glu Ser Leu Trp Asp
Ser Pro Glu Tyr Met
210

<210> 422
<211> 944
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (138)..(704)

<400> 422
gacccccgga aaaagaaaag aaaagaaact cacagctatt gaatttcact tcacttcact      60

tgcatgccaa atgaaaacaa cctcttccca gaatcttgtc ggtatttaac tccttcgatt      120

tcacaacacc aataaca atg aga gtt tca aca gag aca gag ccg gag act      170
Met Arg Val Ser Thr Glu Thr Glu Pro Glu Thr
1 5 10
aaa aag ata aaa cgc att cgc ggc ggc gac tcg agc aag cac cct      218
Lys Lys Ile Lys Arg Ile Arg Gly Gly Asp Ser Ser Lys His Pro
15 20 25
ttg tac cgc ggc gtg cgg atg cgg aac tgg ggc aag tgg gtg tcg gaa      266
Leu Tyr Arg Gly Val Arg Met Arg Asn Trp Gly Lys Trp Val Ser Glu
30 35 40
atc cgc gag ccg agg aag aaa tcg cgg ata tgg cta ggc aca ttc ccc      314
Ile Arg Glu Pro Arg Lys Lys Ser Arg Ile Trp Leu Gly Thr Phe Pro
45 50 55
acg ccg gaa atg gcg gcg aga gcg cac gac gtc gcc gct ctc agc atc      362
Thr Pro Glu Met Ala Arg Ala His Asp Val Ala Ala Leu Ser Ile
60 65 70 75
aaa ggc ccc gcc gcc att ctc aac ttc cct cac ttg gcc aac tcg ctc      410
Lys Gly Pro Ala Ala Ile Leu Asn Phe Pro His Leu Ala Asn Ser Leu
80 85 90
ccc cgc ccg gct tcg ctg gcg ccg cgc gac gtt caa gct gcg gcg gcg      458
Pro Arg Pro Ala Ser Leu Ala Pro Arg Asp Val Gln Ala Ala Ala Ala
95 100 105
aag gcg gcg cac atg gac cct tcc tcc ctc tcc tcc ttg gtc tcc gca      506
Lys Ala Ala His Met Asp Pro Ser Ser Leu Ser Ser Leu Val Ser Ala
110 115 120
atg gac ttg tcc tct gcc tct gac gag ttg agc caa atc ata gag ctt      554
Met Asp Leu Ser Ser Ala Ser Asp Glu Leu Ser Gln Ile Ile Glu Leu
125 130 135
cct tct ttg gaa agc acc gat gat ggc tct gtt gac tta aag aag gag      602
Pro Ser Leu Glu Ser Thr Asp Asp Gly Ser Val Asp Leu Lys Lys Glu
140 145 150 155
ttt gtt ttt gtt gat tcc ctt gat gct tgg atg tat cag cca ccc ttt      650
Phe Val Phe Val Asp Ser Leu Asp Ala Trp Met Tyr Gln Pro Pro Phe
160 165 170
ggt ttt gac acc gaa caa gac act ggt ttc gag ggt ttg atg tgg aat      698
Gly Phe Asp Thr Glu Gln Asp Thr Gly Phe Glu Gly Leu Met Trp Asn
175 180 185
tac taggttcgat ccaagtttct attctatgtc ttgtgtttgt ataaatttat      751
Tyr

atcgatctct tttatgtttt ggtttgtgtg tgtctataag cagtaagcag ccacttgtgg      811

tttttctttc gggggctgcc agtgctactg atcactctcg tattcatcat catgtctctg      871

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PF59082SeqList_PF59082.txt

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agaaattttc tgt 944

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<211> 188
<212> PRT
<213> Glycine max

<400> 423
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1 5 10 15
Ile Arg Gly Gly Gly Asp Ser Ser Lys His Pro Leu Tyr Arg Gly Val
20 25 30
Arg Met Arg Asn Trp Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Arg
35 40 45
Lys Lys Ser Arg Ile Trp Leu Gly Thr Phe Pro Thr Pro Glu Met Ala
50 55 60
Ala Arg Ala His Asp Val Ala Ala Leu Ser Ile Lys Gly Pro Ala Ala
65 70 75 80
Ile Leu Asn Phe Pro His Leu Ala Asn Ser Leu Pro Arg Pro Ala Ser
85 90 95
Leu Ala Pro Arg Asp Val Gln Ala Ala Ala Lys Ala Ala His Met
100 105 110
Asp Pro Ser Ser Leu Ser Ser Leu Val Ser Ala Met Asp Leu Ser Ser
115 120 125
Ala Ser Asp Glu Leu Ser Gln Ile Ile Glu Leu Pro Ser Leu Glu Ser
130 135 140
Thr Asp Asp Gly Ser Val Asp Leu Lys Lys Glu Phe Val Phe Val Asp
145 150 155 160
Ser Leu Asp Ala Trp Met Tyr Gln Pro Pro Phe Gly Phe Asp Thr Glu
165 170 175
Gln Asp Thr Gly Phe Glu Gly Leu Met Trp Asn Tyr
180 185

<210> 424
<211> 919
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (274)..(858)

<220>
<221> misc_feature
<222> (899)..(899)
<223> w i s a o r t

<400> 424
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catttttttc tctctggtgg gtcccatcct cttctgctct gagaaccttt ataagtgtta 120

tatgagtcac tgagaagtga cccagggaaa aagaaaagaa aagaaaaact tcacttcact 180

tgcatgccaa atgagaacaa cctcttctta gaataatttc ctcggtgttt aagccttgtc 240

gatttccgaa caccaatccg agttaattaa aca atg aga gtt tcg aca gaa aag 294
Met Arg Val Ser Thr Glu Lys
Seite 592

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tta	gag	aca	gag	ccg	gag	agc	aaa	aag	ata	aaa	cgc	att	cgt	ggc	ggc	342
Leu	Glu	Thr	Glu	Pro	Glu	Ser	Lys	Lys	Ile	Lys	Arg	Ile	Arg	Gly	Gly	
		10					15					20				
ggc	ggc	ggg	gac	tcg	agc	aat	aag	cac	cct	ttg	tac	cgc	ggc	gtg	cgg	390
Gly	Gly	Gly	Asp	Ser	Ser	Asn	Lys	His	Pro	Leu	Tyr	Arg	Gly	Val	Arg	
	25					30					35					
atg	cgg	aac	tgg	ggg	aaa	tgg	gtg	tcg	gaa	atc	cgc	gag	ccg	cgg	aag	438
Met	Arg	Asn	Trp	Gly	Lys	Trp	Val	Ser	Glu	Ile	Arg	Glu	Pro	Arg	Lys	
	40				45					50					55	
aag	tcg	cgg	ata	tgg	cta	ggc	aca	ttc	ccg	acg	ccg	gaa	atg	gcg	gcg	486
Lys	Ser	Arg	Ile	Trp	Leu	Gly	Thr	Phe	Pro	Thr	Pro	Glu	Met	Ala	Ala	
			60					65						70		
agg	gcg	cac	gac	gtg	gcg	gct	ctc	agc	atc	aaa	ggc	tcc	gcc	gcc	att	534
Arg	Ala	His	Asp	Val	Ala	Ala	Leu	Ser	Ile	Lys	Gly	Ser	Ala	Ala	Ile	
			75					80					85			
ctc	aac	ttc	cct	cac	ttt	gcc	aac	tcg	ctc	cct	cgc	ccg	gct	tct	ctc	582
Leu	Asn	Phe	Pro	His	Phe	Ala	Asn	Ser	Leu	Pro	Arg	Pro	Ala	Ser	Leu	
	90					95					100					
gcg	ccg	cgc	gac	ggt	caa	gcc	gcg	gcg	gcc	aaa	gcg	gcg	cac	atg	gac	630
Ala	Pro	Arg	Asp	Val	Gln	Ala	Ala	Ala	Ala	Lys	Ala	Ala	His	Met	Asp	
	105				110						115					
cct	tct	tcc	ctc	tcc	tcc	ctt	gtc	tcc	gca	atg	gac	ttg	tcc	tct	gcc	678
Pro	Ser	Ser	Leu	Ser	Ser	Leu	Val	Ser	Ala	Met	Asp	Leu	Ser	Ser	Ala	
	120				125					130					135	
tct	gac	gag	ttg	agc	caa	atc	ata	gag	ctt	cct	tct	ttg	gaa	agc	acc	726
Ser	Asp	Glu	Leu	Ser	Gln	Ile	Ile	Glu	Leu	Pro	Ser	Leu	Glu	Ser	Thr	
			140					145						150		
gat	gat	ggc	tcc	gtc	gtc	tta	gag	aaa	gag	ttt	ggt	ttt	ggt	gac	tcc	774
Asp	Asp	Gly	Ser	Val	Val	Leu	Glu	Lys	Glu	Phe	Val	Phe	Val	Asp	Ser	
			155					160					165			
ctt	gat	gct	tgg	atg	tat	cag	cca	ccc	ttt	ggt	ttt	gac	acc	gaa	caa	822
Leu	Asp	Ala	Trp	Met	Tyr	Gln	Pro	Pro	Phe	Gly	Phe	Asp	Thr	Glu	Gln	
		170				175						180				
gac	act	ggt	ttc	gag	ggt	ttg	atg	tgg	aat	tac	tagtttcgat	ccatgtttct				875
Asp	Thr	Gly	Phe	Glu	Gly	Leu	Met	Trp	Asn	Tyr						
	185				190											
gttctattct	atgtcttatg	ttgwataaat	taatattgat	cgtc												919

<210> 425
 <211> 194
 <212> PRT
 <213> Glycine max

<400> 425
 Met Arg Val Ser Thr Glu Lys Leu Glu Thr Glu Pro Glu Ser Lys Lys
 1 5 10 15
 Ile Lys Arg Ile Arg Gly Gly Gly Gly Asp Ser Ser Asn Lys His
 20 25 30
 Pro Leu Tyr Arg Gly Val Arg Met Arg Asn Trp Gly Lys Trp Val Ser
 35 40 45
 Glu Ile Arg Glu Pro Arg Lys Lys Ser Arg Ile Trp Leu Gly Thr Phe
 50 55 60
 Pro Thr Pro Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Ser
 65 70 75 80
 Ile Lys Gly Ser Ala Ala Ile Leu Asn Phe Pro His Phe Ala Asn Ser
 85 90 95
 Leu Pro Arg Pro Ala Ser Leu Ala Pro Arg Asp Val Gln Ala Ala Ala
 100 105 110
 Ala Lys Ala Ala His Met Asp Pro Ser Ser Leu Ser Ser Leu Val Ser
 115 120 125
 Ala Met Asp Leu Ser Ser Ala Ser Asp Glu Leu Ser Gln Ile Ile Glu
 130 135 140
 Leu Pro Ser Leu Glu Ser Thr Asp Asp Gly Ser Val Val Leu Glu Lys
 145 150 155 160
 Glu Phe Val Phe Val Asp Ser Leu Asp Ala Trp Met Tyr Gln Pro Pro
 165 170 175

PF59082SeqList_PF59082.txt

Phe Gly Phe Asp Thr Glu Gln Asp Thr Gly Phe Glu Gly Leu Met Trp
 180 185 190
 Asn Tyr

<210> 426
 <211> 585
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (1)..(585)

<400> 426
 atg aga gtt tcg aca gaa aag tta gag aca gag ccg gag agc aaa aag 48
 Met Arg Val Ser Thr Glu Lys Leu Glu Thr Glu Pro Glu Ser Lys Lys
 1 5 10 15
 ata aaa cgc att cgt ggc ggc ggc ggc ggc gac tcg agc aat aag cac 96
 Ile Lys Arg Ile Arg Gly Gly Gly Gly Gly Asp Ser Ser Asn Lys His
 20 25 30
 cct ttg tac cgc ggc gtg cgg atg cgg aac tgg ggg aaa tgg gtg tcg 144
 Pro Leu Tyr Arg Gly Val Arg Met Arg Asn Trp Gly Lys Trp Val Ser
 35 40 45
 gaa atc cgc gag ccg cgg aag aag tcg cgg ata tgg cta ggc aca ttc 192
 Glu Ile Arg Glu Pro Arg Lys Lys Ser Arg Ile Trp Leu Gly Thr Phe
 50 55 60
 ccg acg ccg gaa atg gcg gcg agg gcg cac gac gtg gcg gct ctc agc 240
 Pro Thr Pro Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Ser
 65 70 75 80
 atc aaa ggc tcc gcc gcc att ctc aac ttc cct cac ttt gcc aac tcg 288
 Ile Lys Gly Ser Ala Ala Ile Leu Asn Phe Pro His Phe Ala Asn Ser
 85 90 95
 ctc cct cgc ccg gct tct ctc gcg ccg cgc gac gtt caa gcc gcg gcg 336
 Leu Pro Arg Pro Ala Ser Leu Ala Pro Arg Asp Val Gln Ala Ala Ala
 100 105 110
 gcc aaa gcg gcg cac atg gac cct tct tcc ctc tcc tcc ctt gtc tcc 384
 Ala Lys Ala Ala His Met Asp Pro Ser Ser Leu Ser Ser Leu Val Ser
 115 120 125
 gca atg gac ttg tcc tct gcc tct gac gag ttg agc caa atc ata gag 432
 Ala Met Asp Leu Ser Ser Ala Ser Asp Glu Leu Ser Gln Ile Ile Glu
 130 135 140
 ctt cct tct ttg gaa agc acc gat gat ggc tcc gtc gtc tta aag aaa 480
 Leu Pro Ser Leu Glu Ser Thr Asp Asp Gly Ser Val Val Leu Lys Lys
 145 150 155 160
 gag ttt gtt ttt gtt gac tcc ctt gat gct tgg atg tat cag cca ccc 528
 Glu Phe Val Phe Val Asp Ser Leu Asp Ala Trp Met Tyr Gln Pro Pro
 165 170 175
 ttt ggt ttt gac acc gaa caa gac act ggt ttc gag ggt ttg atg tgg 576
 Phe Gly Phe Asp Thr Glu Gln Asp Thr Gly Phe Glu Gly Leu Met Trp
 180 185 190
 aat tac tag 585
 Asn Tyr

<210> 427
 <211> 194
 <212> PRT
 <213> Glycine max

<400> 427
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 1 5 10 15
 Ile Lys Arg Ile Arg Gly Gly Gly Gly Gly Asp Ser Ser Asn Lys His
 20 25 30
 Pro Leu Tyr Arg Gly Val Arg Met Arg Asn Trp Gly Lys Trp Val Ser
 35 40 45
 Glu Ile Arg Glu Pro Arg Lys Lys Ser Arg Ile Trp Leu Gly Thr Phe
 50 55 60

PF59082SeqList_PF59082.txt

Pro Thr Pro Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Ser
65 70 75 80
Ile Lys Gly Ser Ala Ala Ile Leu Asn Phe Pro His Phe Ala Asn Ser
85 90 95
Leu Pro Arg Pro Ala Ser Leu Ala Pro Arg Asp Val Gln Ala Ala Ala
100 105 110
Ala Lys Ala Ala His Met Asp Pro Ser Ser Leu Ser Ser Leu Val Ser
115 120 125
Ala Met Asp Leu Ser Ser Ala Ser Asp Glu Leu Ser Gln Ile Ile Glu
130 135 140
Leu Pro Ser Leu Glu Ser Thr Asp Asp Gly Ser Val Val Leu Lys Lys
145 150 155 160
Glu Phe Val Phe Val Asp Ser Leu Asp Ala Trp Met Tyr Gln Pro Pro
165 170 175
Phe Gly Phe Asp Thr Glu Gln Asp Thr Gly Phe Glu Gly Leu Met Trp
180 185 190
Asn Tyr

<210> 428
<211> 702
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (1)..(702)

<400> 428
atg gtc gag cct gca gta gca gca agc tca gaa tta tca gac tca aca 48
Met Val Glu Pro Ala Val Ala Ala Ser Ser Glu Leu Ser Asp Ser Thr
1 5 10 15
cga aac acc aac acc aac acc cct tca ccc tct tcc tca tcg tcg tta 96
Arg Asn Thr Asn Thr Asn Thr Pro Ser Pro Ser Ser Ser Ser Leu
20 25 30
tct ccg tcg cca tca ccg tca tca tca agc tct aaa aag cga gcg aga 144
Ser Pro Ser Pro Ser Pro Ser Ser Ser Ser Ser Lys Lys Arg Ala Arg
35 40 45
gac aac aac aat agt aga aac aac agc aac aag cat tct gtg tat aga 192
Asp Asn Asn Asn Ser Arg Asn Asn Ser Asn Lys His Ser Val Tyr Arg
50 55 60
ggg gtc cga atg cgc acg tgg ggc aaa tgg gtg tcg gaa atc cgc gag 240
Gly Val Arg Met Arg Thr Trp Gly Lys Trp Val Ser Glu Ile Arg Glu
65 70 75 80
ccg cga aag aag aac cga atc tgg ctc ggc acc ttc gcc acc gcc gag 288
Pro Arg Lys Lys Asn Arg Ile Trp Leu Gly Thr Phe Ala Thr Ala Glu
85 90 95
atg gcg gcg cgt gcc cac gac gtg gcg gcg ctg acg ata aaa ggc tca 336
Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Thr Ile Lys Gly Ser
100 105 110
tcc gcc atc ctt aac ttc ccc gaa ctc gcc gcc tcc ctg ccc cgg ccg 384
Ser Ala Ile Leu Asn Phe Pro Glu Leu Ala Ala Ser Leu Pro Arg Pro
115 120 125
gcc tcc aac tcg ccc cgc gac gtg cag gcc gcg gca gcc aag gcg gcg 432
Ala Ser Asn Ser Pro Arg Asp Val Gln Ala Ala Ala Lys Ala Ala
130 135 140
tcc atg gag gcg ccg ccg cgg acc cct ccg tcg ccg gcc gcc acc ccg 480
Ser Met Glu Ala Pro Pro Arg Thr Pro Pro Ser Pro Ala Ala Thr Pro
145 150 155 160
gag gat gac ctc ggc gag atc gtg gag ctg ccg ctc gga acg agt 528
Glu Asp Asp Leu Gly Glu Ile Val Glu Leu Pro Pro Leu Gly Thr Ser
165 170 175
ttc gac tcg ccc gac cgg agt tcc gag ttt gtg ttc ctg gac atg gac 576
Phe Asp Ser Pro Asp Arg Ser Ser Glu Phe Val Phe Leu Asp Met Asp
180 185 190
gac ggg tgg ccc tat tct cac ccg tgg tac cac agc att tat gat ggt 624
Asp Gly Trp Pro Tyr Ser His Pro Trp Tyr His Ser Ile Tyr Asp Gly
195 200 205
ggg tac ttc att agc gac atg aac aac atg gtt tcg atg caa gag tca 672

PF59082SeqList_PF59082.txt

Gly Tyr Phe Ile Ser Asp Met Asn Asn Met Val Ser Met Gln Glu Ser
 210 215 220
 gag agc atg gtt ctt tcc ctg tgg cct tga
 Glu Ser Met Val Leu Ser Leu Trp Pro
 225 230

702

<210> 429
 <211> 233
 <212> PRT
 <213> Glycine max

<400> 429
 Met Val Glu Pro Ala Val Ala Ala Ser Ser Glu Leu Ser Asp Ser Thr
 1 5 10 15
 Arg Asn Thr Asn Thr Asn Thr Pro Ser Ser Ser Ser Ser Leu
 20 25 30
 Ser Pro Ser Pro Ser Pro Ser Ser Ser Ser Lys Lys Arg Ala Arg
 35 40 45
 Asp Asn Asn Asn Ser Arg Asn Asn Ser Asn Lys His Ser Val Tyr Arg
 50 55 60
 Gly Val Arg Met Arg Thr Trp Gly Lys Trp Val Ser Glu Ile Arg Glu
 65 70 75 80
 Pro Arg Lys Lys Asn Arg Ile Trp Leu Gly Thr Phe Ala Thr Ala Glu
 85 90 95
 Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Thr Ile Lys Gly Ser
 100 105 110
 Ser Ala Ile Leu Asn Phe Pro Glu Leu Ala Ala Ser Leu Pro Arg Pro
 115 120 125
 Ala Ser Asn Ser Pro Arg Asp Val Gln Ala Ala Ala Lys Ala Ala
 130 135 140
 Ser Met Glu Ala Pro Pro Arg Thr Pro Pro Ser Pro Ala Ala Thr Pro
 145 150 155 160
 Glu Asp Asp Leu Gly Glu Ile Val Glu Leu Pro Pro Leu Gly Thr Ser
 165 170 175
 Phe Asp Ser Pro Asp Arg Ser Ser Glu Phe Val Phe Leu Asp Met Asp
 180 185 190
 Asp Gly Trp Pro Tyr Ser His Pro Trp Tyr His Ser Ile Tyr Asp Gly
 195 200 205
 Gly Tyr Phe Ile Ser Asp Met Asn Asn Met Val Ser Met Gln Glu Ser
 210 215 220
 Glu Ser Met Val Leu Ser Leu Trp Pro
 225 230

<210> 430
 <211> 570
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (1)..(570)

<400> 430
 atg aga gtt tcg aca gaa aag tta gag aca gag ccg gag agc aaa aag 48
 Met Arg Val Ser Thr Glu Lys Leu Glu Thr Glu Pro Glu Ser Lys Lys
 1 5 10 15
 ata aaa cgc att cgt ggc ggc ggc ggc ggc gac tcg agc aat aag cac 96
 Ile Lys Arg Ile Arg Gly Gly Gly Gly Gly Asp Ser Ser Asn Lys His
 20 25 30
 cct ttg tac cgc ggc gtg cgg atg cgg aac tgg ggc aaa tgg gtg tcg 144
 Pro Leu Tyr Arg Gly Val Arg Met Arg Asn Trp Gly Lys Trp Val Ser
 35 40 45
 gaa atc cgc gag ccg cgg aag aag tcg cgg ata tgg cta ggc aca ttc 192
 Glu Ile Arg Glu Pro Arg Lys Lys Ser Arg Ile Trp Leu Gly Thr Phe
 50 55 60
 ccg acg ccg gaa atg gcg gcg agg gcg cac gac gtg gcg gct ctc agc 240
 Pro Thr Pro Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Ser
 65 70 75 80
 atc aaa ggc tcc gcc gcc att ctc aac ttc cct cac ttt gcc aac tcg 288

PF59082SeqList_PF59082.txt

Ile	Lys	Gly	Ser	Ala	Ala	Ile	Leu	Asn	Phe	Pro	His	Phe	Ala	Asn	Ser		
				85					90					95			
ctc	cct	cgc	ccg	gct	tct	ctc	gcg	ccg	cgc	gac	gtt	caa	gcc	gcg	gcg		336
Leu	Pro	Arg	Pro	Ala	Ser	Leu	Ala	Pro	Arg	Asp	Val	Gln	Ala	Ala	Ala		
			100					105					110				
gcc	aaa	gcg	gcg	cac	atg	gac	cct	tct	tcc	ctc	tcc	tcc	ctt	gtc	tcc		384
Ala	Lys	Ala	Ala	His	Met	Asp	Pro	Ser	Ser	Leu	Ser	Ser	Leu	Val	Ser		
		115					120					125					
gca	atg	gac	ttg	tcc	tct	gcc	tct	gac	gag	ttg	agc	caa	atc	ata	gag		432
Ala	Met	Asp	Leu	Ser	Ser	Ala	Ser	Asp	Glu	Leu	Ser	Gln	Ile	Ile	Glu		
		130				135					140						
ctt	cct	tct	ttg	gaa	agc	acc	gat	gat	ggc	tcc	gtc	gtc	tta	gag	aaa		480
Leu	Pro	Ser	Leu	Glu	Ser	Thr	Asp	Asp	Gly	Ser	Val	Val	Leu	Glu	Lys		
145					150				155						160		
gag	ttt	gtt	ttt	gtt	gac	tcc	ctt	gat	gct	tgg	atg	tat	cag	cca	ccc		528
Glu	Phe	Val	Phe	Val	Asp	Ser	Leu	Asp	Ala	Trp	Met	Tyr	Gln	Pro	Pro		
			165					170						175			
ttt	ggt	ttt	gac	acc	gaa	caa	gac	act	ggt	ttc	gag	gtt	tga				570
Phe	Gly	Phe	Asp	Thr	Glu	Gln	Asp	Thr	Gly	Phe	Glu	Val					
			180					185									

<210> 431
 <211> 189
 <212> PRT
 <213> Glycine max

<400> 431																	
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Ile	Lys	Arg	Ile	Arg	Gly	Gly	Gly	Gly	Gly	Asp	Ser	Ser	Asn	Lys	His		
			20					25					30				
Pro	Leu	Tyr	Arg	Gly	Val	Arg	Met	Arg	Asn	Trp	Gly	Lys	Trp	Val	Ser		
		35				40						45					
Glu	Ile	Arg	Glu	Pro	Arg	Lys	Lys	Ser	Arg	Ile	Trp	Leu	Gly	Thr	Phe		
	50					55				60							
Pro	Thr	Pro	Glu	Met	Ala	Ala	Arg	Ala	His	Asp	Val	Ala	Ala	Leu	Ser		
65					70				75					80			
Ile	Lys	Gly	Ser	Ala	Ala	Ile	Leu	Asn	Phe	Pro	His	Phe	Ala	Asn	Ser		
			85					90						95			
Leu	Pro	Arg	Pro	Ala	Ser	Leu	Ala	Pro	Arg	Asp	Val	Gln	Ala	Ala	Ala		
			100					105				110					
Ala	Lys	Ala	Ala	His	Met	Asp	Pro	Ser	Ser	Leu	Ser	Ser	Leu	Val	Ser		
		115				120						125					
Ala	Met	Asp	Leu	Ser	Ser	Ala	Ser	Asp	Glu	Leu	Ser	Gln	Ile	Ile	Glu		
	130					135				140							
Leu	Pro	Ser	Leu	Glu	Ser	Thr	Asp	Asp	Gly	Ser	Val	Val	Leu	Glu	Lys		
145					150				155						160		
Glu	Phe	Val	Phe	Val	Asp	Ser	Leu	Asp	Ala	Trp	Met	Tyr	Gln	Pro	Pro		
			165					170						175			
Phe	Gly	Phe	Asp	Thr	Glu	Gln	Asp	Thr	Gly	Phe	Glu	Val					
			180					185									

<210> 432
 <211> 567
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (1)..(567)

<400> 432																	
atg	gct	tct	gcc	ggc	tta	ggt	agc	cgg	aga	aag	gat	ccg	gtg	tac	aga		48
Met	Ala	Ser	Ala	Gly	Leu	Gly	Ser	Arg	Arg	Lys	Asp	Pro	Val	Tyr	Arg		
1				5					10					15			
gga	atc	cgg	tgc	cga	agt	ggg	aaa	tgg	gtc	tcc	gag	att	cgt	gag	ccg		96
Gly	Ile	Arg	Cys	Arg	Ser	Gly	Lys	Trp	Val	Ser	Glu	Ile	Arg	Glu	Pro		
			20					25					30				
agg	aaa	acc	acg	aga	atc	tgg	ctt	gga	act	tac	ccc	atg	gca	gag	atg		144

PF59082SeqList_PF59082.txt

Arg	Lys	Thr	Thr	Arg	Ile	Trp	Leu	Gly	Thr	Tyr	Pro	Met	Ala	Glu	Met	
		35					40					45				
gca	gca	gcc	gcc	tat	gat	gtg	gct	gct	atg	gct	ctt	aaa	gga	aga	gaa	192
Ala	Ala	Ala	Ala	Tyr	Asp	Val	Ala	Ala	Met	Ala	Leu	Lys	Gly	Arg	Glu	
	50					55					60					
gct	gtc	ttg	aac	ttc	cct	gga	tcc	gtc	ggg	tca	tac	ccg	gtt	cct	gaa	240
Ala	Val	Leu	Asn	Phe	Pro	Gly	Ser	Val	Gly	Ser	Tyr	Pro	Val	Pro	Glu	
	65				70				75						80	
tca	aca	tcc	gca	gca	gat	ata	cga	gcc	gct	gcg	gca	gcc	gca	gca	gca	288
Ser	Thr	Ser	Ala	Ala	Asp	Ile	Arg	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	
				85				90						95		
atg	aag	gga	tgt	gag	gaa	ggg	gag	gag	gag	aaa	aag	gca	aag	gag	aag	336
Met	Lys	Gly	Cys	Glu	Glu	Gly	Glu	Glu	Glu	Lys	Lys	Ala	Lys	Glu	Lys	
		100				105						110				
aag	agt	agt	agt	tcg	aag	tcg	aga	gcg	cgt	gag	tgc	cac	gta	gat	aat	384
Lys	Ser	Ser	Ser	Ser	Lys	Ser	Arg	Ala	Arg	Glu	Cys	His	Val	Asp	Asn	
		115				120						125				
gat	gtt	gga	tct	tcg	tcg	tgg	tgt	ggg	aca	gag	ttc	atg	gac	gaa	gaa	432
Asp	Val	Gly	Ser	Ser	Ser	Trp	Cys	Gly	Thr	Glu	Phe	Met	Asp	Glu	Glu	
	130					135					140					
gaa	gtc	ttg	aat	atg	cct	aat	ctg	ctg	gct	aat	atg	gca	gaa	ggg	atg	480
Glu	Val	Leu	Asn	Met	Pro	Asn	Leu	Leu	Ala	Asn	Met	Ala	Glu	Gly	Met	
	145				150				155						160	
atg	gtt	gcg	ccg	ccg	tcg	tgg	atg	ggg	tct	cgg	ccg	tcg	gat	gac	tct	528
Met	Val	Ala	Pro	Pro	Ser	Trp	Met	Gly	Ser	Arg	Pro	Ser	Asp	Asp	Ser	
			165					170						175		
ccg	gag	aat	tca	aat	gat	gag	gac	ttg	tgg	ggc	tat	tga				567
Pro	Glu	Asn	Ser	Asn	Asp	Glu	Asp	Leu	Trp	Gly	Tyr					
			180					185								

<210> 433

<211> 188

<212> PRT

<213> Arabidopsis thaliana

<400> 433

Met	Ala	Ser	Ala	Gly	Leu	Gly	Ser	Arg	Arg	Lys	Asp	Pro	Val	Tyr	Arg	
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Gly	Ile	Arg	Cys	Arg	Ser	Gly	Lys	Trp	Val	Ser	Glu	Ile	Arg	Glu	Pro	
			20					25					30			
Arg	Lys	Thr	Thr	Arg	Ile	Trp	Leu	Gly	Thr	Tyr	Pro	Met	Ala	Glu	Met	
		35					40					45				
Ala	Ala	Ala	Ala	Tyr	Asp	Val	Ala	Ala	Met	Ala	Leu	Lys	Gly	Arg	Glu	
	50					55					60					
Ala	Val	Leu	Asn	Phe	Pro	Gly	Ser	Val	Gly	Ser	Tyr	Pro	Val	Pro	Glu	
	65				70					75					80	
Ser	Thr	Ser	Ala	Ala	Asp	Ile	Arg	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	
				85				90						95		
Met	Lys	Gly	Cys	Glu	Glu	Gly	Glu	Glu	Lys	Lys	Ala	Lys	Glu	Lys		
		100						105				110				
Lys	Ser	Ser	Ser	Ser	Lys	Ser	Arg	Ala	Arg	Glu	Cys	His	Val	Asp	Asn	
		115					120					125				
Asp	Val	Gly	Ser	Ser	Ser	Trp	Cys	Gly	Thr	Glu	Phe	Met	Asp	Glu	Glu	
	130					135					140					
Glu	Val	Leu	Asn	Met	Pro	Asn	Leu	Leu	Ala	Asn	Met	Ala	Glu	Gly	Met	
	145				150				155						160	
Met	Val	Ala	Pro	Pro	Ser	Trp	Met	Gly	Ser	Arg	Pro	Ser	Asp	Asp	Ser	
			165					170						175		
Pro	Glu	Asn	Ser	Asn	Asp	Glu	Asp	Leu	Trp	Gly	Tyr					
			180					185								

<210> 434

<211> 435

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(435)

PF59082SeqList_PF59082.txt

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<400> 434
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Met Asp Tyr Arg Glu Ser Thr Gly Glu Ser Gln Ser Lys Tyr Lys Gly
1      5      10      15
atc cgt cgt cgg aaa tgg ggc aaa tgg gta tca gag att aga gtt ccg      96
Ile Arg Arg Arg Lys Trp Gly Lys Trp Val Ser Glu Ile Arg Val Pro
20      25      30
gga act cgt gac cgt ctc tgg tta ggt tca ttc tca aca gca gaa ggt      144
Gly Thr Arg Asp Arg Leu Trp Leu Gly Ser Phe Ser Thr Ala Glu Gly
35      40      45
gcc gcc gta gca cac gac gtt gct ttc ttc tgt tta cac caa cct gat      192
Ala Ala Val Ala His Asp Val Ala Phe Phe Cys Leu His Gln Pro Asp
50      55      60
tct tta gaa tct ctc aat ttc cct cat ttg ctt aat cct tca ctc gtt      240
Ser Leu Glu Ser Leu Asn Phe Pro His Leu Leu Asn Pro Ser Leu Val
65      70      75      80
tcc aga act tct ccg aga tct atc cag caa gct gct tct aac gcc ggc      288
Ser Arg Thr Ser Pro Arg Ser Ile Gln Gln Ala Ala Ser Asn Ala Gly
85      90      95
atg gcc att gac gcc gga atc gtc cac agt acc agc gtg aac tct gga      336
Met Ala Ile Asp Ala Gly Ile Val His Ser Thr Ser Val Asn Ser Gly
100      105      110
tgc gga gat acg acg acg tat tac gag aat gga gct gat caa gtg gag      384
Cys Gly Asp Thr Thr Thr Tyr Tyr Glu Asn Gly Ala Asp Gln Val Glu
115      120      125
ccg ttg aat att tca gtg tat gat tat ctg ggc ggc cac gat cac gtt      432
Pro Leu Asn Ile Ser Val Tyr Asp Tyr Leu Gly Gly His Asp His Val
130      135      140
tga
435

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<210> 435
<211> 144
<212> PRT
<213> Arabidopsis thaliana

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<400> 435
Met Asp Tyr Arg Glu Ser Thr Gly Glu Ser Gln Ser Lys Tyr Lys Gly
1      5      10      15
Ile Arg Arg Arg Lys Trp Gly Lys Trp Val Ser Glu Ile Arg Val Pro
20      25      30
Gly Thr Arg Asp Arg Leu Trp Leu Gly Ser Phe Ser Thr Ala Glu Gly
35      40      45
Ala Ala Val Ala His Asp Val Ala Phe Phe Cys Leu His Gln Pro Asp
50      55      60
Ser Leu Glu Ser Leu Asn Phe Pro His Leu Leu Asn Pro Ser Leu Val
65      70      75      80
Ser Arg Thr Ser Pro Arg Ser Ile Gln Gln Ala Ala Ser Asn Ala Gly
85      90      95
Met Ala Ile Asp Ala Gly Ile Val His Ser Thr Ser Val Asn Ser Gly
100      105      110
Cys Gly Asp Thr Thr Thr Tyr Tyr Glu Asn Gly Ala Asp Gln Val Glu
115      120      125
Pro Leu Asn Ile Ser Val Tyr Asp Tyr Leu Gly Gly His Asp His Val
130      135      140

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<210> 436
<211> 552
<212> DNA
<213> Arabidopsis thaliana

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<220>
<221> CDS
<222> (1)..(552)

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<400> 436
atg gct ggt ctt agg aat tcc ggt aac agc gac aaa gcg caa aac gat      48

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PF59082SeqList_PF59082.txt

Met	Ala	Gly	Leu	Arg	Asn	Ser	Gly	Asn	Ser	Asp	Lys	Ala	Gln	Asn	Asp	
1				5				10					15			
ggc	aaa	ggt	gta	cca	tct	gcc	tac	aga	gga	gtc	cgg	aag	aga	aaa	tgg	96
Gly	Lys	Gly	Val	Pro	Ser	Ala	Tyr	Arg	Gly	Val	Arg	Lys	Arg	Lys	Trp	
			20					25					30			
ggg	aaa	tgg	gtg	tct	gaa	atc	cgt	gaa	ccg	ggg	acc	aag	aac	cgt	atc	144
Gly	Lys	Trp	Val	Ser	Glu	Ile	Arg	Glu	Pro	Gly	Thr	Lys	Asn	Arg	Ile	
		35					40					45				
tgg	cta	ggc	agt	ttc	gag	act	cct	gaa	atg	gct	gca	acc	gca	tac	gac	192
Trp	Leu	Gly	Ser	Phe	Glu	Thr	Pro	Glu	Met	Ala	Ala	Thr	Ala	Tyr	Asp	
		50				55					60					
gtg	gca	gca	ttt	cat	ttc	aga	ggg	aga	gaa	gct	cgt	ctc	aac	ttc	cct	240
Val	Ala	Ala	Phe	His	Phe	Arg	Gly	Arg	Glu	Ala	Arg	Leu	Asn	Phe	Pro	
65					70		75							80		
gag	ctc	gcc	agc	agc	ctt	cca	cgt	cct	gca	gac	tct	agc	tca	gac	agc	288
Glu	Leu	Ala	Ser	Ser	Leu	Pro	Arg	Pro	Ala	Asp	Ser	Ser	Ser	Asp	Ser	
			85				90							95		
att	cgc	atg	gca	gtt	cat	gag	gca	aca	ctc	tgc	cgc	acc	acc	gaa	gga	336
Ile	Arg	Met	Ala	Val	His	Glu	Ala	Thr	Leu	Cys	Arg	Thr	Thr	Glu	Gly	
			100				105						110			
aca	gag	tca	gcc	atg	caa	gtg	gac	agc	tca	agc	tcc	tcc	aat	gta	gct	384
Thr	Glu	Ser	Ala	Met	Gln	Val	Asp	Ser	Ser	Ser	Ser	Ser	Asn	Val	Ala	
		115				120					125					
cca	aca	atg	gtc	aga	ctc	tcg	ccc	agg	gaa	att	caa	gcg	atc	aac	gag	432
Pro	Thr	Met	Val	Arg	Leu	Ser	Pro	Arg	Glu	Ile	Gln	Ala	Ile	Asn	Glu	
		130				135					140					
tca	act	ttg	gga	tct	cct	act	aca	atg	atg	cat	tca	aca	tac	gac	cct	480
Ser	Thr	Leu	Gly	Ser	Pro	Thr	Thr	Met	Met	His	Ser	Thr	Tyr	Asp	Pro	
145					150					155				160		
atg	gag	ttt	gct	aat	gat	gtg	gag	atg	aat	gct	tgg	gaa	aca	tac	cag	528
Met	Glu	Phe	Ala	Asn	Asp	Val	Glu	Met	Asn	Ala	Trp	Glu	Thr	Tyr	Gln	
			165						170					175		
agt	gac	ttt	ctt	tgg	gac	cct	taa									552
Ser	Asp	Phe	Leu	Trp	Asp	Pro										
			180													

<210> 437

<211> 183

<212> PRT

<213> Arabidopsis thaliana

<400> 437

Met	Ala	Gly	Leu	Arg	Asn	Ser	Gly	Asn	Ser	Asp	Lys	Ala	Gln	Asn	Asp	
1				5				10					15			
Gly	Lys	Gly	Val	Pro	Ser	Ala	Tyr	Arg	Gly	Val	Arg	Lys	Arg	Lys	Trp	
			20					25					30			
Gly	Lys	Trp	Val	Ser	Glu	Ile	Arg	Glu	Pro	Gly	Thr	Lys	Asn	Arg	Ile	
		35					40					45				
Trp	Leu	Gly	Ser	Phe	Glu	Thr	Pro	Glu	Met	Ala	Ala	Thr	Ala	Tyr	Asp	
		50				55					60					
val	Ala	Ala	Phe	His	Phe	Arg	Gly	Arg	Glu	Ala	Arg	Leu	Asn	Phe	Pro	
65					70		75							80		
Glu	Leu	Ala	Ser	Ser	Leu	Pro	Arg	Pro	Ala	Asp	Ser	Ser	Ser	Asp	Ser	
			85				90							95		
Ile	Arg	Met	Ala	Val	His	Glu	Ala	Thr	Leu	Cys	Arg	Thr	Thr	Glu	Gly	
		100					105						110			
Thr	Glu	Ser	Ala	Met	Gln	Val	Asp	Ser	Ser	Ser	Ser	Ser	Asn	Val	Ala	
		115				120						125				
Pro	Thr	Met	Val	Arg	Leu	Ser	Pro	Arg	Glu	Ile	Gln	Ala	Ile	Asn	Glu	
		130				135					140					
Ser	Thr	Leu	Gly	Ser	Pro	Thr	Thr	Met	Met	His	Ser	Thr	Tyr	Asp	Pro	
145					150					155				160		
Met	Glu	Phe	Ala	Asn	Asp	Val	Glu	Met	Asn	Ala	Trp	Glu	Thr	Tyr	Gln	
			165						170					175		
Ser	Asp	Phe	Leu	Trp	Asp	Pro										
			180													

<210> 438

<211> 735

PF59082SeqList_PF59082.txt

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(735)

<400> 438

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1 5 10 15	
gag gag gag gat cat cat cat cac caa caa gac tcc cac cga acc aac	96
Glu Glu Glu Asp His His His His Gln Gln Asp Ser His Arg Thr Asn	
20 25 30	
acc aag aaa cgt gta aga tcc gac ccg ggt tac cga ggc gtc cgg atg	144
Thr Lys Lys Arg Val Arg Ser Asp Pro Gly Tyr Arg Gly Val Arg Met	
35 40 45	
cga acg tgg ggc aaa tgg gtc tcc gag atc cga gag cct cgc aag aag	192
Arg Thr Trp Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Arg Lys Lys	
50 55 60	
agc cga atc tgg cta ggc act ttc tcc aca ccg gaa atg gcg gcg cgt	240
Ser Arg Ile Trp Leu Gly Thr Phe Ser Thr Pro Glu Met Ala Ala Arg	
65 70 75 80	
gca cat gac gca gct gct ctc acc att aaa gga act tcc gcc gtc ctc	288
Ala His Asp Ala Ala Leu Thr Ile Lys Gly Thr Ser Ala Val Leu	
85 90 95	
aac ttc ccg gag ctc gcc act tac ctt ccc cgt cca gct tcc tcc tct	336
Asn Phe Pro Glu Leu Ala Thr Tyr Leu Pro Arg Pro Ala Ser Ser Ser	
100 105 110	
cca cgc gac gtt caa gcc gca gcc gcc gta gcg gcc gcc atg gac ttc	384
Pro Arg Asp Val Gln Ala Ala Ala Val Ala Ala Met Asp Phe	
115 120 125	
tcc ccc tcc tcc tcc tct ctc gta gtc tcc gat cca acc acc gtc atc	432
Ser Pro Ser Ser Ser Ser Leu Val Val Ser Asp Pro Thr Thr Val Ile	
130 135 140	
gcc cca gct gag acg cag ttg tct tcc tcg agc tat tca acg tgt acg	480
Ala Pro Ala Glu Thr Gln Leu Ser Ser Ser Ser Tyr Ser Thr Cys Thr	
145 150 155 160	
tca tcg tcg ttg tca ccg tca agc gaa gaa gct gcg tcg acg gcg gaa	528
Ser Ser Ser Leu Ser Pro Ser Ser Glu Ala Ala Ser Thr Ala Glu	
165 170 175	
gaa cta agc gag ata gtg gag tta ccg agt cta gag acg agt tac gat	576
Glu Leu Ser Glu Ile Val Glu Leu Pro Ser Leu Glu Thr Ser Tyr Asp	
180 185 190	
gag tca ttg agc gag ttt gtg tac gtt gac tcg gcg tat cca cct agt	624
Glu Ser Leu Ser Glu Phe Val Tyr Val Asp Ser Ala Tyr Pro Pro Ser	
195 200 205	
tcg cct tgg tat att aat aat tgt tat agc ttt tat tac cac agc gac	672
Ser Pro Trp Tyr Ile Asn Asn Cys Tyr Ser Phe Tyr Tyr His Ser Asp	
210 215 220	
gaa aat ggc att tcg atg gct gaa cct ttc gac tct tcc aat ttt ggc	720
Glu Asn Gly Ile Ser Met Ala Glu Pro Phe Asp Ser Ser Asn Phe Gly	
225 230 235 240	
ccc ctt ttt cct tag	735
Pro Leu Phe Pro	

<210> 439

<211> 244

<212> PRT

<213> Arabidopsis thaliana

<400> 439

Met Thr Glu Ser Ser Ile Ile Ser Val Lys Gln Ser Ser Pro Val Pro
1 5 10 15
Glu Glu Glu Asp His His His His Gln Gln Asp Ser His Arg Thr Asn
20 25 30
Thr Lys Lys Arg Val Arg Ser Asp Pro Gly Tyr Arg Gly Val Arg Met
35 40 45

PF59082SeqList_PF59082.txt

Arg Thr Trp Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Arg Lys Lys
50 55 60
Ser Arg Ile Trp Leu Gly Thr Phe Ser Thr Pro Glu Met Ala Ala Arg
65 70 75 80
Ala His Asp Ala Ala Leu Thr Ile Lys Gly Thr Ser Ala Val Leu
85 90 95
Asn Phe Pro Glu Leu Ala Thr Tyr Leu Pro Arg Pro Ala Ser Ser Ser
100 105 110
Pro Arg Asp Val Gln Ala Ala Ala Val Ala Ala Met Asp Phe
115 120 125
Ser Pro Ser Ser Ser Leu Val Val Ser Asp Pro Thr Thr Val Ile
130 135 140
Ala Pro Ala Glu Thr Gln Leu Ser Ser Ser Ser Tyr Ser Thr Cys Thr
145 150 155 160
Ser Ser Ser Leu Ser Pro Ser Ser Glu Glu Ala Ala Ser Thr Ala Glu
165 170 175
Glu Leu Ser Glu Ile Val Glu Leu Pro Ser Leu Glu Thr Ser Tyr Asp
180 185 190
Glu Ser Leu Ser Glu Phe Val Tyr Val Asp Ser Ala Tyr Pro Pro Ser
195 200 205
Ser Pro Trp Tyr Ile Asn Asn Cys Tyr Ser Phe Tyr Tyr His Ser Asp
210 215 220
Glu Asn Gly Ile Ser Met Ala Glu Pro Phe Asp Ser Ser Asn Phe Gly
225 230 235 240
Pro Leu Phe Pro

<210> 440

<211> 582

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<221> CDS

<222> (1)..(582)

<400> 440

atg gag caa cgg gcg gcg gcg gcg gcg cag cag cgg cag ggg agg agg	48
Met Glu Gln Arg Ala Ala Ala Ala Ala Gln Gln Arg Gln Gly Arg Arg	
1 5 10 15	
cag agc gcg gcg gcg tgc ggg atc agg cgg gcg agg gcg gag acg cgg	96
Gln Ser Ala Ala Ala Cys Gly Ile Arg Arg Ala Arg Ala Glu Thr Arg	
20 25 30	
cac ccg gtg tac cgc ggc gtg cgg ttc agg gcg ggg aag tgg gtg tcg	144
His Pro Val Tyr Arg Gly Val Phe Arg Ala Gly Lys Trp Val Ser	
35 40 45	
gag atc cgg gag ctc cgg aag ccg agc agg ata tgg ctc ggc acg tac	192
Glu Ile Arg Glu Leu Arg Lys Pro Ser Arg Ile Trp Leu Gly Thr Tyr	
50 55 60	
gcc acc ccc gag atg gcc gcg gcg tac gac gcc gca ctg gcg	240
Ala Thr Pro Glu Met Ala Ala Ala Tyr Asp Ala Ala Ala Leu Ala	
65 70 75 80	
ctg cgc ggg cgc ggc gcg gcg ctc aac ttc ccc gac gcc gcg cgg tcg	288
Leu Arg Gly Arg Gly Ala Ala Leu Asn Phe Pro Asp Ala Ala Arg Ser	
85 90 95	
cgc ccc gcc ccg gcg tcc gcg tcc gcc gac gac gtg cgc gcc gcg gcc	336
Arg Pro Ala Pro Ala Ser Ala Ser Ala Asp Asp Val Arg Ala Ala Ala	
100 105 110	
acc gcc gcc gcc gcc gcg atg gca cac cag gag gag gac gac gac agt	384
Thr Ala Ala Ala Ala Met Ala His Gln Glu Glu Asp Asp Asp Ser	
115 120 125	
cgg cgt cag ctc gag gac ggg ggc ggc ggc ggc ggc gtg gtg gac gag	432
Arg Arg Gln Leu Glu Asp Gly Gly Gly Gly Gly Val Val Asp Glu	
130 135 140	
gac gac gtg ctg gag atg ccg agg ctg atg gtg agc atg gcg gag ggg	480
Asp Asp Val Leu Glu Met Pro Arg Leu Met Val Ser Met Ala Glu Gly	
145 150 155 160	
ctg atg atc agc cca ccg ccg gtg atg ctc ggc ctg cag gcg gac ggc	528
Leu Met Ile Ser Pro Pro Pro Val Met Leu Gly Leu Gln Ala Asp Gly	

PF59082SeqList_PF59082.txt

				165					170					175				
ggt	gga	ata	atg	gac	gag	ggc	ggc	ggc	gtg	gtg	agg	ttg	tgg	gat	cac			
Gly	Gly	Ile	Met	Asp	Glu	Gly	Gly	Gly	Val	Val	Arg	Leu	Trp	Asp	His			576
			180				185						190					
agc	tga																	582
Ser																		

<210> 441
 <211> 193
 <212> PRT
 <213> Oryza sativa (japonica cultivar-group)

<400> 441
 Met Glu Gln Arg Ala Ala Ala Ala Gln Gln Arg Gln Gly Arg Arg
 1 5 10 15
 Gln Ser Ala Ala Ala Cys Gly Ile Arg Arg Ala Arg Ala Glu Thr Arg
 20 25 30
 His Pro Val Tyr Arg Gly Val Arg Phe Arg Ala Gly Lys Trp Val Ser
 35 40 45
 Glu Ile Arg Glu Leu Arg Lys Pro Ser Arg Ile Trp Leu Gly Thr Tyr
 50 55 60
 Ala Thr Pro Glu Met Ala Ala Ala Ala Tyr Asp Ala Ala Ala Leu Ala
 65 70 75 80
 Leu Arg Gly Arg Gly Ala Ala Leu Asn Phe Pro Asp Ala Ala Arg Ser
 85 90 95
 Arg Pro Ala Pro Ala Ser Ala Ser Ala Asp Asp Val Arg Ala Ala Ala
 100 105 110
 Thr Ala Ala Ala Ala Met Ala His Gln Glu Glu Asp Asp Asp Ser
 115 120 125
 Arg Arg Gln Leu Glu Asp Gly Gly Gly Gly Gly Val Val Asp Glu
 130 135 140
 Asp Asp Val Leu Glu Met Pro Arg Leu Met Val Ser Met Ala Glu Gly
 145 150 155 160
 Leu Met Ile Ser Pro Pro Val Met Leu Gly Leu Gln Ala Asp Gly
 165 170 175
 Gly Gly Ile Met Asp Glu Gly Gly Gly Val Val Arg Leu Trp Asp His
 180 185 190
 Ser

<210> 442
 <211> 585
 <212> DNA
 <213> Oryza sativa (japonica cultivar-group)

<220>
 <221> CDS
 <222> (1)..(585)

<400> 442	
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Met Leu Ala Ser Leu Ile Gly Arg Ser Val Met Glu Gln Gln Pro Gln	
1 5 10 15	
cag cag caa gcg gcg gcg ccg gcc atg gcg gcg ggc ggc ggc ggc	96
Gln Gln Gln Ala Ala Ala Pro Ala Met Ala Ala Gly Gly Gly Gly Gly	
20 25 30	
ccg cag tac agg ggg gtg agg cgg cgg aag tgg ggg aag tgg gtg tcg	144
Pro Gln Tyr Arg Gly Val Arg Arg Lys Trp Gly Lys Trp Val Ser	
35 40 45	
gag atc agg cag ccc ggg acc aag gtc cgc atc tgg ctg ggg agc ttc	192
Glu Ile Arg Gln Pro Gly Thr Lys Val Arg Ile Trp Leu Gly Ser Phe	
50 55 60	
gac tcg gcg gag atg gcg gtg gcg cac gac gtc gcg gcg ctg cgg	240
Asp Ser Ala Glu Met Ala Val Ala His Asp Val Ala Ala Leu Arg	
65 70 75 80	
ctg cgc ggg agg gac ggc gcg cag ctc aac ttc ccg ggc tcc gtc ggc	288
Leu Arg Gly Arg Asp Gly Ala Gln Leu Asn Phe Pro Gly Ser Val Gly	
85 90 95	

PF59082SeqList_PF59082.txt

Val	Arg	Arg	Arg	Lys	Trp	Gly	Lys	Trp	Val	Ser	Glu	Ile	Arg	Gln	Pro	
			20					25					30			
ggg	acc	aag	acc	cgc	atc	tgg	ctc	ggg	agc	ttc	gag	tcg	gcg	gag	atg	144
Gly	Thr	Lys	Thr	Arg	Ile	Trp	Leu	Gly	Ser	Phe	Glu	Ser	Ala	Glu	Met	
		35					40					45				
gcg	gcg	gtg	gcg	cac	gac	gtg	gcg	gcg	ctc	cgc	ctg	cgc	ggc	cgc	gac	192
Ala	Ala	Val	Ala	His	Asp	Val	Ala	Ala	Leu	Arg	Leu	Arg	Gly	Arg	Asp	
		50				55					60					
gcg	cag	ctc	aac	ttc	ccg	ggc	tcc	gtc	gac	cgc	ctg	ccc	cgc	ccg	gcc	240
Ala	Gln	Leu	Asn	Phe	Pro	Gly	Ser	Val	Asp	Arg	Leu	Pro	Arg	Pro	Ala	
		65			70				75						80	
agc	tcc	cgc	ccg	ggc	gac	atc	cgc	gcc	gcc	gcg	gcg	gag	gct	gcg	gac	288
Ser	Ser	Arg	Pro	Gly	Asp	Ile	Arg	Ala	Ala	Ala	Ala	Glu	Ala	Ala	Asp	
				85				90						95		
cgg	gtg	cgc	cgc	gag	cct	gcg	ctg	gtc	gtg	gtg	cgc	ggc	gcc	gcc	gcc	336
Arg	Val	Arg	Arg	Glu	Pro	Ala	Leu	Val	Val	Val	Arg	Gly	Ala	Ala	Ala	
			100					105					110			
gcc	gcc	ggc	gag	ctc	gcg	gcg	gtg	agg	tgg	gcc	ggc	ctc	gag	gtc	gag	384
Ala	Ala	Gly	Glu	Leu	Ala	Ala	Val	Arg	Trp	Ala	Gly	Leu	Glu	Val	Glu	
		115					120					125				
gtc	gag	cag	cag	ctg	ggc	ggg	agc	gac	gag	gag	ttc	gag	gtg	gac	tcg	432
Val	Glu	Gln	Gln	Leu	Gly	Gly	Ser	Asp	Glu	Glu	Phe	Glu	Val	Asp	Ser	
		130			135						140					
ccg	agg	ctg	tgg	gcc	gag	atg	gcg	gag	gcc	atg	ctg	ctg	gac	cca	ccg	480
Pro	Arg	Leu	Trp	Ala	Glu	Met	Ala	Glu	Ala	Met	Leu	Leu	Asp	Pro	Pro	
					150				155						160	
gta	tgg	gcc	gtg	gat	gtc	agc	gag	atg	gaa	ggc	cca	cac	tgc	tgg	gcc	528
Val	Trp	Ala	Val	Asp	Val	Ser	Glu	Met	Glu	Gly	Pro	His	Cys	Trp	Ala	
				165				170						175		
cac	ggg	tcc	ttg	tgg	gac	gcc	tgc	taa								555
His	Gly	Ser	Leu	Trp	Asp	Ala	Cys									
			180													

<210> 445

<211> 184

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<400> 445

Met	Ala	Ser	Ala	Ala	Ala	Ala	Gly	Gly	Gly	Cys	Gln	Tyr	Arg	Gly	
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Val	Arg	Arg	Arg	Lys	Trp	Gly	Lys	Trp	Val	Ser	Glu	Ile	Arg	Gln	Pro
			20					25					30		
Gly	Thr	Lys	Thr	Arg	Ile	Trp	Leu	Gly	Ser	Phe	Glu	Ser	Ala	Glu	Met
		35					40					45			
Ala	Ala	Val	Ala	His	Asp	Val	Ala	Ala	Leu	Arg	Leu	Arg	Gly	Arg	Asp
		50				55					60				
Ala	Gln	Leu	Asn	Phe	Pro	Gly	Ser	Val	Asp	Arg	Leu	Pro	Arg	Pro	Ala
		65			70				75						80
Ser	Ser	Arg	Pro	Gly	Asp	Ile	Arg	Ala	Ala	Ala	Glu	Ala	Ala	Ala	Asp
				85				90					95		
Arg	Val	Arg	Arg	Glu	Pro	Ala	Leu	Val	Val	Val	Arg	Gly	Ala	Ala	Ala
			100					105					110		
Ala	Ala	Gly	Glu	Leu	Ala	Ala	Val	Arg	Trp	Ala	Gly	Leu	Glu	Val	Glu
		115					120					125			
Val	Glu	Gln	Gln	Leu	Gly	Gly	Ser	Asp	Glu	Glu	Phe	Glu	Val	Asp	Ser
		130			135						140				
Pro	Arg	Leu	Trp	Ala	Glu	Met	Ala	Glu	Ala	Met	Leu	Leu	Asp	Pro	Pro
				150					155						160
Val	Trp	Ala	Val	Asp	Val	Ser	Glu	Met	Glu	Gly	Pro	His	Cys	Trp	Ala
				165				170						175	
His	Gly	Ser	Leu	Trp	Asp	Ala	Cys								
			180												

<210> 446

<211> 955

<212> DNA

<213> Oryza sativa

PF59082SeqList_PF59082.txt

<220>

<221> CDS

<222> (117)..(719)

<400> 446

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tttcagtttc agctgtgtag tagcacactc tgtttgcttc atcgtttgtg ttcgag atg      119
                                     Met
                                     1
gat cga gac gag agc ttg ggc acg cag cca ttg acc ggg agg cgg gtg      167
Asp Arg Asp Glu Ser Leu Gly Thr Gln Pro Leu Thr Gly Arg Arg Val
                                     5
                                     10
                                     15
cgc gcg gac aca agg cac ccg gtg tac cgc ggc atc cgg ctc cgc agc      215
Arg Ala Asp Thr Arg His Pro Val Tyr Arg Gly Ile Arg Leu Arg Ser
                                     20
                                     25
                                     30
ggc aag tgg gtc tcg gag atc cgc gag ccg ggc aag tcc agc agg atc      263
Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Gly Lys Ser Ser Arg Ile
                                     35
                                     40
                                     45
tgg ctc ggc acg tac ccg acg ccc gag atg gcc gcc gcg gcg tac gac      311
Trp Leu Gly Thr Tyr Pro Thr Pro Glu Met Ala Ala Ala Ala Tyr Asp
                                     50
                                     55
                                     60
gcc gcg gca ttg gcg ctg cgc ggc gcc gag gcc gcc gcg ctc aac ttc ccc      359
Ala Ala Ala Leu Ala Leu Arg Gly Ala Asp Ala Ala Leu Asn Phe Pro
                                     70
                                     75
                                     80
ggc acg gcc acg tcg cgc ccg gcg cca gcc tcc ggc tcc ccc gac gac      407
Gly Thr Ala Thr Ser Arg Pro Ala Pro Ala Ser Gly Ser Pro Asp Asp
                                     85
                                     90
                                     95
atc cgc gca gcg gcc gcg gcc gcc gcc gcg atg atc ggc tcc ggt cac      455
Ile Arg Ala Ala Ala Ala Ala Ala Ala Met Ile Gly Ser Gly His
                                     100
                                     105
                                     110
cgt ggc aac cag cgc gcc gcc gcc gcc gcg agc acg tct cgc gcg gcg acg      503
Arg Gly Asn Gln Arg Ala Ala Asp Ala Ser Thr Ser Arg Ala Ala Thr
                                     115
                                     120
                                     125
gcg gcg ccg gag gcc gcc gtc gcc gct ggg gcg ggc gat cag aag cgc      551
Ala Ala Pro Glu Ala Ala Val Ala Ala Gly Ala Gly Asp Gln Lys Arg
                                     130
                                     135
                                     140
                                     145
gtc gtg gac gag gac gtc ttc gag atg ccg cgg ctg ctg gtg agc      599
Val Val Asp Glu Asp Val Phe Glu Met Pro Arg Leu Leu Val Ser
                                     150
                                     155
                                     160
atg gcc gag ggc ttg atg atg agc ccg ccg agg ctg agc ccc tcg acg      647
Met Ala Glu Gly Leu Met Met Ser Pro Pro Arg Leu Ser Pro Ser Thr
                                     165
                                     170
                                     175
gac ggc gtc ggc ggc gtg tcg ccg gag gac gac gag gac gag gac ggc      695
Asp Gly Val Gly Gly Val Ser Pro Glu Asp Asp Glu Asp Glu Asp Gly
                                     180
                                     185
                                     190
atg agc ctg tgg aac cat tcc tgaaatgggc ttacgggtgc atagcatttg      746
Met Ser Leu Trp Asn His Ser
                                     195
                                     200
caggaggaca ccatgtattt tccatgtgtt cgtatgaatt ctgtgcctac gtacagtacg      806

tactcggcac gtatgcgaga taggaacaga gcagagcagg atactgaatt ttatcgtagt      866

tgtcctgtta cgtgtatacg gtatatatgg tcaactccact gatgtataag ccatccgtag      926

acgaattatg gctgaaaacg atgcccctg      955

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<210> 447

<211> 200

<212> PRT

<213> Oryza sativa

<400> 447

PF59082SeqList_PF59082.txt

Met Asp Arg Asp Glu Ser Leu Gly Thr Gln Pro Leu Thr Gly Arg Arg
1 5 10 15
Val Arg Ala Asp Thr Arg His Pro Val Tyr Arg Gly Ile Arg Leu Arg
20 25 30
Ser Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Gly Lys Ser Ser Arg
35 40 45
Ile Trp Leu Gly Thr Tyr Pro Thr Pro Glu Met Ala Ala Ala Tyr
50 55 60
Asp Ala Ala Ala Leu Ala Leu Arg Gly Ala Asp Ala Ala Leu Asn Phe
65 70 75 80
Pro Gly Thr Ala Thr Ser Arg Pro Ala Pro Ala Ser Gly Ser Pro Asp
85 90 95
Asp Ile Arg Ala Ala Ala Ala Ala Ala Met Ile Gly Ser Gly
100 105 110
His Arg Gly Asn Gln Arg Ala Ala Asp Ala Ser Thr Ser Arg Ala Ala
115 120 125
Thr Ala Ala Pro Glu Ala Ala Val Ala Ala Gly Ala Gly Asp Gln Lys
130 135 140
Arg Val Val Asp Glu Asp Asp Val Phe Glu Met Pro Arg Leu Leu Val
145 150 155 160
Ser Met Ala Glu Gly Leu Met Met Ser Pro Pro Arg Leu Ser Pro Ser
165 170 175
Thr Asp Gly Val Gly Gly Val Ser Pro Glu Asp Asp Glu Asp Glu Asp
180 185 190
Gly Met Ser Leu Trp Asn His Ser
195 200

<210> 448

<211> 597

<212> DNA

<213> Glycine max

<220>

<221> CDS

<222> (1)..(597)

<400> 448

atg gcg aaa ccc agc agc gaa aag cca gag gag cat agc gat tcc aag	48
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tac tac aaa ggg gtc cga aag aga aaa tgg ggc aaa tgg gta tcc gaa	96
Tyr Tyr Lys Gly Val Arg Lys Arg Lys Trp Gly Lys Trp Val Ser Glu	
20 25 30	
ata aga cta ccc aac agc cgt cag agg att tgg ttg gga tcc tac gac	144
Ile Arg Leu 35 Pro Asn Ser Arg Gln Arg Ile Trp Leu 45 Gly Ser Tyr Asp	
acc ccc gag aag gcc gcg cgt gcc ttc gac gcg gca atg ttc tgc tta	192
Thr Pro 50 Glu Lys Ala Ala Arg 55 Ala Phe Asp Ala 60 Met Phe Cys Leu	
cgt ggc cgc aac gcc aag ttt aac ttc ccc gac aac cca ccc gac atc	240
Arg 65 Gly Arg Asn Ala Lys 70 Phe Asn Phe Pro Asp 75 Asn Pro Pro Asp 80 Ile	
gcc ggc gga acg tcc atg acg ccg tcg cag att cag atc gcc gcc gca	288
Ala Gly Gly Thr 85 Ser Met Thr Pro Ser Gln 90 Ile Gln Ile Ala 95 Ala Ala	
caa ttc gcc aac gcg ggg ccc cac gag gga cat tcg ggc cga ccc gaa	336
Gln Phe Ala Asn Ala Gly Pro His Glu Gly His Ser Gly Arg Pro Glu	
100 105 110	
cat cct ccc atg gaa tct cca tcg cct tct gtt tcg gaa ggg acc atc	384
His Pro 115 Met Glu Ser Pro 120 Pro Ser Val Ser 125 Glu Gly Thr Ile	
caa acg gac agt gac gtc ccc act ctt aac ggt tca gta acg gat ttg	432
Gln Thr 130 Asp Ser Val Pro 135 Thr Leu Asn Gly Ser 140 Val Thr Asp Leu	
ttc acg ccc gtt ggg tcg agt ggt tac gca tcc gat tac ggg att ttc	480
Phe Thr Pro Val Gly Ser Ser Gly Tyr Ala Ser 155 Asp Tyr Gly Ile Phe	
145 150 160	
ccg ggc ttt gat gat ttc agt ggc gat ttt tat gtg ccg gaa atg ccg	528
Pro Gly Phe Asp Asp Phe Ser Gly Asp Phe Tyr Val Pro Glu Met Pro	

PF59082SeqList_PF59082.txt

aac gtt aat tat gga gaa gaa aac ggg gaa ggg ttc ata gtt gat gaa	165	170	175	576
Asn Val Asn Tyr Gly Glu Glu Asn Gly Glu Gly Phe Ile Val Asp Glu				
tct ttc ttg tgg aat ttt tga	180	185	190	597
Ser Phe Leu Trp Asn Phe	195			

<210> 449
 <211> 198
 <212> PRT
 <213> Glycine max

<400> 449	
Met Ala Lys Pro Ser Ser Glu Lys Pro Glu Glu His Ser Asp Ser Lys	
1 Tyr Tyr Lys Gly Val Arg Lys Arg Lys Trp Gly Lys Trp Val Ser Glu	
Ile Arg Leu Pro Asn Ser Arg Gln Arg Ile Trp Leu Gly Ser Tyr Asp	
Thr Pro Glu Lys Ala Ala Arg Ala Phe Asp Ala Ala Met Phe Cys Leu	
Arg Gly Arg Asn Ala Lys Phe Asn Phe Pro Asp Asn Pro Pro Asp Ile	
65 Ala Gly Gly Thr Ser Met Thr Pro Ser Gln Ile Gln Ile Ala Ala Ala	
Gln Phe Ala Asn Ala Gly Pro His Glu Gly His Ser Gly Arg Pro Glu	
His Pro Pro Met Glu Ser Pro Ser Pro Ser Val Ser Glu Gly Thr Ile	
Gln Thr Asp Ser Asp Val Pro Thr Leu Asn Gly Ser Val Thr Asp Leu	
Phe Thr Pro Val Gly Ser Ser Gly Tyr Ala Ser Asp Tyr Gly Ile Phe	
145 Pro Gly Phe Asp Asp Phe Ser Gly Asp Phe Tyr Val Pro Glu Met Pro	
Asn Val Asn Tyr Gly Glu Glu Asn Gly Glu Gly Phe Ile Val Asp Glu	
Ser Phe Leu Trp Asn Phe	195

<210> 450
 <211> 579
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (1)..(579)

<400> 450		
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Met Asn Ser Ser Met Ala Ser Ala Gly Leu Gly Ser Arg Arg Lys Asp		
1 ccg gtg tac aga gga atc cgg tgc cga agt ggg aaa tgg gtc tcc gag		96
Pro Val Tyr Arg Gly Ile Arg Cys Arg Ser Gly Lys Trp Val Ser Glu		
att cgt gag ccg agg aaa acc acg aga atc tgg ctt gga act tac ccc		144
Ile Arg Glu Pro Arg Lys Thr Thr Arg Ile Trp Leu Gly Thr Tyr Pro		
atg gca gag atg gca gca gcc gcc tat gat gtg gct gct atg gct ctt		192
Met Ala Glu Met Ala Ala Ala Tyr Asp Val Ala Ala Met Ala Leu		
aaa gga aga gaa gct gtc ttg aac ttc cct gga tcc gtc ggg tca tac		240
Lys Gly Arg Glu Ala Val Leu Asn Phe Pro Gly Ser Val Gly Ser Tyr		
65 ccg gtt cct gaa tca aca tcc gca gca gat ata cga gcc gct gcg gca		288
Pro Val Pro Glu Ser Thr Ser Ala Ala Asp Ile Arg Ala Ala Ala Ala		
85	90	95

PF59082SeqList_PF59082.txt

gcc gca gca gca atg aag gga tgt gag gaa ggg gag gag gag aaa aag	336
Ala Ala Ala Ala Met Lys Gly Cys Glu Glu Gly Glu Glu Glu Lys Lys	
100 105 110	
gca aag gag aag aag agt agt agt tcg aag tcg aga gcg cgt gag tgc	384
Ala Lys Glu Lys Lys Ser Ser Ser Ser Lys Ser Arg Ala Arg Glu Cys	
115 120 125	
cac gta gat aat gat gtt gga tct tcg tcg tgg tgt ggg aca gag ttc	432
His Val Asp Asn Asp Val Gly Ser Ser Ser Trp Cys Gly Thr Glu Phe	
130 135 140	
atg gac gaa gaa gaa gtc ttg aat atg cct aat ctg ctg gct aat atg	480
Met Asp Glu Glu Glu Val Leu Asn Met Pro Asn Leu Leu Ala Asn Met	
145 150 155 160	
gca gaa ggg atg atg gtt gcg ccg ccg tcg tgg atg ggt tct ccg ccg	528
Ala Glu Gly Met Met Val Ala Pro Pro Ser Trp Met Gly Ser Arg Pro	
165 170 175	
tcg gat gac tct ccg gag aat tca aat gat gag gac ttg tgg ggc tat	576
Ser Asp Asp Ser Pro Glu Asn Ser Asn Asp Glu Asp Leu Trp Gly Tyr	
180 185 190	
tga	579

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 <211> 192
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 <213> Arabidopsis thaliana

<400> 451

Met Asn Ser Ser Met Ala Ser Ala Gly Leu Gly Ser Arg Arg Lys Asp	
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35 40 45	
Met Ala Glu Met Ala Ala Ala Tyr Asp Val Ala Ala Met Ala Leu	
50 55 60	
Lys Gly Arg Glu Ala Val Leu Asn Phe Pro Gly Ser Val Gly Ser Tyr	
65 70 75 80	
Pro Val Pro Glu Ser Thr Ser Ala Ala Asp Ile Arg Ala Ala Ala	
85 90 95	
Ala Ala Ala Ala Met Lys Gly Cys Glu Glu Gly Glu Glu Glu Lys Lys	
100 105 110	
Ala Lys Glu Lys Lys Ser Ser Ser Ser Lys Ser Arg Ala Arg Glu Cys	
115 120 125	
His Val Asp Asn Asp Val Gly Ser Ser Ser Trp Cys Gly Thr Glu Phe	
130 135 140	
Met Asp Glu Glu Glu Val Leu Asn Met Pro Asn Leu Leu Ala Asn Met	
145 150 155 160	
Ala Glu Gly Met Met Val Ala Pro Pro Ser Trp Met Gly Ser Arg Pro	
165 170 175	
Ser Asp Asp Ser Pro Glu Asn Ser Asn Asp Glu Asp Leu Trp Gly Tyr	
180 185 190	

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 <211> 669
 <212> DNA
 <213> Lycopersicon hirsutum

<220>
 <221> CDS
 <222> (1)..(669)

<400> 452

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1 5 10 15	
tca tct tct tct tca tca tca tcg tca tcg tca ttg ttt tct gag gag	96
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Leu Phe Ser Glu Glu	
20 25 30	

PF59082SeqList_PF59082.txt

gaa	att	att	tta	gct	tcg	aat	aac	ccg	aaa	agg	cca	gct	ggc	agg	aag	144
Glu	Ile	Ile	Leu	Ala	Ser	Asn	Asn	Pro	Lys	Arg	Pro	Ala	Gly	Arg	Lys	
		35					40					45				
aag	ttt	cga	gaa	aca	cga	cat	ccg	ata	tac	agg	gga	atc	agg	aag	agg	192
Lys	Phe	Arg	Glu	Thr	Arg	His	Pro	Ile	Tyr	Arg	Gly	Ile	Arg	Lys	Arg	
	50					55					60					
aat	tca	gga	aaa	tgg	gtt	tgt	gaa	gtc	aga	gag	cca	aat	aag	aag	aca	240
Asn	Ser	Gly	Lys	Trp	Val	Cys	Glu	Val	Arg	Glu	Pro	Asn	Lys	Lys	Thr	
	65				70					75					80	
agg	att	tgg	ctt	ggt	act	ttt	cct	acg	gct	gaa	atg	gcg	gct	aga	gct	288
Arg	Ile	Trp	Leu	Gly	Thr	Phe	Pro	Thr	Ala	Glu	Met	Ala	Ala	Arg	Ala	
				85					90					95		
cat	gac	gtg	gcg	gct	tta	gca	tta	aga	ggc	cgt	tct	gct	tgt	ttg	aat	336
His	Asp	Val	Ala	Ala	Leu	Ala	Leu	Arg	Gly	Arg	Ser	Ala	Cys	Leu	Asn	
			100					105					110			
ttc	tct	gat	tca	gct	tgg	aga	ttg	cct	atc	cct	gct	tcc	tcc	aac	tct	384
Phe	Ser	Asp	Ser	Ala	Trp	Arg	Leu	Pro	Ile	Pro	Ala	Ser	Ser	Asn	Ser	
		115					120					125				
aaa	gat	att	caa	aag	gcg	gcc	gct	gag	gcc	gcc	gaa	atc	ttc	cga	cca	432
Lys	Asp	Ile	Gln	Lys	Ala	Ala	Ala	Glu	Ala	Ala	Glu	Ile	Phe	Arg	Pro	
	130					135					140					
tta	aaa	gag	tcg	gaa	gaa	gtt	tca	gga	gaa	tct	gat	aac	agt	act	tct	480
Leu	Lys	Glu	Ser	Glu	Glu	Val	Ser	Gly	Glu	Ser	Asp	Asn	Ser	Thr	Ser	
	145				150					155					160	
cct	gaa	acg	tca	gaa	aat	gtg	caa	gag	agt	agt	gac	ttc	gtg	gat	gat	528
Pro	Glu	Thr	Ser	Glu	Asn	Val	Gln	Glu	Ser	Ser	Asp	Phe	Val	Asp	Glu	
				165					170					175		
gaa	gcg	atc	ttt	ttc	atg	cca	gga	tta	ctt	gca	aat	atg	gcg	gaa	gga	576
Glu	Ala	Ile	Phe	Phe	Met	Pro	Gly	Leu	Leu	Ala	Asn	Met	Ala	Glu	Gly	
			180					185					190			
ctc	atg	cta	cct	cca	cct	caa	tgt	gca	gaa	atg	gga	gat	cat	tat	gtg	624
Leu	Met	Leu	Pro	Pro	Pro	Gln	Cys	Ala	Glu	Met	Gly	Asp	His	Tyr	Val	
		195					200					205				
gaa	act	gat	gcc	tac	atg	ata	act	tta	tgg	aat	tat	tct	atc	taa		669
Glu	Thr	Asp	Ala	Tyr	Met	Ile	Thr	Leu	Trp	Asn	Tyr	Ser	Ile			
	210					215					220					

<210> 453

<211> 222

<212> PRT

<213> Lycopersicon hirsutum

<400> 453

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			20					25					30			
Glu	Ile	Ile	Leu	Ala	Ser	Asn	Asn	Pro	Lys	Arg	Pro	Ala	Gly	Arg	Lys	
		35					40					45				
Lys	Phe	Arg	Glu	Thr	Arg	His	Pro	Ile	Tyr	Arg	Gly	Ile	Arg	Lys	Arg	
	50					55					60					
Asn	Ser	Gly	Lys	Trp	Val	Cys	Glu	Val	Arg	Glu	Pro	Asn	Lys	Lys	Thr	
	65				70					75					80	
Arg	Ile	Trp	Leu	Gly	Thr	Phe	Pro	Thr	Ala	Glu	Met	Ala	Ala	Arg	Ala	
				85					90					95		
His	Asp	Val	Ala	Ala	Leu	Ala	Leu	Arg	Gly	Arg	Ser	Ala	Cys	Leu	Asn	
			100					105					110			
Phe	Ser	Asp	Ser	Ala	Trp	Arg	Leu	Pro	Ile	Pro	Ala	Ser	Ser	Asn	Ser	
		115					120					125				
Lys	Asp	Ile	Gln	Lys	Ala	Ala	Ala	Glu	Ala	Ala	Glu	Ile	Phe	Arg	Pro	
	130					135					140					
Leu	Lys	Glu	Ser	Glu	Glu	Val	Ser	Gly	Glu	Ser	Asp	Asn	Ser	Thr	Ser	
	145				150					155					160	
Pro	Glu	Thr	Ser	Glu	Asn	Val	Gln	Glu	Ser	Ser	Asp	Phe	Val	Asp	Glu	
				165					170					175		
Glu	Ala	Ile	Phe	Phe	Met	Pro	Gly	Leu	Leu	Ala	Asn	Met	Ala	Glu	Gly	
			180					185					190			
Leu	Met	Leu	Pro	Pro	Pro	Gln	Cys	Ala	Glu	Met	Gly	Asp	His	Tyr	Val	
		195					200					205				

PF59082SeqList_PF59082.txt

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210 215 220

<210> 454
<211> 678
<212> DNA
<213> Arabidopsis thaliana

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<221> CDS
<222> (1)..(678)

<400> 454
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1 5 10 15
aag gag aaa acg aaa gaa aag ggg gta tat cgt ggg gct cgc atg agg 96
Lys Glu Lys Thr Lys Glu Lys Gly Val Tyr Arg Gly Ala Arg Met Arg
20 25 30
agc tgg ggg aaa tgg gtc tcg gag att cgg gag ccc cgt aag aaa tca 144
Ser Trp Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Arg Lys Lys Ser
35 40 45
aga atc tgg ctc ggg act ttc ccc acg gcg gag atg gca gcg cgt gcc 192
Arg Ile Trp Leu Gly Thr Phe Pro Thr Ala Glu Met Ala Ala Arg Ala
50 55 60
cat gat gtt gcg gca ttg agt atc aaa gga agt tcc gca atc ctt aac 240
His Asp Val Ala Ala Leu Ser Ile Lys Gly Ser Ser Ala Ile Leu Asn
65 70 75 80
ttc cct gag ctc gcg gat ttt ctg cca aga cca gtc tcg ctc agc caa 288
Phe Pro Glu Leu Ala Asp Phe Leu Pro Arg Pro Val Ser Leu Ser Gln
85 90 95
cag gat atc cag gcc gca gcc gcc gaa gcc gct ctt atg gat ttc aaa 336
Gln Asp Ile Gln Ala Ala Ala Glu Ala Ala Leu Met Asp Phe Lys
100 105 110
act gta cca ttc cat ctt cag gat gac tca acg ccg ttg caa act agg 384
Thr Val Pro Phe His Leu Gln Asp Asp Ser Thr Pro Leu Gln Thr Arg
115 120 125
tgt gat act gag aag atc gaa aag tgg tca tcc tca tcg tcc tca gcc 432
Cys Asp Thr Glu Lys Ile Glu Lys Trp Ser Ser Ser Ser Ser Ala
130 135 140
tca tcc tca tcc tca tct tcg tcc tcg tcc tca tca tct atg ctt tcg 480
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Met Leu Ser
145 150 155 160
ggg gag cta gga gat att gtg gag ttg ccg agt ctt gaa aac aat gta 528
Gly Glu Leu Gly Asp Ile Val Glu Leu Pro Ser Leu Glu Asn Asn Val
165 170 175
aaa tac gat tgt gcg ctg tat gac tcg ttg gag ggg ctg gtg tcg atg 576
Lys Tyr Asp Cys Ala Leu Tyr Asp Ser Leu Glu Gly Leu Val Ser Met
180 185 190
ccc cca tgg tta gat gct acc gaa aat gat ttt agg tat gga gat gat 624
Pro Pro Trp Leu Asp Ala Thr Glu Asn Asp Phe Arg Tyr Gly Asp Asp
195 200 205
tcg gta ctg ttg gac cca tgt ctc aaa gaa agc ttt ttg tgg aat tat 672
Ser Val Leu Leu Asp Pro Cys Leu Lys Glu Ser Phe Leu Trp Asn Tyr
210 215 220
gag taa 678
Glu
225

<210> 455
<211> 225
<212> PRT
<213> Arabidopsis thaliana

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Lys Glu Lys Thr Lys Glu Lys Gly Val Tyr Arg Gly Ala Arg Met Arg
20 25 30

PF59082SeqList_PF59082.txt

Ser Trp Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Arg Lys Lys Ser
 35 40 45
 Arg Ile Trp Leu Gly Thr Phe Pro Thr Ala Glu Met Ala Ala Arg Ala
 50 55 60
 His Asp Val Ala Ala Leu Ser Ile Lys Gly Ser Ala Ile Leu Asn
 65 70 75 80
 Phe Pro Glu Leu Ala Asp Phe Leu Pro Arg Pro Val Ser Leu Ser Gln
 85 90 95
 Gln Asp Ile Gln Ala Ala Ala Glu Ala Ala Leu Met Asp Phe Lys
 100 105 110
 Thr Val Pro Phe His Leu Gln Asp Ser Thr Pro Leu Gln Thr Arg
 115 120 125
 Cys Asp Thr Glu Lys Ile Glu Lys Trp Ser Ser Ser Ser Ser Ala
 130 135 140
 Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Met Leu Ser
 145 150 155 160
 Gly Glu Leu Gly Asp Ile Val Glu Leu Pro Ser Leu Glu Asn Asn Val
 165 170 175
 Lys Tyr Asp Cys Ala Leu Tyr Asp Ser Leu Glu Gly Leu Val Ser Met
 180 185 190
 Pro Pro Trp Leu Asp Ala Thr Glu Asn Asp Phe Arg Tyr Gly Asp Asp
 195 200 205
 Ser Val Leu Leu Asp Pro Cys Leu Lys Glu Ser Phe Leu Trp Asn Tyr
 210 215 220
 Glu
 225

<210> 456
 <211> 606
 <212> DNA
 <213> Oryza sativa

<220>
 <221> CDS
 <222> (1)..(606)

<400> 456
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 1 5 15
 atg gcg ggg cag tac cga ggg gtg agg aag agg aag tgg ggg aag tgg 96
 Met Ala Gly Gln Tyr Arg Gly Val Arg Lys Arg Lys Trp Gly Lys Trp
 20 25 30
 gtg tcg gag atc agg gag ccc ggg aag aag acg cgc atc tgg ctc ggg 144
 Val Ser Glu Ile Arg Glu Pro Gly Lys Lys Thr Arg Ile Trp Leu Gly
 35 40 45
 agc ttc gag tcg ccg gag atg gcc gcc gtg gcg cac gac gtg gcc gcg 192
 Ser Phe Glu Ser Pro Glu Met Ala Ala Val Ala His Asp Val Ala Ala
 50 55 60
 ctc cgc ctc cgg ggg cgg gac gcg cgc ctc aac ttc ccg gcg atc gcc 240
 Leu Arg Leu Arg Gly Arg Asp Ala Arg Leu Asn Phe Pro Ala Ile Ala
 65 70 75 80
 cac cgc ttc cgc cgc ccg gac acc gcc gag ccc ggc gac gtc cgc gcc 288
 His Arg Phe Arg Arg Pro Asp Thr Ala Glu Pro Gly Asp Val Arg Ala
 85 90 95
 gcc gcg ctc gag gcc gcc gcc cag gtc cgc ttc acc ccc gac ctc ctc 336
 Ala Ala Leu Glu Ala Ala Ala Gln Val Arg Phe Thr Pro Asp Leu Leu
 100 105 110
 gtc gtc gcc ggc gga gac gac gcc aga cga cga tgc tgc tcc gcc ggc 384
 Val Val Ala Gly Gly Asp Asp Ala Arg Arg Arg Cys Cys Ser Ala Gly
 115 120 125
 gag gcc gag gcg gcg gcg gtg gcg gcg gcg gcg tgg gag tgg gac gtg 432
 Glu Ala Glu Ala Ala Val Ala Ala Ala Ala Trp Glu Trp Asp Val
 130 135 140
 gtg gtc ggc ggc ggc ggc gag ctg gag gcc aag tcg ccc aac atg 480
 Val Val Gly Gly Gly Gly Asp Glu Leu Glu Ala Lys Ser Pro Asn Met
 145 150 155 160
 tgg gct gag ctg gcg gag gcc atg ctg atg gcc cca cct gtc tgg gag 528
 Trp Ala Glu Leu Ala Glu Ala Met Leu Met Ala Pro Pro Val Trp Glu

PF59082SeqList_PF59082.txt

cg	cc	gc	cc	gc	tc	gc	tc	gc	ga	ga	gt	cg	gc	gc		336
Arg	Pro	Ala	Pro	Ala	Ser	Ala	Ser	Ala	Asp	Asp	Val	Arg	Ala	Ala	Ala	
			100					105					110			
acc	gcc	gcc	gcc	gcc	gcg	atg	gca	cac	cag	gag	gag	gac	gac	gac	agt	384
Thr	Ala	Ala	Ala	Ala	Ala	Met	Ala	His	Gln	Glu	Glu	Asp	Asp	Asp	Ser	
		115					120					125				
cg	cg	cag	ctc	gag	gac	ggg	ggc	ggc	ggc	ggc	ggc	gtg	gtg	gac	gag	432
Arg	Arg	Gln	Leu	Glu	Asp	Gly	Gly	Gly	Gly	Gly	Gly	Val	Val	Asp	Glu	
	130					135					140					
gac	gac	gtg	ctg	gag	atg	ccg	agg	ctg	atg	gtg	agc	atg	gcg	gag	ggg	480
Asp	Asp	Val	Leu	Glu	Met	Pro	Arg	Leu	Met	Val	Ser	Met	Ala	Glu	Gly	
	145				150					155					160	
ctg	atg	atc	agc	cca	ccg	ccg	gtg	atg	ctc	ggc	ctg	cag	gcg	gac	ggc	528
Leu	Met	Ile	Ser	Pro	Pro	Pro	Val	Met	Leu	Gly	Leu	Gln	Ala	Asp	Gly	
				165			170							175		
ggt	gga	ata	atg	gac	gag	ggc	ggc	agc	gtg	gtg	agg	ttg	tgg	gat	cac	576
Gly	Gly	Ile	Met	Asp	Glu	Gly	Gly	Ser	Val	Val	Arg	Leu	Trp	Asp	His	
			180					185					190			
agc	tga															582
Ser																

<210> 459
 <211> 193
 <212> PRT
 <213> Oryza sativa

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 20 25 30
 His Pro Val Tyr Arg Gly Val Arg Phe Arg Ala Gly Lys Trp Val Ser
 35 40 45
 Glu Ile Arg Glu Leu Arg Lys Pro Ser Arg Ile Trp Leu Gly Thr Tyr
 50 55 60
 Ala Thr Pro Glu Met Ala Ala Ala Ala Tyr Asp Ala Ala Ala Leu Ala
 65 70 75 80
 Leu Arg Gly Arg Gly Ala Ala Leu Asn Phe Pro Asp Ala Ala Arg Ser
 85 90 95
 Arg Pro Ala Pro Ala Ser Ala Ser Ala Asp Asp Val Arg Ala Ala Ala
 100 105 110
 Thr Ala Ala Ala Ala Ala Met Ala His Gln Glu Glu Asp Asp Asp Ser
 115 120 125
 Arg Arg Gln Leu Glu Asp Gly Gly Gly Gly Gly Val Val Asp Glu
 130 135 140
 Asp Asp Val Leu Glu Met Pro Arg Leu Met Val Ser Met Ala Glu Gly
 145 150 155 160
 Leu Met Ile Ser Pro Pro Val Met Leu Gly Leu Gln Ala Asp Gly
 165 170 175
 Gly Gly Ile Met Asp Glu Gly Gly Ser Val Val Arg Leu Trp Asp His
 180 185 190
 Ser

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 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (77)..(778)

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ttctattcct taaacc atg gtc gag cct gca gta gca gca agc tca gaa tta 112
 Seite 614

PF59082SeqList_PF59082.txt
Met Val Glu Pro Ala Val Ala Ala Ser Ser Glu Leu

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1      5      10
tca gac tca aca cga aac acc aac acc aac acc cct tca ccc tct tcc 160
Ser Asp Ser Thr Arg Asn Thr Asn Thr Asn Thr Pro Ser Pro Ser Ser
15      20      25
tca tcg tcg tta tct ccg tcg cca tca ccg tca tca tca agc tct aaa 208
Ser Ser Ser Leu Ser Pro Ser Pro Ser Pro Ser Ser Ser Ser Ser Lys
30      35      40
aag cga gcg aga gac aac aac aat agt aga aac aac agc aac aag cat 256
Lys Arg Ala Arg Asp Asn Asn Asn Ser Arg Asn Asn Ser Asn Lys His
45      50      55      60
tct gtg tat aga ggt gtc cga atg cgc acg tgg ggc aaa tgg gtg tcg 304
Ser Val Tyr Arg Gly Val Arg Met Arg Thr Trp Gly Lys Trp Val Ser
65      70      75
gaa atc cgc gag ccg cga aag aag aac cga atc tgg ctc ggc acc ttc 352
Glu Ile Arg Glu Pro Arg Lys Lys Asn Arg Ile Trp Leu Gly Thr Phe
80      85      90
gcc acc gcc gag atg gcg gcg cgt gcc cac gac gtg gcg gcg ctg acg 400
Ala Thr Ala Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Thr
95      100      105
ata aaa ggc tca tcc gcc atc ctt aac ttc ccc gaa ctc gcc gcc tcc 448
Ile Lys Gly Ser Ser Ala Ile Leu Asn Phe Pro Glu Leu Ala Ala Ser
110      115      120
ctg ccc cgg ccg gcc tcc aac tcg ccc cgc gac gtg cag gcc gcg gca 496
Leu Pro Arg Pro Ala Ser Asn Ser Pro Arg Asp Val Gln Ala Ala Ala
125      130      135
gcc aag gcg gcg tcc atg gag gcg ccg ccg ccg acc cct ccg tcg ccg 544
Ala Lys Ala Ala Ser Met Glu Ala Pro Pro Arg Thr Pro Pro Ser Pro
145      150      155
gcc gcc acg ccg gag gat gac ctc ggc gag atc gtg gag ctg ccg ccg 592
Ala Ala Thr Pro Glu Asp Asp Leu Gly Glu Ile Val Glu Leu Pro Pro
160      165      170
ctc gga acg agt ttc gac tcg ccc gac cgg agt tcc gag ttt gtg ttc 640
Leu Gly Thr Ser Phe Asp Ser Pro Asp Arg Ser Ser Glu Phe Val Phe
175      180      185
ctg gac atg gac gac ggg tgg ccc tat tct cac ccg tgg tac cac agc 688
Leu Asp Met Asp Asp Gly Trp Pro Tyr Ser His Pro Trp Tyr His Ser
190      195      200
att tat gat ggt ggg tac ttc att agc gac atg aac aac atg gtt tcg 736
Ile Tyr Asp Gly Gly Tyr Phe Ile Ser Asp Met Asn Asn Met Val Ser
205      210      215      220
atg caa gag tca gag agc atg gtt ctt tcc ctg tgg cct tga agttaagcca 788
Met Gln Glu Ser Glu Ser Met Val Leu Ser Leu Trp Pro
225      230
atgctactca ttgcagtatg gttatatattt gggtcttttt tttttttttt gcgtgagaca 848

gataatcatg tttctgttct taagtatgcg attagggatt ggattttcat gtccgtatat 908

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aaaaaaaaa 978

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<212> PRT
<213> Glycine max

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20 25 30
Ser Pro Ser Pro Ser Pro Ser Ser Ser Ser Lys Lys Arg Ala Arg
35 40 45

PF59082SeqList_PF59082.txt

Asp Asn Asn Asn Ser Arg Asn Asn Ser Asn Lys His Ser Val Tyr Arg
50 55 60
Gly Val Arg Met Arg Thr Trp Gly Lys Trp Val Ser Glu Ile Arg Glu
65 70 75 80
Pro Arg Lys Lys Asn Arg Ile Trp Leu Gly Thr Phe Ala Thr Ala Glu
85 90 95
Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Thr Ile Lys Gly Ser
100 105 110
Ser Ala Ile Leu Asn Phe Pro Glu Leu Ala Ala Ser Leu Pro Arg Pro
115 120 125
Ala Ser Asn Ser Pro Arg Asp Val Gln Ala Ala Ala Lys Ala Ala
130 135 140
Ser Met Glu Ala Pro Pro Arg Thr Pro Pro Ser Pro Ala Ala Thr Pro
145 150 155 160
Glu Asp Asp Leu Gly Glu Ile Val Glu Leu Pro Pro Leu Gly Thr Ser
165 170 175
Phe Asp Ser Pro Asp Arg Ser Ser Glu Phe Val Phe Leu Asp Met Asp
180 185 190
Asp Gly Trp Pro Tyr Ser His Pro Trp Tyr His Ser Ile Tyr Asp Gly
195 200 205
Gly Tyr Phe Ile Ser Asp Met Asn Asn Met Val Ser Met Gln Glu Ser
210 215 220
Glu Ser Met Val Leu Ser Leu Trp Pro
225 230

<210> 462

<211> 799

<212> DNA

<213> Helianthus annuus

<220>

<221> CDS

<222> (169)..(642)

<400> 462

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tttatttata cacacgacca ctgtatatac tacctcacac ttttcctttt ctttttaaaa 120

ggtgtcgggtg ttttcgacca tcttctcctt ttccaatcac caaaacca atg gaa gcc 177
Met Glu Ala
1

atc atc acc ggc ggc gga gat ggg ccg tgc aac cgt ccg ccg gag aaa 225
Ile Ile Thr Gly Gly Gly Asp Gly Pro Cys Asn Arg Pro Pro Glu Lys
5 10 15

agg aag agt gat caa cgg ccg tac aag ggg ata cgc atg agg aag tgg 273
Arg Lys Ser Asp Gln Arg Pro Tyr Lys Gly Ile Arg Met Arg Lys Trp
20 25 30 35

gga aaa tgg gtg gcg gag att cgg gag ccg aat aag cgg tcc agg att 321
Gly Lys Trp Val Ala Glu Ile Arg Glu Pro Asn Lys Arg Ser Arg Ile
40 45 50

tgg ttg ggg tcc tat tgc acg ccc gtg gcc gct gca cgg gcg tac gac 369
Trp Leu Gly Ser Tyr Ser Thr Pro Val Ala Ala Ala Arg Ala Tyr Asp
55 60 65

acg gcc gta tac tac cta cgg ggc ccg acg gcc agg ttg aat ttt ccc 417
Thr Ala Val Tyr Tyr Leu Arg Gly Pro Thr Ala Arg Leu Asn Phe Pro
70 75 80

gaa tta ttg ggg tct gac gtg ggc ttc ggg gag ttg tcg gcg gcg agt 465
Glu Leu Leu Gly Ser Asp Val Ala Phe Gly Glu Leu Ser Ala Ala Ser
85 90 95

att cgg aaa aag gcg ata gag gtt ggg gcc aga gtg gat gca gag acg 513
Ile Arg Lys Lys Ala Ile Glu Val Gly Ala Arg Val Asp Ala Glu Thr
100 105 110 115

agt tgt acg tcg ttg ctt agg agt ggt acg cgt gta ccc ggg tct ggg 561
Ser Cys Thr Ser Leu Leu Arg Ser Gly Thr Arg Val Pro Gly Ser Gly
120 125 130

ctt aag gcg tgt tgg ttt cag gag aaa ccc gac ttg aat atg aaa ccc 609

PF59082SeqList_PF59082.txt

Leu Lys Ala Cys Trp Phe Gln Glu Lys Pro Asp Leu Asn Met Lys Pro
 135 140 145
 gaa ccc gag gag aat gat gga gat tat tgg tga tggatacaat acgaggatgg 662
 Glu Pro Glu Glu Asn Asp Gly Asp Tyr Trp
 150 155
 gttggtttgg tgggtcggtc ggtcggggca gttggatgga agatattttc tttctttttt 722
 tttttaagtg aagtgttttg ttatcttgga aacagatgaa acaagttttg atgtttacaa 782
 ggaaaaaaaa aaaaaaa 799

<210> 463
 <211> 157
 <212> PRT
 <213> Helianthus annuus

<400> 463
 Met Glu Ala Ile Ile Thr Gly Gly Gly Asp Gly Pro Cys Asn Arg Pro
 1 5 10 15
 Pro Glu Lys Arg Lys Ser Asp Gln Arg Pro Tyr Lys Gly Ile Arg Met
 20 25 30
 Arg Lys Trp Gly Lys Trp Val Ala Glu Ile Arg Glu Pro Asn Lys Arg
 35 40 45
 Ser Arg Ile Trp Leu Gly Ser Tyr Ser Thr Pro Val Ala Ala Ala Arg
 50 55 60
 Ala Tyr Asp Thr Ala Val Tyr Tyr Leu Arg Gly Pro Thr Ala Arg Leu
 65 70 75 80
 Asn Phe Pro Glu Leu Leu Gly Ser Asp Val Ala Phe Gly Glu Leu Ser
 85 90 95
 Ala Ala Ser Ile Arg Lys Lys Ala Ile Glu Val Gly Ala Arg Val Asp
 100 105 110
 Ala Glu Thr Ser Cys Thr Ser Leu Leu Arg Ser Gly Thr Arg Val Pro
 115 120 125
 Gly Ser Gly Leu Lys Ala Cys Trp Phe Gln Glu Lys Pro Asp Leu Asn
 130 135 140
 Met Lys Pro Glu Pro Glu Glu Asn Asp Gly Asp Tyr Trp
 145 150 155

<210> 464
 <211> 534
 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (1)..(534)

<400> 464
 atg gat cag gga ccg tcg tcg tca aag tac aaa ggc gtg agg aag agg 48
 Met Asp Gln Gly Pro Ser Ser Ser Lys Tyr Lys Gly Val Arg Lys Arg
 1 5 10 15
 aag tgg ggg aag tgg gtt tcg gag atc aga ctt ccc aac agc aga gag 96
 Lys Trp Gly Lys Trp Val Ser Glu Ile Arg Leu Pro Asn Ser Arg Glu
 20 25 30
 cgt atc tgg ttg gga tct tac gac tct ccc gag aag gcg gcg cgc gcc 144
 Arg Ile Trp Leu Gly Ser Tyr Asp Ser Pro Glu Lys Ala Ala Arg Ala
 35 40 45
 ttc gac gcc gct ctt tac tgc ctc cga gga agc ggc acc aag ttc aat 192
 Phe Asp Ala Ala Leu Tyr Cys Leu Arg Gly Ser Gly Thr Lys Phe Asn
 50 55 60
 ttc ccg gat aat cct ccg gcg atc agc ggc gga ggg aac atg tcg cga 240
 Phe Pro Asp Asn Pro Pro Ala Ile Ser Gly Gly Gly Asn Met Ser Arg
 65 70 75 80
 tcg gag atc cga gac gcc gcc gcg agg ttc gct aat tcg gaa gag agt 288
 Ser Glu Ile Arg Asp Ala Ala Ala Arg Phe Ala Asn Ser Glu Glu Ser

PF59082SeqList_PF59082.txt

				85				90					95				
gtg	gcg	agt	gag	atg	gtg	gtg	cag	cag	caa	gag	tct	cct	tcg	acg	acg		336
Val	Ala	Ser	Glu	Met	Val	Val	Gln	Gln	Gln	Glu	Ser	Pro	Ser	Thr	Thr		
			100				105						110				
atg	gcg	att	gat	tcg	gag	ttt	ttg	agt	atg	ctt	ccg	acg	gtc	ggg	tcg		384
Met	Ala	Ile	Asp	Ser	Glu	Phe	Leu	Ser	Met	Leu	Pro	Thr	Val	Gly	Ser		
		115					120					125					
ggt	aat	ttt	gct	tcg	gat	ttc	ggg	ttg	ttt	ccc	ggg	ttc	gat	gat	ttc		432
Gly	Asn	Phe	Ala	Ser	Asp	Phe	Gly	Leu	Phe	Pro	Gly	Phe	Asp	Asp	Phe		
	130					135					140						
gcg	gac	gaa	ttt	tta	ggt	gat	cgt	ttt	gta	gaa	cag	ggt	tcg	cct	acg		480
Ala	Asp	Glu	Phe	Leu	Gly	Asp	Arg	Phe	Val	Glu	Gln	Val	Ser	Pro	Thr		
145					150					155					160		
tgg	aat	ggg	gat	gag	agt	tgt	tat	gat	ggc	tct	gtg	tct	ctt	tgg	aat		528
Trp	Asn	Gly	Asp	Glu	Ser	Cys	Tyr	Asp	Gly	Ser	Val	Ser	Leu	Trp	Asn		
				165					170					175			
ttt	tga																534
Phe																	

<210> 465
 <211> 177
 <212> PRT
 <213> Brassica napus

<400>	465																
Met	Asp	Gln	Gly	Pro	Ser	Ser	Ser	Lys	Tyr	Lys	Gly	Val	Arg	Lys	Arg		
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Lys	Trp	Gly	Lys	Trp	Val	Ser	Glu	Ile	Arg	Leu	Pro	Asn	Ser	Arg	Glu		
			20					25					30				
Arg	Ile	Trp	Leu	Gly	Ser	Tyr	Asp	Ser	Pro	Glu	Lys	Ala	Ala	Arg	Ala		
		35					40					45					
Phe	Asp	Ala	Ala	Leu	Tyr	Cys	Leu	Arg	Gly	Ser	Gly	Thr	Lys	Phe	Asn		
	50					55					60						
Phe	Pro	Asp	Asn	Pro	Pro	Ala	Ile	Ser	Gly	Gly	Gly	Asn	Met	Ser	Arg		
65					70					75					80		
Ser	Glu	Ile	Arg	Asp	Ala	Ala	Ala	Arg	Phe	Ala	Asn	Ser	Glu	Glu	Ser		
				85					90					95			
Val	Ala	Ser	Glu	Met	Val	Val	Gln	Gln	Gln	Glu	Ser	Pro	Ser	Thr	Thr		
			100				105						110				
Met	Ala	Ile	Asp	Ser	Glu	Phe	Leu	Ser	Met	Leu	Pro	Thr	Val	Gly	Ser		
		115					120					125					
Gly	Asn	Phe	Ala	Ser	Asp	Phe	Gly	Leu	Phe	Pro	Gly	Phe	Asp	Asp	Phe		
	130					135					140						
Ala	Asp	Glu	Phe	Leu	Gly	Asp	Arg	Phe	Val	Glu	Gln	Val	Ser	Pro	Thr		
145					150					155					160		
Trp	Asn	Gly	Asp	Glu	Ser	Cys	Tyr	Asp	Gly	Ser	Val	Ser	Leu	Trp	Asn		
				165					170					175			
Phe																	

<210> 466
 <211> 630
 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (1)..(630)

<400>	466																
atg	agt	caa	gac	acc	aaa	aaa	gag	aag	acg	aac	gcg	ggt	aga	gat	tcc		48
Met	Ser	Gln	Asp	Thr	Lys	Lys	Glu	Lys	Thr	Asn	Ala	Val	Arg	Asp	Ser		
1				5					10					15			
ggt	aag	cat	ccg	ggt	tac	cga	ggt	gtc	cga	aag	agg	aac	tgg	ggg	aaa		96
Gly	Lys	His	Pro	Val	Tyr	Arg	Gly	Val	Arg	Lys	Arg	Asn	Trp	Gly	Lys		
			20				25					30					
tgg	gtg	tcg	gag	ata	aga	gag	ccg	agg	aag	aaa	tct	cgt	ata	tgg	ctc		144
Trp	Val	Ser	Glu	Ile	Arg	Glu	Pro	Arg	Lys	Lys	Ser	Arg	Ile	Trp	Leu		

PF59082SeqList_PF59082.txt

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      35      40      45
gga acg ttt cct tcc ccg gag atg gcg gcg cgt gca cac gac gta gcc 192
Gly Thr Phe Pro Ser Pro Glu Met Ala Ala Arg Ala His Asp Val Ala
      50      55      60
gct ttg agc atc aaa gga gcc tct gcg ata ctc aac ttc cct gac ctc 240
Ala Leu Ser Ile Lys Gly Ala Ser Ala Ile Leu Asn Phe Pro Asp Leu
      65      70      75      80
gcc ggt tct ttc cca cgg cca agc tct ctc agc cct cga gac atc caa 288
Ala Gly Ser Phe Pro Arg Pro Ser Ser Leu Ser Pro Arg Asp Ile Gln
      85      90      95
gcc gca gct ctc aaa gct gca cac atg gaa atc atc atg acc ccc tca 336
Ala Ala Ala Leu Lys Ala Ala His Met Glu Ile Ile Met Thr Pro Ser
      100      105      110
cag tct tct act tct tct tca tct ttt acg ttt tct tcc tca cag tcg 384
Gln Ser Ser Thr Ser Ser Ser Phe Thr Phe Ser Ser Ser Gln Ser
      115      120      125
tct tct tct ctg gag tct ctt gtg tct tct tca ggg aca ggc tct gag 432
Ser Ser Ser Leu Glu Ser Leu Val Ser Ser Ser Gly Thr Gly Ser Glu
      130      135      140
gag cta ggg gag att gtt gag ctg ccg agt tta ggg tcg agc tat gat 480
Glu Leu Gly Glu Ile Val Glu Leu Pro Ser Leu Gly Ser Ser Tyr Asp
      145      150      155      160
ggc acg act cag cta agt aac gag ttc att ttc tct gac ccg gca gac 528
Gly Thr Thr Gln Leu Ser Asn Glu Phe Ile Phe Ser Asp Pro Ala Asp
      165      170      175
ttt tgg gtt tat cca cct cac cag ttg tta gaa ggt gat tat gag atg 576
Phe Trp Val Tyr Pro Pro His Gln Leu Leu Glu Gly Asp Tyr Glu Met
      180      185      190
att cct ggc tca ttt tca cag gat tgg gat ctt tca gga ctg ttt aat 624
Ile Pro Gly Ser Phe Ser Gln Asp Trp Asp Leu Ser Gly Leu Phe Asn
      195      200      205
tat taa
Tyr

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<210> 467
 <211> 209
 <212> PRT
 <213> Brassica napus

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<400> 467
Met Ser Gln Asp Thr Lys Lys Glu Lys Thr Asn Ala Val Arg Asp Ser
1      5      10      15
Gly Lys His Pro Val Tyr Arg Gly Val Arg Lys Arg Asn Trp Gly Lys
      20      25      30
Trp Val Ser Glu Ile Arg Glu Pro Arg Lys Lys Ser Arg Ile Trp Leu
      35      40      45
Gly Thr Phe Pro Ser Pro Glu Met Ala Ala Arg Ala His Asp Val Ala
      50      55      60
Ala Leu Ser Ile Lys Gly Ala Ser Ala Ile Leu Asn Phe Pro Asp Leu
      65      70      75      80
Ala Gly Ser Phe Pro Arg Pro Ser Ser Leu Ser Pro Arg Asp Ile Gln
      85      90      95
Ala Ala Ala Leu Lys Ala Ala His Met Glu Ile Ile Met Thr Pro Ser
      100      105      110
Gln Ser Ser Thr Ser Ser Ser Ser Phe Thr Phe Ser Ser Ser Gln Ser
      115      120      125
Ser Ser Ser Leu Glu Ser Leu Val Ser Ser Ser Gly Thr Gly Ser Glu
      130      135      140
Glu Leu Gly Glu Ile Val Glu Leu Pro Ser Leu Gly Ser Ser Tyr Asp
      145      150      155      160
Gly Thr Thr Gln Leu Ser Asn Glu Phe Ile Phe Ser Asp Pro Ala Asp
      165      170      175
Phe Trp Val Tyr Pro Pro His Gln Leu Glu Gly Asp Tyr Glu Met
      180      185      190
Ile Pro Gly Ser Phe Ser Gln Asp Trp Asp Leu Ser Gly Leu Phe Asn
      195      200      205
Tyr

```

PF59082SeqList_PF59082.txt

<210> 468
<211> 435
<212> DNA
<213> Brassica napus

<220>
<221> CDS
<222> (1)..(435)

```

<400> 468
atg gat tac atc gac aac acc gtc gaa act caa tca aag tac aaa ggc      48
Met Asp Tyr Ile Asp Asn Thr Val Glu Thr Gln Ser Lys Tyr Lys Gly
1      5      10      15
atc cgt cgc cgg aaa tgg gga aaa tgg gta tcg gag att aga gtt ccg      96
Ile Arg Arg Arg Lys Trp Gly Lys Trp Val Ser Glu Ile Arg Val Pro
20      25      30
gga act cga gac cgt ctc tgg tta ggc tca ttc tcc acc gca gaa ggc      144
Gly Thr Arg Asp Arg Leu Trp Leu Gly Ser Phe Ser Thr Ala Glu Gly
35      40      45
gca gcc gta gcg cac gac gta gct ttc tac tgt tta cac caa cca aac      192
Ala Ala Val Ala His Asp Val Ala Phe Tyr Cys Leu His Gln Pro Asn
50      55      60
tcg ctc gaa tct ctc aac ttc cct cac ttg ctt cct cct tcc ata gtt      240
Ser Leu Glu Ser Leu Asn Phe Pro His Leu Leu Pro Pro Ser Ile Val
65      70      75      80
tcc aag act tcg ccg agg tct atc cag caa gct gct tct aat gcc gga      288
Ser Lys Thr Ser Pro Arg Ser Ile Gln Gln Ala Ala Ser Asn Ala Gly
85      90      95
atg gcc gtt gac gcc gga atc gtt aac agc tgt gat cac gcg tcc ggg      336
Met Ala Val Asp Ala Gly Ile Val Asn Ser Cys Asp His Ala Ser Gly
100      105      110
aac tct ggg aat gga gat aca acg acg gcg tat tgt gag aat gga ggt      384
Asn Ser Gly Asn Gly Asp Thr Thr Thr Ala Tyr Cys Glu Asn Gly Gly
115      120      125
gcg ttg aat ata tca gtg tat gat tat ttg gac ggt cac gat cac gtt      432
Ala Leu Asn Ile Ser Val Tyr Asp Tyr Leu Asp Gly His Asp His Val
130      135      140
tga
435

```

<210> 469
<211> 144
<212> PRT
<213> Brassica napus

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<400> 469
Met Asp Tyr Ile Asp Asn Thr Val Glu Thr Gln Ser Lys Tyr Lys Gly
1      5      10      15
Ile Arg Arg Arg Lys Trp Gly Lys Trp Val Ser Glu Ile Arg Val Pro
20      25      30
Gly Thr Arg Asp Arg Leu Trp Leu Gly Ser Phe Ser Thr Ala Glu Gly
35      40      45
Ala Ala Val Ala His Asp Val Ala Phe Tyr Cys Leu His Gln Pro Asn
50      55      60
Ser Leu Glu Ser Leu Asn Phe Pro His Leu Leu Pro Pro Ser Ile Val
65      70      75      80
Ser Lys Thr Ser Pro Arg Ser Ile Gln Gln Ala Ala Ser Asn Ala Gly
85      90      95
Met Ala Val Asp Ala Gly Ile Val Asn Ser Cys Asp His Ala Ser Gly
100      105      110
Asn Ser Gly Asn Gly Asp Thr Thr Thr Ala Tyr Cys Glu Asn Gly Gly
115      120      125
Ala Leu Asn Ile Ser Val Tyr Asp Tyr Leu Asp Gly His Asp His Val
130      135      140

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<210> 470
<211> 585

PF59082SeqList_PF59082.txt

<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (1)..(585)

<400> 470

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atg gcg aag aaa gcg atg aag gag gaa gaa gaa gag aat cga aac tcg      48
Met Ala Lys Lys Ala Met Lys Glu Glu Glu Glu Glu Asn Arg Asn Ser
 1      5      10      15
tcg atg cag tca aag tac aga ggc gtg agg aag agg aaa tgg ggg aag      96
Ser Met Gln Ser Lys Tyr Arg Gly Val Arg Lys Arg Lys Trp Gly Lys
      20      25      30
tgg gtg tcg gag atc aga ctt cca cac agc aga gaa cgc atc tgg tta     144
Trp Val Ser Glu Ile Arg Leu Pro His Ser Arg Glu Arg Ile Trp Leu
      35      40      45
ggc tct tac gac act ccc gag aag gcg gcg cgt gcc ttc gac gcc gct     192
Gly Ser Tyr Asp Thr Pro Glu Lys Ala Ala Arg Ala Phe Asp Ala Ala
 50      55      60
cag ttt tgt ctc cgc ggc ggc ggt tcc gca ttc aat ttc ccc gat aac     240
Gln Phe Cys Leu Arg Gly Gly Gly Ser Ala Phe Asn Phe Pro Asp Asn
 65      70      75
cca ccg tcg atc tcc ggc gga agg tcg ttg acg gcg acg gag att cga     288
Pro Pro Ser Ile Ser Gly Gly Arg Ser Leu Thr Ala Thr Glu Ile Arg
      85      90      95
gaa gct gct gct agg ttc gcc aac gct cag gac gat gtt att agt gtc     336
Glu Ala Ala Ala Arg Phe Ala Asn Ala Gln Asp Asp Val Ile Ser Val
      100      105      110
cgg gga gaa gaa tcg ggt ttg tcc gaa atc cga ccg gag tct cct tct     384
Arg Gly Glu Glu Ser Gly Leu Ser Glu Ile Arg Pro Glu Ser Pro Ser
      115      120      125
tca acc tcc gtg tct gaa gtg gat aca tcg tca gcg aca acg ctg gat     432
Ser Thr Ser Val Ser Glu Val Asp Thr Ser Ser Ala Thr Thr Leu Asp
      130      135      140
tgc gat ctg tcg ttg ttt gat atg ctt cct gca gat ttt ggg acg ttt     480
Cys Asp Leu Ser Leu Phe Asp Met Leu Pro Ala Asp Phe Gly Thr Phe
      145      150      155
cca ggg tta gat gac ttc tcc tgt gat gga ttt aca gag att tta ccc     528
Pro Gly Leu Asp Asp Phe Ser Cys Asp Gly Phe Thr Glu Ile Leu Pro
      160      165      170      175
att gaa gat tac gga gaa gag att ttt gat gga tct ttt ttt ctt tgg     576
Ile Glu Asp Tyr Gly Glu Glu Ile Phe Asp Gly Ser Phe Phe Leu Trp
      180      185      190
ggc ttt taa
Gly Phe
      585

```

<210> 471

<211> 194

<212> PRT

<213> Brassica napus

<400> 471

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Met Ala Lys Lys Ala Met Lys Glu Glu Glu Glu Glu Asn Arg Asn Ser
 1      5      10      15
Ser Met Gln Ser Lys Tyr Arg Gly Val Arg Lys Arg Lys Trp Gly Lys
      20      25      30
Trp Val Ser Glu Ile Arg Leu Pro His Ser Arg Glu Arg Ile Trp Leu
      35      40      45
Gly Ser Tyr Asp Thr Pro Glu Lys Ala Ala Arg Ala Phe Asp Ala Ala
      50      55      60
Gln Phe Cys Leu Arg Gly Gly Gly Ser Ala Phe Asn Phe Pro Asp Asn
      65      70      75
Pro Pro Ser Ile Ser Gly Gly Arg Ser Leu Thr Ala Thr Glu Ile Arg
      85      90      95
Glu Ala Ala Ala Arg Phe Ala Asn Ala Gln Asp Asp Val Ile Ser Val
      100      105      110
Arg Gly Glu Glu Ser Gly Leu Ser Glu Ile Arg Pro Glu Ser Pro Ser

```

PF59082SeqList_PF59082.txt

115 120 125
 Ser Thr Ser Val Ser Glu Val Asp Thr Ser Ser Ala Thr Thr Leu Asp
 130 135 140
 Cys Asp Leu Ser Leu Phe Asp Met Leu Pro Ala Asp Phe Gly Thr Phe
 145 150 155 160
 Pro Gly Leu Asp Asp Phe Ser Cys Asp Gly Phe Thr Glu Ile Leu Pro
 165 170 175
 Ile Glu Asp Tyr Gly Glu Glu Ile Phe Asp Gly Ser Phe Phe Leu Trp
 180 185 190
 Gly Phe

<210> 472
 <211> 435
 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (1)..(435)

<400> 472
 atg gat tac atc gac aac acc gtc gaa act caa tca aag tac aaa ggc 48
 Met Asp Tyr Ile Asp Asn Thr Val Glu Thr Gln Ser Lys Tyr Lys Gly
 1 5 10 15
 atc cgt cgc cgg aaa tgg ggg aaa tgg gta tcg gag att cga gtt ccg 96
 Ile Arg Arg Arg Lys Trp Gly Lys Trp Val Ser Glu Ile Arg Val Pro
 20 25 30
 gga act cgc gac cgt ctc tgg tta ggc tca ttc tcc acg gcg gaa ggc 144
 Gly Thr Arg Asp Arg Leu Trp Leu Gly Ser Phe Ser Thr Ala Glu Gly
 35 40 45
 gca gcc gtg gcg cac gac gtg gct ttc tac tgt tta cac caa cca aac 192
 Ala Ala Val Ala His Asp Val Ala Phe Tyr Cys Leu His Gln Pro Asn
 50 55 60
 tcg ctc gaa tct ctc aac ttc cct cac ttg ctt cct cct tcc ata gtt 240
 Ser Leu Glu Ser Leu Asn Phe Pro His Leu Leu Pro Pro Ser Ile Val
 65 70 75 80
 tcc aag act tcg ccg agg tct atc cag caa gct gct tct aat gcc gga 288
 Ser Lys Thr Ser Pro Arg Ser Ile Gln Gln Ala Ala Ser Asn Ala Gly
 85 90 95
 atg gcc gtt gac gcc gga atc gtt aac agc tgt gat cac gcg tcc ggg 336
 Met Ala Val Asp Ala Gly Ile Val Asn Ser Cys Asp His Ala Ser Gly
 100 105 110
 aac tct ggg aat gga gat aca acg acg gcg tat tgt gag aat gga ggt 384
 Asn Ser Gly Asn Gly Asp Thr Thr Ala Tyr Cys Glu Asn Gly Gly
 115 120 125
 gcg ttg aat ata tca gtg tat gat tat ttg gac ggt cac gat cac gtt 432
 Ala Leu Asn Ile Ser Val Tyr Asp Tyr Leu Asp Gly His Asp His Val
 130 135 140
 tga 435

<210> 473
 <211> 144
 <212> PRT
 <213> Brassica napus

<400> 473
 Met Asp Tyr Ile Asp Asn Thr Val Glu Thr Gln Ser Lys Tyr Lys Gly
 1 5 10 15
 Ile Arg Arg Arg Lys Trp Gly Lys Trp Val Ser Glu Ile Arg Val Pro
 20 25 30
 Gly Thr Arg Asp Arg Leu Trp Leu Gly Ser Phe Ser Thr Ala Glu Gly
 35 40 45
 Ala Ala Val Ala His Asp Val Ala Phe Tyr Cys Leu His Gln Pro Asn
 50 55 60
 Ser Leu Glu Ser Leu Asn Phe Pro His Leu Leu Pro Pro Ser Ile Val
 65 70 75 80

PF59082SeqList_PF59082.txt

Ser Lys Thr Ser Pro Arg Ser Ile Gln Gln Ala Ala Ser Asn Ala Gly
 85 90 95
 Met Ala Val Asp Ala Gly Ile Val Asn Ser Cys Asp His Ala Ser Gly
 100 105 110
 Asn Ser Gly Asn Gly Asp Thr Thr Ala Tyr Cys Glu Asn Gly Gly
 115 120 125
 Ala Leu Asn Ile Ser Val Tyr Asp Tyr Leu Asp Gly His Asp His Val
 130 135 140

<210> 474
 <211> 594
 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (1)..(594)

<400> 474
 atg gtg aag aaa gcg atg aag gag gaa gaa gaa gca gag atg aga aac 48
 Met Val Lys Lys Ala Met Lys Glu Glu Glu Glu Ala Glu Met Arg Asn
 1 5 10 15
 tcg tcg atg cag tca aag tac aaa ggc gtg agg aag agg aag tgg ggc 96
 Ser Ser Met Gln Ser Lys Tyr Lys Gly Val Arg Lys Arg Lys Trp Gly
 20 25 30
 aaa tgg gtt tcg gag atc aga ctt ccc aac agc aga gag cga atc tgg 144
 Lys Trp Val Ser Glu Ile Arg Leu Pro Asn Ser Arg Glu Arg Ile Trp
 35 40 45
 cta ggc tct ttc gac act ccc gag aag gcg gcg cgt gcc ttc gac gcc 192
 Leu Gly Ser Phe Asp Thr Pro Glu Lys Ala Ala Arg Ala Phe Asp Ala
 50 55 60
 gcc cag ttt tgt ctc cgc ggc tgc caa tcc ggt ttc aat ttc ccc gat 240
 Ala Gln Phe Cys Leu Arg Gly Cys Gln Ser Gly Phe Asn Phe Pro Asp
 65 70 75 80
 aat ccg ccg tcg atc tcc ggc gga agg tcg acg cct ccg gag atc 288
 Asn Pro Pro Ser Ile Ser Gly Gly Arg Ser Leu Thr Pro Pro Glu Ile
 85 90 95
 cgg gaa gcg gct gct cga tac gca aac gct cag gac gac gat att atc 336
 Arg Glu Ala Ala Ala Arg Tyr Ala Asn Ala Gln Asp Asp Asp Ile Ile
 100 105 110
 atc acc acc gga gaa gaa gaa tcg gtt ttg tcc gaa acc cga ccg gag 384
 Ile Thr Thr Gly Glu Glu Glu Ser Val Leu Ser Glu Thr Arg Pro Glu
 115 120 125
 tct cct tca aca acc tcc gtg tct gaa gca gat acg tcg ctg gat tgc 432
 Ser Pro Ser Thr Thr Ser Val Ser Glu Ala Asp Thr Ser Leu Asp Cys
 130 135 140
 gat cta tcg ttc tta gac acg ctt cct aat gat ttc ggg atg ttt tct 480
 Asp Leu Ser Phe Leu Asp Thr Leu Pro Asn Asp Phe Gly Met Phe Ser
 145 150 155 160
 gtg ttt gat gac ttc tcc gac ggc ttc tcc gat cag ttt aca gag 528
 Val Phe Asp Asp Phe Ser Asp Gly Phe Ser Gly Asp Gln Phe Thr Glu
 165 170 175
 gtt tta ccc gtt gaa gat tac gga gat gtg att ttt gat gag tct ctg 576
 Val Leu Pro Val Glu Asp Tyr Gly Asp Val Ile Phe Asp Glu Ser Leu
 180 185 190
 ttt ctt tgg gat ttt taa 594
 Phe Leu Trp Asp Phe
 195

<210> 475
 <211> 197
 <212> PRT
 <213> Brassica napus

<400> 475
 Met Val Lys Lys Ala Met Lys Glu Glu Glu Glu Ala Glu Met Arg Asn
 1 5 10 15
 Ser Ser Met Gln Ser Lys Tyr Lys Gly Val Arg Lys Arg Lys Trp Gly
 20 25 30

PF59082SeqList_PF59082.txt

Lys Trp Val Ser Glu Ile Arg Leu Pro Asn Ser Arg Glu Arg Ile Trp
 35 40 45
 Leu Gly Ser Phe Asp Thr Pro Glu Lys Ala Ala Arg Ala Phe Asp Ala
 50 55 60
 Ala Gln Phe Cys Leu Arg Gly Cys Gln Ser Gly Phe Asn Phe Pro Asp
 65 70 75 80
 Asn Pro Pro Ser Ile Ser Gly Gly Arg Ser Leu Thr Pro Pro Glu Ile
 85 90 95
 Arg Glu Ala Ala Ala Arg Tyr Ala Asn Ala Gln Asp Asp Asp Ile Ile
 100 105 110
 Ile Thr Thr Gly Glu Glu Glu Ser Val Leu Ser Glu Thr Arg Pro Glu
 115 120 125
 Ser Pro Ser Thr Thr Ser Val Ser Glu Ala Asp Thr Ser Leu Asp Cys
 130 135 140
 Asp Leu Ser Phe Leu Asp Thr Leu Pro Asn Asp Phe Gly Met Phe Ser
 145 150 155 160
 Val Phe Asp Asp Phe Ser Asp Gly Phe Ser Gly Asp Gln Phe Thr Glu
 165 170 175
 Val Leu Pro Val Glu Asp Tyr Gly Asp Val Ile Phe Asp Glu Ser Leu
 180 185 190
 Phe Leu Trp Asp Phe
 195

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 <211> 612
 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (1)..(612)

<400> 476
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 Met Asp His Ser Ser Ser Glu Ser His Leu Asp Asp Tyr Arg Arg
 1 5 10 15
 agg cct cag gcc aag gcc aca gcg aga gca gtg aat aat aat aaa aat 96
 Arg Pro Gln Ala Lys Ala Thr Ala Arg Ala Val Asn Asn Asn Lys Asn
 20 25 30
 atc aag aag aaa aga gtc aaa gaa gat ctt gat gat gat gaa aag att 144
 Ile Lys Lys Lys Arg Val Lys Glu Asp Leu Asp Asp Asp Glu Lys Ile
 35 40 45
 aat gtt tca aag cat caa agt ttt aga ggg gtg aga atg agg caa tgg 192
 Asn Val Ser Lys His Gln Ser Phe Arg Gly Val Arg Met Arg Gln Trp
 50 55 60
 gga aaa tgg gtc tcg gag atc aga gag cca aag aag aaa tct aga atc 240
 Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Lys Lys Lys Ser Arg Ile
 65 70 75 80
 tgg ctt ggt acc ttc ccc acg gcg gag atg gct gct cgt gct cac gac 288
 Trp Leu Gly Thr Phe Pro Thr Ala Glu Met Ala Ala Arg Ala His Asp
 85 90 95
 gtg gcg gct tta gcc ata aaa ggt gac tct gct cat ctc aac ttc ccg 336
 Val Ala Ala Leu Ala Ile Lys Gly Asp Ser Ala His Leu Asn Phe Pro
 100 105 110
 gag cta gcc tac cac ctc cct aga ccg gct agt gcc cac cct aaa gac 384
 Glu Leu Ala Tyr His Leu Pro Arg Pro Ala Ser Ala His Pro Lys Asp
 115 120 125
 atc caa gca gcc gca gcg gag gct gca gct tca gta gtc att gat atg 432
 Ile Gln Ala Ala Ala Ala Glu Ala Ala Ala Ser Val Val Ile Asp Met
 130 135 140
 gac ata gag acg tcg tca cct tct acc gga gcc acg gaa ctg tcg cct 480
 Asp Ile Glu Thr Ser Ser Pro Ser Thr Gly Ala Thr Glu Leu Ser Pro
 145 150 155 160
 cct gct gtg gcc tca aca gcc gat gac gcg ttc tcc gac ctt ccg gac 528
 Pro Ala Val Ala Ser Thr Ala Asp Asp Ala Phe Ser Asp Leu Pro Asp
 165 170 175
 ctc ttc ctc gac gtg aac cac aaa aac gat ggc ttt tgg gag tcc ttc 576
 Leu Phe Leu Asp Val Asn His Lys Asn Asp Gly Phe Trp Glu Ser Phe
 180 185 190

cct tac gag gaa ccc ttc ttc tcg gga agt tac tag
 Pro Tyr Glu Glu Pro Phe Phe Ser Gly Ser Tyr
 195 200

<210> 477
 <211> 203
 <212> PRT
 <213> Brassica napus

<400> 477
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 Arg Pro Gln Ala Lys Ala Thr Ala Arg Ala Val Asn Asn Asn Lys Asn
 20 25 30
 Ile Lys Lys Lys Arg Val Lys Glu Asp Leu Asp Asp Glu Lys Ile
 35 40 45
 Asn Val Ser Lys His Gln Ser Phe Arg Gly Val Arg Met Arg Gln Trp
 50 55 60
 Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Lys Lys Lys Ser Arg Ile
 65 70 75 80
 Trp Leu Gly Thr Phe Pro Thr Ala Glu Met Ala Ala Arg Ala His Asp
 85 90 95
 Val Ala Ala Leu Ala Ile Lys Gly Asp Ser Ala His Leu Asn Phe Pro
 100 105 110
 Glu Leu Ala Tyr His Leu Pro Arg Pro Ala Ser Ala His Pro Lys Asp
 115 120 125
 Ile Gln Ala Ala Ala Ala Glu Ala Ala Ala Ser Val Val Ile Asp Met
 130 135 140
 Asp Ile Glu Thr Ser Ser Pro Ser Thr Gly Ala Thr Glu Leu Ser Pro
 145 150 155 160
 Pro Ala Val Ala Ser Thr Ala Asp Asp Ala Phe Ser Asp Leu Pro Asp
 165 170 175
 Leu Phe Leu Asp Val Asn His Lys Asn Asp Gly Phe Trp Glu Ser Phe
 180 185 190
 Pro Tyr Glu Glu Pro Phe Phe Ser Gly Ser Tyr
 195 200

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 <211> 633
 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (1)..(633)

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 1 5 10
 ccg tct tct cca aag atc aag agc aag aag aat aag att aag aag tac 96
 Pro Ser Ser Pro Lys Ile Lys Ser Lys Lys Asn Lys Ile Lys Lys Tyr 20 25 30
 aaa gga gtg agg atg aga agt tgg gga tca tgg gtg tct gag att agg 144
 Lys Gly Val Arg Met Arg Ser Trp Gly Ser Trp Val Ser Glu Ile Arg 35 40 45
 gca cca aat aaa aag ata agg att tgg ttg ggc tct tac tca aca gct 192
 Ala Pro Asn Lys Lys Ile Arg Ile Trp Leu Gly Ser Tyr Ser Thr Ala 50 55 60
 gaa gca gca gct agg gct tat gat gtt gca ctc ttg tgt cta aaa ggc 240
 Glu Ala Ala Ala Arg Ala Tyr Asp Val Ala Leu Leu Cys Leu Lys Gly 65 70 75 80
 cct caa gcc aat ctc aac ttc ccc agc tct gct tct tct cgc ctt ctg 288
 Pro Gln Ala Asn Leu Asn Phe Pro Ser Ser Ala Ser Ser Arg Leu Leu 85 90 95
 tta gat gaa aag acc cat ttg tcc ccc aaa tcc atc caa aaa att gcc 336
 Leu Asp Glu Lys Thr His Leu Ser Pro Lys Ser Ile Gln Lys Ile Ala 100 105 110
 gct caa gca gcc aac aat tca ttt gac ctt ttt gct cca tct tca tcg 384
 115 120 125

PF59082SeqList_PF59082.txt

Ala	Gln	Ala	Ala	Asn	Asn	Ser	Phe	Asp	Leu	Phe	Ala	Pro	Ser	Ser	Ser		
		115					120				125						
gca	gat	tcg	tca	ccg	ttc	gat	cat	gat	caa	cat	cct	gat	gac	atg	caa		432
Ala	Asp	Ser	Ser	Pro	Phe	Asp	His	Asp	Gln	His	Pro	Asp	Asp	Met	Gln		
		130				135					140						
tct	ttg	ata	ggg	tct	ttc	gta	gac	aat	cgt	gtg	tct	ttg	atg	gat	cca		480
Ser	Leu	Ile	Gly	Ser	Phe	Val	Asp	Asn	Arg	Val	Ser	Leu	Met	Asp	Pro		
		145			150					155					160		
tca	tca	tcg	tgg	tat	gat	aat	gat	cat	aat	ggg	atg	ttc	ttc	ttc	gat		528
Ser	Ser	Ser	Trp	Tyr	Asp	Asn	Asp	His	Asn	Gly	Met	Phe	Phe	Phe	Asp		
				165					170					175			
gat	gga	gct	ccg	ttt	aat	tac	tct	cct	cca	ctg	aac	tcg	acc	acg	aat		576
Asp	Gly	Ala	Pro	Phe	Asn	Tyr	Ser	Pro	Pro	Leu	Asn	Ser	Thr	Thr	Asn		
			180					185					190				
atg	gtc	gat	ggg	tat	ttc	tac	gaa	gat	gct	gat	att	cca	ctt	tgg	agt		624
Met	Val	Asp	Gly	Tyr	Phe	Tyr	Glu	Asp	Ala	Asp	Ile	Pro	Leu	Trp	Ser		
		195					200					205					
ttc	agt	tga															633
Phe	Ser																
	210																

<210> 479
 <211> 210
 <212> PRT
 <213> Brassica napus

<400>	479																
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			20					25					30				
Lys	Gly	Val	Arg	Met	Arg	Ser	Trp	Gly	Ser	Trp	Val	Ser	Glu	Ile	Arg		
		35				40					45						
Ala	Pro	Asn	Lys	Lys	Ile	Arg	Ile	Trp	Leu	Gly	Ser	Tyr	Ser	Thr	Ala		
	50					55				60							
Glu	Ala	Ala	Ala	Arg	Ala	Tyr	Asp	Val	Ala	Leu	Leu	Cys	Leu	Lys	Gly		
65					70				75					80			
Pro	Gln	Ala	Asn	Leu	Asn	Phe	Pro	Ser	Ser	Ala	Ser	Ser	Arg	Leu	Leu		
			85					90						95			
Leu	Asp	Glu	Lys	Thr	His	Leu	Ser	Pro	Lys	Ser	Ile	Gln	Lys	Ile	Ala		
		100						105				110					
Ala	Gln	Ala	Ala	Asn	Asn	Ser	Phe	Asp	Leu	Phe	Ala	Pro	Ser	Ser	Ser		
	115					120					125						
Ala	Asp	Ser	Ser	Pro	Phe	Asp	His	Asp	Gln	His	Pro	Asp	Asp	Met	Gln		
	130					135					140						
Ser	Leu	Ile	Gly	Ser	Phe	Val	Asp	Asn	Arg	Val	Ser	Leu	Met	Asp	Pro		
145					150				155						160		
Ser	Ser	Ser	Trp	Tyr	Asp	Asn	Asp	His	Asn	Gly	Met	Phe	Phe	Phe	Asp		
			165					170					175				
Asp	Gly	Ala	Pro	Phe	Asn	Tyr	Ser	Pro	Pro	Leu	Asn	Ser	Thr	Thr	Asn		
		180						185					190				
Met	Val	Asp	Gly	Tyr	Phe	Tyr	Glu	Asp	Ala	Asp	Ile	Pro	Leu	Trp	Ser		
		195					200					205					
Phe	Ser																
	210																

<210> 480
 <211> 705
 <212> DNA
 <213> Glycine max

<220>
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 <222> (1)..(705)

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Met	Val	Lys	Ser	Glu	His	Lys	Ile	Lys	Thr	Glu	Pro	Ser	Ser	Lys	Glu		
1				5					10					15			

PF59082SeqList_PF59082.txt

atg	cgg	tta	tct	tca	ccc	tca	tca	tca	aca	tca	aca	tca	tca	gat	tgc	96
Met	Arg	Leu	Ser	Ser	Pro	Ser	Ser	Ser	Thr	Ser	Thr	Ser	Ser	Asp	Cys	
			20						25				30			
aag	aag	aag	aag	tac	aag	gga	gtg	aga	atg	agg	agc	tgg	gga	tca	tgg	144
Lys	Lys	Lys	Lys	Tyr	Lys	Gly	Val	Arg	Met	Arg	Ser	Trp	Gly	Ser	Trp	
			35				40					45				
gtg	tct	gag	att	aga	gca	cca	aac	cag	aaa	aca	aga	ata	tgg	tta	ggc	192
Val	Ser	Glu	Ile	Arg	Ala	Pro	Asn	Gln	Lys	Thr	Arg	Ile	Trp	Leu	Gly	
			50			55					60					
tct	tat	tca	acc	cca	gaa	gct	gca	gct	aga	gcc	tat	gat	gct	gca	ctt	240
Ser	Tyr	Ser	Thr	Pro	Glu	Ala	Ala	Ala	Arg	Ala	Tyr	Asp	Ala	Ala	Leu	
					70					75					80	
cta	tgc	ctt	aaa	ggc	tcc	tca	gca	aat	ctc	aat	ttc	cct	tta	agc	tct	288
Leu	Cys	Leu	Lys	Gly	Ser	Ser	Ala	Asn	Leu	Asn	Phe	Pro	Leu	Ser	Ser	
				85					90					95		
tca	caa	caa	tac	att	cct	gga	gat	gct	gtc	atg	tcc	ccc	aaa	tca	atc	336
Ser	Gln	Gln	Tyr	Ile	Pro	Gly	Asp	Ala	Val	Met	Ser	Pro	Lys	Ser	Ile	
			100					105					110			
caa	aga	ggt	gct	gcg	gcc	gcc	gca	tat	agt	ttc	atc	gac	aat	gcc	acc	384
Gln	Arg	Val	Ala	Ala	Ala	Ala	Ala	Tyr	Ser	Phe	Ile	Asp	Asn	Ala	Thr	
			115				120					125				
act	ccc	cct	tcc	cca	cct	ccg	gct	tcg	acc	cca	tca	tca	tca	tca	ttg	432
Thr	Pro	Pro	Ser	Pro	Pro	Pro	Ala	Ser	Thr	Pro	Ser	Ser	Ser	Ser	Leu	
						135					140					
gcc	tca	tcc	ccc	tca	ttg	gtt	tct	tct	ccc	tcg	gat	caa	atc	gat	gac	480
Ala	Ser	Ser	Pro	Ser	Leu	Val	Ser	Ser	Pro	Ser	Asp	Gln	Ile	Asp	Asp	
					150					155					160	
gac	gcc	ttg	ctg	ata	tcg	tct	ttc	caa	gcc	tac	act	agt	tgt	ggt	caa	528
Asp	Ala	Leu	Leu	Ile	Ser	Ser	Phe	Gln	Ala	Tyr	Thr	Ser	Cys	Gly	Gln	
				165					170					175		
gca	aat	caa	tca	atg	gct	gtg	aat	gtg	atg	gag	cct	tgg	tac	acc	ttt	576
Ala	Asn	Gln	Ser	Met	Ala	Val	Asn	Val	Met	Glu	Pro	Trp	Tyr	Thr	Phe	
			180					185					190			
ggt	gat	ggt	ctt	caa	tcc	ccc	aag	tat	gct	gat	cag	atg	cta	agt	ggt	624
Gly	Asp	Gly	Leu	Gln	Ser	Pro	Lys	Tyr	Ala	Asp	Gln	Met	Leu	Ser	Gly	
			195				200					205				
gat	ttc	ttc	cat	gtc	gat	tct	tcc	cat	ctg	ctt	gat	gat	cta	tac	gaa	672
Asp	Phe	Phe	His	Val	Asp	Ser	Ser	His	Leu	Leu	Asp	Asp	Leu	Tyr	Glu	
					215						220					
gaa	agt	gac	att	cgt	ttg	agg	ttc	tgc	tga							705
Glu	Ser	Asp	Ile	Arg	Leu	Trp	Ser	Phe	Cys							
					230											

<210> 481

<211> 234

<212> PRT

<213> Glycine max

<400> 481

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Met	Arg	Leu	Ser	Ser	Pro	Ser	Ser	Ser	Thr	Ser	Thr	Ser	Ser	Asp	Cys
			20					25					30		
Lys	Lys	Lys	Lys	Tyr	Lys	Gly	Val	Arg	Met	Arg	Ser	Trp	Gly	Ser	Trp
			35				40					45			
Val	Ser	Glu	Ile	Arg	Ala	Pro	Asn	Gln	Lys	Thr	Arg	Ile	Trp	Leu	Gly
			50			55					60				
Ser	Tyr	Ser	Thr	Pro	Glu	Ala	Ala	Ala	Arg	Ala	Tyr	Asp	Ala	Ala	Leu
65					70					75					80
Leu	Cys	Leu	Lys	Gly	Ser	Ser	Ala	Asn	Leu	Asn	Phe	Pro	Leu	Ser	Ser
				85					90					95	
Ser	Gln	Gln	Tyr	Ile	Pro	Gly	Asp	Ala	Val	Met	Ser	Pro	Lys	Ser	Ile
			100					105					110		
Gln	Arg	Val	Ala	Ala	Ala	Ala	Ala	Tyr	Ser	Phe	Ile	Asp	Asn	Ala	Thr
			115				120					125			
Thr	Pro	Pro	Ser	Pro	Pro	Pro	Ala	Ser	Thr	Pro	Ser	Ser	Ser	Ser	Leu
						135									
Ala	Ser	Ser	Pro	Ser	Leu	Val	Ser	Ser	Pro	Ser	Asp	Gln	Ile	Asp	Asp
145					150					155					160

PF59082SeqList_PF59082.txt

Asp Ala Leu Leu Ile Ser Ser Phe Gln Ala Tyr Thr Ser Cys Gly Gln
 165 170 175
 Ala Asn Gln Ser Met Ala Val Asn Val Met Glu Pro Trp Tyr Thr Phe
 180 185 190
 Gly Asp Gly Leu Gln Ser Pro Lys Tyr Ala Asp Gln Met Leu Ser Gly
 195 200 205
 Asp Phe Phe His Val Asp Ser Ser His Leu Leu Asp Asp Leu Tyr Glu
 210 215 220
 Glu Ser Asp Ile Arg Leu Trp Ser Phe Cys
 225 230

<210> 482
 <211> 567
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (1)..(567)

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 act ggg cgc cac cct gtg tac cgt gga gtg agg cgt agg agt agt ggc 96
 Thr Gly Arg His Pro Val Tyr Arg Gly Val Arg Arg Arg Ser Ser Gly
 20 25 30
 aaa tgg gtt tct gaa atc cgt gaa ccc aaa aaa cct aac agg att tgg 144
 Lys Trp Val Ser Glu Ile Arg Glu Pro Lys Lys Pro Asn Arg Ile Trp
 35 40 45
 tta ggg aca ttt gcc acc cct gaa atg gct gct att gcc tat gac gtg 192
 Leu Gly Thr Phe Ala Thr Pro Glu Met Ala Ala Ile Ala Tyr Asp Val
 50 55 60
 gca gcg ctt gct ctt aag ggt aag gat gct gaa ctc aac ttc cct aac 240
 Ala Ala Leu Ala Leu Lys Gly Lys Asp Ala Glu Leu Asn Phe Pro Asn
 65 70 75 80
 tcg gct tcc tcc ctc ccc gtc ccc aca tca tct gct gct cgc gac att 288
 Ser Ala Ser Ser Leu Pro Val Pro Thr Ser Ser Ala Ala Arg Asp Ile
 85 90 95
 cag atg gct gcg gct agc gcc gca gcc gct gtc gga gct gcg aat gat 336
 Gln Met Ala Ala Ala Ser Ala Ala Ala Val Gly Ala Ala Asn Asp
 100 105 110
 gca ctt gaa gga agc cga gga ggg aat gct tcg gtt tca ttg acg gaa 384
 Ala Leu Glu Gly Ser Arg Gly Gly Asn Ala Ser Val Ser Leu Thr Glu
 115 120 125
 gag ttt tca ggg gga aat ttg aac cac ttt gtg gat gag gac ttg atc 432
 Glu Phe Ser Gly Gly Asn Leu Asn His Phe Val Asp Glu Asp Leu Ile
 130 135 140
 ttt gac atg ccg aat att ctg gtc aat atg gct gaa gga atg cta ctg 480
 Phe Asp Met Pro Asn Ile Leu Val Asn Met Ala Glu Gly Met Leu Leu
 145 150 155 160
 agt cct cct cgt ttt gat aat ttt gct gct acc gac tat gaa tac atg 528
 Ser Pro Pro Arg Phe Asp Asn Phe Ala Ala Thr Asp Tyr Glu Tyr Met
 165 170 175
 gat gaa gat cct aac ctc tgg ggg ttc cct aat tac tag 567
 Asp Glu Asp Pro Asn Leu Trp Gly Phe Pro Asn Tyr
 180 185

<210> 483
 <211> 188
 <212> PRT
 <213> Glycine max

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 20 25 30
 Lys Trp Val Ser Glu Ile Arg Glu Pro Lys Lys Pro Asn Arg Ile Trp
 35 40 45
 Seite 628

PF59082SeqList_PF59082.txt

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      35      40      45
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Ala Ala Leu Ala Leu Lys Gly Lys Asp Ala Glu Leu Asn Phe Pro Asn
65      70      75
Ser Ala Ser Ser Leu Pro Val Pro Thr Ser Ala Ala Arg Asp Ile
      85      90      95
Gln Met Ala Ala Ala Ser Ala Ala Ala Val Gly Ala Ala Asn Asp
      100      105      110
Ala Leu Glu Gly Ser Arg Gly Gly Asn Ala Ser Val Ser Leu Thr Glu
      115      120      125
Glu Phe Ser Gly Gly Asn Leu Asn His Phe Val Asp Glu Asp Leu Ile
      130      135      140
Phe Asp Met Pro Asn Ile Leu Val Asn Met Ala Glu Gly Met Leu Leu
145      150      155
Ser Pro Pro Arg Phe Asp Asn Phe Ala Ala Thr Asp Tyr Glu Tyr Met
      165      170      175
Asp Glu Asp Pro Asn Leu Trp Gly Phe Pro Asn Tyr
      180      185

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 <211> 534
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (1)..(534)

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      1      5      10      15
aca gca gca gca acg agg aag gtg gtg gag ggt gct gat cag aga aga      96
Thr Ala Ala Ala Thr Arg Lys Val Val Glu Gly Ala Asp Gln Arg Arg
      20      25      30
tac aaa gga ata agg atg agg aag tgg ggc aag tgg gtc gct gaa att      144
Tyr Lys Gly Ile Arg Met Arg Lys Trp Gly Lys Trp Val Ala Glu Ile
      35      40      45
aga gaa ccc aat aag cgt tca agg att tgg ctc ggt tcc tat tct acc      192
Arg Glu Pro Asn Lys Arg Ser Arg Ile Trp Leu Gly Ser Tyr Ser Thr
      50      55      60
cct gtc gca gcc gca cgt gcc tac gac acc gcc gtc ttt tac ctt cga      240
Pro Val Ala Ala Ala Arg Ala Tyr Asp Thr Ala Val Phe Tyr Leu Arg
      65      70      75
gga ccc tcc gcg cgt ctt aac ttc ccg gag ctt ctc atc gga gaa ggc      288
Gly Pro Ser Ala Arg Leu Asn Phe Pro Glu Leu Leu Ile Gly Glu Gly
      85      90      95
gcc gcc gcc ctc acc ggc ggc tgt gac atg tca gca gct tct att agg      336
Ala Ala Ala Leu Thr Gly Gly Cys Asp Met Ser Ala Ala Ser Ile Arg
      100      105      110
aag aag gcc tcc gag gtc ggt gct aga gtc gat gct ctt cag gca acc      384
Lys Lys Ala Ser Glu Val Gly Ala Arg Val Asp Ala Leu Gln Ala Thr
      115      120      125
ctt cac cac cat cac cac cat gtt gtg cca cca cgg cag ctt ctc tct      432
Leu His His His His His Val Val Pro Pro Arg Gln Leu Leu Ser
      130      135      140
gcc agc tgt ggc ggt ggg tcc ggt gat ttt gca gtg cgg gtt gtt gac      480
Ala Ser Cys Gly Gly Gly Ser Gly Asp Phe Ala Val Arg Val Val Asp
145      150      155
ctg aat aag atg ccc gaa ccc gag agc tcc gac tgt gag tgg aac gtg      528
Leu Asn Lys Met Pro Glu Pro Glu Ser Ser Asp Cys Glu Trp Asn Val
      165      170      175
aat tga
Asn

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<210> 485
 <211> 177

PF59082SeqList_PF59082.txt

<212> PRT

<213> Glycine max

<400> 485

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      20      25      30
Tyr Lys Gly Ile Arg Met Arg Lys Trp Gly Lys Trp Val Ala Glu Ile
      35      40      45
Arg Glu Pro Asn Lys Arg Ser Arg Ile Trp Leu Gly Ser Tyr Ser Thr
      50      55      60
Pro Val Ala Ala Ala Arg Ala Tyr Asp Thr Ala Val Phe Tyr Leu Arg
65      70      75      80
Gly Pro Ser Ala Arg Leu Asn Phe Pro Glu Leu Leu Ile Gly Glu Gly
      85      90      95
Ala Ala Ala Leu Thr Gly Gly Cys Asp Met Ser Ala Ala Ser Ile Arg
      100      105      110
Lys Lys Ala Ser Glu Val Gly Ala Arg Val Asp Ala Leu Gln Ala Thr
      115      120      125
Leu His His His His His Val Val Pro Pro Arg Gln Leu Leu Ser
130      135      140
Ala Ser Cys Gly Gly Gly Ser Gly Asp Phe Ala Val Arg Val Val Asp
145      150      155      160
Leu Asn Lys Met Pro Glu Pro Glu Ser Ser Asp Cys Glu Trp Asn Val
      165      170      175
Asn

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<210> 486

<211> 642

<212> DNA

<213> Glycine max

<220>

<221> CDS

<222> (1)..(642)

<400> 486

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 1      5      10      15
ata gcc cca aca aca aca acg gca aca tca tcg tat cgt gga gtt cgt      96
Ile Ala Pro Thr Thr Thr Thr Ala Thr Ser Ser Tyr Arg Gly Val Arg
      20      25      30
cag cga aaa tgg ggc aaa tgg gtg tcc gaa atc cgt gag cct gga aag      144
Gln Arg Lys Trp Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Gly Lys
      35      40      45
aag agc aga ata tgg tta ggg agc tat gag tca cca gag atg gct gca      192
Lys Ser Arg Ile Trp Leu Gly Ser Tyr Glu Ser Pro Glu Met Ala Ala
      50      55      60
gca gca tat gac gtg gca gcg tta cac ctt cgg gga cga gct gca aga      240
Ala Ala Tyr Asp Val Ala Ala Leu His Leu Arg Gly Arg Ala Ala Arg
65      70      75      80
ctc aat ttc ccc gaa tta gtt gag acg ctg cca cgt cca acg agt tcg      288
Leu Asn Phe Pro Glu Leu Val Glu Thr Leu Pro Arg Pro Thr Ser Ser
      85      90      95
aaa ccc gaa gat gtc caa gtg gca gca caa caa gcg gcg gtg atg ttc      336
Lys Pro Glu Asp Val Gln Val Ala Ala Gln Gln Ala Ala Val Met Phe
      100      105      110
aga ata tca cca aca atg tca cct att aac aat cat caa gga tgt gtc      384
Arg Ile Ser Pro Thr Met Ser Pro Ile Asn Asn His Gln Gly Cys Val
      115      120      125
aat gac aat aac att att aag ggt agt gtg gtt cct gtg aga gtg gga      432
Asn Asp Asn Asn Ile Ile Lys Gly Ser Val Val Pro Val Arg Val Gly
130      135      140
ctc tca ccc aca caa att cag gcc atc aat gag tcc cca ttg gac tca      480
Leu Ser Pro Thr Gln Ile Gln Ala Ile Asn Glu Ser Pro Leu Asp Ser
145      150      155      160

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PF59082SeqList_PF59082.txt

cca aag atg tgg atg gtg caa atg gca gag gca ctc agg ttt ggt ttc	528
Pro Lys Met Trp Met Val Gln Met Ala Glu Ala Leu Arg Phe Gly Phe	
gat gat cac tct atg atg atg ctg cct tct gat gat gat gat tat gct	576
Asp Asp His Ser Met Met Met Leu Pro Ser Asp Asp Asp Tyr Ala	
ttg gag ttg agt gga tgg gaa gaa ata cag cat gaa tct tta tgg gac	624
Leu Glu Leu Ser Gly Trp Glu Glu Ile Gln His Glu Ser Leu Trp Asp	
tct cca gaa tat atg taa	642
Ser Pro Glu Tyr Met	
210	

<210> 487
 <211> 213
 <212> PRT
 <213> Glycine max

<400> 487	
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20 25 30	
Gln Arg Lys Trp Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Gly Lys	
35 40 45	
Lys Ser Arg Ile Trp Leu Gly Ser Tyr Glu Ser Pro Glu Met Ala Ala	
50 55 60	
Ala Ala Tyr Asp Val Ala Ala Leu His Leu Arg Gly Arg Ala Ala Arg	
65 70 75 80	
Leu Asn Phe Pro Glu Leu Val Glu Thr Leu Pro Arg Pro Thr Ser Ser	
85 90 95	
Lys Pro Glu Asp Val Gln Val Ala Ala Gln Gln Ala Ala Val Met Phe	
100 105 110	
Arg Ile Ser Pro Thr Met Ser Pro Ile Asn Asn His Gln Gly Cys Val	
115 120 125	
Asn Asp Asn Asn Ile Ile Lys Gly Ser Val Val Pro Val Arg Val Gly	
130 135 140	
Leu Ser Pro Thr Gln Ile Gln Ala Ile Asn Glu Ser Pro Leu Asp Ser	
145 150 155 160	
Pro Lys Met Trp Met Val Gln Met Ala Glu Ala Leu Arg Phe Gly Phe	
165 170 175	
Asp Asp His Ser Met Met Met Leu Pro Ser Asp Asp Asp Tyr Ala	
180 185 190	
Leu Glu Leu Ser Gly Trp Glu Glu Ile Gln His Glu Ser Leu Trp Asp	
195 200 205	
Ser Pro Glu Tyr Met	
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 <213> Glycine max

<220>
 <221> CDS
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Met Val Met Glu Glu Ser Asn Pro Leu Asp Asn Glu Val Gln Pro Thr	
1 5 10 15	
act tca tca tcc tct ttc acc att act act ccc tct acc tcc tct tcc	96
Thr Ser Ser Ser Ser Phe Thr Ile Thr Thr Pro Ser Thr Ser Ser Ser	
20 25 30	
tcc tcc ata gaa gaa gcc act aac act act act aag gag aaa aag aag	144
Ser Ser Ile Glu Glu Ala Thr Asn Thr Thr Thr Lys Glu Lys Lys Lys	
35 40 45	
aag aga gcc att agt aat att gaa ggg aag cac cct acg tat aga gga	192
Lys Arg Ala Ile Ser Asn Ile Glu Gly Lys His Pro Thr Tyr Arg Gly	

PF59082SeqList_PF59082.txt

50	55	60		
gta cgt atg cgt caa tgg ggc aaa tgg gta tcc gaa att aga gag cca	240			
Val Arg Met Arg Gln Trp Gly Lys Trp Val Ser Glu Ile Arg Glu Pro				
65	70	75	80	
agg aag aaa tca aga att tgg ctt gga act ttt ccc act ccc gat atg	288			
Arg Lys Lys Ser Arg Ile Trp Leu Gly Thr Phe Pro Thr Pro Asp Met				
85	90	95		
gcg gct cga gcc cat gat gtg gcg gct ctc acg atc aaa ggc agc tcg	336			
Ala Ala Arg Ala His Asp Val Ala Ala Leu Thr Ile Lys Gly Ser Ser				
100	105	110		
gct tac ctc aat ttc ccc gaa tta gcc aag ctg ccc cgc ccc gcc	384			
Ala Tyr Leu Asn Phe Pro Glu Leu Ala Ala Lys Leu Pro Arg Pro Ala				
115	120	125		
agc acc tcc ccc aag gac atc caa gct gcg gcg gct aaa gcc tcc gcc	432			
Ser Thr Ser Pro Lys Asp Ile Gln Ala Ala Ala Lys Ala Ser Ala				
130	135	140		
ttg gat ttc ggt cac caa agc cat gaa gcc gaa tcc gag ctg agc caa	480			
Leu Asp Phe Gly His Gln Ser His Glu Ala Glu Ser Glu Leu Ser Gln				
145	150	155	160	
gcc gtt tcc tcc tca atc caa aca caa tca tca tca tcc aat	528			
Ala Val Ser Ser Ile Gln Thr Gln Ser Ser Ser Ser Ser Ser Asn				
165	170	175		
tca tcg ttg aag ggt gtg gat gac aca ttc ttg gac ctt cct gat ctc	576			
Ser Ser Leu Lys Gly Val Asp Asp Thr Phe Leu Asp Leu Pro Asp Leu				
180	185	190		
tct ctt gac ttg agc cat gga gcc gat gag ttt cat tat tca tcg gct	624			
Ser Leu Asp Leu Ser His Gly Ala Asp Glu Phe His Tyr Ser Ser Ala				
195	200	205		
tggt ctt gta gcc gga gcc gaa cat ata gag ctg ggt ttc cgg ctt gag	672			
Trp Leu Val Ala Gly Ala Glu His Ile Glu Leu Gly Phe Arg Leu Glu				
210	215	220		
gaa cct ttt ctt tgg gaa tca tat taa	699			
Glu Pro Phe Leu Trp Glu Ser Tyr				
225	230			

<210> 489
 <211> 232
 <212> PRT
 <213> Glycine max

<400> 489	
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	15
Ser Ser Ile Glu Glu Ala Thr Asn Thr Thr Thr Lys Glu Lys Lys Lys	20
	25
Lys Arg Ala Ile Ser Asn Ile Glu Gly Lys His Pro Thr Tyr Arg Gly	30
	35
Val Arg Met Arg Gln Trp Gly Lys Trp Val Ser Glu Ile Arg Glu Pro	40
65	45
Arg Lys Lys Ser Arg Ile Trp Leu Gly Thr Phe Pro Thr Pro Asp Met	50
	55
Ala Ala Arg Ala His Asp Val Ala Ala Leu Thr Ile Lys Gly Ser Ser	60
	65
Ala Tyr Leu Asn Phe Pro Glu Leu Ala Ala Lys Leu Pro Arg Pro Ala	70
	75
Ser Thr Ser Pro Lys Asp Ile Gln Ala Ala Ala Ala Lys Ala Ser Ala	80
	85
Leu Asp Phe Gly His Gln Ser His Glu Ala Glu Ser Glu Leu Ser Gln	90
145	95
Ala Val Ser Ser Ser Ile Gln Thr Gln Ser Ser Ser Ser Ser Ser Asn	100
	105
Ser Ser Leu Lys Gly Val Asp Asp Thr Phe Leu Asp Leu Pro Asp Leu	110
	115
Ser Leu Asp Leu Ser His Gly Ala Asp Glu Phe His Tyr Ser Ser Ala	120
	125
Trp Leu Val Ala Gly Ala Glu His Ile Glu Leu Gly Phe Arg Leu Glu	130
	135
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	215
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PF59082SeqList_PF59082.txt

Glu Pro Phe Leu Trp Glu Ser Tyr
225 230

<210> 490
<211> 699
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (1)..(699)

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Met Val Met Glu Glu Ser Asn Pro Leu Asp Asn Glu Val Gln Pro Thr
1      5      10      15
act tca tca tcc tct ttc acc att act act ccc tct acc tcc tct tcc      96
Thr Ser Ser Ser Ser Phe Thr Ile Thr Thr Pro Ser Thr Ser Ser Ser
20      25      30
tcc tcc ata gaa gaa gcc act aac act act act aag gag aaa aag aag      144
Ser Ser Ile Glu Glu Ala Thr Asn Thr Thr Thr Lys Glu Lys Lys Lys
35      40      45
aag aga gcc att agt aat att gaa ggg aag cac cct acg tat aga gga      192
Lys Arg Ala Ile Ser Asn Ile Glu Gly Lys His Pro Thr Tyr Arg Gly
50      55      60
gta cgt atg cgt caa tgg ggc aaa tgg gta tcc gaa att aga gag cca      240
Val Arg Met Arg Gln Trp Gly Lys Trp Val Ser Glu Ile Arg Glu Pro
65      70      75
agg aag aaa tca aga att tgg ctt gga act ttt ccc act ccc gat atg      288
Arg Lys Lys Ser Arg Ile Trp Leu Gly Thr Phe Pro Thr Pro Asp Met
85      90      95
gcg gct cga gcc cat gat gtg gcg gct ctc acg atc aaa ggc agc tcg      336
Ala Ala Arg Ala His Asp Val Ala Ala Leu Thr Ile Lys Gly Ser Ser
100      105      110
gct tac ctc aat ttc ccc gaa tta gcc gac aag ctg ccc cgc gcc gcc      384
Ala Tyr Leu Asn Phe Pro Glu Leu Ala Asp Lys Leu Pro Arg Pro Ala
115      120      125
agc acc tcc ccc aag gac atc caa gct gcg gcg gct aaa gcc tcc gcc      432
Ser Thr Ser Pro Lys Asp Ile Gln Ala Ala Ala Lys Ala Ser Ala
130      135      140
ttg gat ttc ggt cac caa agc cat gaa gcc gaa tcc gag ctg agc caa      480
Leu Asp Phe Gly His Gln Ser His Glu Ala Glu Ser Glu Leu Ser Gln
145      150      155
gcc gtt tcc tcc tca atc caa aca caa cca tca tca tca tcc aat      528
Ala Val Ser Ser Ser Ile Gln Thr Gln Pro Ser Ser Ser Ser Asn
160      165      170
tca tcg ttg aag ggt gtg gat gac aca ttc ttg gac ctt cct gat ctc      576
Ser Ser Leu Lys Gly Val Asp Asp Thr Phe Leu Asp Leu Pro Asp Leu
175      180      185
tct ctt gac ttg agc cat gga gcc gat gag ttt cat tat tca tcg gct      624
Ser Leu Asp Leu Ser His Gly Ala Asp Glu Phe His Tyr Ser Ser Ala
190      195      200
tgg ctt gta gcc gga gcc gaa cat ata gag ctg ggt ttc cgg ctt gag      672
Trp Leu Val Ala Gly Ala Glu His Ile Glu Leu Gly Phe Arg Leu Glu
205      210      215
gaa cct ttt ctt tgg gaa tca tat taa
220      225      230
Glu Pro Phe Leu Trp Glu Ser Tyr
225 230

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<210> 491
<211> 232
<212> PRT
<213> Glycine max

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<400> 491
Met Val Met Glu Glu Ser Asn Pro Leu Asp Asn Glu Val Gln Pro Thr
1      5      10      15
Thr Ser Ser Ser Ser Phe Thr Ile Thr Thr Pro Ser Thr Ser Ser
20      25      30

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PF59082SeqList_PF59082.txt

Ser Ser Ile Glu Glu Ala Thr Asn Thr Thr Thr Lys Glu Lys Lys Lys
 35 40 45
 Lys Arg Ala Ile Ser Asn Ile Glu Gly Lys His Pro Thr Tyr Arg Gly
 50 55 60
 Val Arg Met Arg Gln Trp Gly Lys Trp Val Ser Glu Ile Arg Glu Pro
 65 70 75 80
 Arg Lys Lys Ser Arg Ile Trp Leu Gly Thr Phe Pro Thr Pro Asp Met
 85 90 95
 Ala Ala Arg Ala His Asp Val Ala Ala Leu Thr Ile Lys Gly Ser Ser
 100 105 110
 Ala Tyr Leu Asn Phe Pro Glu Leu Ala Asp Lys Leu Pro Arg Pro Ala
 115 120 125
 Ser Thr Ser Pro Lys Asp Ile Gln Ala Ala Ala Lys Ala Ser Ala
 130 135 140
 Leu Asp Phe Gly His Gln Ser His Glu Ala Glu Ser Glu Leu Ser Gln
 145 150 155 160
 Ala Val Ser Ser Ser Ile Gln Thr Gln Pro Ser Ser Ser Ser Ser Asn
 165 170 175
 Ser Ser Leu Lys Gly Val Asp Asp Thr Phe Leu Asp Leu Pro Asp Leu
 180 185 190
 Ser Leu Asp Leu Ser His Gly Ala Asp Glu Phe His Tyr Ser Ser Ala
 195 200 205
 Trp Leu Val Ala Gly Ala Glu His Ile Glu Leu Gly Phe Arg Leu Glu
 210 215 220
 Glu Pro Phe Leu Trp Glu Ser Tyr
 225 230

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 <213> Glycine max

<220>
 <221> CDS
 <222> (1)..(576)

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 gcc acc acg agc tcc gtt gac aag ccc gcc act cct cac gcc gga ggc 96
 Ala Thr Thr Ser Ser Val Asp Lys Pro Ala Thr Pro His Ala Gly Gly
 20 25 30
 acc cgc cac ccg ctc ttc cgc ggc gtc cgc aag cgc cgc tgg ggc aaa 144
 Thr Arg His Pro Leu Phe Arg Gly Val Arg Lys Arg Arg Trp Gly Lys
 35 40 45
 tgg gtc tcc gaa atc cgg gag ccg agg aaa aag tca cgc ata tgg ctc 192
 Trp Val Ser Glu Ile Arg Glu Pro Arg Lys Lys Ser Arg Ile Trp Leu
 50 55 60
 ggc tcc ttc ccg gcg ccg gag atg gcg gcg aag gcc tac gac gtt gcc 240
 Gly Ser Phe Pro Ala Pro Glu Met Ala Ala Lys Ala Tyr Asp Val Ala
 65 70 75 80
 gcc tac tgc ctc aag ggc tgc aag gcg cag ctc aac ttc ccc gac gag 288
 Ala Tyr Cys Leu Lys Gly Cys Lys Ala Gln Leu Asn Phe Pro Asp Glu
 85 90 95
 gtc cac cgg ctt ccg ccg ctc ccc tcc tcc tgc acc gcc cgg gac atc 336
 Val His Arg Leu Pro Pro Leu Pro Ser Ser Cys Thr Ala Arg Asp Ile
 100 105 110
 cag gcc gcc gca gcc aag gcc gcc cac atg atg atg gtc cag gct gcc 384
 Gln Ala Ala Ala Lys Ala Ala His Met Met Met Val Gln Ala Ala
 115 120 125
 tcc gcc gac tcg ccg gag aaa agc agc agc att acc tcc gac tgc gac 432
 Ser Ala Asp Ser Pro Glu Lys Ser Ser Ser Ile Thr Ser Asp Cys Asp
 130 135 140
 ggc agc ggt ggt gac gac ttc tgg ggc gaa att gag ctg cca gaa ctg 480
 Gly Ser Gly Gly Asp Asp Phe Trp Gly Glu Ile Glu Leu Pro Glu Leu
 145 150 155 160
 ctc aac ggc aag tgg tgg gcc tcc gac cgc cac gta acg ccg tgg ccg 528
 Leu Asn Gly Lys Trp Trp Ala Ser Asp Arg His Val Thr Pro Trp Pro

<div> <div>165</div> <div>170</div> <div>175</div> </div>															
gag	act	gag	ctt	acg	gcc	cag	ctg	ccc	ttc	acc	acg	gcg	tgc	ttg	573
Glu	Thr	Glu	Leu	Thr	Ala	Gln	Leu	Pro	Phe	Thr	Thr	Ala	Cys	Leu	
			180									185	190		
tag															576

<210> 493
<211> 191
<212> PRT
<213> Glycine max

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Met	Glu	Gln	Glu	Leu	Pro	Arg	Ser	Ser	Val	Pro	Asp	Asp	Ala	Thr	Ala	
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Ala	Thr	Thr	Ser	Val	Asp	Lys	Pro	Pro	Ala	Thr	Pro	His	Ala	Gly	Gly	
			20				25						30			
Thr	Arg	His	Pro	Leu	Phe	Arg	Gly	Val	Arg	Lys	Arg	Arg	Trp	Gly	Lys	
		35					40					45				
Trp	Val	Ser	Glu	Ile	Arg	Glu	Pro	Arg	Lys	Lys	Ser	Arg	Ile	Trp	Leu	
	50					55					60					
Gly	Ser	Phe	Pro	Ala	Pro	Glu	Met	Ala	Ala	Lys	Ala	Tyr	Asp	Val	Ala	
65					70					75					80	
Ala	Tyr	Cys	Leu	Lys	Gly	Cys	Lys	Ala	Gln	Leu	Asn	Phe	Pro	Asp	Glu	
				85					90					95		
Val	His	Arg	Leu	Pro	Pro	Leu	Pro	Ser	Ser	Cys	Thr	Ala	Arg	Asp	Ile	
			100					105					110			
Gln	Ala	Ala	Ala	Ala	Lys	Ala	Ala	His	Met	Met	Met	Val	Gln	Ala	Ala	
		115					120					125				
Ser	Ala	Asp	Ser	Pro	Glu	Lys	Ser	Ser	Ser	Ile	Thr	Ser	Asp	Cys	Asp	
	130					135					140					
Gly	Ser	Gly	Gly	Asp	Asp	Phe	Trp	Gly	Glu	Ile	Glu	Leu	Pro	Glu	Leu	
145					150					155					160	
Leu	Asn	Gly	Lys	Trp	Trp	Ala	Ser	Asp	Arg	His	Val	Thr	Pro	Trp	Pro	
				165					170					175		
Glu	Thr	Glu	Leu	Thr	Ala	Gln	Leu	Pro	Phe	Thr	Thr	Ala	Cys	Leu		
			180					185					190			

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<210> 494
<211> 474
<212> DNA
<213> Helianthus annuus
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<220>
<221> CDS
<222> (1)..(474)

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Met	Glu	Ala	Ile	Ile	Thr	Gly	Gly	Gly	Asp	Gly	Pro	Cys	Asn	Arg	Pro			
1				5					10					15				
ccg	gag	aaa	agg	aag	agt	gat	caa	cgg	ccg	tac	aag	ggg	ata	cgc	atg			96
Pro	Glu	Lys	Arg	Lys	Ser	Asp	Gln	Arg	Pro	Tyr	Lys	Gly	Ile	Arg	Met			
			20					25					30					
agg	aag	tgg	gga	aaa	tgg	gtg	gcg	gag	att	cgg	gag	ccg	aat	aag	cgg			144
Arg	Lys	Trp	Gly	Lys	Trp	Val	Ala	Glu	Ile	Arg	Glu	Pro	Asn	Lys	Arg			
			35				40					45						
tcc	agg	att	tgg	ttg	ggg	tcc	tat	tcg	acg	ccc	gtg	gcc	gct	gca	cgg			192
Ser	Arg	Ile	Trp	Leu	Gly	Ser	Tyr	Ser	Thr	Pro	Val	Ala	Ala	Ala	Arg			
	50				55						60							
gcg	tac	gac	acg	gcc	gta	tac	tac	cta	cgg	ggc	ccg	acg	gcc	agg	ttg			240
Ala	Tyr	Asp	Thr	Ala	Val	Tyr	Tyr	Leu	Arg	Gly	Pro	Thr	Ala	Arg	Leu			
	65				70					75					80			
aat	ttt	ccc	gaa	tta	ttg	ggg	tct	gac	gtg	gcg	ttc	ggg	gag	ttg	tcg			288
Asn	Phe	Pro	Glu	Leu	Leu	Gly	Ser	Asp	Val	Ala	Phe	Gly	Glu	Leu	Ser			
				85					90					95				
gcg	gcg	agt	att	cgg	aaa	aag	gcg	ata	gag	gtt	ggg	gcc	aga	gat				336
Ala	Ala	Ser	Ile	Arg	Lys	Lys	Ala	Ile	Glu	Val	Gly	Ala	Arg	Val	Asp			

PF59082SeqList_PF59082.txt

gca	gag	acg	agt	tgt	acg	tcg	ttg	ctt	agg	agt	ggt	acg	cgt	gta	ccc	384
Ala	Glu	Thr	Ser	Cys	Thr	Ser	Leu	Leu	Arg	Ser	Gly	Thr	Arg	Val	Pro	
		115					120					125				
ggg	tct	ggg	ctt	aag	gcg	tgt	tgg	ttt	cag	gag	aaa	ccc	gac	ttg	aat	432
Gly	Ser	Gly	Leu	Lys	Ala	Cys	Trp	Phe	Gln	Glu	Lys	Pro	Asp	Leu	Asn	
		130				135					140					
atg	aaa	ccc	gaa	ccc	gag	gag	aat	gat	gga	gat	tat	tgg	tga			474
Met	Lys	Pro	Glu	Pro	Glu	Glu	Asn	Asp	Gly	Asp	Tyr	Trp				
145					150					155						

<210> 495

<211> 157

<212> PRT

<213> Helianthus annuus

<400> 495

Met	Glu	Ala	Ile	Ile	Thr	Gly	Gly	Gly	Asp	Gly	Pro	Cys	Asn	Arg	Pro
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Pro	Glu	Lys	Arg	Lys	Ser	Asp	Gln	Arg	Pro	Tyr	Lys	Gly	Ile	Arg	Met
			20				25						30		
Arg	Lys	Trp	Gly	Lys	Trp	Val	Ala	Glu	Ile	Arg	Glu	Pro	Asn	Lys	Arg
		35				40						45			
Ser	Arg	Ile	Trp	Leu	Gly	Ser	Tyr	Ser	Thr	Pro	Val	Ala	Ala	Ala	Arg
	50					55					60				
Ala	Tyr	Asp	Thr	Ala	Val	Tyr	Tyr	Leu	Arg	Gly	Pro	Thr	Ala	Arg	Leu
65					70					75					80
Asn	Phe	Pro	Glu	Leu	Leu	Gly	Ser	Asp	Val	Ala	Phe	Gly	Glu	Leu	Ser
				85					90					95	
Ala	Ala	Ser	Ile	Arg	Lys	Lys	Ala	Ile	Glu	Val	Gly	Ala	Arg	Val	Asp
			100					105					110		
Ala	Glu	Thr	Ser	Cys	Thr	Ser	Leu	Leu	Arg	Ser	Gly	Thr	Arg	Val	Pro
		115					120					125			
Gly	Ser	Gly	Leu	Lys	Ala	Cys	Trp	Phe	Gln	Glu	Lys	Pro	Asp	Leu	Asn
	130					135					140				
Met	Lys	Pro	Glu	Pro	Glu	Glu	Asn	Asp	Gly	Asp	Tyr	Trp			
145					150					155					

<210> 496

<211> 618

<212> DNA

<213> Helianthus annuus

<220>

<221> CDS

<222> (1)..(618)

<400> 496

atg	aat	cac	aac	acc	gcc	acc	gct	acc	aca	acc	acc	acc	aaa	cgc	ccc	48
Met	Asn	His	Asn	Thr	Ala	Thr	Ala	Thr	Thr	Thr	Thr	Thr	Lys	Arg	Pro	
1				5					10					15		
aaa	ccc	ggg	gac	ctt	aac	gat	gaa	gtt	aca	aaa	aaa	aca	aag	aaa	acc	96
Lys	Pro	Gly	Asp	Leu	Asn	Asp	Glu	Val	Thr	Lys	Lys	Thr	Lys	Lys	Thr	
			20					25					30			
gac	att	gat	caa	ata	aac	cac	cct	gta	tac	cgc	ggt	gta	cgc	aag	cgg	144
Asp	Ile	Asp	Gln	Ile	Asn	His	Pro	Val	Tyr	Arg	Gly	Val	Arg	Lys	Arg	
		35					40					45				
agt	tgg	gga	aaa	tgg	gtg	tca	gaa	atc	cgc	gag	cca	aag	aaa	aaa	tca	192
Ser	Trp	Gly	Lys	Trp	Val	Ser	Glu	Ile	Arg	Glu	Pro	Lys	Lys	Lys	Ser	
		50				55					60					
aga	ata	tgg	ctt	ggg	act	ttt	gac	acc	cca	gag	atg	gcg	gcc	cgg	gcc	240
Arg	Ile	Trp	Leu	Gly	Thr	Phe	Asp	Thr	Pro	Glu	Met	Ala	Ala	Arg	Ala	
		65			70					75					80	
cat	gat	gta	gct	gcg	gtc	gcc	atc	aaa	ggt	aac	tcg	gcc	atc	ctc	aac	288
His	Asp	Val	Ala	Ala	Val	Ala	Ile	Lys	Gly	Asn	Ser	Ala	Ile	Leu	Asn	
				85					90					95		
ttc	cct	gag	ctg	gct	cac	caa	ctc	ccc	aag	ccg	gct	tca	aac	tcc	cct	336
Phe	Pro	Glu	Leu	Ala	His	Gln	Leu	Pro	Lys	Pro	Ala	Ser	Asn	Ser	Pro	
			100					105					110			

PF59082SeqList_PF59082.txt

aga	gat	atc	caa	gcc	gcg	gct	ctt	aaa	gcc	gcc	acg	ttg	gtc	ctt	cga	384
Arg	Asp	Ile	Gln	Ala	Ala	Ala	Leu	Lys	Ala	Ala	Thr	Leu	Val	Leu	Arg	
		115					120					125				
agc	ctt	aat	tcc	gat	aaa	gat	gat	caa	tcc	gag	cca	acc	cgg	att	gat	432
Ser	Leu	Asn	Ser	Asp	Lys	Asp	Asp	Gln	Ser	Glu	Pro	Thr	Arg	Ile	Asp	
	130					135					140					
caa	ctt	cca	tgt	tct	tcg	tct	tca	tct	tca	tgt	tca	ctt	caa	agt	gat	480
Gln	Leu	Pro	Cys	Ser	Ser	Ser	Ser	Ser	Ser	Cys	Ser	Leu	Gln	Ser	Asp	
	145				150					155					160	
ata	acg	gat	gac	ccg	ttt	ctt	gat	ttg	ccg	gat	ctt	tat	atg	gac	ctc	528
Ile	Thr	Asp	Asp	Pro	Phe	Leu	Asp	Leu	Pro	Asp	Leu	Tyr	Met	Asp	Leu	
				165					170					175		
ggg	tac	cgg	att	ttt	aac	aca	ttg	tca	gag	aag	att	act	ggt	aac	aat	576
Gly	Tyr	Arg	Ile	Phe	Asn	Thr	Leu	Ser	Glu	Lys	Ile	Thr	Gly	Asn	Asn	
			180					185					190			
gaa	ttc	tgg	cca	gaa	gat	cat	ttc	ttg	tgg	agc	tat	agc	taa			618
Glu	Phe	Trp	Pro	Glu	Asp	His	Phe	Leu	Trp	Ser	Tyr	Ser				
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<210> 497
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 <212> PRT
 <213> Helianthus annuus

<400> 497															
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			20				25						30		
Asp	Ile	Asp	Gln	Ile	Asn	His	Pro	Val	Tyr	Arg	Gly	Val	Arg	Lys	Arg
		35					40					45			
Ser	Trp	Gly	Lys	Trp	Val	Ser	Glu	Ile	Arg	Glu	Pro	Lys	Lys	Lys	Ser
	50					55				60					
Arg	Ile	Trp	Leu	Gly	Thr	Phe	Asp	Thr	Pro	Glu	Met	Ala	Ala	Arg	Ala
	65			70						75				80	
His	Asp	Val	Ala	Ala	Val	Ala	Ile	Lys	Gly	Asn	Ser	Ala	Ile	Leu	Asn
			85						90					95	
Phe	Pro	Glu	Leu	Ala	His	Gln	Leu	Pro	Lys	Pro	Ala	Ser	Asn	Ser	Pro
			100					105					110		
Arg	Asp	Ile	Gln	Ala	Ala	Ala	Leu	Lys	Ala	Ala	Thr	Leu	Val	Leu	Arg
		115					120					125			
Ser	Leu	Asn	Ser	Asp	Lys	Asp	Asp	Gln	Ser	Glu	Pro	Thr	Arg	Ile	Asp
	130					135					140				
Gln	Leu	Pro	Cys	Ser	Ser	Ser	Ser	Ser	Cys	Ser	Ser	Leu	Gln	Ser	Asp
	145			150					155					160	
Ile	Thr	Asp	Asp	Pro	Phe	Leu	Asp	Leu	Pro	Asp	Leu	Tyr	Met	Asp	Leu
			165					170					175		
Gly	Tyr	Arg	Ile	Phe	Asn	Thr	Leu	Ser	Glu	Lys	Ile	Thr	Gly	Asn	Asn
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Met	Asp	Gln	Met	Leu	Gly	Lys	His	Leu	Gln	Met	Pro	Ser	Val	Thr	Thr	
	1			5					10					15		
agc	gcc	gcc	tgc	cag	cag	ccg	cag	tcg	ccg	ccg	ccg	tcg	ccg	cag	cag	96
Ser	Ala	Ala	Cys	Gln	Gln	Pro	Gln	Ser	Pro	Pro	Pro	Ser	Pro	Gln	Gln	
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cag	tac	cgg	ggc	gtg	cgg	aag	cgc	aag	tgg	ggc	aag	tgg	gtg	tcg	gag	144

PF59082SeqList_PF59082.txt

Gln	Tyr	Arg	Gly	Val	Arg	Lys	Arg	Lys	Trp	Gly	Lys	Trp	Val	Ser	Glu	
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Ile	Arg	Gln	Pro	Gly	Thr	Lys	Thr	Arg	Ile	Trp	Leu	Gly	Ser	Phe	Glu	
	50					55					60					
tcg	gcc	gag	atg	gcc	gcg	gtg	gcg	cac	gac	gtg	gcg	gcg	ctg	cgc	ctg	240
Ser	Ala	Glu	Met	Ala	Ala	Val	Ala	His	Asp	Val	Ala	Ala	Leu	Arg	Leu	
	65				70					75					80	
cgg	ggc	cgc	gac	gcg	cag	ctc	aac	ttc	ccg	ggc	tgc	gtc	gcc	tgg	ctg	288
Arg	Gly	Arg	Asp	Ala	Gln	Leu	Asn	Phe	Pro	Gly	Cys	Val	Ala	Trp	Leu	
				85					90					95		
ccc	cgc	ccg	gcg	acc	tcg	cac	gcg	cgc	gac	gtc	cgc	gcc	gcg	gcg	gcc	336
Pro	Arg	Pro	Ala	Thr	Ser	His	Ala	Arg	Asp	Val	Arg	Ala	Ala	Ala	Ala	
			100					105				110				
gag	gcc	gcc	gac	cgc	gtg	cgc	tgc	gac	ccg	gcg	ctg	ctg	ctg	ctc	cag	384
Glu	Ala	Ala	Asp	Arg	Val	Arg	Cys	Asp	Pro	Ala	Leu	Leu	Leu	Leu	Gln	
	115					120					125					
cag	gcg	gcg	gca	gcg	cgg	tgc	cac	gac	tac	gac	cac	gac	cac	gag	ttc	432
Gln	Ala	Ala	Ala	Ala	Arg	Cys	His	Asp	Tyr	Asp	His	Asp	His	Glu	Phe	
	130					135				140						
ggg	gcc	ggg	ccg	gcg	ccg	gtg	gtc	gag	ctc	ggg	aac	gac	gag	gag	ttc	480
Gly	Ala	Gly	Pro	Ala	Pro	Val	Val	Glu	Leu	Gly	Asn	Asp	Glu	Glu	Phe	
	145				150					155					160	
gag	ctg	gac	ctg	gac	tcg	ccc	agc	ctc	tgg	gcc	gag	atg	gcg	gag	gcc	528
Glu	Leu	Asp	Leu	Asp	Ser	Pro	Ser	Leu	Trp	Ala	Glu	Met	Ala	Glu	Ala	
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atg	ctc	ctg	gac	ccg	ccg	ggc	tgg	gcc	acc	ggc	gtc	gtc	ggc	gac	ccg	576
Met	Leu	Leu	Asp	Pro	Pro	Gly	Trp	Ala	Thr	Gly	Val	Val	Gly	Asp	Pro	
			180					185					190			
gcg	gag	gtg	gcc	ctg	tgc	tgg	cca	cac	ggc	tcc	ctc	tgg	gac	gcc	tgc	624
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tag																627

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Gln	Tyr	Arg	Gly	Val	Arg	Lys	Arg	Lys	Trp	Gly	Lys	Trp	Val	Ser	Glu	
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Ile	Arg	Gln	Pro	Gly	Thr	Lys	Thr	Arg	Ile	Trp	Leu	Gly	Ser	Phe	Glu	
	50					55					60					
Ser	Ala	Glu	Met	Ala	Ala	Val	Ala	His	Asp	Val	Ala	Ala	Leu	Arg	Leu	
	65				70					75					80	
Arg	Gly	Arg	Asp	Ala	Gln	Leu	Asn	Phe	Pro	Gly	Cys	Val	Ala	Trp	Leu	
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Pro	Arg	Pro	Ala	Thr	Ser	His	Ala	Arg	Asp	Val	Arg	Ala	Ala	Ala	Ala	
			100					105					110			
Glu	Ala	Ala	Asp	Arg	Val	Arg	Cys	Asp	Pro	Ala	Leu	Leu	Leu	Leu	Gln	
		115					120					125				
Gln	Ala	Ala	Ala	Ala	Arg	Cys	His	Asp	Tyr	Asp	His	Asp	His	Glu	Phe	
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Gly	Ala	Gly	Pro	Ala	Pro	Val	Val	Glu	Leu	Gly	Asn	Asp	Glu	Glu	Phe	
	145				150					155					160	
Glu	Leu	Asp	Leu	Asp	Ser	Pro	Ser	Leu	Trp	Ala	Glu	Met	Ala	Glu	Ala	
				165					170				175			
Met	Leu	Leu	Asp	Pro	Pro	Gly	Trp	Ala	Thr	Gly	Val	Val	Gly	Asp	Pro	
			180					185					190			
Ala	Glu	Val	Ala	Leu	Cys	Trp	Pro	His	Gly	Ser	Leu	Trp	Asp	Ala	Cys	
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PF59082SeqList_PF59082.txt

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agc gcc gcc tgc cag cag ccg cag tcg ccg ccg ccg tcc ccg cag cag      96
Ser Ala Ala Cys Gln Gln Pro Gln Ser Pro Pro Pro Ser Pro Gln Gln
          20          25          30
cag cag cag tac cgg ggc gtg cgg aag cgc aag tgg ggc aag tgg gtg     144
Gln Gln Gln Tyr Arg Gly Val Arg Lys Arg Lys Trp Gly Lys Trp Val
          35          40          45
tcg gag atc cgg cag ccg ggc acc aag acg cgc atc tgg ctc ggc agc     192
Ser Glu Ile Arg Gln Pro Gly Thr Lys Thr Arg Ile Trp Leu Gly Ser
          50          55          60
ttc gag tcg gcc gag atg gcc gcg gtg gcg cac gac gtg gcg gcg ctg     240
Phe Glu Ser Ala Glu Met Ala Ala Val Ala His Asp Val Ala Ala Leu
          65          70          75          80
cgc ctg cgg ggc cgc gac gcg cag ctc aac ttc ccg ggc tgc gtc gcc     288
Arg Leu Arg Gly Arg Asp Ala Gln Leu Asn Phe Pro Gly Cys Val Ala
          85          90          95
tgg ctg ccc cgc ccg gcg acc tcg cac gcg cgc gac gtc cgc gcc gcg     336
Trp Leu Pro Arg Pro Ala Thr Ser His Ala Arg Asp Val Arg Ala Ala
          100          105          110
gcg gcc gag gcc gcc gac cgc gtg cgc tgc gac ccg gcg ctg ctg ctg     384
Ala Ala Glu Ala Ala Asp Arg Val Arg Cys Asp Pro Ala Leu Leu Leu
          115          120          125
ctc cag cag gcg gcg gca gcg cgg tgc cac gac tac gac cac gac cac     432
Leu Gln Gln Ala Ala Ala Ala Arg Cys His Asp Tyr Asp His Asp His
          130          135          140
gag ttc ggg gcc ggg ccg gcg ccg gtg gtc gag ctc ggg agc gac gag     480
Glu Phe Gly Ala Gly Pro Ala Pro Val Val Glu Leu Gly Ser Asp Glu
          145          150          155          160
gag ttc gag ctg gac ctg gac tcg ccc agc ctc tgg gcc gag atg gcg     528
Glu Phe Glu Leu Asp Leu Asp Ser Pro Ser Leu Trp Ala Glu Met Ala
          165          170          175
gag gcc atg ctc ctg gac ccg ccg ggc tgg gcc acc ggc gtc gtc ggc     576
Glu Ala Met Leu Leu Asp Pro Pro Gly Trp Ala Thr Gly Val Val Gly
          180          185          190
gac gcg gcg gag gtg gcc ctg tgc tgg cca cac ggc tcc ctc tgg gac     624
Asp Ala Ala Glu Val Ala Leu Cys Trp Pro His Gly Ser Leu Trp Asp
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gcc tgc tag
Ala Cys
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<210> 501
<211> 210
<212> PRT
<213> Zea mays

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          20          25          30
Gln Gln Gln Tyr Arg Gly Val Arg Lys Arg Lys Trp Gly Lys Trp Val
          35          40          45
Ser Glu Ile Arg Gln Pro Gly Thr Lys Thr Arg Ile Trp Leu Gly Ser
          50          55          60
Phe Glu Ser Ala Glu Met Ala Ala Val Ala His Asp Val Ala Ala Leu
          65          70          75          80
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PF59082SeqList_PF59082.txt

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 Trp Leu Pro Arg Pro Ala Thr Ser His Ala Arg Asp Val Arg Ala Ala
 100 105 110
 Ala Ala Glu Ala Ala Asp Arg Val Arg Cys Asp Pro Ala Leu Leu Leu
 115 120 125
 Leu Gln Gln Ala Ala Ala Ala Arg Cys His Asp Tyr Asp His Asp His
 130 135 140
 Glu Phe Gly Ala Gly Pro Ala Pro Val Val Glu Leu Gly Ser Asp Glu
 145 150 155 160
 Glu Phe Glu Leu Asp Leu Asp Ser Pro Ser Leu Trp Ala Glu Met Ala
 165 170 175
 Glu Ala Met Leu Leu Asp Pro Pro Gly Trp Ala Thr Gly Val Val Gly
 180 185 190
 Asp Ala Ala Glu Val Ala Leu Cys Trp Pro His Gly Ser Leu Trp Asp
 195 200 205
 Ala Cys
 210

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<220>
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<210> 503
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<220>
 <223> primer

<400> 503
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<210> 504
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 <212> DNA
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<220>
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<400> 504
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<210> 505
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<220>
 <223> primer

<400> 505
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<210> 506
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<222> (4)..(4)
<223> Xaa in position 4 is any amino acid

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<222> (6)..(6)
<223> Xaa in position 6 is any amino acid

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<222> (8)..(8)
<223> Xaa in position 8 is any amino acid

<220>
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<223> Xaa in position 18 is any amino acid

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<222> (20)..(23)
<223> Xaa in position 20 to 23 is any amino acid

<220>
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<222> (29)..(33)
<223> Xaa in position 29 to 33 is any amino acid

<220>
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<222> (35)..(35)
<223> Xaa in position 35 is any amino acid

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<222> (38)..(38)
<223> Xaa in position 38 is any amino acid

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<222> (40)..(40)
<223> Xaa in position 40 is any amino acid

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<222> (42)..(42)
<223> Xaa in position 42 is any amino acid

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<221> Variant
<222> (44)..(48)
<223> Xaa in position 44 to 48 is any amino acid

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<222> (50)..(51)
<223> Xaa in position 50 to 51 is any amino acid

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<222> (52)..(53)
<223> Xaa in position 52 to 53 is any or no amino acid

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<222> (55)..(55)
<223> Xaa in position 55 is any amino acid

<220>
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<222> (60)..(77)
<223> Xaa in position 60 to 77 is any amino acid

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<222> (78)..(83)
<223> Xaa in position 78 to 83 is any or no amino acid

<220>
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<222> (86)..(87)
<223> Xaa in position 86 to 87 is any amino acid

<400> 510

PF59082SeqList_PF59082.txt

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      20      25      30
Xaa Glu Xaa Ala Ala Xaa Ala Xaa Asp Xaa Ala Xaa Xaa Xaa Xaa Xaa
      35      40      45
Gly Xaa Xaa Xaa Xaa Ala Xaa Leu Asn Phe Pro Xaa Xaa Xaa Xaa Xaa
      50      55      60
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
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<210> 511

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<222> (16)..(16)

<223> Xaa in position 16 is Ile or Leu

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<221> Variant

<222> (20)..(20)

<223> Xaa in position 20 is Ser or Thr

<220>

<221> Variant

<222> (21)..(21)

<223> Xaa in position 21 is Phe or Tyr

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<222> (22)..(23)

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<221> Variant

<222> (25)..(25)

<223> Xaa in position 25 is Asp or Glu

<220>

<221> Variant

<222> (26)..(26)

<223> Xaa in position 26 is any amino acid

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<222> (29)..(29)

<223> Xaa in position 29 is any amino acid

<220>

<221> Variant

<222> (31)..(31)

<223> Xaa in position 31 is Phe, His or Tyr

<220>

<221> Variant

<222> (33)..(33)

<223> Xaa in position 33 is Ala or Val

<220>

<221> Variant

<222> (35)..(37)

<223> Xaa in position 35 to 37 is any amino acid

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<222> (38)..(38)

<223> Xaa in position 38 is Phe, Ile or Leu

<220>

<221> Variant

<222> (39)..(39)

<223> Xaa in position 39 is His, Lys or Arg

<220>

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<222> (40)..(40)

<223> Xaa in position 40 is Gly or Gln

<400> 511

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<213> Arabidopsis thaliana

<220>

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<400> 512

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Gly	Asp	Ala	Tyr	Thr	Val	Ser	Asp	Pro	Thr	Lys	Asn	Val	Asp	Glu	Asp	
			20					25					30			
ggt	cga	gag	aag	cgt	acc	ggg	acg	tgg	ctt	acg	gcg	agt	gcg	cat	att	144
Gly	Arg	Glu	Lys	Arg	Thr	Gly	Thr	Trp	Leu	Thr	Ala	Ser	Ala	His	Ile	
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Ile	Thr	Ala	Val	Ile	Gly	Ser	Gly	Val	Leu	Ser	Leu	Ala	Trp	Ala	Ile	
			50			55		60								
gct	cag	ctt	ggt	tgg	atc	gca	ggg	aca	tcg	atc	tta	ctc	att	ttc	tcg	240
Ala	Gln	Leu	Gly	Trp	Ile	Ala	Gly	Thr	Ser	Ile	Leu	Leu	Ile	Phe	Ser	
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ttc	att	act	tac	ttc	acc	tcc	acc	atg	ctt	gcc	gat	tgc	tac	cgt	gcg	288
Phe	Ile	Thr	Tyr	Phe	Thr	Ser	Thr	Met	Leu	Ala	Asp	Cys	Tyr	Arg	Ala	
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PF59082SeqList_PF59082.txt																
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			100					105					110			
cga	tct	tac	ctc	ggt	ggt	agg	aaa	gtg	cag	ctc	tgt	gga	gtg	gca	caa	384
Arg	Ser		Leu	Gly	Gly	Arg	Lys	Val	Gln	Leu	Cys	Gly	Val	Ala	Gln	
		115					120					125				
tat	ggg	aat	ctg	att	ggg	gtc	act	gtt	ggt	tac	acc	atc	act	gct	tct	432
Tyr	Gly	Asn	Leu	Ile	Gly	Val	Thr	Val	Gly	Tyr	Thr	Ile	Thr	Ala	Ser	
	130					135					140					
att	agt	ttg	gta	gcg	gta	ggg	aaa	tcg	aac	tgc	ttc	cac	gat	aaa	ggg	480
Ile	Ser	Leu	Val	Ala	Val	Gly	Lys	Ser	Asn	Cys	Phe	His	Asp	Lys	Gly	
	145				150					155					160	
cac	act	gcg	gat	tgt	act	ata	tcg	aat	tat	ccg	tat	atg	gcg	gtt	ttt	528
His	Thr	Ala	Asp	Cys	Thr	Ile	Ser	Asn	Tyr	Pro	Tyr	Met	Ala	Val	Phe	
			165						170					175		
ggc	att	att	cag	gtt	att	ctt	agc	cag	atc	cca	aat	ttc	cac	aag	ctc	576
Gly	Ile	Ile	Gln	Val	Ile	Leu	Ser	Gln	Ile	Pro	Asn	Phe	His	Lys	Leu	
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tct	ttt	ctt	tcc	att	atg	gcc	gcg	gtc	atg	tcc	ttt	act	tat	gca	act	624
Ser	Phe		Leu	Ser	Ile	Met	Ala	Val	Met	Ser	Phe	Thr	Tyr	Ala	Thr	
		195					200					205				
att	gga	atc	ggt	cta	gcc	atc	gca	acc	gtc	gca	ggg	ggg	aaa	gtg	ggt	672
Ile	Gly	Ile	Gly	Leu	Ala	Ile	Ala	Thr	Val	Ala	Gly	Gly	Lys	Val	Gly	
	210				215					220						
aag	acg	agt	atg	acg	ggc	aca	gcg	gtt	gga	gta	gat	gta	acc	gca	gct	720
Lys	Thr	Ser	Met	Thr	Gly	Thr	Ala	Val	Gly	Val	Asp	Val	Thr	Ala	Ala	
	225				230				235						240	
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Gln	Lys	Ile	Trp	Arg	Ser	Phe	Gln	Ala	Val	Gly	Asp	Ile	Ala	Phe	Ala	
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Tyr	Ala	Tyr	Ala	Thr	Val	Leu	Ile	Glu	Ile	Gln	Asp	Thr	Leu	Arg	Ser	
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Ser	Pro		Glu	Asn	Lys	Ala	Met	Lys	Arg	Ala	Ser	Leu	Val	Gly	Val	
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Ser	Thr	Thr	Thr	Phe	Phe	Tyr	Ile	Leu	Cys	Gly	Cys	Ile	Gly	Tyr	Ala	
	290					295					300					
gca	ttt	gga	aac	aat	gcc	cct	gga	gat	ttc	ctc	aca	gat	ttc	ggg	ttt	960
Ala	Phe	Gly	Asn	Asn	Ala	Pro	Gly	Asp	Phe	Leu	Thr	Asp	Phe	Gly	Phe	
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ttc	gag	ccc	ttt	tgg	ctc	att	gac	ttt	gca	aac	gct	tgc	atc	gct	gtc	1008
Phe	Glu	Pro	Phe	Trp	Leu	Ile	Asp	Phe	Ala	Asn	Ala	Cys	Ile	Ala	Val	
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cac	ctt	att	ggt	gcc	tat	cag	gtg	ttc	gcg	cag	ccg	ata	ttc	cag	ttt	1056
His	Leu	Ile	Gly	Ala	Tyr	Gln	Val	Phe	Ala	Gln	Pro	Ile	Phe	Gln	Phe	
			340					345					350			
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Val	Glu	Lys	Lys	Cys	Asn	Arg	Asn	Tyr	Pro	Asp	Asn	Lys	Phe	Ile	Thr	
		355					360					365				
tct	gaa	tat	tca	gta	aac	gta	cct	ttc	ctt	gga	aaa	ttc	aac	att	agc	1152
Ser	Glu	Tyr	Ser	Val	Asn	Val	Pro	Phe	Leu	Gly	Lys	Phe	Asn	Ile	Ser	
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ctc	ttc	aga	ttg	gtg	tgg	agg	aca	gct	tat	gtg	gtt	ata	acc	act	gtt	1200
Leu	Phe	Arg	Leu	Val	Trp	Arg	Thr	Ala	Tyr	Val	Val	Ile	Thr	Thr	Val	
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Val	Ala	Met	Ile	Phe	Pro	Phe	Phe	Asn	Ala	Ile	Leu	Gly	Leu	Ile	Gly	
				405					410					415		
gca	gct	tcc	ttc	tgg	cct	tta	acg	gtt	tat	ttc	cct	gtg	gag	atg	cac	1296
Ala	Ala	Ser	Phe	Trp	Pro	Leu	Thr	Val	Tyr	Phe	Pro	Val	Glu	Met	His	
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Ile	Ala	Gln	Thr	Lys	Ile	Lys	Lys	Tyr	Ser	Ala	Arg	Trp	Ile	Ala	Leu	
		435					440					445				
aaa	acg	atg	tgc	tat	gtt	tgc	ttg	atc	gtc	tcg	ctc	tta	gct	gca	gcc	1392
Lys	Thr	Met	Cys	Tyr	Val	Cys	Leu	Ile	Val	Ser	Leu	Leu	Ala	Ala	Ala	
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PF59082SeqList_PF59082.txt

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cgg	act	atg	cat	gag	tga											1458
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 35 40 45
 Ile Thr Ala Val Ile Gly Ser Gly Val Leu Ser Leu Ala Trp Ala Ile
 50 55 60
 Ala Gln Leu Gly Trp Ile Ala Gly Thr Ser Ile Leu Leu Ile Phe Ser
 65 70 75 80
 Phe Ile Thr Tyr Phe Thr Ser Thr Met Leu Ala Asp Cys Tyr Arg Ala
 85 90 95
 Pro Asp Pro Val Thr Gly Lys Arg Asn Tyr Thr Tyr Met Asp Val Val
 100 105 110
 Arg Ser Tyr Leu Gly Gly Arg Lys Val Gln Leu Cys Gly Val Ala Gln
 115 120 125
 Tyr Gly Asn Leu Ile Gly Val Thr Val Gly Tyr Thr Ile Thr Ala Ser
 130 135 140
 Ile Ser Leu Val Ala Val Gly Lys Ser Asn Cys Phe His Asp Lys Gly
 145 150 155 160
 His Thr Ala Asp Cys Thr Ile Ser Asn Tyr Pro Tyr Met Ala Val Phe
 165 170 175
 Gly Ile Ile Gln Val Ile Leu Ser Gln Ile Pro Asn Phe His Lys Leu
 180 185 190
 Ser Phe Leu Ser Ile Met Ala Ala Val Met Ser Phe Thr Tyr Ala Thr
 195 200 205
 Ile Gly Ile Gly Leu Ala Ile Ala Thr Val Ala Gly Lys Val Gly
 210 215 220
 Lys Thr Ser Met Thr Gly Thr Ala Val Gly Val Asp Val Thr Ala Ala
 225 230 235 240
 Gln Lys Ile Trp Arg Ser Phe Gln Ala Val Gly Asp Ile Ala Phe Ala
 245 250 255
 Tyr Ala Tyr Ala Thr Val Leu Ile Glu Ile Gln Asp Thr Leu Arg Ser
 260 265 270
 Ser Pro Ala Glu Asn Lys Ala Met Lys Arg Ala Ser Leu Val Gly Val
 275 280 285
 Ser Thr Thr Thr Phe Phe Tyr Ile Leu Cys Gly Cys Ile Gly Tyr Ala
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 305 310 315 320
 Phe Glu Pro Phe Trp Leu Ile Asp Phe Ala Asn Ala Cys Ile Ala Val
 325 330 335
 His Leu Ile Gly Ala Tyr Gln Val Phe Ala Gln Pro Ile Phe Gln Phe
 340 345 350
 Val Glu Lys Lys Cys Asn Arg Asn Tyr Pro Asp Asn Lys Phe Ile Thr
 355 360 365
 Ser Glu Tyr Ser Val Asn Val Pro Phe Leu Gly Lys Phe Asn Ile Ser
 370 375 380
 Leu Phe Arg Leu Val Trp Arg Thr Ala Tyr Val Val Ile Thr Thr Val
 385 390 395 400
 Val Ala Met Ile Phe Pro Phe Phe Asn Ala Ile Leu Gly Leu Ile Gly
 405 410 415
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 Ile Ala Gln Thr Lys Ile Lys Lys Tyr Ser Ala Arg Trp Ile Ala Leu
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PF59082SeqList_PF59082.txt

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 ctctcctttg acttcattcc ccttctctat ttaaccatt attgtttttc tcgcaaacta 180

 tcatgaattc taattgcctt ttcttttttc tatagttcat tatcttagtt caccaaactc 240

 ttataagtag agccaagcca aaccaaccac accaagtaca agcagagagt tacaacacat 300

 atttcttttt cttttccctt tttcctaggc acagcacacg ccctctcaaa tagaaactga 360

 gag atg aat tct gat cag ttt cag aag aac agc atg ttc gta gaa acc 408
 Met Asn Ser Asp Gln Phe Gln Lys Asn Ser Met Phe Val Glu Thr
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 Pro Glu Asp Gly Gly Lys Asn Phe Asp Asp Gly Arg Val Arg Arg
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 acg ggt aca tgg ata act gcg agt gcc cat atc ata acg gca gtg ata 504
 Thr Gly Thr Trp Ile Thr Ala Ser Ala His Ile Ile Thr Ala Val Ile
 35 40 45
 ggg tca gga gtg ttg tca ctt gca tgg gca att gca caa atg ggt tgg 552
 Gly Ser Gly Val Leu Ser Leu Ala Trp Ala Ile Ala Gln Met Gly Trp
 50 55 60
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 Val Ala Gly Pro Ala Val Leu Phe Ala Phe Ser Phe Ile Thr Tyr Phe
 65 70 75
 act tcc act ctt ctt gcc gac tgt tat cgt tca cct gat cct gtt cat 648
 Thr Ser Thr Leu Leu Ala Asp Cys Tyr Arg Ser Pro Asp Pro Val His
 80 85 90 95
 ggc aag cga aac tac acc tat tcc gat gtt gtc aga tcc gtc tta gga 696
 Gly Lys Arg Asn Tyr Thr Tyr Ser Asp Val Arg Ser Val Leu Gly
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 ggg agg aaa ttt cag ctg tgt gga tta gct cag tac ata aat ctt gtc 744
 Gly Arg Lys Phe Gln Leu Cys Gly Leu Ala Gln Tyr Ile Asn Leu Val
 115 120 125
 ggt gta act atc ggt tac acg ata acg gct tca att agt atg gtg gcg 792
 Gly Val Thr Ile Gly Tyr Thr Ile Thr Ala Ser Ile Ser Met Val Ala
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 gtg aag agg tcg aat tgt ttt cac aaa cat ggt cat cat gtt aag tgc 840
 Val Lys Arg Ser Asn Cys Phe His Lys His Gly His Val Lys Cys

PF59082SeqList_PF59082.txt

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Val	Leu	Ser	Gln	Ile	Pro	Asn	Phe	His	Lys	Leu	Trp	Trp	Leu	Ser	Ile	
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gtt	gca	gca	gtt	atg	tct	ttt	gct	tat	tct	tcc	att	ggc	ctc	ggg	ctc	984
Val	Ala	Ala	Val	Met	Ser	Phe	Ala	Tyr	Ser	Ser	Ile	Gly	Leu	Gly	Leu	
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Ser	Val	Ala	Lys	Val	Ala	Gly	Gly	Gly	Glu	Pro	Val	Arg	Thr	Thr	Leu	
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acg	ggg	gtg	caa	gtt	ggg	gta	gac	gtt	aca	gga	tcc	gag	aag	gtc	tgg	1080
Thr	Gly	Val	Gln	Val	Gly	Val	Asp	Val	Thr	Gly	Ser	Glu	Lys	Val	Trp	
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Arg	Thr	Phe	Gln	Ala	Ile	Gly	Asp	Ile	Ala	Phe	Ala	Tyr	Ala	Tyr	Ser	
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Asn	Val	Leu	Ile	Glu	Ile	Gln	Asp	Thr	Leu	Lys	Ser	Ser	Pro	Pro	Glu	
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Asn	Lys	Val	Met	Lys	Arg	Ala	Ser	Leu	Ile	Gly	Ile	Leu	Thr	Thr	Thr	
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Leu	Phe	Tyr	Val	Leu	Cys	Gly	Cys	Leu	Gly	Tyr	Ala	Ala	Phe	Gly	Asn	
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Asp	Ala	Pro	Gly	Asn	Phe	Leu	Thr	Gly	Phe	Gly	Phe	Tyr	Glu	Pro	Phe	
tgg	ctc	ata	gac	ttt	gct	aac	atc	tgc	ata	gcc	gtg	cac	ttg	gtt	gga	1368
Trp	Leu	Ile	Asp	Phe	Ala	Asn	Ile	Cys	Ile	Ala	Val	His	Leu	Val	Gly	
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Ala	Tyr	Gln	Val	Phe	Cys	Gln	Pro	Ile	Phe	Gly	Phe	Val	Glu	Asn	Trp	
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ggt	aag	gaa	agg	tgg	cca	aat	agc	caa	ttt	gta	aat	gga	gaa	cac	gct	1464
Gly	Lys	Glu	Arg	Trp	Pro	Asn	Ser	Gln	Phe	Val	Asn	Gly	Glu	His	Ala	
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Leu	Asn	Phe	Pro	Leu	Cys	Gly	Thr	Phe	Pro	Val	Asn	Phe	Phe	Arg	Val	
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gtg	tgg	aga	aca	aca	tat	gtc	atc	atc	act	gct	ttg	ata	gct	atg	atg	1560
Val	Trp	Arg	Thr	Thr	Tyr	Val	Ile	Ile	Thr	Ala	Leu	Ile	Ala	Met	Met	
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Phe	Pro	Phe	Phe	Asn	Asp	Phe	Leu	Gly	Leu	Ile	Gly	Ser	Leu	Ser	Phe	
400					405				410						415	
tgg	cca	tta	acc	gtt	tac	ttc	ccc	ata	gaa	atg	tac	att	aag	cag	tca	1656
Trp	Pro	Leu	Thr	Val	Tyr	Phe	Pro	Ile	Glu	Met	Tyr	Ile	Lys	Gln	Ser	
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aag	atg	caa	agg	ttt	tcc	ttc	acg	tgg	aca	tgg	ctc	aag	ata	ctg	agc	1704
Lys	Met	Gln	Arg	Phe	Ser	Phe	Thr	Trp	Thr	Trp	Leu	Lys	Ile	Leu	Ser	
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Trp	Ala	Cys	Leu	Ile	Val	Ser	Ile	Ile	Ser	Ala	Ala	Gly	Ser	Ile	Gln	
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ggc	ctc	gct	caa	gat	ctc	aag	aaa	tat	cag	ccc	ttc	aaa	gcc	cag	caa	1800
Gly	Leu	Ala	Gln	Asp	Leu	Lys	Lys	Tyr	Gln	Pro	Phe	Lys	Ala	Gln	Gln	
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2007

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 35 40 45
 Ser Gly Val Leu Ser Leu Ala Trp Ala Ile Ala Gln Met Gly Trp Val
 50 55 60
 Ala Gly Pro Ala Val Leu Phe Ala Phe Ser Phe Ile Thr Tyr Phe Thr
 65 70 75 80
 Ser Thr Leu Leu Ala Asp Cys Tyr Arg Ser Pro Asp Pro Val His Gly
 85 90 95
 Lys Arg Asn Tyr Thr Tyr Ser Asp Val Arg Ser Val Leu Gly Gly
 100 105 110
 Arg Lys Phe Gln Leu Cys Gly Leu Ala Gln Tyr Ile Asn Leu Val Gly
 115 120 125
 Val Thr Ile Gly Tyr Thr Ile Thr Ala Ser Ile Ser Met Val Ala Val
 130 135 140
 Lys Arg Ser Asn Cys Phe His Lys His Gly His Val Lys Cys Tyr
 145 150 155 160
 Thr Ser Asn Asn Pro Phe Met Ile Leu Phe Ala Cys Ile Gln Ile Val
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 Ala Ala Val Met Ser Phe Ala Tyr Ser Ser Ile Gly Leu Gly Leu Ser
 195 200 205
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 210 215 220
 Gly Val Gln Val Gly Val Asp Val Thr Gly Ser Glu Lys Val Trp Arg
 225 230 235 240
 Thr Phe Gln Ala Ile Gly Asp Ile Ala Phe Ala Tyr Ala Tyr Ser Asn
 245 250 255
 Val Leu Ile Glu Ile Gln Asp Thr Leu Lys Ser Ser Pro Pro Glu Asn
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 Lys Val Met Lys Arg Ala Ser Leu Ile Gly Ile Leu Thr Thr Thr Leu
 275 280 285
 Phe Tyr Val Leu Cys Gly Cys Leu Gly Tyr Ala Ala Phe Gly Asn Asp
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 Leu Ile Asp Phe Ala Asn Ile Cys Ile Ala Val His Leu Val Gly Ala
 325 330 335
 Tyr Gln Val Phe Cys Gln Pro Ile Phe Gly Phe Val Glu Asn Trp Gly
 340 345 350
 Lys Glu Arg Trp Pro Asn Ser Gln Phe Val Asn Gly Glu His Ala Leu
 355 360 365
 Asn Phe Pro Leu Cys Gly Thr Phe Pro Val Asn Phe Phe Arg Val Val
 370 375 380
 Trp Arg Thr Thr Tyr Val Ile Ile Thr Ala Leu Ile Ala Met Met Phe
 385 390 395 400
 Pro Phe Phe Asn Asp Phe Leu Gly Leu Ile Gly Ser Leu Ser Phe Trp
 405 410 415
 Pro Leu Thr Val Tyr Phe Pro Ile Glu Met Tyr Ile Lys Gln Ser Lys
 420 425 430
 Met Gln Arg Phe Ser Phe Thr Trp Thr Trp Leu Lys Ile Leu Ser Trp
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PF59082SeqList_PF59082.txt

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tctcgtttga gcattatata aactcagtcg gtgctcataa cttttcctca cacgactctg 180

ctcactcata tttatatattga acaaacagag atcccaaadc a atg gat att gaa gca 236
Met Asp Ile Glu Ala 5
ggt aaa gat att cct gta aga gac cca gcg cta ctc gat gac gac ggc 284
Gly Lys Asp Ile Pro Val Arg Asp Pro Ala Leu Leu Asp Asp Asp Gly
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Arg Ile Lys Arg Thr Gly Asn Val Phe Thr Ala Thr Thr His Ile Val
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Thr Val Val Val Gly Ala Gly Val Leu Ala Leu Ala Trp Ala Met Ala
40 45 50
cag ctt gga tgg ata gct ggc ata gcc gtt atg atc ctc ttt gca tgc 428
Gln Leu Gly Trp Ile Ala Gly Ile Ala Val Met Ile Leu Phe Ala Cys
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Ile Ser Val Tyr Thr Tyr Asn Leu Val Ala Asp Cys Tyr Arg Phe Pro
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Asp Pro Val Ser Gly Lys Arg Asn Tyr Thr Tyr Met Gln Ala Val Asp
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gcc tac ctt ggt gga aaa atg cac gtg ttc tgc gga tcc gtc cta tat 572
Ala Tyr Leu Gly Gly Lys Met His Val Phe Cys Gly Ser Val Leu Tyr
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ggg aag ctc gcc ggg gtt aca gtg ggc tac act ata act agt tct gtg 620
Gly Lys Leu Ala Gly Val Thr Val Gly Tyr Thr Ile Thr Ser Ser Val
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Ser Leu Val Ala Ile Lys Lys Ala Ile Cys Phe His Lys Lys Gly His
135 140 145
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Trp Leu Ser Thr Ile Ala Ala Ala Thr Ser Phe Gly Tyr Ala Phe Ile
185 190 195
gga agc ggg ctt tct ctt tcg gtg gtg gtc tca ggt aaa gga gaa gca 860
Gly Ser Gly Leu Ser Leu Ser Val Val Val Ser Gly Lys Gly Glu Ala
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acc agt ata ttt gga agc aaa gta gga cca gat tta tct gaa gcg gat 908
Thr Ser Ile Phe Gly Ser Lys Val Gly Pro Asp Leu Ser Glu Ala Asp
215 220 225
aaa gtt tgg aag gtt ttc agt gct ttg gga aac att gca ctt gct tgc 956
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Pro Pro Glu Asn Lys Gln Met Lys Lys Ala Asn Met Leu Gly Ile Thr	265	270	275	
aca atg aca ata ctt ttc ctg cta tgc ggt ggc ctt ggc tat gct gct	280	285	290	1100
Thr Met Thr Ile Leu Phe Leu Leu Cys Gly Gly Leu Gly Tyr Ala Ala				
ttc gga gat gac acg ccg ggg aac atc ctc acc ggc ttt gga ttt tac	295	300	305	1148
Phe Gly Asp Asp Thr Pro Gly Asn Ile Leu Thr Gly Phe Gly Phe Tyr				
gag cca ttc tgg ttg gtc gcc ctt ggc aat gtt ttc att gta gtc cac	310	315	320	1196
Glu Pro Phe Trp Leu Val Ala Leu Gly Asn Val Phe Ile Val Val His				
atg gtt gga gca tat cag gtg atg gct caa cca cta ttt cgt gta att	330	335	340	1244
Met Val Gly Ala Tyr Gln Val Met Ala Gln Pro Leu Phe Arg Val Ile				
gag atg ggt gct aac atg gcg tgg ccg cgt tca gat ttc att aac aag	345	350	355	1292
Glu Met Gly Ala Asn Met Ala Trp Pro Arg Ser Asp Phe Ile Asn Lys				
agc tat ccc atc aaa atg ggc tcc tta aca tgt aac atc aac ttg ttt	360	365	370	1340
Ser Tyr Pro Ile Lys Met Gly Ser Leu Thr Cys Asn Ile Asn Leu Phe				
agg ata att tgg agg tca atg tat gtg gca gtg gcc aca gtt att gcc	375	380	385	1388
Arg Ile Ile Trp Arg Ser Met Tyr Val Ala Val Ala Thr Val Ile Ala				
atg gct atg cca ttt ttc aat gag ttt ctt gcc ttg ctt gga gca ata	390	395	400	1436
Met Ala Met Pro Phe Asn Glu Phe Leu Ala Leu Leu Gly Ala Ile				
ggg ttt tgg cct ctc att gtc ttc ttc cct gta caa atg cac att gca	410	415	420	1484
Gly Phe Trp Pro Leu Ile Val Phe Phe Pro Val Gln Met His Ile Ala				
cag aaa cgg gta aaa aga cta tca ttg aag tgg tgt tgt ctt caa ata	425	430	435	1532
Gln Lys Arg Val Lys Arg Leu Ser Leu Lys Trp Cys Cys Leu Gln Ile				
ttg agc ttc gcg tgc ttc cta gtt aca gtt tcc gcg gca gtt ggt tcg	440	445	450	1580
Leu Ser Phe Ala Cys Phe Leu Val Thr Val Ser Ala Ala Val Gly Ser				
gtt cgt gga att agc aag aat ata aaa aaa tac aaa ctt ttc cag tat	455	460	465	1628
Val Arg Gly Ile Ser Lys Asn Ile Lys Lys Tyr Lys Leu Phe Gln Tyr				
aaa caa tagggcattt gggtgcacat tccagtgtct cacatttgag aaatgtgaaa	470			1684
Lys Gln				
atagctatag ctaggcagaa aaagaaggga gacaagttaa ttaaaacaag gcagtgaaaa				1744
ttatctgaat gcaaaattat ttgtcagcta cattattcca acttacagtg tgagcaacac				1804
tatttcaact agtcaaaata tttctgtctc agttatatca aattactctc attttatgtt				1864
c				1865

<210> 517
 <211> 471
 <212> PRT
 <213> Glycine max

<400> 517
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 Leu Asp Asp Asp Gly Arg Ile Lys Arg Thr Gly Asn Val Phe Thr Ala
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PF59082SeqList_PF59082.txt

Thr Thr His Ile Val Thr Val Val Val Gly Ala Gly Val Leu Ala Leu
 35 40 45
 Ala Trp Ala Met Ala Gln Leu Gly Trp Ile Ala Gly Ile Ala Val Met
 50 55 60
 Ile Leu Phe Ala Cys Ile Ser Val Tyr Thr Tyr Asn Leu Val Ala Asp
 65 70 75 80
 Cys Tyr Arg Phe Pro Asp Pro Val Ser Gly Lys Arg Asn Tyr Thr Tyr
 85 90 95
 Met Gln Ala Val Asp Ala Tyr Leu Gly Gly Lys Met His Val Phe Cys
 100 105 110
 Gly Ser Val Leu Tyr Gly Lys Leu Ala Gly Val Thr Val Gly Tyr Thr
 115 120 125
 Ile Thr Ser Ser Val Ser Leu Val Ala Ile Lys Lys Ala Ile Cys Phe
 130 135 140
 His Lys Lys Gly His Asp Ala Tyr Cys Lys Phe Ser Asn Asn Pro Tyr
 145 150 155 160
 Met Ile Gly Phe Gly Ile Cys Gln Ile Leu Leu Ser Gln Ile Pro Asn
 165 170 175
 Phe His Lys Leu Thr Trp Leu Ser Thr Ile Ala Ala Ala Thr Ser Phe
 180 185 190
 Gly Tyr Ala Phe Ile Gly Ser Gly Leu Ser Leu Ser Val Val Val Ser
 195 200 205
 Gly Lys Gly Glu Ala Thr Ser Ile Phe Gly Ser Lys Val Gly Pro Asp
 210 215 220
 Leu Ser Glu Ala Asp Lys Val Trp Lys Val Phe Ser Ala Leu Gly Asn
 225 230 235 240
 Ile Ala Leu Ala Cys Ser Phe Ala Thr Val Ile Tyr Asp Ile Met Asp
 245 250 255
 Thr Leu Lys Ser Tyr Pro Pro Glu Asn Lys Gln Met Lys Lys Ala Asn
 260 265 270
 Met Leu Gly Ile Thr Thr Met Thr Ile Leu Phe Leu Leu Cys Gly Gly
 275 280 285
 Leu Gly Tyr Ala Ala Phe Gly Asp Asp Thr Pro Gly Asn Ile Leu Thr
 290 295 300
 Gly Phe Gly Phe Tyr Glu Pro Phe Trp Leu Val Ala Leu Gly Asn Val
 305 310 315 320
 Phe Ile Val Val His Met Val Gly Ala Tyr Gln Val Met Ala Gln Pro
 325 330 335
 Leu Phe Arg Val Ile Glu Met Gly Ala Asn Met Ala Trp Pro Arg Ser
 340 345 350
 Asp Phe Ile Asn Lys Ser Tyr Pro Ile Lys Met Gly Ser Leu Thr Cys
 355 360 365
 Asn Ile Asn Leu Phe Arg Ile Ile Trp Arg Ser Met Tyr Val Ala Val
 370 375 380
 Ala Thr Val Ile Ala Met Ala Met Pro Phe Phe Asn Glu Phe Leu Ala
 385 390 395 400
 Leu Leu Gly Ala Ile Gly Phe Trp Pro Leu Ile Val Phe Phe Pro Val
 405 410 415
 Gln Met His Ile Ala Gln Lys Arg Val Lys Arg Leu Ser Leu Lys Trp
 420 425 430
 Cys Cys Leu Gln Ile Leu Ser Phe Ala Cys Phe Leu Val Thr Val Ser
 435 440 445
 Ala Ala Val Gly Ser Val Arg Gly Ile Ser Lys Asn Ile Lys Lys Tyr
 450 455 460
 Lys Leu Phe Gln Tyr Lys Gln
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<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (130)..(1425)

<400> 518

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PF59082SeqList_PF59082.txt

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tccgcgggag	atg acg cag cag gac	gtg gag atg gcg gcg	cgc cac ggg acc			171
	Met Thr Gln Gln Asp	Val Glu Met Ala Ala	Arg His Gly Thr			
	1	5	10			
ggc gcc gac gga gcg gga ttc tac cct cag ccg cgg aac ggc ggc ggc	219					
Gly Ala Asp Gly Ala Gly Phe Tyr Pro Gln Pro Arg Asn Gly Gly Gly						
15	20	25	30			
ggc gag acg ctc gac gac gac ggc aag aag aag cgc acg gga acg gta	267					
Gly Glu Thr Leu Asp Asp Asp Gly Lys Lys Lys Arg Thr Gly Thr Val						
	35	40	45			
tgg acg gca agc gcg cac atc atc aca gcc gtc atc ggc tcc ggc gtg	315					
Trp Thr Ala Ser Ala His Ile Ile Thr Ala Val Ile Gly Ser Gly Val						
	50	55	60			
ctc tcc cta gcc tgg tcg act gca cag ctc ggc tgg gtc gtg ggg ccg	363					
Leu Ser Leu Ala Trp Ser Thr Ala Gln Leu Gly Trp Val Val Gly Pro						
	65	70	75			
ctc acc ctg atg atc ttt gcc ttg atc aca tac tac acc tct agc ctt	411					
Leu Thr Leu Met Ile Phe Ala Leu Ile Thr Tyr Thr Ser Ser Leu						
	80	85	90			
ctt gct gac tgc tac gcg agc ggc gat cag ctc acc ggc aag agg aac	459					
Leu Ala Asp Cys Tyr Arg Ser Gly Asp Gln Leu Thr Gly Lys Arg Asn						
	95	100	105			
tac acc tac atg gac gct gtc gcc gcg tac ctg ggt cga tgg caa gtc	507					
Tyr Thr Tyr Met Asp Ala Val Ala Ala Tyr Leu Gly Arg Trp Gln Val						
	115	120	125			
ctg tcc tgt ggt gtt ttc cag tat gtt aac ttg gtt gga act gcc gtt	555					
Leu Ser Cys Gly Val Phe Gln Tyr Val Asn Leu Val Gly Thr Ala Val						
	130	135	140			
ggg tat aca att aca gcg tcc atc agt gca gcg gcc gtg cac aag gca	603					
Gly Tyr Thr Ile Thr Ala Ser Ile Ser Ala Ala Val His Lys Ala						
	145	150	155			
aac tgc ttc cac aac aag ggc cac gcg gcc gac tgc agc acc tac gac	651					
Asn Cys Phe His Asn Lys Gly His Ala Ala Asp Cys Ser Thr Tyr Asp						
	160	165	170			
acc atg tac atg gtc gta ttt ggg atc gtt cag atc ttc ttc tct cag	699					
Thr Met Tyr Met Val Val Phe Gly Ile Val Gln Ile Phe Phe Ser Gln						
	175	180	185			
ctc cct aac ttc agc gac ctt tcg tgg ctg tcc atc gtc gcc gcc atc	747					
Leu Pro Asn Phe Ser Asp Leu Ser Trp Leu Ser Ile Val Ala Ala Ile						
	195	200	205			
atg tct ttc tct tac tcc agc atc gcc gtc ggc ctc tcg ttg gcg cgg	795					
Met Ser Phe Ser Tyr Ser Ser Ile Ala Val Gly Leu Ser Leu Ala Arg						
	210	215	220			
acc att tca ggc cgt agt ggt acg acc act ctg acc ggc act gag atc	843					
Thr Ile Ser Gly Arg Ser Gly Thr Thr Thr Leu Thr Gly Thr Glu Ile						
	225	230	235			
gga gtc gac gtt gat tca gcc cag aag gtc tgg ctc gcg ctt caa gct	891					
Gly Val Asp Val Asp Ser Ala Gln Lys Val Trp Leu Ala Leu Gln Ala						
	240	245	250			
ctt ggc aac atc gcg ttc gct tac tcc tac tcc atg att ctc atc gaa	939					
Leu Gly Asn Ile Ala Phe Ala Tyr Ser Tyr Ser Met Ile Leu Ile Glu						
	255	260	265			
atc caa gac acg gtg aag tct cct cca gcc gag aac aag acg atg aag	987					
Ile Gln Asp Thr Val Lys Ser Pro Pro Ala Glu Asn Lys Thr Met Lys						
	275	280	285			
aag gcg acg ctg atg ggc gtg acg acc acc acg gcg ttc tac atg ctt	1035					
Lys Ala Thr Met Gly Val Thr Thr Thr Ala Phe Tyr Met Leu						
	290	295	300			
gct ggc tgc ctc ggg tac tcg gcg ttc ggg aac gcg gcg cca ggg aac	1083					
Ala Gly Cys Leu Gly Tyr Ser Ala Phe Gly Asn Ala Ala Pro Gly Asn						
	305	310	315			
atc ctg acc ggg ttc ggc ttc tac gag ccc tac tgg ctg atc gac ttc	1131					
Ile Leu Thr Gly Phe Gly Phe Tyr Glu Pro Tyr Trp Leu Ile Asp Phe						
	320	325	330			
gcc aac gtc tgc atc gtg gtg cac ctg gtg ggc gcg tac cag gtc ttc	1179					
Ala Asn Val Cys Ile Val Val His Leu Val Gly Ala Tyr Gln Val Phe						

PF59082SeqList_PF59082.txt

335		340		345		350	
tcc	cag	ccc	atc	ttc	gcg	gcc	ttg
Ser	Gln	Pro	Ile	Phe	Ala	Ala	Leu
				355			
ccg	aac	gac	cgg	ttc	gtc	acg	cg
Pro	Asn	Asp	Arg	Phe	Val	Thr	Arg
				370			
ttc	cac	gtg	agc	ctg	ctc	agg	ctg
Phe	His	Val	Ser	Leu	Leu	Arg	Leu
				385			
gtg	agc	acg	gtg	ctc	gcc	atc	gtg
Val	Ser	Thr	Val	Leu	Ala	Ile	Ala
				400			
ggc	ttc	ctc	gga	gac	atc	gaa	ttc
Gly	Phe	Leu	Gly	Asp	Ile	Glu	Phe
415				420			
gtg	tagatggaca	tcccggaggg	ccctgaacgc	aaatatacct	ggagggggggg		
Val							
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 <211> 431
 <212> PRT
 <213> Zea mays

<400> 519	
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Asp Gly Ala Gly Phe Tyr Pro Gln Pro Arg Asn Gly Gly Gly Glu	
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Thr Leu Asp Asp Gly Lys Lys Arg Thr Gly Thr Val Trp Thr	
	35
Ala Ser Ala His Ile Ile Thr Ala Val Ile Gly Ser Gly Val Leu Ser	
	50
Leu Ala Trp Ser Thr Ala Gln Leu Gly Trp Val Val Gly Pro Leu Thr	
65	70
Leu Met Ile Phe Ala Leu Ile Thr Tyr Tyr Thr Ser Ser Leu Leu Ala	
	85
Asp Cys Tyr Arg Ser Gly Asp Gln Leu Thr Gly Lys Arg Asn Tyr Thr	
	100
Tyr Met Asp Ala Val Ala Ala Tyr Leu Gly Arg Trp Gln Val Leu Ser	
	115
Cys Gly Val Phe Gln Tyr Val Asn Leu Val Gly Thr Ala Val Gly Tyr	
	130
Thr Ile Thr Ala Ser Ile Ser Ala Ala Ala Val His Lys Ala Asn Cys	
145	150
Phe His Asn Lys Gly His Ala Ala Asp Cys Ser Thr Tyr Asp Thr Met	
	165
Tyr Met Val Val Phe Gly Ile Val Gln Ile Phe Phe Ser Gln Leu Pro	
	180
Asn Phe Ser Asp Leu Ser Trp Leu Ser Ile Val Ala Ala Ile Met Ser	
	195
Phe Ser Tyr Ser Ser Ile Ala Val Gly Leu Ser Leu Ala Arg Thr Ile	
	210
Ser Gly Arg Ser Gly Thr Thr Thr Leu Thr Gly Thr Glu Ile Gly Val	
225	230
Asp Val Asp Ser Ala Gln Lys Val Trp Leu Ala Leu Gln Ala Leu Gly	
	245
Asn Ile Ala Phe Ala Tyr Ser Tyr Ser Met Ile Leu Ile Glu Ile Gln	
	260
Asp Thr Val Lys Ser Pro Pro Ala Glu Asn Lys Thr Met Lys Lys Ala	
	275
Thr Leu Met Gly Val Thr Thr Thr Thr Ala Phe Tyr Met Leu Ala Gly	
	290
Cys Leu Gly Tyr Ser Ala Phe Gly Asn Ala Ala Pro Gly Asn Ile Leu	
305	310
	315
	320

PF59082SeqList_PF59082.txt

Thr Gly Phe Gly Phe Tyr Glu Pro Tyr Trp Leu Ile Asp Phe Ala Asn
 Val Cys Ile Val Val His Leu Val Gly Ala Tyr Gln Val Phe Ser Gln
 Pro Ile Phe Ala Ala Leu Glu Thr Ala Ala Leu Lys Arg Trp Pro Asn
 Asp Arg Phe Val Thr Arg Glu His Pro Leu Val Gly Val Arg Phe His
 Val Ser Leu Leu Arg Leu Thr Trp Arg Thr Ala Phe Val Val Val Ser
 Thr Val Leu Ala Ile Ala Leu Pro Phe Phe Asn Asp Ile Leu Gly Phe
 Leu Gly Asp Ile Glu Phe Trp Pro Leu Thr Leu Asp Tyr Pro Val

<210> 520

<211> 1988

<212> DNA

<213> Zea mays subsp. mays

<220>

<221> CDS

<222> (195)..(1631)

<400> 520

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aactgcagcg gagcctcaca gttgttcgtg tgctgtgtat ttgtcactgg tgggtgctgtg 120

cagaccaagc tactgcggga gggagaaggg tgtgtgccgg cccgccgcca agcactgcta 180

cccgccgggc ggcc atg gag gtg agc tcc gtg gag ttc ggt cat cac gcg 230
 Met Glu Val Ser Ser Val Glu Phe Gly His His Ala

gcg gcc gcc tca aag tgc ttt gac gac gac ggt cgc ctc aag cgc aca 278
 Ala Ala Ala Ser Lys Cys Phe Asp Asp Asp Gly Arg Leu Lys Arg Thr

ggg acg atg tgg acg gcg agc gcg cac att atc acg gcc gtg ata ggg 326
 Gly Thr Met Trp Thr Ala Ser Ala His Ile Ile Thr Ala Val Ile Gly

tcc ggg gtg ctg tgc ctc gcg tgg gcc atc gcg cag ctc ggc tgg gtg 374
 Ser Gly Val Leu Ser Leu Ala Trp Ala Ile Ala Gln Leu Gly Trp Val

gca ggc ccc acc gtc atg ctg ctc ttc tcc ttc gtc acc tac tac aca 422
 Ala Gly Pro Thr Val Met Leu Leu Phe Ser Phe Val Thr Tyr Tyr Thr

tcg gcc cta ctc gcc gac tgc tac cgc tcc ggc gac gcc tgc acc ggc 470
 Ser Ala Leu Leu Ala Asp Cys Tyr Arg Ser Gly Asp Ala Cys Thr Gly

aag cgc aac tac acg tac atg gac gcg gtt aac gcc aat ctc agt ggc 518
 Lys Arg Asn Tyr Thr Tyr Met Asp Ala Val Asn Ala Asn Leu Ser Gly

gtc aag gtc tgg ttc tgc ggc ttc ctg cag tac gcc aac atc gtc gga 566
 Val Lys Val Trp Phe Cys Gly Phe Leu Gln Tyr Ala Asn Ile Val Gly

gtc gcc ata ggc tac acc att gcc gcc tct att agc atg ctg gcg atc 614
 Val Ala Ile Gly Tyr Thr Ile Ala Ala Ser Ile Ser Met Leu Ala Ile

cag agg gcg aac tgc ttc cac gtg gag ggg cac ggg gac ccc tgc aac 662
 Gln Arg Ala Asn Cys Phe His Val Glu Gly His Gly Asp Pro Cys Asn

atc tcc agc acg ccc tac atg atc atc ttc ggc gtc gtg cag att ttc 710
 Ile Ser Ser Thr Pro Tyr Met Ile Ile Phe Gly Val Val Gln Ile Phe

ttc tcg cag atc ccg gac ttc gac cag ata tcg tgg ctc tcc atc ctc 758
 Phe Ser Gln Ile Pro Asp Phe Asp Gln Ile Ser Trp Leu Ser Ile Leu

PF59082SeqList_PF59082.txt

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Ala	Ala	Val	Met	Ser	Phe	Thr	Tyr	Ser	Thr	Ile	Gly	Leu	Gly	Leu	Gly	
190						195					200					
atc	gcg	cag	gtg	gtg	tcc	aac	aag	ggc	gtg	cag	ggc	agc	ctg	acg	ggg	854
Ile	Ala	Gln	Val	Val	Ser	Asn	Lys	Gly	Val	Gln	Gly	Ser	Leu	Thr	Gly	
205					210					215					220	
atc	agc	gtc	ggc	gcg	gtc	acc	ccg	gtc	gac	aag	atg	tgg	cgc	agc	ctg	902
Ile	Ser	Val	Gly	Ala	Val	Thr	Pro	Val	Asp	Lys	Met	Trp	Arg	Ser	Leu	
			225						230					235		
cag	gcg	ttc	ggc	gac	atc	gcc	ttc	gcc	tac	tcc	tac	tcc	ctc	atc	ctc	950
Gln	Ala	Phe	Gly	Asp	Ile	Ala	Phe	Ala	Tyr	Ser	Tyr	Ser	Leu	Ile	Leu	
			240					245					250			
atc	gag	atc	cag	gac	acc	atc	cgc	gcg	ccg	ccg	ccg	tcc	gag	tcc	aag	998
Ile	Glu	Ile	Gln	Asp	Thr	Ile	Arg	Ala	Pro	Pro	Pro	Ser	Glu	Ser	Lys	
		255					260					265				
gtc	atg	cgg	cgc	gcc	acc	gtc	gtc	agc	gtg	gcc	gtc	acc	acg	ttc	ttc	1046
Val	Met	Arg	Arg	Ala	Thr	Val	Val	Ser	Val	Ala	Val	Thr	Thr	Phe	Phe	
		270				275				280						
tac	atg	ctg	tgc	ggg	tgc	atg	ggg	tac	gcc	gcg	ttc	ggg	gac	aac	gcc	1094
Tyr	Met	Leu	Cys	Gly	Cys	Met	Gly	Tyr	Ala	Ala	Phe	Gly	Asp	Asn	Ala	
285					290					295					300	
ccc	ggg	aac	ctc	ctc	acg	ggc	ttc	ggc	ttc	tac	gag	ccc	ttc	tgg	ctc	1142
Pro	Gly	Asn	Leu	Leu	Thr	Gly	Phe	Gly	Phe	Tyr	Glu	Pro	Phe	Trp	Leu	
			305						310					315		
ctc	gac	gtc	gcc	aac	gcc	gcc	atc	gcc	gtg	cac	ctc	gtc	ggc	gcc	tac	1190
Leu	Asp	Val	Ala	Asn	Ala	Ala	Ile	Ala	Val	His	Leu	Val	Gly	Ala	Tyr	
			320					325					330			
cag	gtc	tac	tgc	cag	ccc	ctg	ttc	gcc	ttc	gtc	gag	aag	tgg	gcg	cgc	1238
Gln	Val		Cys	Gln	Pro	Leu	Phe	Ala	Phe	Val	Glu	Lys	Trp	Ala	Arg	
		335				340						345				
cag	agg	tgg	ccc	aag	tcc	cgc	tac	atc	acg	ggc	gag	gtc	gac	gtc	ccg	1286
Gln	Arg	Trp	Pro	Lys	Ser	Arg	Tyr	Ile	Thr	Gly	Glu	Val	Asp	Val	Pro	
		350				355				360						
ctc	ccg	ctc	ggg	acc	gcc	ggc	cgc	tgc	tac	aag	ctc	agc	ctg	ttc	1334	
Leu	Pro	Leu	Gly	Thr	Ala	Gly	Gly	Arg	Cys	Tyr	Lys	Leu	Ser	Leu	Phe	
365					370					375					380	
cgg	ctg	acg	tgg	cgg	acg	gcg	ttc	gtg	gtg	gcc	acg	acg	gtg	gtg	tcc	1382
Arg	Leu	Thr	Trp	Arg	Thr	Ala	Phe	Val	Val	Ala	Thr	Thr	Val	Val	Ser	
			385					390						395		
atg	ctg	ctg	ccc	ttc	ttc	aac	gac	gtg	gtc	ggg	ctc	ctg	ggc	gcg	ctg	1430
Met	Leu	Leu	Pro	Phe	Phe	Asn	Asp	Val	Val	Gly	Leu	Leu	Gly	Ala	Leu	
			400					405					410			
ggg	ttc	tgg	ccg	ctc	acc	gtc	tac	ttc	ccc	gtg	gag	atg	tac	atc	gtg	1478
Gly	Phe	Trp	Pro	Leu	Thr	Val	Tyr	Phe	Pro	Val	Glu	Met	Tyr	Ile	Val	
		415					420					425				
cag	aag	aag	gtg	ccc	agg	tgg	agc	acg	cgg	tgg	gtg	tgc	ctg	cag	ctg	1526
Gln	Lys	Lys	Val	Pro	Arg	Trp	Ser	Thr	Arg	Trp	Val	Cys	Leu	Gln	Leu	
		430				435				440						
ctc	agc	gtc	gcc	tgc	ctc	gtc	atc	acc	gtc	gcc	tcc	gcc	gca	ggc	tcc	1574
Leu	Ser	Val	Ala	Cys	Leu	Val	Ile	Thr	Val	Ala	Ser	Ala	Ala	Gly	Ser	
445					450					455					460	
gtt	gcc	ggg	atc	gtc	tct	gac	ctc	aaa	gtg	tac	aaa	ccg	ttc	gtc	acc	1622
Val	Ala	Gly	Ile	Val	Ser	Asp	Leu	Lys	Val	Tyr	Lys	Pro	Phe	Val	Thr	
			465					470						475		
acc	tcc	tgatggaccg	gcctagcttc	cgtgcagttc	aaaacacaca	tacgcacgaa										1678
Thr	Ser															
cagatcatta	attggcgcct	agtatatatg	tgcagtcctt	aattaaatta	actaggcatt											1738
aatcgatcga	tcaccactac	gcgtcgttct	agtgatgcgc	gtagcttgca	tcaccgctcg											1798
ctgattta	atttccattg	tttctttgat	gatctgggta	gccgaaatgg	ctagtgaatt											1858
aagagaaaac	aaatagtagc	agtactgtgt	gagtaatccc	aagtcaaata	cgttattgaa											1918

PF59082SeqList_PF59082.txt

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tacgtgtttc 1988

<210> 521
<211> 478
<212> PRT
<213> Zea mays subsp. mays

<400> 521
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Lys Cys Phe Asp Asp Asp Gly Arg Leu Lys Arg Thr Gly Thr Met Trp
20 25 30
Thr Ala Ser Ala His Ile Ile Thr Ala Val Ile Gly Ser Gly Val Leu
35 40 45
Ser Leu Ala Trp Ala Ile Ala Gln Leu Gly Trp Val Ala Gly Pro Thr
50 55 60
Val Met Leu Leu Phe Ser Phe Val Thr Tyr Tyr Thr Ser Ala Leu Leu
65 70 75 80
Ala Asp Cys Tyr Arg Ser Gly Asp Ala Cys Thr Gly Lys Arg Asn Tyr
85 90 95
Thr Tyr Met Asp Ala Val Asn Ala Asn Leu Ser Gly Val Lys Val Trp
100 105 110
Phe Cys Gly Phe Leu Gln Tyr Ala Asn Ile Val Gly Val Ala Ile Gly
115 120 125
Tyr Thr Ile Ala Ala Ser Ile Ser Met Leu Ala Ile Gln Arg Ala Asn
130 135 140
Cys Phe His Val Glu Gly His Gly Asp Pro Cys Asn Ile Ser Ser Thr
145 150 155 160
Pro Tyr Met Ile Ile Phe Gly Val Val Gln Ile Phe Phe Ser Gln Ile
165 170 175
Pro Asp Phe Asp Gln Ile Ser Trp Leu Ser Ile Leu Ala Ala Val Met
180 185 190
Ser Phe Thr Tyr Ser Thr Ile Gly Leu Gly Leu Gly Ile Ala Gln Val
195 200 205
Val Ser Asn Lys Gly Val Gln Gly Ser Leu Thr Gly Ile Ser Val Gly
210 215 220
Ala Val Thr Pro Val Asp Lys Met Trp Arg Ser Leu Gln Ala Phe Gly
225 230 235 240
Asp Ile Ala Phe Ala Tyr Ser Tyr Ser Leu Ile Leu Ile Glu Ile Gln
245 250 255
Asp Thr Ile Arg Ala Pro Pro Pro Ser Glu Ser Lys Val Met Arg Arg
260 265 270
Ala Thr Val Val Ser Val Ala Val Thr Thr Phe Phe Tyr Met Leu Cys
275 280 285
Gly Cys Met Gly Tyr Ala Ala Phe Gly Asp Asn Ala Pro Gly Asn Leu
290 295 300
Leu Thr Gly Phe Gly Phe Tyr Glu Pro Phe Trp Leu Leu Asp Val Ala
305 310 315 320
Asn Ala Ala Ile Ala Val His Leu Val Gly Ala Tyr Gln Val Tyr Cys
325 330 335
Gln Pro Leu Phe Ala Phe Val Glu Lys Trp Ala Arg Gln Arg Trp Pro
340 345 350
Lys Ser Arg Tyr Ile Thr Gly Glu Val Asp Val Pro Leu Pro Leu Gly
355 360 365
Thr Ala Gly Gly Arg Cys Tyr Lys Leu Ser Leu Phe Arg Leu Thr Trp
370 375 380
Arg Thr Ala Phe Val Val Ala Thr Thr Val Val Ser Met Leu Leu Pro
385 390 395 400
Phe Phe Asn Asp Val Val Gly Leu Leu Gly Ala Leu Gly Phe Trp Pro
405 410 415
Leu Thr Val Tyr Phe Pro Val Glu Met Tyr Ile Val Gln Lys Lys Val
420 425 430
Pro Arg Trp Ser Thr Arg Trp Val Cys Leu Gln Leu Leu Ser Val Ala
Seite 657

PF59082SeqList_PF59082.txt

	200	205	210	
gcc ttc gcc tac tcc tac tcc ctc atc ctc atc gag atc cag gac acc	215	220	225	968
Ala Phe Ala Tyr Ser Tyr Ser Leu Ile Leu Ile Glu Ile Gln Asp Thr				
atc cgc gcg ccg ccg ccg tcc gag tcc aag gtc atg cgg cgc gcc acc	230	235	240	1016
Ile Arg Ala Pro Pro Pro Ser Glu Ser Lys Val Met Arg Arg Ala Thr				
gtc gtc agc gtg gcc gtc acc acg ttc ttc tac atg ctg tgc ggg tgc	245	250	255	1064
Val Val Ser Val Ala Val Thr Thr Phe Phe Tyr Met Leu Cys Gly Cys				
atg ggg tac gcc gcg ttc ggg gac aac gcc ccc ggg aac ctc ctc acg	265	270	275	1112
Met Gly Tyr Ala Ala Phe Gly Asp Asn Ala Pro Gly Asn Leu Leu Thr				
ggc ttc ggc ttc tac gag ccc ttc tgg ctc ctc gac gtc gcc aac gcc	280	285	290	1160
Gly Phe Gly Phe Tyr Glu Pro Phe Trp Leu Leu Asp Val Ala Asn Ala				
gcc atc gcc gtg cac ctc gtc ggc gcc tac cag gtc tac tgc cag ccc	295	300	305	1208
Ala Ile Ala Val His Leu Val Gly Ala Tyr Gln Val Tyr Cys Gln Pro				
ctg ttc gcc ttc gtc gag aag tgg gcg cgc cag agg tgg ccc aag tcc	310	315	320	1256
Leu Phe Ala Phe Val Glu Lys Trp Ala Arg Gln Arg Trp Pro Lys Ser				
cgc tac atc acg ggc gag gtc gac gtc ccg ctc ccg ctc ggg acc gcc	325	330	335	1304
Arg Tyr Ile Thr Gly Glu Val Asp Val Pro Leu Pro Leu Gly Thr Ala				
ggc ggc cgg tgc tac aag ctc agc ctg ttc cgg ctg acg tgg cgg acg	345	350	355	1352
Gly Gly Arg Cys Tyr Lys Leu Ser Leu Phe Arg Leu Thr Trp Arg Thr				
gcg ttc gtg gtg gcc acg acg gtg gtg tcc atg ctg ctg ccc ttc ttc	360	365	370	1400
Ala Phe Val Val Ala Thr Thr Val Val Ser Met Leu Leu Pro Phe Phe				
aac gac gtg gtc ggg ctc ctg ggc gcg ctg ggg ttc tgg ccg ctc acc	375	380	385	1448
Asn Asp Val Val Gly Leu Leu Gly Ala Leu Gly Phe Trp Pro Leu Thr				
gtc tac ttc ccc gtg gag atg tac atc gtg cag aag aag gtg ccc agg	390	395	400	1496
Val Tyr Phe Pro Val Glu Met Tyr Ile Val Gln Lys Lys Val Pro Arg				
tgg agc acg cgg tgg gtg tgc ctg cag ctg ctc agc gtc gcc tgc ctc	405	410	415	1544
Trp Ser Thr Arg Trp Val Cys Leu Gln Leu Leu Ser Val Ala Cys Leu				
gtc atc acc gtc gcc tcc gcc gca ggc tcc gtt gcc ggg atc gtc tct	425	430	435	1592
Val Ile Thr Val Ala Ser Ala Ala Gly Ser Val Ala Gly Ile Val Ser				
gac ctc aaa gtg tac aaa ccg ttc gtc acc acc tcc tgatggaccg	440	445		1638
Asp Leu Lys Val Tyr Lys Pro Phe Val Thr Thr Ser				
gcctagcttc cgtgcagttc aaaacacaca tacgcacgaa cagatcatta attggcgcct				1698
agtatatatg tgcagtcctt aattaaatta actaggcatt aatcgatcga tcaccactac				1758
gcgtcgttct agtgatgcgc gtagcttgca tcaccgctcg ctgatttaatt ttccattggt				1818
tttctttgat gatctgggta gccgaaatgg ctagtgaatt aagagaaaac aaatagtagc				1878
agtactgtgt gagtaatccc aagtcaaata cgttattgaa gttgtcggcg gtacaaaacg				1938
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PF59082SeqList_PF59082.txt

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25 30
Pro Thr Val Met Leu Leu Phe Ser 40 Phe Val Thr Tyr Tyr Thr Ser Ala
35 45
Leu Leu 50 Ala Asp Cys Tyr Arg 55 Ser Gly Asp Ala Cys 60 Thr Gly Lys Arg
65
Asn Tyr Thr Tyr Met Asp 70 Ala Val Asn Ala Asn 75 Leu Ser Gly Val Lys
80
Val Trp Phe Cys Gly 85 Phe Leu Gln Tyr Ala Asn 90 Ile Val Gly Val Ala
95
Ile Gly Tyr Thr 100 Ile Ala Ala Ser Ile 105 Ser Met Leu Ala Ile Gln Arg
110
Ala Asn Cys Phe His Val Glu Gly His Gly Asp Pro Cys Asn Ile Ser
115 120 125
Ser Thr Pro Tyr Met Ile 130 Ile Phe Gly Val Val Gln Ile Phe Phe Ser
135 140
Gln Ile Pro Asp Phe Asp 150 Gln Ile Ser Trp Leu 155 Ser Ile Leu Ala Ala
160
Val Met Ser Phe Thr Tyr Ser Thr Ile Gly Leu Gly Leu Gly Ile Ala
165 170 175
Gln Val Val Ser 180 Asn Lys Gly Val Gln Gly Ser Leu Thr Gly Ile Ser
185 190
Val Gly Ala Val Thr Pro Val Asp Lys Met Trp Arg Ser Leu Gln Ala
195 200 205
Phe Gly Asp Ile Ala Phe Ala Tyr Ser Tyr Ser Leu Ile Leu Ile Glu
210 220
Ile Gln Asp Thr Ile Arg 230 Ala Pro Pro Pro Ser Glu Ser Lys Val Met
225 235 240
Arg Arg Ala Thr Val Val Ser Val Ala Val Thr Thr Phe Phe Tyr Met
245 250 255
Leu Cys Gly Cys Met Gly Tyr Ala Ala Phe Gly Asp Asn Ala Pro Gly
260 270
Asn Leu Leu Thr Gly Phe Gly Phe Tyr Glu Pro Phe Trp Leu Leu Asp
275 280 285
Val Ala Asn Ala Ala Ile Ala Val His Leu Val Gly Ala Tyr Gln Val
290 300
Tyr Cys Gln Pro Leu Phe Ala Phe Val Glu Lys Trp Ala Arg Gln Arg
305 310 315 320
Trp Pro Lys Ser Arg Tyr Ile Thr Gly Glu Val Asp Val Pro Leu Pro
325 330 335
Leu Gly Thr Ala Gly Gly Arg Cys Tyr Lys Leu Ser Leu Phe Arg Leu
340 345 350
Thr Trp Arg Thr Ala Phe Val Val Ala Thr Thr Val Val Ser Met Leu
355 360 365
Leu Pro Phe Phe Asn Asp Val Val Gly Leu Leu Gly Ala Leu Gly Phe
370 375 380
Trp Pro Leu Thr Val Tyr Phe Pro Val Glu Met Tyr Ile Val Gln Lys
385 390 395 400
Lys Val Pro Arg Trp Ser Thr Arg Trp Val Cys Leu Gln Leu Leu Ser
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Val Ala Cys Leu Val Ile Thr Val Ala Ser Ala Ala Gly Ser Val Ala
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Gly Ile Val Ser Asp Leu Lys Val Tyr Lys Pro Phe Val Thr Thr Ser
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<213> Zea mays

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<220>
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PF59082SeqList_PF59082.txt

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ttagttgctc ttc atg gcc gtg tca cac aac gtt ggg agc aag cac ggt Met Ala Val Ser His Asn Val Gly Ser Lys His Gly	169
gtc gcg ccg ctg gag gtg tcg gtg gag gcc ggg aac ggc gga gcc gcc Val Ala Pro Leu Glu Val Ser Val Glu Ala Gly Asn Gly Gly Ala Ala	217
gag tgg ctg gac gac gat ggc cgg cct cgc cgc acg ggc acg ttc tgg Glu Trp Leu Asp Asp Asp Gly Arg Pro Arg Arg Thr Gly Thr Phe Trp	265
acg gcc agc gcg cac atc gtc acc gcc gtc atc ggc tcc ggg gtg ctc Thr Ala Ser Ala His Ile Val Thr Ala Val Ile Gly Ser Gly Val Leu	313
tcg ctc gcc tgg gcg atc gcg cag ctg ggc tgg gtc gcc ggc ccc gcc Ser Leu Ala Trp Ala Ile Ala Gln Leu Gly Trp Val Ala Gly Pro Ala	361
gcc atg ctc ctc ttc gcc ttc gtc aca tac tac acc gcc acg ctg ctc Ala Met Leu Leu Phe Ala Phe Val Thr Tyr Tyr Thr Ala Thr Leu Leu	409
gcc gag tgc tac cgc acg ggc gac ccg gag acg ggc aag cgc aac tac Ala Glu Cys Tyr Arg Thr Gly Asp Pro Glu Thr Gly Lys Arg Asn Tyr	457
acc tac atg gac gcc gtg cgc tcc aac ctc ggc ggc gcc aag gtc gcg Thr Tyr Met Asp Ala Val Arg Ser Asn Leu Gly Gly Ala Lys Val Ala	505
ttc tgc ggc gtc ata cag tac gcc aac ctc gtc ggc gtc gcc atc ggc Phe Cys Gly Val Ile Gln Tyr Ala Asn Leu Val Gly Val Ala Ile Gly	553
tac acc atc gcg gcg tcc atc agc atg aag gcc gtc agg aga gct ggg Tyr Thr Ile Ala Ala Ser Ile Ser Met Lys Ala Val Arg Arg Ala Gly	601
tgc ttc cac gcc cac ggg cac gct gat ccc tgc aac agc tcc agc acc Cys Phe His Ala His Gly His Ala Asp Pro Cys Asn Ser Ser Ser Thr	649
ccg tac atg atc ctc ttc ggc gtc gtg cag atc ctc ttc tcg cag ata Pro Tyr Met Ile Leu Phe Gly Val Val Gln Ile Leu Phe Ser Gln Ile	697
ccc gac ttc gac cag att tgg tgg ctc tcc att gtc gcc gcc gtc atg Pro Asp Phe Asp Gln Ile Trp Trp Leu Ser Ile Val Ala Ala Val Met	745
tcc ttc act tac tct tcc atc ggg ctc tcc ctc ggc atc gca cag acc Ser Phe Thr Tyr Ser Ser Ile Gly Leu Ser Leu Gly Ile Ala Gln Thr	793
atc tcc aat ggt ggg ttc atg ggc agt ctc act ggc atc agc atc ggc Ile Ser Asn Gly Gly Phe Met Gly Ser Leu Thr Gly Ile Ser Ile Gly	841
gcc ggt gtc acc tcc acg cag aag atc tgg cat acg ctt cag gca ttc Ala Gly Val Thr Ser Thr Gln Lys Ile Trp His Thr Leu Gln Ala Phe	889
gga gac atc gcc ttc gcc tac tcc ttc tcc aac atc ctc atc gag atc Gly Asp Ile Ala Phe Ala Tyr Ser Phe Ser Asn Ile Leu Ile Glu Ile	937
caa gac acg atc aag gca ccg cca ccg tcg gag tcc aag gtg atg cag Gln Asp Thr Ile Lys Ala Pro Pro Pro Ser Glu Ser Lys Val Met Gln	985
aag gcg acg cgc ctc agc gtg gcg acg acc acc atc ttc tac atg ctg Lys Ala Thr Arg Leu Ser Val Ala Thr Thr Thr Ile Phe Tyr Met Leu	1033
tgc ggg tgc atg ggg tac gcg gcg ttc ggc gac aag gcg ccg gac aac Cys Gly Cys Met Tyr Ala Ala Phe Gly Asp Lys Ala Pro Asp Asn	1081
ctc ctc acc ggc ttc ggc ttc ttc gag ccg ttc tgg ctc atc gac atc Leu Leu Thr Gly Phe Gly Phe Phe Glu Pro Phe Trp Leu Ile Asp Ile	1129

PF59082SeqList_PF59082.txt

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Ala	Asn	Val	Ala	Ile	Val	Val	His	Leu	Val	Gly	Ala	Tyr	Gln	Val	Phe	
		335					340					345				
tgc	cag	ccc	atc	ttc	gcc	ttc	gtc	gag	cgc	cgc	gcc	gcc	gcg	gcc	tgg	1225
Cys	Gln	Pro	Ile	Phe	Ala	Phe	Val	Glu	Arg	Arg	Ala	Ala	Ala	Ala	Trp	
		350					355				360					
ccc	gac	agc	gcc	ttc	gtc	tcc	cag	gag	ctc	cgc	gtg	ggc	ccc	ttc	gcg	1273
Pro	Asp	Ser	Ala	Phe	Val	Ser	Gln	Glu	Leu	Arg	Val	Gly	Pro	Phe	Ala	
365					370					375					380	
gtc	agc	gtg	ttc	cgc	ctg	aca	tgg	cgg	tcg	tcc	ttc	gtg	tgc	gtc	acc	1321
Val	Ser	Val	Phe	Arg	Leu	Thr	Trp	Arg	Ser	Ser	Phe	Val	Cys	Val	Thr	
				385					390					395		
acc	gtc	gtt	gcc	atg	ctg	ctg	ccg	ttc	ttc	ggc	aac	gtg	gtg	ggg	ttc	1369
Thr	Val	Val	Ala	Met	Leu	Leu	Pro	Phe	Phe	Gly	Asn	Val	Val	Gly	Phe	
			400					405					410			
ctc	ggc	gcc	gtc	tcc	ttc	tgg	ccg	ctc	acc	gtc	tac	ttc	ccc	gtc	gag	1417
Leu	Gly	Ala	Val	Ser	Phe	Trp	Pro	Leu	Thr	Val	Tyr	Phe	Pro	Val	Glu	
		415					420					425				
atg	tac	atc	aag	cag	cgc	cgc	gtg	ccg	cgc	ggc	agc	acc	aag	tgg	atc	1465
Met	Tyr	Ile	Lys	Gln	Arg	Arg	Val	Pro	Arg	Gly	Ser	Thr	Lys	Trp	Ile	
		430				435					440					
tgt	ctc	cag	acg	ctc	agc	gtc	agc	tgc	ctc	ctc	gtc	tcc	gtg	gcg	gcc	1513
Cys	Leu	Gln	Thr	Leu	Ser	Val	Ser	Cys	Leu	Leu	Val	Ser	Val	Ala	Ala	
445					450					455					460	
gcc	gac	tagtgagctc	gtcgac													1535
Ala	Asp															

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 <212> PRT
 <213> Zea mays

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 Glu Val Ser Val Glu Ala Gly Asn Gly Gly Ala Ala Glu Trp Leu Asp
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 Asp Asp Gly Arg Pro Arg Arg Thr Phe Trp Thr Ala Ser Ala
 35 40 45
 His Ile Val Thr Ala Val Ile Gly Ser Gly Val Leu Ser Leu Ala Trp
 50 55 60
 Ala Ile Ala Gln Leu Gly Trp Val Ala Gly Pro Ala Ala Met Leu Leu
 65 70 75 80
 Phe Ala Phe Val Thr Tyr Tyr Thr Ala Thr Leu Leu Ala Glu Cys Tyr
 85 90 95
 Arg Thr Gly Asp Pro Glu Thr Gly Lys Arg Asn Tyr Thr Tyr Met Asp
 100 105 110
 Ala Val Arg Ser Asn Leu Gly Gly Ala Lys Val Ala Phe Cys Gly Val
 115 120 125
 Ile Gln Tyr Ala Asn Leu Val Gly Val Ala Ile Gly Tyr Thr Ile Ala
 130 135 140
 Ala Ser Ile Ser Met Lys Ala Val Arg Arg Ala Gly Cys Phe His Ala
 145 150 155 160
 His Gly His Ala Asp Pro Cys Asn Ser Ser Thr Pro Tyr Met Ile
 165 170 175
 Leu Phe Gly Val Val Gln Ile Leu Phe Ser Gln Ile Pro Asp Phe Asp
 180 185 190
 Gln Ile Trp Trp Leu Ser Ile Val Ala Ala Val Met Ser Phe Thr Tyr
 195 200 205
 Ser Ser Ile Gly Leu Ser Leu Gly Ile Ala Gln Thr Ile Ser Asn Gly
 210 215 220
 Gly Phe Met Gly Ser Leu Thr Gly Ile Ser Ile Gly Ala Gly Val Thr
 225 230 235 240
 Ser Thr Gln Lys Ile Trp His Thr Leu Gln Ala Phe Gly Asp Ile Ala
 245 250 255
 Phe Ala Tyr Ser Phe Ser Asn Ile Leu Ile Glu Ile Gln Asp Thr Ile
 260 265 270
 Lys Ala Pro Pro Pro Ser Glu Ser Lys Val Met Gln Lys Ala Thr Arg

PF59082SeqList_PF59082.txt

aac	tgc	ttc	cac	gtg	gag	ggg	cac	ggg	gac	ccc	tgc	aac	atc	tcc	agc	660
Asn	Cys	Phe	His	Val	Glu	Gly	His	Gly	Asp	Pro	Cys	Asn	Ile	Ser	Ser	
145						150					155					
acg	ccc	tac	atg	atc	atc	ttc	ggc	gtc	gtg	cag	att	ttc	ttc	tcg	cag	708
Thr	Pro	Tyr	Met	Ile	Ile	Phe	Gly	Val	Val	Gln	Ile	Phe	Phe	Ser	Gln	
160					165					170					175	
atc	ccg	gac	ttc	gac	cag	ata	tcg	tgg	ctc	tcc	atc	ctc	gcc	gcc	gtc	756
Ile	Pro	Asp	Phe	Asp	Gln	Ile	Ser	Trp	Leu	Ser	Ile	Leu	Ala	Ala	Val	
				180					185					190		
atg	tcg	ttc	acc	tac	tcc	acc	atc	ggc	ctg	ggc	ctg	ggc	atc	gcg	cag	804
Met	Ser	Phe	Thr	Tyr	Ser	Thr	Ile	Gly	Leu	Gly	Leu	Gly	Ile	Ala	Gln	
			195					200					205			
gtg	gtg	tcc	aac	aag	ggc	gtg	cag	ggc	agc	ctg	acg	ggg	atc	agc	gtc	852
Val	Val	Ser	Asn	Lys	Gly	Val	Gln	Gly	Ser	Leu	Thr	Gly	Ile	Ser	Val	
		210					215					220				
ggc	ttg	gtc	acc	ccg	gtc	gac	aag	atg	tgg	cgc	agc	ctg	cag	gcg	ttc	900
Gly	Leu	Val	Thr	Pro	Val	Asp	Lys	Met	Trp	Arg	Ser	Leu	Gln	Ala	Phe	
225						230					235					
ggc	gac	atc	gcc	ttc	gcc	tac	tcc	tac	tcg	ctc	atc	ctc	atc	gag	atc	948
Gly	Asp	Ile	Ala	Phe	Ala	Tyr	Ser	Tyr	Ser	Leu	Ile	Leu	Ile	Glu	Ile	
240					245					250					255	
cag	gac	acc	atc	cg	gcg	ccg	ccg	ccg	tcc	gag	tcc	aag	gtc	atg	cgg	996
Gln	Asp	Thr	Ile	Arg	Ala	Pro	Pro	Pro	Ser	Glu	Ser	Lys	Val	Met	Arg	
				260					265					270		
cgc	gcc	acc	gtc	gtc	agc	gtg	gcc	gtc	acc	acg	ttc	ttc	tac	atg	ctg	1044
Arg	Ala	Thr	Val	Val	Ser	Val	Ala	Val	Thr	Thr	Phe	Phe	Tyr	Met	Leu	
			275					280					285			
tgc	ggg	tgc	atg	ggg	tac	gcc	gcg	ttc	ggg	gac	aac	gcc	ccc	ggg	aac	1092
Cys	Gly	Cys	Met	Gly	Tyr	Ala	Ala	Phe	Gly	Asp	Asn	Ala	Pro	Gly	Asn	
		290					295					300				
ctc	ctc	acg	ggc	ttc	ggc	ttc	tac	gag	ccc	ttc	tgg	ctc	ctc	gac	gtc	1140
Leu	Leu	Thr	Gly	Phe	Gly	Phe	Tyr	Glu	Pro	Phe	Trp	Leu	Leu	Asp	Val	
305						310					315					
gcc	aac	gcc	gcc	atc	gcc	gtg	cac	ctc	gtc	ggc	gcc	tac	cag	gtc	tac	1188
Ala	Asn	Ala	Ala	Ile	Ala	Val	His	Leu	Val	Gly	Ala	Tyr	Gln	Val	Tyr	
320					325					330					335	
tgc	cag	ccc	ctg	ttc	gcc	ttc	gtc	gag	aag	tgg	gcg	cg	cag	agg	tgg	1236
Cys	Gln	Pro	Leu	Phe	Ala	Phe	Val	Glu	Lys	Trp	Ala	Arg	Gln	Arg	Trp	
				340					345					350		
ccc	aag	tcc	cg	tac	atc	acg	ggc	gag	gtc	gac	gtc	ccg	ctc	ccg	ctc	1284
Pro	Lys	Ser	Arg	Tyr	Ile	Thr	Gly	Glu	Val	Asp	Val	Pro	Leu	Pro	Leu	
			355					360					365			
ggg	acc	gcc	ggc	ggc	cg	tgc	tac	aag	ctc	agc	ctg	ttc	cg	ctg	acg	1332
Gly	Thr	Ala	Gly	Gly	Arg	Cys	Tyr	Lys	Leu	Ser	Leu	Phe	Arg	Leu	Thr	
		370					375					380				
tgg	cg	acg	gcg	ttc	gtg	gtg	gcc	acg	acg	gtg	gtg	tcc	atg	ctg	ctg	1380
Trp	Arg	Thr	Ala	Phe	Val	Val	Ala	Thr	Thr	Val	Val	Ser	Met	Leu	Leu	
385						390					395					
ccc	ttc	ttc	aac	gac	gtg	gtg	ggg	ctc	ctg	ggc	ctg	ggg	ttc	tgg		1428
Pro	Phe	Phe	Asn	Asp	Val	Val	Gly	Leu	Leu	Gly	Ala	Leu	Gly	Phe	Trp	
400				405						410					415	
ccg	ctc	acc	gtc	tac	ttc	ccc	gtg	gag	atg	tac	atc	gtg	cag	aag	aag	1476
Pro	Leu	Thr	Val	Tyr	Phe	Pro	Val	Glu	Met	Tyr	Ile	Val	Gln	Lys	Lys	
				420					425					430		
gtg	ccc	agg	tgg	agc	acg	cg	tgg	gtg	tgc	ctg	cag	ctg	ctc	agc	gtc	1524
Val	Pro	Arg	Trp	Ser	Thr	Arg	Trp	Val	Cys	Leu	Gln	Leu	Leu	Ser	Val	
			435				440						445			
gcc	tgc	ctc	gtc	atc	acc	gtc	gcc	tcc	gcc	gca	ggc	tcc	gtt	gcc	ggg	1572
Ala	Cys	Leu	Val	Ile	Thr	Val	Ala	Ser	Ala	Ala	Gly	Ser	Val	Ala	Gly	
		450					455					460				
atc	gtc	tct	gac	ctc	aaa	gtg	tac	aaa	ccg	ttc	gtc	acc	acc	tcc		1617
Ile	Val	Ser	Asp	Leu	Lys	Val	Tyr	Lys	Pro	Phe	Val	Thr	Thr	Ser		
465						470					475					
tgatcgaccg	tacgtcctag	cttccgtgca	gttcaaaaca	catacgcacg	aacagatcat											1677
taattggcgc	ctagtatata	tgtgcagtct	ttaattaaat	taactaggca	ttaatcgatc											1737

PF59082SeqList_PF59082.txt

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 aaatagtagc agtactgtgt gagtaatccc aagtcaaata cgttattgaa gttgtcggcg 1917
 gtacaaaacg cttgtaaaat gtttgtgttt caattaatca agaagaattg tacgtgtttc 1977

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 Lys Cys Phe Asp Asp Asp Gly Arg Leu Lys Arg Thr Gly Thr Met Trp
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 Thr Ala Ser Ala His Ile Ile Thr Ala Val Ile Gly Ser Gly Val Leu
 35 40 45
 Ser Leu Ala Trp Ala Ile Ala Gln Leu Gly Trp Val Ala Gly Pro Thr
 50 55 60
 Val Met Leu Leu Phe Ser Phe Val Thr Tyr Tyr Thr Ser Ala Leu Leu
 65 70 75 80
 Ala Asp Cys Tyr Arg Ser Gly Asp Ala Cys Thr Gly Lys Arg Asn Tyr
 85 90 95
 Thr Tyr Met Asp Ala Val Asn Ala Asn Leu Ser Gly Val Lys Val Trp
 100 105 110
 Phe Cys Gly Phe Leu Gln Tyr Ala Asn Ile Val Gly Val Ala Ile Gly
 115 120 125
 Tyr Thr Ile Ala Ala Ser Ile Ser Met Leu Ala Ile Gln Arg Ala Asn
 130 135 140
 Cys Phe His Val Glu Gly His Gly Asp Pro Cys Asn Ile Ser Ser Thr
 145 150 155 160
 Pro Tyr Met Ile Ile Phe Gly Val Val Gln Ile Phe Phe Ser Gln Ile
 165 170 175
 Pro Asp Phe Asp Gln Ile Ser Trp Leu Ser Ile Leu Ala Ala Val Met
 180 185 190
 Ser Phe Thr Tyr Ser Thr Ile Gly Leu Gly Leu Gly Ile Ala Gln Val
 195 200 205
 Val Ser Asn Lys Gly Val Gln Gly Ser Leu Thr Gly Ile Ser Val Gly
 210 215 220
 Leu Val Thr Pro Val Asp Lys Met Trp Arg Ser Leu Gln Ala Phe Gly
 225 230 235 240
 Asp Ile Ala Phe Ala Tyr Ser Tyr Ser Leu Ile Leu Ile Glu Ile Gln
 245 250 255
 Asp Thr Ile Arg Ala Pro Pro Pro Ser Glu Ser Lys Val Met Arg Arg
 260 265 270
 Ala Thr Val Val Ser Val Ala Val Thr Thr Phe Phe Tyr Met Leu Cys
 275 280 285
 Gly Cys Met Gly Tyr Ala Ala Phe Gly Asp Asn Ala Pro Gly Asn Leu
 290 295 300
 Leu Thr Gly Phe Gly Phe Tyr Glu Pro Phe Trp Leu Leu Asp Val Ala
 305 310 315 320
 Asn Ala Ala Ile Ala Val His Leu Val Gly Ala Tyr Gln Val Tyr Cys
 325 330 335
 Gln Pro Leu Phe Ala Phe Val Glu Lys Trp Ala Arg Gln Arg Trp Pro
 340 345 350
 Lys Ser Arg Tyr Ile Thr Gly Glu Val Asp Val Pro Leu Pro Leu Gly
 355 360 365
 Thr Ala Gly Gly Arg Cys Tyr Lys Leu Ser Leu Phe Arg Leu Thr Trp
 370 375 380
 Arg Thr Ala Phe Val Val Ala Thr Thr Val Val Ser Met Leu Leu Pro

PF59082SeqList_PF59082.txt

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Leu Thr Val Tyr Phe Pro Val Glu Met Tyr Ile Val Gln Lys Lys Val
Pro Arg Trp Ser Thr Arg Trp Val Cys Leu Gln Leu Leu Ser Val Ala
Cys Leu Val Ile Thr Val Ala Ser Ala Ala Gly Ser Val Ala Gly Ile
Val Ser Asp Leu Lys Val Tyr Lys Pro Phe Val Thr Thr Ser
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 <212> DNA
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taggccaaat caccaataaa tattatattcc cgttcttttg gcgtgttggc caccactga      180

acacatttgc actcacacat agaagcagag agaggccatt ggttggtttc agag atg      237
                               Met
                               1
gga agc atg cac ata gaa acc cca gaa act ttt gct gat ggt agc aaa      285
Gly Ser Met His Ile Glu Thr Pro Glu Thr Phe Ala Asp Gly Ser Lys
                               5                               10                               15
aac ttc gat gat gat gga cga gct aaa aga act ggg act tgg att act      333
Asn Phe Asp Asp Asp Gly Arg Ala Lys Arg Thr Gly Thr Trp Ile Thr
                               20                               25                               30
gca agt gct cat atc ata acg gct gtg att ggt tct gga gtg cta tct      381
Ala Ser Ala His Ile Ile Thr Ala Val Ile Gly Ser Gly Val Leu Ser
                               35                               40                               45
ctt gca tgg gca att gca cag atg ggt tgg gta gct ggt cct gca gtg      429
Leu Ala Trp Ala Ile Ala Gln Met Gly Trp Val Ala Gly Pro Ala Val
                               50                               55                               60                               65
ctc ttt gtc ttc tct ttg ata aca tac ttc acc tcc act ctt ctc gct      477
Leu Phe Val Phe Ser Leu Ile Thr Tyr Phe Thr Ser Thr Leu Leu Ala
                               70                               75                               80
gac tgt tac cgt tca cct gac cct gta cat ggc aag cga aac tac aca      525
Asp Cys Tyr Arg Ser Pro Asp Pro Val His Gly Lys Arg Asn Tyr Thr
                               85                               90                               95
tat tct gag gtt gtc aaa gcc aac cta gga gga aga aaa ttt cag ctg      573
Tyr Ser Glu Val Val Lys Ala Asn Leu Gly Gly Arg Lys Phe Gln Leu
                               100                               105                               110
tgt gga ttg gct cag tat ata aat ctt gtt ggt gta aca atc ggc tac      621
Cys Gly Leu Ala Gln Tyr Ile Asn Leu Val Gly Val Thr Ile Gly Tyr
                               115                               120                               125
act ata act gca tca ctt agt atg ggg gcg gtg aag aag tcg aac tgt      669
Thr Ile Thr Ala Ser Leu Ser Met Gly Ala Val Lys Lys Ser Asn Cys
                               130                               135                               140                               145
tta cac aaa cat ggc cat caa gac gag tgc aaa gtt aag gac aac gct      717
Leu His Lys His Gly His Gln Asp Glu Cys Lys Val Lys Asp Asn Ala
                               150                               155                               160
ttt atg att gct ttt gcc tgc atc caa att ctt cta agc caa ata cca      765
Phe Met Ile Ala Phe Ala Cys Ile Gln Ile Leu Leu Ser Gln Ile Pro
                               165                               170                               175
aac ttc cat aag ctc tct tgg ctc tct atc gta gca gct gtt atg tct      813
Asn Phe His Lys Leu Ser Trp Leu Ser Ile Val Ala Val Met Ser

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PF59082SeqList_PF59082.txt

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ggg gga cac gtg cga acc tta aca ggg gtg gaa gtt tcg gga	909			
Gly Gly Gly His Val Arg Thr Thr Leu Thr Gly Val Glu Val Ser Gly				
210	215	220		
acg gaa aag gtt tgg aaa atg ttt caa gct atc ggt gac att gcc ttt	957			
Thr Glu Lys Val Trp Lys Met Phe Gln Ala Ile Gly Asp Ile Ala Phe				
230	235	240		
gct tat gct ttt tct aat gtc cta att gag atc cag gac aca ctg aaa	1005			
Ala Tyr Ala Phe Ser Asn Val Leu Ile Glu Ile Gln Asp Thr Leu Lys				
245	250	255		
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Ser Ser Pro Pro Glu Asn Lys Val Met Lys Arg Ala Ser Leu Ile Gly				
260	265	270		
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Ile Met Thr Thr Thr Leu Phe Tyr Val Leu Cys Gly Cys Leu Gly Tyr				
275	280	285		
gct gca ttt gga aat gat gca cca tct aat ttc ctc aca gga ttc ggc	1149			
Ala Ala Phe Gly Asn Asp Ala Pro Ser Asn Phe Leu Thr Gly Phe Gly				
290	295	300		
ttc tat gag ccc ttt tgg cta ata gac ttt gcc aat gtc tgc ata gca	1197			
Phe Tyr Glu Pro Phe Trp Leu Ile Asp Phe Ala Asn Val Cys Ile Ala				
310	315	320		
gtg cac tta gtt ggg gca tac cag gtc ttt gtc caa cct ata ttt ggg	1245			
Val His Leu Val Gly Ala Tyr Gln Val Phe Val Gln Pro Ile Phe Gly				
325	330	335		
ttt gtg gaa aag tgg agc aaa gaa aat tgg aca gaa agc caa ttt ata	1293			
Phe Val Glu Lys Trp Ser Lys Gln Asn Trp Thr Glu Ser Gln Phe Ile				
340	345	350		
aat ggc gag cat act ttg aac att cct cta tgt gga agc tac aat gtg	1341			
Asn Gly Glu His Thr Leu Asn Ile Pro Leu Cys Gly Ser Tyr Asn Val				
355	360	365		
aac ttc ttt agg gta gtg tgg agg act gca tat gtg att atc act gcc	1389			
Asn Phe Phe Arg Val Val Trp Arg Thr Ala Tyr Val Ile Ile Thr Ala				
370	375	380		
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Val Val Ala Met Leu Leu Pro Phe Phe Asn Asp Phe Leu Ala Leu Ile				
390	395	400		
ggg gca ctc tct ttc tgg cca ttg acg gtt tac ttc cct ata gag atg	1485			
Gly Ala Leu Ser Phe Trp Pro Leu Thr Val Tyr Phe Pro Ile Glu Met				
405	410	415		
tac att aag aag tca aat atg caa aga ttt tcc ttc acc tgg act tgg	1533			
Tyr Ile Lys Lys Ser Asn Met Gln Arg Phe Ser Phe Thr Trp Thr Trp				
420	425	430		
ctc aag ata ttg agt tgg gtt tgc ttg atc att tct att atc tca ctt	1581			
Leu Lys Ile Leu Ser Trp Val Cys Leu Ile Ile Ser Ile Ile Ser Leu				
435	440	445		
gtg ggt tcc atc caa ggc ctt tcg gtt agt atc aag aaa tac aag ccc	1629			
Val Gly Ser Ile Gln Gly Leu Ser Val Ser Ile Lys Lys Tyr Lys Pro				
450	455	460		
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Phe Gln Ala Glu Gln				
470				
ttctattgag ggcgacaaaa tttgtattac tatgttttga aatagttggt atattttcaa	1744			
ttctcgaaat cgagacaact tgttatacta aagtaatata ataaaatggt tagtttgcta	1804			
tggttaaaaaa ttttaaactt ggtagctggt tttttttctt ttttgtagg ttatgtttag	1864			
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<212> PRT

<213> Glycine max

<400> 529

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Ser Leu Ala Trp Ala Ile Ala Gln Met Gly Trp Val Ala Gly Pro Ala
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Val Leu Phe Val Phe Ser Leu Ile Thr Tyr Phe Thr Ser Thr Leu Leu
65      70      75      80
Ala Asp Cys Tyr Arg Ser Pro Asp Pro Val His Gly Lys Arg Asn Tyr
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Thr Tyr Ser Glu Val Val Lys Ala Asn Leu Gly Gly Arg Lys Phe Gln
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Leu Cys Gly Leu Ala Gln Tyr Ile Asn Leu Val Gly Val Thr Ile Gly
      115      120      125
Tyr Thr Ile Thr Ala Ser Leu Ser Met Gly Ala Val Lys Lys Ser Asn
      130      135      140
Cys Leu His Lys His Gly His Gln Asp Glu Cys Lys Val Lys Asp Asn
145      150      155      160
Ala Phe Met Ile Ala Phe Ala Cys Ile Gln Ile Leu Leu Ser Gln Ile
      165      170      175
Pro Asn Phe His Lys Leu Ser Trp Leu Ser Ile Val Ala Ala Val Met
      180      185      190
Ser Phe Ala Tyr Ser Ser Ile Gly Leu Gly Leu Ser Ile Ala Lys Ile
      195      200      205
Ile Gly Gly Gly His Val Arg Thr Thr Leu Thr Gly Val Glu Val Ser
      210      215      220
Gly Thr Glu Lys Val Trp Lys Met Phe Gln Ala Ile Gly Asp Ile Ala
225      230      235      240
Phe Ala Tyr Ala Phe Ser Asn Val Leu Ile Glu Ile Gln Asp Thr Leu
      245      250      255
Lys Ser Ser Pro Pro Glu Asn Lys Val Met Lys Arg Ala Ser Leu Ile
      260      265      270
Gly Ile Met Thr Thr Thr Leu Phe Tyr Val Leu Cys Gly Cys Leu Gly
      275      280      285
Tyr Ala Ala Phe Gly Asn Asp Ala Pro Ser Asn Phe Leu Thr Gly Phe
      290      295      300
Gly Phe Tyr Glu Pro Phe Trp Leu Ile Asp Phe Ala Asn Val Cys Ile
305      310      315      320
Ala Val His Leu Val Gly Ala Tyr Gln Val Phe Val Gln Pro Ile Phe
      325      330      335
Gly Phe Val Glu Lys Trp Ser Lys Glu Asn Trp Thr Glu Ser Gln Phe
      340      345      350
Ile Asn Gly Glu His Thr Leu Asn Ile Pro Leu Cys Gly Ser Tyr Asn
      355      360      365
Val Asn Phe Phe Arg Val Val Trp Arg Thr Ala Tyr Val Ile Ile Thr
      370      375      380
Ala Val Val Ala Met Leu Leu Pro Phe Phe Asn Asp Phe Leu Ala Leu
385      390      395      400
Ile Gly Ala Leu Ser Phe Trp Pro Leu Thr Val Tyr Phe Pro Ile Glu
      405      410      415
Met Tyr Ile Lys Lys Ser Asn Met Gln Arg Phe Ser Phe Thr Trp Thr
      420      425      430
Trp Leu Lys Ile Leu Ser Trp Val Cys Leu Ile Ile Ser Ile Ile Ser
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Leu Val Gly Ser Ile Gln Gly Leu Ser Val Ser Ile Lys Lys Tyr Lys
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<212> DNA

PF59082SeqList_PF59082.txt

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<222> (130)..(1593)

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caagacaag atg gtt gag aag gat ggc gtt ggc agc aag tat ctt caa caa 171

Met Val Glu Lys Asp Gly Val Gly Ser Lys Tyr Leu Gln Gln
1 5 10

aca ctt aac gtc tcc atc gac atg cat caa cac gga atc tct aag tgt 219

Thr Leu Asn Val Ser Ile Asp Met His Gln His Gly Ile Ser Lys Cys
15 20 25 30

ttc gac gac gat ggt cgc ccg aaa aga acc ggg acg gtg tgg act tca 267

Phe Asp Asp Asp Gly Arg Pro Lys Arg Thr Gly Thr Val Trp Thr Ser
35 40 45

agt gca cac ata ata act gca gtg att ggg tct ggg gtg cta tct ctg 315

Ser Ala His Ile Ile Thr Ala Val Ile Gly Ser Gly Val Leu Ser Leu
50 55 60

gct tgg gct ata gct cag ctt gga tgg att gct ggt cct att gtc atg 363

Ala Trp Ala Ile Ala Gln Leu Gly Trp Ile Ala Gly Pro Ile Val Met
65 70 75

gtt atc ttt tct gcc atc act tac tac act tcc act ctt ctc gct gat 411

Val Ile Phe Ser Ala Ile Thr Tyr Tyr Thr Ser Thr Leu Leu Ala Asp
80 85 90

tgt tac cgc acc ggt gat cct gta act ggc aag aga aac tac act tac 459

Cys Tyr Arg Thr Gly Asp Pro Val Thr Gly Lys Arg Asn Tyr Thr Tyr
95 100 105 110

atg gac gct att cag tct aac ttt ggt gga aat ggc ttt aag gtc aag 507

Met Asp Ala Ile Gln Ser Asn Phe Gly Gly Asn Gly Phe Lys Val Lys
115 120 125

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Leu Cys Gly Leu Val Gln Tyr Val Asn Leu Phe Gly Val Ala Ile Gly
130 135 140

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Tyr Thr Ile Ala Ala Ser Thr Ser Met Met Ala Ile Glu Arg Ser Asn
145 150 155

tgt ttc cac aag agt gga ggg aaa gat ccg tgc cac att aac agc aac 651

Cys Phe His Lys Ser Gly Lys Asp Pro Cys His Ile Asn Ser Asn
160 165 170

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Met Tyr Met Ile Ser Phe Gly Ile Val Glu Ile Leu Phe Ser Gln Ile
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ccg ggc ttc gat caa ctg tgg tgg ctc tcc att gta gct gct gtc atg 747

Pro Gly Phe Asp Gln Leu Trp Trp Leu Ser Ile Val Ala Ala Val Met
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Ile Glu Asn Gly Gly Val Gly Gly Ser Leu Thr Gly Ile Thr Ile Gly
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acc gtg acc caa act gat aaa gtt tgg aga acc atg caa gct ctt ggt 891

Thr Val Thr Gln Thr Asp Lys Val Trp Arg Thr Met Gln Ala Leu Gly
240 245 250

gac ata gcc ttt gct tat tca tac tcc ctc atc ctt ata gaa att cag 939

Asp Ile Ala Phe Ala Tyr Ser Tyr Ser Leu Ile Leu Ile Glu Ile Gln
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Asp Thr Val Lys Ser Pro Pro Ser Glu Ser Lys Thr Met Lys Lys Ala
275 280 285

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PF59082SeqList_PF59082.txt

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gct Ala 335	gcc Ala	ata Ile	gtg Val	atc Ile	cac His 340	ctt Leu	gtt Val	ggt Gly	tca Ser	tac Tyr 345	caa Gln	gtt Val	tac Tyr	tgc Cys	cag Gln 350	
ccc Pro	ctc Leu	ttc Phe	gcc Ala 355	ttc Phe	gtc Val	gag Glu	aaa Lys	cac His	gcg Ala 360	gcg Ala	caa Gln	atg Met	ttc Phe	cca Pro 365	gat Asp	
agt Ser	gat Asp	ttt Phe	ctg Leu 370	aac Asn	aaa Lys	gaa Glu	att Ile	gaa Glu 375	att Ile	cca Pro	atc Ile	cct Pro	ggt Gly 380	ttc Phe	cat His	
ccc Pro	tac Tyr	agg Arg 385	ctc Leu	aac Asn	ctc Leu	ttc Phe	agg Arg 390	ttg Leu	gtt Val	tgg Trp	agg Arg	aca Thr 395	ata Ile	tat Tyr	gta Val	
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cca Pro	gtg Val	gag Glu	atg Met 435	tac Tyr	att Ile	att Ile	caa Gln	aag Lys	aga Arg 440	ata Ile	cca Pro	aag Lys	tgg Trp 445	agc Ser	aca Thr	
aag Lys	tgg Trp	atc Ile	tgc Cys 450	ctc Leu	caa Gln	ata Ile	ctt Leu	agc Ser 455	atg Met	act Thr	tgc Cys	ctt Leu 460	ttg Leu 460	atg Met	act Thr	
ata Ile	gga Gly 465	gct Ala	gca Ala	gct Ala	ggc Gly	tct Ser	att Ile 470	gct Ala	ggg Gly	att Ile	gcc Ala 475	att Ile 475	gat Asp	ctt Leu	cga Arg	
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35 40 45
His Ile Ile Thr Ala Val Ile Gly Ser Gly Val Leu Ser Leu Ala Trp
50 55 60
Ala Ile Ala Gln Leu Gly Trp Ile Ala Gly Pro Ile Val Met Val Ile
65 70 75 80
Phe Ser Ala Ile Thr Tyr Tyr Thr Ser Thr Leu Leu Ala Asp Cys Tyr
85 90 95
Arg Thr Gly Asp Pro Val Thr Gly Lys Arg Asn Tyr Thr Tyr Met Asp
Seite 670

PF59082SeqList_PF59082.txt

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 Gly Leu Val Gln Tyr Val Asn Leu Phe Gly Val Ala Ile Gly Tyr Thr
 130 135 140
 Ile Ala Ala Ser Thr Ser Met Met Ala Ile Glu Arg Ser Asn Cys Phe
 145 150 155
 His Lys Ser Gly Gly Lys Asp Pro Cys His Ile Asn Ser Asn Met Tyr
 165 170 175
 Met Ile Ser Phe Gly Ile Val Glu Ile Leu Phe Ser Gln Ile Pro Gly
 180 185 190
 Phe Asp Gln Leu Trp Trp Leu Ser Ile Val Ala Ala Val Met Ser Phe
 195 200 205
 Thr Tyr Ser Thr Ile Gly Leu Gly Leu Gly Ile Gly Lys Val Ile Glu
 210 215 220
 Asn Gly Gly Val Gly Gly Ser Leu Thr Gly Ile Thr Ile Gly Thr Val
 225 230 235
 Thr Gln Thr Asp Lys Val Trp Arg Thr Met Gln Ala Leu Gly Asp Ile
 245 250 255
 Ala Phe Ala Tyr Ser Tyr Ser Leu Ile Leu Ile Glu Ile Gln Asp Thr
 260 265 270
 Val Lys Ser Pro Pro Ser Glu Ser Lys Thr Met Lys Lys Ala Ser Phe
 275 280 285
 Ile Ser Val Ala Val Thr Ser Ile Phe Tyr Met Leu Cys Gly Cys Phe
 290 295 300
 Gly Tyr Ala Ala Phe Gly Asp Ala Ser Pro Gly Asn Leu Leu Thr Gly
 305 310 315
 Phe Gly Phe Tyr Asn Pro Tyr Trp Leu Leu Asp Ile Ala Asn Ala Ala
 325 330 335
 Ile Val Ile His Leu Val Gly Ser Tyr Gln Val Tyr Cys Gln Pro Leu
 340 345 350
 Phe Ala Phe Val Glu Lys His Ala Ala Gln Met Phe Pro Asp Ser Asp
 355 360 365
 Phe Leu Asn Lys Glu Ile Glu Ile Pro Ile Pro Gly Phe His Pro Tyr
 370 375 380
 Arg Leu Asn Leu Phe Arg Leu Val Trp Arg Thr Ile Tyr Val Met Leu
 385 390 395
 Ser Thr Val Ile Ser Met Leu Leu Pro Phe Phe Asn Asp Ile Gly Gly
 405 410 415
 Leu Leu Gly Ala Phe Gly Phe Trp Pro Leu Thr Val Tyr Phe Pro Val
 420 425 430
 Glu Met Tyr Ile Ile Gln Lys Arg Ile Pro Lys Trp Ser Thr Lys Trp
 435 440 445
 Ile Cys Leu Gln Ile Leu Ser Met Thr Cys Leu Leu Met Thr Ile Gly
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 Leu Pro Arg Ser Arg Thr Leu Pro Ser Arg Ile His Gln Gly Ile Ile 15

gaa gag agg cac gat gtc agg ccc tac gta caa gta gaa gtg cga ccc 152
 Glu Glu Arg His Asp Val Arg Pro Tyr Val Gln Val Glu Val Arg Pro 20 25 30

PF59082SeqList_PF59082.txt																
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Ser	Lys	Cys	Phe	Asp	Asp	Asp	Gly	Arg	Leu	Lys	Arg	Thr	Gly	Thr	Phe	
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Trp	Thr	Ala	Thr	Ala	His	Ile	Ile	Thr	Ala	Val	Ile	Gly	Ser	Gly	Val	
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ctt	tca	cta	gca	tgg	gcg	gtt	gct	cag	ctt	ggc	tgg	gtt	gct	gga	cct	344
Leu	Ser	Leu	Ala	Trp	Ala	Val	Ala	Gln	Leu	Gly	Trp	Val	Ala	Gly	Pro	
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Val	Val	Met	Phe	Leu	Phe	Ala	Val	Val	Asn	Leu	Tyr	Thr	Ser	Asn	Leu	
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Leu	Thr	Gln	Cys	Tyr	Arg	Thr	Gly	Asp	Ser	Val	Asn	Gly	His	Arg	Asn	
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Tyr	Thr	Tyr	Met	Glu	Ala	Val	Lys	Ser	Ile	Leu	Gly	Gly	Lys	Lys	Val	
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Lys	Leu	Cys	Gly	Leu	Ile	Gln	Tyr	Ile	Asn	Leu	Phe	Gly	Val	Ala	Ile	
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ggg	tac	acc	att	gct	gcc	tct	gtc	agt	atg	atg	gcc	ata	aaa	agg	tcg	584
Gly	Tyr	Thr	Ile	Ala	Ala	Ser	Val	Ser	Met	Met	Ala	Ile	Lys	Arg	Ser	
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Asn	Cys	Tyr	His	Ser	Ser	His	Gly	Lys	Asp	Pro	Cys	His	Met	Ser	Ser	
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Asn	Gly	Tyr	Met	Ile	Thr	Phe	Gly	Ile	Ala	Glu	Val	Ile	Phe	Ser	Gln	
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Ile	Pro	Asp	Phe	Asp	Gln	Val	Trp	Trp	Leu	Ser	Ile	Val	Ala	Ala	Ile	
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Met	Ser	Phe	Thr	Tyr	Ser	Ser	Val	Gly	Leu	Ser	Leu	Gly	Val	Ala	Lys	
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Val	Ala	Glu	Asn	Lys	Thr	Phe	Lys	Ser	Leu	Met	Gly	Ile	Ser	Ile		
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Arg	Ser	Leu	Gln	Ala	Leu	Gly	Ala	Met	Ala	Phe	Ala	Tyr	Ser	Phe	Ser	
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att	atc	ctc	atc	gaa	att	cag	gac	acc	ata	aaa	ttt	cct	cct	gca	gag	968
Ile	Ile	Leu	Ile	Glu	Ile	Gln	Asp	Thr	Ile	Lys	Phe	Pro	Pro	Ala	Glu	
	290				295					300					305	
cac	aag	acc	atg	aga	aag	gcc	aca	aca	ttg	agc	atc	gcg	gtt	acc	aca	1016
His	Lys	Thr	Met	Arg	Lys	Ala	Thr	Thr	Leu	Ser	Ile	Ala	Val	Thr	Thr	
				310					315					320		
gtg	ttc	tat	tta	ctc	tgt	gga	tgc	atg	ggc	tat	gca	gcc	ttc	gga	gat	1064
Val	Phe	Tyr	Leu	Leu	Cys	Gly	Cys	Met	Gly	Tyr	Ala	Ala	Phe	Gly	Asp	
			325					330					335			
aat	gca	cct	gga	aat	ctc	ttg	act	ggc	ttt	ggg	ttc	tat	aac	cct	tat	1112
Asn	Ala	Pro	Gly	Asn	Leu	Leu	Thr	Gly	Phe	Gly	Phe	Tyr	Asn	Pro	Tyr	
		340					345					350				
tgg	ctt	ctg	gac	att	gcc	aac	ctt	gca	att	gtt	atc	cac	cta	gtt	ggg	1160
Trp	Leu	Leu	Asp	Ile	Ala	Asn	Leu	Ala	Ile	Val	Ile	His	Leu	Val	Gly	
	355					360					365					
gca	tat	cag	gtt	ttt	tcc	cag	ccc	tta	ttt	gca	ttt	gtg	gaa	aaa	tgg	1208
Ala	Tyr	Gln	Val	Phe	Ser	Gln	Pro	Leu	Phe	Ala	Phe	Val	Glu	Lys	Trp	
					375					380					385	
agt	gta	cgc	aaa	tgg	cca	aag	agc	aat	ttt	gtc	acg	gca	gaa	tat	gat	1256
Ser	Val	Arg	Lys	Trp	Pro	Lys	Ser	Asn	Phe	Val	Thr	Ala	Glu	Tyr	Asp	
				390					395					400		

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ata ccg att ccc tgc ttt ggt gtg tac caa ctc aac ttc ttc cgc tta	1304
Ile Pro Ile Pro Cys Phe Gly Val Tyr Gln Leu Asn Phe Phe Arg Leu	
405 410 415	
gta tgg aga acc att ttt gtg ctg ttg acg acc ctc ata gcc atg ctc	1352
Val Trp Arg Thr Ile Phe Val Leu Leu Thr Thr Leu Ile Ala Met Leu	
420 425 430	
atg cct ttt ttc aac gat gtg gtt gga ata ctt ggc gct ttt ggg ttc	1400
Met Pro Phe Phe Asn Asp Val Val Gly Ile Leu Gly Ala Phe Gly Phe	
435 440 445	
tgg ccc tta aca gtt tat ttc cct atc gac atg tat att tcg caa aag	1448
Trp Pro Leu Thr Val Tyr Phe Pro Ile Asp Met Tyr Ile Ser Gln Lys	
450 455 460 465	
aag att gga cga tgg act agt cgg tgg att gga ctt caa tta ctt agt	1496
Lys Ile Gly Arg Trp Thr Ser Arg Trp Ile Gly Leu Gln Leu Leu Ser	
470 475 480	
gtc agt tgc ctc atc att tca ttg tta gct gca gtt ggt tcc atg gca	1544
Val Ser Cys Leu Ile Ile Ser Leu Leu Ala Ala Val Gly Ser Met Ala	
485 490 495	
ggg gtt gtt ttg gac ctc aag act tat aag cca ttt aaa act agt tat	1592
Gly Val Val Leu Asp Leu Lys Thr Tyr Lys Pro Phe Lys Thr Ser Tyr	
500 505 510	
taagtgcgat ttaaagaagg tcgtagaat agaagtgttt aagcttgatg atattataga	1652
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Tyr Ser Lys Cys Phe Asp Asp Gly Arg Leu Lys Arg Thr Gly Thr	
50 55 60	
Phe Trp Thr Ala Thr Ala His Ile Ile Thr Ala Val Ile Gly Ser Gly	
65 70 75 80	
Val Leu Ser Leu Ala Trp Ala Val Ala Gln Leu Gly Trp Val Ala Gly	
85 90 95	
Pro Val Val Met Phe Leu Phe Ala Val Asn Leu Tyr Thr Ser Asn	
100 105 110	
Leu Leu Thr Gln Cys Tyr Arg Thr Gly Asp Ser Val Asn Gly His Arg	
115 120 125	
Asn Tyr Thr Tyr Met Glu Ala Val Lys Ser Ile Leu Gly Gly Lys Lys	
130 135 140	
Val Lys Leu Cys Gly Leu Ile Gln Tyr Ile Asn Leu Phe Gly Val Ala	
145 150 155 160	
Ile Gly Tyr Thr Ile Ala Ala Ser Val Ser Met Met Ala Ile Lys Arg	
165 170 175	
Ser Asn Cys Tyr His Ser Ser His Gly Lys Asp Pro Cys His Met Ser	
180 185 190	
Ser Asn Gly Tyr Met Ile Thr Phe Gly Ile Ala Glu Val Ile Phe Ser	
195 200 205	
Gln Ile Pro Asp Phe Asp Gln Val Trp Trp Leu Ser Ile Val Ala Ala	
210 215 220	
Ile Met Ser Phe Thr Tyr Ser Ser Val Gly Leu Ser Leu Gly Val Ala	
225 230 235 240	
Lys Val Ala Glu Asn Lys Thr Phe Lys Gly Ser Leu Met Gly Ile Ser	
245 250 255	

PF59082SeqList_PF59082.txt

Ile Gly Thr Val Thr Gln Ala Gly Thr Val Thr Ser Thr Gln Lys Ile
 260 265 270
 Trp Arg Ser Leu Gln Ala Leu Gly Ala Met Ala Phe Ala Tyr Ser Phe
 275 280 285
 Ser Ile Ile Leu Ile Glu Ile Gln Asp Thr Ile Lys Phe Pro Pro Ala
 290 295 300
 Glu His Lys Thr Met Arg Lys Ala Thr Thr Leu Ser Ile Ala Val Thr
 305 310 315 320
 Thr Val Phe Tyr Leu Leu Cys Gly Cys Met Gly Tyr Ala Ala Phe Gly
 325 330 335
 Asp Asn Ala Pro Gly Asn Leu Leu Thr Thr Phe Gly Phe Tyr Asn Pro
 340 345 350
 Tyr Trp Leu Leu Asp Ile Ala Asn Leu Ala Ile Val Ile His Leu Val
 355 360 365
 Gly Ala Tyr Gln Val Phe Ser Gln Pro Leu Phe Ala Phe Val Glu Lys
 370 375 380
 Trp Ser Val Arg Lys Trp Pro Lys Ser Asn Phe Val Thr Ala Glu Tyr
 385 390 395 400
 Asp Ile Pro Ile Pro Cys Phe Gly Val Tyr Gln Leu Asn Phe Phe Arg
 405 410 415
 Leu Val Trp Arg Thr Ile Phe Val Leu Leu Thr Thr Leu Ile Ala Met
 420 425 430
 Leu Met Pro Phe Phe Asn Asp Val Val Gly Ile Leu Gly Ala Phe Gly
 435 440 445
 Phe Trp Pro Leu Thr Val Tyr Phe Pro Ile Asp Met Tyr Ile Ser Gln
 450 455 460
 Lys Lys Ile Gly Arg Trp Thr Ser Arg Trp Ile Gly Leu Gln Leu Leu
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 Ala Gly Val Val Leu Asp Leu Lys Thr Tyr Lys Pro Phe Lys Thr Ser
 500 505 510
 Tyr

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 Thr Leu Pro Ser Arg Ile His Gln Gly Ile Ile Glu Glu Arg His Asp
 10 15 20
 gtc agg ccc tac gta caa gta gaa gtg cga ccc aat aat atc caa acg 150
 Val Arg Pro Tyr Val Gln Val Glu Val Arg Pro Asn Asn Ile Gln Thr
 25 30 35
 gag acc caa gcg atg aat atc cag tct aac tat tcc aag tgc ttc gat 198
 Glu Thr Gln Ala Met Asn Ile Gln Ser Asn Tyr Ser Lys Cys Phe Asp
 40 45 50
 gat gat ggt cgc ttg aag aga aca gga aca ttt tgg acg gca act gct 246
 Asp Asp Gly Arg Leu Lys Arg Thr Gly Thr Phe Trp Thr Ala Thr Ala
 55 60 65 70
 cat atc atc act gct gtg ata ggg tcg gga gtc ctt tca cta gca tgg 294
 His Ile Ile Thr Ala Val Ile Gly Ser Gly Val Leu Ser Leu Ala Trp
 75 80 85
 gcg gtt gct cag ctt ggt tgg gtt gct gga cct gtt gtc atg ttt ctc 342
 Ala Val Ala Gln Leu Gly Trp Val Ala Gly Pro Val Val Met Phe Leu
 90 95 100
 ttt gcc gtc gtc aat ctc tac act tcc aac cta tta aca cag tgt tac 390
 Phe Ala Val Val Asn Leu Tyr Thr Ser Asn Leu Leu Thr Gln Cys Tyr
 105 110 115

PF59082SeqList_PF59082.txt

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Arg	Thr	Gly	Asp	Ser	Val	Asn	Gly	His	Arg	Asn	Tyr	Thr	Tyr	Met	Glu	
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gct	gtc	aag	tcc	atc	ttg	gga	gga	aaa	aag	gtc	aag	tta	tgt	ggc	ctc	486
Ala	Val	Lys	Ser	Ile	Leu	Gly	Gly	Lys	Lys	Val	Lys	Leu	Cys	Gly	Leu	
135					140					145					150	
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Ile	Gln	Tyr	Ile	Asn	Leu	Phe	Gly	Val	Ala	Ile	Gly	Tyr	Thr	Ile	Ala	
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gcc	tct	gtc	agt	atg	atg	gcc	ata	aaa	agg	tcg	aat	tgc	tat	cac	agc	582
Ala	Ser	Val	Ser	Met	Met	Ala	Ile	Lys	Arg	Ser	Asn	Cys	Tyr	His	Ser	
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Ser	His	Gly	Lys	Asp	Pro	Cys	His	Met	Ser	Ser	Asn	Gly	Tyr	Met	Ile	
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aca	ttt	gga	ata	gca	gaa	gtg	ata	ttt	tcc	caa	atc	cca	gac	ttt	gat	678
Thr	Phe	Gly	Ile	Ala	Glu	Val	Ile	Phe	Ser	Gln	Ile	Pro	Asp	Phe	Asp	
	200					205					210					
cag	gtg	tgg	tgg	cta	tcc	ata	gtt	gca	gct	atc	atg	tcc	ttc	act	tat	726
Gln	Val	Trp	Trp	Leu	Ser	Ile	Val	Ala	Ala	Ile	Met	Ser	Phe	Thr	Tyr	
215					220					225					230	
tct	tca	gtt	gga	ttg	agt	ctt	gga	gtg	gcc	aaa	gta	gca	gaa	aat	aaa	774
Ser	Ser	Val	Gly	Leu	Ser	Leu	Gly	Val	Ala	Lys	Val	Ala	Glu	Asn	Lys	
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act	ttc	aaa	gga	agc	ctg	atg	gga	att	agc	att	ggc	aca	gta	aca	caa	822
Thr	Phe	Lys	Gly	Ser	Leu	Met	Gly	Ile	Ser	Ile	Gly	Thr	Val	Thr	Gln	
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gcc	gga	aca	gtc	acc	agc	aca	cag	aaa	ata	tgg	agg	agt	tta	caa	gct	870
Ala	Gly	Thr	Val	Thr	Ser	Thr	Gln	Lys	Ile	Trp	Arg	Ser	Leu	Gln	Ala	
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ctt	ggg	gca	atg	gcc	ttt	gca	tac	tcc	ttt	tcc	att	atc	ctc	atc	gaa	918
Leu	Gly	Ala	Met	Ala	Phe	Ala	Tyr	Ser	Phe	Ser	Ile	Ile	Leu	Ile	Glu	
	280					285					290					
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Ile	Gln	Asp	Thr	Ile	Lys	Ser	Pro	Pro	Ala	Glu	His	Lys	Thr	Met	Arg	
295					300					305					310	
aag	gcc	aca	aca	ttg	agc	atc	gcg	gtt	acc	aca	gtg	ttc	tat	tta	ctc	1014
Lys	Ala	Thr	Thr	Leu	Ser	Ile	Ala	Val	Thr	Thr	Val	Phe	Tyr	Leu	Leu	
				315					320					325		
tgt	gga	tgc	atg	ggt	tat	gca	gcc	ttc	gga	gat	aat	gca	cct	gga	aat	1062
Cys	Gly	Cys	Met	Gly	Tyr	Ala	Ala	Phe	Gly	Asp	Asn	Ala	Pro	Gly	Asn	
				330				335					340			
ctc	ttg	act	ggt	ttt	ggg	ttc	tat	aac	cct	tat	tgg	ctt	ctg	gac	att	1110
Leu	Leu	Thr	Gly	Phe	Gly	Phe	Tyr	Asn	Pro	Tyr	Trp	Leu	Leu	Asp	Ile	
		345					350					355				
gcc	aac	ctt	gca	att	gtt	atc	cac	cta	gtt	ggg	gca	tat	cag	gtt	ttt	1158
Ala	Asn	Leu	Ala	Ile	Val	Ile	His	Leu	Val	Gly	Ala	Tyr	Gln	Val	Phe	
	360					365				370						
tcc	cag	ccc	tta	ttt	gca	ttt	gtg	gaa	aaa	tgg	agt	gta	cgc	aaa	tgg	1206
Ser	Gln	Pro	Leu	Phe	Ala	Phe	Val	Glu	Lys	Trp	Ser	Val	Arg	Lys	Trp	
375					380					385					390	
cca	aag	agc	aat	ttt	gtc	acg	gca	gaa	tat	gat	ata	ccg	att	ccc	tgc	1254
Pro	Lys	Ser	Asn	Phe	Val	Thr	Ala	Glu	Tyr	Asp	Ile	Pro	Ile	Pro	Cys	
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Phe	Gly	Val	Tyr	Gln	Leu	Asn	Phe	Phe	Arg	Leu	Val	Trp	Arg	Thr	Ile	
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ttt	gtg	ctg	ttg	acg	acc	ctc	ata	gcc	atg	ctc	atg	cct	ttt	ttc	aac	1350
Phe	Val	Leu	Leu	Thr	Thr	Leu	Ile	Ala	Met	Leu	Met	Pro	Phe	Phe	Asn	
		425					430					435				
gat	gtg	gtt	gga	ata	ctt	ggc	gct	ttt	ggg	ttc	tgg	ccc	tta	aca	gtt	1398
Asp	Val	Val	Gly	Ile	Leu	Gly	Ala	Phe	Gly	Phe	Trp	Pro	Leu	Thr	Val	
	440					445				450						
tat	ttc	cct	atc	gac	atg	tat	att	tcg	caa	aag	att	gga	cga	tgg		1446
Tyr	Phe	Pro	Ile	Asp	Met	Tyr	Ile	Ser	Gln	Lys	Ile	Gly	Arg	Trp		
455					460					465				470		
act	agt	cgg	tgg	att	gga	ctt	caa	tta	ctt	agt	gtc	agt	tgc	ctc	atc	1494
Thr	Ser	Arg	Trp	Ile	Gly	Leu	Gln	Leu	Leu	Ser	Val	Ser	Cys	Leu	Ile	
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ctc aag act tat aag cca ttt aaa act agt tat taagtgagat ttaaagaagg      1595
Leu Lys Thr Tyr Lys Pro Phe Lys Thr Ser Tyr
          505          510
tcgtagaaat agaagtgttt aagcttgatg atattataga aaactaatga taagttgggt      1655

tgtgaaattt aagtatatac gctccatgcc gctgctgtta gagcaattga tttgagaaga      1715

agaaaaaaat gataattgga cataacatac ctcagaatth ggacgtatac gtgtctgtgt      1775

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Pro Asn Asn Ile Gln Thr Glu Thr Gln Ala Met Asn Ile Gln Ser Asn
          35      40      45
Tyr Ser Lys Cys Phe Asp Asp Gly Arg Leu Lys Arg Thr Gly Thr
          50      55      60
Phe Trp Thr Ala Thr Ala His Ile Ile Thr Ala Val Ile Gly Ser Gly
65      70      75      80
Val Leu Ser Leu Ala Trp Ala Val Ala Gln Leu Gly Trp Val Ala Gly
          85      90      95
Pro Val Val Met Phe Leu Phe Ala Val Val Asn Leu Tyr Thr Ser Asn
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Leu Leu Thr Gln Cys Tyr Arg Thr Gly Asp Ser Val Asn Gly His Arg
          115     120     125
Asn Tyr Thr Tyr Met Glu Ala Val Lys Ser Ile Leu Gly Gly Lys Lys
          130     135     140
Val Lys Leu Cys Gly Leu Ile Gln Tyr Ile Asn Leu Phe Gly Val Ala
145     150     155     160
Ile Gly Tyr Thr Ile Ala Ala Ser Val Ser Met Met Ala Ile Lys Arg
          165     170     175
Ser Asn Cys Tyr His Ser Ser His Gly Lys Asp Pro Cys His Met Ser
          180     185     190
Ser Asn Gly Tyr Met Ile Thr Phe Gly Ile Ala Glu Val Ile Phe Ser
          195     200     205
Gln Ile Pro Asp Phe Asp Gln Val Trp Trp Leu Ser Ile Val Ala Ala
210     215     220
Ile Met Ser Phe Thr Tyr Ser Ser Val Gly Leu Ser Leu Gly Val Ala
225     230     235     240
Lys Val Ala Glu Asn Lys Thr Phe Lys Gly Ser Leu Met Gly Ile Ser
          245     250     255
Ile Gly Thr Val Thr Gln Ala Gly Thr Val Thr Ser Thr Gln Lys Ile
          260     265     270
Trp Arg Ser Leu Gln Ala Leu Gly Ala Met Ala Phe Ala Tyr Ser Phe
          275     280     285
Ser Ile Ile Leu Ile Glu Ile Gln Asp Thr Ile Lys Ser Pro Pro Ala
290     295     300
Glu His Lys Thr Met Arg Lys Ala Thr Thr Leu Ser Ile Ala Val Thr
305     310     315     320
Thr Val Phe Tyr Leu Leu Cys Gly Cys Met Gly Tyr Ala Ala Phe Gly

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PF59082SeqList_PF59082.txt

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Lys	Arg	Ser	Asn	Cys	Tyr	His	Ser	Ser	Gly	Gly	Lys	Asn	Pro	Cys	Lys	
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Met	Asn	Ser	Asn	Trp	Tyr	Met	Ile	Ser	Tyr	Gly	Val	Ser	Glu	Ile	Ile	
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Phe	Ser	Gln	Ile	Pro	Asp	Phe	His	Glu	Leu	Trp	Trp	Leu	Ser	Ile	Val	
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Ala	Ala	Val	Met	Ser	Phe	Thr	Tyr	Ser	Phe	Ile	Gly	Leu	Gly	Leu	Gly	
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Ile	Gly	Lys	Val	Ile	Gly	Asn	Gly	Arg	Ile	Lys	Gly	Ser	Leu	Thr	Gly	
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gta	act	att	ggg	act	gtg	aca	gaa	tcc	caa	aaa	att	tgg	aga	act	ttc	896
Val	Thr	Ile	Gly	Thr	Val	Thr	Glu	Ser	Gln	Lys	Ile	Trp	Arg	Thr	Phe	
			230						235				240			
caa	gcg	ctt	gga	aac	ata	gcc	ttt	gct	tac	tcc	tac	tca	atg	atc	ctt	944
Gln	Ala	Leu	Gly	Asn	Ile	Ala	Phe	Ala	Tyr	Ser	Tyr	Ser	Met	Ile	Leu	
			245						250				255			
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Ile	Glu	Ile	Gln	Asp	Thr	Ile	Lys	Ser	Pro	Pro	Ala	Glu	Ser	Glu	Thr	
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Met	Ser	Lys	Ala	Thr	Leu	Ile	Ser	Val	Leu	Val	Thr	Thr	Val	Phe	Tyr	
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Met	Leu	Cys	Gly	Cys	Phe	Gly	Tyr	Ala	Ser	Phe	Gly	Asp	Ala	Ser	Pro	
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Gly	Asn	Leu	Leu	Thr	Gly	Phe	Gly	Phe	Tyr	Asn	Pro	Phe	Trp	Leu	Ile	
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Asp	Ile	Ala	Asn	Ala	Gly	Ile	Val	Ile	His	Leu	Val	Gly	Ala	Tyr	Gln	
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ggt	tac	tgc	caa	ccc	ctc	ttc	tca	gtc	gaa	tca	aat	gcg	gca	gaa		1232
Val	Tyr	Cys	Gln	Pro	Leu	Phe	Ser	Phe	Val	Glu	Ser	Asn	Ala	Ala	Glu	
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agg	ttc	cct	aat	agt	gat	ttt	atg	agc	aga	gag	ttt	gaa	gta	cca	atc	1280
Arg	Phe	Pro	Asn	Ser	Asp	Phe	Met	Ser	Arg	Glu	Phe	Glu	Val	Pro	Ile	
355					360					365					370	
cct	ggt	tgc	aaa	ccc	tac	aag	ctc	aac	ctc	ttc	agg	ttg	ggt	tgg	agg	1328
Pro	Gly	Cys	Lys	Pro	Tyr	Lys	Leu	Asn	Leu	Phe	Arg	Leu	Val	Trp	Arg	
				375					380					385		
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Thr	Leu	Phe	Val	Ile	Leu	Ser	Thr	Val	Ile	Ala	Met	Leu	Leu	Pro	Phe	
			390						395				400			
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Phe	Asn	Asp	Ile	Val	Gly	Leu	Ile	Gly	Ala	Ile	Gly	Phe	Trp	Pro	Leu	
			405						410				415			
act	gtg	tat	tta	cca	gtg	gag	atg	tat	ata	act	caa	act	aag	ata	cca	1472
Thr	Val	Tyr	Leu	Pro	Val	Glu	Met	Tyr	Ile	Thr	Gln	Thr	Lys	Ile	Pro	
			420													
aag	tgg	ggc	ata	aaa	tgg	ata	ggc	cta	caa	atg	ctt	agt	ggt	gca	tgc	1520
Lys	Trp	Gly	Ile	Lys	Trp	Ile	Gly	Leu	Gln	Met	Leu	Ser	Val	Ala	Cys	
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Phe	Val	Ile	Thr	Ile	Leu	Ala	Ala	Ala	Gly	Ser	Ile	Ala	Gly	Val	Ile	
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PF59082SeqList_PF59082.txt

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 Trp Ile Ala Gly Pro Val Val Met Ile Leu Phe Ser Ile Val Thr Tyr
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 Tyr Thr Ser Thr Leu Ala Thr Cys Tyr Arg Ser Gly Asp Gln Leu
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 Ser Gly Lys Arg Asn Tyr Thr Tyr Thr Gln Ala Val Arg Ser Tyr Leu
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 Gly Gly Phe Ser Val Lys Phe Cys Gly Trp Val Gln Tyr Ala Asn Leu
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 Phe Gly Val Ala Ile Gly Tyr Thr Ile Ala Ala Ser Ile Ser Met Met
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 Ile Ile Phe Ser Gln Ile Pro Asp Phe His Glu Leu Trp Trp Leu Ser
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 Ile Val Ala Val Met Ser Phe Thr Tyr Ser Phe Ile Gly Leu Gly
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 Thr Gly Val Thr Ile Gly Thr Val Thr Glu Ser Gln Lys Ile Trp Arg
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 Thr Phe Gln Ala Leu Gly Asn Ile Ala Phe Ala Tyr Ser Tyr Ser Met
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 Glu Thr Met Ser Lys Ala Thr Leu Ile Ser Val Leu Val Thr Thr Val
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 Phe Tyr Met Leu Cys Gly Cys Phe Gly Tyr Ala Ser Phe Gly Asp Ala
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 Ser Pro Gly Asn Leu Leu Thr Gly Phe Gly Phe Tyr Asn Pro Phe Trp
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 325 330 335
 Tyr Gln Val Tyr Cys Gln Pro Leu Phe Ser Phe Val Glu Ser Asn Ala
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 355 360 365
 Pro Ile Pro Gly Cys Lys Pro Tyr Lys Leu Asn Leu Phe Arg Leu Val
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 Trp Arg Thr Leu Phe Val Ile Leu Ser Thr Val Ile Ala Met Leu Leu
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PF59082SeqList_PF59082.txt

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 Met Val Gly Ala Met Arg Gly Gly Ala Met Glu Leu Glu Asp
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 Arg Leu Ala Thr Leu Pro Arg Phe Arg Gly Asp His Asp Asp Asp Gly
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 Lys Glu Arg Arg Thr Gly Thr Val Trp Thr Ala Thr Ala His Ile Ile
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acg gcg gtg atc ggc tcc ggc gtg ctg tcg ctg gcg tgg gcg atg gcg 372
 Thr Ala Val Ile Gly Ser Gly Val Leu Ser Leu Ala Trp Ala Met Ala
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cag ctg ggg tgg gtg gcc ggg ccg ttg acc ctg gtg ctc ttc gcg gcg 420
 Gln Leu Gly Trp Val Ala Gly Pro Leu Thr Leu Val Leu Phe Ala Ala
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 Ile Thr Phe Tyr Thr Cys Gly Leu Leu Ala Asp Cys Tyr Arg Val Gly
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 Asp Pro Val Thr Gly Lys Arg Asn Tyr Thr Tyr Thr Glu Ala Val Lys
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 Trp Leu Ser Ile Ile Ala Ala Ile Met Ser Phe Ser Tyr Ser Ala Ile
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PF59082SeqList_PF59082.txt

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Pro	Ala	Glu	Asn	Lys	Thr	Met	Arg	Arg	Ala	Thr	Met	Met	Gly	Ile	Ser	
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Leu	Gly	Ile	Leu	Gly	Ser	Ile	Ala	Phe	Trp	Pro	Leu	Thr	Val	Phe	Phe	
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Lys	Trp	Ile	Ala	Leu	Gln	Ser	Leu	Ser	Phe	Val	Cys	Phe	Leu	Val	Thr	
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acc	tac	gtg	ccg	ttc	aag	acg	agg	tcg	tgagctcctg	ctgcttagtt						1619
Thr	Tyr	Val	Pro	Phe	Lys	Thr	Arg	Ser								
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PF59082SeqList_PF59082.txt

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Phe Tyr Thr Cys Gly Leu Leu Ala Asp Cys Tyr Arg Val Gly Asp Pro
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130     135     140
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165     170     175
Gln Val Ile Phe Ser Gln Leu His Asn Phe His Lys Leu Trp Trp Leu
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355     360     365
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Leu	Pro	Asn	Phe	His	Lys	Leu	Ser	Phe	Leu	Ser	Ile	Ile	Ala	Ala	Val	
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<211> 475

<212> PRT

<213> Arabidopsis thaliana

<400> 541

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Thr	Val	Leu	Val	Ala	Phe	Ala	Ile	Ile	Thr	Tyr	Tyr	Thr	Ser	Thr	Leu	
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Leu	Ala	Asp	Cys	Tyr	Arg	Ser	Pro	Asp	Ser	Ile	Thr	Gly	Thr	Arg	Asn	
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Tyr	Asn	Tyr	Met	Gly	Val	Val	Arg	Ser	Tyr	Leu	Gly	Gly	Lys	Lys	Val	
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Gln	Leu	Cys	Gly	Val	Ala	Gln	Tyr	Val	Asn	Leu	Val	Gly	Val	Thr	Ile	
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PF59082SeqList_PF59082.txt

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 Ala Gln Pro Phe 340 Phe Gln Phe Val Glu 345 Glu Asn Cys Asn Lys 350 Lys Trp
 Pro Gln Ser 355 Asn Phe Ile Asn Lys 360 Glu Tyr Ser Ser Lys 365 Val Pro Leu
 Leu Gly 370 Lys Cys Arg Val Asn 375 Leu Phe Arg Leu Val 380 Trp Arg Thr Cys
 Tyr 385 Val Val Leu Thr Thr 390 Phe Val Ala Met Ile 395 Phe Pro Phe Phe Asn 400
 Ala Ile Leu Gly Leu 405 Leu Gly Ala Phe Ala 410 Phe Trp Pro Leu Thr Val 415
 Tyr Phe Pro Val 420 Ala Met His Ile Ala 425 Gln Ala Lys Val Lys 430 Lys Tyr
 Ser Arg Arg Trp Leu Ala Leu Asn 440 Leu Leu Val Leu Val 445 Cys Leu Ile
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<211> 1443

<212> DNA

<213> Arabidopsis thaliana

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<222> (1)..(1443)

<400> 542

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Trp Thr Ala Ser Ala His Ile Ile Thr Ala Val Ile Gly Ser Gly Val	
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Leu Ser Leu Ala Trp Ala Val Ala Gln Ile Gly Trp Ile Gly Gly Pro	
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ctc tgt tct tgt tac cga tct ggt gac tct gtt acc ggc aaa aga aac	288
Leu Cys Ser Cys Tyr 85 Arg Ser Gly Asp Ser 90 Val Thr Gly Lys Arg Asn	
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Tyr Thr Tyr Met Asp Ala Ile His Ser Asn Leu Gly Gly Ile Lys Val	
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Lys Val Cys Gly Val Val Gln Tyr Val Asn Leu Phe Gly Thr Ala Ile	
115 120 125	
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Gly Tyr Thr Ile Ala Ser Ala Ile Ser Leu Val Ala Ile Gln Arg Thr	
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Ile Pro Asp Phe Asp Gln Leu Trp Trp 185 Leu Ser Ile Val Ala Ala Val	
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Gly	Ile	Val	Ser	Asp	Leu	Lys	Val	Tyr	Lys	Pro	Phe	Gln	Ser	Glu	Phe	
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PF59082SeqList_PF59082.txt

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Leu Cys Ser Cys Tyr Arg Ser Gly Asp Ser Val Thr Gly Lys Arg Asn
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Tyr Thr Tyr Met Asp Ala Ile His Ser Asn Leu Gly Gly Ile Lys Val
      100      105
Lys Val Cys Gly Val Val Gln Tyr Val Asn Leu Phe Gly Thr Ala Ile
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Gly Tyr Thr Ile Ala Ser Ala Ile Ser Leu Val Ala Ile Gln Arg Thr
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Ser Cys Gln Gln Met Asn Gly Pro Asn Asp Pro Cys His Val Asn Gly
145      150      155
Asn Val Tyr Met Ile Ala Phe Gly Ile Val Gln Ile Ile Phe Ser Gln
      165      170
Ile Pro Asp Phe Asp Gln Leu Trp Trp Leu Ser Ile Val Ala Ala Val
      180      185
Met Ser Phe Ala Tyr Ser Ala Ile Gly Leu Gly Leu Gly Val Ser Lys
      195      200
Val Val Glu Asn Lys Glu Ile Lys Gly Ser Leu Thr Gly Val Thr Val
      210      215
Gly Thr Val Thr Leu Ser Gly Thr Val Thr Ser Ser Gln Lys Ile Trp
225      230      235
Arg Thr Phe Gln Ser Leu Gly Asn Ile Ala Phe Ala Tyr Ser Tyr Ser
      245      250
Met Ile Leu Ile Glu Ile Gln Asp Thr Val Lys Ser Pro Pro Ala Glu
      260      265
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      275      280
Val Phe Tyr Met Leu Cys Gly Cys Val Gly Tyr Ala Ala Phe Gly Asp
      290      295
Asn Ala Pro Gly Asn Leu Ala His Gly Gly Phe Arg Asn Pro Tyr
305      310      315
Trp Leu Leu Asp Ile Ala Asn Leu Ala Ile Val Ile His Leu Val Gly
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Ala Tyr Gln Val Tyr Cys Gln Pro Leu Phe Ala Phe Val Glu Lys Glu
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      370      375
Val Trp Arg Thr Phe Phe Val Met Thr Thr Thr Leu Ile Ser Met Leu
385      390      395
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Trp Pro Leu Thr Val Tyr Phe Pro Val Glu Met Tyr Ile Ala Gln Lys
      420      425
Asn Val Pro Arg Trp Gly Thr Lys Trp Val Cys Leu Gln Val Leu Ser
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<222> (1)..(1431)

<400> 544

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Gly	Val	Leu	Ser	Leu	Ala	Trp	Ala	Thr	Ala	Gln	Leu	Gly	Trp	Leu	Ala		
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Arg	Asn	Tyr	Thr	Tyr	Met	Asp	Ala	Val	Arg	Ser	Asn	Leu	Gly	Gly	Val		
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Lys	Val	Thr	Leu	Cys	Gly	Ile	Val	Gln	Tyr	Leu	Asn	Ile	Phe	Gly	Val		
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Asn	Ser	Asn	Pro	Tyr	Met	Ile	Ala	Phe	Gly	Leu	Val	Gln	Ile	Leu	Phe		
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Ala	Val	Met	Ser	Phe	Thr	Tyr	Ser	Ser	Ala	Gly	Leu	Ala	Leu	Gly	Ile		
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Ala	Gln	Val	Val	Val	Asn	Gly	Lys	Val	Lys	Gly	Ser	Leu	Thr	Gly	Ile		
	210				215					220							
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Ser	Ile	Gly	Ala	Val	Thr	Glu	Thr	Gln	Lys	Ile	Trp	Arg	Thr	Phe	Gln		
	225			230					235						240		
gct	ctt	gga	gac	att	gct	ttt	gct	tac	tct	tac	tcc	att	atc	ctc	atc		768
Ala	Leu	Gly	Asp	Ile	Ala	Phe	Ala	Tyr	Ser	Tyr	Ser	Ile	Ile	Leu	Ile		
			245						250					255			
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Glu	Ile	Gln	Asp	Thr	Val	Lys	Ser	Pro	Pro	Ser	Glu	Glu	Lys	Thr	Met		
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Tyr	Cys	Gln	Pro	Leu	Phe	Ala	Phe	Ile	Glu	Lys	Gln	Ala	Ser	Ile	Gln		
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Phe	Pro	Asp	Ser	Glu	Phe	Ile	Ala	Lys	Asp	Ile	Lys	Ile	Pro	Ile	Pro		
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	370					375					380						

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Trp	Ser	Thr	Arg	Trp	Val	Cys	Leu	Gln	Val	Phe	Ser	Leu	Gly	Cys	Leu	
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Val	Val	Ser	Ile	Ala	Ala	Ala	Ala	Gly	Ser	Ile	Ala	Gly	Val	Leu	Leu	
	450				455						460					
gat	cta	aag	tcc	tac	aag	cca	ttt	cga	agc	gaa	tac	tga				1431
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<212> PRT

<213> Arabidopsis thaliana

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 Val Tyr Phe Pro Val Glu Met Tyr Ile Ala Gln Lys Lys Ile Pro Arg
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 Trp Ser Thr Arg Trp Val Cys Leu Gln Val Phe Ser Leu Gly Cys Leu
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<211> 1482

<212> DNA

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Gly His Gln Val Phe Asp Val Ala Ser His Asp Phe Val Pro Pro Gln	
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Pro Ala Phe Lys Cys Phe Asp Asp Gly Arg Leu Lys Arg Thr Gly	
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Thr Val Trp Thr Ala Ser Ala His Ile Ile Thr Ala Val Ile Gly Ser	
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Gly Val Leu Ser Leu Ala Trp Ala Ile Ala Gln Leu Gly Trp Ile Ala	
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Gly Pro Ala Val Met Leu Leu Phe Ser Leu Val Thr Leu Tyr Ser Ser	
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Thr Leu Leu Ser Asp Cys Tyr Arg Thr Gly Asp Ala Val Ser Gly Lys	
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Arg Asn Tyr Thr Tyr Met Asp Ala Val Arg Ser Ile Leu Gly Gly Phe	
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Lys Phe Lys Ile Cys Gly Leu Ile Gln Tyr Leu Asn Leu Phe Gly Ile	
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Ala	Val 210	Met	Ser	Phe	Thr	Tyr 215	Ser	Ala	Ile	Gly	Leu 220	Ala	Leu	Gly	Ile
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Lys	Trp 450	Ser	Thr	Arg	Trp	Val 455	Cys	Leu	Gln	Met	Leu 460	Ser	Val	Ala	Cys
Leu 465	Val	Ile	Ser	Val	Val 470	Ala	Gly	Val	Gly	Ser 475	Ile	Ala	Gly	Val	Met 480
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Seite 692																

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Ser	Tyr	Ser	Gln	Ala	Val	Lys	Leu	Tyr	Leu	Gly	Lys	Lys	Asn	Glu	Ile	
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Asn	Asn	Tyr	Phe	Met	Val	Leu	Phe	Gly	Leu	Thr	Gln	Ile	Phe	Met	Ser	
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Ser	Thr	Val	Ala	Val	Phe	Ile	Gln	Thr	Phe	Phe	Phe	Phe	Cys	Cys	Gly	
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PF59082SeqList_PF59082.txt

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Tyr	Phe	Pro	Val	Glu	Met	Cys	Ile	Leu	Gln	Lys	Lys	Ile	Arg	Ser	Trp	
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Thr	Arg	Pro	Trp	Leu	Leu	Leu	Arg	Gly	Phe	Ser	Phe	Val	Cys	Leu	Leu	
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gtc	tgt	ctc	ttg	tct	ctt	gtt	gga	tct	att	tat	gga	ctt	gtt	gga	gct	1392
Val	Cys	Leu	Leu	Ser	Leu	Val	Gly	Ser	Ile	Tyr	Gly	Leu	Val	Gly	Ala	
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<213> Arabidopsis thaliana

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Asp	Cys	Tyr	Arg	Phe	Pro	Asp	Pro	Asn	Asn	Gly	Pro	Leu	Arg	Leu	Asn	
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Ser	Tyr	Ser	Gln	Ala	Val	Lys	Leu	Tyr	Leu	Gly	Lys	Lys	Asn	Glu	Ile	
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	130					135					140					
Cys	Tyr	His	Arg	Asn	Gly	His	Asn	Ala	Thr	Cys	Ser	Tyr	Gly	Asp	Asn	
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Asn	Asn	Tyr	Phe	Met	Val	Leu	Phe	Gly	Leu	Thr	Gln	Ile	Phe	Met	Ser	
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Gln	Ile	Pro	Asn	Phe	His	Asn	Met	Val	Trp	Leu	Ser	Leu	Val	Ala	Ala	
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Ile	Met	Ser	Phe	Thr	Tyr	Ser	Phe	Ile	Gly	Ile	Gly	Leu	Ala	Leu	Gly	
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Asn	Ile	Ala	Phe	Ser	Tyr	Pro	Phe	Ser	Ile	Ile	Leu	Leu	Glu	Ile	Gln	
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Ser	Thr	Val	Ala	Val	Phe	Ile	Gln	Thr	Phe	Phe	Phe	Phe	Cys	Cys	Gly	
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Cys	Phe	Gly	Tyr	Ala	Ala	Phe	Gly	Asp	Ser	Thr	Pro	Gly	Asn	Leu	Leu	
	290					295					300					
Thr	Gly	Phe	Gly	Phe	Tyr	Glu	Pro	Phe	Trp	Leu	Val	Asp	Phe	Ala	Asn	
305				310					315						320	
Ala	Cys	Ile	Val	Leu	His	Leu	Val	Gly	Gly	Tyr	Gln	Val	Tyr	Ser	Gln	
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Pro	Ile	Phe	Ala	Ala	Glu	Arg	Ser	Leu	Thr	Lys	Lys	Tyr	Pro	Glu		
		340					345					350				
Asn	Lys	Phe	Ile	Ala	Arg	Phe	Tyr	Gly	Phe	Lys	Leu	Pro	Leu	Leu	Arg	
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PF59082SeqList_PF59082.txt

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 420 425 430
 Thr Arg Pro Trp Leu Leu Leu Arg Gly Phe Ser Phe Val Cys Leu Leu
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<400> 550

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Glu Ile Gly Asp Thr Asn Lys Asn Phe Asp Glu Asp Gly Arg Asp Lys	
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aga act ggg aca tgg atg acc ggg agt gca cac ata ata acg gcc gtg	144
Arg Thr Gly Thr Trp Met Thr Gly Ser Ala His Ile Ile Thr Ala Val	
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ata ggg tcg gga gtg ttg tct ttg gcg tgg gca atc gca caa ctt gga	192
Ile Gly Ser Gly Val Leu Ser Leu Ala Trp Ala Ile Ala Gln Leu Gly	
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tgg gtg gca gga ccc gcc gta cta atg gct ttt tct ttc ata aca tat	240
Trp Val Ala Gly Pro Ala Val Leu Met Ala Phe Ser Phe Ile Thr Tyr	
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ttt aca tca acc atg ctt gcc gat tgt tac cgt tcc cct gac cct gtt	288
Phe Thr Ser Thr Met Leu Ala Asp Cys Tyr Arg Ser Pro Asp Pro Val	
85 90 95	
acc ggc aaa cgc aac tac acc tac atg gaa gtt gtc cga tcc tat cta	336
Thr Gly Lys Arg Asn Tyr Thr Tyr Met Glu Val Val Arg Ser Tyr Leu	
100 105 110	
gga gga aga aaa gtg caa tta tgt gga ttg gct caa tac ggg aat ctg	384
Gly Gly Arg Lys Val Gln Leu Cys Gly Leu Ala Gln Tyr Gly Asn Leu	
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Ile Gly Ile Thr Ile Gly Tyr Thr Ile Thr Ala Ser Ile Ser Met Val	
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Ala Val Lys Arg Ser Asn Cys Phe His Lys Asn Gly His Asn Val Lys	
145 150 155 160	
tgt gcc act tca aac act ccc ttc atg atc ata ttt gca atc atc caa	528
Cys Ala Thr Ser Asn Thr Pro Phe Met Ile Phe Ala Ile Ile Gln	
165 170 175	
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Ile Ile Leu Ser Gln Ile Pro Asn Phe His Asn Leu Ser Trp Leu Ser	
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PF59082SeqList_PF59082.txt

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Ser	Thr	Val	Leu	Ile	Glu	Ile	Gln	Asp	Thr	Leu	Lys	Ala	Gly	Pro	Pro	
			260					265					270			
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Ser	Glu	Asn	Lys	Ala	Met	Lys	Arg	Ala	Ser	Leu	Val	Gly	Val	Ser	Thr	
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Pro	Phe	Trp	Leu	Ile	Asp	Phe	Ala	Asn	Val	Cys	Ile	Ala	Val	His	Leu	
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Ile	Gly	Ala	Tyr	Gln	Val	Phe	Cys	Gln	Pro	Ile	Phe	Gln	Phe	Val	Glu	
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Arg	Leu	Val	Trp	Arg	Thr	Ser	Tyr	Val	Val	Val	Thr	Ala	Val	Val	Ala	
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Met	Ile	Phe	Pro	Phe	Phe	Asn	Asp	Phe	Leu	Gly	Leu	Ile	Gly	Ala	Ala	
			405					410						415		
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Ser	Phe	Trp	Pro	Leu	Thr	Val	Tyr	Phe	Pro	Ile	Glu	Met	His	Ile	Ala	
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Gln	Lys	Lys	Ile	Pro	Lys	Phe	Ser	Phe	Thr	Trp	Thr	Trp	Leu	Lys	Ile	
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gtg	caa	gga	ctc	ata	caa	agt	ctc	aag	gat	ttc	aag	cct	ttc	cag	gct	1440
Val	Gln	Gly	Leu	Ile	Gln	Ser	Leu	Lys	Asp	Phe	Lys	Pro	Phe	Gln	Ala	
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Thr	Gly	Lys	Arg	Asn	Tyr	Thr	Tyr	Met	Glu	Val	Val	Arg	Ser	Tyr	Leu	
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Ile Ile Leu Ser Gln Ile Pro Asn Phe His Asn Leu Ser Trp Leu Ser
180      185      190
Ile Leu Ala Val Met Ser Phe Cys Tyr Ala Ser Ile Gly Val Gly
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225      230      235
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245      250      255
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290      295      300
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Pro Phe Trp Leu Ile Asp Phe Ala Asn Val Cys Ile Ala Val His Leu
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Tyr Lys Ile His Val Pro Cys Cys Gly Asp Phe Ser Ile Asn Phe Leu
370      375      380
Arg Leu Val Trp Arg Thr Ser Tyr Val Val Val Thr Ala Val Val Ala
385      390      395
Met Ile Phe Pro Phe Phe Asn Asp Phe Leu Gly Leu Ile Gly Ala Ala
405      410      415
Ser Phe Trp Pro Leu Thr Val Tyr Phe Pro Ile Glu Met His Ile Ala
420      425      430
Gln Lys Lys Ile Pro Lys Phe Ser Phe Thr Trp Thr Trp Leu Lys Ile
435      440      445
Leu Ser Trp Thr Cys Phe Ile Val Ser Leu Val Ala Ala Ala Gly Ser
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ctt aaa cgt tca ggg acg gtt tgg acc gcg agt gcg cat atc ata acc      96
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20      25      30
gcc gtg att gga tct ggt gtt cta tcg ctt gcg tgg gct ata ggt caa      144
Ala Val Ile Gly Ser Gly Val Leu Ser Leu Ala Trp Ala Ile Gly Gln
35      40      45
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85	Pro	Val	Ser	Gly	Lys	Arg	Asn	Tyr	Thr	Tyr	Met	Asp	Ala	Val	Arg	Ser	
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110	Asn	Leu	Phe	Gly	Ile	Thr	Val	Gly	Tyr	Thr	Ile	Ala	Ala	Ser	Ile	Ser	
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120	Met	Met	Ala	Ile	Lys	Arg	Ser	Asn	Cys	Phe	His	Glu	Ser	Gly	Gly	Lys	
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130	Asn	Pro	Cys	His	Met	Ser	Ser	Asn	Pro	Tyr	Met	Ile	Met	Phe	Gly	Val	
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140	Thr	Glu	Ile	Leu	Leu	Ser	Gln	Ile	Lys	Asp	Phe	Asp	Gln	Ile	Trp	Trp	
145	ctc	tcc	att	gtc	gct	gct	atc	atg	tcc	ttc	aca	tac	tct	gca	atc	ggg	576
150	Leu	Ser	Ile	Val	Ala	Ala	Ile	Met	Ser	Phe	Thr	Tyr	Ser	Ala	Ile	Gly	
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160	Leu	Ala	Leu	Gly	Ile	Ile	Gln	Val	Ala	Ala	Asn	Gly	Val	Val	Lys	Gly	
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170	Ser	Leu	Thr	Gly	Ile	Ser	Ile	Gly	Ala	Val	Thr	Gln	Thr	Gln	Lys	Ile	
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180	Trp	Arg	Thr	Phe	Gln	Ala	Leu	Gly	Asp	Ile	Ala	Phe	Ala	Tyr	Ser	Tyr	
185	225	tct	gtt	gtt	ctt	att	gaa	att	cag	gac	act	gta	aga	tct	cca	cca	768
190	Ser	Val	Val	Leu	Ile	Glu	Ile	Gln	Asp	Thr	Val	Arg	Ser	Pro	Pro	Ala	
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200	Glu	Ser	Lys	Thr	Met	Lys	Ile	Ala	Thr	Arg	Ile	Ser	Ile	Ala	Val	Thr	
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215	gat	aaa	gca	ccg	gga	aac	ctc	tta	acc	ggg	ttt	ggg	ttc	tac	aat	ccg	912
220	Asp	Lys	Ala	Pro	Gly	Asn	Leu	Leu	Thr	Gly	Phe	Gly	Phe	Tyr	Asn	Pro	
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230	Phe	Trp	Leu	Leu	Asp	Val	Ala	Asn	Ala	Ala	Ile	Val	Ile	His	Leu	Val	
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240	Gly	Ala	Tyr	Gln	Val	Phe	Ala	Gln	Pro	Ile	Phe	Ala	Phe	Ile	Glu	Lys	
245	caa	gct	gcc	gct	agg	ttt	ccc	gac	agt	gac	ttg	gtg	acc	aag	gaa	tac	1056
250	Gln	Ala	Ala	Ala	Arg	Phe	Pro	Asp	Ser	Asp	Leu	Val	Thr	Lys	Glu	Tyr	
255	gaa	atc	cga	atc	cct	ggg	ttt	agg	tca	ccg	tac	aaa	gtc	aac	gtt	ttc	1104
260	Glu	Ile	Arg	Ile	Pro	Gly	Phe	Arg	Ser	Pro	Tyr	Lys	Val	Asn	Val	Phe	
265	aga	gca	gtt	tac	cga	agc	ggg	ttt	gtg	gtt	ttg	acc	act	gtg	ata	tcc	1152
270	Arg	Ala	Val	Tyr	Arg	Ser	Gly	Phe	Val	Val	Leu	Thr	Thr	Val	Ile	Ser	
275	atg	ctt	atg	ccg	ttt	ttc	aac	gac	gtc	gta	ggg	att	tta	ggg	gcg	tta	1200
280	Met	Leu	Met	Pro	Phe	Phe	Asn	Asp	Val	Val	Gly	Ile	Leu	Gly	Ala	Leu	
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PF59082SeqList_PF59082.txt

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Leu	Ser	Cys	Gly	Cys	Leu	Met	Ile	Thr	Leu	Val	Ala	Gly	Val	Gly	Ser			1344
		435					440				445							
atc	gcc	gga	gta	atg	cta	gac	ctt	aag	gtt	tac	aag	ccg	ttc	aag	act			1392
Ile	Ala	Gly	Val	Met	Leu	Asp	Leu	Lys	Val	Tyr	Lys	Pro	Phe	Lys	Thr			
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<211> 466

<212> PRT

<213> Arabidopsis thaliana

<400> 553

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Ala	Val	Ile	Gly	Ser	Gly	Val	Leu	Ser	Leu	Ala	Trp	Ala	Ile	Gly	Gln			
		35					40					45						
Leu	Gly	Trp	Ile	Ala	Gly	Pro	Thr	Val	Met	Leu	Leu	Phe	Ser	Phe	Val			
	50					55					60							
Thr	Tyr	Tyr	Ser	Ser	Thr	Leu	Leu	Ser	Asp	Cys	Tyr	Arg	Thr	Gly	Asp			
65					70					75					80			
Pro	Val	Ser	Gly	Lys	Arg	Asn	Tyr	Thr	Tyr	Met	Asp	Ala	Val	Arg	Ser			
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Ile	Leu	Gly	Gly	Phe	Arg	Phe	Lys	Ile	Cys	Gly	Leu	Ile	Gln	Tyr	Leu			
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Asn	Leu	Phe	Gly	Ile	Thr	Val	Gly	Tyr	Thr	Ile	Ala	Ala	Ser	Ile	Ser			
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Asn	Pro	Cys	His	Met	Ser	Ser	Asn	Pro	Tyr	Met	Ile	Met	Phe	Gly	Val			
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Thr	Glu	Ile	Leu	Leu	Ser	Gln	Ile	Lys	Asp	Phe	Asp	Gln	Ile	Trp	Trp			
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Leu	Ser	Ile	Val	Ala	Ala	Ile	Met	Ser	Phe	Thr	Tyr	Ser	Ala	Ile	Gly			
			180					185					190					
Leu	Ala	Leu	Gly	Ile	Ile	Gln	Val	Ala	Ala	Asn	Gly	Val	Val	Lys	Gly			
		195					200					205						
Ser	Leu	Thr	Gly	Ile	Ser	Ile	Gly	Ala	Val	Thr	Gln	Thr	Gln	Lys	Ile			
	210					215					220							
Trp	Arg	Thr	Phe	Gln	Ala	Leu	Gly	Asp	Ile	Ala	Phe	Ala	Tyr	Ser	Tyr			
225					230					235					240			
Ser	Val	Val	Leu	Ile	Glu	Ile	Gln	Asp	Thr	Val	Arg	Ser	Pro	Pro	Ala			
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Glu	Ser	Lys	Thr	Met	Lys	Ile	Ala	Thr	Arg	Ile	Ser	Ile	Ala	Val	Thr			
			260					265					270					
Thr	Thr	Phe	Tyr	Met	Leu	Cys	Gly	Cys	Met	Gly	Tyr	Ala	Ala	Phe	Gly			
		275					280					285						
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	290					295					300							
Phe	Trp	Leu	Leu	Asp	Val	Ala	Asn	Ala	Ala	Ile	Val	Ile	His	Leu	Val			
305					310					315					320			
Gly	Ala	Tyr	Gln	Val	Phe	Ala	Gln	Pro	Ile	Phe	Ala	Phe	Ile	Glu	Lys			
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Gln	Ala	Ala	Ala	Arg	Phe	Pro	Asp	Ser	Asp	Leu	Val	Thr	Lys	Glu	Tyr			
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Glu	Ile	Arg	Ile	Pro	Gly	Phe	Arg	Ser	Pro	Tyr	Lys	Val	Asn	Val	Phe			
		355					360					365						
Arg	Ala	Val	Tyr	Arg	Ser	Gly	Phe	Val	Val	Leu	Thr	Thr	Val	Ile	Ser			
	370					375						380						
Met	Leu	Met	Pro	Phe	Phe	Asn	Asp	Val	Val	Gly	Ile	Leu	Gly	Ala	Leu			
385					390					395					400			
Gly	Phe	Trp	Pro	Leu	Thr	Val	Tyr	Phe	Pro	Val	Glu	Met	Tyr	Ile	Arg			
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PF59082SeqList_PF59082.txt

Gln Arg Lys Val Glu Arg Trp Ser Met Lys Trp Val Cys Leu Gln Met
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 450 460
 Thr Tyr
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<210> 554
 <211> 1398
 <212> DNA
 <213> Oryza sativa (japonica cultivar-group)

<220>
 <221> CDS
 <222> (1)..(1398)

<400> 554
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 Arg Thr Gly Thr Val Trp Thr Ala Thr Ala His Ile Val Thr Ala Val
 20 25 30
 atc ggc tcc ggc gtg ctg gcg ctg gcg tgg agc gtg gcg cag ctg ggt 144
 Ile Gly Ser Gly Val Leu Ala Leu Ala Trp Ser Val Ala Gln Leu Gly
 35 40 45
 tgg gtg gcc ggg ccg ctc gcc ctc gcc ggc ttc gcc tgc gtc acc tac 192
 Trp Val Ala Gly Pro Leu Ala Leu Ala Gly Phe Ala Cys Val Thr Tyr
 50 55 60
 tac acc tcc act ctg ctc gcc aac gcc tac cgc gcg ccg cac ccc gtc 240
 Tyr Thr Ser Thr Leu Leu Ala Asn Ala Tyr Arg Ala Pro His Pro Val
 65 70 75 80
 acc ggc acc agg aac cgc aca tac atg gac gcc gtc aga tca tac ctc 288
 Thr Gly Thr Arg Asn Arg Thr Tyr Met Asp Ala Val Arg Ser Tyr Leu
 85 90 95
 agt cct aga gag gtg ttc atg tgc gga atc gcg cag tac gtc aac ctg 336
 Ser Pro Arg Glu Val Phe Met Cys Gly Ile Ala Gln Tyr Val Asn Leu
 100 105 110
 tgg ggc acc atg gtc ggc tac aca atc acc gca acc ata agc atg gtc 384
 Trp Gly Thr Met Val Gly Tyr Thr Ile Thr Ala Thr Ile Ser Met Val
 115 120 125
 gcg atc agg agg tcg gat tgc atc cat cgg aac ggc gcc gcc gcc gcc 432
 Ala Ile Arg Arg Ser Asp Cys Ile His Arg Asn Gly Ala Gly Ala Ala
 130 135 140
 gcg cgg tgc gac aac acg tcg gcg acg gtg ctc atg ctg gcg ttc agc 480
 Ala Arg Cys Asp Asn Thr Ser Ala Thr Val Leu Met Leu Ala Phe Ser
 145 150 155 160
 atc gtg cag gtg gtg ctg tcc cag ttc ccg ggc ctg gag cac atc acc 528
 Ile Val Gln Val Val Leu Ser Gln Phe Pro Gly Leu Glu His Ile Thr
 165 170 175
 tgg ctg tcc gtc gtc gcc gcc gtc atg tcg ttc gcc tac tcc ttc atc 576
 Trp Leu Ser Val Val Ala Ala Val Met Ser Phe Ala Tyr Ser Phe Ile
 180 185 190
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 Gly Leu Gly Leu Ser Val Ala Glu Trp Val Ser His Gly Gly His Leu
 195 200 205
 agc ggc agg atc cag ggc gcc acc gcg gcg tcc tcc agc aag aag ctc 672
 Ser Gly Arg Ile Gln Gly Ala Thr Ala Ala Ser Ser Ser Lys Lys Leu
 210 215 220
 tgg aac gta ctg ctc gca ctg ggg aac atc gcc ttc gcc tac acc ttt 720
 Trp Asn Val Leu Leu Ala Leu Gly Asn Ile Ala Phe Ala Tyr Thr Phe
 225 230 235 240
 gca gaa gtg cta att gag atc cag gac aca ctg aaa ccg tca cca ccg 768
 Ala Glu Val Leu Ile Glu Ile Gln Asp Thr Leu Lys Pro Ser Pro Pro
 245 250 255
 gag aac aag acc atg aag aag gca gcg atg tac ggg att gga gcc acc 816
 Glu Asn Lys Thr Met Lys Lys Ala Ala Met Tyr Gly Ile Gly Ala Thr

PF59082SeqList_PF59082.txt

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tca	gat	gct	ccg	ggc	aac	atc	ctg	acg	gcg	tcc	ggt	atg	ggg	ccc	ttc		912
Ser	Asp	Ala	Pro	Gly	Asn	Ile	Leu	Thr	Ala	Ser	Gly	Met	Gly	Pro	Phe		
	290					295					300						
tgg	ctc	gtc	gac	att	gcc	aac	atg	tgc	ctc	atc	ctc	cat	ctc	atc	gga		960
Trp	Leu	Val	Asp	Ile	Ala	Asn	Met	Cys	Leu	Ile	Leu	His	Leu	Ile	Gly		
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gca	tat	cag	gtt	tat	gca	cag	ccc	ata	ttt	gcg	aca	atg	gag	aga	tgg		1008
Ala	Tyr	Gln	Val	Tyr	Ala	Gln	Pro	Ile	Phe	Ala	Thr	Met	Glu	Arg	Trp		
			325						330					335			
atc	tcc	tcc	cgg	tgg	ccg	gag	gcc	aag	ttc	atc	aac	agc	gag	tac	acc		1056
Ile	Ser	Ser	Arg	Trp	Pro	Glu	Ala	Lys	Phe	Ile	Asn	Ser	Glu	Tyr	Thr		
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gta	aac	gtg	ccg	ctg	atc	cag	cga	gga	tcg	gtg	acc	gtg	gcg	ccg	tac		1104
Val	Asn	Val	Pro	Leu	Ile	Gln	Arg	Gly	Ser	Val	Thr	Val	Ala	Pro	Tyr		
		355					360					365					
aag	ctc	gtc	ctc	cgg	acc	gtc	gta	gtc	atc	gcg	acg	acg	gtg	gtg	gcg		1152
Lys	Leu	Val	Leu	Arg	Thr	Val	Val	Val	Ile	Ala	Thr	Thr	Val	Val	Ala		
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Met	Met	Ile	Pro	Phe	Phe	Asn	Ala	Val	Leu	Gly	Leu	Leu	Gly	Ala	Phe		
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agc	ttc	tgg	cca	ctg	act	gtt	tac	ttc	ccc	atc	agc	atg	cac	att	gcg		1248
Ser	Phe	Trp	Pro	Leu	Thr	Val	Tyr	Phe	Pro	Ile	Ser	Met	His	Ile	Ala		
			405						410					415			
cag	gag	aag	atc	acc	agg	gga	ggg	agg	tgg	tat	ctc	ctg	caa	ggc	ctg		1296
Gln	Glu	Lys	Ile	Thr	Arg	Gly	Gly	Arg	Trp	Tyr	Leu	Leu	Gln	Gly	Leu		
			420				425						430				
agc	atg	gtg	tgc	ttg	atg	atc	tcg	gtg	gca	gtg	ggc	att	ggc	tct	gtc		1344
Ser	Met	Val	Cys	Leu	Met	Ile	Ser	Val	Ala	Val	Gly	Ile	Gly	Ser	Val		
		435					440					445					
act	gac	att	gtt	gat	agc	ctg	aag	gtt	gca	acc	cct	ttc	aaa	act	gtc		1392
Thr	Asp	Ile	Val	Asp	Ser	Leu	Lys	Val	Ala	Thr	Pro	Phe	Lys	Thr	Val		
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<210> 555
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Ile	Gly	Ser	Gly	Val	Leu	Ala	Leu	Ala	Trp	Ser	Val	Ala	Gln	Leu	Gly	
		35					40					45				
Trp	Val	Ala	Gly	Pro	Leu	Ala	Leu	Ala	Gly	Phe	Ala	Cys	Val	Thr	Tyr	
	50					55					60					
Tyr	Thr	Ser	Thr	Leu	Leu	Ala	Asn	Ala	Tyr	Arg	Ala	Pro	His	Pro	Val	
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Thr	Gly	Thr	Arg	Asn	Arg	Thr	Tyr	Met	Asp	Ala	Val	Arg	Ser	Tyr	Leu	
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Trp	Gly	Thr	Met	Val	Gly	Tyr	Thr	Ile	Thr	Ala	Thr	Ile	Ser	Met	Val	
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Ala	Ile	Arg	Arg	Ser	Asp	Cys	Ile	His	Arg	Asn	Gly	Ala	Gly	Ala	Ala	
	130					135					140					
Ala	Arg	Cys	Asp	Asn	Thr	Ser	Ala	Thr	Val	Leu	Met	Leu	Ala	Phe	Ser	
145					150					155					160	
Ile	Val	Gln	Val	Val	Leu	Ser	Gln	Phe	Pro	Gly	Leu	Glu	His	Ile	Thr	
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PF59082SeqList_PF59082.txt

Trp Leu Ser Val Val Ala Ala Val Met Ser Phe Ala Tyr Ser Phe Ile
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 Gly Leu Gly Leu Ser Val Ala Glu Trp Val Ser His Gly Gly His Leu
 195 200 205
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 210 215 220
 Trp Asn Val Leu Leu Ala Leu Gly Asn Ile Ala Phe Ala Tyr Thr Phe
 225 230 235 240
 Ala Glu Val Leu Ile Glu Ile Gln Asp Thr Leu Lys Pro Ser Pro Pro
 245 250 255
 Glu Asn Lys Thr Met Lys Lys Ala Ala Met Tyr Gly Ile Gly Ala Thr
 260 265 270
 Thr Ile Phe Tyr Ile Ser Val Gly Cys Ala Gly Tyr Ala Ala Phe Gly
 275 280 285
 Ser Asp Ala Pro Gly Asn Ile Leu Thr Ala Ser Gly Met Gly Pro Phe
 290 295 300
 Trp Leu Val Asp Ile Ala Asn Met Cys Leu Ile Leu His Leu Ile Gly
 305 310 315 320
 Ala Tyr Gln Val Tyr Ala Gln Pro Ile Phe Ala Thr Met Glu Arg Trp
 325 330 335
 Ile Ser Ser Arg Trp Pro Glu Ala Lys Phe Ile Asn Ser Glu Tyr Thr
 340 345 350
 Val Asn Val Pro Leu Ile Gln Arg Gly Ser Val Thr Val Ala Pro Tyr
 355 360 365
 Lys Leu Val Leu Arg Thr Val Val Ile Ala Thr Thr Val Val Ala
 370 375 380
 Met Met Ile Pro Phe Phe Asn Ala Val Leu Gly Leu Leu Gly Ala Phe
 385 390 395 400
 Ser Phe Trp Pro Leu Thr Val Tyr Phe Pro Ile Ser Met His Ile Ala
 405 410 415
 Gln Glu Lys Ile Thr Arg Gly Gly Arg Trp Tyr Leu Leu Gln Gly Leu
 420 425 430
 Ser Met Val Cys Leu Met Ile Ser Val Ala Val Gly Ile Gly Ser Val
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 Thr Asp Ile Val Asp Ser Leu Lys Val Ala Thr Pro Phe Lys Thr Val
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 Ser
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<210> 556

<211> 1596

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<221> CDS

<222> (1)..(1596)

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Gly Arg Val Arg Thr Asp Leu Arg Ala Ser Val Ile Ala Glu Phe Gly	
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cag aaa cgt gca ttg ctg gcg tac gtt gga ggg tgg tta ttg act tgt	144
Gln Lys Arg Ala Leu Leu Ala Tyr Val Gly Gly Trp Leu Leu Thr Cys	
35 40 45	
gcc tct ctt tca acc gcg ctg ata tgg caa tct ctt caa tgc act gca	192
Ala Ser Leu Ser Thr Ala Leu Ile Trp Gln Ser Leu Gln Cys Thr Ala	
50 55 60	
tct tta ttg atg ttc atg ctt aat cag cca ggt gtt cca aga gac caa	240
Ser Leu Leu Met Phe Met Leu Asn Gln Pro Gly Val Pro Arg Asp Gln	
65 70 75 80	
gaa ggc aag aat gtc aca cga acg gta tgg acg gcg acg cac gcc	288
Glu Gly Lys Asn Val Thr Arg Thr Val Trp Thr Ala Thr Thr His Ala	
85 90 95	
atc acc gcc gtg atc ggg tca ggc gtg ctg gcg ctg ccg tgg agc gtg	336
Ile Thr Ala Val Ile Gly Ser Gly Val Leu Ala Leu Pro Trp Ser Val	

PF59082SeqList_PF59082.txt

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	115						120					125					
tac	atc	acc	tac	tac	acc	gcc	gtc	ctc	ctc	tgc	gac	tgc	tac	cgc	acg		432
Tyr	Ile	Thr	Tyr	Tyr	Thr	Ala	Val	Leu	Leu	Cys	Asp	Cys	Tyr	Arg	Thr		
	130					135					140						
ccg	gac	ccc	gtc	cac	ggc	aag	cgg	aac	tac	acc	tac	atg	gac	gtc	gtc		480
Pro	Asp	Pro	Val	His	Gly	Lys	Arg	Asn	Tyr	Thr	Tyr	Met	Asp	Val	Val		
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cgc	tca	tgc	ctc	ggg	cct	cga	gac	gtg	gtc	gtg	tgt	ggc	att	cgc	cag		528
Arg	Ser	Cys	Leu	Gly	Pro	Arg	Asp	Val	Val	Val	Cys	Gly	Ile	Ala	Gln		
			165					170						175			
tac	gcg	att	ctc	tgg	ggc	gca	atg	gtg	ggg	tac	acc	atc	acg	acc	gct		576
Tyr	Ala	Ile	Leu	Trp	Gly	Ala	Met	Val	Gly	Tyr	Thr	Ile	Thr	Thr	Ala		
			180					185					190				
acg	agc	atc	atg	tca	gtg	gtg	cgc	acg	aac	tgc	cac	cac	tac	aag	ggg		624
Thr	Ser	Ile	Met	Ser	Val	Val	Arg	Thr	Asn	Cys	His	His	Tyr	Lys	Gly		
	195					200					205						
ccg	gac	gcg	acc	tgc	ggc	tcg	tcc	ggg	acg	atg	tac	atg	gtg	ctg	ttc		672
Pro	Asp	Ala	Thr	Cys	Gly	Ser	Ser	Gly	Thr	Met	Tyr	Met	Val	Leu	Phe		
	210					215					220						
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Gly	Leu	Ala	Glu	Val	Val	Leu	Ser	Gln	Cys	Pro	Ser	Leu	Glu	Gly	Val		
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acg	ctc	atc	tcc	gtc	gtc	gcc	gcc	gtc	atg	tcg	ttc	acc	tac	tcc	ttc		768
Thr	Leu	Ile	Ser	Val	Val	Ala	Ala	Val	Met	Ser	Phe	Thr	Tyr	Ser	Phe		
			245					250					255				
gtc	ggg	ctc	ttc	ctc	agc	gcc	gct	aag	gtc	gcg	tcg	cac	ggc	gcg	gcg		816
Val	Gly	Leu	Phe	Leu	Ser	Ala	Ala	Lys	Val	Ala	Ser	His	Gly	Ala	Ala		
			260					265					270				
cac	ggc	acc	ctc	ctc	ggc	gtc	agg	gtc	ggc	gcc	gga	ggc	gtc	acc	gcg		864
His	Gly	Thr	Leu	Leu	Gly	Val	Arg	Val	Gly	Ala	Gly	Gly	Val	Thr	Ala		
	275					280					285						
tcg	acc	aag	gcg	tgg	cac	ttc	ctg	cag	gcg	ctc	ggg	aac	atc	gcc	ttc		912
Ser	Thr	Lys	Ala	Trp	His	Phe	Leu	Gln	Ala	Leu	Gly	Asn	Ile	Ala	Phe		
	290					295					300						
gcg	tac	acc	tac	tcc	atg	ctg	ctc	atc	gag	atc	cag	gac	acg	gtg	aag		960
Ala	Tyr	Thr	Tyr	Ser	Met	Leu	Leu	Ile	Glu	Ile	Gln	Asp	Thr	Val	Lys		
	305				310					315					320		
tcg	ccg	ccg	tcg	gag	aac	gtg	acg	atg	aag	agg	gcg	agc	ctg	tac	ggc		1008
Ser	Pro	Pro	Ser	Glu	Asn	Val	Thr	Met	Lys	Arg	Ala	Ser	Leu	Tyr	Gly		
			325					330					335				
atc	ggc	gtc	acg	acc	gtc	ttc	tac	gtg	tcg	atc	ggg	tgc	gtc	ggg	tac		1056
Ile	Gly	Val	Thr	Thr	Val	Phe	Tyr	Val	Ser	Ile	Gly	Cys	Val	Gly	Tyr		
			340					345					350				
gcg	gcg	ttc	ggc	aac	gcc	gcg	ccc	ggg	aac	gtc	ctc	acc	ggc	ttc	ctc		1104
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		355				360						365					
gag	ccg	ttc	tgg	ctc	gtc	gac	atc	gcc	aac	gtt	gcc	gtc	gtc	atc	cac		1152
Glu	Pro	Phe	Trp	Leu	Val	Asp	Ile	Ala	Asn	Val	Ala	Val	Val	Ile	His		
	370					375					380						
ctg	gtc	gga	gcg	tac	cag	gtg	tac	gcg	cag	ccg	gtg	ttc	gcg	tgc	tac		1200
Leu	Val	Gly	Ala	Tyr	Gln	Val	Tyr	Ala	Gln	Pro	Val	Phe	Ala	Cys	Tyr		
	385				390					395					400		
gag	aag	tgg	ctg	gcg	agc	cgt	tgg	ccg	gag	tcg	gcg	ttc	ttc	cac	cgg		1248
Glu	Lys	Trp	Leu	Ala	Ser	Arg	Trp	Pro	Glu	Ser	Ala	Phe	Phe	His	Arg		
			405					410					415				
gag	tac	gcg	gtg	ccg	ctg	ggc	ggc	ggg	cgc	gcg	gtg	cgg	ttc	acg	ctg		1296
Glu	Tyr	Ala	Val	Pro	Leu	Gly	Gly	Gly	Arg	Ala	Val	Arg	Phe	Thr	Leu		
			420				425						430				
tgc	aag	ctg	gtg	ctg	cgc	acg	gcg	ttc	gtg	gcc	gtg	acg	acg	gtg	gtg		1344
Cys	Lys	Leu	Val	Leu	Arg	Thr	Ala	Phe	Val	Ala	Val	Thr	Thr	Val	Val		
		435				440						445					
tcg	ctg	gtg	ctg	ccg	ttc	ttc	aac	gcc	gtg	ctc	ggg	ctg	ctc	ggc	gcc		1392
Ser	Leu	Val	Leu	Pro	Phe	Phe	Asn	Ala	Val	Leu	Gly	Leu	Leu	Gly	Ala		
	450				455						460						
gtc	gcg	ttc	tgg	ccg	ctc	acg	gtg	tac	ttc	ccg	gtg	acc	atg	tac	atg		1440
Val	Ala	Phe	Trp	Pro	Leu	Thr	Val	Tyr	Phe	Pro	Val	Thr	Met	Tyr	Met		

PF59082SeqList_PF59082.txt

465		470		475		480	
gcg cag gcg aag gtg	cag aga ggc agc cgg aag tgg gtg gcg ctg cag						1488
Ala Gln Ala Lys Val	Gln Arg Gly Ser Arg Lys Trp Val Ala Leu Gln						
		485		490		495	
gcg ctc aac gtc ggc	gcg ctc gtc gtg tgc ctg ctc gcg gcg gtg ggc						1536
Ala Leu Asn Val Gly	Ala Leu Val Val Ser Leu Leu Ala Ala Val Gly						
		500		505		510	
tcg gtg gcc gac atg	gcg cag cgc ctg cgc cac gtc acc atc ttc caa						1584
Ser Val Ala Asp Met	Ala Gln Arg Leu Arg His Val Thr Ile Phe Gln						
		515		520		525	
acg cag ctc tga							1596
Thr Gln Leu							
		530					

<210> 557

<211> 531

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<400> 557

Met Asp Val Glu Lys Val Glu Arg Lys Glu Val Ala Val Asp Asp Asp	
1 Gly Arg Val Arg Thr Asp Leu Arg Ala Ser Val Ile Ala Glu Phe Gly	
	5
Gln Lys Arg Ala Leu Leu Ala Tyr Val Gly Gly Trp Leu Thr Cys	
	10
Ala Ser Leu Ser Thr Ala Leu Ile Trp Gln Ser Leu Gln Cys Thr Ala	
	15
Ser Leu Leu Met Phe Met Leu Asn Gln Pro Gly Val Pro Arg Asp Gln	
65 Glu Gly Lys Asn Val Thr Arg Thr Val Trp Thr Ala Thr Thr His Ala	
	20
Ile Thr Ala Val Ile Gly Ser Gly Val Leu Ala Leu Pro Trp Ser Val	
	25
Ala Gln Met Gly Trp Val Leu Gly Pro Ile Ala Leu Val Val Cys Ala	
	30
Tyr Ile Thr Tyr Tyr Thr Ala Val Leu Leu Cys Asp Cys Tyr Arg Thr	
	35
Pro Asp Pro Val His Gly Lys Arg Asn Tyr Thr Tyr Met Asp Val Val	
145 Arg Ser Cys Leu Gly Pro Arg Asp Val Val Val Cys Gly Ile Ala Gln	
	40
Tyr Ala Ile Leu Trp Gly Ala Met Val Gly Tyr Thr Ile Thr Thr Ala	
	45
Thr Ser Ile Met Ser Val Val Arg Thr Asn Cys His His Tyr Lys Gly	
	50
Pro Asp Ala Thr Cys Gly Ser Ser Gly Thr Met Tyr Met Val Leu Phe	
	55
Gly Leu Ala Glu Val Val Leu Ser Gln Cys Pro Ser Leu Glu Gly Val	
225 Thr Leu Ile Ser Val Val Ala Ala Val Met Ser Phe Thr Tyr Ser Phe	
	60
Val Gly Leu Phe Leu Ser Ala Ala Lys Val Ala Ser His Gly Ala Ala	
	65
His Gly Thr Leu Leu Gly Val Arg Val Gly Ala Gly Gly Val Thr Ala	
	70
Ser Thr Lys Ala Trp His Phe Leu Gln Ala Leu Gly Asn Ile Ala Phe	
	75
Ala Tyr Thr Tyr Ser Met Leu Leu Ile Glu Ile Gln Asp Thr Val Lys	
305 Ser Pro Pro Ser Glu Asn Val Thr Met Lys Arg Ala Ser Leu Tyr Gly	
	80
Ile Gly Val Thr Thr Val Phe Tyr Val Ser Ile Gly Cys Val Gly Tyr	
	85
Ala Ala Phe Gly Asn Ala Ala Pro Gly Asn Val Leu Thr Gly Phe Leu	
	90
Glu Pro Phe Trp Leu Val Asp Ile Ala Asn Val Ala Val Val Ile His	
	95
Leu Val Gly Ala Tyr Gln Val Tyr Ala Gln Pro Val Phe Ala Cys Tyr	
	100

PF59082SeqList_PF59082.txt

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385          390          395          400
Glu Lys Trp Leu Ala Ser Arg Trp Pro Glu Ser Ala Phe Phe His Arg
    405
Glu Tyr Ala Val Pro Leu Gly Gly Gly Arg Ala Val Arg Phe Thr Leu
    420
Cys Lys Leu Val Leu Arg Thr Ala Phe Val Ala Val Thr Thr Val Val
    435
Ser Leu Val Leu Pro Phe Phe Asn Ala Val Leu Gly Leu Leu Gly Ala
    450
Val Ala Phe Trp Pro Leu Thr Val Tyr Phe Pro Val Thr Met Tyr Met
    465
Ala Gln Ala Lys Val Gln Arg Gly Ser Arg Lys Trp Val Ala Leu Gln
    485
Ala Leu Asn Val Gly Ala Leu Val Val Ser Leu Leu Ala Ala Val Gly
    500
Ser Val Ala Asp Met Ala Gln Arg Leu Arg His Val Thr Ile Phe Gln
    515
Thr Gln Leu
    530

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<210> 558

<211> 1467

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<221> CDS

<222> (1)..(1467)

<400> 558

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Met Gly Glu Asn Val Val Gly Thr Tyr Tyr Tyr Pro Pro Ser Ala Ala
  1          5          10          15
gcc atg gac ggc gtg gag ctc ggc cac gcc gcc gcc ggc tcc aag ctc      96
Ala Met Asp Asp Val Glu Leu Gly His Ala Ala Ala Gly Ser Lys Leu
          20          25          30
ttc gac gac gac ggc cgc ccc agg cgc aac ggg acg atg tgg acg gcg      144
Phe Asp Asp Asp Gly Arg Pro Arg Arg Asn Gly Thr Met Trp Thr Ala
          35          40          45
agc gcg cac atc atc acg gcg gtg atc ggc tcc ggc gtg ctg tcg ctg      192
Ser Ala His Ile Ile Thr Ala Val Ile Gly Ser Gly Val Leu Ser Leu
          50          55          60
ggg tgg gcc atc gcg cag ctc ggc tgg gtg gcc ggg ccg gcg gtc atg      240
Gly Trp Ala Ile Ala Gln Leu Gly Trp Val Ala Gly Pro Ala Val Met
          65          70          75
gtg ctc ttc tcc ctc gtc acc tac tac acc tca tcc ctc ctc tcc gat      288
Val Leu Phe Ser Leu Val Thr Tyr Tyr Thr Ser Ser Leu Leu Ser Asp
          80          85          90
tgc tac cgc tcc ggc gac ccc gtc acc ggc aag cgg aac tac acc tac      336
Cys Tyr Arg Ser Gly Asp Pro Val Thr Gly Lys Arg Asn Tyr Thr Tyr
          100          105          110
atg gac gcc gtg aac gcc aac ctg agc ggg ttc aag gtg aag atc tgc      384
Met Asp Ala Val Asn Ala Asn Leu Ser Gly Phe Lys Val Lys Ile Cys
          115          120          125
ggg ttc ttg cag tac gcc aac atc gtc ggc gtc gcc atc ggc tac acc      432
Gly Phe Leu Gln Tyr Ala Asn Ile Val Gly Val Ala Ile Gly Tyr Thr
          130          135          140
atc gcg gcg tcc atc agc atg ctg gcg atc ggg agg gcc aac tgc ttc      480
Ile Ala Ala Ser Ile Ser Met Leu Ala Ile Gly Arg Ala Asn Cys Phe
          145          150          155
cac agg aag ggg cac ggc gac ccg tgc aac gtc tcc agc gtg ccc tac      528
His Arg Lys Gly His Gly Asp Pro Cys Asn Val Ser Ser Val Pro Tyr
          160          165          170
atg atc gtc ttc ggc gtc gcc gag gtc ttc ttc tcg cag atc ccc gac      576
Met Ile Val Phe Gly Val Ala Glu Val Phe Phe Ser Gln Ile Pro Asp
          175          180          185
ttc gat cag atc tcc tgg ctc tcc atg ctc gcc gcc gtc atg tcc ttc      624
Phe Asp Gln Ile Ser Trp Leu Ser Met Leu Ala Ala Val Met Ser Phe
          190          195          200

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PF59082SeqList_PF59082.txt

acc	tac	tcc	gtc	atc	ggc	ctc	agc	ctc	ggc	atc	gtc	caa	gtc	gtc	gcg	672
Thr	Tyr	Ser	Val	Ile	Gly	Leu	Ser	Leu	Gly	Ile	Val	Gln	Val	Val	Ala	
	210					215					220					
aac	gga	ggg	ttg	aag	gga	agc	ctg	acc	ggg	atc	agc	atc	ggc	gtg	gtg	720
Asn	Gly	Gly	Leu	Lys	Gly	Ser	Leu	Thr	Gly	Ile	Ser	Ile	Gly	Val	Val	
	225				230					235					240	
acg	ccg	atg	gac	aag	gtg	tgg	agg	agc	ctg	cag	gcg	ttc	ggc	gac	atc	768
Thr	Pro	Met	Asp	Lys	Val	Trp	Arg	Ser	Leu	Gln	Ala	Phe	Gly	Asp	Ile	
				245					250					255		
gcg	ttc	gcc	tac	tcc	tac	tcg	ctg	atc	ctc	atc	gag	atc	cag	gac	acc	816
Ala	Phe	Ala	Tyr	Ser	Tyr	Ser	Leu	Ile	Leu	Ile	Glu	Ile	Gln	Asp	Thr	
			260					265					270			
atc	cgg	gcg	ccg	ccg	ccg	tcg	gag	tcg	gcg	gtg	atg	aag	cgc	gcc	acg	864
Ile	Arg	Ala	Pro	Pro	Pro	Ser	Glu	Ser	Ala	Val	Met	Lys	Arg	Ala	Thr	
		275					280					285				
gtg	gtg	agc	gtg	gcg	gtg	acc	acg	gtg	ttc	tac	atg	ctc	tgc	ggc	agc	912
Val	Val	Ser	Val	Ala	Val	Thr	Thr	Val	Phe	Tyr	Met	Leu	Cys	Gly	Ser	
	290					295					300					
atg	ggg	tac	gcg	gcg	ttc	ggc	gac	gac	gcg	ccg	ggg	aac	ctc	ctc	acc	960
Met	Gly	Tyr	Ala	Ala	Phe	Gly	Asp	Asp	Ala	Pro	Gly	Asn	Leu	Leu	Thr	
	305				310					315					320	
ggg	ttc	ggc	ttc	tac	gag	ccc	ttc	tgg	ctc	ctc	gac	atc	gcc	aac	gcc	1008
Gly	Phe	Gly	Phe	Tyr	Glu	Pro	Phe	Trp	Leu	Leu	Asp	Ile	Ala	Asn	Ala	
				325					330					335		
gcc	atc	gtc	gtc	cac	ctc	gtc	ggc	gcc	tac	cag	gtg	ttc	tgc	cag	ccg	1056
Ala	Ile	Val	Val	His	Leu	Val	Gly	Ala	Tyr	Gln	Val	Phe	Cys	Gln	Pro	
			340					345					350			
ctc	ttc	gcc	ttc	gtc	gag	aag	tgg	gcg	gcg	cag	cgg	tgg	ccg	gag	tcg	1104
Leu	Phe	Ala	Phe	Val	Glu	Lys	Trp	Ala	Ala	Gln	Arg	Trp	Pro	Glu	Ser	
		355					360					365				
ccg	tac	atc	acc	ggg	gag	gtg	gag	ctc	cgc	ctc	tcg	ccg	tcg	tcg	agg	1152
Pro	Tyr	Ile	Thr	Gly	Glu	Val	Glu	Leu	Arg	Leu	Ser	Pro	Ser	Ser	Arg	
	370					375					380					
cgg	tgc	agg	gtg	aac	ctg	ttc	cgg	tcg	acg	tgg	cgc	acg	gcg	ttc	gtc	1200
Arg	Cys	Arg	Val	Asn	Leu	Phe	Arg	Ser	Thr	Trp	Arg	Thr	Ala	Phe	Val	
	385				390					395					400	
gtc	gcc	acc	acg	gtg	gtg	tcc	atg	ctg	ctg	ccc	ttc	ttc	aac	gac	gtg	1248
Val	Ala	Thr	Thr	Val	Val	Ser	Met	Leu	Leu	Pro	Phe	Phe	Asn	Asp	Val	
				405					410					415		
gtc	ggc	ttc	ctc	ggc	gcg	ctc	gga	ttc	tgg	ccg	ctc	acc	gtc	tac	ttc	1296
Val	Gly	Phe	Leu	Gly	Ala	Leu	Gly	Phe	Trp	Pro	Leu	Thr	Val	Tyr	Phe	
			420					425					430			
ccc	gtg	gag	atg	tac	gtg	gtg	cag	aag	aag	gtg	cca	cgg	tgg	agc	aca	1344
Pro	Val	Glu	Met	Tyr	Val	Val	Gln	Lys	Lys	Val	Pro	Arg	Trp	Ser	Thr	
		435					440					445				
cgg	tgg	gtg	tgc	ctg	cag	atg	ctc	agc	gtc	ggc	tgc	ctc	gtc	atc	tcc	1392
Arg	Trp	Val	Cys	Leu	Gln	Met	Leu	Ser	Val	Gly	Cys	Leu	Val	Ile	Ser	
	450					455					460					
atc	gcc	gcc	gcc	gcg	ggc	tcc	atc	gcc	ggc	gtc	atg	tcg	gat	ctc	aag	1440
Ile	Ala	Ala	Ala	Ala	Gly	Ser	Ile	Ala	Gly	Val	Met	Ser	Asp	Leu	Lys	
	465				470					475					480	
gtt	tac	cgc	ccg	ttc	aag	ggt	tac	tga								1467
Val	Tyr	Arg	Pro	Phe	Lys	Gly	Tyr									
				485												

<210> 559

<211> 488

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<400> 559

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Ala	Met	Asp	Gly	Val	Glu	Leu	Gly	His	Ala	Ala	Ala	Gly	Ser	Lys	Leu	
			20					25					30			
Phe	Asp	Asp	Asp	Gly	Arg	Pro	Arg	Arg	Asn	Gly	Thr	Met	Trp	Thr	Ala	
		35					40					45				
Ser	Ala	His	Ile	Ile	Thr	Ala	Val	Ile	Gly	Ser	Gly	Val	Leu	Ser	Leu	
	50					55					60					

PF59082SeqList_PF59082.txt

Gly Trp Ala Ile Ala Gln Leu Gly Trp Val Ala Gly Pro Ala Val Met
65 70 75 80
Val Leu Phe Ser Leu Val Thr Tyr Tyr Thr Ser Ser Leu Leu Ser Asp
85 90 95
Cys Tyr Arg Ser Gly Asp Pro Val Thr Gly Lys Arg Asn Tyr Thr Tyr
100 105 110
Met Asp Ala Val Asn Ala Asn Leu Ser Gly Phe Lys Val Lys Ile Cys
115 120 125
Gly Phe Leu Gln Tyr Ala Asn Ile Val Gly Val Ala Ile Gly Tyr Thr
130 135 140
Ile Ala Ala Ser Ile Ser Met Leu Ala Ile Gly Arg Ala Asn Cys Phe
145 150 155 160
His Arg Lys Gly His Gly Asp Pro Cys Asn Val Ser Ser Val Pro Tyr
165 170 175
Met Ile Val Phe Gly Val Ala Glu Val Phe Phe Ser Gln Ile Pro Asp
180 185 190
Phe Asp Gln Ile Ser Trp Leu Ser Met Leu Ala Ala Val Met Ser Phe
195 200 205
Thr Tyr Ser Val Ile Gly Leu Ser Leu Gly Ile Val Gln Val Val Ala
210 215 220
Asn Gly Gly Leu Lys Gly Ser Leu Thr Gly Ile Ser Ile Gly Val Val
225 230 235 240
Thr Pro Met Asp Lys Val Trp Arg Ser Leu Gln Ala Phe Gly Asp Ile
245 250 255
Ala Phe Ala Tyr Ser Tyr Ser Leu Ile Leu Ile Glu Ile Gln Asp Thr
260 265 270
Ile Arg Ala Pro Pro Pro Ser Glu Ser Ala Val Met Lys Arg Ala Thr
275 280 285
Val Val Ser Val Ala Val Thr Thr Val Phe Tyr Met Leu Cys Gly Ser
290 295 300
Met Gly Tyr Ala Ala Phe Gly Asp Asp Ala Pro Gly Asn Leu Leu Thr
305 310 315 320
Gly Phe Gly Phe Tyr Glu Pro Phe Trp Leu Leu Asp Ile Ala Asn Ala
325 330 335
Ala Ile Val Val His Leu Val Gly Ala Tyr Gln Val Phe Cys Gln Pro
340 345 350
Leu Phe Ala Phe Val Glu Lys Trp Ala Ala Gln Arg Trp Pro Glu Ser
355 360 365
Pro Tyr Ile Thr Gly Glu Val Glu Leu Arg Leu Ser Pro Ser Ser Arg
370 375 380
Arg Cys Arg Val Asn Leu Phe Arg Ser Thr Trp Arg Thr Ala Phe Val
385 390 395 400
Val Ala Thr Thr Val Val Ser Met Leu Leu Pro Phe Phe Asn Asp Val
405 410 415
Val Gly Phe Leu Gly Ala Leu Gly Phe Trp Pro Leu Thr Val Tyr Phe
420 425 430
Pro Val Glu Met Tyr Val Val Gln Lys Lys Val Pro Arg Trp Ser Thr
435 440 445
Arg Trp Val Cys Leu Gln Met Leu Ser Val Gly Cys Leu Val Ile Ser
450 455 460
Ile Ala Ala Ala Ala Gly Ser Ile Ala Gly Val Met Ser Asp Leu Lys
465 470 475 480
Val Tyr Arg Pro Phe Lys Gly Tyr
485

<210> 560

<211> 1557

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<221> CDS

<222> (1)..(1557)

<400> 560

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48

96

PF59082SeqList_PF59082.txt

Val	Val	Val	Glu 20	Arg	Asp	Val	Arg	Arg	Tyr	Gln	Gln	Leu	Pro 30	Gln	Gln		
gtg	gag	atg	gag	atg	acg	acg	acc	aag	agg	cag	cag	gat	cat	cag	gtg	144	
Val	Glu	Met 35	Glu	Met	Thr	Thr	Thr	Lys	Arg	Gln	Gln	Asp 45	His	Gln	Val		
gag	acg	atg	acg	acg	aag	aag	att	gat	gaa	gaa	gat	gaa	gag	gtg	gac	192	
Glu	Thr	Met	Thr	Thr	Lys	Lys	Ile	Asp	Glu	Glu	Asp	Glu	Glu	Val	Asp		
	50					55					60						
gac	gac	ggt	cgg	gcg	aag	cgg	agg	ggg	acg	gtg	tgg	acg	gcg	gcg	tcg	240	
Asp	Asp	Gly	Arg	Ala	Lys 70	Arg	Arg	Gly	Thr	Val 75	Trp	Thr	Ala	Ala	Ser 80		
cac	atc	atc	acg	gcg	gtg	atc	ggg	tca	ggg	gtg	ctg	tcg	ctg	gcg	tgg	288	
His	Ile	Ile	Thr	Ala	Val	Ile	Gly	Ser	Gly	Val	Leu	Ser	Leu	Ala	Trp		
			85					90						95			
gcg	atc	gcg	cag	ctg	ggc	tgg	gtg	gtg	ggc	ccc	acc	gtc	atg	ctc	ctc	336	
Ala	Ile	Ala	Gln	Leu	Gly	Trp	Val	Val	Gly	Pro	Thr	Val	Met	Leu	Leu		
			100					105						110			
ttt	gct	gcc	gtc	atc	tac	ttc	acc	tcc	aac	ctc	ctc	gcc	gac	tgc	tac	384	
Phe	Ala	Ala	Val	Ile	Tyr	Phe	Thr	Ser	Asn	Leu	Leu	Ala	Asp	Cys	Tyr		
		115					120					125					
cgc	acc	ggc	gac	ccc	gcc	acc	ggc	aga	agg	aac	tac	acc	tac	atg	gac	432	
Arg	Thr	Gly	Asp	Pro	Ala	Thr	Gly	Arg	Arg	Asn	Tyr	Thr	Tyr	Met	Asp		
	130					135					140						
gcc	gtc	aag	gcc	aac	ctc	ggc	ggg	gcc	aag	gtg	aag	ggt	tgc	gga	tgc	480	
Ala	Val	Lys	Ala	Asn	Leu	Gly	Gly	Ala	Lys	Val	Lys	Val	Cys	Gly	Cys		
	145				150					155				160			
att	cag	tac	ctc	aac	ctt	ttg	gga	gtg	gcc	atc	ggg	tac	acc	atc	gcc	528	
Ile	Gln	Tyr	Leu	Asn	Leu	Leu	Gly	Val	Ala	Ile	Gly	Tyr	Thr	Ile	Ala		
				165				170						175			
gcc	tcc	att	agc	atg	atg	gcg	atc	cag	cgt	tcc	aac	tgc	ttc	cac	gcg	576	
Ala	Ser	Ile	Ser	Met	Met	Ala	Ile	Gln	Arg	Ser	Asn	Cys	Phe	His	Ala		
			180					185					190				
aga	gga	gag	cag	gat	cca	tgc	cac	gcc	tcc	agc	aac	gtg	tac	atg	atc	624	
Arg	Gly	Glu	Gln	Asp	Pro	Cys	His	Ala	Ser	Ser	Asn	Val	Tyr	Met	Ile		
		195				200						205					
atg	ttc	ggc	atc	gtc	cag	gtg	ttc	ttc	tcc	cag	atc	ccc	gac	ttc	gac	672	
Met	Phe	Gly	Ile	Val	Gln	Val	Phe	Phe	Ser	Gln	Ile	Pro	Asp	Phe	Asp		
	210					215					220						
caa	gtc	tgg	tgg	ctc	tcc	atc	ctc	gcc	gcc	gtc	atg	tcc	ttc	acc	tac	720	
Gln	Val	Trp	Trp	Leu	Ser	Ile	Leu	Ala	Ala	Val	Met	Ser	Phe	Thr	Tyr		
	225				230					235				240			
tcc	gcc	gtc	ggc	ctc	gcc	ctc	ggc	gcc	gcc	cag	gtc	gcc	cag	aac	cgc	768	
Ser	Ala	Val	Gly	Leu	Ala	Leu	Gly	Ala	Ala	Gln	Val	Ala	Gln	Asn	Arg		
				245				250						255			
acg	ttc	gcc	ggc	agc	gcc	atg	ggc	gtc	gcc	gtg	ggc	ttc	gtc	acc	aag	816	
Thr	Phe	Ala	Gly	Ser	Ala	Met	Gly	Val	Ala	Val	Gly	Phe	Val	Thr	Lys		
			260				265					270					
acc	ggc	gac	gtc	gtc	acc	ccc	gcg	cag	aag	gtg	tgg	cgc	aac	ctg	cag	864	
Thr	Gly	Asp	Val	Val	Thr	Pro	Ala	Gln	Lys	Val	Trp	Arg	Asn	Leu	Gln		
		275					280					285					
gcg	ctg	ggg	gac	atc	gcc	ttc	gcc	tac	tcc	tac	tcc	atc	atc	ctc	atc	912	
Ala	Leu	Gly	Asp	Ile	Ala	Phe	Ala	Tyr	Ser	Tyr	Ser	Ile	Ile	Leu	Ile		
	290					295					300						
gag	atc	cag	gac	acg	ctg	cgg	tcg	ccg	ccg	gcg	gag	gcg	agg	acg	atg	960	
Glu	Ile	Gln	Asp	Thr	Leu	Arg	Ser	Pro	Pro	Ala	Glu	Ala	Arg	Thr	Met		
	305				310					315					320		
cgg	aag	gcg	acg	ggg	atc	agc	gtg	gtg	gtg	acg	agc	gtg	ttc	tac	ctg	1008	
Arg	Lys	Ala	Thr	Gly	Ile	Ser	Val	Val	Val	Thr	Ser	Val	Phe	Tyr	Leu		
				325				330						335			
ctg	tgc	gga	tgc	atg	ggg	tac	gcg	gcg	ttc	ggc	gac	gac	gcg	ccg	ggg	1056	
Leu	Cys	Gly	Cys	Met	Gly	Tyr	Ala	Ala	Phe	Gly	Asp	Asp	Ala	Pro	Gly		
				340				345					350				
aac	ctc	ctc	acc	ggc	ttc	ggc	ttc	tac	aag	ccc	tac	tgg	ctg	ctg	gac	1104	
Asn	Leu	Leu	Thr	Gly	Phe	Gly	Phe	Tyr	Lys	Pro	Tyr	Trp	Leu	Leu	Asp		
		355					360					365					
gtg	gcc	aac	atg	gcg	atc	gtg	gta	cac	ctg	gtg	ggg	gcg	tac	cag	gtg	1152	
Val	Ala	Asn	Met	Ala	Ile	Val	Val	His	Leu	Val	Gly	Ala	Tyr	Gln	Val		
	370					375					380						
tac	tgc	cag	ccg	ctc	ttc	gcc	ttc	gtg	gag	agg	gag	gag	gag	cgg	cgg	1200	

PF59082SeqList_PF59082.txt

Tyr 385	Cys	Gln	Pro	Leu	Phe 390	Ala	Phe	Val	Glu	Arg 395	Arg	Ala	Glu	Arg	Arg 400	
tgg	ccc	aac	ggc	ctc	ccc	ggc	ggc	gac	tac	gac	ctg	ggg	tgg	ata	aag	1248
Trp	Pro	Asn	Gly	Leu 405	Pro	Gly	Gly	Asp	Tyr 410	Asp	Leu	Gly	Trp	Ile 415	Lys	
gtg	agc	gtg	ttc	agg	ttg	gcg	tgg	cgg	acg	tgc	ttc	gtg	gcg	gtg	acg	1296
Val	Ser	Val	Phe	Arg	Leu	Ala	Trp	Arg	Thr	Cys	Phe	Val	Ala	Val	Thr	
			420					425					430			
acg	gtg	gtg	gcg	atg	ctg	ctg	ccc	ttc	ttc	aac	gac	gtg	gtg	ggc	atc	1344
Thr	Val	Val	Ala	Met	Leu	Leu	Pro	Phe	Phe	Asn	Asp	Val	Val	Gly	Ile	
			435				440					445				
ctg	ggg	gcg	ctc	ggc	ttc	tgg	ccg	ctc	acc	gtc	tac	ttc	ccc	gtc	gag	1392
Leu	Gly	Ala	Leu	Gly	Phe	Trp	Pro	Leu	Thr	Val	Tyr	Phe	Pro	Val	Glu	
	450					455					460					
atg	tac	atc	gcc	cac	cgc	atc	cgg	agg	tgg	aca	acc	acc	tgg	gtc		1440
Met	Tyr	Ile	Ala	His	Arg	Ile	Arg	Arg	Trp	Thr	Thr	Thr	Trp	Val		
465					470				475					480		
ggc	ctg	cag	gcg	ctc	agc	ctc	gcc	tgc	ctt	ctc	gtc	tcg	ctc	gcc	gcc	1488
Gly	Leu	Gln	Ala	Leu	Ser	Leu	Ala	Cys	Leu	Leu	Val	Ser	Leu	Ala	Ala	
			485						490					495		
gcc	gtc	ggc	tcc	atc	gcc	ggc	gtc	ctg	ctc	gac	ctc	aag	tcc	tac	cgt	1536
Ala	Val	Gly	Ser	Ile	Ala	Gly	Val	Leu	Leu	Asp	Leu	Lys	Ser	Tyr	Arg	
			500					505					510			
cca	ttc	cgc	tcc	acc	tac	taa										1557
Pro	Phe	Arg	Ser	Thr	Tyr											
			515													

<210> 561

<211> 518

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<400> 561

Met	Leu	Pro	Arg	Ser	Arg	Thr	Leu	Pro	Pro	Arg	Ile	His	Asp	Gly	Val	
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Val	Val	Val	Glu	Arg	Asp	Val	Arg	Arg	Tyr	Gln	Gln	Leu	Pro	Gln	Gln	
			20					25					30			
Val	Glu	Met	Glu	Met	Thr	Thr	Thr	Lys	Arg	Gln	Gln	Asp	His	Gln	Val	
		35					40					45				
Glu	Thr	Met	Thr	Thr	Lys	Lys	Ile	Asp	Glu	Glu	Asp	Glu	Glu	Val	Asp	
	50					55					60					
Asp	Asp	Gly	Arg	Ala	Lys	Arg	Arg	Gly	Thr	Val	Trp	Thr	Ala	Ala	Ser	
65					70					75					80	
His	Ile	Ile	Thr	Ala	Val	Ile	Gly	Ser	Gly	Val	Leu	Ser	Leu	Ala	Trp	
			85					90						95		
Ala	Ile	Ala	Gln	Leu	Gly	Trp	Val	Val	Gly	Pro	Thr	Val	Met	Leu	Leu	
			100				105						110			
Phe	Ala	Ala	Val	Ile	Tyr	Phe	Thr	Ser	Asn	Leu	Leu	Ala	Asp	Cys	Tyr	
		115					120					125				
Arg	Thr	Gly	Asp	Pro	Ala	Thr	Gly	Arg	Arg	Asn	Tyr	Thr	Tyr	Met	Asp	
	130					135					140					
Ala	Val	Lys	Ala	Asn	Leu	Gly	Gly	Ala	Lys	Val	Lys	Val	Cys	Gly	Cys	
145					150					155					160	
Ile	Gln	Tyr	Leu	Asn	Leu	Leu	Gly	Val	Ala	Ile	Gly	Tyr	Thr	Ile	Ala	
			165					170						175		
Ala	Ser	Ile	Ser	Met	Met	Ala	Ile	Gln	Arg	Ser	Asn	Cys	Phe	His	Ala	
			180					185					190			
Arg	Gly	Glu	Gln	Asp	Pro	Cys	His	Ala	Ser	Ser	Asn	Val	Tyr	Met	Ile	
		195					200					205				
Met	Phe	Gly	Ile	Val	Gln	Val	Phe	Phe	Ser	Gln	Ile	Pro	Asp	Phe	Asp	
	210					215					220					
Gln	Val	Trp	Trp	Leu	Ser	Ile	Leu	Ala	Ala	Val	Met	Ser	Phe	Thr	Tyr	
225					230					235					240	
Ser	Ala	Val	Gly	Leu	Ala	Leu	Gly	Ala	Ala	Gln	Val	Ala	Gln	Asn	Arg	
			245					250						255		
Thr	Phe	Ala	Gly	Ser	Ala	Met	Gly	Val	Ala	Val	Gly	Phe	Val	Thr	Lys	
			260					265					270			
Thr	Gly	Asp	Val	Val	Thr	Pro	Ala	Gln	Lys	Val	Trp	Arg	Asn	Leu	Gln	
		275					280					285				

PF59082SeqList_PF59082.txt

Ala Leu Gly Asp Ile Ala Phe 295 Ala Tyr Ser Tyr Ser Ile Ile Leu Ile
 290 300
 Glu Ile Gln Asp Thr Leu Arg Ser Pro Pro Ala Glu Ala Arg Thr Met
 305 310 315 320
 Arg Lys Ala Thr Gly Ile Ser Val Val Val Thr Ser Val Phe Tyr Leu
 325 330 335
 Leu Cys Gly Cys Met Gly Tyr Ala Ala Phe Gly Asp Asp Ala Pro Gly
 340 345 350
 Asn Leu Leu Thr Gly Phe Gly Phe Tyr Lys Pro Tyr Trp Leu Leu Asp
 355 360 365
 Val Ala Asn Met Ala Ile Val Val His Leu Val Gly Ala Tyr Gln Val
 370 375 380
 Tyr Cys Gln Pro Leu Phe Ala Phe Val Glu Arg Arg Ala Glu Arg Arg
 385 390 395 400
 Trp Pro Asn Gly Leu Pro Gly Gly Asp Tyr Asp Leu Gly Trp Ile Lys
 405 410 415
 Val Ser Val Phe Arg Leu Ala Trp Arg Thr Cys Phe Val Ala Val Thr
 420 425 430
 Thr Val Val Ala Met Leu Leu Pro Phe Phe Asn Asp Val Val Gly Ile
 435 440 445
 Leu Gly Ala Leu Gly Phe Trp Pro Leu Thr Val Tyr Phe Pro Val Glu
 450 455 460
 Met Tyr Ile Ala His Arg Arg Ile Arg Arg Trp Thr Thr Thr Trp Val
 465 470 475 480
 Gly Leu Gln Ala Leu Ser Leu Ala Cys Leu Val Ser Leu Ala Ala
 485 490 495
 Ala Val Gly Ser Ile Ala Gly Val Leu Leu Asp Leu Lys Ser Tyr Arg
 500 505 510
 Pro Phe Arg Ser Thr Tyr
 515

<210> 562

<211> 1401

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<221> CDS

<222> (1)..(1401)

<400> 562

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Met Ala Leu Gly Asp 5 Gly Asp Asp Gly Ala Ala Ala Ala Val Pro	
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ctc atc tcg gat cgc ccc aag cat gcc gcc atc gtc aga agc ggg acg	96
Leu Ile Ser Asp Arg Pro Lys His Ala Ala Ile Val Arg Ser Gly Thr	
20 25 30	
gag tgg acg gcg gcg gcg cac gtg atc acg gcg gtg atc ggg tcc ggg	144
Glu Trp Thr Ala Ala Ala His Val Ile Thr Ala Val Ile Gly Ser Gly	
35 40 45	
gtg ctg tcg ctg gcg tgg agc gtg gcg cag ctg ggg tgg ctg gcg ggg	192
Val Leu Ser Leu Ala Trp Ser Val Ala Gln Leu Gly Trp Leu Ala Gly	
50 55 60	
ccg ggg atg atg ctc gtg ttc gcg gcc gtg acg gcg ctg cag tcg gcg	240
Pro Gly Met Met Leu Val Phe Ala Ala Val Thr Ala Leu Gln Ser Ala	
65 70 75 80	
ctg ttc gcc gac tgc tac cgc tcg ccg gac ccg gag gtc ggc ccg cac	288
Leu Phe Ala Asp Cys Tyr Arg Ser Pro Asp Pro Glu Val Gly Pro His	
85 90 95	
cgc aac cgc acc tac gcc aac gcc gtc gag cgc aac cta ggt agc tcg	336
Arg Asn Arg Thr Tyr Ala Asn Ala Val Glu Arg Asn Leu Gly Ser Ser	
100 105 110	
agc gcg tgg gtc tgc ttg ttg ctg cag caa acg gcc ttg ttc ggc tac	384
Ser Ala Trp Val Cys Leu Leu Leu Gln Gln Thr Ala Leu Phe Gly Tyr	
115 120 125	
ggc atc gcc tac acc atc acc gcc tcc atc agt tgc agg gcg atc ctg	432
Gly Ile Ala Tyr Thr Ile Thr Ala Ser Ile Ser Cys Arg Ala Ile Leu	
130 135 140	
agg tcc aac tgc tac cac acg cac ggc cac gag gcg ccc tgc aaa tac	480

PF59082SeqList_PF59082.txt

Arg 145	Ser	Asn	Cys	Tyr	His 150	Thr	His	Gly	His	Asp 155	Ala	Pro	Cys	Lys	Tyr 160	
ggg	ggt	agc	tac	tac	atg	ctc	atg	ttc	ggc	gcg	gcg	cag	ctg	ttc	ctc	528
Gly	Gly	Ser	Tyr	Tyr 165	Met	Leu	Met	Phe	Gly 170	Ala	Ala	Gln	Leu	Phe 175	Leu	
tcc	ttc	ata	ccg	gac	ttc	cac	gac	atg	gcg	tgg	ctg	tcg	gtc	ctc	gcc	576
Ser	Phe	Ile	Pro	Asp	Phe	His	Asp	Met	Ala	Trp	Leu	Ser	Val 190	Leu	Ala	
gcg	gtc	atg	tcg	ttc	tcc	tac	tcg	ttc	atc	ggc	ctc	ggc	ctc	ggc	ctc	624
Ala	Val	Met 195	Ser	Phe	Ser	Tyr	Ser	Phe	Ile	Gly	Leu	Gly 205	Leu	Gly	Leu	
gcc	aac	aca	att	gct	aat	gga	acg	atc	aaa	gga	agc	ata	aca	ggt	gct	672
Ala	Asn	Thr	Ile	Ala	Asn	Gly 215	Thr	Ile	Lys	Gly	Ser 220	Ile	Thr	Gly	Ala	
cca	acg	aga	acc	cct	gtg	cag	aag	gtc	tgg	cac	gtc	tcg	cag	gcc	atc	720
Pro	Thr	Arg	Thr	Pro	Val 230	Gln	Lys	Val	Trp	His 235	Val	Ser	Gln	Ala	Ile 240	
ggc	gac	atc	gca	ttc	gcg	tac	ccg	tac	tca	tta	atc	ctc	ttg	gaa	att	768
Gly	Asp	Ile	Ala	Phe 245	Ala	Tyr	Pro	Tyr	Ser 250	Leu	Ile	Leu	Leu	Glu 255	Ile	
cag	gac	aca	ctg	aag	gct	cca	ccg	gcc	gag	aac	aag	acg	atg	aag	aag	816
Gln	Asp	Thr	Leu	Lys	Ala	Pro	Pro	Ala	Glu 265	Asn	Lys	Thr	Met 270	Lys	Lys	
gcg	tcc	atc	atc	tcg	atc	gtc	gtc	acc	acc	ttc	ttc	tac	ctc	tgc	tgc	864
Ala	Ser	Ile 275	Ile	Ser	Ile	Val	Val	Thr	Thr	Phe	Phe	Tyr 285	Leu	Cys	Cys	
ggc	tgc	ttc	ggc	tac	gcc	gcc	ttc	ggg	agc	gac	gcc	cct	ggc	aac	ctc	912
Gly	Cys 290	Phe	Gly	Tyr	Ala	Ala 295	Phe	Gly	Ser	Asp	Ala 300	Pro	Gly	Asn	Leu	
ctc	acc	ggc	ttc	ggc	ttc	tac	gag	ccc	tac	tgg	ctc	atc	gac	ttc	gcc	960
Leu	Thr	Gly	Phe	Gly	Phe 310	Tyr	Glu	Pro	Tyr	Trp 315	Leu	Ile	Asp	Phe	Ala 320	
aac	gcc	tgc	atc	atc	ctc	cac	ctg	ctc	ggc	ggc	tac	cag	gtg	tac	agc	1008
Asn	Ala	Cys	Ile	Ile 325	Leu	His	Leu	Leu	Gly 330	Gly	Tyr	Gln	Val	Tyr 335	Ser	
cag	ccg	ata	tac	cag	ttc	gcg	gac	agg	ttc	ttc	gcg	gag	agg	tac	ccg	1056
Gln	Pro	Ile	Tyr	Gln	Phe	Ala	Asp	Arg	Phe 345	Phe	Ala	Glu	Arg 350	Tyr	Pro	
gcg	agc	cgg	ttc	gtg	aac	gac	ttc	cac	acg	gtg	aag	ctg	ccg	ctg	ctg	1104
Ala	Ser	Arg 355	Phe	Val	Asn	Asp	Phe 360	His	Thr	Val	Lys	Leu	Pro	Leu	Leu	
ccg	ccg	tgt	cgg	gtg	aac	ctc	ctg	cgg	gtg	tgc	ttc	cgg	acg	gtg	tac	1152
Pro	Pro	Cys	Arg	Val	Asn 375	Leu	Leu	Arg	Val	Cys	Phe 380	Arg	Thr	Val	Tyr	
gtg	gcg	agc	acc	acg	gcg	gtg	gcg	ctc	gcc	ttc	ccc	tac	ttc	aac	gag	1200
Val	Ala	Ser	Thr	Thr	Ala 390	Val	Ala	Leu	Ala	Phe 395	Pro	Tyr	Phe	Asn	Glu 400	
gtg	ctc	gcg	ctg	ctc	ggc	gcc	ctc	aac	ttc	tgg	ccg	ctc	gcc	atc	tac	1248
Val	Leu	Ala	Leu	Leu 405	Gly	Ala	Leu	Asn	Phe 410	Trp	Pro	Leu	Ala	Ile 415	Tyr	
ttc	ccc	gtg	gag	atg	tac	ttc	atc	cag	cgc	cat	gtc	ccg	cgg	tgg	tcg	1296
Phe	Pro	Val	Glu	Met	Tyr	Phe	Ile	Gln	Arg	His	Val	Pro	Arg 430	Trp	Ser	
ccc	cgg	tgg	gtc	gtg	ctg	cag	tcg	ttc	agc	gtc	ctc	tgc	ctc	ctc	gtc	1344
Pro	Arg	Trp 435	Val	Val	Leu	Gln	Ser 440	Phe	Ser	Val	Leu	Cys 445	Leu	Leu	Val	
agc	gcc	ttc	gcg	ctc	gtc	ggc	tcc	atc	cag	ggc	ctc	atc	agc	cag	aag	1392
Ser	Ala	Phe	Ala	Leu	Val 455	Gly	Ser	Ile	Gln	Gly	Leu 460	Ile	Ser	Gln	Lys	
cta	ggc	taa														1401
Leu	Gly															
465																

<210> 563

<211> 466

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<400> 563

PF59082SeqList_PF59082.txt

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      20      25      30
Glu Trp Thr Ala Ala Ala His Val Ile Thr Ala Val Ile Gly Ser Gly
      35      40      45
Val Leu Ser Leu Ala Trp Ser Val Ala Gln Leu Gly Trp Leu Ala Gly
      50      55      60
Pro Gly Met Met Leu Val Phe Ala Ala Val Thr Ala Leu Gln Ser Ala
65      70      75      80
Leu Phe Ala Asp Cys Tyr Arg Ser Pro Asp Pro Glu Val Gly Pro His
      85      90      95
Arg Asn Arg Thr Tyr Ala Asn Ala Val Glu Arg Asn Leu Gly Ser Ser
      100      105      110
Ser Ala Trp Val Cys Leu Leu Leu Gln Gln Thr Ala Leu Phe Gly Tyr
      115      120      125
Gly Ile Ala Tyr Thr Ile Thr Ala Ser Ile Ser Cys Arg Ala Ile Leu
      130      135      140
Arg Ser Asn Cys Tyr His Thr His Gly His Asp Ala Pro Cys Lys Tyr
145      150      155      160
Gly Gly Ser Tyr Tyr Met Leu Met Phe Gly Ala Ala Gln Leu Phe Leu
      165      170      175
Ser Phe Ile Pro Asp Phe His Asp Met Ala Trp Leu Ser Val Leu Ala
      180      185      190
Ala Val Met Ser Phe Ser Tyr Ser Phe Ile Gly Leu Gly Leu Gly Leu
      195      200      205
Ala Asn Thr Ile Ala Asn Gly Thr Ile Lys Gly Ser Ile Thr Gly Ala
      210      215      220
Pro Thr Arg Thr Pro Val Gln Lys Val Trp His Val Ser Gln Ala Ile
225      230      235      240
Gly Asp Ile Ala Phe Ala Tyr Pro Tyr Ser Leu Ile Leu Leu Glu Ile
      245      250      255
Gln Asp Thr Leu Lys Ala Pro Pro Ala Glu Asn Lys Thr Met Lys Lys
      260      265      270
Ala Ser Ile Ile Ser Ile Val Val Thr Thr Phe Phe Tyr Leu Cys Cys
      275      280      285
Gly Cys Phe Gly Tyr Ala Ala Phe Gly Ser Asp Ala Pro Gly Asn Leu
      290      295      300
Leu Thr Gly Phe Gly Phe Tyr Glu Pro Tyr Trp Leu Ile Asp Phe Ala
305      310      315      320
Asn Ala Cys Ile Ile Leu His Leu Leu Gly Gly Tyr Gln Val Tyr Ser
      325      330      335
Gln Pro Ile Tyr Gln Phe Ala Asp Arg Phe Phe Ala Glu Arg Tyr Pro
      340      345      350
Ala Ser Arg Phe Val Asn Asp Phe His Thr Val Lys Leu Pro Leu Leu
      355      360      365
Pro Pro Cys Arg Val Asn Leu Leu Arg Val Cys Phe Arg Thr Val Tyr
      370      375      380
Val Ala Ser Thr Thr Ala Val Ala Leu Ala Phe Pro Tyr Phe Asn Glu
385      390      395      400
Val Leu Ala Leu Leu Gly Ala Leu Asn Phe Trp Pro Leu Ala Ile Tyr
      405      410      415
Phe Pro Val Glu Met Tyr Phe Ile Gln Arg His Val Pro Arg Trp Ser
      420      425      430
Pro Arg Trp Val Val Leu Gln Ser Phe Ser Val Leu Cys Leu Leu Val
      435      440      445
Ser Ala Phe Ala Leu Val Gly Ser Ile Gln Gly Leu Ile Ser Gln Lys
      450      455      460
Leu Gly
465

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<210> 564

<211> 1467

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<221> CDS

<222> (1)..(1467)

PF59082SeqList_PF59082.txt

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Val Pro Ser Lys Ala Ala Gly Val Asp Gly Asp Gly Glu Pro Arg Arg
20 25 30
acg ggc acc atg tgg acg gcg agc gcg cac atc atc acg gcg gtg atc      144
Thr Gly Thr Met Trp Thr Ala Ser Ala His Ile Ile Thr Ala Val Ile
35 40 45
ggg tcc ggc gtg ctg tcg ctg gcg tgg ggc gtc gcg cag ctg ggg tgg      192
Gly Ser Gly Val Leu Ser Leu Ala Trp Gly Val Ala Gln Leu Gly Trp
50 55 60
gtg gcc ggc ccc gcg gtg atg ctg ctg ttc ggc gtc atc tac tgc      240
Val Ala Gly Pro Ala Val Met Leu Leu Phe Gly Ala Val Ile Tyr Cys
65 70 75 80
tgc tcc gtg ctc ctc gtc gag tgc tac cgc acc ggc gac ccg tac acc      288
Cys Ser Val Leu Leu Val Glu Cys Tyr Arg Thr Gly Asp Pro Tyr Thr
85 90 95
ggc cag cgc aac cgc acc tac atg gac gcc gtc cgc gcc aac ctc ggc      336
Gly Gln Arg Asn Arg Thr Tyr Met Asp Ala Val Arg Ala Asn Leu Gly
100 105 110
ggg acc aag gtg agg ctc tgc ggc gtg ctg cag ttc gcc aac ttc ttc      384
Gly Thr Lys Val Arg Leu Cys Gly Val Leu Gln Phe Ala Asn Phe Phe
115 120 125
ggc gtc tgc gtc ggc atc acc atc gcc tcc tcc atc agc atg ctg gcg      432
Gly Val Cys Val Gly Ile Thr Ile Ala Ser Ser Ile Ser Met Leu Ala
130 135 140
atc aag agg gcg ggg tgc ttc cac gtg aga ggc cac gac cag agg gag      480
Ile Lys Arg Ala Gly Cys Phe His Val Arg Gly His Asp Gln Arg Glu
145 150 155 160
gcg tgc ggc ggc tcg agc cgg ccg tac atg gtg gtg tac ggc gcg ctg      528
Ala Cys Gly Gly Ser Ser Arg Pro Tyr Met Val Val Tyr Gly Ala Leu
165 170 175
cag gtc gtg ttc tcg cag atc ccc aac ctc cac aag atg tgg tgg ctc      576
Gln Val Val Phe Ser Gln Ile Pro Asn Leu His Lys Met Trp Trp Leu
180 185 190
tcc acg ctc gcc tcc gcc atg tcg ctg tcc tac tcc gcc atc ggc atc      624
Ser Thr Leu Ala Ser Ala Met Ser Leu Ser Tyr Ser Ala Ile Gly Ile
195 200 205
gcc ctc ggc gtc gcg cag atc gta gcg aac ggc gga atc agg ggc acc      672
Ala Leu Gly Val Ala Gln Ile Val Ala Asn Gly Gly Ile Arg Gly Thr
210 215 220
atc acg ggc gtc ttc gtc ggc ggc gcc ggc ggc gtc acc tcg atg cag      720
Ile Thr Gly Val Phe Val Gly Ala Gly Ala Gly Val Thr Ser Met Gln
225 230 235 240
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Lys Val Trp Arg Ser Phe Gln Ala Phe Gly Asn Ile Ala Phe Ala Tyr
245 250 255
ggc ttc tcg ttc atc ctc ctc gag atc cat gac acg gtg aag ccg gtg      816
Gly Phe Ser Phe Ile Leu Leu Glu Ile His Asp Thr Val Lys Pro Val
260 265 270
gcg ccg ccg tcg acg gag acg aag gtg atg agg aaa gcg gtg gcg gtg      864
Ala Pro Pro Ser Thr Glu Thr Lys Val Met Arg Lys Ala Val Ala Val
275 280 285
agc gtg gcg acg acg acg gcg gtg tac ctg atg tgc ggc tgc gtc ggc      912
Ser Val Ala Thr Thr Thr Ala Val Tyr Leu Met Cys Gly Cys Val Gly
290 295 300
tac gcg gcg ttc ggg aac gac tcg ccg gac aac ctc acc ggc ttc      960
Tyr Ala Ala Phe Gly Asn Asp Ser Pro Asp Asn Leu Leu Thr Gly Phe
305 310 315 320
ggg ttc ttc gag ccc ttc tgg ctg ctc gac ctc gcc aac gcc ggc gtc      1008
Gly Phe Phe Glu Pro Phe Trp Leu Leu Asp Leu Ala Asn Ala Gly Val
325 330 335
gtg gtg cac ctc gta ggc acg tac cag gtg gtg gcg cag ccg gtg ttc      1056
Val Val His Leu Val Gly Thr Tyr Gln Val Val Ala Gln Pro Val Phe
340 345 350 355
gcg ttc ctc gac ggg cgc gcc gcg gcg ggc gcg tgg ccc ggc agc gcg      1104

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PF59082SeqList_PF59082.txt

Ala	Phe	Leu	Asp	Gly	Arg	Ala	Ala	Gly	Ala	Trp	Pro	Gly	Ser	Ala	
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Ala	Leu	Gly	Lys	Arg	Arg	Arg	Val	Leu	Arg	Val	Gly	Ser	Leu	Ala	Glu
		370				375					380				
atc	gag	gtg	agc	ccg	ttc	cgt	ctg	gcg	tgg	cgc	acg	gcg	ttc	gtg	tgc
Ile	Glu	Val	Ser	Pro	Phe	Arg	Leu	Ala	Trp	Arg	Thr	Ala	Phe	Val	Cys
		385			390					395					400
gtg	acc	acg	gcg	gcg	tcc	acg	ctg	ctc	ccg	ttc	ttc	ggc	tcc	atg	gtg
Val	Thr	Thr	Ala	Ala	Ser	Thr	Leu	Leu	Pro	Phe	Phe	Gly	Ser	Met	Val
				405					410					415	
ggg	ctc	atc	ggc	gcg	gcg	tcg	ttc	tgg	ccg	ctc	acc	gtc	tac	ttc	ccc
Gly	Leu	Ile	Gly	Ala	Ala	Ser	Phe	Trp	Pro	Leu	Thr	Val	Tyr	Phe	Pro
			420					425					430		
gtg	gag	atg	tac	atc	gcg	cag	cgc	cgg	gtg	ccg	cgg	ggg	agc	gcg	cag
Val	Glu	Met	Tyr	Ile	Ala	Gln	Arg	Arg	Val	Pro	Arg	Gly	Ser	Ala	Gln
		435				440						445			
tgg	ctg	tcc	ctc	cag	gcg	ctc	agc	gcc	ggg	tgc	ctc	gtc	gtg	tcc	gtc
Trp	Leu	Ser	Leu	Gln	Ala	Leu	Ser	Ala	Gly	Cys	Leu	Val	Val	Ser	Val
		450				455					460				
gcc	gcc	tcg	gcg	gga	tcc	atc	gcc	ggc	gtc	gtg	gag	gcg	ttc	aag	gcg
Ala	Ala	Ser	Ala	Gly	Ser	Ile	Ala	Gly	Val	Val	Glu	Ala	Phe	Lys	Ala
					470					475					480
cac	aac	ccg	ttc	tgc	tgg	acg	tgc	tga							
His	Asn	Pro	Phe	Cys	Trp	Thr	Cys								
				485											

<210> 565

<211> 488

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<400> 565

Met	Ser	Leu	Ala	Asp	Asp	Leu	Ala	Ala	Val	Glu	Arg	Gly	Gly	His	Met
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Val	Pro	Ser	Lys	Ala	Ala	Gly	Val	Asp	Gly	Asp	Gly	Glu	Pro	Arg	Arg
			20					25					30		
Thr	Gly	Thr	Met	Trp	Thr	Ala	Ser	Ala	His	Ile	Ile	Thr	Ala	Val	Ile
		35				40						45			
Gly	Ser	Gly	Val	Leu	Ser	Leu	Ala	Trp	Gly	Val	Ala	Gln	Leu	Gly	Trp
		50				55					60				
Val	Ala	Gly	Pro	Ala	Val	Met	Leu	Leu	Phe	Gly	Ala	Val	Ile	Tyr	Cys
					70					75					80
Cys	Ser	Val	Leu	Leu	Val	Glu	Cys	Tyr	Arg	Thr	Gly	Asp	Pro	Tyr	Thr
				85					90					95	
Gly	Gln	Arg	Asn	Arg	Thr	Tyr	Met	Asp	Ala	Val	Arg	Ala	Asn	Leu	Gly
			100					105					110		
Gly	Thr	Lys	Val	Arg	Leu	Cys	Gly	Val	Leu	Gln	Phe	Ala	Asn	Phe	Phe
		115					120					125			
Gly	Val	Cys	Val	Gly	Ile	Thr	Ile	Ala	Ser	Ser	Ile	Ser	Met	Leu	Ala
		130				135					140				
Ile	Lys	Arg	Ala	Gly	Cys	Phe	His	Val	Arg	Gly	His	Asp	Gln	Arg	Glu
				150						155					160
Ala	Cys	Gly	Gly	Ser	Arg	Pro	Tyr	Met	Val	Val	Tyr	Gly	Ala	Leu	
				165				170					175		
Gln	Val	Val	Phe	Ser	Gln	Ile	Pro	Asn	Leu	His	Lys	Met	Trp	Trp	Leu
			180					185					190		
Ser	Thr	Leu	Ala	Ser	Ala	Met	Ser	Leu	Ser	Tyr	Ser	Ala	Ile	Gly	Ile
		195					200					205			
Ala	Leu	Gly	Val	Ala	Gln	Ile	Val	Ala	Asn	Gly	Gly	Ile	Arg	Gly	Thr
		210				215					220				
Ile	Thr	Gly	Val	Phe	Val	Gly	Ala	Gly	Ala	Gly	Val	Thr	Ser	Met	Gln
				230						235					240
Lys	Val	Trp	Arg	Ser	Phe	Gln	Ala	Phe	Gly	Asn	Ile	Ala	Phe	Ala	Tyr
				245					250					255	
Gly	Phe	Ser	Phe	Ile	Leu	Leu	Glu	Ile	His	Asp	Thr	Val	Lys	Pro	Val
			260					265					270		
Ala	Pro	Pro	Ser	Thr	Glu	Thr	Lys	Val	Met	Arg	Lys	Ala	Val	Ala	Val
		275					280					285			

PF59082SeqList_PF59082.txt

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Ser Val Ala Thr Thr Thr Ala Val Tyr Leu Met Cys Gly Cys Val Gly
290 295 300
Tyr Ala Ala Phe Gly Asn Asp Ser Pro Asp Asn Leu Leu Thr Gly Phe
305 310 315 320
Gly Phe Phe Glu Pro Phe Trp Leu Leu Asp Leu Ala Asn Ala Gly Val
325 330 335
Val Val His Leu Val Gly Thr Tyr Gln Val Val Ala Gln Pro Val Phe
340 345 350
Ala Phe Leu Asp Gly Arg Ala Ala Ala Gly Ala Trp Pro Gly Ser Ala
355 360 365
Ala Leu Gly Lys Arg Arg Arg Val Leu Arg Val Gly Ser Leu Ala Glu
370 375 380
Ile Glu Val Ser Pro Phe Arg Leu Ala Trp Arg Thr Ala Phe Val Cys
385 390 395 400
Val Thr Thr Ala Ala Ser Thr Leu Leu Pro Phe Phe Gly Ser Met Val
405 410 415
Gly Leu Ile Gly Ala Ala Ser Phe Trp Pro Leu Thr Val Tyr Phe Pro
420 425 430
Val Glu Met Tyr Ile Ala Gln Arg Arg Val Pro Arg Gly Ser Ala Gln
435 440 445
Trp Leu Ser Leu Gln Ala Leu Ser Ala Gly Cys Leu Val Val Ser Val
450 455 460
Ala Ala Ser Ala Gly Ser Ile Ala Gly Val Val Glu Ala Phe Lys Ala
465 470 475 480
His Asn Pro Phe Cys Trp Thr Cys
485

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<210> 566

<211> 1464

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<221> CDS

<222> (1)..(1464)

<400> 566

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Met Gly Met Glu Arg Pro Gln Glu Lys Val Ala Thr Thr Thr Thr Ala
1 5 10 15
gcc ttc aac ctc gcc gag tcc ggc tac gcc gac cgc ccc gac ctc gac
Ala Phe Asn Leu Ala Glu Ser Gly Tyr Ala Asp Arg Pro Asp Leu Asp
20 25 30
gac gac ggc cgc gag aag cgc aca ggg acg ctg gtg acg gcg agc gcg
Asp Asp Gly Arg Glu Lys Arg Thr Gly Thr Leu Val Thr Ala Ser Ala
35 40 45
cac ata ata acg gcg gtg atc ggc tcc ggc gtg ctg tcg ctg gcg tgg
His Ile Ile Thr Ala Val Ile Gly Ser Gly Val Leu Ser Leu Ala Trp
50 55 60
gcg ata gcg cag ctg ggg tgg gtg atc ggg ccg gcc gtg ctg gtg gcg
Ala Ile Ala Gln Leu Gly Trp Val Ile Gly Pro Ala Val Leu Val Ala
65 70 75 80
ttc tcg gtc ata acc tgg ttc tgc tcc agc ctc ctc gcc gac tgc tac
Phe Ser Val Ile Thr Trp Phe Cys Ser Ser Leu Leu Ala Asp Cys Tyr
85 90 95
cga tct ccc gac ccc gtc cat ggc aag cgc aac tac acc tac ggc caa
Arg Ser Pro Asp Pro Val His Gly Lys Arg Asn Tyr Thr Tyr Gly Gln
100 105 110
gcc gtc agg gcc aac cta ggt gtg gcc aag tac agg ctc tgc tcg gtg
Ala Val Arg Ala Asn Leu Gly Val Ala Lys Tyr Arg Leu Cys Ser Val
115 120 125
gca cag tac gtc aat ctc gtc ggc gtc acc att ggc tac acc atc act
Ala Gln Tyr Val Asn Leu Val Gly Val Thr Ile Gly Tyr Thr Ile Thr
130 135 140
acg gcc atc agc atg ggt gcg atc aaa cgg tcc aac tgg ttc cat cgc
Thr Ala Ile Ser Met Gly Ala Ile Lys Arg Ser Asn Trp Phe His Arg
145 150 155 160
aac ggc cac gac gca gcc tgc ttg gca tct gac acg acc aac atg atc
Asn Gly His Asp Ala Ala Cys Leu Ala Ser Asp Thr Thr Asn Met Ile

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PF59082SeqList_PF59082.txt

				165				170				175					
ata	ttt	gct	ggc	atc	caa	atc	ctc	ctc	tcg	cag	ctg	ccg	aat	ttt	cac		576
Ile	Phe	Ala	Gly	Ile	Gln	Ile	Leu	Leu	Ser	Gln	Leu	Pro	Asn	Phe	His		
			180					185					190				
aaa	att	tgg	tgg	ctc	tcc	att	gtc	gct	gct	gtc	atg	tca	ctg	gcc	tac		624
Lys	Ile	Trp	Trp	Leu	Ser	Ile	Val	Ala	Ala	Val	Met	Ser	Leu	Ala	Tyr		
			195				200					205					
tca	acc	att	ggc	ctt	ggc	ctc	tcc	att	gca	aaa	att	gca	ggg	ggg	gcc		672
Ser	Thr	Ile	Gly	Leu	Gly	Leu	Ser	Ile	Ala	Lys	Ile	Ala	Gly	Gly	Ala		
			210			215					220						
cac	ccc	gag	gca	acc	ctc	aca	ggg	gtg	act	gtt	gga	gtg	gat	gtg	tct		720
His	Pro	Glu	Ala	Thr	Leu	Thr	Gly	Val	Thr	Val	Gly	Val	Asp	Val	Ser		
					230					235					240		
gca	agt	gag	aaa	atc	tgg	aga	act	ttt	cag	tca	ctt	ggg	gac	att	gcc		768
Ala	Ser	Glu	Lys	Ile	Trp	Arg	Thr	Phe	Gln	Ser	Leu	Gly	Asp	Ile	Ala		
				245					250					255			
ttt	gca	tac	tcc	tac	tcc	aat	gtc	ctc	ata	gaa	att	cag	gac	acg	ctg		816
Phe	Ala	Tyr	Ser	Tyr	Ser	Asn	Val	Leu	Ile	Glu	Ile	Gln	Asp	Thr	Leu		
			260				265						270				
cgg	tcg	agc	ccg	gcg	gag	aac	gag	gtg	atg	aag	aag	gcg	tcg	ttc	atc		864
Arg	Ser	Ser	Pro	Ala	Glu	Asn	Glu	Val	Met	Lys	Lys	Ala	Ser	Phe	Ile		
			275			280						285					
gga	gtc	tcg	acg	acg	acg	acg	ttc	tac	atg	ctg	tgc	ggc	gtg	ctc	ggc		912
Gly	Val	Ser	Thr	Thr	Thr	Thr	Phe	Tyr	Met	Leu	Cys	Gly	Val	Leu	Gly		
			290			295					300						
tac	gcg	gcg	ttc	ggc	aac	gcg	ccg	ggg	aac	ctc	acc	ggc	ttc				960
Tyr	Ala	Ala	Phe	Gly	Asn	Arg	Ala	Pro	Gly	Asn	Phe	Leu	Thr	Gly	Phe		
				310					315					320			
ggc	ttc	tac	gag	ccc	ttc	tgg	ctc	gtc	gac	gtc	ggc	aac	gtc	tgc	atc		1008
Gly	Phe	Tyr	Glu	Pro	Phe	Trp	Leu	Val	Asp	Val	Gly	Asn	Val	Cys	Ile		
				325					330					335			
gtc	gtc	cac	ctc	gtc	ggc	gcc	tac	cag	gtc	ttc	tgc	cag	ccc	atc	tac		1056
Val	Val	His	Leu	Val	Gly	Ala	Tyr	Gln	Val	Phe	Cys	Gln	Pro	Ile	Tyr		
			340				345					350					
cag	ttc	gcc	gag	gcc	tgg	gcg	cg	tcg	cg	tgg	ccg	gac	agc	gcc	ttc		1104
Gln	Phe	Ala	Glu	Ala	Trp	Ala	Arg	Ser	Arg	Trp	Pro	Asp	Ser	Ala	Phe		
			355			360					365						
gtc	aac	ggc	gag	cg	gtg	ctc	cg	ctg	ccg	ctc	ggc	gcc	ggc	gac	ttc		1152
Val	Asn	Gly	Glu	Arg	Val	Leu	Arg	Leu	Pro	Leu	Gly	Ala	Gly	Asp	Phe		
			370		375					380							
ccc	gtc	agc	gcg	ctc	cg	ctc	gtc	tgg	cg	acg	gcc	tac	gtc	gtg	ctc		1200
Pro	Val	Ser	Ala	Leu	Arg	Leu	Val	Trp	Arg	Thr	Ala	Tyr	Val	Val	Leu		
				390					395					400			
acc	gcc	gtc	gcc	gcc	atg	gcg	ttc	ccc	ttc	aac	gac	ttc	ctc	ggc			1248
Thr	Ala	Val	Ala	Ala	Met	Ala	Phe	Pro	Phe	Asn	Asp	Phe	Leu	Gly			
				405				410					415				
ctc	atc	ggc	gcc	gtc	tcc	ttc	tgg	ccg	ctc	acc	gtc	tac	ttc	ccc	gtc		1296
Leu	Ile	Gly	Ala	Val	Ser	Phe	Trp	Pro	Leu	Thr	Val	Tyr	Phe	Pro	Val		
			420				425					430					
cag	atg	tac	tct	cag	gcc	aag	gtc	cg	cg	ttc	tcg	ccg	acg	tgg			1344
Gln	Met	Tyr	Met	Ser	Gln	Lys	Val	Arg	Arg	Phe	Ser	Pro	Thr	Trp			
			435			440				445							
acg	tgg	atg	aac	gtg	ctc	agc	ctc	gcc	tgc	ctc	gtc	gtc	tcc	ctc	ctc		1392
Thr	Trp	Met	Asn	Val	Leu	Ser	Leu	Ala	Cys	Leu	Val	Val	Ser	Leu	Leu		
			450		455					460							
gcc	gcc	gcc	ggc	tcc	atc	cag	ggc	ctc	atc	aaa	tcc	gtc	gca	cat	tac		1440
Ala	Ala	Ala	Gly	Ser	Ile	Gln	Gly	Leu	Ile	Lys	Ser	Val	Ala	His	Tyr		
				470					475						480		
aag	cca	ttc	agc	gtc	tcc	tca	tga										1464
Lys	Pro	Phe	Ser	Val	Ser												
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<210> 567

<211> 487

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<400> 567

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PF59082SeqList_PF59082.txt

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Asp Asp Gly Arg Glu Lys Arg Thr Gly Thr Leu Val Thr Ala Ser Ala
      35
His Ile Ile Thr Ala Val Ile Gly Ser Gly Val Leu Ser Leu Ala Trp
      50
Ala Ile Ala Gln Leu Gly Trp Val Ile Gly Pro Ala Val Leu Val Ala
      65
Phe Ser Val Ile Thr Trp Phe Cys Ser Ser Leu Leu Ala Asp Cys Tyr
      85
Arg Ser Pro Asp Pro Val His Gly Lys Arg Asn Tyr Thr Tyr Gly Gln
      100
Ala Val Arg Ala Asn Leu Gly Val Ala Lys Tyr Arg Leu Cys Ser Val
      115
Ala Gln Tyr Val Asn Leu Val Gly Val Thr Ile Gly Tyr Thr Ile Thr
      130
Thr Ala Ile Ser Met Gly Ala Ile Lys Arg Ser Asn Trp Phe His Arg
      145
Asn Gly His Asp Ala Cys Leu Ala Ser Asp Thr Thr Asn Met Ile
      165
Ile Phe Ala Gly Ile Gln Ile Leu Leu Ser Gln Leu Pro Asn Phe His
      180
Lys Ile Trp Trp Leu Ser Ile Val Ala Ala Val Met Ser Leu Ala Tyr
      195
Ser Thr Ile Gly Leu Gly Leu Ser Ile Ala Lys Ile Ala Gly Gly Ala
      210
His Pro Glu Ala Thr Leu Thr Gly Val Thr Val Gly Val Asp Val Ser
      225
Ala Ser Glu Lys Ile Trp Arg Thr Phe Gln Ser Leu Gly Asp Ile Ala
      245
Phe Ala Tyr Ser Tyr Ser Asn Val Leu Ile Glu Ile Gln Asp Thr Leu
      260
Arg Ser Ser Pro Ala Glu Asn Glu Val Met Lys Lys Ala Ser Phe Ile
      275
Gly Val Ser Thr Thr Thr Thr Phe Tyr Met Leu Cys Gly Val Leu Gly
      290
Tyr Ala Ala Phe Gly Asn Arg Ala Pro Gly Asn Phe Leu Thr Gly Phe
      305
Gly Phe Tyr Glu Pro Phe Trp Leu Val Asp Val Gly Asn Val Cys Ile
      325
Val Val His Leu Val Gly Ala Tyr Gln Val Phe Cys Gln Pro Ile Tyr
      340
Gln Phe Ala Glu Ala Trp Ala Arg Ser Arg Trp Pro Asp Ser Ala Phe
      355
Val Asn Gly Glu Arg Val Leu Arg Leu Pro Leu Gly Ala Gly Asp Phe
      370
Pro Val Ser Ala Leu Arg Leu Val Trp Arg Thr Ala Tyr Val Val Leu
      385
Thr Ala Val Ala Ala Met Ala Phe Pro Phe Phe Asn Asp Phe Leu Gly
      405
Leu Ile Gly Ala Val Ser Phe Trp Pro Leu Thr Val Tyr Phe Pro Val
      420
Gln Met Tyr Met Ser Gln Ala Lys Val Arg Arg Phe Ser Pro Thr Trp
      435
Thr Trp Met Asn Val Leu Ser Leu Ala Cys Leu Val Val Ser Leu Leu
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Ala Ala Ala Gly Ser Ile Gln Gly Leu Ile Lys Ser Val Ala His Tyr
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Lys Pro Phe Ser Val Ser
      485

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<210> 568

<211> 1383

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<221> CDS

<222> (1)..(1383)

<400> 568

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1				5					10					15		
gtg	acg	gcg	agc	gcg	cac	ata	ata	acg	gcg	gtg	atc	ggc	tcc	ggc	gtg	96
Val	Thr	Ala	Ser	Ala	His	Ile	Ile	Thr	Ala	Val	Ile	Gly	Ser	Gly	Val	
			20					25					30			
ctg	tcg	ctg	gcg	tgg	gcg	ata	gcg	cag	ctg	ggg	tgg	gtg	atc	ggg	ccg	144
Leu	Ser	Leu	Ala	Trp	Ala	Ile	Ala	Gln	Leu	Gly	Trp	Val	Ile	Gly	Pro	
			35				40					45				
gcc	gtg	ctg	gtg	gcg	ttc	tcg	gtc	ata	acc	tgg	ttc	tgc	tcc	agc	ctc	192
Ala	Val	Leu	Val	Ala	Phe	Ser	Val	Ile	Thr	Trp	Phe	Cys	Ser	Ser	Leu	
	50					55					60					
ctc	gcc	gac	tgc	tac	cga	tct	ccc	gac	ccc	gtc	cat	ggc	aag	cgc	aac	240
Leu	Ala	Asp	Cys	Tyr	Arg	Ser	Pro	Asp	Pro	Val	His	Gly	Lys	Arg	Asn	
					70					75					80	
tac	acc	tac	ggc	caa	gcc	gtc	agg	gcc	aac	cta	ggt	gtg	gcc	aag	tac	288
Tyr	Thr	Tyr	Gly	Gln	Ala	Val	Arg	Ala	Asn	Leu	Gly	Val	Ala	Lys	Tyr	
				85					90					95		
agg	ctc	tgc	tcg	gtg	gca	cag	tac	gtc	aat	ctc	gtc	ggc	gtc	acc	att	336
Arg	Leu	Cys	Ser	Val	Ala	Gln	Tyr	Val	Asn	Leu	Val	Gly	Val	Thr	Ile	
			100					105					110			
ggc	tac	acc	atc	act	acg	gcc	atc	agc	atg	ggt	gcg	atc	aaa	cgg	tcc	384
Gly	Tyr	Thr	Ile	Thr	Thr	Ala	Ile	Ser	Met	Gly	Ala	Ile	Lys	Arg	Ser	
			115				120					125				
aac	tgg	ttc	cat	cgc	aac	ggc	cac	gac	gca	gcc	tgc	ttg	gca	tct	gac	432
Asn	Trp	Phe	His	Arg	Asn	Gly	His	Asp	Ala	Ala	Cys	Leu	Ala	Ser	Asp	
	130					135					140					
acg	acc	aac	atg	atc	ata	ata	gct	ggc	atc	caa	ctc	ctc	tcg	cag		480
Thr	Thr	Asn	Met	Ile	Ile	Phe	Ala	Gly	Ile	Gln	Ile	Leu	Leu	Ser	Gln	
					150					155					160	
ctg	ccg	aat	ttt	cac	aaa	att	tgg	tgg	ctc	tcc	att	gtc	gct	gct	gtc	528
Leu	Pro	Asn	Phe	His	Lys	Ile	Trp	Trp	Leu	Ser	Ile	Val	Ala	Ala	Val	
				165					170				175			
atg	tca	ctg	gcc	tac	tca	acc	att	ggc	ctt	ggc	ctc	tcc	att	gca	aaa	576
Met	Ser	Leu	Ala	Tyr	Ser	Thr	Ile	Gly	Leu	Gly	Leu	Ser	Ile	Ala	Lys	
			180					185					190			
att	gca	ggt	ggg	gcc	cac	ccc	gag	gca	acc	ctc	aca	ggg	gtg	act	gtt	624
Ile	Ala	Gly	Gly	Ala	His	Pro	Glu	Ala	Thr	Leu	Thr	Gly	Val	Thr	Val	
			195				200					205				
gga	gtg	gat	gtg	tct	gca	agt	gag	aaa	atc	tgg	aga	act	ttt	cag	tca	672
Gly	Val	Asp	Val	Ser	Ala	Ser	Glu	Lys	Ile	Trp	Arg	Thr	Phe	Gln	Ser	
	210					215					220					
ctt	ggt	gac	att	gcc	ttt	gca	tac	tcc	tac	tcc	aat	gtc	ctc	ata	gaa	720
Leu	Gly	Asp	Ile	Ala	Phe	Ala	Tyr	Ser	Tyr	Ser	Asn	Val	Leu	Ile	Glu	
					230					235					240	
att	cag	gac	acg	ctg	cgg	tcg	agc	ccg	gcg	gag	aac	gag	gtg	atg	aag	768
Ile	Gln	Asp	Thr	Leu	Arg	Ser	Ser	Pro	Ala	Glu	Asn	Glu	Val	Met	Lys	
				245					250					255		
aag	gcg	tcg	ttc	atc	gga	gtc	tcg	acg	acg	acg	acg	ttc	tac	atg	ctg	816
Lys	Ala	Ser	Phe	Ile	Gly	Val	Ser	Thr	Thr	Thr	Thr	Phe	Tyr	Met	Leu	
			260					265					270			
tgc	ggc	gtg	ctc	ggc	tac	gcg	gcg	ttc	ggc	aac	cgc	gcg	ccg	ggg	aac	864
Cys	Gly	Val	Leu	Gly	Tyr	Ala	Ala	Phe	Gly	Asn	Arg	Ala	Pro	Gly	Asn	
						280						285				
ttc	ctc	acc	ggc	ttc	ggc	ttc	tac	gag	ccc	ttc	tgg	ctc	gtc	gac	gtc	912
Phe	Leu	Thr	Gly	Phe	Gly	Phe	Tyr	Glu	Pro	Phe	Trp	Leu	Val	Asp	Val	
						295					300					
ggc	aac	gtc	tgc	atc	gtc	gtc	cac	ctc	gtc	ggc	gcc	tac	cag	gtc	ttc	960
Gly	Asn	Val	Cys	Ile	Val	Val	His	Leu	Val	Gly	Ala	Tyr	Gln	Val	Phe	
					310					315					320	
tgc	cag	ccc	atc	tac	cag	ttc	gcc	gag	gcc	tgg	gcg	cgc	tcg	cgg	tgg	1008
Cys	Gln	Pro	Ile	Tyr	Gln	Phe	Ala	Glu	Ala	Trp	Ala	Arg	Ser	Arg	Trp	
				325					330					335		
ccg	gac	agc	gcc	ttc	gtc	aac	ggc	gag	cgc	gtg	ctc	cgg	ctg	ccg	ctc	1056
Pro	Asp	Ser	Ala	Phe	Val	Asn	Gly	Glu	Arg	Val	Leu	Arg	Leu	Pro	Leu	
			340					345					350			

PF59082SeqList_PF59082.txt

ggc	gcc	ggc	gac	ttc	ccc	gtc	agc	gcg	ctc	cg	ctc	gtc	tgg	cg	acg	1104
Gly	Ala	Gly	Asp	Phe	Pro	Val	Ser	Ala	Leu	Arg	Leu	Val	Trp	Arg	Thr	
		355					360					365				
gcc	tac	gtc	gtg	ctc	acc	gcc	gtc	gcc	gcc	atg	gcg	ttc	ccc	ttc	ttc	1152
Ala	Tyr	Val	Val	Leu	Thr	Ala	Val	Ala	Ala	Met	Ala	Phe	Pro	Phe	Phe	
	370					375					380					
aac	gac	ttc	ctc	ggc	ctc	atc	ggc	gcc	gtc	tcc	ttc	tgg	ccg	ctc	acc	1200
Asn	Asp	Phe	Leu	Gly	Leu	Ile	Gly	Ala	Val	Ser	Phe	Trp	Pro	Leu	Thr	
385				390						395					400	
gtc	tac	ttc	ccc	gtc	cag	atg	tac	atg	tct	cag	gcc	aag	gtc	cgg	cga	1248
Val	Tyr	Phe	Pro	Val	Gln	Met	Tyr	Met	Ser	Gln	Ala	Lys	Val	Arg	Arg	
				405					410					415		
ttc	tcg	ccg	acg	tgg	acg	tgg	atg	aac	gtg	ctc	agc	ctc	gcc	tgc	ctc	1296
Phe	Ser	Pro	Thr	Trp	Thr	Trp	Met	Asn	Val	Leu	Ser	Leu	Ala	Cys	Leu	
			420					425					430			
gtc	gtc	tcc	ctc	ctc	gcc	gcc	ggc	tcc	atc	cag	ggc	ctc	atc	aaa		1344
Val	Val	Ser	Leu	Leu	Ala	Ala	Ala	Gly	Ser	Ile	Gln	Gly	Leu	Ile	Lys	
		435				440					445					
tcc	gtc	gca	cat	tac	aag	cca	ttc	agc	gtc	tcc	tca	tga				1383
Ser	Val	Ala	His	Tyr	Lys	Pro	Phe	Ser	Val	Ser						
	450					455					460					

<210> 569

<211> 460

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<400> 569

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Val	Thr	Ala	Ser	Ala	His	Ile	Ile	Thr	Ala	Val	Ile	Gly	Ser	Gly	Val	
			20					25					30			
Leu	Ser	Leu	Ala	Trp	Ala	Ile	Ala	Gln	Leu	Gly	Trp	Val	Ile	Gly	Pro	
		35					40					45				
Ala	Val	Leu	Val	Ala	Phe	Ser	Val	Ile	Thr	Trp	Phe	Cys	Ser	Ser	Leu	
	50					55					60					
Leu	Ala	Asp	Cys	Tyr	Arg	Ser	Pro	Asp	Pro	Val	His	Gly	Lys	Arg	Asn	
65					70				75						80	
Tyr	Thr	Tyr	Gly	Gln	Ala	Val	Arg	Ala	Asn	Leu	Gly	Val	Ala	Lys	Tyr	
			85						90					95		
Arg	Leu	Cys	Ser	Val	Ala	Gln	Tyr	Val	Asn	Leu	Val	Gly	Val	Thr	Ile	
			100					105					110			
Gly	Tyr	Thr	Ile	Thr	Thr	Ala	Ile	Ser	Met	Gly	Ala	Ile	Lys	Arg	Ser	
		115				120						125				
Asn	Trp	Phe	His	Arg	Asn	Gly	His	Asp	Ala	Ala	Cys	Leu	Ala	Ser	Asp	
	130					135					140					
Thr	Thr	Asn	Met	Ile	Ile	Phe	Ala	Gly	Ile	Gln	Ile	Leu	Leu	Ser	Gln	
145					150				155						160	
Leu	Pro	Asn	Phe	His	Lys	Ile	Trp	Trp	Leu	Ser	Ile	Val	Ala	Ala	Val	
			165						170					175		
Met	Ser	Leu	Ala	Tyr	Ser	Thr	Ile	Gly	Leu	Gly	Leu	Ser	Ile	Ala	Lys	
			180					185					190			
Ile	Ala	Gly	Gly	Ala	His	Pro	Glu	Ala	Thr	Leu	Thr	Gly	Val	Thr	Val	
		195					200					205				
Gly	Val	Asp	Val	Ser	Ala	Ser	Glu	Lys	Ile	Trp	Arg	Thr	Phe	Gln	Ser	
	210					215					220					
Leu	Gly	Asp	Ile	Ala	Phe	Ala	Tyr	Ser	Tyr	Ser	Asn	Val	Leu	Ile	Glu	
225					230					235					240	
Ile	Gln	Asp	Thr	Leu	Arg	Ser	Ser	Pro	Ala	Glu	Asn	Glu	Val	Met	Lys	
			245						250					255		
Lys	Ala	Ser	Phe	Ile	Gly	Val	Ser	Thr	Thr	Thr	Thr	Phe	Tyr	Met	Leu	
			260					265					270			
Cys	Gly	Val	Leu	Gly	Tyr	Ala	Ala	Phe	Gly	Asn	Arg	Ala	Pro	Gly	Asn	
	275						280					285				
Phe	Leu	Thr	Gly	Phe	Gly	Phe	Tyr	Glu	Pro	Phe	Trp	Leu	Val	Asp	Val	
	290					295					300					
Gly	Asn	Val	Cys	Ile	Val	Val	His	Leu	Val	Gly	Ala	Tyr	Gln	Val	Phe	
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Cys	Gln	Pro	Ile	Tyr	Gln	Phe	Ala	Glu	Ala	Trp	Ala	Arg	Ser	Arg	Trp	

PF59082SeqList_PF59082.txt

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          325          330          335
Pro Asp Ser Ala Phe Val Asn Gly Glu Arg Val Leu Arg Leu Pro Leu
          340          345          350
Gly Ala Gly Asp Phe Pro Val Ser Ala Leu Arg Leu Val Trp Arg Thr
          355          360          365
Ala Tyr Val Val Leu Thr Ala Val Ala Ala Met Ala Phe Pro Phe Phe
          370          375          380
Asn Asp Phe Leu Gly Leu Ile Gly Ala Val Ser Phe Trp Pro Leu Thr
          385          390          395
Val Tyr Phe Pro Val Gln Met Tyr Met Ser Gln Ala Lys Val Arg Arg
          400          405          410
Phe Ser Pro Thr Trp Thr Trp Met Asn Val Leu Ser Leu Ala Cys Leu
          415          420          425
Val Val Ser Leu Leu Ala Ala Ala Gly Ser Ile Gln Gly Leu Ile Lys
          430          435          440
Ser Val Ala His Tyr Lys Pro Phe Ser Val Ser Ser
          445          450          455          460

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<210> 570
 <211> 1461
 <212> DNA
 <213> Ricinus communis

<220>
 <221> CDS
 <222> (1)..(1461)

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Met Val Glu Asn Thr Ala Ala Lys Asn His Pro His Gln Val Phe Asp
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gta tcc att aac atg caa act caa gtt gtt ggc tct aaa tgg ctt gat      96
Val Ser Ile Asn Met Gln Thr Gln Val Val Gly Ser Lys Trp Leu Asp
20          25          30
gat gat ggc cgt acc aag aga act ggg acc gtg tgg act gca agt gcc      144
Asp Asp Gly Arg Thr Lys Arg Thr Gly Thr Val Trp Thr Ala Ser Ala
35          40          45
cac atc ata aca gca gtg ata ggg tct gga gtt ctg tct tta gct tgg      192
His Ile Ile Thr Ala Val Ile Gly Ser Gly Val Leu Ser Leu Ala Trp
50          55          60
gca atc gct cag ctt ggg tgg att gct ggc cct gct gtt atg ttc ttg      240
Ala Ile Ala Gln Leu Gly Trp Ile Ala Gly Pro Ala Val Met Phe Leu
65          70          75          80
ttc tct tta gtc act tac tat act tct act ctt cta tct gcc tgc tac      288
Phe Ser Leu Val Thr Tyr Tyr Thr Ser Thr Leu Leu Ser Ala Cys Tyr
85          90          95
cgt tct ggt gat cct gtc aat ggc aag agg aac tat act tat atg gac      336
Arg Ser Gly Asp Pro Val Asn Gly Lys Arg Asn Tyr Thr Tyr Met Asp
100          105          110
gct gtt cgc acc aat ctt ggt gga gct aag gtc aag tta tgt gga ttt      384
Ala Val Arg Thr Asn Leu Gly Gly Ala Lys Val Lys Leu Cys Gly Phe
115          120          125
gtt cag tat ctg aat ctt ttc gga gtt gcc att gga tac act atc gcg      432
Val Gln Tyr Leu Asn Leu Phe Gly Val Ala Ile Gly Tyr Thr Ile Ala
130          135          140
tcg tct att agt atg atg gct ata aag agg tct aat tgt ttt cac aag      480
Ser Ser Ile Ser Met Met Ala Ile Lys Arg Ser Asn Cys Phe His Lys
145          150          155          160
agc gga ggc aaa aac cca tgc cat ata aat gcc aat cct tac atg att      528
Ser Gly Gly Lys Asn Pro Cys His Ile Asn Ala Asn Pro Tyr Met Ile
165          170          175
gca ttc gga att gct gaa atc att ttc tct caa att cct gat ttt gat      576
Ala Phe Gly Ile Ala Glu Ile Ile Phe Ser Gln Ile Pro Asp Phe Asp
180          185          190
cag cta tgg tgg ctc tcc att ctt gct gca gtc atg tcc ttt act tac      624
Gln Leu Trp Trp Leu Ser Ile Leu Ala Ala Val Met Ser Phe Thr Tyr
195          200          205
tca acc att ggt ctt gga ctt gga att gct caa gtt gta gaa aat gga      672
Ser Thr Ile Gly Leu Gly Leu Gly Ile Ala Gln Val Val Glu Asn Gly

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PF59082SeqList_PF59082.txt

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225	cca acc cag aag ata tgg agg agc ttc caa gct ctt ggt gac att gct	768
Pro Thr Gln Lys Ile Trp Arg Ser Phe Gln Ala Leu Gly Asp Ile Ala		
230	ttc gcc tat tct tat tcc ata atc ctt att gaa att cag gac aca gtc	816
Phe Ala Tyr Ser Tyr Ser Ile Ile Leu Ile Glu Ile Gln Asp Thr Val		
235	aga tcc cca cct tca gag tcc aag aca atg aag aaa gca act ctg ata	864
Arg Ser Pro Pro Ser Glu Ser Lys Thr Met Lys Lys Ala Thr Leu Ile		
240	agt gtg gca gta aca acc ctt ttc tac atg cta tgt ggt tgc ttt ggc	912
Ser Val Ala Val Thr Thr Leu Phe Tyr Met Leu Cys Gly Cys Phe Gly		
245	tat gct gct ttt gga gac atg tct cct gga aat cta cta aca ggg ttt	960
Tyr Ala Ala Phe Gly Asp Met Ser Pro Gly Asn Leu Leu Thr Gly Phe		
250	ggc ttc tac aac cca tat tgg cta ctt gac att gct aat gtt gca atc	1008
Gly Phe Tyr Asn Pro Tyr Trp Leu Leu Asp Ile Ala Asn Val Ala Ile		
255	gta gtc cat ctt gtt ggc gcg tac caa gtc tat tgc caa ccc ttg ttt	1056
Val Val His Leu Val Gly Ala Tyr Gln Val Tyr Cys Gln Pro Leu Phe		
260	gcc ttc gtt gaa aaa gca gct gca caa aga tat cca gac agt gga ttc	1104
Ala Phe Val Glu Lys Ala Ala Ala Gln Arg Tyr Pro Asp Ser Gly Phe		
265	att act aaa gat atc aaa atc cca gtt cct ggt ttc cgc ccc ttt aat	1152
Ile Thr Lys Asp Ile Lys Ile Pro Val Pro Gly Phe Arg Pro Phe Asn		
270	ctt aac ctc ttt aga tcg gta tgg agg aca ctt ttt gtg gtc ttc aca	1200
Leu Asn Leu Phe Arg Ser Val Trp Arg Thr Leu Phe Val Val Phe Thr		
275	act gtg att tcc atg ctc ctt ccg ttc ttt aac gac ata gtt ggt ttg	1248
Thr Val Ile Ser Met Leu Leu Pro Phe Phe Asn Asp Ile Val Gly Leu		
280	ctt gga gct ttg gga ttt tgg cca ctc acg gtt tac ttc cca gta gaa	1296
Leu Gly Ala Leu Gly Phe Trp Pro Leu Thr Val Tyr Phe Pro Val Glu		
285	atg tat ata gca caa aag aag atc cca aaa tgg agc aca aga tgg ctc	1344
Met Tyr Ile Ala Gln Lys Lys Ile Pro Lys Trp Ser Thr Arg Trp Leu		
290	tgc ctg caa ata cta agc gct gct tgc ctt gtt att aca ata gct gct	1392
Cys Leu Gln Ile Leu Ser Ala Ala Cys Leu Val Ile Thr Ile Ala Ala		
295	gct gct gga tcc att gct ggg gtt gtt ggt gat ctc aag tct gtc aag	1440
Ala Ala Gly Ser Ile Ala Gly Val Val Gly Asp Leu Lys Ser Val Lys		
300	cca ttc cag acc tct tac tga	1461
Pro Phe Gln Thr Ser Tyr		

<210> 571

<211> 486

<212> PRT

<213> Ricinus communis

<400> 571

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35 His Ile Ile Thr Ala Val Ile Gly Ser Gly Val Leu Ser Leu Ala Trp	
50 Ala Ile Ala Gln Leu Gly Trp Ile Ala Gly Pro Ala Val Met Phe Leu	
65 65 70 75 80	

PF59082SeqList_PF59082.txt

Phe Ser Leu Val Thr Tyr Tyr Thr Ser Thr Leu Leu Ser Ala Cys Tyr
 85 90 95
 Arg Ser Gly Asp Pro Val Asn Gly Lys Arg Asn Tyr Thr Tyr Met Asp
 100 105 110
 Ala Val Arg Thr Asn Leu Gly Gly Ala Lys Val Lys Leu Cys Gly Phe
 115 120 125
 Val Gln Tyr Leu Asn Leu Phe Gly Val Ala Ile Gly Tyr Thr Ile Ala
 130 135 140
 Ser Ser Ile Ser Met Met Ala Ile Lys Arg Ser Asn Cys Phe His Lys
 145 150 155 160
 Ser Gly Gly Lys Asn Pro Cys His Ile Asn Ala Asn Pro Tyr Met Ile
 165 170 175
 Ala Phe Gly Ile Ala Glu Ile Ile Phe Ser Gln Ile Pro Asp Phe Asp
 180 185 190
 Gln Leu Trp Trp Leu Ser Ile Leu Ala Ala Val Met Ser Phe Thr Tyr
 195 200 205
 Ser Thr Ile Gly Leu Gly Leu Gly Ile Ala Gln Val Val Glu Asn Gly
 210 215 220
 Lys Ala Met Gly Ser Val Thr Gly Ile Ser Ile Gly Ala Asn Val Thr
 225 230 235 240
 Pro Thr Gln Lys Ile Trp Arg Ser Phe Gln Ala Leu Gly Asp Ile Ala
 245 250 255
 Phe Ala Tyr Ser Tyr Ser Ile Ile Leu Ile Glu Ile Gln Asp Thr Val
 260 265 270
 Arg Ser Pro Ser Glu Ser Lys Thr Met Lys Lys Ala Thr Leu Ile
 275 280 285
 Ser Val Ala Val Thr Thr Leu Phe Tyr Met Leu Cys Gly Cys Phe Gly
 290 295 300
 Tyr Ala Ala Phe Gly Asp Met Ser Pro Gly Asn Leu Leu Thr Gly Phe
 305 310 315 320
 Gly Phe Tyr Asn Pro Tyr Trp Leu Leu Asp Ile Ala Asn Val Ala Ile
 325 330 335
 Val Val His Leu Val Gly Ala Tyr Gln Val Tyr Cys Gln Pro Leu Phe
 340 345 350
 Ala Phe Val Glu Lys Ala Ala Ala Gln Arg Tyr Pro Asp Ser Gly Phe
 355 360 365
 Ile Thr Lys Asp Ile Lys Ile Pro Val Pro Gly Phe Arg Pro Phe Asn
 370 375 380
 Leu Asn Leu Phe Arg Ser Val Trp Arg Thr Leu Phe Val Val Phe Thr
 385 390 395 400
 Thr Val Ile Ser Met Leu Leu Pro Phe Phe Asn Asp Ile Val Gly Leu
 405 410 415
 Leu Gly Ala Leu Gly Phe Trp Pro Leu Thr Val Tyr Phe Pro Val Glu
 420 425 430
 Met Tyr Ile Ala Gln Lys Lys Ile Pro Lys Trp Ser Thr Arg Trp Leu
 435 440 445
 Cys Leu Gln Ile Leu Ser Ala Ala Cys Leu Val Ile Thr Ile Ala Ala
 450 455 460
 Ala Ala Gly Ser Ile Ala Gly Val Val Gly Asp Leu Lys Ser Val Lys
 465 470 475 480
 Pro Phe Gln Thr Ser Tyr
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 <211> 1410
 <212> DNA
 <213> Solanum tuberosum

<220>
 <221> CDS
 <222> (1)..(1410)

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 gaa aat gga gac gtt caa aaa aac ttt gat gat gat gga cgt gaa aaa 96
 Glu Asn Gly Asp Val Gln Lys Asn Phe Asp Asp Asp Gly Arg Glu Lys
 20 25 30

PF59082SeqList_PF59082.txt																
aga	aca	ggg	act	ttg	ttg	act	gct	agt	gca	cat	att	att	act	gct	gtg	144
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att	ggt	tca	gga	gta	ctt	tca	cta	gca	tggt	gct	ata	gct	caa	tta	gga	192
Ile	Gly	Ser	Gly	Val	Leu	Ser	Leu	Ala	Trp	Ala	Ile	Ala	Gln	Leu	Gly	
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Trp	Val	Ala	Gly	Pro	Ala	Val	Leu	Phe	Ala	Phe	Ser	Phe	Ile	Thr	Tyr	
	65				70				75						80	
ttc	act	tcc	aca	ctt	gct	gcc	gac	tgt	tac	agg	tct	ccg	gga	ccg	att	288
Phe	Thr	Ser	Thr	Leu	Leu	Ala	Asp	Cys	Tyr	Arg	Ser	Pro	Gly	Pro	Ile	
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tcc	ggc	aag	aga	aac	tat	act	tat	atg	gac	gtt	gtc	cgc	tct	cac	tta	336
Ser	Gly	Lys	Arg	Asn	Tyr	Thr	Tyr	Met	Asp	Val	Val	Arg	Ser	His	Leu	
		100						105					110			
gga	ggt	gtg	aag	gtg	aca	ttg	tgt	gga	att	gca	caa	tat	gct	aac	ctt	384
Gly	Gly	Val	Lys	Val	Thr	Leu	Cys	Gly	Ile	Ala	Gln	Tyr	Ala	Asn	Leu	
		115					120					125				
gtt	gga	gtt	aca	att	gga	tat	aca	att	aca	gca	tct	att	agt	atg	gtg	432
Val	Gly	Val	Thr	Ile	Gly	Tyr	Thr	Ile	Thr	Ala	Ser	Ile	Ser	Met	Val	
	130					135					140					
gct	gta	aag	agg	tca	aat	tgt	ttt	cac	aaa	aat	ggg	cat	gaa	gca	agt	480
Ala	Val	Lys	Arg	Ser	Asn	Cys	Phe	His	Lys	Asn	Gly	His	Glu	Ala	Ser	
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tcg	tca	att	gaa	agt	tac	cca	tac	atg	ata	ata	ttt	gca	gta	att	caa	528
Cys	Ser	Ile	Glu	Ser	Tyr	Pro	Tyr	Met	Ile	Ile	Phe	Ala	Val	Ile	Gln	
				165				170						175		
ata	gtt	ctt	agc	caa	att	cca	aat	ttc	cac	aag	ctc	tca	tggt	tta	tca	576
Ile	Val	Leu	Ser	Gln	Ile	Pro	Asn	Phe	His	Lys	Leu	Ser	Trp	Leu	Ser	
			180					185					190			
att	ctt	gct	gct	gtt	atg	tca	ttt	act	tat	gct	tct	att	gggt	ctt	gga	624
Ile	Leu	Ala	Ala	Val	Met	Ser	Phe	Thr	Tyr	Ala	Ser	Ile	Gly	Leu	Gly	
		195					200					205				
cta	tcc	ata	gcc	aaa	gcc	tca	gggt	gtg	ggg	cac	cat	gtg	aag	aca	gcc	672
Leu	Ser	Ile	Ala	Lys	Ala	Ser	Gly	Val	Gly	His	His	Val	Lys	Thr	Ala	
	210					215					220					
cta	aca	ggg	gtg	gta	gta	gggt	gtg	gat	gta	tct	gga	aca	gaa	aaa	gta	720
Leu	Thr	Gly	Val	Val	Val	Gly	Val	Asp	Val	Ser	Gly	Thr	Glu	Lys	Val	
	225				230				235						240	
tggt	aga	agt	ttc	caa	gct	att	gga	gat	att	gca	ttt	gct	tat	gct	tat	768
Trp	Arg	Ser	Phe	Gln	Ala	Ile	Gly	Asp	Ile	Ala	Phe	Ala	Tyr	Ala	Tyr	
				245				250						255		
tcc	aca	gtt	ctt	att	gaa	ata	cag	gac	aca	ctg	aaa	tca	tca	cca	tca	816
Ser	Thr	Val	Leu	Ile	Glu	Ile	Gln	Asp	Thr	Leu	Lys	Ser	Ser	Pro	Ser	
			260					265					270			
gaa	agc	aag	gta	atg	aag	aga	gcc	tca	cta	gct	gga	gtt	tcc	acc	aca	864
Glu	Ser	Lys	Val	Met	Lys	Arg	Ala	Ser	Leu	Ala	Gly	Val	Ser	Thr	Thr	
		275					280					285				
act	tta	ttc	tat	gta	ctt	tgt	gggt	acc	att	ggc	tat	gca	gcc	ttt	gga	912
Thr	Leu	Phe	Tyr	Val	Leu	Cys	Gly	Thr	Ile	Gly	Tyr	Ala	Ala	Phe	Gly	
	290					295					300					
aac	aat	gct	cca	gga	aat	ttt	ctt	act	gga	ttt	gggt	ttc	tat	gaa	cct	960
Asn	Asn	Ala	Pro	Gly	Asn	Phe	Leu	Thr	Gly	Phe	Gly	Phe	Tyr	Glu	Pro	
				310						315				320		
ttt	tggt	cta	att	gac	ttt	gcc	aac	gtc	tcg	atc	gct	gtc	cac	ctt	gtc	1008
Phe	Trp	Leu	Ile	Asp	Phe	Ala	Asn	Val	Cys	Ile	Ala	Val	His	Leu	Val	
				325				330						335		
gga	gct	tat	cag	gtt	ttc	tcg	caa	cca	tta	tat	gga	ttc	gtg	gag	gggt	1056
Gly	Ala	Tyr	Gln	Val	Phe	Cys	Gln	Pro	Leu	Tyr	Gly	Phe	Val	Glu	Gly	
			340					345					350			
cgt	tcg	agc	gaa	cga	tggt	cca	gac	agc	aaa	ttc	ata	acc	tca	gaa	tac	1104
Arg	Cys	Ser	Glu	Arg	Trp	Pro	Asp	Ser	Lys	Phe	Ile	Thr	Ser	Glu	Tyr	
		355					360					365				
gcg	atg	caa	gtt	cca	tggt	tgt	ggc	act	tac	aac	ctc	aac	tta	ttc	agg	1152
Ala	Met	Gln	Val	Pro	Trp	Cys	Gly	Thr	Tyr	Asn	Leu	Asn	Leu	Phe	Arg	
	370					375					380					
ctg	gtg	tggt	aga	aca	aca	tat	gtt	ata	gtg	aca	gcg	gtg	att	gca	atg	1200
Leu	Val	Trp	Arg	Thr	Thr	Tyr	Val	Ile	Val	Thr	Ala	Val	Ile	Ala	Met	
	385				390					395					400	

PF59082SeqList_PF59082.txt

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Ile Phe Pro Phe Phe Asn Asp Phe Leu Gly Leu Ile Gly Ala Ala Ser	
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ttc tat cca tta acc gtt tac ttc cca ata gag atg tac att gct cag	1296
Phe Tyr Pro Leu Thr Val Tyr Phe Pro Ile Glu Met Tyr Ile Ala Gln	
	420
aga aag ata cca aag tat tct ttc aca tgg gta tgg ctg aaa ata ttg	1344
Arg Lys Ile Pro Lys Tyr Ser Phe Thr Trp Val Trp Leu Lys Ile Leu	
	435
agt tgg act tgt ttg atc agt atc act tgt tgc agc tgc tgg atc gat	1392
Ser Trp Thr Cys Leu Ile Ser Ile Thr Cys Cys Ser Cys Trp Ile Asp	
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cca ggg act tgc cac tga	1410
Pro Gly Thr Cys His	
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<211> 469

<212> PRT

<213> Solanum tuberosum

<400> 573

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Ile Gly Ser Gly Val Leu Ser Leu Ala Trp Ala Ile Ala Gln Leu Gly	
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Trp Val Ala Gly Pro Ala Val Leu Phe Ala Phe Ser Phe Ile Thr Tyr	
	65
Phe Thr Ser Thr Leu Leu Ala Asp Cys Tyr Arg Ser Pro Gly Pro Ile	
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Ser Gly Lys Arg Asn Tyr Thr Tyr Met Asp Val Val Arg Ser His Leu	
	95
Gly Gly Val Lys Val Thr Leu Cys Gly Ile Ala Gln Tyr Ala Asn Leu	
	110
Val Gly Val Thr Ile Gly Tyr Thr Ile Thr Ala Ser Ile Ser Met Val	
	125
Ala Val Lys Arg Ser Asn Cys Phe His Lys Asn Gly His Glu Ala Ser	
	140
Cys Ser Ile Glu Ser Tyr Pro Tyr Met Ile Ile Phe Ala Val Ile Gln	
	155
Ile Val Leu Ser Gln Ile Pro Asn Phe His Lys Leu Ser Trp Leu Ser	
	170
Ile Leu Ala Ala Val Met Ser Phe Thr Tyr Ala Ser Ile Gly Leu Gly	
	185
Leu Ser Ile Ala Lys Ala Ser Gly Val Gly His His Val Lys Thr Ala	
	200
Leu Thr Gly Val Val Val Gly Val Asp Val Ser Gly Thr Glu Lys Val	
	215
Trp Arg Ser Phe Gln Ala Ile Gly Asp Ile Ala Phe Ala Tyr Ala Tyr	
	230
Ser Thr Val Leu Ile Glu Ile Gln Asp Thr Leu Lys Ser Ser Pro Ser	
	245
Glu Ser Lys Val Met Lys Arg Ala Ser Leu Ala Gly Val Ser Thr Thr	
	260
Thr Leu Phe Tyr Val Leu Cys Gly Thr Ile Gly Tyr Ala Ala Phe Gly	
	275
Asn Asn Ala Pro Gly Asn Phe Leu Thr Gly Phe Gly Phe Tyr Glu Pro	
	290
Phe Trp Leu Ile Asp Phe Ala Asn Val Cys Ile Ala Val His Leu Val	
	305
Gly Ala Tyr Gln Val Phe Cys Gln Pro Leu Tyr Gly Phe Val Glu Gly	
	320
Arg Cys Ser Glu Arg Trp Pro Asp Ser Lys Phe Ile Thr Ser Glu Tyr	
	335
Ala Met Gln Val Pro Trp Cys Gly Thr Tyr Asn Leu Asn Leu Phe Arg	
	350

PF59082SeqList_PF59082.txt

370
 Leu Val Trp Arg Thr Thr Tyr Val Ile Val Thr Ala Val Ile Ala Met
 385 390 400
 Ile Phe Pro Phe Phe Asn Asp Phe Leu Gly Leu Ile Gly Ala Ala Ser
 410 415
 Phe Tyr Pro Leu Thr Val Tyr Phe Pro Ile Glu Met Tyr Ile Ala Gln
 420 425 430
 Arg Lys Ile Pro Lys Tyr Ser Phe Thr Trp Val Trp Leu Lys Ile Leu
 435 440 445
 Ser Trp Thr Cys Leu Ile Ser Ile Thr Cys Cys Ser Cys Trp Ile Asp
 450 455 460
 Pro Gly Thr Cys His
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<210> 574

<211> 1452

<212> DNA

<213> Medicago truncatula

<220>

<221> CDS

<222> (1)..(1452)

<400> 574

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gtt ggc atg gag ggg ggt aca tct tta caa gat gac tcc aaa tac tat	96
Val Gly Met Glu Gly Gly Thr Ser Leu Gln Asp Asp Ser Lys Tyr Tyr	
20 25 30	
gac gat gat ggc cgt gtt aaa cgg aca gga acc att tgg act aca tgc	144
Asp Asp Asp Gly Arg Val Lys Arg Thr Gly Thr Ile Trp Thr Thr Cys	
35 40 45	
tcc cac ata ata aca gct gtg ata gga tct ggg gtg ctc tcc tta gcc	192
Ser His Ile Ile Thr Ala Val Ile Gly Ser Gly Val Leu Ser Leu Ala	
50 55 60	
tgg tct ata gct cag atg ggt tgg gtt gct ggt cct gga gcc atg ata	240
Trp Ser Ile Ala Gln Met Gly Trp Val Ala Gly Pro Gly Ala Met Ile	
65 70 75 80	
ttt ttc agc atc atc act ctg tat act tca tca ttt ctc gct gat tgt	288
Phe Phe Ser Ile Ile Thr Leu Tyr Thr Ser Ser Phe Leu Ala Asp Cys	
85 90 95	
tat cgt tgt ggt gac acc gaa ttt gga aag aga aac tat act ttc atg	336
Tyr Arg Cys Gly Asp Thr Glu Phe Gly Lys Arg Asn Tyr Thr Phe Met	
100 105 110	
gat gca gtt agt aac att ctt ggc ggg ccc agt gtt aag att tgt ggg	384
Asp Ala Val Ser Asn Ile Leu Gly Gly Pro Ser Val Lys Ile Cys Gly	
115 120 125	
ata gtt cag tat ttg aat ctt ttc gga agt gca ata ggg tac aat att	432
Ile Val Gln Tyr Leu Asn Leu Phe Gly Ser Ala Ile Gly Tyr Asn Ile	
130 135 140	
gca gct gcc atg agc atg atg gaa atc aaa aag tct tta tgt gtc cat	480
Ala Ala Ala Met Ser Met Met Glu Ile Lys Lys Ser Leu Cys Val His	
145 150 155 160	
aca tct gat gga aaa gac gca tgt cat att tca ggc aac cca tac atg	528
Thr Ser Asp Gly Lys Asp Ala Cys His Ile Ser Gly Asn Pro Tyr Met	
165 170 175	
att gct ttt ggc gtg gca caa ctt ttc ctt tct caa att cca gat ttt	576
Ile Ala Phe Gly Val Ala Gln Leu Phe Leu Ser Gln Ile Pro Asp Phe	
180 185 190	
cat aac atg tgg tgg ctc tca ata gtt gct gca gtc atg tct ttc ttc	624
His Asn Met Trp Trp Leu Ser Ile Val Ala Ala Val Met Ser Phe Phe	
195 200 205	
tac tcc aca att gct ctt gct ctt gga att tcc aaa gtt gca gaa aac	672
Tyr Ser Thr Ile Ala Leu Ala Leu Gly Ile Ser Lys Val Ala Glu Asn	
210 215 220	
ggt act gtt atg ggt agc ctc aca gga gta agc gtc gga aca gtg acc	720
Gly Thr Val Met Gly Ser Leu Thr Gly Val Ser Val Gly Thr Val Thr	
225 230 235 240	

PF59082SeqList_PF59082.txt

ccg	gcc	caa	aaa	gta	tgg	ggg	ggt	ttc	caa	ggt	ctt	gga	aac	atc	gcc	768
Pro	Ala	Gln	Lys	Val	Trp	Gly	Val	Phe	Gln	Gly	Leu	Gly	Asn	Ile	Ala	
				245				250						255		
ttt	gct	tat	tca	tat	tct	ttt	ggt	ctc	ctg	gaa	att	cag	gac	aca	atc	816
Phe	Ala	Tyr	Ser	Tyr	Ser	Phe	Val	Leu	Leu	Glu	Ile	Gln	Asp	Thr	Ile	
			260					265					270			
aaa	tct	cca	cca	tca	gaa	gga	aaa	gca	atg	aag	ata	gct	gcg	aag	ata	864
Lys	Ser	Pro	Pro	Ser	Glu	Gly	Lys	Ala	Met	Lys	Ile	Ala	Ala	Lys	Ile	
		275				280						285				
agt	att	gca	gta	act	aca	aca	ttt	tat	ttg	ctc	tgt	ggc	tgc	atg	gga	912
Ser	Ile	Ala	Val	Thr	Thr	Thr	Phe	Tyr	Leu	Leu	Cys	Gly	Cys	Met	Gly	
	290					295					300					
tat	gct	gct	ttt	gga	gac	aat	gcg	cca	ggc	aac	ctg	ctc	gcc	gga	ttt	960
Tyr	Ala	Ala	Phe	Gly	Asp	Asn	Ala	Pro	Gly	Asn	Leu	Leu	Ala	Gly	Phe	
305				310					315						320	
ggt	gtc	tca	aaa	gca	tat	tgg	ggt	gta	gat	gct	gcc	aat	gct	gct	atc	1008
Gly	Val	Ser	Lys	Ala	Tyr	Trp	Val	Val	Asp	Ala	Ala	Asn	Ala	Ala	Ile	
			325						330				335			
ggt	att	cac	ctt	ttt	gga	gca	tac	caa	gtg	tat	gcc	caa	ccc	cta	ttt	1056
Val	Ile	His	Leu	Phe	Gly	Ala	Tyr	Gln	Val	Tyr	Ala	Gln	Pro	Leu	Phe	
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gct	ttc	gtc	gag	aaa	gag	gca	gca	aaa	aaa	tgg	ccc	aaa	att	gac	aga	1104
Ala	Phe	Val	Glu	Lys	Glu	Ala	Ala	Lys	Lys	Trp	Pro	Lys	Ile	Asp	Arg	
		355				360						365				
gaa	ttc	aaa	ggt	aaa	atc	cct	ggt	ttg	cca	gtc	tac	agt	caa	aac	ata	1152
Glu	Phe	Lys	Val	Lys	Ile	Pro	Gly	Leu	Pro	Val	Tyr	Ser	Gln	Asn	Ile	
	370					375					380					
ttt	tcg	tta	ggt	tgg	agg	aca	gtg	ttt	ggt	atc	atc	tcc	act	ctc	atc	1200
Phe	Ser	Leu	Val	Trp	Arg	Thr	Val	Phe	Val	Ile	Ile	Ser	Thr	Leu	Ile	
385					390									400		
gca	atg	ttg	att	cca	ttt	ttc	aac	gac	gtt	ttg	gga	gtg	att	ggg	gca	1248
Ala	Met	Leu	Ile	Pro	Phe	Phe	Asn	Asp	Val	Leu	Gly	Val	Ile	Gly	Ala	
			405					410						415		
ttg	gga	ttt	tgg	cct	tta	act	gtt	tac	ttt	cct	gtg	gag	atg	tat	atc	1296
Leu	Gly	Phe	Trp	Pro	Leu	Thr	Val	Tyr	Phe	Pro	Val	Glu	Met	Tyr	Ile	
			420					425					430			
gta	caa	atg	aag	atc	cca	aaa	tgg	agt	agg	aag	tgg	att	att	ctg	gaa	1344
Val	Gln	Met	Lys	Ile	Pro	Lys	Trp	Ser	Arg	Lys	Trp	Ile	Ile	Leu	Glu	
		435					440					445				
ata	atg	agt	act	ttc	tgc	ctc	att	gta	tct	att	gtg	gct	ggg	ctt	ggc	1392
Ile	Met	Ser	Thr	Phe	Cys	Leu	Ile	Val	Ser	Ile	Val	Ala	Gly	Leu	Gly	
	450				455						460					
tca	ttg	gtc	ggt	gtc	tgg	atc	gac	ctg	cag	aaa	tac	aaa	cca	ttc	agc	1440
Ser	Leu	Val	Gly	Val	Trp	Ile	Asp	Leu	Gln	Lys	Tyr	Lys	Pro	Phe	Ser	
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Leu	Ser	Asn														

<210> 575

<211> 483

<212> PRT

<213> Medicago truncatula

<400> 575

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Val	Gly	Met	Glu	Gly	Gly	Thr	Ser	Leu	Gln	Asp	Asp	Ser	Lys	Tyr	Tyr	
			20					25					30			
Asp	Asp	Asp	Gly	Arg	Val	Lys	Arg	Thr	Gly	Thr	Ile	Trp	Thr	Thr	Cys	
		35					40					45				
Ser	His	Ile	Ile	Thr	Ala	Val	Ile	Gly	Ser	Gly	Val	Leu	Ser	Leu	Ala	
	50				55						60					
Trp	Ser	Ile	Ala	Gln	Met	Gly	Trp	Val	Ala	Gly	Pro	Gly	Ala	Met	Ile	
65					70					75					80	
Phe	Phe	Ser	Ile	Ile	Thr	Leu	Tyr	Thr	Ser	Ser	Phe	Leu	Ala	Asp	Cys	
			85						90					95		
Tyr	Arg	Cys	Gly	Asp	Thr	Glu	Phe	Gly	Lys	Arg	Asn	Tyr	Thr	Phe	Met	
			100					105					110			

PF59082SeqList_PF59082.txt

Asp Ala Val Ser Asn Ile Leu Gly Gly Pro Ser Val Lys Ile Cys Gly
 115 120 125
 Ile Val Gln Tyr Leu Asn Leu Phe Gly Ser Ala Ile Gly Tyr Asn Ile
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 Ala Ala Ala Met Ser Met Met Glu Ile Lys Lys Ser Leu Cys Val His
 145 150 155 160
 Thr Ser Asp Gly Lys Asp Ala Cys His Ile Ser Gly Asn Pro Tyr Met
 165 170 175
 Ile Ala Phe Gly Val Ala Gln Leu Phe Leu Ser Gln Ile Pro Asp Phe
 180 185 190
 His Asn Met Trp Trp Leu Ser Ile Val Ala Ala Val Met Ser Phe Phe
 195 200 205
 Tyr Ser Thr Ile Ala Leu Ala Leu Gly Ile Ser Lys Val Ala Glu Asn
 210 215 220
 Gly Thr Val Met Gly Ser Leu Thr Gly Val Ser Val Gly Thr Val Thr
 225 230 235 240
 Pro Ala Gln Lys Val Trp Gly Val Phe Gln Gly Leu Gly Asn Ile Ala
 245 250 255
 Phe Ala Tyr Ser Tyr Ser Phe Val Leu Glu Ile Gln Asp Thr Ile
 260 265 270
 Lys Ser Pro Pro Ser Glu Gly Lys Ala Met Lys Ile Ala Ala Lys Ile
 275 280 285
 Ser Ile Ala Val Thr Thr Thr Phe Tyr Leu Leu Cys Gly Cys Met Gly
 290 295 300
 Tyr Ala Ala Phe Gly Asp Asn Ala Pro Gly Asn Leu Leu Ala Gly Phe
 305 310 315 320
 Gly Val Ser Lys Ala Tyr Trp Val Val Asp Ala Ala Asn Ala Ala Ile
 325 330 335
 Val Ile His Leu Phe Gly Ala Tyr Gln Val Tyr Ala Gln Pro Leu Phe
 340 345 350
 Ala Phe Val Glu Lys Glu Ala Ala Lys Lys Trp Pro Lys Ile Asp Arg
 355 360 365
 Glu Phe Lys Val Lys Ile Pro Gly Leu Pro Val Tyr Ser Gln Asn Ile
 370 375 380
 Phe Ser Leu Val Trp Arg Thr Val Phe Val Ile Ile Ser Thr Leu Ile
 385 390 395 400
 Ala Met Leu Ile Pro Phe Phe Asn Asp Val Leu Gly Val Ile Gly Ala
 405 410 415
 Leu Gly Phe Trp Pro Leu Thr Val Tyr Phe Pro Val Glu Met Tyr Ile
 420 425 430
 Val Gln Met Lys Ile Pro Lys Trp Ser Arg Lys Trp Ile Ile Leu Glu
 435 440 445
 Ile Met Ser Thr Phe Cys Leu Ile Val Ser Ile Val Ala Gly Leu Gly
 450 455 460
 Ser Leu Val Gly Val Trp Ile Asp Leu Gln Lys Tyr Lys Pro Phe Ser
 465 470 475 480
 Leu Ser Asn

<210> 576

<211> 1401

<212> DNA

<213> Medicago truncatula

<220>

<221> CDS

<222> (1)..(1401)

<400> 576

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Met Glu Val Glu His Ser Ile Glu Ala Val Pro Ser His Lys Asp Ser	
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aaa ttg tac gat gat gat gac cgt ctc aaa aga aca gga acg gtt tgg	96
Lys Leu Tyr Asp Asp Asp Arg Leu Lys Arg Thr Gly Thr Val Trp	
20 25 30	
aca aca agt tcg cac ata ata aca gca gtt gta gga tca gga gtg ttg	144
Thr Thr Ser Ser His Ile Ile Thr Ala Val Val Gly Ser Gly Val Leu	
35 40 45	
tcg tta gca tgg gcc ata gct cag ttg ggt tgg gta att ggt cct tct	192

PF59082SeqList_PF59082.txt

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Val	Met	Ile	Phe	Phe	Ser	Leu	Ile	Thr	Trp	Tyr	Thr	Ser	Ser	Leu	Leu	
65					70					75					80	
gct	gaa	tgt	tat	cga	att	ggt	gat	cct	cat	tac	gga	aag	agg	aac	tat	288
Ala	Glu	Cys	Tyr	Arg	Ile	Gly	Asp	Pro	His	Tyr	Gly	Lys	Arg	Asn	Tyr	
				85					90					95		
act	ttc	atg	gaa	gct	ggt	cac	acc	att	cta	gga	ggt	ttc	aat	gac	acc	336
Thr	Phe	Met	Glu	Ala	Val	His	Thr	Ile	Leu	Gly	Gly	Phe	Asn	Asp	Thr	
			100					105					110			
ctt	tgt	ggg	ata	ggt	cag	tac	aca	aat	ctt	tac	gga	act	gca	ata	gga	384
Leu	Cys	Gly	Ile	Val	Gln	Tyr	Thr	Asn	Leu	Tyr	Gly	Thr	Ala	Ile	Gly	
		115				120						125				
tac	aca	att	gcg	ggt	gcc	att	agc	atg	atg	gca	ata	aaa	agg	tct	gac	432
Tyr	Thr	Ile	Ala	Gly	Ala	Ile	Ser	Met	Met	Ala	Ile	Lys	Arg	Ser	Asp	
		130				135					140					
tgt	ttg	cat	tcc	tca	gga	gga	aaa	gac	tca	tgt	cac	att	tca	agc	aat	480
Cys	Leu	His	Ser	Ser	Gly	Gly	Lys	Asp	Ser	Cys	His	Ile	Ser	Ser	Asn	
145					150					155					160	
cca	tac	atg	ata	gca	ttt	gga	gta	atc	caa	att	ttc	ttt	tct	caa	att	528
Pro	Tyr	Met	Ile	Ala	Phe	Gly	Val	Ile	Gln	Ile	Phe	Phe	Ser	Gln	Ile	
			165					170						175		
cca	gat	ttt	gat	aaa	atg	tgg	tgg	ctc	tca	ata	ggt	gca	gca	atc	atg	576
Pro	Asp	Phe	Asp	Lys	Met	Trp	Trp	Leu	Ser	Ile	Val	Ala	Ala	Ile	Met	
			180					185					190			
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Ser	Phe	Thr	Tyr	Ser	Phe	Ile	Gly	Leu	Gly	Leu	Ala	Ile	Ala	Lys	Val	
		195				200						205				
gca	gaa	aat	ggt	tcc	ttc	aag	ggt	agc	ctc	aca	gga	gta	agc	att	gga	672
Ala	Glu	Asn	Gly	Ser	Phe	Lys	Gly	Ser	Leu	Thr	Gly	Val	Ser	Ile	Gly	
	210					215					220					
act	gtg	aca	aaa	gcc	caa	aaa	gta	tgg	gga	act	ttc	caa	gct	ctt	ggc	720
Thr	Val	Thr	Lys	Ala	Gln	Lys	Val	Trp	Gly	Thr	Phe	Gln	Ala	Leu	Gly	
225					230					235					240	
aac	ata	gcc	ttt	gca	tat	tca	tat	tct	caa	att	ctc	att	gaa	att	cag	768
Asn	Ile	Ala	Phe	Ala	Tyr	Ser	Tyr	Ser	Gln	Ile	Leu	Ile	Glu	Ile	Gln	
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gac	acc	ata	aaa	aat	cca	cca	tct	gaa	gta	aaa	aca	atg	aag	caa	gcc	816
Asp	Thr	Ile	Lys	Asn	Pro	Pro	Ser	Glu	Val	Lys	Thr	Met	Lys	Gln	Ala	
		260						265					270			
aca	aag	ata	agt	ata	ggc	gtg	aca	act	gca	ttt	tat	atg	ctt	tgt	ggc	864
Thr	Lys	Ile	Ser	Ile	Gly	Val	Thr	Thr	Ala	Phe	Tyr	Met	Leu	Cys	Gly	
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Cys	Met	Gly	Tyr	Ala	Ala	Phe	Gly	Asp	Thr	Ala	Pro	Gly	Asn	Leu	Leu	
	290					295					300					
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Thr	Gly	Ile	Phe	Asn	Pro	Tyr	Trp	Leu	Ile	Asp	Ile	Ala	Asn	Ala	Ala	
305					310					315					320	
atc	gta	att	cac	ctt	gtg	gga	gca	tac	caa	gta	tac	gcg	caa	ccc	ttc	1008
Ile	Val	Ile	His	Leu	Val	Gly	Ala	Tyr	Gln	Val	Tyr	Ala	Gln	Pro	Phe	
			325					330						335		
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Phe	Ala	Phe	Val	Glu	Lys	Ile	Val	Ile	Lys	Arg	Trp	Pro	Lys	Ile	Asn	
			340					345					350			
aaa	gaa	tac	aga	att	cca	att	cct	ggt	ttt	cat	cct	tac	aat	cta	aat	1104
Lys	Glu	Tyr	Arg	Ile	Pro	Ile	Pro	Gly	Phe	His	Pro	Tyr	Asn	Leu	Asn	
		355					360					365				
cta	ttc	aga	tta	ata	tgg	agg	act	ata	ttt	gtg	atc	aca	acc	act	gtg	1152
Leu	Phe	Arg	Leu	Ile	Trp	Arg	Thr	Ile	Phe	Val	Ile	Thr	Thr	Thr	Val	
		370				375					380					
ata	gca	atg	ctg	att	cct	ttc	ttc	aat	gat	gtt	ttg	gga	tta	ctt	gga	1200
Ile	Ala	Met	Leu	Ile	Pro	Phe	Phe	Asn	Asp	Val	Leu	Gly	Leu	Leu	Gly	
385					390					395					400	
gca	gta	ggg	ttt	tgg	cct	tta	aca	gtc	tat	ttt	cca	gtg	gag	atg	tat	1248
Ala	Val	Gly	Phe	Trp	Pro	Leu	Thr	Val	Tyr	Phe	Pro	Val	Glu	Met	Tyr	
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PF59082SeqList_PF59082.txt

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Gln	Ile	Leu	Ser	Val	Val	Cys	Leu	Val	Val	Ser	Val	Val	Ala	Val	Val	
ggg	tca	gtg	gca	agt	att	cag	ctt	gat	ctg	aag	aaa	tac	aaa	cca	ttc	1392
Gly	Ser	Val	Ala	Ser	Ile	Gln	Leu	Asp	Leu	Lys	Lys	Tyr	Lys	Pro	Phe	
acc	atg	taa														1401
Thr	Met															
465																

<210> 577

<211> 466

<212> PRT

<213> Medicago truncatula

<400> 577

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Thr	Thr	Ser	Ser	His	Ile	Ile	Thr	Ala	Val	Val	Gly	Ser	Gly	Val	Leu	
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Ser	Leu	Ala	Trp	Ala	Ile	Ala	Gln	Leu	Gly	Trp	Val	Ile	Gly	Pro	Ser	
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Val	Met	Ile	Phe	Phe	Ser	Leu	Ile	Thr	Trp	Tyr	Thr	Ser	Ser	Leu	Leu	
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Thr	Phe	Met	Glu	Ala	Val	His	Thr	Ile	Leu	Gly	Gly	Phe	Asn	Asp	Thr	
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Leu	Cys	Gly	Ile	Val	Gln	Tyr	Thr	Asn	Leu	Tyr	Gly	Thr	Ala	Ile	Gly	
		115					120					125				
Tyr	Thr	Ile	Ala	Gly	Ala	Ile	Ser	Met	Met	Ala	Ile	Lys	Arg	Ser	Asp	
	130					135					140					
Cys	Leu	His	Ser	Ser	Gly	Gly	Lys	Asp	Ser	Cys	His	Ile	Ser	Ser	Asn	
145					150					155					160	
Pro	Tyr	Met	Ile	Ala	Phe	Gly	Val	Ile	Gln	Ile	Phe	Phe	Ser	Gln	Ile	
				165					170					175		
Pro	Asp	Phe	Asp	Lys	Met	Trp	Trp	Leu	Ser	Ile	Val	Ala	Ala	Ile	Met	
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Asn	Ile	Ala	Phe	Ala	Tyr	Ser	Tyr	Ser	Gln	Ile	Leu	Ile	Glu	Ile	Gln	
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			260					265					270			
Thr	Lys	Ile	Ser	Ile	Gly	Val	Thr	Thr	Ala	Phe	Tyr	Met	Leu	Cys	Gly	
		275					280					285				
Cys	Met	Gly	Tyr	Ala	Ala	Phe	Gly	Asp	Thr	Ala	Pro	Gly	Asn	Leu	Leu	
	290					295					300					
Thr	Gly	Ile	Phe	Asn	Pro	Tyr	Trp	Leu	Ile	Asp	Ile	Ala	Asn	Ala	Ala	
305					310					315					320	
Ile	Val	Ile	His	Leu	Val	Gly	Ala	Tyr	Gln	Val	Tyr	Ala	Gln	Pro	Phe	
				325					330					335		
Phe	Ala	Phe	Val	Glu	Lys	Ile	Val	Ile	Lys	Arg	Trp	Pro	Lys	Ile	Asn	
			340					345					350			
Lys	Glu	Tyr	Arg	Ile	Pro	Ile	Pro	Gly	Phe	His	Pro	Tyr	Asn	Leu	Asn	
		355					360					365				
Leu	Phe	Arg	Leu	Ile	Trp	Arg	Thr	Ile	Phe	Val	Ile	Thr	Thr	Thr	Val	
	370					375					380					
Ile	Ala	Met	Leu	Ile	Pro	Phe	Phe	Asn	Asp	Val	Leu	Gly	Leu	Leu	Gly	
385					390					395					400	
Ala	Val	Gly	Phe	Trp	Pro	Leu	Thr	Val	Tyr	Phe	Pro	Val	Glu	Met	Tyr	

PF59082SeqList_PF59082.txt

Ile Lys Gln Lys Lys 405 Ile Pro Lys Trp Ser Tyr Lys Trp Ile Ser Met
 Gln Ile Leu 420 Ser Val Val Cys Leu 425 Val Val Ser Val Val 430 Ala Val Val
 Gly Ser 435 Val Ala Ser Ile Gln 440 Leu Asp Leu Lys Lys 445 Tyr Lys Pro Phe
 Thr Met 450
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<211> 1434

<212> DNA

<213> Medicago truncatula

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<221> CDS

<222> (1)..(1434)

<400> 578

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atc	cct	tca	caa	ctt	gat	cct	gaa	tac	ttc	gat	gac	gat	ggt	cgt	cct	96
Ile	Pro	Ser	Gln	Leu	Asp	Pro	Glu	Tyr	Phe	Asp	Asp	Asp	Gly	Arg	Pro	
			20					25					30			
aaa	cga	aca	gga	aca	ata	tgg	aca	aca	agc	tct	cat	ata	ata	aca	gct	144
Lys	Arg	Thr	Gly	Thr	Ile	Trp	Thr	Thr	Ser	Ser	His	Ile	Ile	Thr	Ala	
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gtg	att	ggg	tct	ggg	gtg	cta	tcc	tta	gca	tgg	gct	act	gca	caa	ttg	192
Val	Ile	Gly	Ser	Gly	Val	Leu	Ser	Leu	Ala	Trp	Ala	Thr	Ala	Gln	Leu	
		50				55					60					
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Gly	Trp	Ile	Gly	Gly	Pro	Leu	Ala	Met	Ile	Leu	Phe	Ser	Leu	Ile	Thr	
		65			70					75				80		
ttg	tat	act	tca	tca	atg	cta	gct	gaa	tgt	tat	cgt	tgt	gga	gat	cct	288
Leu	Tyr	Thr	Ser	Ser	Met	Leu	Ala	Glu	Cys	Tyr	Arg	Cys	Gly	Asp	Pro	
			85					90						95		
gtg	tat	gga	aag	aga	agc	tat	act	ttt	gtg	gat	gca	ggt	cgt	agc	att	336
Val	Tyr	Gly	Lys	Arg	Ser	Tyr	Thr	Phe	Val	Asp	Ala	Val	Arg	Ser	Ile	
			100					105					110			
ctt	ggc	ggg	cgc	caa	tac	acg	gtt	tgt	gga	ata	ggt	cag	tac	atg	tat	384
Leu	Gly	Gly	Arg	Gln	Tyr	Thr	Val	Cys	Gly	Ile	Val	Gln	Tyr	Met	Tyr	
		115				120						125				
ctt	tat	ggc	agt	gca	ata	gga	tac	tcg	att	gca	gct	ccc	atc	agc	atg	432
Leu	Tyr	Gly	Ser	Ala	Ile	Gly	Tyr	Ser	Ile	Ala	Ala	Pro	Ile	Ser	Met	
		130				135					140					
atg	gaa	ata	aaa	aag	tct	aga	tgt	ctc	cat	tta	tca	gga	gga	aaa	gat	480
Met	Glu	Ile	Lys	Lys	Ser	Arg	Cys	Leu	His	Leu	Ser	Gly	Gly	Lys	Asp	
145				150						155				160		
cca	tgt	cac	att	tca	agc	aac	cca	tac	atg	atc	ggt	ttt	gga	gta	atc	528
Pro	Cys	His	Ile	Ser	Ser	Asn	Pro	Tyr	Met	Ile	Gly	Phe	Gly	Val	Ile	
			165					170						175		
gaa	att	ttc	gtt	tct	caa	att	cca	gag	ttt	cat	aat	acg	tgg	tgg	ctc	576
Glu	Ile	Phe	Val	Ser	Gln	Ile	Pro	Glu	Phe	His	Asn	Thr	Trp	Trp	Leu	
			180					185					190			
tca	gta	ata	gct	gca	ata	atg	tct	ttt	ggc	tat	tcc	aca	att	ggc	gtc	624
Ser	Val	Ile	Ala	Ala	Ile	Met	Ser	Phe	Gly	Tyr	Ser	Thr	Ile	Gly	Val	
		195				200						205				
ttt	tta	gca	att	tct	caa	aca	gca	gaa	aat	ggt	acc	ttc	aag	ggt	act	672
Phe	Leu	Ala	Ile	Ser	Gln	Thr	Ala	Glu	Asn	Gly	Thr	Phe	Lys	Gly	Thr	
		210				215					220					
ctc	act	gga	gga	agc	act	gaa	aat	gtg	tca	aca	aca	aca	gaa	gtg	tgg	720
Leu	Thr	Gly	Gly	Ser	Thr	Glu	Asn	Val	Ser	Thr	Thr	Thr	Glu	Val	Trp	
225				230						235				240		
gga	att	ttc	caa	gct	ctt	ggt	gac	ata	gcc	ttt	gct	tat	tca	tac	tct	768
Gly	Ile	Phe	Gln	Ala	Leu	Gly	Asp	Ile	Ala	Phe	Ala	Tyr	Ser	Tyr	Ser	
			245					250						255		
caa	att	ctc	att	gaa	att	cag	gac	acc	ata	aaa	agt	cca	cca	tcc	gaa	816

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Gln	Ile	Leu	Ile	Glu	Ile	Gln	Asp	Thr	Ile	Lys	Ser	Pro	Ser	Glu	
260			260				265					270			
ata	aaa	acg	atg	aag	aat	gca	gca	gct	tta	agt	ggt	gct	gct	act	aca
Ile	Lys	Thr	Met	Lys	Asn	Ala	Ala	Ala	Leu	Ser	Val	Ala	Val	Thr	Thr
275						280						285			
gca	ttt	tat	ttg	ctt	tgt	ggc	tgc	atg	ggc	tat	gct	gca	ttc	gga	gaa
Ala	Phe	Tyr	Leu	Leu	Cys	Gly	Cys	Met	Gly	Tyr	Ala	Ala	Phe	Gly	Glu
290						295					300				
caa	gca	cca	ggg	aac	ttg	ctc	act	gga	ttt	agt	atg	tac	aat	cca	gcc
Gln	Ala	Pro	Gly	Asn	Leu	Leu	Thr	Gly	Phe	Ser	Met	Tyr	Asn	Pro	Ala
305					310					315					320
tg	ctc	atc	gat	ttt	g	aat	gct	gcc	gtc	gta	atc	cac	ctt	gtg	gga
Trp	Leu	Ile	Asp	Phe	Ala	Asn	Ala	Ala	Val	Val	Ile	His	Leu	Val	Gly
			325				330							335	
gca	tac	caa	gta	tat	gtt	caa	cct	gtc	ttt	gcc	ttc	gta	gag	aaa	gga
Ala	Tyr	Gln	Val	Tyr	Val	Gln	Pro	Val	Phe	Ala	Phe	Val	Glu	Lys	Gly
			340				345					350			
gca	gca	aaa	aga	tgg	ccc	caa	aca	aaa	gtg	gaa	cac	aaa	att	cca	atc
Ala	Ala	Lys	Arg	Trp	Pro	Gln	Thr	Lys	Val	Glu	His	Lys	Ile	Pro	Ile
355						360						365			
ccg	ggt	ttt	cgt	cct	tac	aat	cta	aat	cta	ttt	aga	tta	ggt	tgg	aga
Pro	Gly	Phe	Arg	Pro	Tyr	Asn	Leu	Asn	Leu	Phe	Arg	Leu	Val	Trp	Arg
370						375					380				
aca	gca	ttt	atg	atc	cta	act	act	ttt	gtt	gca	atg	ttg	att	cct	ttt
Thr	Ala	Phe	Met	Ile	Leu	Thr	Thr	Phe	Val	Ala	Met	Leu	Ile	Pro	Phe
385					390					395					400
ttt	aat	gat	gtt	ctg	gga	ttt	ctt	gga	gca	gtg	gga	ttt	tgg	cct	ttg
Phe	Asn	Asp	Val	Leu	Gly	Phe	Leu	Gly	Ala	Val	Gly	Phe	Trp	Pro	Leu
			405					410						415	
aca	gtt	tat	tat	cca	gtg	gag	atg	tat	atc	ttg	caa	agg	aag	atc	cca
Thr	Val	Tyr	Tyr	Pro	Val	Glu	Met	Tyr	Ile	Leu	Gln	Arg	Lys	Ile	Pro
			420				425					430			
aaa	tgg	agt	cct	aaa	tgg	att	ttg	ttg	caa	atc	ata	agt	ggt	ata	tgc
Lys	Trp	Ser	Pro	Lys	Trp	Ile	Leu	Leu	Gln	Ile	Ile	Ser	Val	Ile	Cys
435						440						445			
ttt	att	gta	tcg	ggt	g	gct	gct	ctt	ggc	tca	acc	gcc	agt	att	ata
Phe	Ile	Val	Ser	Gly	Ala	Ala	Ala	Leu	Gly	Ser	Thr	Ala	Ser	Ile	Ile
450					455						460				
gag	gac	cta	aag	cat	tac	aag	cca	ttc	agc	tca	gag	tat	tga		
Glu	Asp	Leu	Lys	His	Tyr	Lys	Pro	Phe	Ser	Ser	Glu	Tyr			
465					470					475					

<210> 579

<211> 477

<212> PRT

<213> Medicago truncatula

<400> 579

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Ile	Pro	Ser	Gln	Leu	Asp	Pro	Glu	Tyr	Phe	Asp	Asp	Asp	Gly	Arg	Pro
			20					25					30		
Lys	Arg	Thr	Gly	Thr	Ile	Trp	Thr	Thr	Ser	Ser	His	Ile	Ile	Thr	Ala
		35				40						45			
Val	Ile	Gly	Ser	Gly	Val	Leu	Ser	Leu	Ala	Trp	Ala	Thr	Ala	Gln	Leu
	50					55					60				
Gly	Trp	Ile	Gly	Gly	Pro	Leu	Ala	Met	Ile	Leu	Phe	Ser	Leu	Ile	Thr
65					70				75						80
Leu	Tyr	Thr	Ser	Ser	Met	Leu	Ala	Glu	Cys	Tyr	Arg	Cys	Gly	Asp	Pro
			85						90					95	
Val	Tyr	Gly	Lys	Arg	Ser	Tyr	Thr	Phe	Val	Asp	Ala	Val	Arg	Ser	Ile
			100					105					110		
Leu	Gly	Gly	Arg	Gln	Tyr	Thr	Val	Cys	Gly	Ile	Val	Gln	Tyr	Met	Tyr
		115				120						125			
Leu	Tyr	Gly	Ser	Ala	Ile	Gly	Tyr	Ser	Ile	Ala	Ala	Pro	Ile	Ser	Met
		130				135					140				
Met	Glu	Ile	Lys	Lys	Ser	Arg	Cys	Leu	His	Leu	Ser	Gly	Gly	Lys	Asp
145					150					155					160
Pro	Cys	His	Ile	Ser	Ser	Asn	Pro	Tyr	Met	Ile	Gly	Phe	Gly	Val	Ile

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165 170 175
 Glu Ile Phe Val Ser Gln Ile Pro Glu Phe His Asn Thr Trp Trp Leu
 180 185 190
 Ser Val Ile Ala Ala Ile Met Ser Phe Gly Tyr Ser Thr Ile Gly Val
 195 200 205
 Phe Leu Ala Ile Ser Gln Thr Ala Glu Asn Gly Thr Phe Lys Gly Thr
 210 215 220
 Leu Thr Gly Gly Ser Thr Glu Asn Val Ser Thr Thr Thr Glu Val Trp
 225 230 235 240
 Gly Ile Phe Gln Ala Leu Gly Asp Ile Ala Phe Ala Tyr Ser Tyr Ser
 245 250 255
 Gln Ile Leu Ile Glu Ile Gln Asp Thr Ile Lys Ser Pro Pro Ser Glu
 260 265 270
 Ile Lys Thr Met Lys Asn Ala Ala Ala Leu Ser Val Ala Val Thr Thr
 275 280 285
 Ala Phe Tyr Leu Leu Cys Gly Cys Met Gly Tyr Ala Phe Gly Glu
 290 295 300
 Gln Ala Pro Gly Asn Leu Leu Thr Gly Phe Ser Met Tyr Asn Pro Ala
 305 310 315 320
 Trp Leu Ile Asp Phe Ala Asn Ala Ala Val Ile His Leu Val Gly
 325 330 335
 Ala Tyr Gln Val Tyr Val Gln Pro Val Phe Ala Phe Val Glu Lys Gly
 340 345 350
 Ala Ala Lys Arg Trp Pro Gln Thr Lys Val Glu His Lys Ile Pro Ile
 355 360 365
 Pro Gly Phe Arg Pro Tyr Asn Leu Asn Leu Phe Arg Leu Val Trp Arg
 370 375 380
 Thr Ala Phe Met Ile Leu Thr Thr Phe Val Ala Met Leu Ile Pro Phe
 385 390 395 400
 Phe Asn Asp Val Leu Gly Phe Leu Gly Ala Val Gly Phe Trp Pro Leu
 405 410 415
 Thr Val Tyr Tyr Pro Val Glu Met Tyr Ile Leu Gln Arg Lys Ile Pro
 420 425 430
 Lys Trp Ser Pro Lys Trp Ile Leu Gln Ile Ile Ser Val Ile Cys
 435 440 445
 Phe Ile Val Ser Gly Ala Ala Ala Leu Gly Ser Thr Ala Ser Ile Ile
 450 455 460
 Glu Asp Leu Lys His Tyr Lys Pro Phe Ser Ser Glu Tyr
 465 470 475

<210> 580
 <211> 1407
 <212> DNA
 <213> Oryza sativa

<220>
 <221> CDS
 <222> (1)..(1407)

<400> 580
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 1 5 10 15
 gcg gac tcg gcg ttg ctc gac gac gac ggg cgg ccg cgc cgc acc ggc 96
 Ala Asp Ser Ala Leu Leu Asp Asp Asp Gly Arg Pro Arg Arg Thr Gly
 20 25 30
 acg ttc tgg acg gcg agc gcg cac atc atc acc gcc gtg atc ggc tcc 144
 Thr Phe Trp Thr Ala Ser Ala His Ile Ile Thr Ala Val Ile Gly Ser
 35 40 45
 ggg gtg ctg tcg ctg ccg tgg gcg acg gcg cag ctc ggg tgg gtc ggc 192
 Gly Val Leu Ser Leu Pro Trp Ala Thr Ala Gln Leu Gly Trp Val Gly
 50 55 60
 ggg ccc gcc gtg atg gtg ttc ggc ggc gtc acc tac ttc acc gcc 240
 Gly Pro Ala Val Met Val Val Phe Gly Gly Val Thr Tyr Phe Thr Ala
 65 70 75 80
 acg ctc cag gcc gag tgc tac cgc acc ggc gac gag gag acc ggc gcc 288
 Thr Leu Gln Ala Glu Cys Tyr Arg Thr Gly Asp Glu Glu Thr Gly Ala
 85 90 95
 cgc aac tac acc tac atc ggc gcc gtc cgc gcc atc ctc ggc ggc gcc 336
 100 105 110 115 120 125 130 135 140 145 150

PF59082SeqList_PF59082.txt

Arg	Asn	Tyr	Thr	Tyr	Ile	Gly	Ala	Val	Arg	Ala	Ile	Leu	Gly	Gly	Ala	
			100					105					110			
aac	gcc	aag	ctc	tgc	ggc	atc	atc	cag	tac	gcc	aac	ctc	gtc	ggc	acc	384
Asn	Ala	Lys	Leu	Cys	Gly	Ile	Ile	Gln	Tyr	Ala	Asn	Leu	Val	Gly	Thr	
		115					120					125				
gcc	gtc	ggc	tac	acc	atc	gcc	gcc	tcc	atc	agc	atg	cag	gcc	atc	aag	432
Ala	Val	Gly	Tyr	Thr	Ile	Ala	Ala	Ser	Ile	Ser	Met	Gln	Ala	Ile	Lys	
	130					135					140					
agg	gcg	ggc	tgc	ttc	cac	gcc	aat	ggc	cac	aac	gtc	ccg	tgc	cac	atc	480
Arg	Ala	Gly	Cys	Phe	His	Ala	Asn	Gly	His	Asn	Val	Pro	Cys	His	Ile	
	145				150					155					160	
tcg	agc	acc	ccg	tac	atg	ctc	atc	ttc	ggc	gcc	ttc	gag	atc	gtc	ttc	528
Ser	Ser	Thr	Pro	Tyr	Met	Leu	Ile	Phe	Gly	Ala	Phe	Glu	Ile	Val	Phe	
			165					170						175		
tcg	cag	atc	ccc	gac	ttc	cac	gag	atc	tgg	tgg	ctg	tcc	atc	gtc	gcc	576
Ser	Gln	Ile	Pro	Asp	Phe	His	Glu	Ile	Trp	Trp	Leu	Ser	Ile	Val	Ala	
			180					185						190		
gcc	gtc	atg	tcc	ttc	acc	tac	tcc	ggc	gtc	ggc	ctc	ggc	ctc	ggc	atc	624
Ala	Val	Met	Ser	Phe	Thr	Tyr	Ser	Gly	Val	Gly	Leu	Gly	Leu	Gly	Ile	
		195					200					205				
gcc	cag	acc	gtc	gcc	gac	ggc	ggg	ttc	cgc	ggc	acg	atc	gcc	ggc	gtc	672
Ala	Gln	Thr	Val	Ala	Asp	Gly	Gly	Phe	Arg	Gly	Thr	Ile	Ala	Gly	Val	
	210					215					220					
acc	aac	gtc	acc	gcc	acg	cag	aag	gcg	tgg	cgg	tcg	ctg	cag	gcg	ctg	720
Thr	Asn	Val	Thr	Ala	Thr	Gln	Lys	Ala	Trp	Arg	Ser	Leu	Gln	Ala	Leu	
	225				230					235					240	
ggc	aac	atc	gcc	ttc	gcg	ttc	gcc	ttc	tcc	aac	gtg	tac	acc	gag	atc	768
Gly	Asn	Ile	Ala	Phe	Ala	Phe	Ala	Phe	Ser	Asn	Val	Tyr	Thr	Glu	Ile	
			245					250						255		
cag	gac	acg	atc	aag	gcg	ccg	ccg	ccg	tcg	gag	gcg	aag	gtg	atg	aag	816
Gln	Asp	Thr	Ile	Lys	Ala	Pro	Pro	Pro	Ser	Glu	Ala	Lys	Val	Met	Lys	
			260					265						270		
cag	gcg	tcg	ctg	ctg	agc	atc	gtg	gcg	acg	tcg	gtg	ttc	tac	gcg	ctg	864
Gln	Ala	Ser	Leu	Leu	Ser	Ile	Val	Ala	Thr	Ser	Val	Phe	Tyr	Ala	Leu	
		275					280						285			
tgc	ggg	tgg	atg	ggc	tac	gcg	gcg	ttc	ggc	aac	gcg	gcg	ccg	gac	aac	912
Cys	Gly	Trp	Met	Gly	Tyr	Ala	Ala	Phe	Gly	Asn	Ala	Ala	Pro	Asp	Asn	
	290					295					300					
ctc	ctc	acc	gga	ttc	ggc	ttc	ttc	gag	ccg	ttc	tgg	ctc	gtc	gac	gcc	960
Leu	Leu	Thr	Gly	Phe	Gly	Phe	Phe	Glu	Pro	Phe	Trp	Leu	Val	Asp	Ala	
	305				310					315					320	
gcc	aac	gtc	gcc	atc	gcc	gtg	cac	ctc	atc	ggc	gcc	tac	cag	gtg	tac	1008
Ala	Asn	Val	Ala	Ile	Ala	Val	His	Leu	Ile	Gly	Ala	Tyr	Gln	Val	Tyr	
			325					330						335		
tgc	cag	ccg	gtc	ttc	gcc	ttc	gtc	gag	cgc	aag	gcg	tcg	cgc	ccg	tgg	1056
Cys	Gln	Pro	Val	Phe	Ala	Phe	Val	Glu	Arg	Lys	Ala	Ser	Arg	Arg	Trp	
			340					345						350		
ccc	gac	agc	ggc	ttc	gtc	aac	agc	gag	ctc	cgg	gtg	tgg	ccc	ttc	gcc	1104
Pro	Asp	Ser	Gly	Phe	Val	Asn	Ser	Glu	Leu	Arg	Val	Trp	Pro	Phe	Ala	
		355					360						365			
atc	agc	gcg	ttc	cgg	ctg	gcg	tgg	cgc	tcg	gtg	ttc	gtc	tgc	ttc	acc	1152
Ile	Ser	Ala	Phe	Arg	Leu	Ala	Trp	Arg	Ser	Val	Phe	Val	Cys	Phe	Thr	
	370					375					380					
acc	gtg	gtc	gcc	atg	gcg	ctg	ccc	ttc	ttc	ggc	gtc	atc	gtc	ggc	ctc	1200
Thr	Val	Val	Ala	Met	Ala	Leu	Pro	Phe	Phe	Gly	Val	Ile	Val	Gly	Leu	
	385				390					395					400	
ctc	ggt	gcc	atc	tcc	ttc	tgg	ccg	ctc	acc	gtc	tac	ctc	ccc	acg	gag	1248
Leu	Gly	Ala	Ile	Ser	Phe	Trp	Pro	Leu	Thr	Val	Tyr	Leu	Pro	Thr	Glu	
			405					410						415		
atg	tac	atc	gcg	cag	cgc	ggc	gtg	cgg	cgc	ggc	agc	gca	ctg	tgg	atc	1296
Met	Tyr	Ile	Ala	Gln	Arg	Gly	Val	Arg	Arg	Gly	Ser	Ala	Leu	Trp	Ile	
			420					425						430		
ggg	ctc	agg	gcg	ctc	gcc	gtc	gcc	ggc	ttc	gtc	gtg	tcg	gcc	gcc	gcc	1344
Gly	Leu	Arg	Ala	Leu	Ala	Val	Ala	Gly	Phe	Val	Val	Ser	Ala	Ala	Ala	
		435				440							445			
acc	acg	ggc	gcc	gtc	gcc	aac	ttc	gtc	ggc	gac	ttc	atg	aaa	ttc	cgt	1392
Thr	Thr	Gly	Ala	Val	Ala	Asn	Phe	Val	Gly	Asp	Phe	Met	Lys	Phe	Arg	
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ccc	ttc	agt	gga	tag												1407

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Pro Phe Ser Gly
465

<210> 581
<211> 468
<212> PRT
<213> Oryza sativa

<400> 581
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Thr Phe Trp Thr Ala Ser Ala His Ile Ile Thr Ala Val Ile Gly Ser
35 40 45
Gly Val Leu Ser Leu Pro Trp Ala Thr Ala Gln Leu Gly Trp Val Gly
50 55 60
Gly Pro Ala Val Met Val Val Phe Gly Gly Val Thr Tyr Phe Thr Ala
65 70 75 80
Thr Leu Gln Ala Glu Cys Tyr Arg Thr Gly Asp Glu Glu Thr Gly Ala
85 90 95
Arg Asn Tyr Thr Tyr Ile Gly Ala Val Arg Ala Ile Leu Gly Gly Ala
100 105 110
Asn Ala Lys Leu Cys Gly Ile Ile Gln Tyr Ala Asn Leu Val Gly Thr
115 120 125
Ala Val Gly Tyr Thr Ile Ala Ser Ile Ser Met Gln Ala Ile Lys
130 135 140
Arg Ala Gly Cys Phe His Ala Asn Gly His Asn Val Pro Cys His Ile
145 150 155 160
Ser Ser Thr Pro Tyr Met Leu Ile Phe Gly Ala Phe Glu Ile Val Phe
165 170 175
Ser Gln Ile Pro Asp Phe His Glu Ile Trp Trp Leu Ser Ile Val Ala
180 185 190
Ala Val Met Ser Phe Thr Tyr Ser Gly Val Gly Leu Gly Leu Gly Ile
195 200 205
Ala Gln Thr Val Ala Asp Gly Gly Phe Arg Gly Thr Ile Ala Gly Val
210 215 220
Thr Asn Val Thr Ala Thr Gln Lys Ala Trp Arg Ser Leu Gln Ala Leu
225 230 235 240
Gly Asn Ile Ala Phe Ala Phe Ala Phe Ser Asn Val Tyr Thr Glu Ile
245 250 255
Gln Asp Thr Ile Lys Ala Pro Pro Pro Ser Glu Ala Lys Val Met Lys
260 265 270
Gln Ala Ser Leu Leu Ser Ile Val Ala Thr Ser Val Phe Tyr Ala Leu
275 280 285
Cys Gly Trp Met Gly Tyr Ala Ala Phe Gly Asn Ala Ala Pro Asp Asn
290 295 300
Leu Leu Thr Gly Phe Gly Phe Phe Glu Pro Phe Trp Leu Val Asp Ala
305 310 315 320
Ala Asn Val Ala Ile Ala Val His Leu Ile Gly Ala Tyr Gln Val Tyr
325 330 335
Cys Gln Pro Val Phe Ala Phe Val Glu Arg Lys Ala Ser Arg Arg Trp
340 345 350
Pro Asp Ser Gly Phe Val Asn Ser Glu Leu Arg Val Trp Pro Phe Ala
355 360 365
Ile Ser Ala Phe Arg Leu Ala Trp Arg Ser Val Phe Val Cys Phe Thr
370 375 380
Thr Val Val Ala Met Ala Leu Pro Phe Phe Gly Val Ile Val Gly Leu
385 390 395 400
Leu Gly Ala Ile Ser Phe Trp Pro Leu Thr Val Tyr Leu Pro Thr Glu
405 410 415
Met Tyr Ile Ala Gln Arg Gly Val Arg Arg Gly Ser Ala Leu Trp Ile
420 425 430
Gly Leu Arg Ala Leu Ala Val Ala Gly Phe Val Val Ser Ala Ala Ala
435 440 445
Thr Thr Gly Ala Val Ala Asn Phe Val Gly Asp Phe Met Lys Phe Arg
450 455 460
Pro Phe Ser Gly
465

PF59082SeqList_PF59082.txt

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 <211> 1773
 <212> DNA
 <213> Oryza sativa

<220>
 <221> CDS
 <222> (74)..(1501)

<400> 582
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 Met Ala Ser Gly Gln Lys Val Val Lys Pro Met Glu
 1 5 10
 gtg tcg gtg gag gcc ggg aac gcc ggg gag gcg gcg tgg ctg gac gac 157
 Val Ser Val Glu Ala Gly Asn Ala Gly Glu Ala Ala Trp Leu Asp Asp
 15 20 25
 gac ggg cgg gcg cgg cgg acg ggc acg ttc tgg acg gcg agc gcg cac 205
 Asp Gly Arg Ala Arg Arg Thr Gly Thr Phe Trp Thr Ala Ser Ala His
 30 35 40
 atc atc acc gcc gtc atc ggc tcc ggc gtg ctg tcg ctg gcg tgg gcg 253
 Ile Ile Thr Ala Val Ile Gly Ser Gly Val Leu Ser Leu Ala Trp Ala
 45 50 55 60
 atc gcg cag ctg ggc tgg gtg gcc ggc ccc gcc gtg atg ctc ctc ttc 301
 Ile Ala Gln Leu Gly Trp Val Ala Gly Pro Ala Val Met Leu Leu Phe
 65 70 75
 gcc ttc gtc atc tac acc tcc acc ctc ctc gcc gag tgc tac cgc 349
 Ala Phe Val Ile Tyr Tyr Thr Ser Thr Leu Leu Ala Glu Cys Tyr Arg
 80 85 90
 acc ggc gac cct gcc acc ggc aag cgc aac tac acc tac atg gac gcc 397
 Thr Gly Asp Pro Ala Thr Gly Lys Arg Asn Tyr Thr Tyr Met Asp Ala
 95 100 105
 gtg cgc gcc aac ctc ggc ggc gcc aag gtc acc ttc tgc ggc gtc atc 445
 Val Arg Ala Asn Leu Gly Gly Ala Lys Val Thr Phe Cys Gly Val Ile
 110 115 120
 cag tac gcc aac ctc gtc ggc gtc gcc atc ggc tac acc atc gcg tcg 493
 Gln Tyr Ala Asn Leu Val Gly Val Ala Ile Gly Tyr Thr Ile Ala Ser
 125 130 135 140
 tcc atc agc atg cgc gcc atc agg agg gcc ggc tgc ttc cac cac aac 541
 Ser Ile Ser Met Arg Ala Ile Arg Arg Ala Gly Cys Phe His His Asn
 145 150 155
 ggc cat ggt gac ccg tgc cgc agc tcc acc aac cct tac atg atc ctc 589
 Gly His Gly Asp Pro Cys Arg Ser Ser Ser Asn Pro Tyr Met Ile Leu
 160 165 170
 ttc ggc gcc gtg cag atc gtc ttc tcg cag atc cct gac ttc gac cag 637
 Phe Gly Ala Val Gln Ile Val Phe Ser Gln Ile Pro Asp Phe Asp Gln
 175 180 185
 att tgg tgg ctg tcc atc gtc gcc gcc gtc atg tcc ttc acc tac tcc 685
 Ile Trp Trp Leu Ser Ile Val Ala Ala Val Met Ser Phe Thr Tyr Ser
 190 195 200
 ggc atc ggc ctc tcc ctc ggc atc gtc cag aca atc tcc aat ggc ggc 733
 Gly Ile Gly Leu Ser Leu Gly Ile Val Gln Thr Ile Ser Asn Gly Gly
 205 210 215 220
 atc cag ggc agc ctc acc gga atc agc atc ggc gtc ggc gtc agc tca 781
 Ile Gln Gly Ser Leu Thr Gly Ile Ser Ile Gly Val Gly Val Ser Ser
 225 230 235
 acg cag aag gtg tgg cgc agc ctg cag gca ttc ggc gac atc gcc ttc 829
 Thr Gln Lys Val Trp Arg Ser Leu Gln Ala Phe Gly Asp Ile Ala Phe
 240 245 250
 gca tac tcc ttc tcc aac atc ctc atc gag atc caa gac acg atc aag 877
 Ala Tyr Ser Phe Ser Asn Ile Leu Ile Glu Ile Gln Asp Thr Ile Lys
 255 260 265
 gcg ccg ccg ccg tcg gag gcg aag gtg atg aag agc gcg acg agg ctg 925
 Ala Pro Pro Pro Ser Glu Ala Lys Val Met Lys Ser Ala Thr Arg Leu
 270 275 280
 agc gtg gcg acg acc acg gtg ttc tac atg ctg tgc ggg tgc atg ggc 973

PF59082SeqList_PF59082.txt

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Tyr	Ala	Ala	Phe	Gly 305	Asp	Ala	Ala	Pro	Asp 310	Asn	Leu	Leu	Thr	Gly 315	Phe	
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Gly	Phe	Tyr	Glu 320	Pro	Phe	Trp	Leu	Leu	Asp 325	Val	Ala	Asn	Val 330	Ala	Ile	
gtc	gtg	cac	ctc	gtc	ggc	gcc	tac	cag	gtg	ttc	gtc	cag	cca	atc	ttc	1117
Val	Val	His 335	Leu	Val	Gly	Ala	Tyr 340	Gln	Val	Phe	Val	Gln 345	Pro	Ile	Phe	
gcc	ttc	gtc	gag	cgc	tgg	gcc	tcc	cgc	cgg	tgg	ccg	gac	agc	gcg	ttc	1165
Ala	Phe	Val	Glu	Arg	Trp	Ala 355	Ser	Arg	Arg	Trp 360	Pro	Asp	Ser	Ala	Phe	
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Ile 365	Ala	Lys	Glu	Leu	Arg 370	Val	Gly	Pro	Phe	Ala 375	Leu	Ser	Leu	Phe	Arg 380	
ctg	acg	tgg	cgc	tgc	gcg	ttc	gtc	tgc	ctc	acc	acc	gtc	gtc	gcc	atg	1261
Leu	Thr	Trp	Arg	Ser 385	Ala	Phe	Val	Cys	Leu 390	Thr	Thr	Val	Val	Ala 395	Met	
ctc	ctc	ccc	ttc	ggc	aac	gtg	gtg	ggg	ctc	ctc	ggc	gcc	gtc	tcc		1309
Leu	Leu	Pro	Phe 400	Phe	Gly	Asn	Val 405	Val	Gly	Leu	Leu	Gly 410	Ala	Val	Ser	
ttc	tgg	ccg	ctc	acc	gtc	tac	ttc	ccc	gtc	gag	atg	tac	atc	gcg	cag	1357
Phe	Trp	Pro 415	Leu	Thr	Val	Tyr 420	Phe	Pro	Val	Glu	Met	Tyr 425	Ile	Ala	Gln	
cgc	ggc	gtg	cca	cgt	ggc	agc	gcg	agg	tgg	gtc	tca	ctc	aag	acg	ctc	1405
Arg	Gly 430	Val	Pro	Arg	Gly 435	Ser	Ala	Arg	Trp	Val 440	Ser	Leu	Lys	Thr	Leu	
agc	gcg	tgc	tgc	ctc	gtc	tcc	atc	gcc	gcc	gcc	gcg	ggc	tcc	att		1453
Ser 445	Ala	Cys	Cys	Leu	Val 450	Val	Ser	Ile	Ala 455	Ala	Ala	Ala	Gly	Ser	Ile 460	
gct	gac	gtc	atc	gac	gcg	ctc	aag	gtg	tac	agg	ccg	ttc	agc	gga		1498
Ala	Asp	Val	Ile	Asp 465	Ala	Leu	Lys	Val 470	Tyr	Arg	Pro	Phe	Ser	Gly 475		
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<212> PRT

<213> Oryza sativa

<400> 583

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Val	Ile	Gly	Ser	Gly	Val	Leu	Ser	Leu	Ala	Trp	Ala	Ile	Ala	Gln	Leu	
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Gly	Trp	Val	Ala	Gly	Pro	Ala	Val	Met	Leu	Leu	Phe	Ala	Phe	Val	Ile	
65					70				75						80	
Tyr	Tyr	Thr	Ser	Thr	Leu	Leu	Ala	Glu	Cys	Tyr	Arg	Thr	Gly	Asp	Pro	
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PF59082SeqList_PF59082.txt

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115 120 125
Leu Val Gly Val Ala Ile Gly Tyr Thr Ile Ala Ser Ile Ser Met
130 135 140
Arg Ala Ile Arg Arg Ala Gly Cys Phe His His Asn Gly His Gly Asp
145 150 155 160
Pro Cys Arg Ser Ser Asn Pro Tyr Met Ile Leu Phe Gly Ala Val
165 170 175
Gln Ile Val Phe Ser Gln Ile Pro Asp Phe Asp Gln Ile Trp Trp Leu
180 185 190
Ser Ile Val Ala Ala Val Met Ser Phe Thr Tyr Ser Gly Ile Gly Leu
195 200 205
Ser Leu Gly Ile Val Gln Thr Ile Ser Asn Gly Gly Ile Gln Gly Ser
210 215 220
Leu Thr Gly Ile Ser Ile Gly Val Gly Val Ser Ser Thr Gln Lys Val
225 230 235 240
Trp Arg Ser Leu Gln Ala Phe Gly Asp Ile Ala Phe Ala Tyr Ser Phe
245 250 255
Ser Asn Ile Leu Ile Glu Ile Gln Asp Thr Ile Lys Ala Pro Pro Pro
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Ser Glu Ala Lys Val Met Lys Ser Ala Thr Arg Leu Ser Val Ala Thr
275 280 285
Thr Thr Val Phe Tyr Met Leu Cys Gly Cys Met Gly Tyr Ala Ala Phe
290 295 300
Gly Asp Ala Ala Pro Asp Asn Leu Leu Thr Gly Phe Gly Phe Tyr Glu
305 310 315 320
Pro Phe Trp Leu Leu Asp Val Ala Asn Val Ala Ile Val Val His Leu
325 330 335
Val Gly Ala Tyr Gln Val Phe Val Gln Pro Ile Phe Ala Phe Val Glu
340 345 350
Arg Trp Ala Ser Arg Arg Trp Pro Asp Ser Ala Phe Ile Ala Lys Glu
355 360 365
Leu Arg Val Gly Pro Phe Ala Leu Ser Leu Phe Arg Leu Thr Trp Arg
370 375 380
Ser Ala Phe Val Cys Leu Thr Thr Val Val Ala Met Leu Leu Pro Phe
385 390 395 400
Phe Gly Asn Val Val Gly Leu Leu Gly Ala Val Ser Phe Trp Pro Leu
405 410 415
Thr Val Tyr Phe Pro Val Glu Met Tyr Ile Ala Gln Arg Gly Val Pro
420 425 430
Arg Gly Ser Ala Arg Trp Val Ser Leu Lys Thr Leu Ser Ala Cys Cys
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<212> DNA

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<400> 584

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Met Ala Ser Gly Gln Lys
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gtg gtg aag ccg atg gag gtg tcg gtg gag gcc ggg aac gcc ggg gag 161

Val Val Lys Pro Met Glu Val Ser Val Glu Ala Gly Asn Ala Gly Glu
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PF59082SeqList_PF59082.txt

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Trp	Thr	Ala	Ser	Ala	His	Ile	Ile	Thr	Ala	Val	Ile	Gly	Ser	Gly	Val	
40						45					50					
ctg	tcg	ctg	gcg	tgg	gcg	atc	gcg	cag	ctg	ggc	tgg	gtg	gcc	ggg	ccc	305
Leu	Ser	Leu	Ala	Trp	Ala	Ile	Ala	Gln	Leu	Gly	Trp	Val	Ala	Gly	Pro	
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gcc	gtg	atg	ctc	ctc	ttc	gcc	ttc	gtc	atc	tac	tac	acc	tcc	acc	ctc	353
Ala	Val	Met	Leu	Leu	Phe	Ala	Phe	Val	Ile	Tyr	Tyr	Thr	Ser	Thr	Leu	
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ctc	gcc	gag	tgc	tac	cgc	acc	ggc	gac	ccg	gcc	acc	ggc	aag	cga	aac	401
Leu	Ala	Glu	Cys	Tyr	Arg	Thr	Gly	Asp	Pro	Ala	Thr	Gly	Lys	Arg	Asn	
			90					95					100			
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Tyr	Thr	Tyr	Met	Asp	Ala	Val	Arg	Ala	Asn	Leu	Gly	Gly	Ala	Lys	Val	
			105				110					115				
acc	ttc	tgc	ggc	gtc	atc	cag	tac	gcc	aac	ctc	gtc	ggc	gtc	gcc	atc	497
Thr	Phe	Cys	Gly	Val	Ile	Gln	Tyr	Ala	Asn	Leu	Val	Gly	Val	Ala	Ile	
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Gly	Tyr	Thr	Ile	Ala	Ser	Ser	Ile	Ser	Met	Arg	Ala	Ile	Arg	Arg	Ala	
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Gly	Cys	Phe	His	His	Asn	Gly	His	Gly	Asp	Pro	Cys	Arg	Ser	Ser	Ser	
					155				160					165		
aac	cct	tac	atg	atc	ctc	ttc	ggc	gtc	gtg	cag	atc	gtc	ttc	tcg	cag	641
Asn	Pro	Tyr	Met	Ile	Leu	Phe	Gly	Val	Val	Gln	Ile	Val	Phe	Ser	Gln	
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atc	ccg	gac	ttc	gac	cag	att	tgg	tgg	ctg	tcc	atc	gtc	gcc	gcc	gtc	689
Ile	Pro	Asp	Phe	Asp	Gln	Ile	Trp	Trp	Leu	Ser	Ile	Val	Ala	Ala	Val	
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Met	Ser	Phe	Thr	Tyr	Ser	Gly	Ile	Gly	Leu	Ser	Leu	Gly	Ile	Val	Gln	
	200					205					210					
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Thr	Ile	Ser	Asn	Gly	Gly	Ile	Gln	Gly	Ser	Leu	Thr	Gly	Ile	Ser	Ile	
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ggc	gtc	ggc	gtc	agc	tca	acg	cag	aag	gtg	tgg	cgc	agc	ctg	cag	gca	833
Gly	Val	Gly	Val	Ser	Ser	Thr	Gln	Lys	Val	Trp	Arg	Ser	Leu	Gln	Ala	
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ttc	ggc	gac	atc	gcc	ttc	gca	tac	tcc	ttc	tcc	aac	atc	ctc	atc	gag	881
Phe	Gly	Asp	Ile	Ala	Phe	Ala	Tyr	Ser	Phe	Ser	Asn	Ile	Leu	Ile	Glu	
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Ile	Gln	Asp	Thr	Ile	Lys	Ala	Pro	Pro	Pro	Ser	Glu	Ala	Lys	Val	Met	
			265				270					275				
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Lys	Ser	Ala	Thr	Arg	Leu	Ser	Val	Ala	Thr	Thr	Thr	Val	Phe	Tyr	Met	
	280					285					290					
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Leu	Cys	Gly	Cys	Met	Gly	Tyr	Ala	Ala	Phe	Gly	Asp	Ala	Ala	Pro	Asp	
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aac	ctc	ctc	acg	ggc	ttc	ggc	ttc	tac	gag	ccc	ttc	tgg	ctg	ctc	gac	1073
Asn	Leu	Leu	Thr	Gly	Phe	Gly	Phe	Tyr	Glu	Pro	Phe	Trp	Leu	Leu	Asp	
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gtc	gcc	aac	gtc	gcc	atc	gtc	gtg	cac	ctc	gtc	ggc	gcc	tac	cag	gtg	1121
Val	Ala	Asn	Val	Ala	Ile	Val	Val	His	Leu	Val	Gly	Ala	Tyr	Gln	Val	
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Phe	Val	Gln	Pro	Ile	Phe	Ala	Phe	Val	Glu	Arg	Trp	Ala	Ser	Arg	Arg	
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Trp	Pro	Asp	Ser	Ala	Phe	Ile	Ala	Lys	Glu	Leu	Arg	Val	Gly	Pro	Phe	
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Ala	Leu	Ser	Leu	Phe	Arg	Leu	Thr	Trp	Arg	Ser	Ala	Phe	Val	Cys	Leu	
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PF59082SeqList_PF59082.txt

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Leu	Leu	Gly	Ala	Val	Ser	Phe	Trp	Pro	Leu	Thr	Val	Tyr	Phe	Pro	Val	
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Glu	Met	Tyr	Ile	Ala	Gln	Arg	Gly	Val	Pro	Arg	Gly	Ser	Ala	Arg	Trp	
		425					430					435				
gtc	tcg	ctc	aag	acg	ctc	agc	gcg	tgc	tgc	ctc	gtc	gtc	tcc	atc	gcc	1457
Val	Ser	Leu	Lys	Thr	Leu	Ser	Ala	Cys	Cys	Leu	Val	Val	Ser	Ile	Ala	
	440					445					450					
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Ala	Ala	Ala	Gly	Ser	Ile	Ala	Asp	Val	Ile	Asp	Ala	Leu	Lys	Val	Tyr	
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Arg	Pro	Phe	Ser	Gly												
			475													
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			245					250						255		
Ser	Asn	Ile	Leu	Ile	Glu	Ile	Gln	Asp	Thr	Ile	Lys	Ala	Pro	Pro	Pro	
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PF59082SeqList_PF59082.txt

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<211> 1401

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<400> 586

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Ala Val Ile Gly Ser Gly Val Leu Ser Leu Ala Trp Ala Ile Gly Gln	
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ctc ggt tgg atc gca ggt cct aca gtg atg ttg ttg ttc tct ttt gtc	192
Leu Gly Trp Ile Ala Gly Pro Thr Val Met Leu Leu Phe Ser Phe Val	
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Thr Tyr Tyr Ser Ser Thr Leu Leu Ser Asp Cys Tyr Arg Thr Gly Asp	
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Pro Val Ser Gly Lys Arg Asn Tyr Thr Tyr Met Asp Ala Val Arg Ser	
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atc cta ggt ggc ttt agg ttc aag att tgt ggg ctg att cag tat ttg	336
Ile Leu Gly Gly Phe Arg Phe Lys Ile Cys Gly Leu Ile Gln Tyr Leu	
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Asn Leu Phe Gly Ile Thr Val Gly Tyr Thr Ile Ala Ala Ser Ile Ser	
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Met Met Ala Ile Lys Arg Ser Asn Cys Phe His Glu Ser Gly Gly Lys	
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aac ccg tgt cac atg tcg agc aat cca tac atg atc atg ttt ggt gtg	480
Asn Pro Cys His Met Ser Ser Asn Pro Tyr Met Ile Met Phe Gly Val	
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acc gag atc ttg ctc tct cag atc aaa gat ttt gac cag att tgg tgg	528
Thr Glu Ile Leu Leu Ser Gln Ile Lys Asp Phe Asp Gln Ile Trp Trp	
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PF59082SeqList_PF59082.txt

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Leu	Ala	Leu	Gly	Ile	Ile	Gln	Val	Ala	Ala	Asn	Gly	Val	Val	Lys	Gly	
agt	ctc	acc	gga	att	agc	atc	ggc	gca	gtg	act	cag	acc	caa	aaa	ata	672
Ser	Leu	Thr	Gly	Ile	Ser	Ile	Gly	Ala	Val	Thr	Gln	Thr	Gln	Lys	Ile	
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Trp	Arg	Thr	Phe	Gln	Ala	Leu	Gly	Asp	Ile	Ala	Phe	Ala	Tyr	Ser	Tyr	
225					230					235					240	
tct	ggt	ggt	ctt	att	gaa	att	cag	gac	act	gta	aga	tct	cca	cca	gca	768
Ser	Val	Val	Leu	Ile	Glu	Ile	Gln	Asp	Thr	Val	Arg	Ser	Pro	Pro	Ala	
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Glu	Ser	Lys	Thr	Met	Lys	Ile	Ala	Thr	Arg	Ile	Ser	Ile	Ala	Val	Thr	
			260					265								
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Thr	Thr	Phe	Tyr	Met	Leu	Cys	Gly	Cys	Met	Gly	Tyr	Ala	Ala	Phe	Gly	
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Phe	Trp	Leu	Leu	Asp	Val	Ala	Asn	Ala	Ala	Ile	Val	Ile	His	Leu	Val	
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gga	gct	tat	caa	gtc	ttt	gct	cag	ccc	atc	ttc	gcc	ttt	att	gag	aaa	1008
Gly	Ala	Tyr	Gln	Val	Phe	Ala	Gln	Pro	Ile	Phe	Ala	Phe	Ile	Glu	Lys	
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caa	ctg	gcc	gct	agg	ttt	ccc	gac	agt	gac	ttg	gtg	acc	aag	gaa	tac	1056
Gln	Leu	Ala	Ala	Arg	Phe	Pro	Asp	Ser	Asp	Leu	Val	Thr	Lys	Glu	Tyr	
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gaa	atc	cga	atc	cct	ggt	ttt	agg	tca	ccg	tac	aaa	gtc	aac	ggt	ttc	1104
Glu	Ile	Arg	Ile	Pro	Gly	Phe	Arg	Ser	Pro	Tyr	Lys	Val	Asn	Val	Phe	
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aga	gca	ggt	tac	cga	agc	ggg	ttt	gtg	ggt	ttg	acc	act	gtg	ata	tcc	1152
Arg	Ala	Val	Tyr	Arg	Ser	Gly	Phe	Val	Val	Leu	Thr	Thr	Val	Ile	Ser	
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Met	Leu	Met	Pro	Phe	Asn	Asp	Val	Val	Gly	Ile	Leu	Gly	Ala	Leu		
385					390				395						400	
ggg	ttt	tgg	cct	ttg	acg	ggt	tac	ttt	ccg	gtg	gag	atg	tat	ata	aga	1248
Gly	Phe	Trp	Pro	Leu	Thr	Val	Tyr	Phe	Pro	Val	Glu	Met	Tyr	Ile	Arg	
			405						410					415		
cag	agg	aag	ggt	gag	aga	tgg	agt	atg	aag	tgg	ggt	tgt	ctg	cag	atg	1296
Gln	Arg	Lys	Val	Glu	Arg	Trp	Ser	Met	Lys	Trp	Val	Cys	Leu	Gln	Met	
			420					425					430			
ttg	agc	tgt	ggt	tgt	ttg	atg	atc	acg	ttg	gtc	gcc	gga	ggt	ggc	tcc	1344
Leu	Ser	Cys	Gly	Cys	Leu	Met	Ile	Thr	Leu	Val	Ala	Gly	Val	Gly	Ser	
			435				440					445				
atc	gcc	gga	gta	atg	cta	gac	ctt	aag	ggt	tac	aag	ccg	ttc	aag	act	1392
Ile	Ala	Gly	Val	Met	Leu	Asp	Leu	Lys	Val	Tyr	Lys	Pro	Phe	Lys	Thr	
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Thr	Tyr															
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<211> 466

<212> PRT

<213> Arabidopsis thaliana

<400> 587

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Ala Val Ile Gly Ser Gly Val Leu Ser Leu Ala Trp Ala Ile Gly Gln

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PF59082SeqList_PF59082.txt

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Pro Val Ser Gly Lys Arg Asn Tyr Thr Tyr Met Asp Ala Val Arg Ser
85 90 95
Ile Leu Gly Gly Phe Arg Phe Lys Ile Cys Gly Leu Ile Gln Tyr Leu
100 105 110
Asn Leu Phe Gly Ile Thr Val Gly Tyr Thr Ile Ala Ala Ser Ile Ser
115 120 125
Met Met Ala Ile Lys Arg Ser Asn Cys Phe His Glu Ser Gly Gly Lys
130 135 140
Asn Pro Cys His Met Ser Ser Asn Pro Tyr Met Ile Met Phe Gly Val
145 150 155 160
Thr Glu Ile Leu Leu Ser Gln Ile Lys Asp Phe Asp Gln Ile Trp Trp
165 170 175
Leu Ser Ile Val Ala Ala Ile Met Ser Phe Thr Tyr Ser Ala Ile Gly
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195 200 205
Ser Leu Thr Gly Ile Ser Ile Gly Ala Val Thr Gln Thr Gln Lys Ile
210 215 220
Trp Arg Thr Phe Gln Ala Leu Gly Asp Ile Ala Phe Ala Tyr Ser Tyr
225 230 235 240
Ser Val Val Leu Ile Glu Ile Gln Asp Thr Val Arg Ser Pro Pro Ala
245 250 255
Glu Ser Lys Thr Met Lys Ile Ala Thr Arg Ile Ser Ile Ala Val Thr
260 265 270
Thr Thr Phe Tyr Met Leu Cys Gly Cys Met Gly Tyr Ala Ala Phe Gly
275 280 285
Asp Lys Ala Pro Gly Asn Leu Leu Thr Gly Phe Gly Phe Tyr Asn Pro
290 295 300
Phe Trp Leu Leu Asp Val Ala Asn Ala Ala Ile Val Ile His Leu Val
305 310 315 320
Gly Ala Tyr Gln Val Phe Ala Gln Pro Ile Phe Ala Phe Ile Glu Lys
325 330 335
Gln Leu Ala Ala Arg Phe Pro Asp Ser Asp Leu Val Thr Lys Glu Tyr
340 345 350
Glu Ile Arg Ile Pro Gly Phe Arg Ser Pro Tyr Lys Val Asn Val Phe
355 360 365
Arg Ala Val Tyr Arg Ser Gly Phe Val Val Leu Thr Thr Val Ile Ser
370 375 380
Met Leu Met Pro Phe Phe Asn Asp Val Val Gly Ile Leu Gly Ala Leu
385 390 395 400
Gly Phe Trp Pro Leu Thr Val Tyr Phe Pro Val Glu Met Tyr Ile Arg
405 410 415
Gln Arg Lys Val Glu Arg Trp Ser Met Lys Trp Val Cys Leu Gln Met
420 425 430
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Thr Tyr
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<211> 1443

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1443)

<400> 588

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tcc gat tca ttc gat gat gat ggt cgt ccc aag cga acc ggg acg gtg
48 96

PF59082SeqList_PF59082.txt

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Trp	Thr	Ala	Ser	Ala	His	Ile	Ile	Thr	Ala	Val	Ile	Gly	Ser	Gly	Val		
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ttg	tca	gca	tgg	gcc	gtt	gct	cag	att	ggt	tgg	att	ggg	ggt	ggt	cca	192	
Leu	Ser	Leu	Ala	Trp	Ala	Val	Ala	Gln	Ile	Gly	Trp	Ile	Gly	Gly	Pro		
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gtg	gct	atg	tta	ctc	ttt	tct	ttc	gtt	act	ttt	tac	aca	tct	acc	ctt	240	
Val	Ala	Met	Leu	Leu	Phe	Ser	Phe	Val	Thr	Phe	Tyr	Thr	Ser	Thr	Leu		
65					70					75					80		
ctc	tgt	tct	tgt	tac	cga	tct	ggg	gac	tct	gtt	acc	ggc	aaa	aga	aac	288	
Leu	Cys	Ser	Cys	Tyr	Arg	Ser	Gly	Asp	Ser	Val	Thr	Gly	Lys	Arg	Asn		
85								90						95			
tac	act	tac	atg	gac	gct	att	cac	tcc	aac	ctc	ggg	ggg	att	aag	gtg	336	
Tyr	Thr	Tyr	Met	Asp	Ala	Ile	His	Ser	Asn	Leu	Gly	Gly	Ile	Lys	Val		
100								105									
aaa	gta	tgt	gga	gtt	gtg	caa	tat	gtt	aat	cta	ttt	ggg	aca	gca	att	384	
Lys	Val	Cys	Gly	Val	Val	Gln	Tyr	Val	Asn	Leu	Phe	Gly	Thr	Ala	Ile		
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Ser	Cys	Gln	Gln	Met	Asn	Gly	Pro	Asn	Asp	Pro	Cys	His	Val	Asn	Gly		
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Asn	Val	Tyr	Met	Ile	Ala	Phe	Gly	Ile	Val	Gln	Ile	Ile	Phe	Ser	Gln		
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Ile	Pro	Asp	Phe	Asp	Gln	Leu	Trp	Trp	Leu	Ser	Ile	Val	Ala	Ala	Val		
180							185							190			
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195							200										
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Arg	Thr	Phe	Gln	Ser	Leu	Gly	Asn	Ile	Ala	Phe	Ala	Tyr	Ser	Tyr	Ser		
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Met	Ile	Leu	Ile	Glu	Ile	Gln	Asp	Thr	Val	Lys	Ser	Pro	Pro	Ala	Glu		
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Val	Asn	Thr	Met	Arg	Lys	Ala	Thr	Phe	Val	Ser	Val	Ala	Val	Thr	Thr		
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Trp	Leu	Leu	Asp	Ile	Ala	Asn	Leu	Ala	Ile	Val	Ile	His	Leu	Val	Gly		
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Ala	Tyr	Gln	Val	Tyr	Cys	Gln	Pro	Leu	Phe	Ala	Phe	Val	Glu	Lys	Glu		
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Ala	Ser	Arg	Arg	Phe	Pro	Glu	Ser	Glu	Phe	Val	Thr	Lys	Glu	Ile	Lys		
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PF59082SeqList_PF59082.txt

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Trp	Pro	Leu	Thr	Val	Tyr	Phe	Pro	Val	Glu	Met	Tyr	Ile	Ala	Gln	Lys	
aat	ggt	ccg	aga	tgg	ggc	aca	aag	tgg	ggt	tgt	cta	caa	gtc	ttg	agt	1344
Asn	Val	Pro	Arg	Trp	Gly	Thr	Lys	Trp	Val	Cys	Leu	Gln	Val	Leu	Ser	
gtg	aca	tgt	ctt	ttt	gtg	tcc	gta	gcc	gcg	gcc	gcg	gga	tct	ggt	att	1392
Val	Thr	Cys	Leu	Phe	Val	Ser 455	Val	Ala	Ala	Ala	Ala	Gly	Ser	Val	Ile	
ggc	att	ggt	agt	gat	ctc	aag	gtc	tac	aaa	cct	ttc	cag	tct	gaa	ttc	1440
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<213> Arabidopsis thaliana

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Trp	Thr	Ala 35	Ser	Ala	His	Ile	Ile 40	Thr	Ala	Val	Ile	Gly 45	Ser	Gly	Val	
Leu	Ser	Leu	Ala	Trp	Ala	Val 55	Ala	Gln	Ile	Gly	Trp 60	Ile	Gly	Gly	Pro	
Val 65	Ala	Met	Leu	Leu	Phe 70	Ser	Phe	Val	Thr	Phe 75	Tyr	Thr	Ser	Thr	Leu 80	
Leu	Cys	Ser	Cys	Tyr 85	Arg	Ser	Gly	Asp	Ser 90	Val	Thr	Gly	Lys	Arg 95	Asn	
Tyr	Thr	Tyr	Met 100	Asp	Ala	Ile	His	Ser 105	Asn	Leu	Gly	Gly	Ile 110	Lys	Val	
Lys	Val	Cys 115	Gly	Val	Val	Gln	Tyr 120	Val	Asn	Leu	Phe	Gly 125	Thr	Ala	Ile	
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Ser 145	Cys	Gln	Gln	Met	Asn 150	Gly	Pro	Asn	Asp	Pro 155	Cys	His	Val	Asn	Gly 160	
Asn	Val	Tyr	Met	Ile 165	Ala	Phe	Gly	Ile	Val 170	Gln	Ile	Ile	Phe	Ser 175	Gln	
Ile	Pro	Asp	Phe 180	Asp	Gln	Leu	Trp	Trp 185	Leu	Ser	Ile	Val	Ala 190	Ala	Val	
Met	Ser	Phe 195	Ala	Tyr	Ser	Ala	Ile 200	Gly	Leu	Gly	Leu	Gly 205	Val	Ser	Lys	
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Asn 305	Ala	Pro	Gly	Asn	Leu 310	Leu	Ala	His	Gly	Gly 315	Phe	Arg	Asn	Pro	Tyr 320	
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PF59082SeqList_PF59082.txt

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 Ile Gln Leu Phe Pro Gly Lys Pro Phe Asn Leu Asn Leu Phe Arg Leu
 370 375 380
 Val Trp Arg Thr Phe Phe Val Ile Thr Thr Thr Leu Ile Ser Met Leu
 385 390 400
 Met Pro Phe Phe Asn Asp Val Val Gly Leu Leu Gly Ala Ile Gly Phe
 405 410 415
 Trp Pro Leu Thr Val Tyr Phe Pro Val Glu Met Tyr Ile Ala Gln Lys
 420 425 430
 Asn Val Pro Arg Trp Gly Thr Lys Trp Val Cys Leu Gln Val Leu Ser
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<212> DNA

<213> Oryza sativa

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<400> 590

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Ala Gly Met Met Val Gly His Gly Glu Trp Arg Asp Asp Asp Gly Arg	
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Ala Arg Arg Met Gly Thr Val Trp Thr Ala Ser Ala His Ile Ile Thr	
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Ala Val Ile Gly Ser Gly Val Leu Ser Leu Ala Trp Ala Ile Ala Gln	
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ctc ggc tgg gtg gcc ggc ccc gcc gtc atg ctg ctc ttc gcc ttc gtc	240
Leu Gly Trp Val Ala Gly Pro Ala Val Met Leu Leu Phe Ala Phe Val	
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Ile Tyr Tyr Thr Ser Thr Leu Leu Ala Glu Cys Tyr Arg Ser Gly Asp	
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Pro Cys Thr Gly Lys Arg Asn Tyr Thr Tyr Met Asp Ala Val Arg Ala	
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Asn Leu Gly Gly Ser Lys Val Arg Leu Cys Gly Val Ile Gln Tyr Ala	
115 120 125	
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Asn Leu Phe Gly Val Ala Ile Gly Tyr Thr Ile Ala Ala Ser Ile Ser	
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Met Leu Ala Ile Lys Arg Ala Asp Cys Phe His Glu Lys Gly His Lys	
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Asn Pro Cys Arg Ser Ser Ser Asn Pro Tyr Met Ile Leu Phe Gly Val	
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Val Gln Ile Val Phe Ser Gln Ile Pro Asp Phe Asp Gln Ile Trp Trp	
180 185 190	
ctg tcc atc gtc gcc gcc atc atg tcc ttc acc tat tcg acg att ggc	624
Leu Ser Ile Val Ala Ala Ile Met Ser Phe Thr Tyr Ser Thr Ile Gly	
195 200 205	
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PF59082SeqList_PF59082.txt

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225					230					235					240		
gtc	tgg	cgc	agc	ctc	cag	gcc	ttc	ggt	gac	atc	gcg	ttc	gcc	tac	tcc		768
Val	Trp	Arg	Ser	Leu	Gln	Ala	Phe	Gly	Asp	Ile	Ala	Phe	Ala	Tyr	Ser		
				245					250					255			
tac	tcc	atc	atc	ctc	atc	gag	atc	cag	gac	acg	atc	aag	gcg	ccg	ccg		816
Tyr	Ser	Ile	Ile	Leu	Ile	Glu	Ile	Gln	Asp	Thr	Ile	Lys	Ala	Pro	Pro		
				260					265					270			
cca	tcg	gag	ggc	aag	gtg	atg	aag	cgc	gcg	acg	atg	gtg	agc	gtg	gcg		864
Pro	Ser	Glu	Ala	Lys	Val	Met	Lys	Arg	Ala	Thr	Met	Val	Ser	Val	Ala		
		275					280					285					
acg	acg	acg	gtg	ttc	tac	atg	ctg	tgc	ggg	tgc	atg	ggg	tac	gcg	gcg		912
Thr	Thr	Thr	Val	Phe	Tyr	Met	Leu	Cys	Gly	Cys	Met	Gly	Tyr	Ala	Ala		
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Phe	Gly	Asp	Lys	Ser	Pro	Asp	Asn	Leu	Leu	Thr	Gly	Phe	Gly	Phe	Tyr		
305					310					315					320		
gag	ccg	ttc	tgg	ctg	ctc	gac	gtc	gcc	aac	gct	gcc	atc	gtc	gtg	cac		1008
Glu	Pro	Phe	Trp	Leu	Leu	Asp	Val	Ala	Asn	Ala	Ala	Ile	Val	Val	His		
				325					330					335			
ctc	gtc	ggc	gcc	tac	cag	gtg	ttc	gtc	cag	ccg	atc	ttc	gcg	ttc	gtc		1056
Leu	Val	Gly	Ala	Tyr	Gln	Val	Phe	Val	Gln	Pro	Ile	Phe	Ala	Phe	Val		
				340					345					350			
gag	cgg	tgg	ggc	ggc	ggc	agg	tgg	ccg	gac	ggc	ggc	ttc	atc	tcc	cgg		1104
Glu	Arg	Trp	Ala	Ala	Ala	Arg	Trp	Pro	Asp	Gly	Gly	Phe	Ile	Ser	Arg		
		355					360					365					
gag	ctc	cgc	gtg	ggc	ccc	ttc	tcg	ctc	agc	gtg	ttc	cgc	ctg	aca	tgg		1152
Glu	Leu	Arg	Val	Gly	Pro	Phe	Ser	Leu	Ser	Val	Phe	Arg	Leu	Thr	Trp		
					375						380						
cgc	acg	ggc	ttc	gtc	tgc	gcc	acc	acc	gtc	gtg	tcc	atg	ctc	ctc	ccg		1200
Arg	Thr	Ala	Phe	Val	Cys	Ala	Thr	Thr	Val	Val	Ser	Met	Leu	Leu	Pro		
385					390					395					400		
ttc	ttc	ggc	gac	gtg	gtg	ggg	ctc	ctc	ggc	gcc	gtc	tcg	ttc	tgg	ccg		1248
Phe	Phe	Gly	Asp	Val	Val	Gly	Leu	Leu	Gly	Ala	Val	Ser	Phe	Trp	Pro		
				405					410					415			
ctc	acc	gtc	tac	ttc	ccc	gtc	gag	atg	tac	atc	gcg	cag	cgc	ggc	gtg		1296
Leu	Thr	Val	Tyr	Phe	Pro	Val	Glu	Met	Tyr	Ile	Ala	Gln	Arg	Gly	Val		
				420					425					430			
cgg	cga	ggg	agc	ggc	cgg	tgg	ctc	tgc	ctc	aag	gtc	ctc	agc	gcc	gcc		1344
Arg	Arg	Gly	Ser	Ala	Arg	Trp	Leu	Cys	Leu	Lys	Val	Leu	Ser	Ala	Ala		
		435					440					445					
tgc	ctc	gtc	gtc	tcc	gtc	gcc	gcc	gcc	ggc	tcc	atc	gcc	gac	gtg			1392
Cys	Leu	Val	Val	Ser	Val	Ala	Ala	Ala	Gly	Ser	Ile	Ala	Asp	Val			
					455					460							
gtc	gac	ggc	ctc	aag	gtg	tac	cgg	ccg	ttc	agc	ggg	tag					1431
Val	Asp	Ala	Leu	Lys	Val	Tyr	Arg	Pro	Phe	Ser	Gly						
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<210> 591

<211> 476

<212> PRT

<213> Oryza sativa

<400> 591

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			20					25					30			
Ala	Arg	Arg	Met	Gly	Thr	Val	Trp	Thr	Ala	Ser	Ala	His	Ile	Ile	Thr	
			35				40					45				
Ala	Val	Ile	Gly	Ser	Gly	Val	Leu	Ser	Leu	Ala	Trp	Ala	Ile	Ala	Gln	
			50			55					60					
Leu	Gly	Trp	Val	Ala	Gly	Pro	Ala	Val	Met	Leu	Leu	Phe	Ala	Phe	Val	
65					70				75						80	
Ile	Tyr	Tyr	Thr	Ser	Thr	Leu	Leu	Ala	Glu	Cys	Tyr	Arg	Ser	Gly	Asp	
				85					90					95		

PF59082SeqList_PF59082.txt

Pro Cys Thr Gly Lys Arg Asn Tyr Thr Tyr Met Asp Ala Val Arg Ala
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 Asn Leu Gly Gly Ser Lys Val Arg Leu Cys Gly Val Ile Gln Tyr Ala
 115 120 125
 Asn Leu Phe Gly Val Ala Ile Gly Tyr Thr Ile Ala Ala Ser Ile Ser
 130 135 140
 Met Leu Ala Ile Lys Arg Ala Asp Cys Phe His Glu Lys Gly His Lys
 145 150 155 160
 Asn Pro Cys Arg Ser Ser Ser Asn Pro Tyr Met Ile Leu Phe Gly Val
 165 170 175
 Val Gln Ile Val Phe Ser Gln Ile Pro Asp Phe Asp Gln Ile Trp Trp
 180 185 190
 Leu Ser Ile Val Ala Ala Ile Met Ser Phe Thr Tyr Ser Thr Ile Gly
 195 200 205
 Leu Ser Leu Gly Ile Ala Gln Thr Val Ala Asn Gly Gly Phe Met Gly
 210 215 220
 Ser Leu Thr Gly Ile Ser Val Gly Thr Gly Val Thr Ser Met Gln Lys
 225 230 235 240
 Val Trp Arg Ser Leu Gln Ala Phe Gly Asp Ile Ala Phe Ala Tyr Ser
 245 250 255
 Tyr Ser Ile Ile Leu Ile Glu Ile Gln Asp Thr Ile Lys Ala Pro Pro
 260 265 270
 Pro Ser Glu Ala Lys Val Met Lys Arg Ala Thr Met Val Ser Val Ala
 275 280 285
 Thr Thr Thr Val Phe Tyr Met Leu Cys Gly Cys Met Gly Tyr Ala Ala
 290 295 300
 Phe Gly Asp Lys Ser Pro Asp Asn Leu Leu Thr Gly Phe Gly Phe Tyr
 305 310 315 320
 Glu Pro Phe Trp Leu Asp Val Ala Asn Ala Ala Ile Val Val His
 325 330 335
 Leu Val Gly Ala Tyr Gln Val Phe Val Gln Pro Ile Phe Ala Phe Val
 340 345 350
 Glu Arg Trp Ala Ala Ala Arg Trp Pro Asp Gly Gly Phe Ile Ser Arg
 355 360 365
 Glu Leu Arg Val Gly Pro Phe Ser Leu Ser Val Phe Arg Leu Thr Trp
 370 375 380
 Arg Thr Ala Phe Val Cys Ala Thr Thr Val Val Ser Met Leu Leu Pro
 385 390 395 400
 Phe Phe Gly Asp Val Gly Leu Leu Gly Ala Val Ser Phe Trp Pro
 405 410 415
 Leu Thr Val Tyr Phe Pro Val Glu Met Tyr Ile Ala Gln Arg Gly Val
 420 425 430
 Arg Arg Gly Ser Ala Arg Trp Leu Cys Leu Lys Val Leu Ser Ala Ala
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 Val Asp Ala Leu Lys Val Tyr Arg Pro Phe Ser Gly
 465 470 475

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 <211> 1449
 <212> DNA
 <213> Pisum sativum

<220>
 <221> CDS
 <222> (1)..(1449)

<400> 592
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 gat gta tcc att gat caa caa ctc gat tct aag ttt ttc gat gat gac 96
 Asp Val Ser Ile Asp Gln Gln Leu Asp Ser Lys Phe Phe Asp Asp 20 25 30
 20 25 30
 ggt cgc gtc aaa cga acc ggc aca tct tgg act gca agt gcc cat gta 144
 Gly Arg Val Lys Arg Thr Gly Thr Ser Trp Thr Ala Ser Ala His Val 35 40 45
 35 40 45
 ata aca gca gta att ggc tct gga gtg ctg tct cta gct tgg gct ata 192
 40 45 50 55 60
 Seite 747

PF59082SeqList_PF59082.txt

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Ala	Gln	Leu	Gly	Trp	Ile	Ala	Gly	Pro	Val	Val	Met	Ile	Leu	Phe	Ala	
65					70					75					80	
tgg	gtt	act	tat	tac	acc	tcg	gtt	ctt	ctc	gct	gaa	tgt	tat	cg	aat	288
Trp	Val	Thr	Tyr	Tyr	Thr	Ser	Val	Leu	Leu	Ala	Glu	Cys	Tyr	Arg	Asn	
				85					90					95		
ggt	gat	cca	gta	aat	ggc	aag	aga	aac	tac	act	tac	atg	gaa	gtt	gtt	336
Gly	Asp	Pro	Val	Asn	Gly	Lys	Arg	Asn	Tyr	Thr	Tyr	Met	Glu	Val	Val	
			100					105					110			
cat	tcg	aat	ctt	ggt	ggt	tta	caa	gtc	cag	ttt	tgt	ggg	ttc	att	cag	384
His	Ser	Asn	Leu	Gly	Gly	Leu	Gln	Val	Gln	Phe	Cys	Gly	Phe	Ile	Gln	
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tat	ctc	aac	ctt	att	ggg	gtc	gcg	att	gga	tac	acg	gta	gct	tct	gcc	432
Tyr	Leu	Asn	Leu	Ile	Gly	Val	Ala	Ile	Gly	Tyr	Thr	Val	Ala	Ser	Ala	
			130			135					140					
ata	agc	atg	atg	gcg	att	gaa	agg	tca	aat	tgt	tat	cat	agg	agt	gga	480
Ile	Ser	Met	Met	Ala	Ile	Glu	Arg	Ser	Asn	Cys	Tyr	His	Arg	Ser	Gly	
145					150					155					160	
gga	aaa	gat	cca	tgt	cat	atg	aac	agc	aac	gct	tac	atg	att	gct	ttt	528
Gly	Lys	Asp	Pro	Cys	His	Met	Asn	Ser	Asn	Ala	Tyr	Met	Ile	Ala	Phe	
				165				170						175		
ggt	gct	gtg	caa	att	ata	gtc	tct	caa	att	cca	gat	ttt	gat	cag	tta	576
Gly	Ala	Val	Gln	Ile	Ile	Val	Ser	Gln	Ile	Pro	Asp	Phe	Asp	Gln	Leu	
			180					185					190			
tgg	tgg	ctt	tcc	att	gtt	gct	gct	gtt	atg	tcc	ttt	aca	tat	tcg	acg	624
Trp	Trp	Leu	Ser	Ile	Val	Ala	Ala	Val	Met	Ser	Phe	Thr	Tyr	Ser	Thr	
			195			200						205				
att	ggt	cta	ggc	ctt	ggt	atc	gga	aaa	gtt	atg	gag	aac	aaa	aag	ttt	672
Ile	Gly	Leu	Gly	Leu	Gly	Ile	Gly	Lys	Val	Met	Glu	Asn	Lys	Lys	Phe	
						215					220					
gct	gga	acc	att	act	gga	gta	aat	gat	gtg	aca	aaa	gct	cag	aaa	act	720
Ala	Gly	Thr	Ile	Thr	Gly	Val	Asn	Asp	Val	Thr	Lys	Ala	Gln	Lys	Thr	
225					230					235					240	
tgg	ggg	agt	ttg	caa	gct	ctt	ggg	gac	ata	gct	ttt	gct	tat	tca	ttc	768
Trp	Gly	Ser	Leu	Gln	Ala	Leu	Gly	Asp	Ile	Ala	Phe	Ala	Tyr	Ser	Phe	
				245					250					255		
tcc	atg	att	ctt	ata	gaa	att	cag	gac	acg	gta	aaa	gca	cca	cca	ccg	816
Ser	Met	Ile	Leu	Ile	Glu	Ile	Gln	Asp	Thr	Val	Lys	Ala	Pro	Pro	Pro	
				260				265					270			
tca	gag	tcg	aaa	acc	atg	aag	aag	gct	aca	ttg	atc	agt	ggt	ata	gtg	864
Ser	Glu	Ser	Lys	Thr	Met	Lys	Lys	Ala	Thr	Leu	Ile	Ser	Val	Ile	Val	
				275				280				285				
aca	aca	ttt	ttc	tac	atg	ctt	tgc	ggt	tgt	tta	gga	tac	gca	gcg	ttt	912
Thr	Thr	Phe	Phe	Tyr	Met	Leu	Cys	Gly	Cys	Leu	Gly	Tyr	Ala	Ala	Phe	
				290		295					300					
gga	aat	tca	agt	ccc	gga	aac	ctt	tta	acc	ggt	ttc	gga	ttc	tat	aac	960
Gly	Asn	Ser	Ser	Pro	Gly	Asn	Leu	Leu	Thr	Gly	Phe	Gly	Phe	Tyr	Asn	
305					310					315					320	
cca	ttt	tgg	ctc	ctt	gac	ata	gcc	aat	gct	gcc	ata	gtg	att	cac	ctt	1008
Pro	Phe	Trp	Leu	Leu	Asp	Ile	Ala	Asn	Ala	Ala	Ile	Val	Ile	His	Leu	
				325					330					335		
att	ggt	gca	tac	caa	gtc	tat	tgc	caa	ccc	ctt	tat	gct	ttc	gtc	gaa	1056
Ile	Gly	Ala	Tyr	Gln	Val	Tyr	Cys	Gln	Pro	Leu	Tyr	Ala	Phe	Val	Glu	
				340				345					350			
aac	tac	atg	gtg	aaa	aga	ttt	cca	gac	aat	tat	ttt	ttg	aac	aag	aac	1104
Asn	Tyr	Met	Val	Lys	Arg	Phe	Pro	Asp	Asn	Tyr	Phe	Leu	Asn	Lys	Asn	
				355			360					365				
ata	aag	att	cca	atc	ccg	ggt	tta	gat	atg	tat	aaa	ctc	aac	ctt	ttc	1152
Ile	Lys	Ile	Pro	Ile	Pro	Gly	Leu	Asp	Met	Tyr	Lys	Leu	Asn	Leu	Phe	
						375					380					
aaa	ttg	gtt	tgg	agg	aca	gtt	ttt	gta	ata	tta	aca	act	ttg	gtc	tca	1200
Lys	Leu	Val	Trp	Arg	Thr	Val	Phe	Val	Ile	Leu	Thr	Thr	Leu	Val	Ser	
385					390					395					400	
atg	ctt	ctt	cca	ttc	ttc	aat	gat	att	gtt	gga	ctt	ctt	ggt	gca	ctt	1248
Met	Leu	Leu	Pro	Phe	Phe	Asn	Asp	Ile	Val	Gly	Leu	Leu	Gly	Ala	Leu	
				405					410					415		
gga	ttt	tgg	cct	cta	acg	gtt	tat	ttt	ccg	gtg	gag	atg	tat	ata	att	1296

PF59082SeqList_PF59082.txt

Gly	Phe	Trp	Pro	Leu	Thr	Val	Tyr	Phe	Pro	Val	Glu	Met	Tyr	Ile	Ile	
			420					425					430			
caa	aag	aaa	ata	cca	aag	tgg	agc	aca	aaa	tgg	aca	tgc	ctt	caa	ttg	1344
Gln	Lys	Lys	Ile	Pro	Lys	Trp	Ser	Thr	Lys	Trp	Thr	Cys	Leu	Gln	Leu	
		435					440					445				
ctt	agt	ggg	gct	tgt	ctt	ata	atc	act	ata	gca	gct	tca	gtt	ggg	tct	1392
Leu	Ser	Gly	Ala	Cys	Leu	Ile	Ile	Thr	Ile	Ala	Ala	Ser	Val	Gly	Ser	
	450					455				460						
att	gct	ggg	att	tat	ctt	gat	ctt	aaa	gtg	ttt	aag	cca	ttc	aag	act	1440
Ile	Ala	Gly	Ile	Tyr	Leu	Asp	Leu	Lys	Val	Phe	Lys	Pro	Phe	Lys	Thr	
465					470					475					480	
atc	tat	tga														1449
Ile	Tyr															

<210> 593
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 <212> PRT
 <213> Pisum sativum

<400> 593

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			20					25					30			
Gly	Arg	Val	Lys	Arg	Thr	Gly	Thr	Ser	Trp	Thr	Ala	Ser	Ala	His	Val	
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Ile	Thr	Ala	Val	Ile	Gly	Ser	Gly	Val	Leu	Ser	Leu	Ala	Trp	Ala	Ile	
	50				55						60					
Ala	Gln	Leu	Gly	Trp	Ile	Ala	Gly	Pro	Val	Val	Met	Ile	Leu	Phe	Ala	
65				70					75						80	
Trp	Val	Thr	Tyr	Tyr	Thr	Ser	Val	Leu	Leu	Ala	Glu	Cys	Tyr	Arg	Asn	
			85					90						95		
Gly	Asp	Pro	Val	Asn	Gly	Lys	Arg	Asn	Tyr	Thr	Tyr	Met	Glu	Val	Val	
		100						105					110			
His	Ser	Asn	Leu	Gly	Gly	Leu	Gln	Val	Gln	Phe	Cys	Gly	Phe	Ile	Gln	
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Tyr	Leu	Asn	Leu	Ile	Gly	Val	Ala	Ile	Gly	Tyr	Thr	Val	Ala	Ser	Ala	
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Ile	Ser	Met	Met	Ala	Ile	Glu	Arg	Ser	Asn	Cys	Tyr	His	Arg	Ser	Gly	
145				150					155						160	
Gly	Lys	Asp	Pro	Cys	His	Met	Asn	Ser	Asn	Ala	Tyr	Met	Ile	Ala	Phe	
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Gly	Ala	Val	Gln	Ile	Ile	Val	Ser	Gln	Ile	Pro	Asp	Phe	Asp	Gln	Leu	
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Trp	Trp	Leu	Ser	Ile	Val	Ala	Ala	Val	Met	Ser	Phe	Thr	Tyr	Ser	Thr	
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Ile	Gly	Leu	Gly	Leu	Gly	Ile	Gly	Lys	Val	Met	Glu	Asn	Lys	Lys	Phe	
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Ala	Gly	Thr	Ile	Thr	Gly	Val	Asn	Asp	Val	Thr	Lys	Ala	Gln	Lys	Thr	
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Trp	Gly	Ser	Leu	Gln	Ala	Leu	Gly	Asp	Ile	Ala	Phe	Ala	Tyr	Ser	Phe	
		245						250					255			
Ser	Met	Ile	Leu	Ile	Glu	Ile	Gln	Asp	Thr	Val	Lys	Ala	Pro	Pro	Pro	
		260					265						270			
Ser	Glu	Ser	Lys	Thr	Met	Lys	Lys	Ala	Thr	Leu	Ile	Ser	Val	Ile	Val	
		275				280						285				
Thr	Thr	Phe	Phe	Tyr	Met	Leu	Cys	Gly	Cys	Leu	Gly	Tyr	Ala	Ala	Phe	
	290				295						300					
Gly	Asn	Ser	Ser	Pro	Gly	Asn	Leu	Leu	Thr	Gly	Phe	Gly	Phe	Tyr	Asn	
305				310					315						320	
Pro	Phe	Trp	Leu	Leu	Asp	Ile	Ala	Asn	Ala	Ala	Ile	Val	Ile	His	Leu	
		325					330						335			
Ile	Gly	Ala	Tyr	Gln	Val	Tyr	Cys	Gln	Pro	Leu	Tyr	Ala	Phe	Val	Glu	
		340					345						350			
Asn	Tyr	Met	Val	Lys	Arg	Phe	Pro	Asp	Asn	Tyr	Phe	Leu	Asn	Lys	Asn	
	355						360					365				
Ile	Lys	Ile	Pro	Ile	Pro	Gly	Leu	Asp	Met	Tyr	Lys	Leu	Asn	Leu	Phe	
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PF59082SeqList_PF59082.txt

Lys Leu Val Trp Arg Thr Val Phe Val Ile Leu Thr Thr Leu Val Ser
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 405 410 415
 Gly Phe Trp Pro Leu Thr Val Tyr Phe Pro Val Glu Met Tyr Ile Ile
 420 425 430
 Gln Lys Lys Ile Pro Lys Trp Ser Thr Lys Trp Thr Cys Leu Gln Leu
 435 440 445
 Leu Ser Gly Ala Cys Leu Ile Ile Thr Ile Ala Ala Ser Val Gly Ser
 450 455 460
 Ile Ala Gly Ile Tyr Leu Asp Leu Lys Val Phe Lys Pro Phe Lys Thr
 465 470 475 480
 Ile Tyr

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 <212> DNA
 <213> Oryza sativa

<220>
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 Thr Ala Val Ile Gly Ser Gly Val Leu Ala Leu Pro Trp Ser Val Ala
 35 40 45
 cag atg ggg tgg gtg ctc ggc ccc atc gcc ctc gtc tgc gcc tac 192
 Gln Met Gly Trp Val Leu Gly Pro Ile Ala Leu Val Val Cys Ala Tyr
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 Ile Thr Tyr Tyr Thr Ala Val Leu Leu Cys Asp Cys Tyr Arg Thr Pro
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 gac ccc gtc cac ggc aag cgg aac tac acc tac atg gac gtc gtc cgc 288
 Asp Pro Val His Gly Lys Arg Asn Tyr Thr Tyr Met Asp Val Val Arg
 85 90 95
 tca tgc ctc ggg cct cga gac gtg gtc gtg tgt ggc att gcg cag tac 336
 Ser Cys Leu Gly Pro Arg Asp Val Val Val Cys Gly Ile Ala Gln Tyr
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 gcg att ctc tgg ggc gca atg gtg ggt tac acc atc acg acc gct acg 384
 Ala Ile Leu Trp Gly Ala Met Val Gly Tyr Thr Ile Thr Thr Ala Thr
 115 120 125
 agc atc atg tca gtg gtg cgc acg aac tgc cac cac tac aag ggg ccg 432
 Ser Ile Met Ser Val Val Arg Thr Asn Cys His His Tyr Lys Gly Pro
 130 135 140
 gac gcg acc tgc ggc tcg tcc ggg acg atg tac atg gtg ctg ttc ggc 480
 Asp Ala Thr Cys Gly Ser Ser Gly Thr Met Tyr Met Val Leu Phe Gly
 145 150 155 160
 ctc gcg gag gtc gtc ctg tcc cag tgc ccg agc ctg gag ggg gtg acg 528
 Leu Ala Glu Val Val Leu Ser Gln Cys Pro Ser Leu Glu Gly Val Thr
 165 170 175
 ctc atc tcc gtc gtc gcc gcc gtc atg tcg ttc acc tac tcc ttc gtc 576
 Leu Ile Ser Val Val Ala Ala Val Met Ser Phe Thr Tyr Ser Phe Val
 180 185 190
 ggg ctc ttc ctc agc gcc gct aag gtc gcg tcg cac ggc gcg gcg cac 624
 Gly Leu Phe Leu Ser Ala Ala Lys Val Ala Ser His Gly Ala Ala His
 195 200 205
 ggc acc ctc ctc ggc gtc agg gtc ggc gcc gga ggc gtc acc gcg tcg 672
 Gly Thr Leu Leu Gly Val Arg Val Gly Ala Gly Gly Val Thr Ala Ser
 210 215 220
 acc aag gcg tgg cac ttc ctg cag gcg ctc ggg aac atc gcc ttc gcg 720
 Thr Lys Ala Trp His Phe Leu Gln Ala Leu Gly Asn Ile Ala Phe Ala

PF59082SeqList_PF59082.txt

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ccg	ccg	tcg	gag	aac	gtg	acg	atg
Pro	Pro	Ser	Glu	Asn	Val	Thr	Met
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ggc	gtc	acg	acc	gtc	ttc	tac	gtg
Gly	Val	Thr	Thr	Val	Phe	Tyr	Val
				275			
gcg	ttc	ggc	aac	gcc	gcg	ccc	ggg
Ala	Phe	Gly	Asn	Ala	Ala	Pro	Gly
				290			
ccg	ttc	tgg	ctc	gtc	gac	atc	gcc
Pro	Phe	Trp	Leu	Val	Asp	Ile	Ala
				305			
gtc	gga	gcg	tac	cag	gtg	tac	gcg
Val	Gly	Ala	Tyr	Gln	Val	Tyr	Ala
				325			
aag	tgg	ctg	gcg	agc	cgt	tgg	ccg
Lys	Trp	Leu	Ala	Ser	Arg	Trp	Pro
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tac	gcg	gtg	ccg	ctg	ggc	ggc	ggg
Tyr	Ala	Val	Pro	Leu	Gly	Gly	Gly
				355			
aag	ctg	gtg	ctg	cgc	acg	gcg	ttc
Lys	Leu	Val	Leu	Arg	Thr	Ala	Phe
				370			
ctg	gtg	ctg	ccg	ttc	ttc	aac	gcc
Leu	Val	Leu	Pro	Phe	Asn	Ala	Val
				385			
gcg	ttc	tgg	ccg	ctc	acg	gtg	tac
Ala	Phe	Trp	Pro	Leu	Thr	Val	Tyr
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cag	gcg	aag	gtg	cag	aga	ggc	agc
Gln	Ala	Lys	Val	Gln	Arg	Gly	Ser
				420			
ctc	aac	gtc	ggc	gcg	ctc	gtc	gtg
Leu	Asn	Val	Gly	Ala	Leu	Val	Val
				435			
gtg	gcc	gac	atg	gcg	cag	cgc	ctg
Val	Ala	Asp	Met	Ala	Gln	Arg	Leu
				450			
cag	ctc	tga					
Gln	Leu						
465							

768

816

864

912

960

1008

1056

1104

1152

1200

1248

1296

1344

1392

1401

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 <212> PRT
 <213> Oryza sativa

<400> 595
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 20 Thr Ala Val Ile Gly Ser Gly Val Leu Ala Leu Pro Trp Ser Val Ala
 35 Gln Met Gly Trp Val Leu Gly Pro Ile Ala Leu Val Val Cys Ala Tyr
 50 Ile Thr Tyr Tyr Thr Ala Val Leu Leu Cys Asp Cys Tyr Arg Thr Pro
 65 Asp Pro Val His Gly Lys Arg Asn Tyr Thr Tyr Met Asp Val Val Arg
 80 Ser Cys Leu Gly Pro Arg Asp Val Val Val Cys Gly Ile Ala Gln Tyr
 95 Ala Ile Leu Trp Gly Ala Met Val Gly Tyr Thr Thr Thr Ala Thr
 110 115 120 125

PF59082SeqList_PF59082.txt

Ser Ile Met Ser Val Val Arg Thr Asn Cys His His Tyr Lys Gly Pro
130 135 140
Asp Ala Thr Cys Gly Ser Ser Gly Thr Met Tyr Met Val Leu Phe Gly
145 150 155 160
Leu Ala Glu Val Val Leu Ser Gln Cys Pro Ser Leu Glu Gly Val Thr
165 170 175
Leu Ile Ser Val Val Ala Ala Val Met Ser Phe Thr Tyr Ser Phe Val
180 185 190
Gly Leu Phe Leu Ser Ala Ala Lys Val Ala Ser His Gly Ala Ala His
195 200 205
Gly Thr Leu Leu Gly Val Arg Val Gly Ala Gly Gly Val Thr Ala Ser
210 215 220
Thr Lys Ala Trp His Phe Leu Gln Ala Leu Gly Asn Ile Ala Phe Ala
225 230 235 240
Tyr Thr Tyr Ser Met Leu Leu Ile Glu Ile Gln Asp Thr Val Lys Ser
245 250 255
Pro Pro Ser Glu Asn Val Thr Met Lys Arg Ala Ser Leu Tyr Gly Ile
260 265 270
Gly Val Thr Thr Val Phe Tyr Val Ser Ile Gly Cys Val Gly Tyr Ala
275 280 285
Ala Phe Gly Asn Ala Ala Pro Gly Asn Val Leu Thr Gly Phe Leu Glu
290 295 300
Pro Phe Trp Leu Val Asp Ile Ala Asn Val Ala Val Val Ile His Leu
305 310 315 320
Val Gly Ala Tyr Gln Val Tyr Ala Gln Pro Val Phe Ala Cys Tyr Glu
325 330 335
Lys Trp Leu Ala Ser Arg Trp Pro Glu Ser Ala Phe Phe His Arg Glu
340 345 350
Tyr Ala Val Pro Leu Gly Gly Gly Arg Ala Val Arg Phe Thr Leu Cys
355 360 365
Lys Leu Val Leu Arg Thr Ala Phe Val Ala Val Thr Thr Val Val Ser
370 375 380
Leu Val Leu Pro Phe Phe Asn Ala Val Leu Gly Leu Leu Gly Ala Val
385 390 395 400
Ala Phe Trp Pro Leu Thr Val Tyr Phe Pro Val Thr Met Tyr Met Ala
405 410 415
Gln Ala Lys Val Gln Arg Gly Ser Arg Lys Trp Val Ala Leu Gln Ala
420 425 430
Leu Asn Val Gly Ala Leu Val Val Ser Leu Leu Ala Ala Val Gly Ser
435 440 445
Val Ala Asp Met Ala Gln Arg Leu Arg His Val Thr Ile Phe Gln Thr
450 455 460
Gln Leu
465

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<222> (1)..(1380)

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aag gag agg agg aca ggg acg gtg tgg acg gcg acg gcg cac ata atc 96
Lys Glu Arg Arg Thr Gly Thr Val Trp Thr Ala Thr Ala His Ile Ile
20 25 30
acg gcg gtg atc ggg tcc ggc gtg ctg tcg ctg gcg tgg gcg atg gcg 144
Thr Ala Val Ile Gly Ser Gly Val Leu Ser Leu Ala Trp Ala Met Ala
35 40 45
cag ctg ggg tgg gtg gct ggc ccc atc acc ctc ctc ttc gcc gcc 192
Gln Leu Gly Trp Val Ala Gly Pro Ile Thr Leu Leu Leu Phe Ala Ala
50 55 60
atc acc ttc tac acc tgc ggc ctc ctc tcc gac tgc tac cgc gtc ggc 240
Ile Thr Phe Tyr Thr Cys Gly Leu Leu Ser Asp Cys Tyr Arg Val Gly
Seite 752

PF59082SeqList_PF59082.txt

65																70																75																80
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Asp	Pro	Ala	Thr	Gly	Lys	Arg	Asn	Tyr	Thr	Tyr	Thr	Asp	Ala	Val	Lys																																	
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tcc	tac	ctc	ggt	ggc	tgg	cac	gtc	tgg	ttc	tgc	ggc	ttc	tgc	cag	tac	336																																
Ser	Tyr	Leu	Gly	Gly	Trp	His	Val	Trp	Phe	Cys	Gly	Phe	Cys	Gln	Tyr																																	
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145					150					155					160																																	
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tgg	ctg	tcc	atc	atc	gcc	gcc	gtc	atg	tcc	ttc	tcg	tac	gcc	gcc	atc	576																																
Trp	Leu	Ser	Ile	Ile	Ala	Ala	Val	Met	Ser	Phe	Ser	Tyr	Ala	Ala	Ile																																	
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Thr	Thr	Leu	Thr	Gly	Thr	Val	Val	Gly	Val	Asp	Val	Asp	Ala	Thr	Gln																																	
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Lys	Val	Trp	Leu	Thr	Phe	Gln	Ala	Leu	Gly	Asn	Val	Ala	Phe	Ala	Tyr																																	
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Phe	Val	Ala	Val	Ile	Thr	Leu	Leu	Ala	Ile	Leu	Met	Pro	Phe	Phe	Asn																																	
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Phe	Phe	Pro	Val	Glu	Met	Tyr	Ile	Arg	Gln	Arg	Gln	Leu	Pro	Arg	Phe																																	
			405					410						415																																		
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Ser	Ala	Lys	Trp	Val	Ala	Leu	Gln	Ser	Leu	Ser	Leu	Val	Cys	Phe	Leu																																	
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PF59082SeqList_PF59082.txt

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1380

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<212> PRT
<213> Oryza sativa

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Thr Ala Val Ile Gly Ser Gly Val Leu Ser Leu Ala Trp Ala Met Ala
35 40 45
Gln Leu Gly Trp Val Ala Gly Pro Ile Thr Leu Leu Leu Phe Ala Ala
50 55 60
Ile Thr Phe Tyr Thr Cys Gly Leu Leu Ser Asp Cys Tyr Arg Val Gly
65 70 75 80
Asp Pro Ala Thr Gly Lys Arg Asn Tyr Thr Tyr Thr Asp Ala Val Lys
85 90 95
Ser Tyr Leu Gly Gly Trp His Val Trp Phe Cys Gly Phe Cys Gln Tyr
100 105 110
Val Asn Met Phe Gly Thr Gly Ile Gly Tyr Thr Ile Thr Ala Ser Ile
115 120 125
Ser Ala Ala Ala Ile Asn Lys Ser Asn Cys Tyr His Trp Arg Gly His
130 135 140
Gly Thr Asp Cys Ser Gln Asn Thr Ser Ala Tyr Ile Ile Gly Phe Gly
145 150 155 160
Val Leu Gln Ala Leu Phe Cys Gln Leu Pro Asn Phe His Gln Leu Trp
165 170 175
Trp Leu Ser Ile Ile Ala Ala Val Met Ser Phe Ser Tyr Ala Ala Ile
180 185 190
Ala Val Gly Leu Ser Leu Ala Gln Thr Ile Met Asp Pro Leu Gly Arg
195 200 205
Thr Thr Leu Thr Gly Thr Val Val Gly Val Asp Val Asp Ala Thr Gln
210 215 220
Lys Val Trp Leu Thr Phe Gln Ala Leu Gly Asn Val Ala Phe Ala Tyr
225 230 235 240
Ser Tyr Ala Ile Ile Leu Ile Glu Ile Gln Asp Thr Leu Arg Ser Pro
245 250 255
Pro Pro Glu Asn Ala Thr Met Arg Arg Ala Thr Ala Ala Gly Ile Ser
260 265 270
Thr Thr Thr Gly Phe Tyr Leu Leu Cys Gly Cys Leu Gly Tyr Ser Ala
275 280 285
Phe Gly Asn Ala Ala Pro Gly Asn Ile Leu Thr Gly Phe Gly Phe Tyr
290 295 300
Glu Pro Tyr Trp Leu Val Asp Val Ala Asn Ala Cys Ile Val Val His
305 310 315 320
Leu Val Gly Gly Phe Gln Val Phe Cys Gln Pro Leu Phe Ala Ala Val
325 330 335
Glu Gly Gly Val Ala Arg Arg Cys Pro Gly Leu Leu Gly Gly Ala
340 345 350
Gly Arg Ala Ser Gly Val Asn Val Phe Arg Leu Val Trp Arg Thr Ala
355 360 365
Phe Val Ala Val Ile Thr Leu Leu Ala Ile Leu Met Pro Phe Phe Asn
370 375 380
Ser Ile Leu Gly Ile Leu Gly Ser Ile Ala Phe Trp Pro Leu Thr Val
385 390 400
Phe Phe Pro Val Glu Met Tyr Ile Arg Gln Arg Gln Leu Pro Arg Phe
405 410 415
Ser Ala Lys Trp Val Ala Leu Gln Ser Leu Ser Leu Val Cys Phe Leu
420 425 430
Val Thr Val Ala Ala Cys Ala Ala Ser Ile Gln Gly Val Leu Asp Ser
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Leu Lys Thr Tyr Val Pro Phe Lys Thr Arg Ser
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PF59082SeqList_PF59082.txt

<210> 598
 <211> 1464
 <212> DNA
 <213> Oryza sativa

<220>
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 <222> (1)..(1464)

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ggc ggc ggc tac tac gcc acc cac ccg cac ggc ggc gcc ggc ggc gag      96
Gly Gly Gly Tyr Tyr Ala Thr His Pro His Gly Gly Ala Gly Gly Glu
20      25      30
gac gtc gac gac gac ggc aag cag cgg cga acc ggt aac gta tgg acg      144
Asp Val Asp Asp Asp Gly Lys Gln Arg Arg Thr Gly Asn Val Trp Thr
35      40      45
gcg agc gcg cac atc atc acg gcg gtg atc ggc tcc ggc gtg ctc tct      192
Ala Ser Ala His Ile Ile Thr Ala Val Ile Gly Ser Gly Val Leu Ser
50      55      60
ctc gca tgg gca acg gcg cag ctc ggc tgg gtg gtc ggc ccg gtg act      240
Leu Ala Trp Ala Thr Ala Gln Leu Gly Trp Val Val Gly Pro Val Thr
65      70      75
ctg atg ctc ttc gcc ctc atc acg tac tac acc tct ggc ctc ctc gcc      288
Leu Met Leu Phe Ala Leu Ile Thr Tyr Tyr Thr Ser Gly Leu Leu Ala
85      90      95
gac tgc tac cgc act ggc gat ccg gtc agc ggc aag cgc aac tac acc      336
Asp Cys Tyr Arg Thr Gly Asp Pro Val Ser Gly Lys Arg Asn Tyr Thr
100      105      110
tac atg gat gcc gtt gcg gcc tac tta ggt ggc tgg caa gtc tgg tcc      384
Tyr Met Asp Ala Val Ala Ala Tyr Leu Gly Gly Trp Gln Val Trp Ser
115      120      125
tgt ggt gtt ttc caa tat gtc aac ctg gtt ggc aca gca att ggc tac      432
Cys Gly Val Phe Gln Tyr Val Asn Leu Val Gly Thr Ala Ile Gly Tyr
130      135      140
aca atc aca gca tcc atc agc gca gcg gct gtg cac aag gcc aac tgc      480
Thr Ile Thr Ala Ser Ile Ser Ala Ala Ala Val His Lys Ala Asn Cys
145      150      155
tac cac aag aac ggc cac gat gcc gat tgc ggt gtc tac gac acc acg      528
Tyr His Lys Asn Gly His Asp Ala Asp Cys Gly Val Tyr Asp Thr Thr
165      170      175
tac atg atc gtc ttt gga gtc gtc cag atc ttc ttc tcc atg ctg ccc      576
Tyr Met Ile Val Phe Gly Val Val Gln Ile Phe Phe Ser Met Leu Pro
180      185      190
aac ttc agt gac ctc tca tgg ctt tcc atc ctc gcc gcg gtc atg tca      624
Asn Phe Ser Asp Leu Ser Trp Leu Ser Ile Leu Ala Ala Val Met Ser
195      200      205
ttc tca tac tcg acc att gcc gtt ggc ctc tcg ctt gcg cga aca ata      672
Phe Ser Tyr Ser Thr Ile Ala Val Gly Leu Ser Leu Ala Arg Thr Ile
210      215      220
tca ggt gct act ggt aag act act ctg act ggc gtt gag gtt gga gtt      720
Ser Gly Ala Thr Gly Lys Thr Thr Leu Thr Gly Val Glu Val Gly Val
225      230      235
gac gtc act tca gcc cag aag atc tgg ctc gcg ttc caa gcg ctc ggt      768
Asp Val Thr Ser Ala Gln Lys Ile Trp Leu Ala Phe Gln Ala Leu Gly
245      250      255
gac atc gcg ttc gcc tac tcc tac tcc atg atc ctt ata gaa att cag      816
Asp Ile Ala Phe Ala Tyr Ser Tyr Ser Met Ile Leu Ile Glu Ile Gln
260      265      270
gac acg gtg aag tct cca ccg gcg gag aac aag acg atg aag aag gca      864
Asp Thr Val Lys Ser Pro Pro Ala Glu Asn Lys Thr Met Lys Lys Ala
275      280      285
acg ctg ctg ggg gtg tcg acc acg acg gcg ttc tac atg ctg tgc ggg      912
Thr Leu Leu Gly Val Ser Thr Thr Thr Ala Phe Tyr Met Leu Cys Gly
290      295      300
tgc ctg ggg tac gcg gcg ttc ggg aac gcg gcg ccg ggg aac atg ctc      960

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PF59082SeqList_PF59082.txt

Cys 305	Leu	Gly	Tyr	Ala	Ala 310	Phe	Gly	Asn	Ala 315	Pro	Gly	Asn	Met	Leu 320	
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gtc tgc atc gtg gtc cac ctg gtc ggc gcc tac cag gtg ttc tgc cag	Val Cys Ile Val Val His Leu Val Gly Ala Tyr Gln Val Phe Cys Gln	1056													
ccc atc ttc ggc gcc gtc gag acg ttc gcc gcc agg cgg tgg ccg ggc	Pro Ile Phe Ala Ala Val Glu Thr Phe Ala Ala Arg Trp Pro Gly	1104													
tcg gag ttc atc acc cgg gag cgc ccc gtc gtg gcc ggc agg tcg ttc	Ser Glu Phe Ile Thr Arg Glu Arg Pro Val Val Ala Gly Arg Ser Phe	1152													
agc gtc aac atg ttc agg ctg acg tgg cgg acg gcg ttc gtg gtc gtc	Ser Val Asn Met Phe Arg Leu Thr Trp Arg Thr Ala Phe Val Val Val	1200													
agc acg gtg ctc gcc atc gtg atg ccc ttc ttc aac gac atc ctg ggc	Ser Thr Val Leu Ala Ile Val Met Pro Phe Phe Asn Asp Ile Leu Gly	1248													
ttc ctc ggc gcc gtc ggg ttc tgg ccg ctg acg gtg tac tac ccg gtg	Phe Leu Gly Ala Val Gly Phe Trp Pro Leu Thr Val Tyr Tyr Pro Val	1296													
gag atg tac atc cgg cag cgg cgg ata cag cgg tac acg tcc agg tgg	Glu Met Tyr Ile Arg Gln Arg Ile Gln Arg Tyr Thr Ser Arg Trp	1344													
gtg gcg ctg cag acg ctc agc ctc ctc tgc ttc ctc gtc tcg ctc gcc	Val Ala Leu Gln Thr Leu Ser Leu Leu Cys Phe Leu Val Ser Leu Ala	1392													
tcc gcc gtc gcc tcc atc gag ggc gtc agc gag tgc ctc aag cac tac	Ser Ala Val Ala Ser Ile Glu Gly Val Ser Glu Ser Leu Lys His Tyr	1440													
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<210> 599

<211> 487

<212> PRT

<213> Oryza sativa

<400> 599

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Asp	Val	Asp 35	Asp	Asp	Gly	Lys	Gln 40	Arg	Arg	Thr	Gly	Asn 45	Val	Trp	Thr
Ala	Ser 50	Ala	His	Ile	Ile	Thr 55	Ala	Val	Ile	Gly	Ser 60	Gly	Val	Leu	Ser
Leu 65	Ala	Trp	Ala	Thr	Ala 70	Gln	Leu	Gly	Trp	Val 75	Val	Gly	Pro	Val	Thr 80
Leu	Met	Leu	Phe	Ala 85	Leu	Ile	Thr	Tyr	Tyr 90	Thr	Ser	Gly	Leu	Leu 95	Ala
Asp	Cys	Tyr	Arg 100	Thr	Gly	Asp	Pro	Val 105	Ser	Gly	Lys	Arg	Asn 110	Tyr	Thr
Tyr	Met	Asp 115	Ala	Val	Ala	Ala	Tyr 120	Leu	Gly	Gly	Trp	Gln 125	Val	Trp	Ser
Cys	Gly 130	Val	Phe	Gln	Tyr	Val 135	Asn	Leu	Val	Gly	Thr 140	Ala	Ile	Gly	Tyr
Thr 145	Ile	Thr	Ala	Ser	Ile 150	Ser	Ala	Ala	Ala	Val 155	His	Lys	Ala	Asn	Cys 160
Tyr	His	Lys	Asn 165	Gly	His	Asp	Ala	Asp	Cys 170	Gly	Val	Tyr	Asp	Thr 175	Thr
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Asn	Phe	Ser 195	Asp	Leu	Ser	Trp	Leu 200	Ser	Ile	Leu	Ala	Ala 205	Val	Met	Ser
Phe	Ser	Tyr	Ser	Thr	Ile	Ala	Val	Gly	Leu	Ser	Leu	Ala	Arg	Thr	Ile

PF59082SeqList_PF59082.txt

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Asp Ile Ala Phe Ala Tyr Ser Tyr Ser Met Ile Leu Ile Glu Ile Gln
245
Asp Thr Val Lys Ser Pro Pro Ala Glu Asn Lys Thr Met Lys Lys Ala
250
Thr Leu Leu Gly Val Ser Thr Thr Thr Ala Phe Tyr Met Leu Cys Gly
260
Cys Leu Gly Tyr Ala Ala Phe Gly Asn Ala Ala Pro Gly Asn Met Leu
270
Thr Gly Phe Gly Phe Tyr Glu Pro Tyr Trp Leu Ile Asp Phe Ala Asn
285
Val Cys Ile Val Val His Leu Val Gly Ala Tyr Gln Val Phe Cys Gln
290
Pro Ile Phe Ala Ala Val Glu Thr Phe Ala Ala Arg Arg Trp Pro Gly
300
Ser Glu Phe Ile Thr Arg Glu Arg Pro Val Val Ala Gly Arg Ser Phe
310
Ser Val Asn Met Phe Arg Leu Thr Trp Arg Thr Ala Phe Val Val Val
320
Ser Thr Val Leu Ala Ile Val Met Pro Phe Phe Asn Asp Ile Leu Gly
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Phe Leu Gly Ala Val Gly Phe Trp Pro Leu Thr Val Tyr Tyr Pro Val
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Glu Met Tyr Ile Arg Gln Arg Arg Ile Gln Arg Tyr Thr Ser Arg Trp
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Val Ala Leu Gln Thr Leu Ser Leu Leu Cys Phe Leu Val Ser Leu Ala
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Ser Ala Val Ala Ser Ile Glu Gly Val Ser Glu Ser Leu Lys His Tyr
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<220>
 <221> CDS
 <222> (1)..(1491)

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Ala Met Glu Val Val Ala Ala Glu Leu Gly His Thr Ala Gly Ser Lys
20
ctg tac gac gac gac ggc cgc ctc aag cgc acc ggg acg atg tgg acg      144
Leu Tyr Asp Asp Asp Gly Arg Leu Lys Arg Thr Gly Thr Met Trp Thr
35
gcg agc gcg cac atc atc acg gcg gtg atc ggc tcc ggc gtg ctg tcg      192
Ala Ser Ala His Ile Ile Thr Ala Val Ile Gly Ser Gly Val Leu Ser
50
ctg ggg tgg gcg atc gcg cag ctg ggt tgg gtg gcc ggc ccc gcc gtc      240
Leu Gly Trp Ala Ile Ala Gln Leu Gly Trp Val Ala Gly Pro Ala Val
65
atg ctg ctc ttc tgc ttc gtc acc tac tac acc tcc gcg ctg ctc gcc      288
Met Leu Leu Phe Ser Phe Val Thr Tyr Tyr Thr Ser Ala Leu Leu Ala
85
gac tgc tac cgc tcc ggc gac gag agc acc ggc aag cgc aac tac acc      336
Asp Cys Tyr Arg Ser Gly Asp Glu Ser Thr Gly Lys Arg Asn Tyr Thr
100
tac atg gac gcc gtg aac gcc aac ctg agt ggc atc aag gtc cag gtc      384
Tyr Met Asp Ala Val Asn Ala Asn Leu Ser Gly Ile Lys Val Gln Val

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PF59082SeqList_PF59082.txt

[illegible]

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 <213> Oryza sativa

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 Leu Tyr Asp Asp Gly Arg Leu Lys Arg Thr Gly Thr Met Trp Thr
 35 40 45
 Ala Ser Ala His Ile Ile Thr Ala Val Ile Gly Ser Gly Val Leu Ser
 50 55 60
 Leu Gly Trp Ala Ile Ala Gln Leu Gly Trp Val Ala Gly Pro Ala Val
 65 70 75 80
 Met Leu Leu Phe Ser Phe Val Thr Tyr Tyr Thr Ser Ala Leu Leu Ala
 85 90 95
 Asp Cys Tyr Arg Ser Gly Asp Glu Ser Thr Gly Lys Arg Asn Tyr Thr
 100 105 110
 Tyr Met Asp Ala Val Asn Ala Asn Leu Ser Gly Ile Lys Val Gln Val
 115 120 125
 Cys Gly Phe Leu Gln Tyr Ala Asn Ile Val Gly Val Ala Ile Gly Tyr
 130 135 140
 Thr Ile Ala Ala Ser Ile Ser Met Leu Ala Ile Lys Arg Ala Asn Cys
 145 150 155 160
 Phe His Val Glu Gly His Gly Asp Pro Cys Asn Ile Ser Ser Thr Pro
 165 170 175
 Tyr Met Ile Ile Phe Gly Val Ala Glu Ile Phe Phe Ser Gln Ile Pro
 180 185 190
 Asp Phe Asp Gln Ile Ser Trp Leu Ser Ile Leu Ala Ala Val Met Ser
 195 200 205
 Phe Thr Tyr Ser Thr Ile Gly Leu Gly Leu Gly Val Val Gln Val Val
 210 215 220
 Ala Asn Gly Gly Val Lys Gly Ser Leu Thr Gly Ile Ser Ile Gly Val
 225 230 235 240
 Val Thr Pro Met Asp Lys Val Trp Arg Ser Leu Gln Ala Phe Gly Asp
 245 250 255
 Ile Ala Phe Ala Tyr Ser Tyr Ser Leu Ile Leu Ile Glu Ile Gln Asp
 260 265 270
 Thr Ile Arg Ala Pro Pro Pro Ser Glu Ser Arg Val Met Arg Arg Ala
 275 280 285
 Thr Val Val Ser Val Ala Val Thr Thr Leu Phe Tyr Met Leu Cys Gly
 290 295 300
 Cys Thr Gly Tyr Ala Ala Phe Gly Asp Ala Ala Pro Gly Asn Leu Leu
 305 310 315 320
 Thr Gly Phe Gly Phe Tyr Glu Pro Phe Trp Leu Leu Asp Val Ala Asn
 325 330 335
 Ala Ala Ile Val Val His Leu Val Gly Ala Tyr Gln Val Tyr Cys Gln
 340 345 350
 Pro Leu Phe Ala Phe Val Glu Lys Trp Ala Gln Gln Arg Trp Pro Lys
 355 360 365
 Ser Trp Tyr Ile Thr Lys Asp Ile Asp Val Pro Leu Ser Leu Ser Gly
 370 375 380
 Gly Gly Gly Gly Gly Arg Cys Tyr Lys Leu Asn Leu Phe Arg Leu
 385 390 395 400
 Thr Trp Arg Ser Ala Phe Val Val Ala Thr Thr Val Val Ser Met Leu
 405 410 415
 Leu Pro Phe Phe Asn Asp Val Val Gly Phe Leu Gly Ala Val Gly Phe
 420 425 430
 Trp Pro Leu Thr Val Tyr Phe Pro Val Glu Met Tyr Ile Val Gln Lys
 435 440 445
 Arg Ile Pro Arg Trp Ser Thr Arg Trp Val Cys Leu Gln Leu Leu Ser
 450 455 460

PF59082SeqList_PF59082.txt

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<213> Oryza sativa

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<222> (1)..(1455)

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gcg gcg tac cct cct ccg ctg cgg cgg agc atc aac gac gac gac gtt 96
Ala Ala Tyr Pro Pro Pro Leu Arg Arg Ser Ile Asn Asp Asp Asp Val
20 25 30
gac gac gac ggg aag ccc aag cga aca gga acg gag tgg acg gcg agc 144
Asp Asp Asp Gly Lys Pro Lys Arg Thr Gly Thr Glu Trp Thr Ala Ser
35 40 45
gcg cac atc gtc acg gcg gtg ggc tcc ggc gtg ctg tcg ctg gca 192
Ala His Ile Val Thr Ala Val Val Gly Ser Gly Val Leu Ser Leu Ala
50 55 60
tgg tcc acg gcg cag ctg ggc tgg gtc gcc ggc ccg gcc acc ctg gtc 240
Trp Ser Thr Ala Gln Leu Gly Trp Val Ala Gly Pro Ala Thr Leu Val
65 70 75 80
gtg ttc gcg gtc atc acc tac tac acc tcc gtg ctc ctc gcc gac tgc 288
Val Phe Ala Val Ile Thr Tyr Tyr Thr Ser Val Leu Leu Ala Asp Cys
85 90 95
tac cgc gcc ggc ggc gat cag gtc tcc ggg aag agg aac tac aca tac 336
Tyr Arg Ala Gly Gly Asp Gln Val Ser Gly Lys Arg Asn Tyr Thr Tyr
100 105 110
atg gac gcc gtc gag tcc tat cta ggt ggt cgg caa gtg tgg ttc tgt 384
Met Asp Ala Val Glu Ser Tyr Leu Gly Gly Arg Gln Val Trp Phe Cys
115 120 125
ggt ctc tgt cag tac gtt aac ctg gtt gga act gca atc ggg tac acc 432
Gly Leu Cys Gln Tyr Val Asn Leu Val Gly Thr Ala Ile Gly Tyr Thr
130 135 140
atc aca gca tcc atc agt gcc gcg gcg gtg tac aag tcc aac tgc ttc 480
Ile Thr Ala Ser Ile Ser Ala Ala Ala Val Tyr Lys Ser Asn Cys Phe
145 150 155 160
cac aag aac ggc cac tcc gcc gac tgc agc gtc ttc acc acc tcg tac 528
His Lys Asn Gly His Ser Ala Asp Cys Ser Val Phe Thr Thr Ser Tyr
165 170 175
atg gtg gtg ttc ggc gtt gtc cag gtc ttc ttc tcc cag ctg cag agc 576
Met Val Val Phe Gly Val Val Gln Val Phe Phe Ser Gln Leu Gln Ser
180 185 190
ctc cac gag gtg gcg tgg ctg tcc gtg ctc gcc gcc gtc atg tcc ttc 624
Leu His Glu Val Ala Trp Leu Ser Val Leu Ala Ala Val Met Ser Phe
195 200 205
tcc tac tcg gcc atc gcc gtc ggc ctc tcc ttg gca caa acc ata tca 672
Ser Tyr Ser Ala Ile Ala Val Gly Leu Ser Leu Ala Gln Thr Ile Ser
210 215 220
ggt cct act ggt atg acg act atg tct ggg act gta atc gga ata gat 720
Gly Pro Thr Gly Met Thr Thr Met Ser Gly Thr Val Ile Gly Ile Asp
225 230 235 240
gtt gat ttg tcg cac aag ata tgg cag gca ctg caa gcc ctc gga aac 768
Val Asp Leu Ser His Lys Ile Trp Gln Ala Leu Gln Ala Leu Gly Asn
245 250 255
atc gcg ttc gca tat tcc tac tcc ctg gtt ctc att gaa atc cag gac 816
Ile Ala Phe Ala Tyr Ser Tyr Ser Leu Val Leu Ile Glu Ile Gln Asp
260 265 270 275
acg atc agg tcg ccg ccg gcg gag agc aag acg atg agg aag gcg aac 864
Thr Ile Arg Ser Pro Pro Ala Glu Ser Lys Thr Met Arg Lys Ala Asn
275 280 285

PF59082SeqList_PF59082.txt

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	290					295					300					
ctc	ggc	tac	gcg	gcg	ttc	ggg	aac	gcg	gcg	ccg	ggg	aac	atg	ctc	acg	960
Leu	Gly	Tyr	Ala	Ala	Phe	Gly	Asn	Ala	Ala	Pro	Gly	Asn	Met	Leu	Thr	
305					310					315					320	
ggc	ttc	ggc	ttc	tac	gac	ccc	tac	tgg	ctc	gtc	ggc	ctc	gcc	aac	gcc	1008
Gly	Phe	Gly	Phe	Tyr	Asp	Pro	Tyr	Trp	Leu	Val	Gly	Leu	Ala	Asn	Ala	
				325				330						335		
tgc	atc	gtc	gtg	cac	ctc	gtc	ggc	gcc	tac	cag	gtg	atg	tcc	cag	ccc	1056
Cys	Ile	Val	Val	His	Leu	Val	Gly	Ala	Tyr	Gln	Val	Met	Ser	Gln	Pro	
				340				345						350		
gtc	ttc	acc	gcc	gtc	gag	tcc	tgg	gcg	tcc	tcc	cgg	tgg	ccc	cgg	tgc	1104
Val	Phe	Thr	Ala	Val	Glu	Ser	Trp	Ala	Ser	Ser	Arg	Trp	Pro	Arg	Cys	
		355					360					365				
ggc	ttc	ttc	gtc	acc	ggc	ggc	ggc	gga	acg	agg	ctg	atc	agc	gtg	aac	1152
Gly	Phe	Phe	Val	Thr	Gly	Gly	Gly	Gly	Thr	Arg	Leu	Ile	Ser	Val	Asn	
	370				375						380					
gcg	ttc	agg	ctc	gcg	tgg	cgc	acg	gcg	tac	gtc	gtg	gcg	tgc	acc	gcg	1200
Ala	Phe	Arg	Leu	Ala	Trp	Arg	Thr	Ala	Tyr	Val	Val	Ala	Cys	Thr	Ala	
385					390					395					400	
gtc	gcc	gcc	gtg	gtg	ccg	ttc	ttc	aac	gac	gtg	ctc	ggc	ctc	ctc	ggc	1248
Val	Ala	Ala	Val	Val	Pro	Phe	Phe	Asn	Asp	Val	Leu	Gly	Leu	Leu	Gly	
				405				410						415		
gcc	gtc	ggg	ttc	tgg	ccg	ctc	acc	gtg	tac	ttc	ccc	gtg	gag	atg	tac	1296
Ala	Val	Gly	Phe	Trp	Pro	Leu	Thr	Val	Tyr	Phe	Pro	Val	Glu	Met	Tyr	
				420				425						430		
atc	cgg	cgg	cgg	aag	ctg	gag	agg	tcg	tcc	aag	agg	tgg	gtg	gcg	ctg	1344
Ile	Arg	Arg	Arg	Lys	Leu	Glu	Arg	Ser	Ser	Lys	Arg	Trp	Val	Ala	Leu	
		435					440					445				
cag	agc	ctc	aac	gcc	gtg	tgc	ttc	gtg	gtg	acg	ctc	gcc	tca	gcg	gtc	1392
Gln	Ser	Leu	Asn	Ala	Val	Cys	Phe	Val	Val	Thr	Leu	Ala	Ser	Ala	Val	
	450					455					460					
gcg	tcc	gtg	cag	ggg	atc	gcc	gaa	tcg	atg	gcg	cac	tat	gta	ccg	ttc	1440
Ala	Ser	Val	Gln	Gly	Ile	Ala	Glu	Ser	Met	Ala	His	Tyr	Val	Pro	Phe	
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Lys	Ser	Lys	Leu													

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 <212> PRT
 <213> Oryza sativa

<400> 603
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 Asp Asp Asp Gly Lys Pro Lys Arg Thr Gly Thr Glu Trp Thr Ala Ser
 35 40 45
 Ala His Ile Val Thr Ala Val Val Gly Ser Gly Val Leu Ser Leu Ala
 50 55 60
 Trp Ser Thr Ala Gln Leu Gly Trp Val Ala Gly Pro Ala Thr Leu Val
 65 70 75 80
 Val Phe Ala Val Ile Thr Tyr Tyr Thr Ser Val Leu Leu Ala Asp Cys
 85 90 95
 Tyr Arg Ala Gly Asp Gln Val Ser Gly Lys Arg Asn Tyr Thr Tyr
 100 105 110
 Met Asp Ala Val Glu Ser Tyr Leu Gly Gly Arg Gln Val Trp Phe Cys
 115 120 125
 Gly Leu Cys Gln Tyr Val Asn Leu Val Gly Thr Ala Ile Gly Tyr Thr
 130 135 140
 Ile Thr Ala Ser Ile Ser Ala Ala Ala Val Tyr Lys Ser Asn Cys Phe
 145 150 155 160
 His Lys Asn Gly His Ser Ala Asp Cys Ser Val Phe Thr Thr Ser Tyr
 165 170 175
 Met Val Val Phe Gly Val Val Gln Val Phe Phe Ser Gln Leu Gln Ser
 Seite 761

PF59082SeqList_PF59082.txt

180 185 190
 Leu His Glu Val Ala Trp Leu Ser Val Leu Ala Ala Val Met Ser Phe
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 Ser Tyr Ser Ala Ile Ala Val Gly Leu Ser Leu Ala Gln Thr Ile Ser
 210 215 220
 Gly Pro Thr Gly Met Thr Thr Met Ser Gly Thr Val Ile Gly Ile Asp
 225 230 235 240
 Val Asp Leu Ser His Lys Ile Trp Gln Ala Leu Gln Ala Leu Gly Asn
 245 250 255
 Ile Ala Phe Ala Tyr Ser Tyr Ser Leu Val Leu Ile Glu Ile Gln Asp
 260 265 270
 Thr Ile Arg Ser Pro Pro Ala Glu Ser Lys Thr Met Arg Lys Ala Asn
 275 280 285
 Ala Leu Ala Met Pro Val Ile Thr Ala Phe Tyr Thr Leu Cys Gly Cys
 290 295 300
 Leu Gly Tyr Ala Ala Phe Gly Asn Ala Ala Pro Gly Asn Met Leu Thr
 305 310 315 320
 Gly Phe Gly Phe Tyr Asp Pro Tyr Trp Leu Val Gly Leu Ala Asn Ala
 325 330 335
 Cys Ile Val Val His Leu Val Gly Ala Tyr Gln Val Met Ser Gln Pro
 340 345 350
 Val Phe Thr Ala Val Glu Ser Trp Ala Ser Ser Arg Trp Pro Arg Cys
 355 360 365
 Gly Phe Phe Val Thr Gly Gly Gly Gly Thr Arg Leu Ile Ser Val Asn
 370 375 380
 Ala Phe Arg Leu Ala Trp Arg Thr Ala Tyr Val Val Ala Cys Thr Ala
 385 390 395 400
 Val Ala Ala Val Val Pro Phe Phe Asn Asp Val Leu Gly Leu Leu Gly
 405 410 415
 Ala Val Gly Phe Trp Pro Leu Thr Val Tyr Phe Pro Val Glu Met Tyr
 420 425 430
 Ile Arg Arg Arg Lys Leu Glu Arg Ser Ser Lys Arg Trp Val Ala Leu
 435 440 445
 Gln Ser Leu Asn Ala Val Cys Phe Val Val Thr Leu Ala Ser Ala Val
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 <212> DNA
 <213> Brassica napus

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 <222> (1)..(1464)

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 Gln Val Phe Asp Ala Tyr Val Pro Gln Pro Ala Phe Lys Cys Phe
 20 25 30
 gac gat gat ggc cgt ctc aaa aga acc ggg act gtt tgg acc gca agc 144
 Asp Asp Asp Gly Arg Leu Lys Arg Thr Gly Thr Val Trp Thr Ala Ser
 35 40 45
 gct cat ata att aca gca gtg atc gga tcc ggc gtt ctc tcg ttg gca 192
 Ala His Ile Ile Thr Ala Val Ile Gly Ser Gly Val Leu Ser Leu Ala
 50 55 60
 tgg gcc att gca cag ctc gga tgg gtc gct gga cct gcg gtg atg cta 240
 Trp Ala Ile Ala Gln Leu Gly Trp Val Ala Gly Pro Ala Val Met Leu
 65 70 75 80
 gtg ttc tct tta gtt act ctc tac tct tcc aca ctt ctc agc gac tgc 288
 Val Phe Ser Leu Val Thr Leu Tyr Ser Ser Thr Leu Leu Ser Asp Cys
 85 90 95
 tac aga acc gga gat gca gtc tcc ggc aag aga aac tac act tac atg 336
 762

PF59082SeqList_PF59082.txt

Tyr	Arg	Thr	Gly	Asp	Ala	Val	Ser	Gly	Lys	Arg	Asn	Tyr	Thr	Tyr	Met	
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Asp	Ala	Val	Arg	Ser	Ile	Leu	Gly	Gly	Phe	Lys	Phe	Lys	Ile	Cys	Gly	
ctg	att	caa	tac	ttg	aat	ctc	ttt	ggt	atc	gcg	atc	gga	tac	aca	ata	432
Leu	Ile	Gln	Tyr	Leu	Asn	Leu	Phe	Gly	Ile	Ala	Ile	Gly	Tyr	Thr	Ile	
gca	gca	tcc	ata	agc	atg	atg	gcg	atc	aag	aga	tcg	aac	tgt	ttc	cac	480
Ala	Ala	Ser	Ile	Ser	Met	Met	Ala	Ile	Lys	Arg	Ser	Asn	Cys	Phe	His	
145					150					155					160	
aag	agc	gga	gga	aaa	gac	ccg	tgt	cac	atg	tcg	agc	aac	cct	tac	atg	528
Lys	Ser	Gly	Gly	Lys	Asp	Pro	Cys	His	Met	Ser	Ser	Asn	Pro	Tyr	Met	
atc	atc	ttc	ggt	gtg	aca	gag	atc	ttg	ctc	tct	cag	gtt	cct	gac	ttc	576
Ile	Ile	Phe	Gly	Val	Thr	Glu	Ile	Leu	Leu	Ser	Gln	Val	Pro	Asp	Phe	
gac	cag	att	tgg	tgg	atc	tcc	att	gta	gca	gct	gtt	atg	tct	ttc	act	624
Asp	Gln	Ile	Trp	Trp	Ile	Ser	Ile	Val	Ala	Ala	Val	Met	Ser	Phe	Thr	
tac	tct	gcc	att	ggt	cta	gct	cta	ggg	atc	gtt	caa	ggt	gct	gct	aat	672
Tyr	Ser	Ala	Ile	Gly	Leu	Ala	Leu	Gly	Ile	Val	Gln	Val	Ala	Ala	Asn	
gga	gtg	ttc	aaa	gga	agt	ctc	act	gga	ata	agc	att	gga	aca	gtg	act	720
Gly	Val	Phe	Lys	Gly	Ser	Leu	Thr	Gly	Ile	Ser	Ile	Gly	Thr	Val	Thr	
225					230					235					240	
caa	aca	cag	aag	ata	tgg	aga	acc	ttc	caa	gca	ctt	gga	gat	att	gcc	768
Gln	Thr	Gln	Lys	Ile	Trp	Arg	Thr	Phe	Gln	Ala	Leu	Gly	Asp	Ile	Ala	
ttt	gct	tac	tca	tac	tct	gtt	gtc	cta	ata	gag	att	cag	gat	act	gta	816
Phe	Ala	Tyr	Ser	Tyr	Ser	Val	Val	Leu	Ile	Glu	Ile	Gln	Asp	Thr	Val	
aga	tca	cca	cca	tca	gaa	tca	aaa	acg	atg	aag	aaa	gct	aca	aaa	ctc	864
Arg	Ser	Pro	Pro	Ser	Glu	Ser	Lys	Thr	Met	Lys	Lys	Ala	Thr	Lys	Leu	
agt	att	gca	atc	aca	acc	atc	ttc	tac	atg	cta	tgt	ggc	tca	atg	ggt	912
Ser	Ile	Ala	Ile	Thr	Thr	Ile	Phe	Tyr	Met	Leu	Cys	Gly	Ser	Met	Gly	
290					295					300						
tac	gca	gcc	ttt	gga	gat	gca	gca	cca	gga	aac	ctc	ctc	acc	ggt	ttc	960
Tyr	Ala	Ala	Phe	Gly	Asp	Ala	Ala	Pro	Gly	Asn	Leu	Leu	Thr	Gly	Phe	
305					310					315					320	
gga	ttc	tac	aac	ccc	ttt	tgg	ctc	ctc	gac	ata	gcc	aac	gcc	gcc	atc	1008
Gly	Phe	Tyr	Asn	Pro	Phe	Trp	Leu	Leu	Asp	Ile	Ala	Asn	Ala	Ala	Ile	
gta	gtc	cac	ctc	ata	gga	gct	tac	caa	gtc	ttc	tcc	cag	ccc	atc	ttc	1056
Val	Val	His	Leu	Ile	Gly	Ala	Tyr	Gln	Val	Phe	Ser	Gln	Pro	Ile	Phe	
gcc	ttc	gct	gaa	aaa	tca	gcc	tcg	gag	agg	ttt	cca	gac	aat	gac	ttg	1104
Ala	Phe	Ala	Glu	Lys	Ser	Ala	Ser	Glu	Arg	Phe	Pro	Asp	Asn	Asp	Leu	
ctc	acc	aag	gaa	ctc	gag	ttc	aag	atc	cca	ggg	ttt	agg	tct	ccg	tac	1152
Leu	Thr	Lys	Glu	Leu	Glu	Phe	Lys	Ile	Pro	Gly	Phe	Arg	Ser	Pro	Tyr	
370					375					380						
aaa	acc	aac	gtt	ttc	agg	gta	gtg	ttc	agg	tgc	tct	ttc	gtc	gtt	cta	1200
Lys	Thr	Asn	Val	Phe	Arg	Val	Val	Phe	Arg	Cys	Ser	Phe	Val	Val	Leu	
385					390					395					400	
acc	acg	gtg	ata	tcg	atg	ctg	atg	ccg	ttc	ttc	aac	gac	gtg	gtg	ggg	1248
Thr	Thr	Val	Ile	Ser	Met	Leu	Met	Pro	Phe	Phe	Asn	Asp	Val	Val	Gly	
atc	ttg	ggg	gcc	tta	ggg	ttt	tgg	ccc	ttg	acg	gtt	tat	ttc	ccg	gtg	1296
Ile	Leu	Gly	Ala	Leu	Gly	Phe	Trp	Pro	Leu	Thr	Val	Tyr	Phe	Pro	Val	
gag	atg	tat	ata	aag	cag	agg	aag	gtg	gag	aaa	tgg	agc	acg	agg	tgg	1344
Glu	Met	Tyr	Ile	Lys	Gln	Arg	Lys	Val	Glu	Lys	Trp	Ser	Thr	Arg	Trp	
gtt	tgt	tta	cag	atg	ctt	agt	gtt	gct	tgt	cta	gtg	atc	tcg	gtg	gtc	1392
Val	Cys	Leu	Gln	Met	Leu	Ser	Val	Ala	Cys	Leu	Val	Ile	Ser	Val	Val	
gcc	gga	gtt	gga	tca	atc	gct	gga	gta	atg	ctt	gat	ctt	aag	gtc	tac	1440

PF59082SeqList_PF59082.txt

Ala Gly Val Gly Ser Ile Ala Gly Val Met Leu Asp Leu Lys Val Tyr
 465 470 475 480
 aag ccc ttc cag tct acg tat tga
 Lys Pro Phe Gln Ser Thr Tyr
 485

1464

<210> 605
 <211> 487
 <212> PRT
 <213> Brassica napus

<400> 605
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 Gln Val Phe Asp Ala Tyr Val Pro Pro Gln Pro Ala Phe Lys Cys Phe
 20 25 30
 Asp Asp Asp Gly Arg Leu Lys Arg Thr Gly Thr Val Trp Thr Ala Ser
 35 40 45
 Ala His Ile Ile Thr Ala Val Ile Gly Ser Gly Val Leu Ser Leu Ala
 50 55 60
 Trp Ala Ile Ala Gln Leu Gly Trp Val Ala Gly Pro Ala Val Met Leu
 65 70 75 80
 Val Phe Ser Leu Val Thr Leu Tyr Ser Ser Thr Leu Leu Ser Asp Cys
 85 90 95
 Tyr Arg Thr Gly Asp Ala Val Ser Gly Lys Arg Asn Tyr Thr Tyr Met
 100 105 110
 Asp Ala Val Arg Ser Ile Leu Gly Gly Phe Lys Phe Lys Ile Cys Gly
 115 120 125
 Leu Ile Gln Tyr Leu Asn Leu Phe Gly Ile Ala Ile Gly Tyr Thr Ile
 130 135 140
 Ala Ala Ser Ile Ser Met Met Ala Ile Lys Arg Ser Asn Cys Phe His
 145 150 155 160
 Lys Ser Gly Gly Lys Asp Pro Cys His Met Ser Ser Asn Pro Tyr Met
 165 170 175
 Ile Ile Phe Gly Val Thr Glu Ile Leu Ser Gln Val Pro Asp Phe
 180 185 190
 Asp Gln Ile Trp Trp Ile Ser Ile Val Ala Ala Val Met Ser Phe Thr
 195 200 205
 Tyr Ser Ala Ile Gly Leu Ala Leu Gly Ile Val Gln Val Ala Ala Asn
 210 215 220
 Gly Val Phe Lys Gly Ser Leu Thr Gly Ile Ser Ile Gly Thr Val Thr
 225 230 235 240
 Gln Thr Gln Lys Ile Trp Arg Thr Phe Gln Ala Leu Gly Asp Ile Ala
 245 250 255
 Phe Ala Tyr Ser Tyr Ser Val Val Leu Ile Glu Ile Gln Asp Thr Val
 260 265 270
 Arg Ser Pro Pro Ser Glu Ser Lys Thr Met Lys Lys Ala Thr Lys Leu
 275 280 285
 Ser Ile Ala Ile Thr Thr Ile Phe Tyr Met Leu Cys Gly Ser Met Gly
 290 295 300
 Tyr Ala Ala Phe Gly Asp Ala Ala Pro Gly Asn Leu Leu Thr Gly Phe
 305 310 315 320
 Gly Phe Tyr Asn Pro Phe Trp Leu Leu Asp Ile Ala Asn Ala Ala Ile
 325 330 335
 Val Val His Leu Ile Gly Ala Tyr Gln Val Phe Ser Gln Pro Ile Phe
 340 345 350
 Ala Phe Ala Glu Lys Ser Ala Ser Glu Arg Phe Pro Asp Asn Asp Leu
 355 360 365
 Leu Thr Lys Glu Leu Glu Phe Lys Ile Pro Gly Phe Arg Ser Pro Tyr
 370 375 380
 Lys Thr Asn Val Phe Arg Val Val Phe Arg Cys Ser Phe Val Val Leu
 385 390 395 400
 Thr Thr Val Ile Ser Met Leu Met Pro Phe Phe Asn Asp Val Val Gly
 405 410 415
 Ile Leu Gly Ala Leu Gly Phe Trp Pro Leu Thr Val Tyr Phe Pro Val
 420 425 430
 Glu Met Tyr Ile Lys Gln Arg Lys Val Glu Lys Trp Ser Thr Arg Trp
 435 440 445
 Val Cys Leu Gln Met Leu Ser Val Ala Cys Leu Val Ile Ser Val Val
 450 455 460
 Seite 764

PF59082SeqList_PF59082.txt

450 455 460
Ala Gly Val Gly Ser Ile Ala Gly Val Met Leu Asp Leu Lys Val Tyr
465 470 475 480
Lys Pro Phe Gln Ser Thr Tyr

<210> 606
<211> 1446
<212> DNA
<213> Brassica napus

<220>
<221> CDS
<222> (1)..(1446)

<400> 606
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agt ggc gat atg aac aaa aac ttt gac gat gat gga cgc cag aaa aga 96
Ser Gly Asp Met Asn Lys Asn Phe Asp Asp Gly Arg Gln Lys Arg
20 25 30
aca ggg act tgg atg acg ggg agc gcc cat ata ata aca gcg gtg ata 144
Thr Gly Thr Trp Met Thr Gly Ser Ala His Ile Ile Thr Ala Val Ile
35 40 45
gga tca gga gtg ttg tca ctg gcg tgg gca att gca cag ctc gga tgg 192
Gly Ser Gly Val Leu Ser Leu Ala Trp Ala Ile Ala Gln Leu Gly Trp
50 55 60
gtg gca gga ccc gcc gta ctt atg gct ttt tcc ttc ata aca tac ttt 240
Val Ala Gly Pro Ala Val Leu Met Ala Phe Ser Phe Ile Thr Tyr Phe
65 70 75 80
aca tca acc atg ctt gcc gac tgt tat cgt tcc ccg gat cct gtc act 288
Thr Ser Thr Met Leu Ala Asp Cys Tyr Arg Ser Pro Asp Pro Val Thr
85 90 95
gga aaa cga aac tat acc tac atg gaa aat gtc cgc tct tac tta gga 336
Gly Lys Arg Asn Tyr Thr Tyr Met Glu Val Val Arg Ser Tyr Leu Gly
100 105 110
gga aga aaa gtg atg tta tgt gga ttg gct caa tac ggg aat ctg att 384
Gly Arg Lys Val Met Leu Cys Gly Leu Ala Gln Tyr Gly Asn Leu Ile
115 120 125
gga ata aca atc ggc tac aca atc aca gcg tcg att agc atg gtg gca 432
Gly Ile Thr Ile Gly Tyr Thr Ile Thr Ala Ser Ile Ser Met Val Ala
130 135 140
gtg aag agg tcg aat tgt ttc cac aag aat gga cat aat gtg aaa tgt 480
Val Lys Arg Ser Asn Cys Phe His Lys Asn Gly His Asn Val Lys Cys
145 150 155 160
tcc act tca aac act ccc ttc atg atc ata ttc gca tgc atc caa att 528
Ser Thr Ser Asn Thr Pro Phe Met Ile Ile Phe Ala Cys Ile Gln Ile
165 170 175
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Val Leu Ser Gln Ile Pro Asn Phe His Asn Leu Ser Trp Leu Ser Ile
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cta gcg gcc gta atg tcc ttt tct tac gcc tcc att ggt atc ggt ctc 624
Leu Ala Ala Val Met Ser Phe Ser Tyr Ala Ser Ile Gly Ile Gly Leu
195 200 205
tcc atc gcc aaa gtg gcc ggt ggc ggt gtg cac gca agg acg gcc ctg 672
Ser Ile Ala Lys Val Ala Gly Gly Gly Val His Ala Arg Thr Ala Leu
210 215 220
aca gga gtt acg gtc gga gtt gat gtt act ggt tct gag aaa gta tgg 720
Thr Gly Val Thr Val Gly Val Asp Val Thr Gly Ser Glu Lys Val Trp
225 230 235 240
aga aca ttc caa gcg gtt gga gat atc gca ttt gct tat gcc tac tca 768
Arg Thr Phe Gln Ala Val Gly Asp Ile Ala Phe Ala Tyr Ala Tyr Ser
245 250 255
acc gta ctt att gag ata cag gac acc tta aaa gca agt cca cca tca 816
Thr Val Leu Ile Glu Ile Gln Asp Thr Leu Lys Ala Ser Pro Pro Ser
260 265 270
gaa aac aaa gcc atg aaa aga gca agc ctt gtg ggt gta tcc aca acg 864
Glu Asn Lys Ala Met Lys Arg Ala Ser Leu Val Gly Val Ser Thr Thr

PF59082SeqList_PF59082.txt

275	280	285	
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Thr Phe Phe Tyr Met Leu Cys Gly Cys Val Gly Tyr Ala Ala Phe Gly			
290	295	300	
aat aat gcg cct gga aat ttc cta acc ggt ttt ggt ttt tat gag ccc			960
Asn Asn Ala Pro Gly Asn Phe Leu Thr Gly Phe Gly Phe Tyr Glu Pro			
305	310	315	
ttc tgg cta atc gac ttt gcc aat gtc tgc atc gct gtg cat ctt gtt			1008
Phe Trp Leu Ile Asp Phe Ala Asn Val Cys Ile Ala Val His Leu Val			
325	330	335	
ggg gcc tat cag gtc ttt tgc cag cca atc ttc caa ttt gta gag agc			1056
Gly Ala Tyr Gln Val Phe Cys Gln Pro Ile Phe Gln Phe Val Glu Ser			
340	345	350	
cag agt gca aaa cgt tgg cca gat aac aag ttt att aca gga gag tac			1104
Gln Ser Ala Lys Arg Trp Pro Asp Asn Lys Phe Ile Thr Gly Glu Tyr			
355	360	365	
aaa atg aac gtc cct tgc ggt ggt gat ttt ggt atc agc ttg ttt aga			1152
Lys Met Asn Val Pro Cys Gly Gly Asp Phe Gly Ile Ser Leu Phe Arg			
370	375	380	
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Leu Val Trp Arg Thr Ser Tyr Val Val Val Thr Ala Val Val Ala Met			
385	390	395	
atc ttc cct ttc ttc aac gat ttc ttg ggt ctt att gga gca gct tcc			1248
Ile Phe Pro Phe Phe Asn Asp Phe Leu Gly Leu Ile Gly Ala Ala Ser			
405	410	415	
ttt tgg cct ttg act gtt tac ttt ccc att gag atg cat att gct cag			1296
Phe Trp Pro Leu Thr Val Tyr Phe Pro Ile Glu Met His Ile Ala Gln			
420	425	430	
aaa aat atg aag aaa ttt tct ttc act tgg aca tgg ctg aaa atc ttg			1344
Lys Asn Met Lys Lys Phe Ser Phe Thr Trp Thr Trp Leu Lys Ile Leu			
435	440	445	
agc tgg gct tgt ttc ctc gtc tcc ctc gtt gct gct gct gga tct gtg			1392
Ser Trp Ala Cys Phe Leu Val Ser Leu Val Ala Ala Ala Gly Ser Val			
450	455	460	
caa gga ctc ata caa agt ctt aag gat ttc aag cct ttc cag gct ccc			1440
Gln Gly Leu Ile Gln Ser Leu Lys Asp Phe Lys Pro Phe Gln Ala Pro			
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gag tag			1446
glu			

<210> 607
 <211> 481
 <212> PRT
 <213> Brassica napus

<400> 607

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			20					25					30		
Thr	Gly	Thr	Trp	Met	Thr	Gly	Ser	Ala	His	Ile	Ile	Thr	Ala	Val	Ile
			35				40					45			
Gly	Ser	Gly	Val	Leu	Ser	Leu	Ala	Trp	Ala	Ile	Ala	Gln	Leu	Gly	Trp
			50			55					60				
Val	Ala	Gly	Pro	Ala	Val	Leu	Met	Ala	Phe	Ser	Phe	Ile	Thr	Tyr	Phe
65					70				75						80
Thr	Ser	Thr	Met	Leu	Ala	Asp	Cys	Tyr	Arg	Ser	Pro	Asp	Pro	Val	Thr
				85					90					95	
Gly	Lys	Arg	Asn	Tyr	Thr	Tyr	Met	Glu	Val	Val	Arg	Ser	Tyr	Leu	Gly
			100					105					110		
Gly	Arg	Lys	Val	Met	Leu	Cys	Gly	Leu	Ala	Gln	Tyr	Gly	Asn	Leu	Ile
			115				120					125			
Gly	Ile	Thr	Ile	Gly	Tyr	Thr	Ile	Thr	Ala	Ser	Ile	Ser	Met	Val	Ala
			130			135					140				
Val	Lys	Arg	Ser	Asn	Cys	Phe	His	Lys	Asn	Gly	His	Asn	Val	Lys	Cys
145				150					155						160
Ser	Thr	Ser	Asn	Thr	Pro	Phe	Met	Ile	Ile	Phe	Ala	Cys	Ile	Gln	Ile
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PF59082SeqList_PF59082.txt

Val Leu Ser Gln Ile Pro Asn Phe His Asn Leu Ser Trp Leu Ser Ile
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 Leu Ala Ala Val Met Ser Phe Ser Tyr Ala Ser Ile Gly Ile Gly Leu
 195 200 205
 Ser Ile Ala Lys Val Ala Gly Gly Val His Ala Arg Thr Ala Leu
 210 215 220
 Thr Gly Val Thr Val Gly Val Asp Val Thr Gly Ser Glu Lys Val Trp
 225 230 235 240
 Arg Thr Phe Gln Ala Val Gly Asp Ile Ala Phe Ala Tyr Ala Tyr Ser
 245 250 255
 Thr Val Leu Ile Glu Ile Gln Asp Thr Leu Lys Ala Ser Pro Pro Ser
 260 265 270
 Glu Asn Lys Ala Met Lys Arg Ala Ser Leu Val Gly Val Ser Thr Thr
 275 280 285
 Thr Phe Phe Tyr Met Leu Cys Gly Cys Val Gly Tyr Ala Ala Phe Gly
 290 295 300
 Asn Asn Ala Pro Gly Asn Phe Leu Thr Gly Phe Gly Phe Tyr Glu Pro
 305 310 315 320
 Phe Trp Leu Ile Asp Phe Ala Asn Val Cys Ile Ala Val His Leu Val
 325 330 335
 Gly Ala Tyr Gln Val Phe Cys Gln Pro Ile Phe Gln Phe Val Glu Ser
 340 345 350
 Gln Ser Ala Lys Arg Trp Pro Asp Asn Lys Phe Ile Thr Gly Glu Tyr
 355 360 365
 Lys Met Asn Val Pro Cys Gly Gly Asp Phe Gly Ile Ser Leu Phe Arg
 370 375 380
 Leu Val Trp Arg Thr Ser Tyr Val Val Val Thr Ala Val Val Ala Met
 385 390 395 400
 Ile Phe Pro Phe Phe Asn Asp Phe Leu Gly Leu Ile Gly Ala Ala Ser
 405 410 415
 Phe Trp Pro Leu Thr Val Tyr Phe Pro Ile Glu Met His Ile Ala Gln
 420 425 430
 Lys Asn Met Lys Lys Phe Ser Phe Thr Trp Thr Trp Leu Lys Ile Leu
 435 440 445
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 450 455 460
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 <213> Brassica napus

<220>
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 ggc gac gtc tac gcc atg tcc gat cca aca aag aac gtt gat gac gat 96
 Gly Asp Val Tyr Ala Met Ser Asp Pro Thr Lys Asn Val Asp Asp Asp
 20 25 30
 ggc cga gag aag agg acg ggg acg tgg ctt acg gcg agt gcg cat att 144
 Gly Arg Glu Lys Arg Thr Gly Thr Trp Leu Thr Ala Ser Ala His Ile
 35 40 45
 atc acg gcg gta ata ggc tca gga gtg ttg tcg ttg gca tgg gcc ata 192
 Ile Thr Ala Val Ile Gly Ser Gly Val Leu Ser Leu Ala Trp Ala Ile
 50 55 60
 gct cag ctt ggt tgg ata gca ggg act ttg att ctg atc att ttc tcg 240
 Ala Gln Leu Gly Trp Ile Ala Gly Thr Leu Ile Leu Ile Ile Phe Ser
 65 70 75 80
 ttt atc acg tac ttc act tct acg atg ctc gct gat tgc tac cgt gcg 288
 Phe Ile Thr Tyr Phe Thr Ser Thr Met Leu Ala Asp Cys Tyr Arg Ala
 85 90 95

PF59082SeqList_PF59082.txt																
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			100					105					110			
cga	tct	tac	ctc	ggt	ggt	agg	aaa	gtg	cag	ctt	tgt	gga	gtg	gca	cag	384
Arg	Ser		Leu	Gly	Gly	Arg	Lys	Val	Gln	Leu	Cys	Gly	Val	Ala	Gln	
		115					120					125				
tat	ggg	aat	ctg	ata	gga	atc	act	gtt	ggg	tac	acc	atc	act	gct	tct	432
Tyr	Gly	Asn	Leu	Ile	Gly	Ile	Thr	Val	Gly	Tyr	Thr	Ile	Thr	Ala	Ser	
	130					135					140					
att	agt	ttg	gta	gcg	atc	ggg	aaa	gcg	aac	tgt	tac	cac	aat	aaa	ggg	480
Ile	Ser	Leu	Val	Ala	Ile	Gly	Lys	Ala	Asn	Cys	Tyr	His	Asn	Lys	Gly	
	145				150					155					160	
cac	cat	gca	gat	tgt	aca	ata	tca	aac	tat	cca	tat	atg	gcg	gcc	ttc	528
His	His	Ala	Asp	Cys	Thr	Ile	Ser	Asn	Tyr	Pro	Tyr	Met	Ala	Ala	Phe	
			165						170					175		
ggg	atc	att	caa	atc	ctt	ctt	agc	cag	atc	ccc	aac	ttt	cac	aag	ctc	576
Gly	Ile	Ile	Gln	Ile	Leu	Leu	Ser	Gln	Ile	Pro	Asn	Phe	His	Lys	Leu	
			180					185					190			
tct	ttt	ctc	tcc	ctt	atg	gct	gcg	gtt	atg	tct	ttc	gct	tac	gca	agt	624
Ser	Phe	Leu	Ser	Leu	Met	Ala	Ala	Val	Met	Ser	Phe	Ala	Tyr	Ala	Ser	
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att	ggg	att	ggc	cta	gcc	atc	gcg	acg	gtc	gca	ggg	ggg	aaa	gtg	ggt	672
Ile	Gly	Ile	Gly	Leu	Ala	Ile	Ala	Thr	Val	Ala	Gly	Gly	Lys	Val	Gly	
	210				215					220						
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Lys	Thr	Asn	Met	Thr	Gly	Thr	Val	Val	Gly	Val	Asp	Val	Thr	Ala	Ala	
	225				230				235						240	
cag	aag	ata	tgg	aga	tcg	ttt	caa	gcg	gtt	gga	gac	ata	gcg	ttt	gca	768
Gln	Lys	Ile	Trp	Arg	Ser	Phe	Gln	Ala	Val	Gly	Asp	Ile	Ala	Phe	Ala	
			245					250						255		
tat	gct	tac	gcc	acg	gtt	ctc	att	gag	att	cag	gac	aca	ttg	aga	tct	816
Tyr	Ala	Tyr	Ala	Thr	Val	Leu	Ile	Glu	Ile	Gln	Asp	Thr	Leu	Arg	Ser	
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Ser	Pro	Ala	Glu	Asn	Lys	Ala	Met	Lys	Arg	Ala	Ser	Phe	Val	Gly	Val	
		275				280						285				
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Ser	Thr	Thr	Thr	Phe	Phe	Tyr	Ile	Leu	Cys	Gly	Cys	Leu	Gly	Tyr	Ala	
	290					295					300					
gca	ttt	gga	aac	aaa	gcc	cct	gga	gat	ttc	ctc	acc	aat	ttc	gga	ttc	960
Ala	Phe	Gly	Asn	Lys	Ala	Pro	Gly	Asp	Phe	Leu	Thr	Asn	Phe	Gly	Phe	
	305				310					315					320	
tac	gag	cca	ttt	tgg	ctc	att	gac	ttt	gca	aac	gct	tgc	att	gct	ttc	1008
Tyr	Glu	Pro	Phe	Trp	Leu	Ile	Asp	Phe	Ala	Asn	Ala	Cys	Ile	Ala	Phe	
			325						330					335		
cat	ctc	att	ggt	gcc	tat	cag	gtg	ttc	gcg	cag	ccc	ata	ttc	cag	ttt	1056
His	Leu	Ile	Gly	Ala	Tyr	Gln	Val	Phe	Ala	Gln	Pro	Ile	Phe	Gln	Phe	
		340						345					350			
gtt	gag	aag	aaa	tgc	aat	aga	aac	tgg	cct	gac	aac	aag	ttc	atc	aca	1104
Val	Glu	Lys	Lys	Cys	Asn	Arg	Asn	Trp	Pro	Asp	Asn	Lys	Phe	Ile	Thr	
		355					360					365				
tct	gaa	tat	tca	gta	aac	ata	cca	ttc	ctt	gga	aaa	ttt	agc	atc	aac	1152
Ser	Glu	Tyr	Ser	Val	Asn	Ile	Pro	Phe	Leu	Gly	Lys	Phe	Ser	Ile	Asn	
	370					375					380					
ctc	ttc	aga	cta	gtg	tgg	agg	aca	gct	tat	gtg	gtt	ata	aca	act	ttg	1200
Leu	Phe	Arg	Leu	Val	Trp	Arg	Thr	Ala	Tyr	Val	Val	Ile	Thr	Thr	Leu	
			385		390					395					400	
gta	gct	atg	ata	ttc	cct	ttc	ttc	aac	gcc	atc	ttg	ggg	ctt	atc	gga	1248
Val	Ala	Met	Ile	Phe	Pro	Phe	Phe	Asn	Ala	Ile	Leu	Gly	Leu	Ile	Gly	
			405						410					415		
gca	gct	tcc	ttc	tgg	cct	tta	acg	gtt	tat	ttc	ccc	gtg	gag	atg	cac	1296
Ala	Ala	Ser	Phe	Trp	Pro	Leu	Thr	Val	Tyr	Phe	Pro	Val	Glu	Met	His	
			420					425					430			
ata	gca	caa	act	aag	gtt	aag	aaa	tac	tct	tct	aga	tgg	att	ggg	ctg	1344
Ile	Ala	Gln	Thr	Lys	Val	Lys	Lys	Tyr	Ser	Ser	Arg	Trp	Ile	Gly	Leu	
		435					440					445				
aaa	atg	ttg	tgc	tgg	gtt	tgc	ttg	atc	gtc	tcc	ctg	tta	gcc	gct	gct	1392
Lys	Met	Leu	Cys	Trp	Val	Cys	Leu	Ile	Val	Ser	Leu	Leu	Ala	Ala	Ala	
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cgg	act	atc	cat	gag	tga											1458
Arg	Thr	Ile	His	Glu												
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<210> 609
 <211> 485
 <212> PRT
 <213> Brassica napus

<400> 609

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Gly	Asp	Val	Tyr	Ala	Met	Ser	Asp	Pro	Thr	Lys	Asn	Val	Asp	Asp	
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Gly	Arg	Glu	Lys	Arg	Thr	Gly	Thr	Trp	Leu	Thr	Ala	Ser	Ala	His	Ile
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Ile	Thr	Ala	Val	Ile	Gly	Ser	Gly	Val	Leu	Ser	Leu	Ala	Trp	Ala	Ile
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Ala	Gln	Leu	Gly	Trp	Ile	Ala	Gly	Thr	Leu	Ile	Leu	Ile	Ile	Phe	Ser
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Phe	Ile	Thr	Tyr	Phe	Thr	Ser	Thr	Met	Leu	Ala	Asp	Cys	Tyr	Arg	Ala
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Pro	Asp	Pro	Leu	Thr	Gly	Lys	Arg	Asn	Tyr	Thr	Tyr	Met	Asp	Val	Val
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Arg	Ser	Tyr	Leu	Gly	Gly	Arg	Lys	Val	Gln	Leu	Cys	Gly	Val	Ala	Gln
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Tyr	Gly	Asn	Leu	Ile	Gly	Ile	Thr	Val	Gly	Tyr	Thr	Ile	Thr	Ala	Ser
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His	His	Ala	Asp	Cys	Thr	Ile	Ser	Asn	Tyr	Pro	Tyr	Met	Ala	Ala	Phe
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Gly	Ile	Ile	Gln	Ile	Leu	Leu	Ser	Gln	Ile	Pro	Asn	Phe	His	Lys	Leu
			180					185					190		
Ser	Phe	Leu	Ser	Leu	Met	Ala	Ala	Val	Met	Ser	Phe	Ala	Tyr	Ala	Ser
		195				200						205			
Ile	Gly	Ile	Gly	Leu	Ala	Ile	Ala	Thr	Val	Ala	Gly	Gly	Lys	Val	Gly
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Lys	Thr	Asn	Met	Thr	Gly	Thr	Val	Val	Gly	Val	Asp	Val	Thr	Ala	Ala
225					230				235						240
Gln	Lys	Ile	Trp	Arg	Ser	Phe	Gln	Ala	Val	Gly	Asp	Ile	Ala	Phe	Ala
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Tyr	Ala	Tyr	Ala	Thr	Val	Leu	Ile	Glu	Ile	Gln	Asp	Thr	Leu	Arg	Ser
			260					265					270		
Ser	Pro	Ala	Glu	Asn	Lys	Ala	Met	Lys	Arg	Ala	Ser	Phe	Val	Gly	Val
		275				280						285			
Ser	Thr	Thr	Thr	Phe	Phe	Tyr	Ile	Leu	Cys	Gly	Cys	Leu	Gly	Tyr	Ala
	290					295					300				
Ala	Phe	Gly	Asn	Lys	Ala	Pro	Gly	Asp	Phe	Leu	Thr	Asn	Phe	Gly	Phe
305					310					315					320
Tyr	Glu	Pro	Phe	Trp	Leu	Ile	Asp	Phe	Ala	Asn	Ala	Cys	Ile	Ala	Phe
				325					330					335	
His	Leu	Ile	Gly	Ala	Tyr	Gln	Val	Phe	Ala	Gln	Pro	Ile	Phe	Gln	Phe
			340					345					350		
Val	Glu	Lys	Lys	Cys	Asn	Arg	Asn	Trp	Pro	Asp	Asn	Lys	Phe	Ile	Thr
		355					360					365			
Ser	Glu	Tyr	Ser	Val	Asn	Ile	Pro	Phe	Leu	Gly	Lys	Phe	Ser	Ile	Asn
	370					375					380				
Leu	Phe	Arg	Leu	Val	Trp	Arg	Thr	Ala	Tyr	Val	Val	Ile	Thr	Thr	Leu
385					390					395					400
Val	Ala	Met	Ile	Phe	Pro	Phe	Phe	Asn	Ala	Ile	Leu	Gly	Leu	Ile	Gly
				405					410					415	
Ala	Ala	Ser	Phe	Trp	Pro	Leu	Thr	Val	Tyr	Phe	Pro	Val	Glu	Met	His
				420				425					430		
Ile	Ala	Gln	Thr	Lys	Val	Lys	Lys	Tyr	Ser	Ser	Arg	Trp	Ile	Gly	Leu
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PF59082SeqList_PF59082.txt

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 Arg Thr Ile His Glu
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 <212> DNA
 <213> Lycopersicon esculentum

<220>
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 <222> (1)..(1416)

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 Cys Phe Asp Asp Asp Gly Arg Ile Lys Arg Thr Gly Ser Val Trp Thr
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 gca agt gct cac atc ata act gct gtg ata gga tca gga gtt tta tca 144
 Ala Ser Ala His Ile Ile Thr Ala Val Ile Gly Ser Gly Val Leu Ser
 35 40 45
 ttg gct tgg gct act gct cag ctt gga tgg gta gct ggg cca act gta 192
 Leu Ala Trp Ala Thr Ala Gln Leu Gly Trp Val Ala Gly Pro Thr Val
 50 55 60
 ttg cta ctt ttc tcc ttt gtt act tac tat acc tct gct ttg ctt tcc 240
 Leu Leu Leu Phe Ser Phe Val Thr Tyr Tyr Thr Ser Ala Leu Leu Ser
 65 70 75 80
 gat tgt tac cgg acc ggt gat cca gtt acc gga aaa aga aat tat act 288
 Asp Cys Tyr Arg Thr Gly Asp Pro Val Thr Gly Lys Arg Asn Tyr Thr
 85 90 95
 tat atg gat gct gtt cga gcc aat cta ggt gga ttt cag gtt aag att 336
 Tyr Met Asp Ala Val Arg Ala Asn Leu Gly Gly Phe Gln Val Lys Ile
 100 105 110
 tgt ggt gtg att cag tat gca aat ctt ttt gga gtt gca att ggt tat 384
 Cys Gly Val Ile Gln Tyr Ala Asn Leu Phe Gly Val Ala Ile Gly Tyr
 115 120 125
 acc ata gcg tct tcc att agt atg gtg gct gtg aat agg tct aat tgt 432
 Thr Ile Ala Ser Ser Ile Ser Met Val Ala Val Asn Arg Ser Asn Cys
 130 135 140
 ttc cat aaa caa ggt cat gct gct tgc aat gtt tca agt act ccc 480
 Phe His Lys Gln Gly His His Ala Ala Cys Asn Val Ser Ser Thr Pro
 145 150 155 160
 tat atg atc atg ttt ggt gtg atg gaa att atc ttc tca caa atc ccg 528
 Tyr Met Ile Met Phe Gly Val Met Glu Ile Ile Phe Ser Gln Ile Pro
 165 170 175
 gat ttc gat cag att tct tgg ctt tcg att gtt gct gct gtt atg tcg 576
 Asp Phe Asp Gln Ile Ser Trp Leu Ser Ile Val Ala Ala Val Met Ser
 180 185 190
 ttt act tac tct aca att ggt ctt ggc tta gga gtt gct caa gtt gca 624
 Phe Thr Tyr Ser Thr Ile Gly Leu Gly Leu Gly Val Ala Gln Val Ala
 195 200 205
 gaa aca gga aaa att gaa gga agt tta act ggg att agc att gga act 672
 Glu Thr Gly Lys Ile Glu Gly Ser Leu Thr Gly Ile Ser Ile Gly Thr
 210 215 220
 gaa gta act gaa atg cag aag att tgg aga agc ttt caa gct ctt gga 720
 Glu Val Thr Glu Met Gln Lys Ile Trp Arg Ser Phe Gln Ala Leu Gly
 225 230 235 240
 gct ata gct ttt gct tat tcc tac tcc cta atc ctt atc gaa att cag 768
 Ala Ile Ala Phe Ala Tyr Ser Tyr Ser Leu Ile Leu Ile Glu Ile Gln
 245 250 255
 gat aca ctc aaa tca cca cca gca gaa gca aag aca atg aaa agg gca 816
 Asp Thr Leu Lys Ser Pro Pro Ala Glu Ala Lys Thr Met Lys Arg Ala
 260 265 270
 aca cta att agt gtg gca gtt aca aca gta ttc tac atg ctt tgt ggt 864

PF59082SeqList_PF59082.txt

Thr	Leu	Ile	Ser	Val	Ala	Val	Thr	Val	Phe	Tyr	Met	Leu	Cys	Gly	
275							280				285				
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Cys	Phe	Gly	Tyr	Ala	Ala	Phe	Gly	Asp	Gln	Ser	Pro	Gly	Asn	Leu	Leu
290						295				300					
aca	gga	ttc	gga	ttc	tac	aac	ccc	tat	tgg	ctt	ctt	gac	atc	gcg	aac
Thr	Gly	Phe	Gly	Phe	Tyr	Asn	Pro	Tyr	Trp	Leu	Leu	Asp	Ile	Ala	Asn
305					310					315					320
ata	gcc	atg	gtt	gtt	cac	cta	gta	ggg	gca	tac	caa	gtt	tac	tgt	caa
Ile	Ala	Met	Val	Val	His	Leu	Val	Gly	Ala	Tyr	Gln	Val	Tyr	Cys	Gln
				325					330					335	
ccc	ctt	ttc	gcc	ttt	gtt	gaa	aaa	aca	gca	gct	gaa	tgg	tac	cct	gac
Pro	Leu	Phe	Ala	Phe	Val	Glu	Lys	Thr	Ala	Ala	Glu	Trp	Tyr	Pro	Asp
			340					345					350		
agc	aaa	atc	ata	aca	aaa	gaa	atc	gat	gtc	cca	atc	ccg	gga	ttc	aaa
Ser	Lys	Ile	Ile	Thr	Lys	Glu	Ile	Asp	Val	Pro	Ile	Pro	Gly	Phe	Lys
		355				360						365			
cct	ttc	aag	ctc	aac	ctt	ttc	cgt	cta	gtc	tgg	agg	gca	ata	ttc	gtg
Pro	Phe	Lys	Leu	Asn	Leu	Phe	Arg	Leu	Val	Trp	Arg	Ala	Ile	Phe	Val
370					375						380				
atc	atc	acc	aca	gtc	ata	tca	atg	ttg	atg	ccc	ttc	ttt	aac	gac	gtc
Ile	Ile	Thr	Thr	Val	Ile	Ser	Met	Leu	Met	Pro	Phe	Phe	Asn	Asp	Val
385					390					395					400
gtt	ggc	att	ctt	gga	gca	ttt	gga	ttt	tgg	cca	ctt	aca	gta	tac	ttc
Val	Gly	Ile	Leu	Gly	Ala	Phe	Gly	Phe	Trp	Pro	Leu	Thr	Val	Tyr	Phe
				405					410					415	
cca	gtg	gaa	atg	tac	att	gtg	caa	aag	aga	att	acc	aaa	tgg	agt	gca
Pro	Val	Glu	Met	Tyr	Ile	Val	Gln	Lys	Arg	Ile	Thr	Lys	Trp	Ser	Ala
			420					425					430		
aga	tgg	ata	tgt	cta	caa	ata	ctt	agt	ggg	gct	tgc	ctt	gtt	atc	tca
Arg	Trp	Ile	Cys	Leu	Gln	Ile	Leu	Ser	Gly	Ala	Cys	Leu	Val	Ile	Ser
		435				440						445			
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Ile	Ala	Ala	Ala	Ala	Gly	Ser	Phe	Ala	Gly	Val	Val	Ser	Asp	Leu	Lys
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Val	Tyr	Arg	Pro	Phe	Gln	Ser									
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<210> 611

<211> 471

<212> PRT

<213> Lycopersicon esculentum

<400> 611

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Cys	Phe	Asp	Asp	Asp	Gly	Arg	Ile	Lys	Arg	Thr	Gly	Ser	Val	Trp	Thr
			20					25					30		
Ala	Ser	Ala	His	Ile	Ile	Thr	Ala	Val	Ile	Gly	Ser	Gly	Val	Leu	Ser
		35					40					45			
Leu	Ala	Trp	Ala	Thr	Ala	Gln	Leu	Gly	Trp	Val	Ala	Gly	Pro	Thr	Val
	50					55					60				
Leu	Leu	Leu	Phe	Ser	Phe	Val	Thr	Tyr	Tyr	Thr	Ser	Ala	Leu	Leu	Ser
65					70					75					80
Asp	Cys	Tyr	Arg	Thr	Gly	Asp	Pro	Val	Thr	Gly	Lys	Arg	Asn	Tyr	Thr
				85					90					95	
Tyr	Met	Asp	Ala	Val	Arg	Ala	Asn	Leu	Gly	Gly	Phe	Gln	Val	Lys	Ile
			100				105						110		
Cys	Gly	Val	Ile	Gln	Tyr	Ala	Asn	Leu	Phe	Gly	Val	Ala	Ile	Gly	Tyr
		115					120					125			
Thr	Ile	Ala	Ser	Ser	Ile	Ser	Met	Val	Ala	Val	Asn	Arg	Ser	Asn	Cys
	130					135					140				
Phe	His	Lys	Gln	Gly	His	His	Ala	Ala	Cys	Asn	Val	Ser	Ser	Thr	Pro
145					150				155						160
Tyr	Met	Ile	Met	Phe	Gly	Val	Met	Glu	Ile	Ile	Phe	Ser	Gln	Ile	Pro
				165					170					175	
Asp	Phe	Asp	Gln	Ile	Ser	Trp	Leu	Ser	Ile	Val	Ala	Ala	Val	Met	Ser
			180					185					190		

PF59082SeqList_PF59082.txt

Phe Thr Tyr Ser Thr Ile Gly Leu Gly Leu Gly Val Ala Gln Val Ala
195 200 205
Glu Thr Gly Lys Ile Glu Gly Ser Leu Thr Gly Ile Ser Ile Gly Thr
210 215 220
Glu Val Thr Glu Met Gln Lys Ile Trp Arg Ser Phe Gln Ala Leu Gly
225 230 235 240
Ala Ile Ala Phe Ala Tyr Ser Tyr Ser Leu Ile Leu Ile Glu Ile Gln
245 250 255
Asp Thr Leu Lys Ser Pro Pro Ala Glu Ala Lys Thr Met Lys Arg Ala
260 265 270
Thr Leu Ile Ser Val Ala Val Thr Thr Val Phe Tyr Met Leu Cys Gly
275 280 285
Cys Phe Gly Tyr Ala Ala Phe Gly Asp Gln Ser Pro Gly Asn Leu Leu
290 295 300
Thr Gly Phe Gly Phe Tyr Asn Pro Tyr Trp Leu Asp Ile Ala Asn
305 310 315 320
Ile Ala Met Val Val His Leu Val Gly Ala Tyr Gln Val Tyr Cys Gln
325 330 335
Pro Leu Phe Ala Phe Val Glu Lys Thr Ala Ala Glu Trp Tyr Pro Asp
340 345 350
Ser Lys Ile Ile Thr Lys Glu Ile Asp Val Pro Ile Pro Gly Phe Lys
355 360 365
Pro Phe Lys Leu Asn Leu Phe Arg Leu Val Trp Arg Ala Ile Phe Val
370 375 380
Ile Ile Thr Thr Val Ile Ser Met Leu Met Pro Phe Phe Asn Asp Val
385 390 395 400
Val Gly Ile Leu Gly Ala Phe Gly Phe Trp Pro Leu Thr Val Tyr Phe
405 410 415
Pro Val Glu Met Tyr Ile Val Gln Lys Arg Ile Thr Lys Trp Ser Ala
420 425 430
Arg Trp Ile Cys Leu Gln Ile Leu Ser Gly Ala Cys Leu Val Ile Ser
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Val Tyr Arg Pro Phe Gln Ser
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<212> DNA

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<222> (1)..(1398)

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aga ccc aaa aga act gga acg gtg ttg act aca agt gct cat ata ata	96
Arg Pro Lys Arg Thr Gly Thr Val Leu Thr Thr Ser Ala His Ile Ile	
20 25 30	
aca gca gtg ata ggt tca gga gtg tta tct ttg gca tgg gct aca gcc	144
Thr Ala Val Ile Gly Ser Gly Val Leu Ser Leu Ala Trp Ala Thr Ala	
35 40 45	
caa ttg gga tgg ata gca gga cca gtt gca ctc att gct ttc tca gcc	192
Gln Leu Gly Trp Ile Ala Gly Pro Val Ala Leu Ile Ala Phe Ser Ala	
50 55 60	
ata aca tgg ttt gct tct atc ctc ctt gct gat tgc tat cgc gcc ccc	240
Ile Thr Trp Phe Ala Ser Ile Leu Leu Ala Asp Cys Tyr Arg Ala Pro	
65 70 75 80	
gat ggc tct cgt agc tac acc tat atg gat gct gtt cga gcc cat cta	288
Asp Gly Ser Arg Ser Tyr Thr Tyr Met Asp Ala Val Arg Ala His Leu	
85 90 95	
gga gga agg aaa gtc cag ctt tgt gga tta gct caa tat agt aac ctt	336
Gly Gly Arg Lys Val Gln Leu Cys Gly Leu Ala Gln Tyr Ser Asn Leu	
100 105 110	
ttt ggt gtt acc att gga tat gca atc acc aca tcc ata agc atg gtg	384

PF59082SeqList_PF59082.txt

Phe	Gly	Val	Thr	Ile	Gly	Tyr	Ala	Ile	Thr	Thr	Ser	Ile	Ser	Met	Val		
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Ala	Ile	Lys	Arg	Ser	Asn	Cys	Phe	His	Arg	Lys	Gly	His	Asp	Ala	Gly		
130						135					140						
tgt	cat	gag	tca	aac	aat	ccc	ttc	ata	att	atc	ttt	ggg	gtt	atg	caa	480	
Cys	His	Glu	Ser	Asn	Asn	Pro	Phe	Ile	Ile	Ile	Phe	Gly	Val	Met	Gln		
145					150					155					160		
atc	ctt	cta	tcc	caa	atc	cca	aat	ttt	cac	aag	ctt	tca	ttc	ctt	tcc	528	
Ile	Leu	Leu	Ser	Gln	Ile	Pro	Asn	Phe	His	Lys	Leu	Ser	Phe	Leu	Ser		
				165					170					175			
atc	att	gct	gct	gcc	atg	tcc	ttt	gct	tat	tct	ttc	att	gga	ctt	ggt	576	
Ile	Ile	Ala	Ala	Ala	Met	Ser	Phe	Ala	Tyr	Ser	Phe	Ile	Gly	Leu	Gly		
				180				185					190				
cta	tcc	att	gcc	aag	att	gca	aag	gat	gga	gta	agt	gca	aat	aca	agc	624	
Leu	Ser	Ile	Ala	Lys	Ile	Ala	Lys	Asp	Gly	Val	Ser	Ala	Asn	Thr	Ser		
				195			200					205					
tta	aca	ggg	aca	ata	gtt	gga	aaa	gat	gta	tca	agc	aga	gac	aag	atg	672	
Leu	Thr	Gly	Thr	Ile	Val	Gly	Lys	Asp	Val	Ser	Ser	Arg	Asp	Lys	Met		
						215					220						
tgg	aac	acc	ttc	tct	gct	gga	gat	att	gcc	ttt	gcc	tat	gct	ttc		720	
Trp	Asn	Thr	Phe	Ser	Ala	Leu	Gly	Asp	Ile	Ala	Phe	Ala	Tyr	Ala	Phe		
225					230					235				240			
tct	att	gtt	ctt	att	gaa	att	cag	gac	act	ttg	aaa	tcc	cat	cca	cca	768	
Ser	Ile	Val	Leu	Ile	Glu	Ile	Gln	Asp	Thr	Leu	Lys	Ser	His	Pro	Pro		
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gaa	aat	aag	tcc	atg	aag	aaa	gct	aca	ttc	act	ggg	atc	tct	gtg	tca	816	
Glu	Asn	Lys	Ser	Met	Lys	Lys	Ala	Thr	Phe	Thr	Gly	Ile	Ser	Val	Ser		
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aca	ata	ttt	tac	tta	ctc	tgt	gga	ctt	cta	ggg	tat	gct	gca	ttt	gga	864	
Thr	Ile	Phe	Tyr	Leu	Leu	Cys	Gly	Leu	Leu	Gly	Tyr	Ala	Ala	Phe	Gly		
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aac	aaa	gcg	cct	gga	aac	ttt	cta	aca	gga	ttt	gga	ttc	tat	gaa	cct	912	
Asn	Lys	Ala	Pro	Gly	Asn	Phe	Leu	Thr	Gly	Phe	Gly	Phe	Tyr	Glu	Pro		
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ttc	tgg	ctt	att	gat	ttc	gct	aat	gta	tgc	atc	gtg	att	cat	ctc	gtt	960	
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gga	gct	tac	cag	gtg	ttc	tgt	caa	cct	ata	ttt	gga	ttt	gta	gag	ggt	1008	
Gly	Ala	Tyr	Gln	Val	Phe	Cys	Gln	Pro	Ile	Phe	Gly	Phe	Val	Glu	Gly		
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tgg	agc	aga	cag	aaa	tgg	cca	gaa	agt	aaa	ttc	ata	aca	aaa	gaa	tac	1056	
Trp	Ser	Arg	Gln	Lys	Trp	Pro	Glu	Ser	Lys	Phe	Ile	Thr	Lys	Glu	Tyr		
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Met	Ile	Asn	Leu	Ser	His	Leu	Gly	Leu	Phe	Asn	Phe	Asn	Phe	Tyr	Arg		
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Leu	Val	Trp	Arg	Thr	Leu	Tyr	Val	Val	Phe	Thr	Thr	Ile	Leu	Ala	Met		
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Leu	Phe	Pro	Phe	Phe	Asn	Asp	Phe	Val	Gly	Phe	Ile	Gly	Ala	Ala	Ser		
385					390				395					400			
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Phe	Trp	Pro	Leu	Thr	Val	Tyr	Phe	Pro	Ile	Gln	Met	Tyr	Ile	Ala	Gln		
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gcc	aag	ata	cct	aaa	tat	tca	ttt	acc	tgg	att	tgg	ttg	aat	ata	ttg	1296	
Ala	Lys	Ile	Pro	Lys	Tyr	Ser	Phe	Thr	Trp	Ile	Trp	Leu	Asn	Ile	Leu		
				420				425					430				
agt	ttt	gtg	tgc	ctg	atc	atc	tca	ctt	ctt	gct	gct	gct	gga	tct	gtt	1344	
Ser	Phe	Val	Cys	Leu	Ile	Ile	Ser	Leu	Leu	Ala	Ala	Ala	Gly	Ser	Val		
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aga	ggc	ctt	ata	aaa	tct	ctc	cag	gaa	ttc	gag	ccc	ttc	caa	tct	cgg	1392	
Arg	Gly	Leu	Ile	Lys	Ser	Leu	Gln	Glu	Phe	Glu	Pro	Phe	Gln	Ser	Arg		
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Ser																	
465																	

PF59082SeqList_PF59082.txt

<210> 613

<211> 465

<212> PRT

<213> Lycopersicon esculentum

<400> 613

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      35      40      45
Gln Leu Gly Trp Ile Ala Gly Pro Val Ala Leu Ile Ala Phe Ser Ala
      50      55      60
Ile Thr Trp Phe Ala Ser Ile Leu Leu Ala Asp Cys Tyr Arg Ala Pro
65      70      75
Asp Gly Ser Arg Ser Tyr Thr Tyr Met Asp Ala Val Arg Ala His Leu
      85      90      95
Gly Gly Arg Lys Val Gln Leu Cys Gly Leu Ala Gln Tyr Ser Asn Leu
      100      105      110
Phe Gly Val Thr Ile Gly Tyr Ala Ile Thr Thr Ser Ile Ser Met Val
      115      120      125
Ala Ile Lys Arg Ser Asn Cys Phe His Arg Lys Gly His Asp Ala Gly
      130      135      140
Cys His Glu Ser Asn Asn Pro Phe Ile Ile Ile Phe Gly Val Met Gln
145      150      155
Ile Leu Leu Ser Gln Ile Pro Asn Phe His Lys Leu Ser Phe Leu Ser
      165      170      175
Ile Ile Ala Ala Met Ser Phe Ala Tyr Ser Phe Ile Gly Leu Gly
      180      185      190
Leu Ser Ile Ala Lys Ile Ala Lys Asp Gly Val Ser Ala Asn Thr Ser
      195      200      205
Leu Thr Gly Thr Ile Val Gly Lys Asp Val Ser Ser Arg Asp Lys Met
      210      215      220
Trp Asn Thr Phe Ser Ala Leu Gly Asp Ile Ala Phe Ala Tyr Ala Phe
225      230      235
Ser Ile Val Leu Ile Glu Ile Gln Asp Thr Leu Lys Ser His Pro Pro
      245      250      255
Glu Asn Lys Ser Met Lys Lys Ala Thr Phe Thr Gly Ile Ser Val Ser
      260      265      270
Thr Ile Phe Tyr Leu Leu Cys Gly Leu Leu Gly Tyr Ala Ala Phe Gly
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Asn Lys Ala Pro Gly Asn Phe Leu Thr Gly Phe Gly Phe Tyr Glu Pro
      290      295      300
Phe Trp Leu Ile Asp Phe Ala Asn Val Cys Ile Val Ile His Leu Val
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      355      360      365
Leu Val Trp Arg Thr Leu Tyr Val Val Phe Thr Thr Ile Leu Ala Met
      370      375      380
Leu Phe Pro Phe Phe Asn Asp Phe Val Gly Phe Ile Gly Ala Ala Ser
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Phe Trp Pro Leu Thr Val Tyr Phe Pro Ile Gln Met Tyr Ile Ala Gln
      405      410      415
Ala Lys Ile Pro Lys Tyr Ser Phe Thr Trp Ile Trp Leu Asn Ile Leu
      420      425      430
Ser Phe Val Cys Leu Ile Ile Ser Leu Leu Ala Ala Ala Gly Ser Val
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Ser
465

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<210> 614

<211> 1431

PF59082SeqList_PF59082.txt

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<213> Lycopersicon esculentum

<220>

<221> CDS

<222> (1)..(1431)

<400> 614

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Ile Thr Glu Ser Lys Leu Phe Asp Asp Asp Gly Arg Ile Lys Arg Ser	
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gga agt gtt tgg act gca agt gct cat atc ata act gct gtg att ggt	144
Gly Ser Val Trp Thr Ala Ser Ala His Ile Ile Thr Ala Val Ile Gly	
35 40 45	
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Ser Gly Val Leu Ser Leu Ala Trp Ala Val Ala Gln Leu Gly Trp Ile	
50 55 60	
gct ggt cct att gtt atg ctt tta ttc tct ttt gtt act tat tac acc	240
Ala Gly Pro Ile Val Met Leu Leu Phe Ser Phe Val Thr Tyr Tyr Thr	
65 70 75 80	
tct tct ctg ctc tcc gat tgt tac cgc tcc ggc gac cca ctt ttc ggc	288
Ser Ser Leu Leu Ser Asp Cys Tyr Arg Ser Gly Asp Pro Leu Phe Gly	
85 90 95	
aag aga aac tat act tac atg gat gtt gta caa gca aat ctc agt ggc	336
Lys Arg Asn Tyr Thr Tyr Met Asp Val Val Gln Ala Asn Leu Ser Gly	
100 105 110	
tta cag gta aag att tgt gga tgg att cag tat gtg aat ctg ttt gga	384
Leu Gln Val Lys Ile Cys Gly Trp Ile Gln Tyr Val Asn Leu Phe Gly	
115 120 125	
gtt gct att ggg tac aca att gct tct tca att agc ctg atg gct gtt	432
Val Ala Ile Gly Tyr Thr Ile Ala Ser Ser Ile Ser Leu Met Ala Val	
130 135 140	
aaa agg tca gat tgt ttt cat aaa cat ggt cat aaa gca cct tgt tta	480
Lys Arg Ser Asp Cys Phe His Lys His Gly His Lys Ala Pro Cys Leu	
145 150 155 160	
caa cca aat act cca tat atg atc ata ttt gga gta ata gaa atc atc	528
Gln Pro Asn Thr Pro Tyr Met Ile Ile Phe Gly Val Ile Glu Ile Ile	
165 170 175	
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Phe Ser Gln Ile Pro Asp Phe Asp Gln Ile Trp Trp Leu Ser Ile Val	
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gct gct gta atg tct ttc act tac tcc acc atc ggc tta ggt tta ggc	624
Ala Ala Val Met Ser Phe Thr Tyr Ser Thr Ile Gly Leu Gly Leu Gly	
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Ile Ala His Val Ala Glu Thr Gly Lys Ile Gly Gly Ser Leu Thr Gly	
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Val Ser Ile Gly Thr Val Thr Glu Met Gln Lys Val Trp Arg Thr Phe	
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Gln Ala Leu Gly Ala Ile Ala Phe Ala Tyr Ser Tyr Ser Leu Ile Leu	
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Ile Glu Ile Gln Asp Thr Ile Lys Ser Pro Pro Ser Glu Ala Lys Thr	
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Met Lys Asn Ala Thr Ile Ile Ser Val Ser Val Thr Thr Val Phe Tyr	
275 280 285	
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290 295 300	
gac aat tta cta act ggt ttt gga ttt tac gac cct tat tgg cta cta	960
Asp Asn Leu Leu Thr Gly Phe Gly Phe Tyr Asp Pro Tyr Trp Leu Leu	
305 310 315 320	
gat ata gcc aac ata gcc atc ttc gtt cat ctt gta ggt gca tac cag	1008

PF59082SeqList_PF59082.txt

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Val	Tyr	Cys	Gln	Pro	Leu	Phe	Ala	Phe	Ile	Glu	Lys	Thr	Ala	Ala	Glu	
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tgg	tac	cct	aac	agt	aaa	atc	atc	acc	aag	aat	att	agt	gtg	cca	atc	1104
Trp	Tyr	Pro	Asn	Ser	Lys	Ile	Ile	Thr	Lys	Asn	Ile	Ser	Val	Pro	Ile	
		355					360					365				
cct	ggc	ttt	aaa	tcg	tac	aac	att	tac	cta	ttc	aga	cta	gtt	tgg	agg	1152
Pro	Gly	Phe	Lys	Ser	Tyr	Asn	Ile	Tyr	Leu	Phe	Arg	Leu	Val	Trp	Arg	
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acg	atc	ttt	gtt	atc	ata	tcc	act	atc	atc	tct	atg	ttg	ttg	cca	ttc	1200
Thr	Ile	Phe	Val	Ile	Ile	Ser	Thr	Ile	Ile	Ser	Met	Leu	Leu	Pro	Phe	
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ttc	agc	gac	atc	gtt	gga	ata	ctt	gga	gca	ttt	gga	ttt	tgg	ccg	ttg	1248
Phe	Ser	Asp	Ile	Val	Gly	Ile	Leu	Gly	Ala	Phe	Gly	Phe	Trp	Pro	Leu	
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act	gtt	tat	tat	cca	gtg	gaa	ata	tac	att	gtg	caa	aag	aag	ata	cca	1296
Thr	Val	Tyr	Tyr	Pro	Val	Glu	Ile	Tyr	Ile	Val	Gln	Lys	Lys	Ile	Pro	
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aaa	tgg	agt	aga	aaa	tgg	ttt	ggc	ctt	caa	att	ctg	agt	gtt	act	tgt	1344
Lys	Trp	Ser	Arg	Lys	Trp	Phe	Gly	Leu	Gln	Ile	Leu	Ser	Val	Thr	Cys	
		435				440						445				
ctt	att	gtc	tca	att	gct	gca	gct	gtt	ggc	tct	ttt	gct	ggc	gtt	gta	1392
Leu	Ile	Val	Ser	Ile	Ala	Ala	Ala	Val	Gly	Ser	Phe	Ala	Gly	Val	Val	
	450				455						460					
tct	gat	ctt	aaa	gtt	tac	aag	cct	ttc	aaa	ttt	act	tag				1431
Ser	Asp	Leu	Lys	Val	Tyr	Lys	Pro	Phe	Lys	Phe	Thr					
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<211> 476

<212> PRT

<213> Lycopersicon esculentum

<400> 615

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Ser	Gly	Val	Leu	Ser	Leu	Ala	Trp	Ala	Val	Ala	Gln	Leu	Gly	Trp	Ile	
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Ala	Gly	Pro	Ile	Val	Met	Leu	Leu	Phe	Ser	Phe	Val	Thr	Tyr	Tyr	Thr	
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Ser	Ser	Leu	Leu	Ser	Asp	Cys	Tyr	Arg	Ser	Gly	Asp	Pro	Leu	Phe	Gly	
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Lys	Arg	Asn	Tyr	Thr	Tyr	Met	Asp	Val	Gln	Ala	Asn	Leu	Ser	Gly		
		100						105				110				
Leu	Gln	Val	Lys	Ile	Cys	Gly	Trp	Ile	Gln	Tyr	Val	Asn	Leu	Phe	Gly	
		115					120					125				
Val	Ala	Ile	Gly	Tyr	Thr	Ile	Ala	Ser	Ser	Ile	Ser	Leu	Met	Ala	Val	
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Lys	Arg	Ser	Asp	Cys	Phe	His	Lys	His	Gly	His	Lys	Ala	Pro	Cys	Leu	
145					150					155					160	
Gln	Pro	Asn	Thr	Pro	Tyr	Met	Ile	Ile	Phe	Gly	Val	Ile	Glu	Ile	Ile	
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Phe	Ser	Gln	Ile	Pro	Asp	Phe	Asp	Gln	Ile	Trp	Trp	Leu	Ser	Ile	Val	
		180						185					190			
Ala	Ala	Val	Met	Ser	Phe	Thr	Tyr	Ser	Thr	Ile	Gly	Leu	Gly	Leu	Gly	
		195					200					205				
Ile	Ala	His	Val	Ala	Glu	Thr	Gly	Lys	Ile	Gly	Gly	Ser	Leu	Thr	Gly	
	210					215					220					
Val	Ser	Ile	Gly	Thr	Val	Thr	Glu	Met	Gln	Lys	Val	Trp	Arg	Thr	Phe	
225					230					235					240	
Gln	Ala	Leu	Gly	Ala	Ile	Ala	Phe	Ala	Tyr	Ser	Tyr	Ser	Leu	Ile	Leu	
			245						250					255		
Ile	Glu	Ile	Gln	Asp	Thr	Ile	Lys	Ser	Pro	Pro	Ser	Glu	Ala	Lys	Thr	

PF59082SeqList_PF59082.txt

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Asp Asn Leu Leu Thr Gly Phe Gly Phe Tyr Asp Pro Tyr Trp Leu Leu
      305      310      315
Asp Ile Ala Asn Ile Ala Ile Phe Val His Leu Val Gly Ala Tyr Gln
      320      325      330
Val Tyr Cys Gln Pro Leu Phe Ala Phe Ile Glu Lys Thr Ala Ala Glu
      335      340      345
Trp Tyr Pro Asn Ser Lys Ile Ile Thr Lys Asn Ile Ser Val Pro Ile
      350      355      360
Pro Gly Phe Lys Ser Tyr Asn Ile Tyr Leu Phe Arg Leu Val Trp Arg
      365      370      375
Thr Ile Phe Val Ile Ile Ser Thr Ile Ile Ser Met Leu Leu Pro Phe
      380      385      390
Phe Ser Asp Ile Val Gly Ile Leu Gly Ala Phe Gly Phe Trp Pro Leu
      395      400      405
Thr Val Tyr Tyr Pro Val Glu Ile Tyr Ile Val Gln Lys Lys Ile Pro
      410      415      420
Lys Trp Ser Arg Lys Trp Phe Gly Leu Gln Ile Leu Ser Val Thr Cys
      425      430      435
Leu Ile Val Ser Ile Ala Ala Ala Val Gly Ser Phe Ala Gly Val Val
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Ser Asp Leu Lys Val Tyr Lys Pro Phe Lys Phe Thr
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      470      475

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<210> 616

<211> 1431

<212> DNA

<213> Arabidopsis thaliana

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<222> (1)..(1431)

<400> 616

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ggc ggc tcc aag tac ttg gac gac gac ggg aaa aac aaa aga act ggg      96
Gly Gly Ser Lys Tyr Leu Asp Asp Asp Gly Lys Asn Lys Arg Thr Gly
      20      25      30
agt gtt tgg acg gcg agt gca cac ata ata acg gca gtg ata ggt tcg      144
Ser Val Trp Thr Ala Ser Ala His Ile Ile Thr Ala Val Ile Gly Ser
      35      40      45
gga gtt ttg tca cta gcg tgg gct acg gcg cag cta ggt tgg ctc gcc      192
Gly Val Leu Ser Leu Ala Trp Ala Thr Ala Gln Leu Gly Trp Leu Ala
      50      55      60
gga ccg gtg gtg atg ttg ctc ttc tct gtc gtc act tat ttc act tct      240
Gly Pro Val Val Met Leu Leu Phe Ser Val Val Thr Tyr Phe Thr Ser
      65      70      75      80
tct ctt ctt gct gct tgt tac cgc tcc ggc gac cct atc tcc ggc aag      288
Ser Leu Leu Ala Ala Cys Tyr Arg Ser Gly Asp Pro Ile Ser Gly Lys
      85      90      95
agg aac tac act tat atg gat gct gtc cga tca aat ctc ggt ggc gtg      336
Arg Asn Tyr Thr Tyr Met Asp Ala Val Arg Ser Asn Leu Gly Gly Val
      100      105      110
aag gtg acg cta tgt ggg att gtt cag tat ctt aat atc ttt ggt gtt      384
Lys Val Thr Leu Cys Gly Ile Val Gln Tyr Leu Asn Ile Phe Gly Val
      115      120      125
gct att ggc tac aca att gct tcg gct ata agc atg atg gca ata aag      432
Ala Ile Gly Tyr Thr Ile Ala Ser Ala Ile Ser Met Met Ala Ile Lys
      130      135      140
aga tca aac tgt ttc cac aag agt gga ggg aaa gat cca tgt cac atg      480
Arg Ser Asn Cys Phe His Lys Ser Gly Gly Lys Asp Pro Cys His Met
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PF59082SeqList_PF59082.txt

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Ser	Gln	Ile	Pro	Asp	Phe	Asp	Gln	Leu	Trp	Trp	Leu	Ser	Ile	Leu	Ala	
			180					185					190			
gcc	gtt	atg	tcc	ttc	act	tat	tcc	tca	gcc	ggt	ctc	gcc	ctc	ggc	ata	624
Ala	Val	Met	Ser	Phe	Thr	Tyr	Ser	Ser	Ala	Gly	Leu	Ala	Leu	Gly	Ile	
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gcc	caa	gtt	gtc	gtt	aat	ggg	aag	gtg	aag	gga	agt	ctc	act	ggg	att	672
Ala	Gln	Val	Val	Val	Asn	Gly	Lys	Val	Lys	Gly	Ser	Leu	Thr	Gly	Ile	
	210					215					220					
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Ser	Ile	Gly	Ala	Val	Thr	Glu	Thr	Gln	Lys	Ile	Trp	Arg	Thr	Phe	Gln	
225					230					235					240	
gct	ctt	gga	gac	att	gct	ttt	gct	tac	tct	tac	tcc	att	atc	ctc	atc	768
Ala	Leu	Gly	Asp	Ile	Ala	Phe	Ala	Tyr	Ser	Tyr	Ser	Ile	Ile	Leu	Ile	
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Glu	Ile	Gln	Asp	Thr	Val	Lys	Ser	Pro	Pro	Ser	Glu	Glu	Lys	Thr	Met	
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Lys	Lys	Ala	Thr	Leu	Val	Ser	Val	Ser	Val	Thr	Thr	Met	Phe	Tyr	Met	
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Leu	Cys	Gly	Cys	Met	Gly	Tyr	Ala	Ala	Phe	Gly	Asp	Leu	Ser	Pro	Gly	
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Asn	Leu	Leu	Thr	Gly	Phe	Gly	Phe	Tyr	Asn	Pro	Tyr	Trp	Leu	Leu	Asp	
305				310					315						320	
att	gca	aat	gca	gcc	att	gtg	att	cac	ctt	att	ggg	gca	tac	caa	gtc	1008
Ile	Ala	Asn	Ala	Ala	Ile	Val	Ile	His	Leu	Ile	Gly	Ala	Tyr	Gln	Val	
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tat	tgc	caa	cct	ctg	ttt	gct	ttc	atc	gag	aag	caa	gct	tgc	att	caa	1056
Tyr	Cys	Gln	Pro	Leu	Phe	Ala	Phe	Ile	Glu	Lys	Gln	Ala	Ser	Ile	Gln	
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Phe	Pro	Asp	Ser	Glu	Phe	Ile	Ala	Lys	Asp	Ile	Lys	Ile	Pro	Ile	Pro	
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Gly	Phe	Lys	Pro	Leu	Arg	Leu	Asn	Val	Phe	Arg	Leu	Ile	Trp	Arg	Thr	
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Val	Phe	Val	Ile	Ile	Thr	Thr	Val	Ile	Ser	Met	Leu	Leu	Pro	Phe	Phe	
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aac	gac	gtt	gtg	ggg	ctg	ctc	ggg	gca	cta	ggg	ttt	tgg	cca	ttg	acg	1248
Asn	Asp	Val	Val	Gly	Leu	Leu	Gly	Ala	Leu	Gly	Phe	Trp	Pro	Leu	Thr	
				405					410					415		
gtg	tat	ttt	cca	gtg	gaa	atg	tac	atc	gcg	cag	aag	aag	ata	cct	aga	1296
Val	Tyr	Phe	Pro	Val	Glu	Met	Tyr	Ile	Ala	Gln	Lys	Lys	Ile	Pro	Arg	
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tgg	agc	acc	aga	tgg	gtt	tgc	ctt	caa	gtc	ttc	agc	tta	ggg	tgt	cta	1344
Trp	Ser	Thr	Arg	Trp	Val	Cys	Leu	Gln	Val	Phe	Ser	Leu	Gly	Cys	Leu	
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gta	gtt	agc	att	gct	gca	gct	gca	ggg	tcc	ata	gct	gga	gta	ctt	ctt	1392
Val	Val	Ser	Ile	Ala	Ala	Ala	Ala	Gly	Ser	Ile	Ala	Gly	Val	Leu	Leu	
	450				455						460					
gat	cta	aag	tcc	tac	aag	cca	ttt	cga	agc	gaa	tac	tga				1431
Asp	Leu	Lys	Ser	Tyr	Lys	Pro	Phe	Arg	Ser	Glu	Tyr					
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<212> PRT

<213> Arabidopsis thaliana

<400> 617

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Gly Pro Val Val Met Leu Phe Ser Val Val Thr Tyr Phe Thr Ser
65      70      75      80
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      85      90      95
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      100      105      110
Lys Val Thr Leu Cys Gly Ile Val Gln Tyr Leu Asn Ile Phe Gly Val
      115      120      125
Ala Ile Gly Tyr Thr Ile Ala Ser Ala Ile Ser Met Met Ala Ile Lys
130      135      140
Arg Ser Asn Cys Phe His Lys Ser Gly Gly Lys Asp Pro Cys His Met
145      150      155      160
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Ser Gln Ile Pro Asp Phe Asp Gln Leu Trp Trp Leu Ser Ile Leu Ala
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      195      200      205
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210      215      220
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Glu Ile Gln Asp Thr Val Lys Ser Pro Pro Ser Glu Glu Lys Thr Met
      260      265      270
Lys Lys Ala Thr Leu Val Ser Val Ser Val Thr Thr Met Phe Tyr Met
      275      280      285
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305      310      315      320
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      325      330      335
Tyr Cys Gln Pro Leu Phe Ala Phe Ile Glu Lys Gln Ala Ser Ile Gln
      340      345      350
Phe Pro Asp Ser Glu Phe Ile Ala Lys Asp Ile Lys Ile Pro Ile Pro
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Gly Phe Lys Pro Leu Arg Leu Asn Val Phe Arg Leu Ile Trp Arg Thr
370      375      380
Val Phe Val Ile Ile Thr Thr Val Ile Ser Met Leu Leu Pro Phe Phe
385      390      395      400
Asn Asp Val Val Gly Leu Leu Gly Ala Leu Gly Phe Trp Pro Leu Thr
      405      410      415
Val Tyr Phe Pro Val Glu Met Tyr Ile Ala Gln Lys Lys Ile Pro Arg
      420      425      430
Trp Ser Thr Arg Trp Val Cys Leu Gln Val Phe Ser Leu Gly Cys Leu
      435      440      445
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450      455      460
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Leu Lys Arg Ser Gly Thr Val Trp Thr Ala Ser Ala His Ile Ile Thr	
20 25 30	
gcc gtg att gga tct ggt gtt cta tcg ctt gcg tgg gct ata ggt caa	144
Ala Val Ile Gly Ser Gly Val Leu Ser Leu Ala Trp Ala Ile Gly Gln	
35 40 45	
ctc ggt tgg atc gca ggt cct aca gtg atg tts ytg ttc tct ttt gtc	192
Leu Gly Trp Ile Ala Gly Pro Thr Val Met Xaa Leu Phe Ser Phe Val	
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Thr Tyr Tyr Ser Ser Thr Leu Leu Ser Asp Cys Tyr Arg Thr Gly Asp	
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cct gtc tct ggg aag aga aac tat act tac atg gac gct gtc cga tca	288
Pro Val Ser Gly Lys Arg Asn Tyr Thr Tyr Met Asp Ala Val Arg Ser	
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Ile Leu Gly Gly Phe Arg Phe Lys Ile Cys Gly Leu Ile Gln Tyr Leu	
100 105 110	
aat ctg ttt ggt atc acg gtc ggg tac aca atc gca gca tct ata agt	384
Asn Leu Phe Gly Ile Thr Val Gly Tyr Thr Ile Ala Ala Ser Ile Ser	
115 120 125	
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Met Met Ala Ile Lys Arg Ser Asn Cys Phe His Glu Ser Gly Gly Lys	
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Asn Pro Cys His Met Ser Ser Asn Pro Tyr Met Ile Met Phe Gly Val	
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acc gag atc ttg ctc tct cag atc aaa gat ttt gac cag att tgg tgg	528
Thr Glu Ile Leu Leu Ser Gln Ile Lys Asp Phe Asp Gln Ile Trp Trp	
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Leu Ala Leu Gly Ile Ile Gln Val Ala Ala Asn Gly Val Val Lys Gly	
195 200 205	
agt ctc acc gga att agc atc ggc gca gtg act cak acc caa aaa ata	672
Ser Leu Thr Gly Ile Ser Ile Gly Ala Val Thr Xaa Thr Gln Lys Ile	
210 215 220	
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225 230 235 240	

PF59082SeqList_PF59082.txt

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gaa	tca	aaa	acg	atg	aag	atc	gcc	aca	aga	atc	agc	atc	gct	ggt	aca	816
Glu	Ser	Lys	Thr	Met	Lys	Ile	Ala	Thr	Arg	Ile	Ser	Ile	Ala	Val	Thr	
			260						265						270	
acg	aca	ttt	tac	atg	cta	tgt	ggt	tgt	atg	ggc	tat	gcc	gcc	ttc	gga	864
Thr	Thr	Phe	Tyr	Met	Leu	Cys	Gly	Cys	Met	Gly	Tyr	Ala	Ala	Phe	Gly	
			275						280							
gat	aaa	gca	ccg	gga	aac	ctc	tta	acc	ggt	ttt	ggt	ttc	tac	aat	ccg	912
Asp	Lys	Ala	Pro	Gly	Asn	Leu	Leu	Thr	Gly	Phe	Gly	Phe	Tyr	Asn	Pro	
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Gly	Ala	Tyr	Gln	Val	Phe	Ala	Gln	Pro	Ile	Phe	Ala	Phe	Ile	Glu	Lys	
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Gln	Ala	Ala	Ala	Arg	Phe	Pro	Asp	Ser	Asp	Leu	Val	Thr	Lys	Glu	Tyr	
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gaa	atc	cga	atc	cct	ggt	ttt	agg	tca	ccg	tac	aaa	gtc	aac	ggt	ttc	1104
Glu	Ile	Arg	Ile	Pro	Gly	Phe	Arg	Ser	Pro	Tyr	Lys	Val	Asn	Val	Phe	
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aga	gca	ggt	tac	cga	agc	ggg	ttt	gtg	ggt	ttg	acc	act	gtg	ata	tcc	1152
Arg	Ala	Val	Tyr	Arg	Ser	Gly	Phe	Val	Val	Leu	Thr	Thr	Val	Ile	Ser	
atg	ctt	atg	ccg	ttt	ttc	aac	gac	gtc	gta	ggg	att	tta	ggt	gcg	tta	1200
Met	Leu	Met	Pro	Phe	Phe	Asn	Asp	Val	Val	Gly	Ile	Leu	Gly	Ala	Leu	
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Gly	Phe	Trp	Pro	Leu	Thr	Val	Tyr	Phe	Pro	Val	Glu	Met	Tyr	Ile	Arg	
									410						415	
cag	agg	aag	ggt	gag	aga	tgg	agt	atg	aag	tgg	ggt	tgt	ctg	cag	atg	1296
Gln	Arg	Lys	Val	Glu	Arg	Trp	Ser	Met	Lys	Trp	Val	Cys	Leu	Gln	Met	
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Leu	Ser	Cys	Gly	Cys	Leu	Met	Ile	Thr	Leu	Val	Ala	Gly	Val	Gly	Ser	
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atc	gcc	gga	gta	atg	cta	gac	ctt	aag	ggt	yhc	aag	ccg	ttc	aag	act	1392
Ile	Ala	Gly	Val	Met	Leu	Asp	Leu	Lys	Val	Xaa	Lys	Pro	Phe	Lys	Thr	
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Thr	Tyr															

<210> 619
 <211> 466
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 <222> (59)..(59)
 <223> The Xaa at location 59 stands for Leu, or Phe.

<220>
 <221> misc_feature
 <222> (220)..(220)
 <223> The Xaa at location 220 stands for Gln, or His.

<220>
 <221> misc_feature
 <222> (459)..(459)
 <223> The Xaa at location 459 stands for His, Leu, Phe, Pro, Ser, or Tyr.

<400> 619
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PF59082SeqList_PF59082.txt

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 Ala Val Ile Gly Ser Gly Val Leu Ser Leu Ala Trp Ala Ile Gly Gln
 Leu Gly Trp Ile Ala Gly Pro Thr Val Met Xaa Leu Phe Ser Phe Val
 Thr Tyr Tyr Ser Ser Thr Leu Leu Ser Asp Cys Tyr Arg Thr Gly Asp
 65 Pro Val Ser Gly Lys Arg Asn Tyr Thr Tyr Met Asp Ala Val Arg Ser
 Ile Leu Gly Gly Phe Arg Phe Lys Ile Cys Gly Leu Ile Gln Tyr Leu
 Asn Leu Phe Gly Ile Thr Val Gly Tyr Thr Ile Ala Ala Ser Ile Ser
 Met Met Ala Ile Lys Arg Ser Asn Cys Phe His Glu Ser Gly Gly Lys
 130 Asn Pro Cys His Met Ser Ser Asn Pro Tyr Met Ile Met Phe Gly Val
 145 Thr Glu Ile Leu Leu Ser Gln Ile Lys Asp Phe Asp Gln Ile Trp Trp
 Leu Ser Ile Val Ala Ala Ile Met Ser Phe Thr Tyr Ser Ala Ile Gly
 Leu Ala Leu Gly Ile Ile Gln Val Ala Ala Asn Gly Val Val Lys Gly
 Ser Leu Thr Gly Ile Ser Ile Gly Ala Val Thr Xaa Thr Gln Lys Ile
 210 Trp Arg Thr Phe Gln Ala Leu Gly Asp Ile Ala Phe Ala Tyr Ser Tyr
 225 Ser Val Val Leu Ile Glu Ile Gln Asp Thr Val Arg Ser Pro Pro Ala
 Glu Ser Lys Thr Met Lys Ile Ala Thr Arg Ile Ser Ile Ala Val Thr
 Thr Thr Phe Tyr Met Leu Cys Gly Cys Met Gly Tyr Ala Ala Phe Gly
 275 Asp Lys Ala Pro Gly Asn Leu Thr Gly Phe Gly Phe Tyr Asn Pro
 290 Phe Trp Leu Leu Asp Val Ala Asn Ala Ala Ile Val Ile His Leu Val
 305 Gly Ala Tyr Gln Val Phe Ala Gln Pro Ile Phe Ala Phe Ile Glu Lys
 Gln Ala Ala Ala Arg Phe Pro Asp Ser Asp Leu Val Thr Lys Glu Tyr
 340 Glu Ile Arg Ile Pro Gly Phe Arg Ser Pro Tyr Lys Val Asn Val Phe
 355 Arg Ala Val Tyr Arg Ser Gly Phe Val Val Leu Thr Thr Val Ile Ser
 370 Met Leu Met Pro Phe Phe Asn Asp Val Val Gly Ile Leu Gly Ala Leu
 385 Gly Phe Trp Pro Leu Thr Val Tyr Phe Pro Val Glu Met Tyr Ile Arg
 405 Gln Arg Lys Val Glu Arg Trp Ser Met Lys Trp Val Cys Leu Gln Met
 420 Leu Ser Cys Gly Cys Leu Met Ile Thr Leu Val Ala Gly Val Gly Ser
 435 Ile Ala Gly Val Met Leu Asp Leu Lys Val Xaa Lys Pro Phe Lys Thr
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<212> DNA

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ggc Gly	cac His	cag Gln	gtc Val 20	ttt Phe	gac Asp	gtg Val	gcc Ala	agc Ser 25	cac His	gat Asp	ttc Phe	gtc Val	cct Pro 30	cca Pro	caa Gln	96
ccg Pro	gct Ala	ttt Phe 35	aaa Lys	tgc Cys	ttc Phe	gat Asp	gat Asp 40	gat Asp	ggc Gly	cgc Arg	ctc Leu	aaa Lys 45	aga Arg	act Thr	ggg Gly	144
act Thr 50	gtt Val	tgg Trp	acc Thr	gcg Ala	agc Ser	gct Ala 55	cat His	ata Ile	ata Ile	act Thr	gcg Ala 60	gtt Val	atc Ile	gga Gly	tcc Ser	192
ggc Gly 65	gtt Val	ttg Leu	tca Ser	ttg Leu	gcg Ala 70	tgg Trp	gcg Ala	att Ile	gca Ala	cag Gln 75	ctc Leu	gga Gly	tgg Trp	atc Ile	gct Ala 80	240
ggc Gly	cct Pro	gct Ala	gtg Val	atg Met 85	cta Leu	ttg Leu	ttc Phe	tct Ser	ctt Leu 90	gtt Val	act Thr	ctt Leu	tac Tyr	tcc Ser 95	tcc Ser	288
aca Thr	ctt Leu	ctt Leu	agc Ser 100	gac Asp	tgc Cys	tac Tyr	aga Arg	acc Thr 105	ggc Gly	gat Asp	gca Ala	gtg Val	tct Ser 110	ggc Gly	aag Lys	336
aga Arg	aac Asn	tac Tyr 115	act Thr	tac Tyr	atg Met	gat Asp	gcc Ala 120	gtt Val	cga Arg	tca Ser	att Ile	ctc Leu 125	ggg Gly	ggg Gly	ttc Phe	384
aag Lys 130	ttc Phe	aag Lys	att Ile	tgt Cys	ggg Gly	ttg Leu 135	att Ile	caa Gln	tac Tyr	ttg Leu	aat Asn 140	ctc Leu	ttt Phe	gtt Val	atc Ile	432
gca Ala 145	att Ile	gga Gly	tac Tyr	acg Thr	ata Ile 150	gca Ala	gct Ala	tcc Ser	ata Ile	agc Ser 155	atg Met	atg Met	gcg Ala	atc Ile	aag Lys 160	480
aga Arg	tcc Ser	aac Asn	tgc Cys	ttc Phe 165	cac His	aag Lys	agt Ser	gga Gly 170	gga Gly	aaa Lys	gac Asp	cca Pro	tgt Cys 175	cac His	atg Met	528
tcc Ser	agt Ser	aat Asn	cct Pro 180	tac Tyr	atg Met	atc Ile	gta Val	ttt Phe 185	ggg Gly	gtg Val	gca Ala	gag Glu	atc Ile 190	ttg Leu	ctc Leu	576
tct Ser	cag Gln	gtt Val 195	cct Pro	gat Asp	ttc Phe	gat Asp	cag Gln 200	att Ile	tgg Trp	tgg Trp	atc Ile	tcc Ser 205	att Ile	gtt Val	gca Ala	624
gct Ala 210	gtt Val	atg Met	tcc Ser	ttc Phe	act Thr	tac Tyr 215	tct Ser	gcc Ala	att Ile	ggg Gly	cta Leu 220	gct Ala	ctt Leu	gga Gly	atc Ile	672
gtt Val 225	caa Gln	gtt Val	gca Ala	gcg Ala	aat Asn 230	gga Gly	gtt Val	ttc Phe	aaa Lys	gga Gly 235	agt Ser	ctc Leu	act Thr	gga Gly	ata Ile 240	720
agc Ser	atc Ile	gga Gly	aca Thr	gtg Val 245	act Thr	caa Gln	aca Thr	cag Gln	aag Lys 250	ata Ile	tgg Trp	aga Arg	acc Thr	ttc Phe 255	caa Gln	768
gca Ala	ctt Leu	gga Gly	gac Asp 260	att Ile	gcc Ala	ttt Phe	gcg Ala	tac Tyr 265	tca Ser	tac Tyr	tct Ser	gtt Val 270	gtc Val	cta Leu	atc Ile	816
gag Glu	att Ile	cag Gln	gat Asp	act Thr	gta Val	aga Arg	tcc Ser 280	cca Pro	ccg Pro	gcg Ala	gaa Glu	tcg Ser 285	aaa Lys	acg Thr	atg Met	864
aag Lys 290	aaa Lys	gca Ala	aca Thr	aaa Lys	atc Ile	agt Ser 295	att Ile	gcc Ala	gtc Val	aca Thr	act Thr 300	atc Ile	ttc Phe	tac Tyr	atg Met	912
cta Leu 305	tgt Cys	ggc Gly	tca Ser	atg Met	ggg Gly 310	tat Tyr	gcc Ala	gct Ala	ttt Phe	gga Gly 315	gat Asp	gca Ala	gca Ala	ccg Pro	gga Gly 320	960
aac Asn	ctc Leu	ctc Leu	acc Thr	ggg Gly 325	ttt Phe	gga Gly	ttc Phe	tac Tyr	aac Asn 330	ccg Pro	ttt Phe	tgg Trp	ctc Leu	ctt Leu 335	gac Asp	1008
ata Ile	gct Ala	aac Asn	gcc Ala 340	gcc Ala	att Ile	gtt Val	gtc Val	cac His 345	ctc Leu	gtt Val	gga Gly	gct Ala	tac Tyr 350	caa Gln	gtc Val	1056
ttt Phe	gct Ala	cag Gln 355	ccc Pro	atc Ile	ttt Phe	gcc Ala	ttt Phe 360	att Ile	gaa Glu	aaa Lys	tca Ser	gtc Val 365	gca Ala	gag Glu	aga Arg	1104

PF59082SeqList_PF59082.txt

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Gly	Phe	Lys	Ser	Pro	Tyr	Lys	Val	Asn	Val	Phe	Arg	Met	Val	Tyr	Arg	
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agt	ggc	ttt	gtc	gtt	aca	acc	acc	gtg	ata	tcg	atg	ctg	atg	ccg	ttt	1248
Ser	Gly	Phe	Val	Val	Thr	Thr	Thr	Val	Ile	Ser	Met	Leu	Met	Pro	Phe	
			405					410						415		
ttt	aac	gac	gtg	gtc	ggg	atc	tta	ggg	gcg	tta	ggg	ttt	tggt	ccc	ttg	1296
Phe	Asn	Asp	Val	Val	Gly	Ile	Leu	Gly	Ala	Leu	Gly	Phe	Trp	Pro	Leu	
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acg	gtt	tat	ttt	ccg	gtg	gag	atg	tat	att	aag	cag	agg	aag	gtt	gag	1344
Thr	Val	Tyr	Phe	Pro	Val	Glu	Met	Tyr	Ile	Lys	Gln	Arg	Lys	Val	Glu	
		435				440					445					
aaa	tggt	agc	acg	aga	tggt	gtg	tgt	tta	cag	atg	ctt	act	gtt	gct	tgt	1392
Lys	Trp	Ser	Thr	Arg	Trp	Val	Cys	Leu	Gln	Met	Leu	Thr	Val	Ala	Cys	
	450					455					460					
ctt	gtg	atc	tcg	gtg	gtc	gcc	ggg	gtt	gga	tca	atc	gcc	gga	gtg	atg	1440
Leu	Val	Ile	Ser	Val	Val	Ala	Gly	Val	Gly	Ser	Ile	Ala	Gly	Val	Met	
	465				470				475						480	
ctt	gat	ctt	aag	gtc	tat	aag	cca	ttc	aag	tct	aca	tat	tga			1482
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Pro	Ala	Phe	Lys	Cys	Phe	Asp	Asp	Asp	Gly	Arg	Leu	Lys	Arg	Thr	Gly	
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Thr	Val	Trp	Thr	Ala	Ser	Ala	His	Ile	Ile	Thr	Ala	Val	Ile	Gly	Ser	
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Gly	Val	Leu	Ser	Leu	Ala	Trp	Ala	Ile	Ala	Gln	Leu	Gly	Trp	Ile	Ala	
	65				70					75					80	
Gly	Pro	Ala	Val	Met	Leu	Leu	Phe	Ser	Leu	Val	Thr	Leu	Tyr	Ser	Ser	
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Thr	Leu	Leu	Ser	Asp	Cys	Tyr	Arg	Thr	Gly	Asp	Ala	Val	Ser	Gly	Lys	
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Arg	Asn	Tyr	Thr	Tyr	Met	Asp	Ala	Val	Arg	Ser	Ile	Leu	Gly	Gly	Phe	
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Lys	Phe	Lys	Ile	Cys	Gly	Leu	Ile	Gln	Tyr	Leu	Asn	Leu	Phe	Val	Ile	
	130					135					140					
Ala	Ile	Gly	Tyr	Thr	Ile	Ala	Ala	Ser	Ile	Ser	Met	Met	Ala	Ile	Lys	
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Arg	Ser	Asn	Cys	Phe	His	Lys	Ser	Gly	Gly	Lys	Asp	Pro	Cys	His	Met	
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Ser	Ser	Asn	Pro	Tyr	Met	Ile	Val	Phe	Gly	Val	Ala	Glu	Ile	Leu	Leu	
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Ser	Gln	Val	Pro	Asp	Phe	Asp	Gln	Ile	Trp	Trp	Ile	Ser	Ile	Val	Ala	
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Val	Gln	Val	Ala	Ala	Asn	Gly	Val	Phe	Lys	Gly	Ser	Leu	Thr	Gly	Ile	
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Ser	Ile	Gly	Thr	Val	Thr	Gln	Thr	Gln	Lys	Ile	Trp	Arg	Thr	Phe	Gln	
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Ala	Leu	Gly	Asp	Ile	Ala	Phe	Ala	Tyr	Ser	Tyr	Ser	Val	Val	Leu	Ile	
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Glu	Ile	Gln	Asp	Thr	Val	Arg	Ser	Pro	Pro	Ala	Glu	Ser	Lys	Thr	Met	
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Lys	Lys	Ala	Thr	Lys	Ile	Ser	Ile	Ala	Val	Thr	Thr	Ile	Phe	Tyr	Met	
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PF59082SeqList_PF59082.txt

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 325 330 335
 Ile Ala Asn Ala Ala Ile Val Val His Leu Val Gly Ala Tyr Gln Val
 340 345 350
 Phe Ala Gln Pro Ile Phe Ala Phe Ile Glu Lys Ser Val Ala Glu Arg
 355 360 365
 Tyr Pro Asp Asn Asp Phe Leu Ser Lys Glu Phe Glu Ile Arg Ile Pro
 370 375 380
 Gly Phe Lys Ser Pro Tyr Lys Val Asn Val Phe Arg Met Val Tyr Arg
 385 390 395 400
 Ser Gly Phe Val Val Thr Thr Thr Val Ile Ser Met Leu Met Pro Phe
 405 410 415
 Phe Asn Asp Val Val Gly Ile Leu Gly Ala Leu Gly Phe Trp Pro Leu
 420 425 430
 Thr Val Tyr Phe Pro Val Glu Met Tyr Ile Lys Gln Arg Lys Val Glu
 435 440 445
 Lys Trp Ser Thr Arg Trp Val Cys Leu Gln Met Leu Thr Val Ala Cys
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Leu Lys Arg Ser Gly Thr Val Trp Thr Ala Ser Ala His Ile Ile Thr	
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gcc gtg att gga tct ggt gtt cta tcg ctt gcg tgg gct ata ggt caa	144
Ala Val Ile Gly Ser Gly Val Leu Ser Leu Ala Trp Ala Ile Gly Gln	
35 40 45	
ctc ggt tgg atc gca ggt cct aca gtg atg ttg ttg ttc tct ttt gtc	192
Leu Gly Trp Ile Ala Gly Pro Thr Val Met Leu Leu Phe Ser Phe Val	
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act tac tac tct tcc acg ctt ctt agc gac tgc tac aga acc gga gat	240
Thr Tyr Tyr Ser Ser Thr Leu Leu Ser Asp Cys Tyr Arg Thr Gly Asp	
65 70 75 80	
cct gtc tct ggg aag aga aac tat act tac atg gac gct gtc cga tca	288
Pro Val Ser Gly Lys Arg Asn Tyr Thr Tyr Met Asp Ala Val Arg Ser	
85 90 95	
atc cta ggt ggc ttt agg ttc aag att tgt ggg ctg att cag tat ttg	336
Ile Leu Gly Gly Phe Arg Phe Lys Ile Cys Gly Leu Ile Gln Tyr Leu	
100 105 110	
aat ctg ttt ggt atc acg gtc ggg tac aca atc gca gca tct ata agt	384
Asn Leu Phe Gly Ile Thr Val Gly Tyr Thr Ile Ala Ala Ser Ile Ser	
115 120 125	
atg atg gcg atc aag agg tcc aac tgt ttc cac gag agc gga ggg aaa	432
Met Met Ala Ile Lys Arg Ser Asn Cys Phe His Glu Ser Gly Gly Lys	
130 135 140	
aac ccg tgt cac atg tcg agc aat cca tac atg atc atg ttt ggt gtg	480
Asn Pro Cys His Met Ser Ser Asn Pro Tyr Met Ile Met Phe Gly Val	
145 150 155 160	
acc gag atc ttg ctc tct cag atc aaa gat ttt gac cag att tgg tgg	528
Thr Glu Ile Leu Leu Ser Gln Ile Lys Asp Phe Asp Gln Ile Trp Trp	
165 170 175	
ctc tcc att gtc gct gct atc atg tcc ttc aca tac tct gca atc ggt	576

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Leu	Ala	Leu	Gly	Ile	Ile	Gln	Val	Ala	Ala	Asn	Gly	Val	Val	Lys	Gly	
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Ser	Leu	Thr	Gly	Ile	Ser	Ile	Gly	Ala	Val	Thr	Gln	Thr	Gln	Lys	Ile	
210			215								220					
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Trp	Arg	Thr	Phe	Gln	Ala	Leu	Gly	Asp	Ile	Ala	Phe	Ala	Tyr	Ser	Tyr	
225			230							235					240	
tct	gtt	gtt	ctt	att	gaa	att	cag	gac	act	gta	aga	tct	cca	cca	gca	768
Ser	Val	Val	Leu	Ile	Glu	Ile	Gln	Asp	Thr	Val	Arg	Ser	Pro	Pro	Ala	
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gaa	tca	aaa	acg	atg	aag	atc	gcc	aca	aga	atc	agc	atc	gct	gtt	aca	816
Glu	Ser	Lys	Thr	Met	Lys	Ile	Ala	Thr	Arg	Ile	Ser	Ile	Ala	Val	Thr	
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acg	aca	ttt	tac	atg	cta	tgt	ggc	tgt	atg	ggc	tat	gcc	gcc	ttc	gga	864
Thr	Thr	Phe	Tyr	Met	Leu	Cys	Gly	Cys	Met	Gly	Tyr	Ala	Ala	Phe	Gly	
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gat	aaa	gca	ccg	gga	aac	ctc	tta	acc	ggc	ttt	ggc	ttc	tac	aat	ccg	912
Asp	Lys	Ala	Pro	Gly	Asn	Leu	Leu	Thr	Gly	Phe	Gly	Phe	Tyr	Asn	Pro	
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Phe	Trp	Leu	Leu	Asp	Val	Ala	Asn	Ala	Ala	Ile	Val	Ile	His	Leu	Val	
305			310							315					320	
gga	gct	tat	caa	gtc	ttt	gct	cag	ccc	atc	ttc	gcc	ttt	att	gag	aaa	1008
Gly	Ala	Tyr	Gln	Val	Phe	Ala	Gln	Pro	Ile	Phe	Ala	Phe	Ile	Glu	Lys	
			325						330					335		
caa	gct	gcc	gct	agt	ttt	ccc	gac	agt	gac	ttg	gtg	acc	aag	gaa	tac	1056
Gln	Ala	Ala	Ala	Ser	Phe	Pro	Asp	Ser	Asp	Leu	Val	Thr	Lys	Glu	Tyr	
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gaa	atc	cga	atc	cct	ggt	ttt	agg	tca	ccg	tac	aaa	gtc	aac	gtt	ttc	1104
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Met	Leu	Met	Pro	Phe	Asn	Asp	Val	Val	Gly	Ile	Leu	Gly	Ala	Leu		
385			390						395					400		
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Gly	Phe	Trp	Pro	Leu	Thr	Val	Tyr	Phe	Pro	Val	Glu	Met	Tyr	Ile	Arg	
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cag	agg	aag	gtt	gag	aga	tgg	agt	atg	aag	tgg	gtt	tgt	ctg	cag	atg	1296
Gln	Arg	Lys	Val	Glu	Arg	Trp	Ser	Met	Lys	Trp	Val	Cys	Leu	Gln	Met	
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ttg	agc	tgt	ggc	tgt	ttg	atg	atc	acg	ttg	gtc	gcc	gga	gtt	ggc	tcc	1344
Leu	Ser	Cys	Gly	Cys	Leu	Met	Ile	Thr	Leu	Val	Ala	Gly	Val	Gly	Ser	
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atc	gcc	gga	gta	atg	cta	gac	ctt	aag	gtt	tac	aag	ccg	ttc	aag	act	1392
Ile	Ala	Gly	Val	Met	Leu	Asp	Leu	Lys	Val	Tyr	Lys	Pro	Phe	Lys	Thr	
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Thr	Tyr															
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 35 40 45

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65 70 75 80
Pro Val Ser Gly Lys Arg Asn Tyr Thr Tyr Met Asp Ala Val Arg Ser
85 90 95
Ile Leu Gly Gly Phe Arg Phe Lys Ile Cys Gly Leu Ile Gln Tyr Leu
100 105 110
Asn Leu Phe Gly Ile Thr Val Gly Tyr Thr Ile Ala Ala Ser Ile Ser
115 120 125
Met Met Ala Ile Lys Arg Ser Asn Cys Phe His Glu Ser Gly Gly Lys
130 135 140
Asn Pro Cys His Met Ser Ser Asn Pro Tyr Met Ile Met Phe Gly Val
145 150 155 160
Thr Glu Ile Leu Leu Ser Gln Ile Lys Asp Phe Asp Gln Ile Trp Trp
165 170 175
Leu Ser Ile Val Ala Ala Ile Met Ser Phe Thr Tyr Ser Ala Ile Gly
180 185 190
Leu Ala Leu Gly Ile Ile Gln Val Ala Ala Asn Gly Val Val Lys Gly
195 200 205
Ser Leu Thr Gly Ile Ser Ile Gly Ala Val Thr Gln Thr Gln Lys Ile
210 215 220
Trp Arg Thr Phe Gln Ala Leu Gly Asp Ile Ala Phe Ala Tyr Ser Tyr
225 230 235 240
Ser Val Val Leu Ile Glu Ile Gln Asp Thr Val Arg Ser Pro Pro Ala
245 250 255
Glu Ser Lys Thr Met Lys Ile Ala Thr Arg Ile Ser Ile Ala Val Thr
260 265 270
Thr Thr Phe Tyr Met Leu Cys Gly Cys Met Gly Tyr Ala Ala Phe Gly
275 280 285
Asp Lys Ala Pro Gly Asn Leu Leu Thr Gly Phe Gly Phe Tyr Asn Pro
290 295 300
Phe Trp Leu Leu Asp Val Ala Asn Ala Ala Ile Val Ile His Leu Val
305 310 315 320
Gly Ala Tyr Gln Val Phe Ala Gln Pro Ile Phe Ala Phe Ile Glu Lys
325 330 335
Gln Ala Ala Ala Ser Phe Pro Asp Ser Asp Leu Val Thr Lys Glu Tyr
340 345 350
Glu Ile Arg Ile Pro Gly Phe Arg Ser Pro Tyr Lys Val Asn Val Phe
355 360 365
Arg Ala Val Tyr Arg Ser Gly Phe Val Val Leu Thr Thr Val Ile Ser
370 375 380
Met Leu Met Pro Phe Phe Asn Asp Val Val Gly Ile Leu Gly Ala Leu
385 390 395 400
Gly Phe Trp Pro Leu Thr Val Tyr Phe Pro Val Glu Met Tyr Ile Arg
405 410 415
Gln Arg Lys Val Glu Arg Trp Ser Met Lys Trp Val Cys Leu Gln Met
420 425 430
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Thr Tyr
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<212> DNA
<213> Vicia faba var

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Seite 787

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Arg	Val	Lys	Arg	Thr	Gly	Thr	Ser	Trp	Thr	Ala	Ser	Ala	His	Val	Ile	
aca	gct	gtg	ata	gga	tct	gga	gtg	ctg	tct	cta	gct	tgg	gct	ata	gct	192
Thr	Ala	Val	Ile	Gly	Ser	Gly	Val	Leu	Ser	Leu	Ala	Trp	Ala	Ile	Ala	
cag	ctt	gga	tgg	att	gct	ggt	cct	att	gtc	atg	ttt	ctc	ttt	gct	tgg	240
Gln	Leu	Gly	Trp	Ile	Ala	Gly	Pro	Ile	Val	Met	Phe	Leu	Phe	Ala	Trp	
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Val	Thr	Tyr	Tyr	Thr	Ser	Val	Leu	Leu	Cys	Glu	Cys	Tyr	Arg	Asn	Gly	
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Asp	Pro	Val	Asn	Gly	Lys	Arg	Asn	Tyr	Thr	Tyr	Met	Glu	Val	Val	His	
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Ser	Asn	Leu	Gly	Gly	Phe	Gln	Val	Gln	Leu	Cys	Gly	Leu	Ile	Gln	Tyr	
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Leu	Asn	Leu	Val	Gly	Val	Ala	Ile	Gly	Tyr	Thr	Val	Ala	Ser	Ala	Ile	
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Ser	Met	Met	Ala	Ile	Val	Arg	Ser	Asn	Cys	Phe	His	Arg	Ser	Gly	Gly	
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Lys	Asp	Pro	Cys	His	Met	Asn	Ser	Asn	Ile	Tyr	Met	Ile	Ala	Phe	Gly	
gct	gtg	caa	att	ata	ttc	tct	caa	att	cct	gat	ttt	gat	caa	tta	tgg	576
Ala	Val	Gln	Ile	Ile	Phe	Ser	Gln	Ile	Pro	Asp	Phe	Asp	Gln	Leu	Trp	
tgg	ctt	tcc	atc	gtt	gct	gtt	gtt	atg	tcc	ttt	aca	tat	tcc	aca	att	624
Trp	Leu	Ser	Ile	Val	Ala	Val	Val	Met	Ser	Phe	Thr	Tyr	Ser	Thr	Ile	
ggt	ctt	ggc	ctt	ggt	att	gga	aaa	gtt	ata	gag	aac	aaa	aag	ttt	gct	672
Gly	Leu	Gly	Leu	Gly	Ile	Gly	Lys	Val	Ile	Glu	Asn	Lys	Lys	Phe	Ala	
gga	acc	att	act	ggg	ata	aat	gat	gtg	aca	aaa	gct	caa	aaa	act	tgg	720
Gly	Thr	Ile	Thr	Gly	Ile	Asn	Asp	Val	Thr	Lys	Ala	Gln	Lys	Thr	Trp	
ggg	agt	ttg	caa	gct	ctt	ggt	gac	ata	gct	ttt	gct	tac	tca	ttc	tcc	768
Gly	Ser	Leu	Gln	Ala	Leu	Gly	Asp	Ile	Ala	Phe	Ala	Tyr	Ser	Phe	Ser	
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Glu	Ser	Lys	Thr	Met	Lys	Lys	Ala	Thr	Leu	Ile	Ser	Val	Ile	Val	Thr	
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Thr	Phe	Phe	Tyr	Met	Leu	Cys	Gly	Cys	Phe	Gly	Tyr	Ala	Ala	Phe	Gly	
aat	tca	agt	ccc	gga	aat	ctt	tta	acc	ggt	ttc	gga	ttc	tat	aac	cca	960
Asn	Ser	Ser	Pro	Gly	Asn	Leu	Leu	Thr	Gly	Phe	Gly	Phe	Tyr	Asn	Pro	
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Phe	Trp	Leu	Leu	Asp	Ile	Ala	Asn	Ala	Ala	Ile	Val	Ile	His	Leu	Ile	
ggt	gca	tac	caa	gtt	tat	tgt	caa	ccc	ctt	ttt	gct	ttt	gtc	gaa	aat	1056
Gly	Ala	Tyr	Gln	Val	Tyr	Cys	Gln	Pro	Leu	Phe	Ala	Phe	Val	Glu	Asn	
tac	acg	gcg	aaa	aga	ttc	cca	gac	agt	gat	ttt	gtg	aac	aag	gac	gta	1104
Tyr	Thr	Lys	Lys	Arg	Phe	Pro	Asp	Ser	Asp	Phe	Val	Asn	Lys	Asp	Val	
aag	att	cca	att	ccc	ggt	tta	gat	agg	tat	aaa	ctc	aac	ctt	ttt	aga	1152
Lys	Ile	Pro	Ile	Pro	Gly	Leu	Asp	Arg	Tyr	Lys	Leu	Asn	Leu	Phe	Arg	
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Leu	Leu	Pro	Phe	Phe 405	Asn	Asp	Ile	Val	Gly 410	Leu	Leu	Gly	Ala	Ile 415	Gly	
ttt	tgg	cct	cta	act	gtt	tat	ttt	ccg	gtg	gag	atg	tat	ata	att	caa	1296
Phe	Trp	Pro	Leu	Thr	Val	Tyr	Phe	Pro	Val	Glu	Met	Tyr	Ile	Ile	Gln	
aag	aaa	ata	cca	aag	tgg	agc	aca	aaa	tgg	att	tgc	ctt	caa	ttg	ctt	1344
Lys	Lys	Ile 435	Pro	Lys	Trp	Ser	Thr	Lys	Trp	Ile	Cys	Leu	Gln	Leu	Leu	
agt	ggt	gcg	tgt	ctt	ata	atc	act	ata	gca	gct	aca	att	ggt	tct	att	1392
Ser	Gly 450	Ala	Cys	Leu	Ile	Ile 455	Thr	Ile	Ala	Ala	Thr	Ile	Gly	Ser	Ile	
gct	ggc	ctt	atc	ctt	gat	ctt	aaa	gtt	ttt	aag	cca	ttc	aag	act	atc	1440
Ala 465	Gly	Leu	Ile	Leu	Asp 470	Leu	Lys	Val	Phe	Lys 475	Pro	Phe	Lys	Thr	Ile 480	
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Tyr																

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 <211> 481
 <212> PRT
 <213> Vicia faba var

<400> 625

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Arg	Val	Lys 35	Arg	Thr	Gly	Thr	Ser	Trp 40	Thr	Ala	Ser	Ala	His	Val	Ile
Thr	Ala 50	Val	Ile	Gly	Ser	Gly 55	Val	Leu	Ser	Leu	Ala	Trp	Ala	Ile	Ala
Gln 65	Leu	Gly	Trp	Ile	Ala	Gly 70	Pro	Ile	Val	Met 75	Phe	Leu	Phe	Ala	Trp 80
Val	Thr	Tyr	Tyr	Thr 85	Ser	Val	Leu	Leu	Cys 90	Glu	Cys	Tyr	Arg	Asn 95	Gly
Asp	Pro	Val	Asn 100	Gly	Lys	Arg	Asn	Tyr 105	Thr	Tyr	Met	Glu	Val	Val	His
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Leu	Asn	Leu	Val	Gly	Val	Ala 135	Ile	Gly	Tyr	Thr	Val	Ala	Ser	Ala	Ile
Ser 145	Met	Met	Ala	Ile	Val	Arg	Ser	Asn	Cys	Phe 155	His	Arg	Ser	Gly	Gly 160
Lys	Asp	Pro	Cys	His 165	Met	Asn	Ser	Asn	Ile 170	Tyr	Met	Ile	Ala	Phe	Gly 175
Ala	Val	Gln	Ile	Ile	Phe	Ser	Gln	Ile 185	Pro	Asp	Phe	Asp	Gln	Leu	Trp
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Gly	Ser	Leu	Gln	Ala 245	Leu	Gly	Asp	Ile	Ala	Phe	Ala	Tyr	Ser	Phe	Ser 255
Met	Ile	Leu	Ile	Glu	Ile	Gln	Asp	Thr 265	Ile	Lys	Ala	Pro	Pro	Pro	Ser
Glu	Ser	Lys 275	Thr	Met	Lys	Lys	Ala	Thr	Leu	Ile	Ser	Val	Ile	Val	Thr
Thr	Phe	Phe	Tyr	Met	Leu	Cys 295	Gly	Cys	Phe	Gly	Tyr	Ala	Ala	Phe	Gly
Asn 305	Ser	Ser	Pro	Gly	Asn	Leu	Leu	Thr	Gly	Phe 315	Gly	Phe	Tyr	Asn	Pro 320
Phe	Trp	Leu	Leu	Asp 325	Ile	Ala	Asn	Ala	Ala	Ile 330	Val	Ile	His	Leu	Ile 335

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 Leu Val Trp Arg Thr Val Tyr Val Ile Leu Thr Thr Leu Ile Ser Met
 Leu Leu Pro Phe Phe Asn Asp Ile Val Gly Leu Leu Gly Ala Ile Gly
 Phe Trp Pro Leu Thr Val Tyr Phe Pro Val Glu Met Tyr Ile Ile Gln
 Lys Lys Ile Pro Lys Trp Ser Thr Lys Trp Ile Cys Leu Gln Leu Leu
 Ser Gly Ala Cys Leu Ile Ile Thr Ile Ala Ala Thr Ile Gly Ser Ile
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 <213> Vicia faba var

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 Gly Gly Ile Glu Glu Ala Ile Asp Asp Ala Pro Leu Gln Thr Asp Ser
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 aaa ttc tat gat gac gat ggc cgt gtt aaa cga aca ggc act gtt tgg 144
 Lys Phe Tyr Asp Asp Asp Gly Arg Val Lys Arg Thr Gly Thr Val Trp
 35 40 45
 act aca tgc tcc cac ata ata aca ggt gtg ata gga tct gga gtg ctc 192
 Thr Thr Cys Ser His Ile Ile Thr Gly Val Ile Gly Ser Gly Val Leu
 50 55 60
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 Ser Leu Ala Trp Ser Val Ala Gln Met Gly Trp Ile Ala Gly Pro Ala
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 Thr Met Ile Phe Phe Ser Ile Ile Thr Leu Tyr Thr Ser Ser Phe Leu
 85 90 95
 gct gat tgt tat cgt agt ggc gac acc gaa ttt gga aag aga aac tat 336
 Ala Asp Cys Tyr Arg Ser Gly Asp Thr Glu Phe Gly Lys Arg Asn Tyr
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 act ttc atg gat gca gtt cac aat att ctt ggt ggg ccc agt gtt aag 384
 Thr Phe Met Asp Ala Val His Asn Ile Leu Gly Gly Pro Ser Val Lys
 115 120 125
 att tgt ggg gta gtt cag tac ttg aat ctt ttc gga agt gca ata gga 432
 Ile Cys Gly Val Val Gln Tyr Leu Asn Leu Phe Gly Ser Ala Ile Gly
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 tac aat att gcg gct gcc atg agc atg atg gaa atc aga aag tct tac 480
 Tyr Asn Ile Ala Ala Met Ser Met Met Glu Ile Arg Lys Ser Tyr
 145 150 155 160
 tgt gtc cat tcc tct cat ggc gaa gac ccg tgt cac gtt tgc ggc aac 528
 Cys Val His Ser Ser His Gly Glu Asp Pro Cys His Val Ser Gly Asn
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 gct tac atg ata gct ttt ggt gtg gca caa ctt ttc ttt tct caa att 576
 Ala Tyr Met Ile Ala Phe Gly Val Ala Gln Leu Phe Phe Ser Gln Ile
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PF59082SeqList_PF59082.txt

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Thr	Val	Thr	Pro	Ala	Gln	Lys	Val	Trp	Gly	Val	Phe	Gln	Ala	Leu	Gly	
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Asn	Ile	Ala	Phe	Ala	Tyr	Ser	Tyr	Ser	Phe	Ile	Leu	Leu	Glu	Ile	Gln	
				260				265					270			
gac	acc	atc	aaa	tct	cca	cca	tcg	gaa	gga	aaa	gca	atg	aag	aag	gct	864
Asp	Thr	Ile	Lys	Ser	Pro	Pro	Ser	Glu	Gly	Lys	Ala	Met	Lys	Lys	Ala	
				275			280					285				
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gct	gct	att	gta	ggt	cac	ctt	ttc	gga	gca	tac	caa	gtg	tat	gcc	caa	1056
Ala	Ala	Ile	Val	Val	His	Leu	Phe	Gly	Ala	Tyr	Gln	Val	Tyr	Ala	Gln	
				340				345					350			
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Pro	Leu	Phe	Ala	Phe	Val	Glu	Lys	Glu	Ala	Gly	Lys	Lys	Trp	Pro	Lys	
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Ile	Asp	Lys	Gly	Phe	Glu	Val	Lys	Ile	Pro	Gly	Leu	Pro	Val	Tyr	Asn	
370					375					380						
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Gln	Asn	Ile	Phe	Met	Leu	Val	Trp	Arg	Thr	Ile	Phe	Val	Ile	Val	Pro	
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Thr	Leu	Ile	Ala	Met	Leu	Ile	Pro	Phe	Phe	Asn	Asp	Val	Leu	Gly	Val	
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att	gga	gca	ttg	gga	ttt	tgg	cct	tta	act	gtt	tac	ttt	cct	gtg	gag	1296
Ile	Gly	Ala	Leu	Gly	Phe	Trp	Pro	Leu	Thr	Val	Tyr	Phe	Pro	Val	Glu	
				420			425						430			
atg	tat	att	att	cag	aag	aag	atc	cca	aaa	tgg	agt	agg	aaa	tgg	att	1344
Met	Tyr	Ile	Ile	Gln	Lys	Lys	Ile	Pro	Lys	Trp	Ser	Arg	Lys	Trp	Ile	
				435			440					445				
tgt	ctg	gaa	ata	atg	agt	act	ttc	tgc	ctc	ttc	gtt	tct	gtt	gtg	gct	1392
Cys	Leu	Glu	Ile	Met	Ser	Thr	Phe	Cys	Leu	Phe	Val	Ser	Val	Val	Ala	
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Gly	Leu	Gly	Ser	Leu	Ile	Gly	Val	Trp	Ile	Asp	Leu	Lys	Lys	Tyr	Lys	
465					470					475					480	
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<211> 486

<212> PRT

<213> Vicia faba var

<400> 627

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			20					25					30		
Lys	Phe	Tyr	Asp	Asp	Asp	Gly	Arg	Val	Lys	Arg	Thr	Gly	Thr	Val	Trp
		35					40					45			
Thr	Thr	Cys	Ser	His	Ile	Ile	Thr	Gly	Val	Ile	Gly	Ser	Gly	Val	Leu

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Ala Asp Cys Tyr Arg Ser Gly Asp Thr Glu Phe Gly Lys Arg Asn Tyr
100 105 110
Thr Phe Met Asp Ala Val His Asn Ile Leu Gly Gly Pro Ser Val Lys
115 120 125
Ile Cys Gly Val Val Gln Tyr Leu Asn Leu Phe Gly Ser Ala Ile Gly
130 135 140
Tyr Asn Ile Ala Ala Ala Met Ser Met Met Glu Ile Arg Lys Ser Tyr
145 150 155 160
Cys Val His Ser Ser His Gly Glu Asp Pro Cys His Val Ser Gly Asn
165 170 175
Ala Tyr Met Ile Ala Phe Gly Val Ala Gln Leu Phe Phe Ser Gln Ile
180 185 190
Pro Asp Phe His Asn Thr Trp Trp Leu Ser Ile Val Ala Ala Val Met
195 200 205
Ser Phe Phe Tyr Ser Thr Ile Ala Leu Ala Leu Gly Ile Ser Lys Val
210 215 220
Ala Glu Thr Gly Thr Val Met Gly Ser Leu Thr Gly Ile Ser Ile Gly
225 230 235 240
Thr Val Thr Pro Ala Gln Lys Val Trp Gly Val Phe Gln Ala Leu Gly
245 250 255
Asn Ile Ala Phe Ala Tyr Ser Tyr Ser Phe Ile Leu Leu Glu Ile Gln
260 265 270
Asp Thr Ile Lys Ser Pro Pro Ser Glu Gly Lys Ala Met Lys Lys Ala
275 280 285
Ala Lys Leu Ser Ile Gly Val Thr Thr Thr Phe Tyr Leu Leu Cys Gly
290 295 300
Cys Thr Gly Tyr Ala Ala Phe Gly Asp Ala Ala Pro Gly Asn Leu Leu
305 310 315 320
Ala Gly Phe Gly Val Ser Lys Ala Tyr Ile Leu Val Asp Met Ala Asn
325 330 335
Ala Ala Ile Val Val His Leu Phe Gly Ala Tyr Gln Val Tyr Ala Gln
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Ile Asp Lys Gly Phe Glu Val Lys Ile Pro Gly Leu Pro Val Tyr Asn
370 375 380
Gln Asn Ile Phe Met Leu Val Trp Arg Thr Ile Phe Val Ile Val Pro
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Thr Leu Ile Ala Met Leu Ile Pro Phe Phe Asn Asp Val Leu Gly Val
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Ile Gly Ala Leu Gly Phe Trp Pro Leu Thr Val Tyr Phe Pro Val Glu
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Met Tyr Ile Ile Gln Lys Lys Ile Pro Lys Trp Ser Arg Lys Trp Ile
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Cys Leu Glu Ile Met Ser Thr Phe Cys Leu Phe Val Ser Val Val Ala
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Thr	Ser	Ser	Leu	Leu	Ser	Glu	Cys	Tyr	Arg	Thr	Gly	Asp	Pro	His	Phe	
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Gly	Thr	Ala	Val	Gly	Tyr	Thr	Ile	Gly	Ala	Ser	Ile	Ser	Met	Met	Ala	
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Phe	Phe	Ser	Gln	Ile	Pro	Asp	Phe	His	Glu	Met	Trp	Trp	Leu	Ser	Ile	
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Val	Ala	Ala	Ile	Met	Ser	Phe	Thr	Tyr	Ser	Leu	Ile	Gly	Leu	Gly	Leu	
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Gln	Val	Tyr	Ala	Gln	Pro	Leu	Phe	Ala	Phe	Val	Glu	Lys	Ile	Met	Ile	
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Tyr	Phe	Pro	Val	Glu	Met	Tyr	Ile	Lys	Gln	Lys	Lys	Ile	Thr	Lys	Trp	
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Pro	Gly	Asn	Leu	Leu	Thr	Gly	Phe	Gly	Phe	Tyr	Asn	Pro	Tyr	Trp	Leu	
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 385 390 395 400
 Asp Val Leu Gly Leu Ile Gly Ala Ala Gly Phe Trp Pro Leu Thr Val
 405 410 415
 Tyr Phe Pro Val Glu Met Tyr Ile Lys Gln Lys Lys Ile Thr Lys Trp
 420 425 430
 Ser Tyr Lys Trp Ile Ser Met Gln Thr Leu Ser Val Ile Cys Phe Val
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 Ile Glu Glu Arg His Asn Val Arg His Tyr Leu Gln Val Glu Val Arg 20
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 ccc aat aat acc caa acg gag acc gaa gcg atg aat atc cag tct aac 144
 Pro Asn Asn Thr Gln Thr Glu Thr Glu Ala Met Asn Ile Gln Ser Asn 35
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 Tyr Ser Lys Cys Phe Asp Asp Asp Gly Arg Leu Lys Arg Thr Gly Thr 50
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 ttt tgg atg gca act gct cat atc atc act gct gtg ata ggc tca gga 240
 Phe Trp Met Ala Thr Ala His Ile Ile Thr Ala Val Ile Gly Ser Gly 65
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 gtc ctt tca cta gca tgg gcg gtt gct cag ctt ggt tgg gtt gct gga 288
 Val Leu Ser Leu Ala Trp Ala Val Ala Gln Leu Gly Trp Val Ala Gly 85
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 cct att gtc atg ttt ctc ttt gcc gtc gtc aat ctc tac act tcc aac 336
 Pro Ile Val Met Phe Leu Phe Ala Val Val Asn Leu Tyr Thr Ser Asn 100
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 Leu Leu Thr Gln Cys Tyr Arg Thr Gly Asp Ser Val Ser Gly His Arg 115
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 aat tac acc tac atg gag gca gtc aac tcc atc ttg gga gga aaa aag 432
 Asn Tyr Thr Tyr Met Glu Ala Val Asn Ser Ile Leu Gly Gly Lys Lys 130
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 gtc aag tta tgt ggc ctc acc caa tat atc aat ctg ttt gga gtt gca 480
 Val Lys Leu Cys Gly Leu Thr Gln Tyr Ile Asn Leu Phe Gly Val Ala 145
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 Ile Gly Tyr Thr Ile Ala Ala Ser Val Ser Met Met Ala Ile Lys Arg 165
 170
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 Ser Asn Cys Tyr His Ser Ser His Gly Lys Asp Pro Cys His Met Ser 180
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 Ser Asn Gly Tyr Met Ile Thr Phe Gly Ile Ala Glu Val Ile Phe Ser 195
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PF59082SeqList_PF59082.txt

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tac	tgg	ctt	ctg	gac	att	gcc	aac	ctt	gca	att	gtt	atc	cac	cta	gtt	1104
Tyr	Trp	Leu	Leu	Asp	Ile	Ala	Asn	Leu	Ala	Ile	Val	Ile	His	Leu	Val	
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Phe	Trp	Pro	Leu	Thr	Val	Tyr	Phe	Pro	Ile	Asp	Met	Tyr	Ile	Ser	Gln	
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Lys	Lys	Ile	Gly	Arg	Trp	Thr	Ser	Arg	Trp	Leu	Gly	Leu	Gln	Leu	Leu	
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agt	gcc	agt	tgc	ctc	atc	att	tca	ttg	tta	gct	gca	gtt	ggt	tcc	atg	1488
Ser	Ala	Ser	Cys	Leu	Ile	Ile	Ser	Leu	Leu	Ala	Ala	Val	Gly	Ser	Met	
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Ala	Gly	Val	Val	Leu	Asp	Leu	Lys	Thr	Tyr	Lys	Pro	Phe	Lys	Thr	Ser	
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Tyr																

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Asp Ile Pro Ile Pro Cys Phe Gly Val Tyr Gln Leu Asn Phe Phe Arg
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Trp Thr Ala Ser Ala His Ile Ile Thr Ala Val Ile Gly Ser Gly Val	
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Leu Ser Leu Ala Trp Ala Val Ala Gln Ile Gly Trp Ile Gly Gly Pro	
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Leu Cys Ser Cys Tyr Arg Ser Gly Asp Ser Val Thr Gly Lys Arg Asn	
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Tyr Thr Tyr Met Asp Ala Ile His Ser Asn Leu Gly Gly Ile Lys Val	
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Lys Val Cys Gly Val Val Gln Tyr Val Asn Leu Phe Gly Thr Ala Ile	
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Gly Tyr Thr Ile Ala Ser Ala Ile Ser Leu Val Thr Ser Cys Gln Gln	
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Arg Lys Ala Thr Phe Val Ser Val Ala Val Thr Thr Val Phe Tyr Met	
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Trp	Gly	Thr	Lys	Trp	Val	Cys	Leu	Gln	Val	Leu	Ser	Val	Thr	Cys	Leu	
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 Tyr 305 Cys 310 Gln 315 Pro 320 Leu 325 Phe 330 Ala 335 Phe 340 Val 345 Thr 350 Lys 355 Glu 360 Ile 365 Lys 370 Ile 375 Gln 380 Leu 385 Phe 390 Arg 395 Thr 400
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 Pro 305 Gly 310 Lys 315 Pro 320 Phe 325 Asn 330 Leu 335 Asn 340 Leu 345 Phe 350 Arg 355 Leu 360 Val 365 Trp 370 Arg 375 Thr 380
 Phe 385 Phe 390 Val 395 Met 400 Thr 405 Thr 410 Thr 415 Thr 420 Thr 425 Thr 430 Thr 435 Thr 440 Thr 445 Thr 450 Thr 455 Thr 460 Thr 465 Thr 470
 Asn 305 Asp 310 Val 315 Val 320 Gly 325 Leu 330 Leu 335 Gly 340 Ala 345 Ile 350 Gly 355 Phe 360 Trp 365 Pro 370 Leu 375 Thr 380
 Val 305 Tyr 310 Phe 315 Pro 320 Val 325 Glu 330 Met 335 Tyr 340 Ile 345 Ala 350 Gln 355 Lys 360 Asn 365 Val 370 Thr 375 Cys 380 Leu 385
 Trp 305 Gly 310 Thr 315 Lys 320 Trp 325 Val 330 Cys 335 Leu 340 Gln 345 Val 350 Leu 355 Ser 360 Val 365 Thr 370 Cys 375 Leu 380
 Phe 385 Val 390 Ser 395 Val 400 Ala 405 Ala 410 Ala 415 Ala 420 Gly 425 Ser 430 Val 435 Ile 440 Gly 445 Ile 450 Val 455 Ser 460
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 Ile 10 Glu 15 Glu 20 Arg 25 Lys 30 Asp 35 Gly 40 Arg 45 His 50 Tyr 55 Ile 60 Glu 65 Leu 70 Pro 75 Val 80
 cct aaa atg gaa act gag act aaa cca atc acc att cag tct aag tgc 144
 Pro 10 Lys 15 Met 20 Glu 25 Thr 30 Glu 35 Thr 40 Lys 45 Pro 50 Ile 55 Thr 60 Ile 65 Gln 70 Ser 75 Lys 80 Cys 85
 ctc gat gac gat ggt cgc gtc aag aga aca gga aca ttt tgg aca gct 192
 Leu 10 Asp 15 Asp 20 Asp 25 Gly 30 Arg 35 Val 40 Lys 45 Arg 50 Thr 55 Gly 60 Thr 65 Phe 70 Trp 75 Thr 80 Ala 85
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 Cys 10 Tyr 15 Arg 20 Ser 25 Asp 30 Asp 35 Ser 40 Val 45 Ala 50 Gly 55 Pro 60 Arg 65 Asn 70 Tyr 75 Thr 80 Tyr 85
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 Thr 10 Asp 15 Ala 20 Val 25 Lys 30 Ser 35 Ile 40 Leu 45 Gly 50 Gly 55 Lys 60 Lys 65 Phe 70 Lys 75 Ile 80 Cys 85
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Thr	Pro	Ala	Gly	Thr	Val	Thr	Gly	Thr	Gln	Lys	Val	Trp	Arg	Ser	Leu	
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caa	gct	tta	gga	gca	atg	gct	ttt	gca	tac	tcc	ttt	tca	att	atc	ctc	864
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Phe	Asn	Asp	Val	Val	Gly	Leu	Leu	Gly	Ala	Phe	Gly	Phe	Trp	Pro	Leu	
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Thr	Val	Tyr	Phe	Pro	Ile	Asp	Met	Tyr	Ile	Ser	Gln	Lys	Lys	Ile	Gly	
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Leu	Ile	Ile	Ser	Thr	Leu	Ala	Ala	Val	Gly	Ser	Ile	Ala	Gly	Val	Val	
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 85 90 95
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 115 120 125
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 Thr Tyr Ser Ala Val Gly Leu Gly Leu Gly Val Ala Lys Val Ala Glu
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 Thr Pro Ala Gly Thr Val Thr Gly Thr Gln Lys Val Trp Arg Ser Leu
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 Ile Glu Ile Gln Asp Thr Ile Lys Ser Pro Pro Ala Glu His Lys Thr
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 Met Lys Lys Ala Thr Met Leu Ser Ile Met Val Thr Thr Val Phe Tyr
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 Val Phe Ser Gln Pro Phe Phe Ala Phe Val Glu Lys Trp Ser Ala His
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 Pro Cys Ile Gly Val Tyr Lys Leu Asn Leu Phe Arg Leu Ile Trp Arg
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 Arg Trp Thr Asn Arg Trp Leu Gly Leu Gln Met Leu Ser Gly Cys Cys
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<213> Ricinus communis

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aag	cgg	act	gga	act	gtt	tgg	act	gct	agt	gct	cac	ata	att	aca	gct	96
Lys	Arg	Thr	Gly	Thr	Val	Trp	Thr	Ala	Ser	Ala	His	Ile	Ile	Thr	Ala	
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gtg	att	ggg	tct	gga	gtt	ctg	tct	ttg	gct	tgg	gct	gtt	gct	cag	ctt	144
Val	Ile	Gly	Ser	Gly	Val	Leu	Ser	Leu	Ala	Trp	Ala	Val	Ala	Gln	Leu	
		35				40						45				
gga	tgg	gtt	gct	ggc	cct	gct	gtt	atg	ttc	ttg	ttc	tct	tta	gtc	act	192
Gly	Trp	Val	Ala	Gly	Pro	Ala	Val	Met	Phe	Leu	Phe	Ser	Leu	Val	Thr	
	50					55					60					
tac	tat	act	tct	act	ctg	ctc	tcc	gct	tgc	tac	cga	act	ggc	gat	cct	240
Tyr	Tyr	Thr	Ser	Thr	Leu	Leu	Ser	Ala	Cys	Tyr	Arg	Thr	Gly	Asp	Pro	
	65				70					75					80	
gtc	aat	ggc	aag	agg	aac	tat	act	tat	atg	gac	gct	gtt	cgg	tcc	aat	288
Val	Asn	Gly	Lys	Arg	Asn	Tyr	Thr	Tyr	Met	Asp	Ala	Val	Arg	Ser	Asn	
			85					90						95		
ctt	ggt	ggt	gct	aag	ttt	aag	ata	tgt	gga	tat	gtt	caa	tac	gtg	aat	336
Leu	Gly	Gly	Ala	Lys	Phe	Lys	Ile	Cys	Gly	Tyr	Val	Gln	Tyr	Val	Asn	
			100					105					110			
ctt	att	ggc	gtt	gcc	att	ggt	tac	aca	ata	gca	tca	tct	atc	agt	atg	384
Leu	Ile	Gly	Val	Ala	Ile	Gly	Tyr	Thr	Ile	Ala	Ser	Ser	Ile	Ser	Met	
		115				120						125				
atg	gct	gtc	aag	agg	tct	aat	tgt	ttc	cat	aag	agt	gag	gca	aaa	aat	432
Met	Ala	Val	Lys	Arg	Ser	Asn	Cys	Phe	His	Lys	Ser	Glu	Ala	Lys	Asn	
	130					135					140					
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Pro	Cys	His	Met	Lys	Cys	Gln	Ser	Leu	His	Asp	Cys	Ile	Leu	Glu	Val	
	145				150					155					160	
gtt	gaa	tca	tct	tct	tct	cag	att	cct	gac	ttt	gat	caa	act	atg	ggc	528
Val	Glu	Ser	Ser	Ser	Ser	Gln	Ile	Pro	Asp	Phe	Asp	Gln	Thr	Met	Gly	
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ggc	cta	tcc	att	gtt	gct	gca	atc	atg	tcc	ttt	act	tac	tca	aca	att	576
Gly	Leu	Ser	Ile	Val	Ala	Ala	Ile	Met	Ser	Phe	Thr	Tyr	Ser	Thr	Ile	
			180					185					190			
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Gly	Leu	Gly	Leu	Gly	Ile	Ala	Glu	Val	Thr	Lys	Asn	Gly	Lys	Ala	Met	
		195				200						205				
gga	agt	atg	acc	ggt	att	agc	att	gga	act	gtg	act	gaa	aca	caa	aag	672
Gly	Ser	Met	Thr	Gly	Ile	Ser	Ile	Gly	Thr	Val	Thr	Glu	Thr	Gln	Lys	
	210					215					220					
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Ile	Trp	Arg	Ser	Phe	Gln	Ala	Leu	Gly	Asp	Ile	Ala	Phe	Ala	Tyr	Ser	
	225				230					235					240	
tat	tcc	ctt	atc	ctc	att	gaa	att	cag	gac	acg	atc	aga	tct	cca	cca	768
Tyr	Ser	Leu	Ile	Leu	Ile	Glu	Ile	Gln	Asp	Thr	Ile	Arg	Ser	Pro	Pro	
				245				250						255		
gca	gag	tcc	aaa	aca	atg	agg	aaa	gca	act	cta	ata	agt	gta	tca	gta	816
Ala	Glu	Ser	Lys	Thr	Met	Arg	Lys	Ala	Thr	Leu	Ile	Ser	Val	Ser	Val	
			260					265					270			
aca	acc	ctt	ttc	tac	atg	cta	tgt	ggt	tgc	ttt	ggc	tat	gct	gcc	ttt	864
Thr	Thr	Leu	Phe	Tyr	Met	Leu	Cys	Gly	Cys	Phe	Gly	Tyr	Ala	Ala	Phe	
			275					280				285				
gga	gac	atg	tct	ccg	gga	aat	ctc	tta	act	ggt	ttc	ggt	ttt	tac	aac	912
Gly	Asp	Met	Ser	Pro	Gly	Asn	Leu	Leu	Thr	Gly	Phe	Gly	Phe	Tyr	Asn	
	290					295					300					
cca	tat	tgg	cta	cta	gac	att	gct	aac	gtt	gca	ata	gta	gtc	cac	ctt	960
Pro	Tyr	Trp	Leu	Leu	Asp	Ile	Ala	Asn	Val	Ala	Ile	Val	Val	His	Leu	
	305				310					315					320	
gtt	ggt	gca	tac	caa	gtc	tac	tgc	caa	ccc	ttg	ttc	gca	ttc	gtc	gaa	1008
Val	Gly	Ala	Tyr	Gln	Val	Tyr	Cys	Gln	Pro	Leu	Phe	Ala	Phe	Val	Glu	
				325				330						335		
aaa	gca	gca	gta	caa	aga	ttc	ccg	gac	agt	gaa	ttc	ata	ctt	aaa	gat	1056
Lys	Ala	Ala	Val	Gln	Arg	Phe	Pro	Asp	Ser	Glu	Phe	Ile	Leu	Lys	Asp	

PF59082SeqList_PF59082.txt

[illegible]

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<212> PRT
<213> Ricinus communis

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Val	Ile	Gly	Ser	Gly	Val	Leu	Ser	Leu	Ala	Trp	Ala	Val	Ala	Gln	Leu
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Gly	Trp	Val	Ala	Gly	Pro	Ala	Val	Met	Phe	Leu	Phe	Ser	Leu	Val	Thr
	50					55					60				
Tyr	Tyr	Thr	Ser	Thr	Leu	Leu	Ser	Ala	Cys	Tyr	Arg	Thr	Gly	Asp	Pro
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Val	Asn	Gly	Lys	Arg	Asn	Tyr	Thr	Tyr	Met	Asp	Ala	Val	Arg	Ser	Asn
				85					90					95	
Leu	Gly	Gly	Ala	Lys	Phe	Lys	Ile	Cys	Gly	Tyr	Val	Gln	Tyr	Val	Asn
			100					105					110		
Leu	Ile	Gly	Val	Ala	Ile	Gly	Tyr	Thr	Ile	Ala	Ser	Ser	Ile	Ser	Met
		115					120					125			
Met	Ala	Val	Lys	Arg	Ser	Asn	Cys	Phe	His	Lys	Ser	Glu	Ala	Lys	Asn
	130					135					140				
Pro	Cys	His	Met	Lys	Cys	Gln	Ser	Leu	His	Asp	Cys	Ile	Leu	Glu	Val
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Val	Glu	Ser	Ser	Ser	Ser	Gln	Ile	Pro	Asp	Phe	Asp	Gln	Thr	Met	Gly
				165					170					175	
Gly	Leu	Ser	Ile	Val	Ala	Ala	Ile	Met	Ser	Phe	Thr	Tyr	Ser	Thr	Ile
			180					185					190		
Gly	Leu	Gly	Leu	Gly	Ile	Ala	Glu	Val	Thr	Lys	Asn	Gly	Lys	Ala	Met
		195					200					205			
Gly	Ser	Met	Thr	Gly	Ile	Ser	Ile	Gly	Thr	Val	Thr	Glu	Thr	Gln	Lys
	210					215					220				
Ile	Trp	Arg	Ser	Phe	Gln	Ala	Leu	Gly	Asp	Ile	Ala	Phe	Ala	Tyr	Ser
225					230					235					240
Tyr	Ser	Leu	Ile	Leu	Ile	Glu	Ile	Gln	Asp	Thr	Ile	Arg	Ser	Pro	Pro
				245					250					255	
Ala	Glu	Ser	Lys	Thr	Met	Arg	Lys	Ala	Thr	Leu	Ile	Ser	Val	Ser	Val
			260					265					270		
Thr	Thr	Leu	Phe	Tyr	Met	Leu	Cys	Gly	Cys	Phe	Gly	Tyr	Ala	Ala	Phe
		275					280					285			
Gly	Asp	Met	Ser	Pro	Gly	Asn	Leu	Leu	Thr	Gly	Phe	Gly	Phe	Tyr	Asn

PF59082SeqList_PF59082.txt

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 Pro Tyr Trp Leu Leu Asp
 305 Val Gly Ala Tyr Gln Val Tyr Cys Gln Pro Leu Phe Ala Phe Val His Leu
 310
 Lys Ala Ala Val Gln Arg Phe Pro Asp Ser Glu Phe Ile Leu Lys Asp
 325
 Ile Lys Ile Pro Ile Pro Gly Cys Lys Pro Tyr Asn Leu Asn Leu Phe
 340
 Arg Met Val Trp Arg Thr Val Phe Val Ile Phe Thr Thr Val Ile Ser
 355
 Met Leu Leu Pro Phe Phe Asn Asp Ile Val Gly Leu Leu Gly Ala Leu
 370
 Gly Phe Trp Pro Leu Thr Val Tyr Phe Pro Val Glu Met Tyr Ile Ala
 385
 Gln Lys Lys Ile Pro Lys Trp Ser Thr Arg Trp Leu Cys Leu Gln Ile
 405
 Leu Ser Ala Ala Cys Leu Ile Ile Thr Ile Ala Ala Ala Ala Gly Ser
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 Thr Tyr
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 <211> 1464
 <212> DNA
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<220>
 <221> CDS
 <222> (1)..(1464)

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 Gln Val Phe Asp Ala Ser Val Pro Gln Gln Pro Ala Phe Lys Cys Phe
 20 25 30
 gac gat gat ggc cgt ctc aaa aga aca ggg act gtt tgg acc gca agc 144
 Asp Asp Asp Gly Arg Leu Lys Arg Thr Gly Thr Val Trp Thr Ala Ser
 35 40 45
 gct cat atc ata aca gca gtg atc gga tca ggc gtt ctc tca ttg gca 192
 Ala His Ile Ile Thr Ala Val Ile Gly Ser Gly Val Leu Ser Leu Ala
 50 55 60
 tgg gcc att gca cag ctc gga tgg atc gct gga cct gcg gtg atg cta 240
 Trp Ala Ile Ala Gln Leu Gly Trp Ile Ala Gly Pro Ala Val Met Leu
 65 70 75 80
 ttg ttc tct tta gtt act cta tac tct tca aca ctt ctc agc gac tgc 288
 Leu Phe Ser Leu Val Thr Leu Tyr Ser Ser Thr Leu Leu Ser Asp Cys
 85 90 95
 tac aga acc gga gac gca gtc tcc ggc aag aga aac tac act tac atg 336
 Tyr Arg Thr Gly Asp Ala Val Ser Gly Lys Arg Asn Tyr Thr Tyr Met
 100 105 110
 gac gca gtc cga tcc att ctc ggt gga ttc aag ttc aag aaa tgt ggg 384
 Asp Ala Val Arg Ser Ile Leu Gly Gly Phe Lys Phe Lys Lys Cys Gly
 115 120 125
 ctg att caa tac ttg aat ctc ttt ggt att gcc gtc ggt tac aca atc 432
 Leu Ile Gln Tyr Leu Asn Leu Phe Gly Ile Ala Val Gly Tyr Thr Ile
 130 135 140
 gca gca tcc ata agc atg atg gcg atc aag aga tcg aac tgt ttc cac 480
 Ala Ala Ser Ile Ser Met Met Ala Ile Lys Arg Ser Asn Cys Phe His
 145 150 155 160
 aag agc gga gga aaa gac ccg tgt cac atg tcg agc aac cct tac atg 528
 Lys Ser Gly Gly Lys Asp Pro Cys His Met Ser Ser Asn Pro Tyr Met
 165 170 175
 atc atc ttc ggt gtg aca gag atc ttg ctc tcc cag gtt cct gat ttc 576
 Ile Ile Phe Gly Val Thr Glu Ile Leu Leu Ser Gln Val Pro Asp Phe

PF59082SeqList_PF59082.txt

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185																672
tac Tyr	tct Ser 210	gcc Ala	att Ile	ggg Gly	cta Leu	tct Ser 215	ctc Leu	ggc Gly	att Ile	ggt Val	caa Gln 220	ggt Val	gct Ala	gca Ala	aat Asn	672
190																720
gga Gly 225	gta Val	ttc Phe	aaa Lys	gga Gly	agt Ser 230	cta Leu	aca Thr	ggg Gly	ata Ile	agc Ser 235	ata Ile	gga Gly	gca Ala	gtg Val	act Thr 240	720
768																
caa Gln	aca Thr	cag Gln	aag Lys 245	ata Ile	tgg Trp	aga Arg	aca Thr	ttt Phe 250	caa Gln	gct Ala	ctt Leu	gga Gly	gac Asp	att Ile 255	gcc Ala	768
816																
ttt Phe	gct Ala	tac Tyr	tct Ser 260	tct Tyr	tct Ser	gtt Val	gtc Val	cta Leu 265	att Ile	gag Glu	att Ile	cag Gln 270	gat Asp	act Thr	gta Val	816
864																
aga Arg	tca Ser	ccg Pro 275	cca Pro	tca Ser	gaa Glu	tca Ser	aaa Lys 280	acg Thr	atg Met	aag Lys	aaa Lys	gct Ala 285	aca Thr	aaa Lys	ctc Leu	864
912																
agc Ser	att Ile 290	gca Ala	atc Ile	aca Thr	acc Thr	atc Ile 295	ttc Phe	tac Tyr	atg Met	cta Leu	tgc Cys 300	ggc Gly	tca Ser	atg Met	gga Gly	912
960																
tac Tyr 305	gca Ala	gcc Ala	ttt Phe	gga Gly	gat Asp 310	gca Ala	gca Ala	cca Pro	gga Gly	aac Asn 315	ctc Leu	ctc Leu	acc Thr	ggg Gly	ttc Phe 320	960
1008																
gga Gly	ttc Phe	tac Tyr	aac Asn 325	ccg Pro	ttt Phe	tgg Trp	ctc Leu	ctc Leu	gac Asp 330	ata Ile	gcc Ala	aac Asn	gca Ala	gcc Ala 335	atc Ile	1008
1056																
gta Val	gtc Val	cac His	ctc Leu 340	atc Ile	gga Gly	gct Ala	tac Tyr	caa Gln 345	gtc Val	ttc Phe	tcc Ser	cag Gln 350	ccc Pro	atc Ile	ttc Phe	1056
1104																
gcc Ala	ttc Phe	gct Ala 355	gaa Glu	aaa Lys	tca Ser	gcc Ala	tcg Ser 360	gag Glu	agg Arg	ttt Phe	cca Pro	gac Asp 365	aat Asn	gac Asp	ttg Leu	1104
1152																
ctc Leu	acc Thr 370	aag Lys	gaa Glu	ctc Leu	caa Gln	atc Ile 375	aaa Lys	atc Ile	cca Pro	ggg Gly	tta Leu 380	agg Arg	tct Ser	cca Pro	tac Tyr	1152
1200																
aaa Lys 385	aca Thr	aac Asn	gtt Val	ttc Phe	agg Arg 390	gta Val	gtg Val	ttc Phe	agg Arg	tgc Cys 395	tct Ser	ttc Phe	gtc Val	gtt Val	cta Leu 400	1200
1248																
acc Thr	acc Thr	gtg Val	ata Ile	tca Ser 405	atg Met	cta Leu	atg Met	ccg Pro	ttc Phe 410	ttc Phe	aac Asn	gac Asp	gtg Val	gtt Val 415	ggg Gly	1248
1296																
atc Ile	tta Leu	gga Gly	gcc Ala 420	tta Leu	ggg Gly	ttc Phe	tgg Trp	ccc Pro 425	ttg Leu	acg Thr	gtt Val	tat Tyr 430	ttc Phe	ccg Pro	gtg Val	1296
1344																
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1392																
gtt Val	tgt Cys 450	tta Leu	cag Gln	atg Met	ctt Leu	agt Ser 455	gtt Val	gct Ala	tgt Cys	cta Leu	gtg Val 460	atc Ile	tcg Ser	gtg Val	gtc Val	1392
1440																
gcc Ala 465	gga Gly	gtt Val	gga Gly	tca Ser	atc Ile 470	gcc Ala	gga Gly	gta Val	atg Met	ctt Leu 475	gat Asp	ctt Leu	aag Lys	gtc Val	tac Tyr 480	1440
1464																
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<210> 639

<211> 487

<212> PRT

<213> Brassica napus

<400> 639

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Gln Val Phe Asp Ala Ser Val Pro Gln Gln Pro Ala Phe Lys Cys Phe
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PF59082SeqList_PF59082.txt

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 Ala His Ile Ile Thr Ala Val Ile Gly Ser Gly Val Leu Ser Leu Ala
 50 55 60
 Trp Ala Ile Ala Gln Leu Gly Trp Ile Ala Gly Pro Ala Val Met Leu
 65 70 75 80
 Leu Phe Ser Leu Val Thr Leu Tyr Ser Ser Thr Leu Leu Ser Asp Cys
 85 90 95
 Tyr Arg Thr Gly Asp Ala Val Ser Gly Lys Arg Asn Tyr Thr Tyr Met
 100 105 110
 Asp Ala Val Arg Ser Ile Leu Gly Gly Phe Lys Phe Lys Lys Cys Gly
 115 120 125
 Leu Ile Gln Tyr Leu Asn Leu Phe Gly Ile Ala Val Gly Tyr Thr Ile
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 Ala Ala Ser Ile Ser Met Met Ala Ile Lys Arg Ser Asn Cys Phe His
 145 150 155 160
 Lys Ser Gly Gly Lys Asp Pro Cys His Met Ser Ser Asn Pro Tyr Met
 165 170 175
 Ile Ile Phe Gly Val Thr Glu Ile Leu Leu Ser Gln Val Pro Asp Phe
 180 185 190
 Asp Gln Ile Trp Trp Ile Ser Ile Val Ala Ala Val Met Ser Phe Thr
 195 200 205
 Tyr Ser Ala Ile Gly Leu Ser Leu Gly Ile Val Gln Val Ala Ala Asn
 210 215 220
 Gly Val Phe Lys Gly Ser Leu Thr Gly Ile Ser Ile Gly Ala Val Thr
 225 230 235 240
 Gln Thr Gln Lys Ile Trp Arg Thr Phe Gln Ala Leu Gly Asp Ile Ala
 245 250 255
 Phe Ala Tyr Ser Tyr Ser Val Val Leu Ile Glu Ile Gln Asp Thr Val
 260 265 270
 Arg Ser Pro Pro Ser Glu Ser Lys Thr Met Lys Lys Ala Thr Lys Leu
 275 280 285
 Ser Ile Ala Ile Thr Thr Ile Phe Tyr Met Leu Cys Gly Ser Met Gly
 290 295 300
 Tyr Ala Ala Phe Gly Asp Ala Ala Pro Gly Asn Leu Leu Thr Gly Phe
 305 310 315 320
 Gly Phe Tyr Asn Pro Phe Trp Leu Leu Asp Ile Ala Asn Ala Ala Ile
 325 330 335
 Val Val His Leu Ile Gly Ala Tyr Gln Val Phe Ser Gln Pro Ile Phe
 340 345 350
 Ala Phe Ala Glu Lys Ser Ala Ser Glu Arg Phe Pro Asp Asn Asp Leu
 355 360 365
 Leu Thr Lys Glu Leu Gln Ile Lys Ile Pro Gly Leu Arg Ser Pro Tyr
 370 375 380
 Lys Thr Asn Val Phe Arg Val Val Phe Arg Cys Ser Phe Val Val Leu
 385 390 395 400
 Thr Thr Val Ile Ser Met Leu Met Pro Phe Phe Asn Asp Val Val Gly
 405 410 415
 Ile Leu Gly Ala Leu Gly Phe Trp Pro Leu Thr Val Tyr Phe Pro Val
 420 425 430
 Glu Met Tyr Ile Lys Gln Arg Lys Val Glu Lys Trp Ser Thr Arg Trp
 435 440 445
 Val Cys Leu Gln Met Leu Ser Val Ala Cys Leu Val Ile Ser Val Val
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<211> 1458

<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (1)..(1458)

<400> 640

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ggc Gly	gac Asp	gtc Val	tac Tyr 20	gcc Ala	atg Met	tcc Ser	gat Asp	cca Pro 25	aca Thr	aag Lys	aac Asn	gtt Val 30	gat Asp	gac Asp	gat Asp	96
ggc Gly	cga Arg	gag Glu 35	aag Lys	agg Arg	acg Thr	ggg Gly	acg Thr 40	tgg Trp	ctt Leu	acg Thr	gcg Ala	agt Ser 45	gcg Ala	cat His	att Ile	144
atc Ile 50	acg Thr	gcg Ala	gta Val	ata Ile	ggc Gly	tca Ser 55	gga Gly	gtg Val	ttg Leu	tcg Ser	ttg Leu 60	gca Ala	tgg Trp	gcc Ala	ata Ile	192
gct Ala 65	cag Gln	ctt Leu	ggg Gly	tgg Trp	ata Ile 70	gca Ala	ggg Gly	act Thr	ttg Leu	att Ile 75	ctg Leu	atc Ile	att Ile	ttc Phe	tcg Ser 80	240
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ccg Pro	gat Asp	ccc Pro	ctc Leu 100	acc Thr	gga Gly	aaa Lys	cga Arg	aac Asn 105	tac Tyr	act Thr	tac Tyr	atg Met	gac Asp 110	gtt Val	gtt Val	336
cga Arg	tct Ser	tac Tyr 115	ctc Leu	ggg Gly	ggg Gly	agg Arg	aaa Lys 120	gtg Val	cag Gln	ctt Leu	tgt Cys	gga Gly 125	gtg Val	gca Ala	cag Gln	384
tat Tyr	ggg Gly 130	aat Asn	ctg Leu	ata Ile	gga Gly	atc Ile 135	act Thr	gtt Val	ggg Gly	tac Tyr	acc Thr 140	atc Ile	act Thr	gct Ala	tct Ser	432
att Ile 145	agt Ser	ttg Leu	gta Val	gcg Ala	atc Ile 150	ggg Gly	aaa Lys	gcg Ala	aac Asn	tgt Cys 155	tac Tyr	cac His	aat Asn	aaa Lys	ggg Gly 160	480
cac His	cat His	gca Ala	gat Asp	tgt Cys 165	aca Thr	ata Ile	tcg Ser	aac Asn	tat Tyr 170	cca Pro	tat Tyr	atg Met	gcg Ala	gcc Ala 175	ttc Phe	528
ggg Gly	atc Ile	att Ile	cag Gln 180	atc Ile	ctt Leu	ctt Leu	agc Ser	cag Gln 185	atc Ile	cca Pro	aac Asn	ttt Phe 190	cac His	aag Lys	ctc Leu	576
tct Ser	ttt Phe 195	ctc Leu	tcc Ser	ctt Leu	atg Met	gct Ala	gcg Ala 200	gtt Val	atg Met	tct Ser	ttc Phe	gct Ala 205	tac Tyr	gca Ala	agt Ser	624
att Ile 210	ggg Gly	att Ile	ggc Gly	cta Leu	gcc Ala	atc Ile 215	gcg Ala	acg Thr	gtc Val	gca Ala	ggg Gly 220	ggg Gly	aaa Lys	gtg Val	ggg Gly	672
aag Lys 225	acg Thr	aat Asn	ata Ile	acg Thr	gga Gly 230	acg Thr	gtg Val	gta Val	gaa Glu	gtt Val 235	gat Asp	gta Val	acc Thr	gcg Ala	act Thr 240	720
cag Gln	aag Lys	ata Ile	tgg Trp	aga Arg 245	tcg Ser	ttt Phe	caa Gln	gcg Ala	gtt Val 250	gga Gly	gac Asp	ata Ile	gcg Ala	ttt Phe 255	gca Ala	768
tat Tyr	gct Ala	tac Tyr	gcc Ala 260	acc Thr	gtt Val	ctc Leu	att Ile	gag Glu 265	att Ile	cag Gln	gac Asp	aca Thr	ctg Leu 270	aaa Lys	tct Ser	816
agc Ser	cca Pro	gca Ala 275	gaa Glu	aac Asn	aaa Lys	gct Ala	atg Met 280	aaa Lys	aga Arg	gca Ala	agc Ser	ctt Leu 285	ctg Leu	gga Gly	gta Val	864
tca Ser	acc Thr 290	acc Thr	act Thr	ttc Phe	ttc Phe	tac Tyr 295	ata Ile	tta Leu	tgt Cys	ggg Gly 300	tgt Cys	ctc Leu	ggc Gly	tat Tyr	gct Ala	912
gca Ala 305	ttt Phe	gga Gly	aac Asn	aaa Lys	gcg Ala 310	cct Pro	gga Gly	gat Asp	ttc Phe	ctc Leu 315	aca Thr	gat Asp	ttc Phe	ggg Gly	ttt Phe 320	960
tac Tyr	gag Glu	ccc Pro	ttt Phe	tgg Trp 325	ctc Leu	att Ile	gac Asp	ttt Phe	gca Ala 330	aac Asn	gca Ala	tgc Cys	att Ile	gct Ala 335	ttc Phe	1008
cac His	ctt Leu	atc Ile	ggg Gly 340	gct Ala	tat Tyr	cag Gln	gtg Val 345	ttt Phe 350	gcg Ala	cag Gln	ccc Pro	atc Ile	ttc Phe 355	cag Gln	ttt Phe	1056
gtt Val	gag Glu	aag Lys 355	aaa Lys	tgc Cys	aat Asn	aga Arg	aac Asn 360	tgg Trp	cct Pro	gac Asp	aac Asn	aag Lys 365	ttc Phe	atc Ile	act Thr	1104

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tct	gaa	tat	tca	gta	aac	ata	cct	ttc	ctt	gga	aaa	ttt	aac	atc	agc	1152
Ser	Glu	Tyr	Ser	Val	Asn	Ile	Pro	Phe	Leu	Gly	Lys	Phe	Asn	Ile	Ser	
	370					375					380					
ctc	ttc	aga	ttg	gtg	tgg	agg	aca	gct	tac	gtg	ggt	ata	aca	act	ttg	1200
Leu	Phe	Arg	Leu	Val	Trp	Arg	Thr	Ala	Tyr	Val	Val	Ile	Thr	Thr	Leu	
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gta	gct	atg	ata	ttc	cct	ttc	ttc	aac	gcc	atc	ttg	ggt	ctt	atc	gga	1248
Val	Ala	Met	Ile	Phe	Pro	Phe	Phe	Asn	Ala	Ile	Leu	Gly	Leu	Ile	Gly	
				405					410					415		
gca	gct	tcg	ttc	tgg	cct	tta	acg	gtt	tat	ttc	cct	gtc	gag	atg	cat	1296
Ala	Ala	Ser	Phe	Trp	Pro	Leu	Thr	Val	Tyr	Phe	Pro	Val	Glu	Met	His	
				420				425					430			
att	gca	cag	act	aag	gtt	aag	aag	tac	tct	cct	aga	tgg	att	ggg	ctg	1344
Ile	Ala	Gln	Thr	Lys	Val	Lys	Lys	Tyr	Ser	Pro	Arg	Trp	Ile	Gly	Leu	
		435				440						445				
aaa	atg	atg	tgc	tgg	gtt	tgc	ctg	atc	gta	tca	ctc	tta	gct	gct	gct	1392
Lys	Met	Met	Cys	Trp	Val	Cys	Leu	Ile	Val	Ser	Leu	Leu	Ala	Ala	Ala	
	450					455					460					
gga	tcc	atc	gca	gga	ctg	ata	agt	agt	gtc	aag	aca	tac	aag	cct	ttc	1440
Gly	Ser	Ile	Ala	Gly	Leu	Ile	Ser	Ser	Val	Lys	Thr	Tyr	Lys	Pro	Phe	
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cgg	act	atc	cat	gag	tga											1458
Arg	Thr	Ile	His	Glu												
				485												

<210> 641

<211> 485

<212> PRT

<213> Brassica napus

<400> 641

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			20					25					30			
Gly	Arg	Glu	Lys	Arg	Thr	Gly	Thr	Trp	Leu	Thr	Ala	Ser	Ala	His	Ile	
		35				40						45				
Ile	Thr	Ala	Val	Ile	Gly	Ser	Gly	Val	Leu	Ser	Leu	Ala	Trp	Ala	Ile	
	50				55				60							
Ala	Gln	Leu	Gly	Trp	Ile	Ala	Gly	Thr	Leu	Ile	Leu	Ile	Ile	Phe	Ser	
65				70					75						80	
Phe	Ile	Thr	Tyr	Phe	Thr	Ser	Thr	Met	Leu	Ala	Asp	Cys	Tyr	Arg	Ala	
			85					90					95			
Pro	Asp	Pro	Leu	Thr	Gly	Lys	Arg	Asn	Tyr	Thr	Tyr	Met	Asp	Val	Val	
		100						105					110			
Arg	Ser	Tyr	Leu	Gly	Gly	Arg	Lys	Val	Gln	Leu	Cys	Gly	Val	Ala	Gln	
		115				120						125				
Tyr	Gly	Asn	Leu	Ile	Gly	Ile	Thr	Val	Gly	Tyr	Thr	Ile	Thr	Ala	Ser	
	130				135						140					
Ile	Ser	Leu	Val	Ala	Ile	Gly	Lys	Ala	Asn	Cys	Tyr	His	Asn	Lys	Gly	
145				150					155						160	
His	His	Ala	Asp	Cys	Thr	Ile	Ser	Asn	Tyr	Pro	Tyr	Met	Ala	Ala	Phe	
			165					170					175			
Gly	Ile	Ile	Gln	Ile	Leu	Leu	Ser	Gln	Ile	Pro	Asn	Phe	His	Lys	Leu	
		180						185					190			
Ser	Phe	Leu	Ser	Leu	Met	Ala	Ala	Val	Met	Ser	Phe	Ala	Tyr	Ala	Ser	
		195				200						205				
Ile	Gly	Ile	Gly	Leu	Ala	Ile	Ala	Thr	Val	Ala	Gly	Gly	Lys	Val	Gly	
	210				215						220					
Lys	Thr	Asn	Ile	Thr	Gly	Thr	Val	Val	Glu	Val	Asp	Val	Thr	Ala	Thr	
225				230					235						240	
Gln	Lys	Ile	Trp	Arg	Ser	Phe	Gln	Ala	Val	Gly	Asp	Ile	Ala	Phe	Ala	
			245					250					255			
Tyr	Ala	Tyr	Ala	Thr	Val	Leu	Ile	Glu	Ile	Gln	Asp	Thr	Leu	Lys	Ser	
		260						265					270			
Ser	Pro	Ala	Glu	Asn	Lys	Ala	Met	Lys	Arg	Ala	Ser	Leu	Leu	Gly	Val	
		275				280						285				
Ser	Thr	Thr	Thr	Phe	Phe	Tyr	Ile	Leu	Cys	Gly	Cys	Leu	Gly	Tyr	Ala	
	290					295					300					

PF59082SeqList_PF59082.txt

Ala Phe Gly Asn Lys Ala Pro Gly Asp Phe Leu Thr Asp Phe Gly Phe
 305 310 315 320
 Tyr Glu Pro Phe Trp Leu Ile Asp Phe Ala Asn Ala Cys Ile Ala Phe
 325 330 335
 His Leu Ile Gly Ala Tyr Gln Val Phe Ala Gln Pro Ile Phe Gln Phe
 340 345 350
 Val Glu Lys Lys Cys Asn Arg Asn Trp Pro Asp Asn Lys Phe Ile Thr
 355 360 365
 Ser Glu Tyr Ser Val Asn Ile Pro Phe Leu Gly Lys Phe Asn Ile Ser
 370 375 380
 Leu Phe Arg Leu Val Trp Arg Thr Ala Tyr Val Val Ile Thr Thr Leu
 385 390 395 400
 Val Ala Met Ile Phe Pro Phe Phe Asn Ala Ile Leu Gly Leu Ile Gly
 405 410 415
 Ala Ala Ser Phe Trp Pro Leu Thr Val Tyr Phe Pro Val Glu Met His
 420 425 430
 Ile Ala Gln Thr Lys Val Lys Lys Tyr Ser Pro Arg Trp Ile Gly Leu
 435 440 445
 Lys Met Met Cys Trp Val Cys Leu Ile Val Ser Leu Leu Ala Ala Ala
 450 455 460
 Gly Ser Ile Ala Gly Leu Ile Ser Ser Val Lys Thr Tyr Lys Pro Phe
 465 470 475 480
 Arg Thr Ile His Glu
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<210> 642
 <211> 1386
 <212> DNA
 <213> Glycine max

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 <221> CDS
 <222> (1)..(1386)

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 tat gac gat gac ggg cgt gct aaa agg act gga act tta tgg agt gct 96
 Tyr Asp Asp Gly Arg Ala Lys Arg Thr Gly Thr Leu Trp Ser Ala
 20 25 30
 gtg gct cat atc atc aca gcc att atc ggt gct ggt gtt ctg tct tta 144
 Val Ala His Ile Ile Thr Ala Ile Ile Gly Ala Gly Val Leu Ser Leu
 35 40 45
 gct tgg agt act tcc caa ttg gga ttg att gca gga cca gtt tgc ttg 192
 Ala Trp Ser Thr Ser Gln Leu Gly Trp Ile Ala Gly Pro Val Cys Leu
 50 55 60
 ctt ttt tgt gca att gtc acc tat gtt tct tca ttc ctc ctt tcc gat 240
 Leu Phe Cys Ala Ile Val Thr Tyr Val Ser Ser Phe Leu Leu Ser Asp
 65 70 75 80
 tgt tac aga act ctg gat cct gta act gtg aaa aga aac tac tct tac 288
 Cys Tyr Arg Thr Leu Asp Pro Val Thr Val Lys Arg Asn Tyr Ser Tyr
 85 90 95
 atg gat gct gtt aga gtc tat ctt ggc aat aag agg aca tgg ttg gct 336
 Met Asp Ala Val Arg Val Tyr Leu Gly Asn Lys Arg Thr Trp Leu Ala
 100 105 110
 ggt tcc ctt caa tat ttg agc ttg tat ggg gtt agt act gct tat gta 384
 Gly Ser Leu Gln Tyr Leu Ser Leu Tyr Gly Val Ser Thr Ala Tyr Val
 115 120 125
 att acc aca aca acc tgt ttg aga gca ata ctg aaa tca aat tgt tat 432
 Ile Thr Thr Thr Thr Cys Leu Arg Ala Ile Leu Lys Ser Asn Cys Tyr
 130 135 140
 cac aag gaa ggg cat cag gct cct tgt aaa tat ggg gat gca gta tat 480
 His Lys Glu Gly His Gln Ala Pro Cys Lys Tyr Gly Asp Ala Val Tyr
 145 150 155 160
 atg atg ctg ttt gga cta gtt cag atc ata atg tca ttc ata cca gat 528
 Met Met Leu Phe Gly Leu Val Gln Ile Ile Met Ser Phe Ile Pro Asp
 165 170 175
 ctc cac aac atg gca tgg gtt tca att gtt gcg gcc ata atg tcc ttt 576
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PF59082SeqList_PF59082.txt

Leu	His	Asn	Met	Ala	Trp	Val	Ser	Ile	Val	Ala	Ala	Ile	Met	Ser	Phe	
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Thr	Tyr	Ser	Ser	Ile	Gly	Leu	Gly	Leu	Gly	Ile	Thr	Thr	Val	Ile	Glu	
		195					200					205				
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Asn	Gly	Arg	Ile	Met	Gly	Ser	Leu	Thr	Gly	Val	Pro	Ala	Ser	Asn	Ile	
	210					215					220					
gct	gac	aag	tta	tgg	tta	gtc	ttc	caa	gca	att	ggt	gat	att	gcc	ttt	720
Ala	Asp	Lys	Leu	Trp	Leu	Val	Phe	Gln	Ala	Ile	Gly	Asp	Ile	Ala	Phe	
	225				230					235					240	
gcc	tat	cca	tac	aca	gtc	atc	ctc	ctt	gag	ata	cag	gac	act	cta	gag	768
Ala	Tyr	Pro	Tyr	Thr	Val	Ile	Leu	Leu	Glu	Ile	Gln	Asp	Thr	Leu	Glu	
			245					250						255		
tct	cct	cca	cca	gaa	aac	aag	acc	atg	aaa	aag	gcc	tcc	atg	att	gct	816
Ser	Pro	Pro	Pro	Glu	Asn	Lys	Thr	Met	Lys	Lys	Ala	Ser	Met	Ile	Ala	
			260					265					270			
atc	ctc	att	aca	aca	ttc	ttc	tac	ctc	tgc	tgt	gga	tgc	ttt	gga	tat	864
Ile	Leu	Ile	Thr	Thr	Phe	Phe	Tyr	Leu	Cys	Cys	Gly	Cys	Phe	Gly	Tyr	
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gcg	gct	ttt	gga	aat	caa	aca	cca	gga	aac	ctc	ttg	aca	ggg	ttt	gga	912
Ala	Ala	Phe	Gly	Asn	Gln	Thr	Pro	Gly	Asn	Leu	Leu	Thr	Gly	Phe	Gly	
	290					295					300					
ttt	tac	gag	cct	tac	tgg	ctc	att	gac	ttt	gcc	aat	gct	tgc	att	gtt	960
Phe	Tyr	Glu	Pro	Tyr	Trp	Leu	Ile	Asp	Phe	Ala	Asn	Ala	Cys	Ile	Val	
	305				310				315						320	
ctt	cac	ttg	gta	gga	gga	tat	cag	att	tac	agt	cag	ccg	ata	tat	ggt	1008
Leu	His	Leu	Val	Gly	Gly	Tyr	Gln	Ile	Tyr	Ser	Gln	Pro	Ile	Tyr	Gly	
			325					330						335		
gct	gtt	gac	aga	tgg	tgt	tca	aaa	aga	tac	ccc	aac	agt	gga	ttt	gtg	1056
Ala	Val	Asp	Arg	Trp	Cys	Ser	Lys	Arg	Tyr	Pro	Asn	Ser	Gly	Phe	Val	
			340					345					350			
aat	aat	ttc	tac	caa	ttg	aaa	ctg	cct	cgg	ttg	cca	gct	ttt	cag	cta	1104
Asn	Asn	Phe	Tyr	Gln	Leu	Lys	Leu	Pro	Arg	Leu	Pro	Ala	Phe	Gln	Leu	
		355					360					365				
aac	atg	ttc	agg	ata	tgt	ttt	aga	aca	gct	tat	gtg	ggt	tcc	acg	act	1152
Asn	Met	Phe	Arg	Ile	Cys	Phe	Arg	Thr	Ala	Tyr	Val	Val	Ser	Thr	Thr	
	370				375						380					
gga	ctt	gcg	atc	cta	ttt	cct	tac	ttc	aat	caa	ggt	ata	gga	gtg	tta	1200
Gly	Leu	Ala	Ile	Leu	Phe	Pro	Tyr	Phe	Asn	Gln	Val	Ile	Gly	Val	Leu	
	385				390					395					400	
gga	gcc	tta	ggc	ttt	tgg	cca	ttg	gct	ata	tat	ttc	ccg	gta	gag	atg	1248
Gly	Ala	Leu	Gly	Phe	Trp	Pro	Leu	Ala	Ile	Tyr	Phe	Pro	Val	Glu	Met	
			405					410						415		
tac	ttt	gtg	cag	agg	aaa	gtt	gaa	gct	tgg	tct	aga	aaa	tgg	att	gtc	1296
Tyr	Phe	Val	Gln	Arg	Lys	Val	Glu	Ala	Trp	Ser	Arg	Lys	Trp	Ile	Val	
			420					425					430			
ctc	agg	acc	ttc	agc	ttt	att	tgc	ttt	ctg	gtg	tca	tta	ctg	ggt	ctc	1344
Leu	Arg	Thr	Phe	Ser	Phe	Ile	Cys	Phe	Leu	Val	Ser	Leu	Leu	Gly	Leu	
		435					440					445				
att	gga	tca	ctt	gaa	gga	atc	ata	agc	gag	aaa	cta	agc	taa			1386
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<210> 643

<211> 461

<212> PRT

<213> Glycine max

<400> 643

Met	Ala	Val	Gln	Asn	Ser	Leu	Gln	Ile	Thr	Arg	Ser	Gly	Ser	Gly	Gly	
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Tyr	Asp	Asp	Asp	Gly	Arg	Ala	Lys	Arg	Thr	Gly	Thr	Leu	Trp	Ser	Ala	
			20					25					30			
Val	Ala	His	Ile	Ile	Thr	Ala	Ile	Ile	Gly	Ala	Gly	Val	Leu	Ser	Leu	
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Ala	Trp	Ser	Thr	Ser	Gln	Leu	Gly	Trp	Ile	Ala	Gly	Pro	Val	Cys	Leu	
	50					55					60					
Leu	Phe	Cys	Ala	Ile	Val	Thr	Tyr	Val	Ser	Ser	Phe	Leu	Leu	Ser	Asp	

PF59082SeqList_PF59082.txt

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65          70          75          80
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Met Asp Ala Val Arg Val Tyr Leu Gly Asn Lys Arg Thr Trp Leu Ala
      100
Gly Ser Leu Gln Tyr Leu Ser Leu Tyr Gly Val Ser Thr Ala Tyr Val
      115
Ile Thr Thr Thr Thr Cys Leu Arg Ala Ile Leu Lys Ser Asn Cys Tyr
      130
His Lys Glu Gly His Gln Ala Pro Cys Lys Tyr Gly Asp Ala Val Tyr
      145
Met Met Leu Phe Gly Leu Val Gln Ile Ile Met Ser Phe Ile Pro Asp
      165
Leu His Asn Met Ala Trp Val Ser Ile Val Ala Ala Ile Met Ser Phe
      180
Thr Tyr Ser Ile Gly Leu Gly Leu Gly Ile Thr Thr Val Ile Glu
      195
Asn Gly Arg Ile Met Gly Ser Leu Thr Gly Val Pro Ala Ser Asn Ile
      210
Ala Asp Lys Leu Trp Leu Val Phe Gln Ala Ile Gly Asp Ile Ala Phe
      225
Ala Tyr Pro Tyr Thr Val Ile Leu Leu Glu Ile Gln Asp Thr Leu Glu
      245
Ser Pro Pro Glu Asn Lys Thr Met Lys Lys Ala Ser Met Ile Ala
      260
Ile Leu Ile Thr Thr Phe Phe Tyr Leu Cys Cys Gly Cys Phe Gly Tyr
      275
Ala Ala Phe Gly Asn Gln Thr Pro Gly Asn Leu Leu Thr Gly Phe Gly
      290
Phe Tyr Glu Pro Tyr Trp Leu Ile Asp Phe Ala Asn Ala Cys Ile Val
      305
Leu His Leu Val Gly Gly Tyr Gln Ile Tyr Ser Gln Pro Ile Tyr Gly
      325
Ala Val Asp Arg Trp Cys Ser Lys Arg Tyr Pro Asn Ser Gly Phe Val
      340
Asn Asn Phe Tyr Gln Leu Lys Leu Pro Arg Leu Pro Ala Phe Gln Leu
      355
Asn Met Phe Arg Ile Cys Phe Arg Thr Ala Tyr Val Val Ser Thr Thr
      370
Gly Leu Ala Ile Leu Phe Pro Tyr Phe Asn Gln Val Ile Gly Val Leu
      385
Gly Ala Leu Gly Phe Trp Pro Leu Ala Ile Tyr Phe Pro Val Glu Met
      405
Tyr Phe Val Gln Arg Lys Val Glu Ala Trp Ser Arg Lys Trp Ile Val
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Leu Arg Thr Phe Ser Phe Ile Cys Phe Leu Val Ser Leu Leu Gly Leu
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 <212> DNA
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<220>
 <221> CDS
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gaa gat ggt ggc aaa aac ttc gac gat gga cga gtc aga aga acg      96
Glu Asp Gly Lys Asn Phe Asp Asp Gly Arg Val Arg Arg Thr
20      25      30
ggt aca tgg ata act gcg agt gcc cat atc ata acg gca gtg ata ggg      144
Gly Thr Trp Ile Thr Ala Ser Ala His Ile Ile Thr Ala Val Ile Gly
35      40      45

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PF59082SeqList_PF59082.txt

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Ala	Gly	Pro	Ala	Val	Leu	Phe	Ala	Phe	Ser	Phe	Ile	Thr	Tyr	Phe	Thr	
	65				70					75					80	
tcc	act	ctt	ctt	gcc	gac	tgt	tat	cgt	tca	cct	gat	cct	gtt	cat	ggc	288
Ser	Thr	Leu	Leu	Ala	Asp	Cys	Tyr	Arg	Ser	Pro	Asp	Pro	Val	His	Gly	
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aag	cga	aac	tac	acc	tat	tcc	gat	gtt	gtc	aga	tcc	gtc	tta	gga	ggg	336
Lys	Arg	Asn	Tyr	Thr	Tyr	Ser	Asp	Val	Val	Arg	Ser	Val	Leu	Gly	Gly	
			100					105					110			
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Arg	Lys	Phe	Gln	Leu	Cys	Gly	Leu	Ala	Gln	Tyr	Ile	Asn	Leu	Val	Gly	
		115				120					125					
gta	act	atc	ggg	tac	acg	ata	acg	gct	tca	att	agt	atg	gtg	gcg	gtg	432
Val	Thr	Ile	Gly	Tyr	Thr	Ile	Thr	Ala	Ser	Ile	Ser	Met	Val	Ala	Val	
	130					135					140					
aag	agg	tcg	aat	tgt	ttt	cac	aaa	cat	ggg	cat	cat	ggt	aag	tgc	tat	480
Lys	Arg	Ser	Asn	Cys	Phe	His	Lys	His	Gly	His	His	Val	Lys	Cys	Tyr	
	145				150					155					160	
acg	tca	aac	aac	cct	ttc	atg	atc	ctc	ttt	gcc	tgc	att	caa	atc	gtg	528
Thr	Ser	Asn	Asn	Pro	Phe	Met	Ile	Leu	Phe	Ala	Cys	Ile	Gln	Ile	Val	
				165					170					175		
ctt	agc	cag	ata	cca	aat	ttc	cat	aag	ctc	tgg	tgg	ctc	tcc	att	gtt	576
Leu	Ser	Gln	Ile	Pro	Asn	Phe	His	Lys	Leu	Trp	Trp	Leu	Ser	Ile	Val	
			180					185					190			
gca	gca	gtt	atg	tct	ttt	gct	tat	tct	tcc	att	ggc	ctc	ggg	ctc	tca	624
Ala	Ala	Val	Met	Ser	Phe	Ala	Tyr	Ser	Ser	Ile	Gly	Leu	Gly	Leu	Ser	
		195				200					205					
gta	gct	aaa	gtg	gca	ggg	ggg	gga	gag	cct	gta	cgg	aca	acc	tta	acg	672
Val	Ala	Lys	Val	Ala	Gly	Gly	Gly	Glu	Pro	Val	Arg	Thr	Thr	Leu	Thr	
	210				215					220						
ggg	gtg	caa	gtt	ggg	gta	gac	gtt	aca	gga	tcc	gag	aag	gtc	tgg	agg	720
Gly	Val	Gln	Val	Gly	Val	Asp	Val	Thr	Gly	Ser	Glu	Lys	Val	Trp	Arg	
	225			230					235					240		
acg	ttt	caa	gct	att	ggg	gac	att	gcc	ttc	gct	tac	gct	tat	tct	aac	768
Thr	Phe	Gln	Ala	Ile	Gly	Asp	Ile	Ala	Phe	Ala	Tyr	Ala	Tyr	Ser	Asn	
				245				250						255		
gtg	ctc	atc	gag	ata	cag	gat	acc	ctg	aaa	tcg	agc	cct	cca	gaa	aac	816
Val	Leu	Ile	Glu	Ile	Gln	Asp	Thr	Leu	Lys	Ser	Ser	Pro	Pro	Glu	Asn	
			260					265				270				
aag	gtc	atg	aaa	aga	gca	agt	ttg	att	ggc	atc	ttg	act	aca	acc	ttg	864
Lys	Val	Met	Lys	Arg	Ala	Ser	Leu	Ile	Gly	Ile	Leu	Thr	Thr	Thr	Leu	
		275					280					285				
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Phe	Tyr	Val	Leu	Cys	Gly	Cys	Leu	Gly	Tyr	Ala	Ala	Phe	Gly	Asn	Asp	
	290				295					300						
gca	cca	gga	aat	ttc	ctc	aca	ggg	ttc	ggc	ttc	tac	gag	ccc	ttt	tgg	960
Ala	Pro	Gly	Asn	Phe	Leu	Thr	Gly	Phe	Gly	Phe	Tyr	Glu	Pro	Phe	Trp	
	305				310			315							320	
ctc	ata	gac	ttt	gct	aac	atc	tgc	ata	gcc	gtg	cac	ttg	gtt	gga	gca	1008
Leu	Ile	Asp	Phe	Ala	Asn	Ile	Cys	Ile	Ala	Val	His	Leu	Val	Gly	Ala	
				325				330						335		
tat	cag	gtc	ttc	tgt	cag	ccc	ata	ttt	ggg	ttc	gta	gag	aac	tgg	ggt	1056
Tyr	Gln	Val	Phe	Cys	Gln	Pro	Ile	Phe	Gly	Phe	Val	Glu	Asn	Trp	Gly	
			340					345				350				
aag	gaa	agg	tgg	cca	aat	agc	caa	ttt	gta	aat	gga	gaa	cac	gct	ttg	1104
Lys	Glu	Arg	Trp	Pro	Asn	Ser	Gln	Phe	Val	Asn	Gly	Glu	His	Ala	Leu	
		355					360					365				
aac	ttt	cca	cta	tgt	gga	acc	ttc	cct	gtg	aac	ttc	ttc	agg	gtg	gtg	1152
Asn	Phe	Pro	Leu	Cys	Gly	Thr	Phe	Pro	Val	Asn	Phe	Phe	Arg	Val	Val	
	370				375					380						
tgg	aga	aca	aca	tat	gtc	atc	atc	act	gct	ttg	gct	atg	atg	ttt		1200
Trp	Arg	Thr	Thr	Tyr	Val	Ile	Ile	Thr	Ala	Leu	Ile	Ala	Met	Met	Phe	
	385				390					395					400	
cca	ttc	ttc	aat	gac	ttc	cta	ggc	ctg	att	ggg	tca	ctg	tcc	ttt	tgg	1248
Pro	Phe	Phe	Asn	Asp	Phe	Leu	Gly	Leu	Ile	Gly	Ser	Leu	Ser	Phe	Trp	
				405					410					415		

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cca	tta	acc	gtt	tac	ttc	ccc	ata	gaa	atg	tac	att	aag	cag	tca	aag	1296
Pro	Leu	Thr	Val	Tyr	Phe	Pro	Ile	Glu	Met	Tyr	Ile	Lys	Gln	Ser	Lys	
			420					425					430			
atg	caa	agg	ttt	tcc	ttc	acg	tgg	aca	tgg	ctc	aag	ata	ctg	agc	tgg	1344
Met	Gln	Arg	Phe	Ser	Phe	Thr	Trp	Thr	Trp	Leu	Lys	Ile	Leu	Ser	Trp	
		435					440					445				
gct	tgc	ttg	atc	gtt	tct	att	atc	tca	gct	gct	ggg	tcc	atc	caa	ggc	1392
Ala	Cys	Leu	Ile	Val	Ser	Ile	Ile	Ser	Ala	Ala	Gly	Ser	Ile	Gln	Gly	
	450					455					460					
ctc	gct	caa	gat	ctc	aag	aaa	tat	cag	ccc	ttc	aaa	gcc	cag	caa		1437
Leu	Ala	Gln	Asp	Leu	Lys	Lys	Tyr	Gln	Pro	Phe	Lys	Ala	Gln	Gln		
465					470					475						
taa																1440

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 <211> 479
 <212> PRT
 <213> Glycine max

<400> 645

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Glu	Asp	Gly	Gly	Lys	Asn	Phe	Asp	Asp	Gly	Arg	Val	Arg	Arg	Thr		
			20					25				30				
Gly	Thr	Trp	Ile	Thr	Ala	Ser	Ala	His	Ile	Ile	Thr	Ala	Val	Ile	Gly	
		35					40					45				
Ser	Gly	Val	Leu	Ser	Leu	Ala	Trp	Ala	Ile	Ala	Gln	Met	Gly	Trp	Val	
	50					55					60					
Ala	Gly	Pro	Ala	Val	Leu	Phe	Ala	Phe	Ser	Phe	Ile	Thr	Tyr	Phe	Thr	
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Ser	Thr	Leu	Leu	Ala	Asp	Cys	Tyr	Arg	Ser	Pro	Asp	Pro	Val	His	Gly	
				85					90					95		
Lys	Arg	Asn	Tyr	Thr	Tyr	Ser	Asp	Val	Arg	Ser	Val	Leu	Gly	Gly		
			100					105				110				
Arg	Lys	Phe	Gln	Leu	Cys	Gly	Leu	Ala	Gln	Tyr	Ile	Asn	Leu	Val	Gly	
		115					120					125				
Val	Thr	Ile	Gly	Tyr	Thr	Ile	Thr	Ala	Ser	Ile	Ser	Met	Val	Ala	Val	
	130					135					140					
Lys	Arg	Ser	Asn	Cys	Phe	His	Lys	His	Gly	His	His	Val	Lys	Cys	Tyr	
145					150					155					160	
Thr	Ser	Asn	Asn	Pro	Phe	Met	Ile	Leu	Phe	Ala	Cys	Ile	Gln	Ile	Val	
				165					170					175		
Leu	Ser	Gln	Ile	Pro	Asn	Phe	His	Lys	Leu	Trp	Trp	Leu	Ser	Ile	Val	
			180					185					190			
Ala	Ala	Val	Met	Ser	Phe	Ala	Tyr	Ser	Ser	Ile	Gly	Leu	Gly	Leu	Ser	
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Val	Ala	Lys	Val	Ala	Gly	Gly	Glu	Pro	Val	Arg	Thr	Thr	Leu	Thr		
	210					215				220						
Gly	Val	Gln	Val	Gly	Val	Asp	Val	Thr	Gly	Ser	Glu	Lys	Val	Trp	Arg	
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Thr	Phe	Gln	Ala	Ile	Gly	Asp	Ile	Ala	Phe	Ala	Tyr	Ala	Tyr	Ser	Asn	
			245						250					255		
Val	Leu	Ile	Glu	Ile	Gln	Asp	Thr	Leu	Lys	Ser	Ser	Pro	Pro	Glu	Asn	
			260					265					270			
Lys	Val	Met	Lys	Arg	Ala	Ser	Leu	Ile	Gly	Ile	Leu	Thr	Thr	Thr	Leu	
		275					280					285				
Phe	Tyr	Val	Leu	Cys	Gly	Cys	Leu	Gly	Tyr	Ala	Ala	Phe	Gly	Asn	Asp	
	290					295					300					
Ala	Pro	Gly	Asn	Phe	Leu	Thr	Gly	Phe	Gly	Phe	Tyr	Glu	Pro	Phe	Trp	
305					310					315					320	
Leu	Ile	Asp	Phe	Ala	Asn	Ile	Cys	Ile	Ala	Val	His	Leu	Val	Gly	Ala	
			325						330					335		
Tyr	Gln	Val	Phe	Cys	Gln	Pro	Ile	Phe	Gly	Phe	Val	Glu	Asn	Trp	Gly	
			340					345					350			
Lys	Glu	Arg	Trp	Pro	Asn	Ser	Gln	Phe	Val	Asn	Gly	Glu	His	Ala	Leu	
		355					360					365				
Asn	Phe	Pro	Leu	Cys	Gly	Thr	Phe	Pro	Val	Asn	Phe	Arg	Val	Val		

PF59082SeqList_PF59082.txt

370 375 380
 Trp Arg Thr Thr Tyr Val Ile Ile Thr Ala Leu Ile Ala Met Met Phe
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 Pro Phe Phe Asn Asp Phe Leu Gly Leu Ile Gly Ser Leu Ser Phe Trp
 405 410 415
 Pro Leu Thr Val Tyr Phe Pro Ile Glu Met Tyr Ile Lys Gln Ser Lys
 420 425 430
 Met Gln Arg Phe Ser Phe Thr Trp Thr Trp Leu Lys Ile Leu Ser Trp
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 Ala Cys Leu Ile Val Ser Ile Ser Ala Ala Gly Ser Ile Gln Gly
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 Leu Ala Gln Asp Leu Lys Lys Tyr Gln Pro Phe Lys Ala Gln Gln
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 gaa gat ggt ggc aaa aac ttc gac gat gat gga cga gtc aga aga act 96
 Glu Asp Gly Gly Lys Asn Phe Asp Asp Gly Arg Val Arg Arg Thr
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 ggt aca tgg ata act gcg agt gcc cat atc ata acg gca gtg ata ggt 144
 Gly Thr Trp Ile Thr Ala Ser Ala His Ile Ile Thr Ala Val Ile Gly
 35 40 45
 tct gga gtg ttg tca ctt gca tgg gca att gca caa atg ggt tgg gtg 192
 Ser Gly Val Leu Ser Leu Ala Trp Ala Ile Ala Gln Met Gly Trp Val
 50 55 60
 gca ggc cct gcg gtt ctc ttt gcc ttc tct ttc atc aca tac ttc act 240
 Ala Gly Pro Ala Val Leu Phe Ala Phe Ser Phe Ile Thr Tyr Phe Thr
 65 70 75 80
 tcc act ctt ctt gcc gac tgt tat cgt tca cct gat cct gtt cat ggc 288
 Ser Thr Leu Leu Ala Asp Cys Tyr Arg Ser Pro Asp Pro Val His Gly
 85 90 95
 aag cga aac tac acc tat tca gat gtt gtc aga tcc gtc tta gga ggt 336
 Lys Arg Asn Tyr Thr Tyr Ser Asp Val Val Arg Ser Val Leu Gly Gly
 100 105 110
 agg aaa ttt cag ctg tgt gga tta gct cag tac ata aat ctt gtc ggt 384
 Arg Lys Phe Gln Leu Cys Gly Leu Ala Gln Tyr Ile Asn Leu Val Gly
 115 120 125
 gta act atc ggt tac acg ata acg gct tca att agt atg gtg gcg gtg 432
 Val Thr Ile Gly Tyr Thr Ile Thr Ala Ser Ile Ser Met Val Ala Val
 130 135 140
 aag agg tcc aac tgt ttt cac aaa cat ggt cat cat gat aag tgc tac 480
 Lys Arg Ser Asn Cys Phe His Lys His Gly His His Asp Lys Cys Tyr
 145 150 155 160
 acg tca aac aac cct ttc atg atc ctc ttt gcc tgc att caa atc gtg 528
 Thr Ser Asn Asn Pro Phe Met Ile Leu Phe Ala Cys Ile Gln Ile Val
 165 170 175
 ctt agc caa ata cca aat ttc cat aag ctc tgg tgg ctc tcc att gtt 576
 Leu Ser Gln Ile Pro Asn Phe His Lys Leu Trp Trp Leu Ser Ile Val
 180 185 190
 gca gca gtt atg tct ttt gct tat tct tcc att ggc ctc ggg ctc tca 624
 Ala Ala Val Met Ser Phe Ala Tyr Ser Ser Ile Gly Leu Gly Leu Ser
 195 200 205
 gta gct aaa gtg gca ggt ggt gga gaa cct gta cgg aca acc tta acg 672
 Val Ala Lys Val Ala Gly Gly Gly Glu Pro Val Arg Thr Thr Leu Thr
 210 215 220
 ggg gtg caa gtt ggg gtg gac gtt acg gga tcc gag aag gtc tgg agg 720
 Gly Val Gln Val Gly Val Asp Val Thr Gly Ser Glu Lys Val Trp Arg
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PF59082SeqList_PF59082.txt

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Thr	Phe	Gln	Ala	Ile	Gly	Asp	Ile	Ala	Phe	Ala	Tyr	Ala	Tyr	Ser	Asn	
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gtg	ctc	att	gag	ata	cag	gat	acc	ctg	aaa	tcg	agc	cct	cca	gaa	aac	816
Val	Leu	Ile	Glu	Ile	Gln	Asp	Thr	Leu	Lys	Ser	Ser	Pro	Pro	Glu	Asn	
			260					265					270			
aag	gtc	atg	aaa	aga	gca	agt	ttg	att	ggc	atc	ttg	act	aca	acc	ttg	864
Lys	Val	Met	Lys	Arg	Ala	Ser	Leu	Ile	Gly	Ile	Leu	Thr	Thr	Thr	Leu	
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ttc	tat	gtg	cta	tgt	ggc	tgc	cta	ggg	tat	gca	gca	ttt	gga	aac	gat	912
Phe	Tyr	Val	Leu	Cys	Gly	Cys	Leu	Gly	Tyr	Ala	Ala	Phe	Gly	Asn	Asp	
	290					295					300					
gca	cca	gga	aat	ttc	ctc	aca	ggg	ttc	ggc	ttc	tac	gag	ccc	ttt	tgg	960
Ala	Pro	Gly	Asn	Phe	Leu	Thr	Gly	Phe	Gly	Phe	Tyr	Glu	Pro	Phe	Trp	
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ctc	ata	gac	ttt	gct	aac	atc	tgc	ata	gcc	gta	cac	ttg	gtt	gga	gca	1008
Leu	Ile	Asp	Phe	Ala	Asn	Ile	Cys	Ile	Ala	Val	His	Leu	Val	Gly	Ala	
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Tyr	Gln	Val	Phe	Cys	Gln	Pro	Ile	Phe	Gly	Phe	Val	Glu	Asn	Trp	Gly	
			340					345					350			
aag	gaa	agg	tgg	cca	aat	agc	caa	ttt	gta	aat	gga	gaa	cac	gct	ttg	1104
Lys	Glu	Arg	Trp	Pro	Asn	Ser	Gln	Phe	Val	Asn	Gly	Glu	His	Ala	Leu	
		355					360					365				
aac	ttt	cca	cta	tgt	gga	acc	ttc	cct	gtg	aac	ttc	ttc	agg	gtg	gtg	1152
Asn	Phe	Pro	Leu	Cys	Gly	Thr	Phe	Pro	Val	Asn	Phe	Phe	Arg	Val	Val	
	370					375					380					
tgg	aga	aca	aca	tat	gtc	atc	atc	act	gct	ttg	ata	gct	atg	atg	ttt	1200
Trp	Arg	Thr	Thr	Tyr	Val	Ile	Ile	Thr	Ala	Leu	Ile	Ala	Met	Met	Phe	
385					390					395					400	
cca	ttc	ttc	aat	gac	ttc	cta	ggc	ctg	att	ggg	tca	ctg	tca	ttt	tgg	1248
Pro	Phe	Phe	Asn	Asp	Phe	Leu	Gly	Leu	Ile	Gly	Ser	Leu	Ser	Phe	Trp	
			405						410					415		
cca	tta	acg	gtt	tac	ttc	ccc	ata	gag	atg	tac	att	aag	cag	tca	aag	1296
Pro	Leu	Thr	Val	Tyr	Phe	Pro	Ile	Glu	Met	Tyr	Ile	Lys	Gln	Ser	Lys	
			420					425					430			
atg	caa	aag	ttt	tcc	ttc	act	tgg	aca	tgg	ctc	aag	ata	ttg	agc	tgg	1344
Met	Gln	Lys	Phe	Ser	Phe	Thr	Trp	Thr	Trp	Leu	Lys	Ile	Leu	Ser	Trp	
		435					440					445				
gct	tgc	ttg	atc	gtt	tct	att	atc	tca	gct	gct	ggc	tcc	atc	caa	ggc	1392
Ala	Cys	Leu	Ile	Val	Ser	Ile	Ile	Ser	Ala	Ala	Gly	Ser	Ile	Gln	Gly	
	450					455					460					
ctc	gct	caa	gat	ctc	aag	aaa	tat	cag	ccc	ttc	aaa	gcc	cag	caa		1437
Leu	Ala	Gln	Asp	Leu	Lys	Lys	Tyr	Gln	Pro	Phe	Lys	Ala	Gln	Gln		
465					470					475						
taa																1440

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 Gly Thr Trp Ile Thr Ala Ser Ala His Ile Ile Thr Ala Val Ile Gly
 35 40 45
 Ser Gly Val Leu Ser Leu Ala Trp Ala Ile Ala Gln Met Gly Trp Val
 50 55 60
 Ala Gly Pro Ala Val Leu Phe Ala Phe Ser Phe Ile Thr Tyr Phe Thr
 65 70 75 80
 Ser Thr Leu Leu Ala Asp Cys Tyr Arg Ser Pro Asp Pro Val His Gly
 85 90 95
 Lys Arg Asn Tyr Thr Tyr Ser Asp Val Val Arg Ser Val Leu Gly Gly
 100 105 110

PF59082SeqList_PF59082.txt

Arg Lys Phe Gln Leu Cys Gly Leu Ala Gln Tyr Ile Asn Leu Val Gly
 115 120 125
 Val Thr Ile Gly Tyr Thr Ile Thr Ala Ser Ile Ser Met Val Ala Val
 130 135 140
 Lys Arg Ser Asn Cys Phe His Lys His Gly His His Asp Lys Cys Tyr
 145 150 155 160
 Thr Ser Asn Asn Pro Phe Met Ile Leu Phe Ala Cys Ile Gln Ile Val
 165 170 175
 Leu Ser Gln Ile Pro Asn Phe His Lys Leu Trp Trp Leu Ser Ile Val
 180 185 190
 Ala Ala Val Met Ser Phe Ala Tyr Ser Ser Ile Gly Leu Gly Leu Ser
 195 200 205
 Val Ala Lys Val Ala Gly Gly Gly Glu Pro Val Arg Thr Thr Leu Thr
 210 215 220
 Gly Val Gln Val Gly Val Asp Val Thr Gly Ser Glu Lys Val Trp Arg
 225 230 235 240
 Thr Phe Gln Ala Ile Gly Asp Ile Ala Phe Ala Tyr Ala Tyr Ser Asn
 245 250 255
 Val Leu Ile Glu Ile Gln Asp Thr Leu Lys Ser Ser Pro Pro Glu Asn
 260 265 270
 Lys Val Met Lys Arg Ala Ser Leu Ile Gly Ile Leu Thr Thr Thr Leu
 275 280 285
 Phe Tyr Val Leu Cys Gly Cys Leu Gly Tyr Ala Ala Phe Gly Asn Asp
 290 295 300
 Ala Pro Gly Asn Phe Leu Thr Gly Phe Gly Phe Tyr Glu Pro Phe Trp
 305 310 315 320
 Leu Ile Asp Phe Ala Asn Ile Cys Ile Ala Val His Leu Val Gly Ala
 325 330 335
 Tyr Gln Val Phe Cys Gln Pro Ile Phe Gly Phe Val Glu Asn Trp Gly
 340 345 350
 Lys Glu Arg Trp Pro Asn Ser Gln Phe Val Asn Gly Glu His Ala Leu
 355 360 365
 Asn Phe Pro Leu Cys Gly Thr Phe Pro Val Asn Phe Phe Arg Val Val
 370 375 380
 Trp Arg Thr Thr Tyr Val Ile Ile Thr Ala Leu Ile Ala Met Met Phe
 385 390 395 400
 Pro Phe Phe Asn Asp Phe Leu Gly Leu Ile Gly Ser Leu Ser Phe Trp
 405 410 415
 Pro Leu Thr Val Tyr Phe Pro Ile Glu Met Tyr Ile Lys Gln Ser Lys
 420 425 430
 Met Gln Lys Phe Ser Phe Thr Trp Thr Trp Leu Lys Ile Leu Ser Trp
 435 440 445
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 Leu Ala Gln Asp Leu Lys Tyr Gln Pro Phe Lys Ala Gln Gln
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<211> 1464

<212> DNA

<213> Triticum aestivum

<220>

<221> CDS

<222> (1)..(1464)

<400> 648

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ccg	atg	gag	gtg	tcg	gtg	gag	gcc	ggg	aac	ggc	agg	gag	tcc	gac	tgg	96
Pro	Met	Glu	Val	Ser	Val	Glu	Ala	Gly	Asn	Gly	Arg	Glu	Ser	Asp	Trp	
			20					25					30			
ctt	gac	gac	gac	ggg	cgc	ccg	cgt	cgg	tcg	ggc	acg	gtg	tgg	acg	gcg	144
Leu	Asp	Asp	Asp	Gly	Arg	Pro	Arg	Arg	Ser	Gly	Thr	Val	Trp	Thr	Ala	
			35				40					45				
agc	gcc	cac	atc	atc	acc	gcc	gtc	atc	ggc	tcg	ggc	gtc	ctc	tcg	ctg	192
Ser	Ala	His	Ile	Ile	Thr	Ala	Val	Ile	Gly	Ser	Gly	Val	Leu	Ser	Leu	
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PF59082SeqList_PF59082.txt

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ctc	ctg	ttc	gcg	ctc	gtc	atc	tac	tac	acc	tcc	acg	ctc	ctc	gcc	gag	288
Leu	Leu	Phe	Ala	Leu	Val	Ile	Tyr	Tyr	Thr	Ser	Thr	Leu	Leu	Ala	Glu	
				85					90					95		
tgc	tac	cgc	tcc	ggc	gac	ccg	gag	acc	ggc	aag	cgc	aac	tac	acc	tac	336
Cys	Tyr	Arg	Ser	Gly	Asp	Pro	Glu	Thr	Gly	Lys	Arg	Asn	Tyr	Thr	Tyr	
			100				105						110			
atg	gac	gcc	gtc	cgc	tcc	tac	ctc	ccg	ggc	acc	aag	gtg	aag	ctc	tgc	384
Met	Asp	Ala	Val	Arg	Ser	Tyr	Leu	Pro	Gly	Thr	Lys	Val	Lys	Leu	Cys	
		115					120					125				
ggc	gtc	atc	cag	tac	gcc	aac	ctc	gtc	ggc	gtc	gcc	atc	ggc	tac	acc	432
Gly	Val	Ile	Gln	Tyr	Ala	Asn	Leu	Val	Gly	Val	Ala	Ile	Gly	Tyr	Thr	
	130					135					140					
atc	gcc	gcc	tcc	atc	agc	atg	cgg	gcg	atc	ggg	agg	gcg	gac	tgc	ttc	480
Ile	Ala	Ala	Ser	Ile	Ser	Met	Arg	Ala	Ile	Gly	Arg	Ala	Asp	Cys	Phe	
145				150						155					160	
cac	tac	cac	gac	gtc	agg	ggc	cgc	agc	ggg	aag	gac	gag	tgc	aag	agc	528
His	Tyr	His	Asp	Val	Arg	Gly	Arg	Ser	Gly	Lys	Asp	Glu	Cys	Lys	Ser	
				165					170					175		
tcc	agc	aac	ccg	tac	atg	atc	gtc	ttc	ggg	gtg	gtg	cag	atc	ctc	ttc	576
Ser	Ser	Asn	Pro	Tyr	Met	Ile	Val	Phe	Gly	Val	Val	Gln	Ile	Leu	Phe	
			180				185					190				
tcg	cag	ata	ccg	gac	ttc	gac	cag	ata	tgg	tgg	ctc	tcc	atc	gtc	gcc	624
Ser	Gln	Ile	Pro	Asp	Phe	Asp	Gln	Ile	Trp	Trp	Leu	Ser	Ile	Val	Ala	
		195					200					205				
gcc	gtc	atg	tcc	ttc	acc	tac	tcc	acc	atc	ggg	ctc	ggg	ctc	ggc	atc	672
Ala	Val	Met	Ser	Phe	Thr	Tyr	Ser	Thr	Ile	Gly	Leu	Gly	Leu	Gly	Ile	
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gcg	cag	acc	gtc	gcc	aac	ggt	ggc	atc	cag	gga	agc	ctc	acc	ggc	ctc	720
Ala	Gln	Thr	Val	Ala	Asn	Gly	Gly	Ile	Gln	Gly	Ser	Leu	Thr	Gly	Leu	
225				230					235					240		
agc	gtc	ggc	ccg	ggc	gtg	acc	tcc	atg	cag	aag	gtg	tgg	cgc	agc	ctc	768
Ser	Val	Gly	Pro	Gly	Val	Thr	Ser	Met	Gln	Lys	Val	Trp	Arg	Ser	Leu	
				245				250						255		
cag	gcc	ttc	ggc	aac	atc	gcc	ttc	gcc	tac	tcc	tac	tcc	atc	atc	ctc	816
Gln	Ala	Phe	Gly	Asn	Ile	Ala	Phe	Ala	Tyr	Ser	Tyr	Ser	Ile	Ile	Leu	
			260				265					270				
atc	gaa	atc	cag	gac	acg	gtg	aag	gcg	ccg	ccg	ccg	tcg	gag	gcg	aag	864
Ile	Glu	Ile	Gln	Asp	Thr	Val	Lys	Ala	Pro	Pro	Pro	Ser	Glu	Ala	Lys	
		275					280					285				
gtg	atg	aag	aag	gcg	acg	ggg	ata	agc	gtg	gcg	acg	acg	acg	gtg	ttc	912
Val	Met	Lys	Lys	Ala	Thr	Gly	Ile	Ser	Val	Ala	Thr	Thr	Thr	Val	Phe	
	290					295					300					
tac	atg	ctg	tgc	ggg	tgc	atg	ggg	tac	gcg	gcg	ttc	ggc	gac	gca	gcc	960
Tyr	Met	Leu	Cys	Gly	Cys	Met	Gly	Tyr	Ala	Ala	Phe	Gly	Asp	Ala	Ala	
305				310					315					320		
ccc	gac	aac	ctc	ctc	acc	ggg	ttc	gga	ttc	tac	gag	ccc	ttc	tgg	ctg	1008
Pro	Asp	Asn	Leu	Leu	Thr	Gly	Phe	Gly	Phe	Tyr	Glu	Pro	Phe	Trp	Leu	
				325				330						335		
ctg	gac	atc	gcc	aac	gtg	gcc	atc	gtc	gtg	cac	ctc	gtc	ggc	gcc	tac	1056
Leu	Asp	Ile	Ala	Asn	Val	Ala	Ile	Val	Val	His	Leu	Val	Gly	Ala	Tyr	
			340				345					350				
cag	gtc	ttc	tgc	cag	ccc	atc	ttc	gcc	ttc	gtc	gag	cgc	tgg	gcc	gcg	1104
Gln	Val	Phe	Cys	Gln	Pro	Ile	Phe	Ala	Phe	Val	Glu	Arg	Trp	Ala	Ala	
		355				360					365					
tcc	aca	tgg	cca	gac	agc	gcc	ttc	atc	tcc	cgc	gag	ttc	cgg	gtg	ggg	1152
Ser	Thr	Trp	Pro	Asp	Ser	Ala	Phe	Ile	Ser	Arg	Glu	Phe	Arg	Val	Gly	
	370					375					380					
cca	ttc	gcg	ctc	agc	gtg	ttc	cgg	ctg	acg	tgg	cgg	tcg	gcc	ttc	gtc	1200
Pro	Phe	Ala	Leu	Ser	Val	Phe	Arg	Leu	Thr	Trp	Arg	Ser	Ala	Phe	Val	
385				390				395						400		
tgc	ctc	acc	acc	gtc	ttc	gcc	atg	ctg	ctc	ccg	ttc	ttc	ggc	aac	gtg	1248
Cys	Leu	Thr	Thr	Val	Phe	Ala	Met	Leu	Leu	Pro	Phe	Phe	Gly	Asn	Val	
				405				410						415		
gtg	gga	ctc	ctc	ggc	gcc	gtc	tcc	ttc	tgg	ccg	ctc	acc	gtc	tac	ttc	1296
Val	Gly	Leu	Leu	Gly	Ala	Val	Ser	Phe	Trp	Pro	Leu	Thr	Val	Tyr	Phe	
			420				425					430				

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ccc	gtc	gag	atg	tac	atc	agg	cag	cgc	ggc	gtg	ccc	ggc	cgg	agc	atg	1344
Pro	Val	Glu	Met	Tyr	Ile	Arg	Gln	Arg	Gly	Val	Pro	Gly	Arg	Ser	Met	
		435					440					445				
cag	ggg	atc	tgc	ctt	agg	atg	ctc	agc	gtc	gga	tgc	ctc	atc	gtt	tcc	1392
Gln	Gly	Ile	Cys	Leu	Arg	Met	Leu	Ser	Val	Gly	Cys	Leu	Ile	Val	Ser	
	450					455					460					
atc	gcc	gcc	gcg	gcg	ggc	tcc	atc	gcc	aac	gtc	atc	gaa	gct	ctc	aaa	1440
Ile	Ala	Ala	Ala	Ala	Gly	Ser	Ile	Ala	Asn	Val	Ile	Glu	Ala	Leu	Lys	
465					470					475					480	
gtg	tac	aag	ccg	ttc	agc	ggc	tga									1464
Val	Tyr	Lys	Pro	Phe	Ser	Gly										
				485												

<210> 649

<211> 487

<212> PRT

<213> Triticum aestivum

<400> 649

Met	Glu	Lys	Lys	Gln	Ala	Ser	Tyr	Gly	Lys	Gly	Ala	Ala	Arg	Met	Ala	
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Pro	Met	Glu	Val	Ser	Val	Glu	Ala	Gly	Asn	Gly	Arg	Glu	Ser	Asp	Trp	
			20					25					30			
Leu	Asp	Asp	Asp	Gly	Arg	Pro	Arg	Arg	Ser	Gly	Thr	Val	Trp	Thr	Ala	
		35					40					45				
Ser	Ala	His	Ile	Ile	Thr	Ala	Val	Ile	Gly	Ser	Gly	Val	Leu	Ser	Leu	
	50					55					60					
Ala	Trp	Ala	Ile	Ala	Gln	Leu	Gly	Trp	Val	Ala	Gly	Pro	Ala	Ile	Met	
65					70				75						80	
Leu	Leu	Phe	Ala	Leu	Val	Ile	Tyr	Tyr	Thr	Ser	Thr	Leu	Leu	Ala	Glu	
				85					90					95		
Cys	Tyr	Arg	Ser	Gly	Asp	Pro	Glu	Thr	Gly	Lys	Arg	Asn	Tyr	Thr	Tyr	
			100					105					110			
Met	Asp	Ala	Val	Arg	Ser	Tyr	Leu	Pro	Gly	Thr	Lys	Val	Lys	Leu	Cys	
		115					120					125				
Gly	Val	Ile	Gln	Tyr	Ala	Asn	Leu	Val	Gly	Val	Ala	Ile	Gly	Tyr	Thr	
	130					135					140					
Ile	Ala	Ala	Ser	Ile	Ser	Met	Arg	Ala	Ile	Gly	Arg	Ala	Asp	Cys	Phe	
145					150					155					160	
His	Tyr	His	Asp	Val	Arg	Gly	Arg	Ser	Gly	Lys	Asp	Glu	Cys	Lys	Ser	
				165					170					175		
Ser	Ser	Asn	Pro	Tyr	Met	Ile	Val	Phe	Gly	Val	Val	Gln	Ile	Leu	Phe	
			180					185					190			
Ser	Gln	Ile	Pro	Asp	Phe	Asp	Gln	Ile	Trp	Trp	Leu	Ser	Ile	Val	Ala	
		195					200					205				
Ala	Val	Met	Ser	Phe	Thr	Tyr	Ser	Thr	Ile	Gly	Leu	Gly	Leu	Gly	Ile	
	210					215					220					
Ala	Gln	Thr	Val	Ala	Asn	Gly	Gly	Ile	Gln	Gly	Ser	Leu	Thr	Gly	Leu	
225					230					235					240	
Ser	Val	Gly	Pro	Gly	Val	Thr	Ser	Met	Gln	Lys	Val	Trp	Arg	Ser	Leu	
				245					250					255		
Gln	Ala	Phe	Gly	Asn	Ile	Ala	Phe	Ala	Tyr	Ser	Tyr	Ser	Ile	Ile	Leu	
			260					265					270			
Ile	Glu	Ile	Gln	Asp	Thr	Val	Lys	Ala	Pro	Pro	Pro	Ser	Glu	Ala	Lys	
		275					280					285				
Val	Met	Lys	Lys	Ala	Thr	Gly	Ile	Ser	Val	Ala	Thr	Thr	Thr	Val	Phe	
	290					295					300					
Tyr	Met	Leu	Cys	Gly	Cys	Met	Gly	Tyr	Ala	Ala	Phe	Gly	Asp	Ala	Ala	
305					310					315					320	
Pro	Asp	Asn	Leu	Leu	Thr	Gly	Phe	Gly	Phe	Tyr	Glu	Pro	Phe	Trp	Leu	
			325						330					335		
Leu	Asp	Ile	Ala	Asn	Val	Ala	Ile	Val	Val	His	Leu	Val	Gly	Ala	Tyr	
			340					345					350			
Gln	Val	Phe	Cys	Gln	Pro	Ile	Phe	Ala	Phe	Val	Glu	Arg	Trp	Ala	Ala	
		355					360					365				
Ser	Thr	Trp	Pro	Asp	Ser	Ala	Phe	Ile	Ser	Arg	Glu	Phe	Arg	Val	Gly	
	370					375					380					
Pro	Phe	Ala	Leu	Ser	Val	Phe	Arg	Leu	Thr	Trp	Arg	Ser	Ala	Phe	Val	
385					390					395					400	

PF59082SeqList_PF59082.txt

Cys Leu Thr Thr Val Phe Ala Met Leu Leu Pro Phe Phe Gly Asn Val
 Val Gly Leu Leu Gly Ala Val Ser Phe Trp Pro Leu Thr Val Tyr Phe
 Pro Val Glu Met Tyr Ile Arg Gln Arg Gly Val Pro Gly Arg Ser Met
 Gln Gly Ile Cys Leu Arg Met Leu Ser Val Gly Cys Leu Ile Val Ser
 Ile Ala Ala Ala Ala Gly Ser Ile Ala Asn Val Ile Glu Ala Leu Lys
 Val Tyr Lys Pro Phe Ser Gly

<210> 650
 <211> 1416
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (1)..(1416)

<400> 650
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 ctc gat gac gac ggc aga atc aaa aga acc ggg aac gtg ttc act gct 96
 Leu Asp Asp Asp Gly Arg Ile Lys Arg Thr Gly Asn Val Phe Thr Ala
 20 25 30
 acc acg cac ata gta acg gtg gtg ggt gca gga gtg ctg gct ctg 144
 Thr Thr His Ile Val Thr Val Val Gly Ala Gly Val Leu Ala Leu
 35 40 45
 gca tgg gcc atg gct cag ctt gga tgg ata gct ggc ata gcc gtt atg 192
 Ala Trp Ala Met Ala Gln Leu Gly Trp Ile Ala Gly Ile Ala Val Met
 50 55 60
 atc ctc ttt gca tgc att tct gtt tac act tac ctt gta gct gat 240
 Ile Leu Phe Ala Cys Ile Ser Val Tyr Thr Tyr Asn Leu Val Ala Asp
 65 70 75 80
 tgc tac aga ttt cct gac cca gtc agt ggc aag aga aac tac act tac 288
 Cys Tyr Arg Phe Pro Asp Pro Val Ser Gly Lys Arg Asn Tyr Thr Tyr
 85 90 95
 atg cag gcc gtt gat gcc tac ctt ggt gga aaa atg cac gtg ttc tgc 336
 Met Gln Ala Val Asp Ala Tyr Leu Gly Gly Lys Met His Val Phe Cys
 100 105 110
 gga tcc gtc cta tat ggg aag ctc gcc ggt gtt aca gtg ggc tac act 384
 Gly Ser Val Leu Tyr Gly Lys Leu Ala Gly Val Thr Val Gly Tyr Thr
 115 120 125
 ata act agt tct gtg agc ttg gtg gct ata aag aaa gct att tgc ttt 432
 Ile Thr Ser Ser Val Ser Leu Val Ala Ile Lys Lys Ala Ile Cys Phe
 130 135 140
 cac aaa aaa ggc cat gat gct tat tgc aag ttt tca aac aat ccc tat 480
 His Lys Lys Gly His Asp Ala Tyr Cys Lys Phe Ser Asn Asn Pro Tyr
 145 150 155 160
 atg att ggt ttt ggg att tgc caa att tta ttg tct caa atc cca aat 528
 Met Ile Gly Phe Gly Ile Cys Gln Ile Leu Ser Gln Ile Pro Asn
 165 170 175
 ttc cac aag tta acg tgg ctt tca acc att gct gct gct acc tct ttc 576
 Phe His Lys Leu Thr Trp Leu Ser Thr Ile Ala Ala Thr Ser Phe
 180 185 190
 ggt tat gca ttc att gga agc ggg ctt tct ctt tcg gtg gtc tca 624
 Gly Tyr Ala Phe Ile Gly Ser Gly Leu Ser Leu Ser Val Val Val Ser
 195 200 205
 ggt aaa gga gaa gca acc agt ata ttt gga agc aaa gta gga cca gat 672
 Gly Lys Gly Glu Ala Thr Ser Ile Phe Gly Ser Lys Val Gly Pro Asp
 210 215 220
 tta tct gaa gcg gat aaa gtt tgg aag gtt ttc agt gct ttg gga aac 720
 Leu Ser Glu Ala Asp Lys Val Trp Lys Val Phe Ser Ala Leu Gly Asn
 225 230 235 240
 att gca ctt gct tgc tca ttt gct act gtt att tat gac ata atg gat 768

PF59082SeqList_PF59082.txt

Ile	Ala	Leu	Ala	Cys	Ser	Phe	Ala	Thr	Val	Ile	Tyr	Asp	Ile	Met	Asp	
				245					250					255		
aca	ttg	aag	tcc	tat	cca	cca	gaa	aac	aaa	cag	atg	aaa	aag	gcc	aat	816
Thr	Leu	Lys	Ser	Tyr	Pro	Pro	Glu	Asn	Lys	Gln	Met	Lys	Lys	Ala	Asn	
			260					265					270			
atg	tta	gga	atc	aca	aca	atg	aca	ata	ctt	ttc	ctg	cta	tgc	ggg	ggc	864
Met	Leu	Gly	Ile	Thr	Thr	Met	Thr	Ile	Leu	Phe	Leu	Leu	Cys	Gly	Gly	
		275					280					285				
ctt	ggc	tat	gct	gct	ttc	gga	gat	gac	acg	ccg	ggg	aac	atc	ctc	acc	912
Leu	Gly	Tyr	Ala	Ala	Phe	Gly	Asp	Asp	Thr	Pro	Gly	Asn	Ile	Leu	Thr	
	290					295					300					
ggc	ttt	gga	ttt	tac	gag	cca	ttc	tgg	ttg	gtc	gcc	ctt	ggc	aat	ggt	960
Gly	Phe	Gly	Phe	Tyr	Glu	Pro	Phe	Trp	Leu	Val	Ala	Leu	Gly	Asn	Val	
305					310					315					320	
ttc	att	gta	gtc	cac	atg	gtt	gga	gca	tat	cag	gtg	atg	gct	caa	cca	1008
Phe	Ile	Val	Val	His	Met	Val	Gly	Ala	Tyr	Gln	Val	Met	Ala	Gln	Pro	
				325					330					335		
cta	ttt	cgt	gta	att	gag	atg	ggg	gct	aac	atg	gcg	tgg	ccg	cgt	tca	1056
Leu	Phe	Arg	Val	Ile	Glu	Met	Gly	Ala	Asn	Met	Ala	Trp	Pro	Arg	Ser	
			340					345					350			
gat	ttc	att	aac	aag	agc	tat	ccc	atc	aaa	atg	ggc	tcc	tta	aca	tgt	1104
Asp	Phe	Ile	Asn	Lys	Ser	Tyr	Pro	Ile	Lys	Met	Gly	Ser	Leu	Thr	Cys	
		355					360					365				
aac	atc	aac	ttg	ttt	agg	ata	att	tgg	agg	tca	atg	tat	gtg	gca	gtg	1152
Asn	Ile	Asn	Leu	Phe	Arg	Ile	Ile	Trp	Arg	Ser	Met	Tyr	Val	Ala	Val	
	370					375					380					
gcc	aca	gtt	att	gcc	atg	gct	atg	cca	ttt	ttc	aat	gag	ttt	ctt	gcc	1200
Ala	Thr	Val	Ile	Ala	Met	Ala	Met	Pro	Phe	Phe	Asn	Glu	Phe	Leu	Ala	
385					390					395					400	
ttg	ctt	gga	gca	ata	ggg	ttt	tgg	cct	ctc	att	gtc	ttc	ttc	cct	gta	1248
Leu	Leu	Gly	Ala	Ile	Gly	Phe	Trp	Pro	Leu	Ile	Val	Phe	Phe	Pro	Val	
				405				410						415		
caa	atg	cac	att	gca	cag	aaa	cgg	gta	aaa	aga	cta	tca	ttg	aag	tgg	1296
Gln	Met	His	Ile	Ala	Gln	Lys	Arg	Val	Lys	Arg	Leu	Ser	Leu	Lys	Trp	
			420					425					430			
tgt	tgt	ctt	caa	ata	ttg	agc	ttc	gcg	tgc	ttc	cta	gtt	aca	gtt	tcc	1344
Cys	Cys	Leu	Gln	Ile	Leu	Ser	Phe	Ala	Cys	Phe	Leu	Val	Thr	Val	Ser	
		435					440					445				
gcg	gca	gtt	ggg	tcg	gtt	cgt	gga	att	agc	aag	aat	ata	aaa	aaa	tac	1392
Ala	Ala	Val	Gly	Ser	Val	Arg	Gly	Ile	Ser	Lys	Asn	Ile	Lys	Lys	Tyr	
	450					455					460					
aaa	ctt	ttc	cag	tat	aaa	caa	tag									1416
Lys	Leu	Phe	Gln	Tyr	Lys	Gln										
465					470											

<210> 651

<211> 471

<212> PRT

<213> Glycine max

<400> 651

Met	Asp	Ile	Glu	Ala	Gly	Lys	Asp	Ile	Pro	Val	Arg	Asp	Pro	Ala	Leu	
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Leu	Asp	Asp	Asp	Gly	Arg	Ile	Lys	Arg	Thr	Gly	Asn	Val	Phe	Thr	Ala	
			20					25					30			
Thr	Thr	His	Ile	Val	Thr	Val	Val	Val	Gly	Ala	Gly	Val	Leu	Ala	Leu	
		35				40						45				
Ala	Trp	Ala	Met	Ala	Gln	Leu	Gly	Trp	Ile	Ala	Gly	Ile	Ala	Val	Met	
	50				55					60						
Ile	Leu	Phe	Ala	Cys	Ile	Ser	Val	Tyr	Thr	Tyr	Asn	Leu	Val	Ala	Asp	
65					70				75						80	
Cys	Tyr	Arg	Phe	Pro	Asp	Pro	Val	Ser	Gly	Lys	Arg	Asn	Tyr	Thr	Tyr	
			85						90					95		
Met	Gln	Ala	Val	Asp	Ala	Tyr	Leu	Gly	Gly	Lys	Met	His	Val	Phe	Cys	
		100						105					110			
Gly	Ser	Val	Leu	Tyr	Gly	Lys	Leu	Ala	Gly	Val	Thr	Val	Gly	Tyr	Thr	
		115					120					125				
Ile	Thr	Ser	Ser	Val	Ser	Leu	Val	Ala	Ile	Lys	Lys	Ala	Ile	Cys	Phe	
	130					135					140					

PF59082SeqList_PF59082.txt

His Lys Lys Gly His Asp Ala Tyr Cys Lys Phe Ser Asn Asn Pro Tyr
 145 150 155 160
 Met Ile Gly Phe Gly Ile Cys Gln Ile Leu Leu Ser Gln Ile Pro Asn
 165 170 175
 Phe His Lys Leu Thr Trp Leu Ser Thr Ile Ala Ala Ala Thr Ser Phe
 180 185 190
 Gly Tyr Ala Phe Ile Gly Ser Gly Leu Ser Leu Ser Val Val Val Ser
 195 200 205
 Gly Lys Gly Glu Ala Thr Ser Ile Phe Gly Ser Lys Val Gly Pro Asp
 210 215 220
 Leu Ser Glu Ala Asp Lys Val Trp Lys Val Phe Ser Ala Leu Gly Asn
 225 230 235 240
 Ile Ala Leu Ala Cys Ser Phe Ala Thr Val Ile Tyr Asp Ile Met Asp
 245 250 255
 Thr Leu Lys Ser Tyr Pro Pro Glu Asn Lys Gln Met Lys Lys Ala Asn
 260 265 270
 Met Leu Gly Ile Thr Thr Met Thr Ile Leu Phe Leu Leu Cys Gly Gly
 275 280 285
 Leu Gly Tyr Ala Ala Phe Gly Asp Asp Thr Pro Gly Asn Ile Leu Thr
 290 295 300
 Gly Phe Gly Phe Tyr Glu Pro Phe Trp Leu Val Ala Leu Gly Asn Val
 305 310 315 320
 Phe Ile Val Val His Met Val Gly Ala Tyr Gln Val Met Ala Gln Pro
 325 330 335
 Leu Phe Arg Val Ile Glu Met Gly Ala Asn Met Ala Trp Pro Arg Ser
 340 345 350
 Asp Phe Ile Asn Lys Ser Tyr Pro Ile Lys Met Gly Ser Leu Thr Cys
 355 360 365
 Asn Ile Asn Leu Phe Arg Ile Ile Trp Arg Ser Met Tyr Val Ala Val
 370 375 380
 Ala Thr Val Ile Ala Met Ala Met Pro Phe Phe Asn Glu Phe Leu Ala
 385 390 395 400
 Leu Leu Gly Ala Ile Gly Phe Trp Pro Leu Ile Val Phe Phe Pro Val
 405 410 415
 Gln Met His Ile Ala Gln Lys Arg Val Lys Arg Leu Ser Leu Lys Trp
 420 425 430
 Cys Cys Leu Gln Ile Leu Ser Phe Ala Cys Phe Leu Val Thr Val Ser
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 Ala Ala Val Gly Ser Val Arg Gly Ile Ser Lys Asn Ile Lys Lys Tyr
 450 455 460
 Lys Leu Phe Gln Tyr Lys Gln
 465 470

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 <211> 1440
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (1)..(1440)

<400> 652
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 gtg tcc gtg gag gcc ggg aac ggc gga gcc gcc gag tgg ctg gac gac 96
 Val Ser Val Glu Ala Gly Asn Gly Gly Ala Ala Glu Trp Leu Asp Asp
 20 25 30
 gac ggc cgg cct cgc cgc acg ggc acg ttc tgg acg gcc agc gcg cac 144
 Asp Gly Arg Pro Arg Arg Thr Gly Thr Phe Trp Thr Ala Ser Ala His
 35 40 45
 atc atc acc gcc gtc atc ggc tcc ggc gtg ctg tcc ctg gcc tgg gcc 192
 Ile Ile Thr Ala Val Ile Gly Ser Gly Val Leu Ser Leu Ala Trp Ala
 50 55 60
 atc gcg cag ctg ggc tgg gtc gcc ggc ccc gcc gcc atg ctc ctc ttc 240
 Ile Ala Gln Leu Gly Trp Val Ala Gly Pro Ala Ala Met Leu Leu Phe
 65 70 75 80
 gcc ttc gtc acc tac tac acc gcc acg ctg ctc gcc gag tgc tac cgc 288

PF59082SeqList_PF59082.txt

Ala	Phe	Val	Thr	Tyr 85	Tyr	Thr	Ala	Thr	Leu 90	Leu	Ala	Glu	Cys	Tyr 95	Arg	
acg	ggc	gac	ccg	gac	acg	ggc	aag	cgc	aac	tac	acc	tac	atg	gac	gcc	336
Thr	Gly	Asp	Pro	Asp	Thr	Gly	Lys	Arg	Asn	Tyr	Thr	Tyr	Met	Asp	Ala	
		100						105					110			
gtg	cgc	tcc	aac	ctc	ggc	ggc	gcc	aag	gtc	gcc	ttc	tgc	ggc	gtc	atc	384
Val	Arg	Ser	Asn	Leu	Gly	Gly	Ala	Lys	Val	Ala	Phe	Cys	Gly	Val	Ile	
		115					120					125				
cag	tac	gcc	aac	ctc	gtc	ggc	gtc	gcc	atc	ggc	tac	acc	atc	gcg	tcg	432
Gln	Tyr	Ala	Asn	Leu	Val	Gly	Val	Ala	Ile	Gly	Tyr	Thr	Ile	Ala	Ser	
	130					135					140					
tcc	atc	agc	atg	aag	gcc	gtc	agg	agg	gcc	ggg	tgc	ttc	cac	acc	cac	480
Ser	Ile	Ser	Met	Lys	Ala	Val	Arg	Arg	Ala	Gly	Cys	Phe	His	Thr	His	
145					150					155					160	
ggg	cac	gcc	gac	ccc	tgc	aag	agc	tcc	agc	acc	ccc	tac	atg	atc	ctc	528
Gly	His	Ala	Asp	Pro	Cys	Lys	Ser	Ser	Ser	Thr	Pro	Tyr	Met	Ile	Leu	
				165				170						175		
ttc	ggc	gcc	gtg	cag	atc	ctc	ttc	tcc	cag	ata	ccc	gac	ttc	gac	cag	576
Phe	Gly	Ala	Val	Gln	Ile	Leu	Phe	Ser	Gln	Ile	Pro	Asp	Phe	Asp	Gln	
			180					185					190			
att	tgg	tgg	ctc	tcc	att	gtc	gcc	gca	gtc	atg	tcc	ttc	act	tac	tcc	624
Ile	Trp	Trp	Leu	Ser	Ile	Val	Ala	Ala	Val	Met	Ser	Phe	Thr	Tyr	Ser	
		195					200					205				
tcc	atc	gga	ctc	tcc	ctc	ggc	atc	gca	cag	acc	gtc	tcc	aac	ggc	ggg	672
Ser	Ile	Gly	Leu	Ser	Leu	Gly	Ile	Ala	Gln	Thr	Val	Ser	Asn	Gly	Gly	
	210					215					220					
ttc	aag	ggc	agc	ctc	acc	ggc	atc	agc	atc	ggc	gcc	ggc	gtc	acc	tcc	720
Phe	Lys	Gly	Ser	Leu	Thr	Gly	Ile	Ser	Ile	Gly	Ala	Gly	Val	Thr	Ser	
225					230					235					240	
acg	cag	aag	atc	tgg	cac	acg	ctg	cag	gcc	ttc	ggc	gac	atc	gcg	ttc	768
Thr	Gln	Lys	Ile	Trp	His	Thr	Leu	Gln	Ala	Phe	Gly	Asp	Ile	Ala	Phe	
				245					250					255		
gcc	tac	tcc	ttc	tcc	aac	atc	ctc	atc	gag	atc	caa	gac	acg	atc	aag	816
Ala	Tyr	Ser	Phe	Ser	Asn	Ile	Leu	Ile	Glu	Ile	Gln	Asp	Thr	Ile	Lys	
			260					265					270			
gcg	ccg	cca	ccg	tcg	gag	tcg	aag	gtg	atg	cag	aag	gcg	acg	cgc	ctc	864
Ala	Pro	Pro	Pro	Ser	Glu	Ser	Lys	Val	Met	Gln	Lys	Ala	Thr	Arg	Leu	
		275					280					285				
agc	gtg	gcg	acg	acg	acc	atc	ttc	tac	atg	ctg	tgc	ggg	tgc	atg	ggg	912
Ser	Val	Ala	Thr	Thr	Thr	Ile	Phe	Tyr	Met	Leu	Cys	Gly	Cys	Met	Gly	
	290					295					300					
tac	gcg	gcg	ttc	ggc	gac	aag	gcg	ccg	gac	aac	ctg	ctc	acc	ggc	ttc	960
Tyr	Ala	Ala	Phe	Gly	Asp	Lys	Ala	Pro	Asp	Asn	Leu	Leu	Thr	Gly	Phe	
305					310					315					320	
ggc	ttc	ttc	gag	cca	ttc	tgg	ctg	atc	gac	gtg	gcc	aac	gtg	gcc	atc	1008
Gly	Phe	Phe	Glu	Pro	Phe	Trp	Leu	Ile	Asp	Val	Ala	Asn	Val	Ala	Ile	
				325					330					335		
gtg	gtg	cac	ctg	gtg	ggc	gcg	tac	cag	gtg	ttc	tgc	cag	ccc	atc	ttc	1056
Val	Val	His	Leu	Val	Gly	Ala	Tyr	Gln	Val	Phe	Cys	Gln	Pro	Ile	Phe	
			340					345					350			
gcc	ttc	gtc	gag	cgc	cgc	gcc	gcc	gcg	gcc	tgg	ccc	gac	agc	gcc	ttc	1104
Ala	Phe	Val	Glu	Arg	Arg	Ala	Ala	Ala	Ala	Trp	Pro	Asp	Ser	Ala	Phe	
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gtc	tcg	cgg	gag	ctc	cgc	gtg	ggc	ccc	ttc	gcc	ctc	agc	gtg	ttc	cgc	1152
Val	Ser	Arg	Glu	Leu	Arg	Val	Gly	Pro	Phe	Ala	Leu	Ser	Val	Phe	Arg	
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ctc	acg	tgg	cgg	tcg	gcg	ttc	gtg	tgc	gtc	acc	acc	gtc	gtc	gcc	atg	1200
Leu	Thr	Trp	Arg	Ser	Ala	Phe	Val	Cys	Val	Thr	Thr	Val	Val	Ala	Met	
					390					395					400	
ctg	ctg	ccg	ttc	ttc	ggc	aac	gtg	gtg	ggg	ctc	ggc	gcc	gtc	tcc		1248
Leu	Leu	Pro	Phe	Phe	Gly	Asn	Val	Val	Gly	Phe	Leu	Gly	Ala	Val	Ser	
				405					410					415		
ttc	tgg	ccg	ctc	acc	gtc	tac	ttc	ccc	gtc	gag	atg	tac	atc	aag	cag	1296
Phe	Trp	Pro	Leu	Thr	Val	Tyr	Phe	Pro	Val	Glu	Met	Tyr	Ile	Lys	Gln	
				420				425						430		
cgc	cgc	gtg	ccc	cgc	ggc	agc	acc	aag	tgg	atc	tgc	ctc	cag	acg	ctc	1344
Arg	Arg	Val	Pro	Arg	Gly	Ser	Thr	Lys	Trp	Ile	Cys	Leu	Gln	Thr	Leu	
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agc	gtc	acg	tgc	ctc	ctc	gtc	tcc	atc	gcc	gcc	gcc	ggc	ggc	tcc	atc	1392

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1437

1440

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 Ala Phe Val Thr Tyr Tyr Thr Ala Thr Leu Ala Glu Cys Tyr Arg
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 115 120 125
 Gln Tyr Ala Asn Leu Val Gly Val Ala Ile Gly Tyr Thr Ile Ala Ser
 130 135 140
 Ser Ile Ser Met Lys Ala Val Arg Arg Ala Gly Cys Phe His Thr His
 145 150 155 160
 Gly His Ala Asp Pro Cys Lys Ser Ser Ser Thr Pro Tyr Met Ile Leu
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 Ile Trp Trp Leu Ser Ile Val Ala Val Met Ser Phe Thr Tyr Ser
 195 200 205
 Ser Ile Gly Leu Ser Leu Gly Ile Ala Gln Thr Val Ser Asn Gly Gly
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 Phe Lys Gly Ser Leu Thr Gly Ile Ser Ile Gly Ala Gly Val Thr Ser
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 Thr Gln Lys Ile Trp His Thr Leu Gln Ala Phe Gly Asp Ile Ala Phe
 245 250 255
 Ala Tyr Ser Phe Ser Asn Ile Leu Ile Glu Ile Gln Asp Thr Ile Lys
 260 265 270
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 Ser Val Ala Thr Thr Thr Ile Phe Tyr Met Leu Cys Gly Cys Met Gly
 290 295 300
 Tyr Ala Ala Phe Gly Asp Lys Ala Pro Asp Asn Leu Leu Thr Gly Phe
 305 310 315 320
 Gly Phe Phe Glu Pro Phe Trp Leu Ile Asp Val Ala Asn Val Ala Ile
 325 330 335
 Val Val His Leu Val Gly Ala Tyr Gln Val Phe Cys Gln Pro Ile Phe
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 Ala Phe Val Glu Arg Arg Ala Ala Ala Trp Pro Asp Ser Ala Phe
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Thr Xaa Xaa Xaa His Ile Ile Thr Ala Val Xaa Gly Ser Gly Val Leu
1      5      10      15
Ser Leu Xaa Trp Xaa Xaa Gln Xaa Gly Trp Xaa Xaa Gly Xaa Xaa
      20      25      30
Xaa Xaa Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu
      35      40      45
Xaa Xaa Cys Tyr Arg Xaa Xaa Xaa
      50      55

<210> 665
<211> 31
<212> PRT
<213> Artificial sequence

<220>
<223> protein pattern

<220>
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<222> (2)..(2)
<223> Xaa in position 2 is any amino acid

<220>
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<222> (3)..(3)
<223> Xaa in position 3 is Ala, Asn, Ser, Thr or Val

<220>
<221> Variant
<222> (4)..(4)
<223> Xaa in position 4 is Phe, Leu or Met

<220>
<221> Variant
<222> (5)..(5)
<223> Xaa in position 5 is any amino acid

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<220>
<221> Variant
<222> (6)..(6)
<223> Xaa in position 6 is Ala or Ser

<220>
<221> Variant
<222> (7)..(7)
<223> Xaa in position 7 is Phe, Ile, Leu or Val

<220>
<221> Variant
<222> (9)..(9)
<223> Xaa in position 9 is Ala, Asp or Asn

<220>
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<222> (10)..(10)
<223> Xaa in position 10 is Ile, Met or Val

<220>
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<222> (15)..(15)
<223> Xaa in position 15 is Ala, Ser or Thr

<220>
<221> Variant
<222> (16)..(16)
<223> Xaa in position 16 is Phe or Tyr

<220>
<221> Variant
<222> (17)..(17)
<223> Xaa in position 17 is Ala or Ser

<220>
<221> Variant
<222> (18)..(18)
<223> Xaa in position 18 is any amino acid

<220>
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<222> (19)..(19)
<223> Xaa in position 19 is Ile or Val

<220>
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<222> (27)..(29)
<223> Xaa in position 27 to 29 is any amino acid

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<222> (30)..(30)
<223> Xaa in position 30 is any or no amino acid

<400> 665
Trp Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Ala Phe Ala Tyr Xaa Xaa
1      5      10      15
Xaa Xaa Xaa Leu Ile Glu Ile Gln Asp Thr Xaa Xaa Xaa Xaa Pro
      20      25      30

<210> 666
<211> 23
<212> PRT
<213> Artificial sequence

<220>

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<223> protein pattern

<220>

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<222> (2)..(2)

<223> Xaa in position 2 is Phe, Ile, Leu or Val

<220>

<221> Variant

<222> (3)..(3)

<223> Xaa in position 3 is Ile or Leu

<220>

<221> Variant

<222> (5)..(5)

<223> Xaa in position 5 is Ala or Ser

<220>

<221> Variant

<222> (6)..(6)

<223> Xaa in position 6 is any amino acid

<220>

<221> Variant

<222> (7)..(7)

<223> Xaa in position 7 is Ala, Gly or Ser

<220>

<221> Variant

<222> (15)..(15)

<223> Xaa in position 15 is any amino acid

<220>

<221> Variant

<222> (17)..(17)

<223> Xaa in position 17 is Ile or Val

<220>

<221> Variant

<222> (18)..(18)

<223> Xaa in position 18 is Ala, Asp, Glu, Gln, Ser or Thr

<220>

<221> Variant

<222> (20)..(20)

<223> Xaa in position 20 is His or Tyr

<220>

<221> Variant

<222> (21)..(21)

<223> Xaa in position 21 is Ile, Met or Val

<220>

<221> Variant

<222> (22)..(22)

<223> Xaa in position 22 is any amino acid

<400> 666

Gly	Xaa	Xaa	Gly	Xaa	Xaa	Xaa	Phe	Trp	Pro	Leu	Thr	Val	Tyr	Xaa	Pro
1				5					10					15	
Xaa	Xaa	Met	Xaa	Xaa	Xaa	Gln									
			20												

<210> 667

<211> 41

<212> PRT

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<220>
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<220>
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<223> Xaa in position 2 to 3 is any amino acid

<220>
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<222> (4)..(4)
<223> Xaa in position 4 is Ala, Thr or Val

<220>
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<222> (6)..(7)
<223> Xaa in position 6 to 7 is any amino acid

<220>
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<222> (9)..(9)
<223> Xaa in position 9 is Ala, Asn, Ser or Thr

<220>
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<222> (10)..(10)
<223> Xaa in position 10 is any amino acid

<220>
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<222> (11)..(11)
<223> Xaa in position 11 is Ala, Ile, Leu or Val

<220>
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<222> (12)..(12)
<223> Xaa in position 12 is Ala, Gly or Ser

<220>
<221> Variant
<222> (13)..(13)
<223> Xaa in position 13 is Ile, Met or Val

<220>
<221> Variant
<222> (14)..(16)
<223> Xaa in position 14 to 16 is any amino acid

<220>
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<222> (17)..(17)
<223> Xaa in position 17 is Ser or Thr

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<222> (18)..(18)
<223> Xaa in position 18 is any amino acid

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<222> (21)..(21)
<223> Xaa in position 21 is any amino acid

<220>
<221> Variant
<222> (25)..(26)
<223> Xaa in position 25 to 26 is any amino acid

<220>

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<222> (33)..(33)
<223> Xaa in position 33 is Asp, Glu or Asn

<220>
<221> Variant
<222> (34)..(34)
<223> Xaa in position 34 is any amino acid

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<223> Xaa in position 37 to 38 is any amino acid

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<222> (39)..(39)
<223> Xaa in position 39 is any or no amino acid

<220>
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<223> Xaa in position 41 is Ala or Thr

<400> 667
Glu Xaa Xaa Xaa Met Xaa Xaa Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1      5      10      15
Xaa Xaa Phe Tyr Xaa Leu Cys Gly Xaa Xaa Gly Tyr Ala Ala Phe Gly
      20      25      30
Xaa Xaa Xaa Pro Xaa Xaa Xaa Leu Xaa
      35      40

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<222> (8)..(8)
<223> Xaa in position 8 is Ile, Leu or Met

<220>
<221> Variant
<222> (9)..(9)
<223> Xaa in position 9 is any amino acid

<220>
<221> Variant
<222> (11)..(12)

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<223> Xaa in position 11 to 12 is any amino acid

<220>

<221> Variant

<222> (13)..(13)

<223> Xaa in position 13 is Ile or Val

<220>

<221> Variant

<222> (16)..(16)

<223> Xaa in position 16 is Ala, Asn or Thr

<220>

<221> Variant

<222> (18)..(18)

<223> Xaa in position 18 is Ala, Gly or Thr

<220>

<221> Variant

<222> (19)..(19)

<223> Xaa in position 19 is Ala, Gly, Ser or Thr

<220>

<221> Variant

<222> (20)..(20)

<223> Xaa in position 20 is Ala, Ser or Thr

<220>

<221> Variant

<222> (21)..(21)

<223> Xaa in position 21 is any amino acid

<220>

<221> Variant

<222> (23)..(24)

<223> Xaa in position 23 to 24 is any amino acid

<220>

<221> Variant

<222> (25)..(25)

<223> Xaa in position 25 is Ala, Glu or Thr

<400> 668

Gly	Xaa	Xaa	Gln	Tyr	Xaa	Asn	Xaa	Xaa	Gly	Xaa	Xaa	Xaa	Gly	Tyr	Xaa
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Ile	Xaa	Xaa	Xaa	Xaa	Ser	Xaa	Xaa	Xaa							
			20					25							

<210> 669

<211> 26

<212> PRT

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<220>

<223> protein pattern

<220>

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<222> (2)..(2)

<223> Xaa in position 2 is Ile or Leu

<220>

<221> Variant

<222> (3)..(3)

<223> Xaa in position 3 is any amino acid

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<221> Variant

<222> (4)..(4)
<223> Xaa in position 4 is Asp, Glu, Gly or Asn

<220>
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<222> (6)..(6)
<223> Xaa in position 6 is Asp or His

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<222> (7)..(9)
<223> Xaa in position 7 to 9 is any amino acid

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<223> Xaa in position 10 is Phe or Trp

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<222> (13)..(13)
<223> Xaa in position 13 is any amino acid

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<222> (14)..(14)
<223> Xaa in position 14 is Ile, Leu, Met or Val

<220>
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<222> (16)..(16)
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<220>
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<223> Xaa in position 17 is Ala, Ile or Val

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<222> (18)..(18)
<223> Xaa in position 18 is any amino acid

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<222> (20)..(20)
<223> Xaa in position 20 is Phe or Leu

<220>
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<222> (21)..(21)
<223> Xaa in position 21 is any amino acid

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<222> (23)..(23)
<223> Xaa in position 23 is Ala or Ser

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<223> Xaa in position 24 is any amino acid

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<223> Xaa in position 25 is Ala, Ile or Val

<220>

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 <400> 669
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 1 5 10 15
 Xaa Xaa Ser Xaa Xaa Tyr Xaa Xaa Xaa Xaa
 20 25

 <210> 670
 <211> 16
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 <223> Xaa in position 7 is Phe or Tyr

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 <223> Xaa in position 8 is any amino acid

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 <223> Xaa in position 9 is Asp, Glu or Gln

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 <223> Xaa in position 12 is any amino acid

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 <223> Xaa in position 13 is Ala, Asn, Ser or Thr

 <220>
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 <222> (14)..(14)
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 <223> Xaa in position 15 is Phe or Leu

 <220>
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 <222> (16)..(16)
 <223> Xaa in position 16 is Gly, Pro or Ser

PF59082SeqList_PF59082.txt

<400> 670

Gly Lys Arg Asn Tyr Thr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

<210> 671

<211> 13

<212> PRT

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<223> Xaa in position 2 is Asp, Glu or Gly

<220>

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<222> (5)..(6)

<223> Xaa in position 5 to 6 is any or no amino acid

<220>

<221> Variant

<222> (8)..(9)

<223> Xaa in position 8 to 9 is any or no amino acid

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<222> (11)..(11)

<223> Xaa in position 11 is any amino acid

<220>

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<222> (13)..(13)

<223> Xaa in position 13 is Asn, Ser or Thr

<400> 671

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1 5 10

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<222> (2)..(3)

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<222> (4)..(4)

<223> Xaa in position 4 is any or no amino acid

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<222> (6)..(8)

<223> Xaa in position 6 to 8 is any amino acid

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PF59082SeqList_PF59082.txt

<222> (9)..(9)

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<222> (11)..(11)

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<222> (12)..(12)

<223> Xaa in position 12 is Phe, Ile, Leu or Met

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<222> (16)..(16)

<223> Xaa in position 16 is Gly or Asn

<400> 672

Val Xaa Xaa Xaa Thr Xaa Xaa Xaa Xaa Met Xaa Xaa Pro Phe Phe Xaa
1 5 10 15

<210> 673

<211> 1812

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1812)

<400> 673

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1 5 10 15	
aaa tgg cga gcg gaa gct gaa att ggt ggc aac gag aga gct ctg caa	96
Lys Trp Arg Ala Glu Ala Glu Ile Gly Gly Asn Glu Arg Ala Leu Gln	
20 25 30	
gcg ctt cga gaa ctc att atc ttc cct ttt cgt tac cct ctc gaa gct	144
Ala Leu Arg Glu Leu Ile Ile Phe Pro Phe Arg Tyr Pro Leu Glu Ala	
35 40 45	
cga act ctt ggt ctc aaa tgg cct aga gga ttg ctt ctc tac ggt cct	192
Arg Thr Leu Gly Leu Lys Trp Pro Arg Gly Leu Leu Tyr Gly Pro	
50 55 60	
cct gga acc ggc aag aca agc ttg gtc cgt gct gtt gtc cag gaa tgt	240
Pro Gly Thr Gly Lys Thr Ser Leu Val Arg Ala Val Val Gln Glu Cys	
65 70 75 80	
gat gca cat ttg att gtt tta agc cct cat tct gta cat cga gca cat	288
Asp Ala His Leu Ile Val Leu Ser Pro His Ser Val His Arg Ala His	
85 90 95	
gct gga gaa agc gag aaa gtc tta agg gaa gct ttc gct gag gct tct	336
Ala Gly Glu Ser Glu Lys Val Leu Arg Glu Ala Phe Ala Glu Ala Ser	
100 105 110	
tct cac gct gtt tca gac aag cct tct gtg att ttt att gat gaa atc	384
Ser His Ala Val Ser Asp Lys Pro Ser Val Ile Phe Ile Asp Glu Ile	
115 120 125	
gat gtt ctt tgt cct cgt cgt gat gct aga cga gaa caa gat gtt cgt	432
Asp Val Leu Cys Pro Arg Arg Asp Ala Arg Arg Glu Gln Asp Val Arg	
130 135 140	
att gct tct caa ctg ttt aca ctt atg gac tca aac aag cct tca tca	480
Ile Ala Ser Gln Leu Phe Thr Leu Met Asp Ser Asn Lys Pro Ser Ser	
145 150 155 160	
tct gca cca aga gtt gtt gta gca tcc aca aat agg gtg gat gcg	528
Ser Ala Pro Arg Val Val Val Ala Ser Thr Asn Arg Val Asp Ala	
165 170 175	
att gac cca gcg cta aga aga gcg gga cga ttt gat gct tta gtt gaa	576
Ile Asp Pro Ala Leu Arg Arg Ala Gly Arg Phe Asp Ala Leu Val Glu	
180 185 190	

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Val	Ser	Thr	Pro	Asn	Glu	Glu	Asp	Arg	Leu	Lys	Ile	Leu	Gln	Leu	Tyr	
		195					200				205					
aca	aag	aaa	gtc	aat	tta	gat	cct	agt	gtc	gat	ctt	caa	gcc	att	gca	672
Thr	Lys	Lys	Val	Asn	Leu	Asp	Pro	Ser	Val	Asp	Leu	Gln	Ala	Ile	Ala	
	210					215					220					
ata	tct	tgc	aac	ggc	tat	gtt	gga	gca	gat	ttg	gaa	gct	tta	tgt	cgt	720
Ile	Ser	Cys	Asn	Gly	Tyr	Val	Gly	Ala	Asp	Leu	Glu	Ala	Leu	Cys	Arg	
225				230					235						240	
gaa	gcg	aca	ata	tct	gca	agt	aaa	aga	tct	tca	gat	tct	ctt	att	cta	768
Glu	Ala	Thr	Ile	Ser	Ala	Ser	Lys	Arg	Ser	Ser	Asp	Ser	Leu	Ile	Leu	
				245					250					255		
aca	tct	caa	gac	ttc	aag	att	gca	aaa	tct	gtg	gtt	ggc	cca	agt	ata	816
Thr	Ser	Gln	Asp	Phe	Lys	Ile	Ala	Lys	Ser	Val	Val	Gly	Pro	Ser	Ile	
			260					265					270			
aac	aga	ggc	atc	aca	gtt	gaa	atc	cct	aaa	gtg	aca	tgg	gac	gat	gtt	864
Asn	Arg	Gly	Ile	Thr	Val	Glu	Ile	Pro	Lys	Val	Thr	Trp	Asp	Asp	Val	
		275					280					285				
ggc	ggc	ctt	aaa	gac	tta	aag	aaa	aag	ctc	cag	caa	gct	gtt	gaa	tgg	912
Gly	Gly	Leu	Lys	Asp	Leu	Lys	Lys	Lys	Leu	Gln	Ala	Val	Glu	Trp		
	290				295					300						
cca	atc	aaa	cat	tca	gct	gca	ttt	gta	aaa	atg	ggc	ata	tcg	cca	atg	960
Pro	Ile	Lys	His	Ser	Ala	Ala	Phe	Val	Lys	Met	Gly	Ile	Ser	Pro	Met	
305				310					315						320	
cgt	ggg	ata	ctt	cta	cat	ggc	cct	cca	ggc	tgc	tca	aag	aca	act	ctt	1008
Arg	Gly	Ile	Leu	Leu	His	Gly	Pro	Pro	Gly	Cys	Ser	Lys	Thr	Thr	Leu	
				325					330					335		
gct	aaa	gcc	gct	gca	aat	gct	gct	caa	gcc	tcc	ttc	ttt	tcc	tta	agc	1056
Ala	Lys	Ala	Ala	Ala	Asn	Ala	Ala	Gln	Ala	Ser	Phe	Phe	Ser	Leu	Ser	
			340					345					350			
tgt	gcg	gag	cta	ttt	tct	atg	tat	gtt	gga	gaa	ggc	gaa	gca	tta	ttg	1104
Cys	Ala	Glu	Leu	Phe	Ser	Met	Tyr	Val	Gly	Glu	Gly	Glu	Ala	Leu	Leu	
		355				360						365				
cgg	aat	aca	ttt	caa	aga	gct	cga	ctt	gct	tct	cca	agt	ata	ata	ttc	1152
Arg	Asn	Thr	Phe	Gln	Arg	Ala	Arg	Leu	Ala	Ser	Pro	Ser	Ile	Ile	Phe	
	370					375					380					
ttt	gat	gaa	gct	gat	gtc	gtt	gcc	tgt	aaa	aga	ggc	gat	gag	agc	tca	1200
Phe	Asp	Glu	Ala	Asp	Val	Val	Ala	Cys	Lys	Arg	Gly	Asp	Glu	Ser	Ser	
385				390					395						400	
agc	aat	agt	tct	aca	gtt	gga	gaa	agg	ctt	cta	tct	aca	ctg	tta	acc	1248
Ser	Asn	Ser	Ser	Thr	Val	Gly	Glu	Arg	Leu	Leu	Ser	Thr	Leu	Leu	Thr	
				405					410					415		
gaa	atg	gac	ggc	ctt	gaa	gaa	gca	aag	gga	atc	ctc	gtc	ttg	gct	gcc	1296
Glu	Met	Asp	Gly	Leu	Glu	Glu	Ala	Lys	Gly	Ile	Leu	Val	Leu	Ala	Ala	
			420					425					430			
aca	aac	cgc	ccg	tat	gca	att	gat	gct	gct	cta	atg	cga	cct	ggc	cga	1344
Thr	Asn	Arg	Pro	Tyr	Ala	Ile	Asp	Ala	Ala	Leu	Met	Arg	Pro	Gly	Arg	
		435					440				445					
ttt	gat	ctc	gtg	cta	tac	gtg	cca	ccg	cct	gat	cta	gaa	gcc	cgg	ttt	1392
Phe	Asp	Leu	Val	Leu	Tyr	Val	Pro	Pro	Pro	Asp	Leu	Glu	Ala	Arg	Phe	
	450					455					460					
gaa	ata	ctg	caa	gtg	cat	aca	cgc	aac	atg	aca	cta	gga	gac	gac	gtt	1440
Glu	Ile	Leu	Gln	Val	His	Thr	Arg	Asn	Met	Thr	Leu	Gly	Asp	Asp	Val	
465				470					475						480	
gat	ctc	aga	aaa	atc	gct	gaa	gaa	acc	gat	ctc	ttc	aca	ggc	gcc	gag	1488
Asp	Leu	Arg	Lys	Ile	Ala	Glu	Glu	Thr	Asp	Leu	Phe	Thr	Gly	Ala	Glu	
				485					490					495		
ctc	gag	ggc	cta	tgc	aga	gaa	agc	gga	act	gtc	tca	ctt	aga	gaa	aac	1536
Leu	Glu	Gly	Leu	Cys	Arg	Glu	Ser	Gly	Thr	Val	Ser	Leu	Arg	Glu	Asn	
			500					505					510			
atc	gca	gca	acc	gct	gtc	ttc	aat	cgc	cat	ttc	caa	acc	gca	aaa	agc	1584
Ile	Ala	Ala	Thr	Ala	Val	Phe	Asn	Arg	His	Phe	Gln	Thr	Ala	Lys	Ser	
		515				520						525				
tcg	ctt	aaa	cca	gcg	tta	aca	atc	gaa	gaa	gtc	gaa	act	tat	tca	tca	1632
Ser	Leu	Lys	Pro	Ala	Leu	Thr	Ile	Glu	Glu	Val	Glu	Thr	Tyr	Ser	Ser	
	530					535					540					
ttc	agg	aag	gcg	gcg	aaa	aga	tct	gat	tcg	aaa	ccg	att	ccg	att	aac	1680
Phe	Arg	Lys	Ala	Ala	Lys	Arg	Ser	Asp	Ser	Lys	Pro	Ile	Pro	Ile	Asn	
545					550					555					560	

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			565					570						575		
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act	aaa	cat	gaa	tta	cta	gta	gct	tct	gct	aca	tga					1812
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<212> PRT

<213> Arabidopsis thaliana

<400> 674

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PF59082SeqList_PF59082.txt

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Asp Leu Arg Lys Ile Ala Glu Glu Thr Asp Leu Phe Thr Gly Ala Glu
      485      490      495
Leu Glu Gly Leu Cys Arg Glu Ser Gly Thr Val Ser Leu Arg Glu Asn
      500      505      510
Ile Ala Ala Thr Ala Val Phe Asn Arg His Phe Gln Thr Ala Lys Ser
      515      520      525
Ser Leu Lys Pro Ala Leu Thr Ile Glu Glu Val Glu Thr Tyr Ser Ser
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Phe Arg Lys Ala Ala Lys Arg Ser Asp Ser Lys Pro Ile Pro Ile Asn
      545      550      555
Lys Lys Lys Ala Thr Ser Thr Val Phe Gly Phe Ser Trp Gln Leu Gly
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Asp Glu Ala Ile Asn Asp Asp Asn Ser Val Val Ser Leu His Pro Ala
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Thr Met Glu Lys Leu Gln Phe Arg Gly Asp Thr Ile Leu Ile Lys
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Gly Lys Lys Arg Lys Asp Thr Ile Cys Ile Ala Leu Ala Asp Glu Ser
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Cys Glu Glu Pro Lys Ile Arg Met Asn Lys Val Val Arg Ser Asn Leu
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Arg Val Arg Leu Gly Asp Val Ile Ser Val His Gln Cys Pro Asp Val
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Lys Tyr Gly Lys Arg Val His Ile Leu Pro Val Asp Asp Thr Val Glu
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Gly Met Arg Ser Val Glu Phe Lys Val Ile Glu Thr Asp Pro Ala Glu
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PF59082SeqList_PF59082.txt

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Leu	Cys	Thr	Glu	Ala	Ala	Leu	Gln	Cys	Ile	Arg	Glu	Lys	Met	Asp	Val		
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Gln	Tyr	Pro	Val	Glu	His	Pro	Glu	Lys	Phe	Glu	Lys	Phe	Gly	Met	Ser		
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Leu	Leu	Ala	Lys	Ala	Ile	Ala	Asn	Glu	Cys	Gln	Ala	Asn	Phe	Ile	Ser		
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gtc	aaa	ggt	cct	gag	ctt	ctc	acc	atg	tgg	ttt	gga	gag	agt	gaa	gcc		1680
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PF59082SeqList_PF59082.txt

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Ser Gly Gly Asp Ala Gly Gly Ala Ala Asp Arg Val Leu Asn Gln Leu					
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Gly Arg Leu Asp Gln Leu Ile Tyr Ile Pro Leu Pro Asp Glu Asp Ser					
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Ala Asp Ile Thr Glu Ile Cys Gln Arg Ala Cys Lys Tyr Ala Ile Arg					
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Glu Asn Ile Glu Lys Asp Ile Glu Lys Glu Lys Arg Arg Ser Glu Asn					
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Ala Ala His Phe Glu Glu Ser Met Lys Tyr Ala Arg Arg Ser Val Ser					
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Asp Ala Asp Ile Arg Lys Tyr Gln Ala Phe Ala Gln Thr Leu Gln Gln					
tct aga ggg ttt ggt tct gag ttc agg ttc gag act aat gct ggt tca					2352
Ser Arg Gly Phe Gly Ser Glu Phe Arg Phe Glu Thr Asn Ala Gly Ser					
ggt gca acc act gga gtc gct gat cct ttt gcc acc tct gca gct gct					2400
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Glu	Ile	Asp	Ile	Gly	Val	Pro	Asp	Glu	Ile	Gly	Arg	Leu	Glu	Val	Leu
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Arg	Ile	Ser	Lys	Asp	Thr	His	Gly	Tyr	Val	Gly	Ala	Asp	Leu	Ala	Ala
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Asn	Val	Arg	Glu	Ile	Phe	Asp	Lys	Ala	Arg	Gln	Ser	Ala	Pro	Cys	Val
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 690 700
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 740 745 750
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 755 760 765
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ctctcgagct cggcggcctc ccccttaggg cagaagcgga cgaggcga atg gaa gag 177
 Met Glu Glu
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gtt agg ggc agg gag agc aaa gac cac cgc ggc ggc ggc ggc ggc ggc 225
 Val Arg Gly Arg Glu Ser Lys Asp His Arg Gly Gly Gly Gly Gly Gly
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gga ggt gat ggg gac ggc gag cgg acg gga cgg tgg cgc gcc gag gag 273
 Gly Gly Asp Gly Asp Gly Glu Arg Thr Gly Arg Trp Arg Ala Glu Glu
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 Val Ile Ala Gly Asn Arg Ala Val Leu Glu Ala Leu Arg Glu Leu Val
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atg tat cct gtc ctc tac gca cgg gag gcc cgc gtg ctc ggc ctc aat 369
 Met Tyr Pro Val Leu Tyr Ala Arg Glu Ala Arg Val Leu Gly Leu Asn
 55 60 65

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 Phe Pro Arg Gly Leu Leu Leu His Gly Pro Ser Gly Thr Gly Lys Lys
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agc atg gtc cga gct gtt gtt cga gaa tgt aat gcc cac ctc aca gtg 465
 Ser Met Val Arg Ala Val Val Arg Glu Cys Asn Ala His Leu Thr Val
 85 90 95

att gat tca att tct gtg cat aaa ccc cac gct gga gag ggg gag aag 513
 Ile Asp Ser Ile Ser Val His Lys Pro His Ala Gly Glu Gly Glu Lys
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 Phe Met Arg Glu Ala Phe Thr Glu Ala Tyr Ser Gln Ala Ser Gln Gly
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 Arg Pro Ala Val Ile Phe Ile Asp Glu Leu Asp Asp Ile Cys Pro Pro
 135 140 145

cgt ggc agt agg aga gag caa ggg tcc cgc att gtt ggt cag ctg ttg 657
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PF59082SeqList_PF59082.txt

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Met	Glu	Asp	Trp	Glu	Ser	Ala	Lys	Ser	Val	Ala	Lys	Asn	Ser	Val	Thr	
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Ile	Lys	His	Ala	Ala	Ser	Phe	Asp	Arg	Leu	Gly	Ile	Ser	Pro	Ile	Arg	
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Gly	Val	Leu	Leu	His	Gly	Pro	Pro	Gly	Cys	Ser	Lys	Thr	Thr	Leu	Ala	
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Tyr	Glu	Ile	Leu	Arg	Ile	His	Thr	Arg	Lys	Met	Pro	Leu	Gly	Asp	Asp	
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PF59082SeqList_PF59082.txt

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Ala Leu Arg Ser Leu Arg Pro Ser Leu Thr Gln Ser Val Val Asp Glu
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Tyr Ser Asn Ala Ala Ile His Gly Pro Leu Thr Arg Arg Lys His
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Gly Leu Asn Phe Pro Arg Gly Leu Leu Leu His Gly Pro Ser Gly Thr
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Gly Lys Lys Ser Met Val Arg Ala Val Val Arg Glu Cys Asn Ala His
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Cys Pro Pro Arg Gly Ser Arg Arg Glu Gln Gly Ser Arg Ile Val Gly
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Gln Leu Leu Thr Leu Met Asp Gly Lys Ser Ser Lys Leu Leu Pro His
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Leu Val Val Val Ala Ser Ala Thr Arg Val Asp Ala Ile Glu Ser Ala
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Leu Arg Arg Pro Gly Arg Phe Asp Ser Glu Ile Glu Val Thr Val Pro
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PF59082SeqList_PF59082.txt

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 Ile Phe Phe Asp Glu Ala Asp Ala Ile Ala Pro Lys Arg Thr Gly Pro
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PF59082SeqList_PF59082.txt

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Pro	Asp	Ile	Lys	Tyr	Ala	Lys	Arg	Ile	Ala	Val	Leu	Pro	Met	Ala	Asp	
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Tyr	Phe	Arg	Glu	Ala	Tyr	Arg	Pro	Leu	Arg	Gln	Gly	Asp	Leu	Phe	Thr	
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Gly	Glu	Ser	Glu	Ser	Asn	Ile	Arg	Asp	Ile	Phe	Asp	Lys	Ala	Arg	Ala	
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Ala	Ala	Pro	Cys	Val	Val	Phe	Leu	Asp	Glu	Leu	Asp	Ser	Ile	Ala	Lys	
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Ser	Arg	Gly	Gly	Ser	Gln	Gly	Asp	Ala	Gly	Gly	Ala	Ser	Asp	Arg	Val	
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Val	Asn	Gln	Leu	Leu	Thr	Glu	Met	Asp	Gly	Met	Thr	Ser	Lys	Lys	Asn	
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Leu	Cys	Arg	Pro	Gly	Arg	Leu	Asp	Thr	Leu	Val	Tyr	Val	Pro	Leu	Pro	
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Asp	Gln	Pro	Gly	Arg	Glu	Ser	Ile	Leu	Lys	Ala	Gln	Leu	Arg	Lys	Thr	
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Pro	Val	Ala	Lys	Asp	Val	Asp	Leu	Ser	Tyr	Ile	Ala	Ser	Lys	Thr	His	
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Arg	Glu	Ala	Ala	Glu	Gly	Asp	Asp	Thr	Lys	Met	Asp	Glu	Asp	Val	Asp	
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Met	Ser	Met	Ala	Arg	Arg	Ser	Val	Thr	Asp	Thr	Glu	Ile	Arg	Arg	Tyr	
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gag	gcc	ttc	gcg	cag	agg	atg	aag	aac	agg	gct	ggc	ggc	agg	gct	ttc	2581
Glu	Ala	Phe	Ala	Gln	Ser	Met	Lys	Asn	Ser	Ala	Gly	Gly	Ser	Ala	Phe	
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Phe	Arg	Phe	Pro	Glu	Gly	Gly	Ala	Glu	Gly	Ala	Ala	Ala	Glu	Ala	Gln	
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Gln	Asn	Gly	Ala	Gly	Glu	Glu	Asp	Leu	Tyr	Asp						
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 Gly Ile Val Ala Gln Asp Thr Val Ile His Cys Glu Gly Glu Pro Ile
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Met His Pro Gln Thr Met Glu Lys Leu Gln	
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Leu Phe Arg Gly Asp Thr Ile Leu Ile Lys Gly Lys Lys Arg Lys Asp	
15 20 25	
acc att tgc ata gct ctt gct gat gag aac tgt gag gag ccg aag atc	329
Thr Ile Cys Ile Ala Leu Ala Asp Glu Asn Cys Glu Glu Pro Lys Ile	
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agg atg aat aaa gtt gtg agg tca aat ttg cgg gtt cgg ctt gga gat	377
Arg Met Asn Lys Val Val Arg Ser Asn Leu Arg Val Arg Leu Gly Asp	
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Val Val Ser Val His Gln Cys Pro Asp Val Lys Tyr Gly Lys Arg Val	
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His Ile Leu Pro Ile Asp Asp Thr Ile Glu Gly Val Thr Gly Asn Leu	
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Phe Asp Ala Phe Leu Lys Pro Tyr Phe Leu Glu Ala Tyr Arg Pro Val	
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Arg Lys Gly Asp Leu Phe Leu Val Arg Gly Gly Met Arg Ser Val Glu	
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Phe Lys Val Val Glu Thr Asp Pro Gly Glu Tyr Cys Val Val Ala Pro	
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Asp Thr Glu Ile Phe Cys Glu Gly Glu Pro Leu Lys Arg Glu Asp Glu	
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Glu Arg Leu Asp Glu Val Gly Tyr Asp Asp Val Gly Gly Val Arg Lys	
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Gln Leu Phe Lys Ser Ile Gly Val Lys Pro Pro Lys Gly Ile Leu Leu	
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Tyr Gly Pro Pro Gly Ser Gly Lys Thr Leu Ile Ala Arg Ala Val Ala	
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Asn Glu Thr Gly Ala Phe Phe Phe Cys Ile Asn Gly Pro Glu Ile Met	
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Glu Ala Glu Lys Asn Ala Pro Ser Ile Ile Phe Ile Asp Glu Ile Asp	
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Ser Ile Ala Pro Lys Arg Glu Lys Thr His Gly Glu Val Glu Arg Arg	
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Ile Val Ser Gln Leu Leu Thr Leu Met Asp Gly Leu Lys Ser Arg Ala	
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His Val Ile Val Ile Gly Ala Thr Asn Arg Pro Asn Ser Ile Asp Pro	
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gca ttg aga agg ttt ggt aga ttt gat agg gaa att gat att ggt gtt	1193
Ala Leu Arg Arg Phe Gly Arg Phe Asp Arg Glu Ile Asp Ile Gly Val	
315 320 325 330	
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His	Gly	Tyr	Val	Gly	Ala	Asp	Leu	Ala	Ala	Leu	Cys	Thr	Glu	Ala	Ala	
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Leu	Gln	Cys	Ile	Arg	Glu	Lys	Met	Asp	Val	Ile	Asp	Leu	Glu	Asp	Glu	
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Thr	Ile	Asp	Ala	Glu	Val	Leu	Asn	Ser	Met	Ala	Val	Thr	Asn	Glu	His	
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Phe	Gln	Thr	Ala	Leu	Gly	Thr	Ser	Asn	Pro	Ser	Ala	Leu	Arg	Glu	Thr	
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Val	Val	Glu	Val	Pro	Asn	Val	Ser	Trp	Glu	Asp	Ile	Gly	Gly	Leu	Glu	
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Asn	Val	Lys	Arg	Glu	Leu	Gln	Glu	Thr	Val	Gln	Tyr	Pro	Val	Glu	His	
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Pro	Glu	Lys	Phe	Glu	Lys	Phe	Gly	Met	Ser	Pro	Ser	Lys	Gly	Val	Leu	
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Phe	Tyr	Gly	Pro	Pro	Gly	Cys	Gly	Lys	Thr	Leu	Leu	Ala	Lys	Ala	Ile	
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Ala	Asn	Glu	Cys	Gln	Ala	Asn	Phe	Ile	Ser	Val	Lys	Gly	Pro	Glu	Leu	
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Leu	Thr	Met	Trp	Phe	Gly	Glu	Ser	Glu	Ala	Asn	Val	Arg	Glu	Ile	Phe	
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Asp	Ser	Ile	Ala	Thr	Gln	Arg	Gly	Ser	Ser	Val	Gly	Asp	Ala	Gly	Gly	
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Gln	Arg	Ala	Cys	Lys	Tyr	Ala	Ile	Arg	Glu	Asn	Ile	Glu	Lys	Asp	Ile	
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Glu	Arg	Glu	Arg	Lys	Ser	Arg	Glu	Asn	Pro	Glu	Ala	Met	Asp	Glu	Asp	
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Thr	Val	Asp	Asp	Glu	Val	Ala	Glu	Ile	Lys	Ala	Ala	His	Phe	Glu	Glu	
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PF59082SeqList_PF59082.txt

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Tyr	Gln	Ala	Phe	Ala	Gln	Thr	Leu	Gln	Gln	Ser	Arg	Gly	Phe	Gly	Ser		
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Glu	Phe	Arg	Phe	Pro	Glu	Ser	Gly	Asp	Arg	Thr	Thr	Thr	Gly	Ser	Asp		
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Pro	Phe	Ala	Ala	Ser	Ala	Gly	Gly	Ala	Asp	Glu	Asp	Asp	Leu	Tyr	Ser		
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PF59082SeqList_PF59082.txt

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 370 375 380
 Lys Met Asp Val Ile Asp Leu Glu Asp Glu Thr Ile Asp Ala Glu Val
 385 390 395 400
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 Thr Ser Asn Pro Ser Ala Leu Arg Glu Thr Val Val Glu Val Pro Asn
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 Val Ser Trp Glu Asp Ile Gly Gly Leu Glu Asn Val Lys Arg Glu Leu
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 Gln Glu Thr Val Gln Tyr Pro Val Glu His Pro Glu Lys Phe Glu Lys
 450 455 460
 Phe Gly Met Ser Pro Ser Lys Gly Val Leu Phe Tyr Gly Pro Pro Gly
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 Cys Gly Lys Thr Leu Ala Lys Ala Ile Ala Asn Glu Cys Gln Ala
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 Glu Ser Glu Ala Asn Val Arg Glu Ile Phe Asp Lys Ala Arg Gln Ser
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 Arg Gly Ser Ser Val Gly Asp Ala Gly Gly Ala Ala Asp Arg Val Leu
 545 550 555 560
 Asn Gln Leu Leu Thr Glu Met Asp Gly Met Ser Ala Lys Lys Thr Val
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 Phe Ile Ile Gly Ala Thr Asn Arg Pro Asp Ile Ile Asp Pro Ala Leu
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 Leu Arg Pro Gly Arg Leu Asp Gln Leu Ile Tyr Ile Pro Leu Pro Asp
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 Glu Asp Ser Arg His Gln Ile Phe Lys Ala Cys Leu Arg Lys Ser Pro
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 Seite 865

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PF59082SeqList_PF59082.txt

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Met Glu Lys Leu Gln Leu

ttc cga ggg gac act atc ctc atc aag ggt aag aaa cgg aag gat acc 284
Phe Arg Gly Asp Thr Ile Leu Ile Lys Gly Lys Lys Arg Lys Asp Thr

att tgc ata gct ctt gct gat gag aac tgt gag gag ccg aag atc agg 332
Ile Cys Ile Ala Leu Ala Asp Glu Asn Cys Glu Glu Pro Lys Ile Arg

atg aat aaa gtt gtg agg tca aat ttg cgg gtt cgg ctt gga gat gtt 380
Met Asn Lys Val Val Arg Ser Asn Leu Arg Val Arg Leu Gly Asp Val

gtg tct gtg cac cag tgc ccg gat gtt aaa tat ggg aaa cgt gtg cac 428
Val Ser Val His Gln Cys Pro Asp Val Lys Tyr Gly Lys Arg Val His

att ctg cct att gat gat acc att gaa ggt gtc act ggc aat ctg ttt 476
Ile Leu Pro Ile Asp Asp Thr Ile Glu Gly Val Thr Gly Asn Leu Phe

gat gct ttc ttg aaa ccc tat ttc ttg gaa gct tac cgt cct gtc aga 524
Asp Ala Phe Leu Lys Pro Tyr Phe Leu Glu Ala Tyr Arg Pro Val Arg

aaa gga gat cta ttt ctt gtc cgg gga ggg atg aga agt gta gag ttc 572
Lys Gly Asp Leu Phe Leu Val Arg Gly Gly Met Arg Ser Val Glu Phe

aag gtg gtt gaa acc gat cct gga gaa tat tgt gtt gtt gct cca gac 620
Lys Val Val Glu Thr Asp Pro Gly Glu Tyr Cys Val Val Ala Pro Asp

act gaa att ttc tgt gag ggg gag cct ttg aaa aga gaa gat gaa gag 668
Thr Glu Ile Phe Cys Glu Gly Glu Pro Leu Lys Arg Glu Asp Glu Glu

aga ctg gat gaa gtc ggg tat gat gat gtg ggt ggt gtc agg aaa caa 716
Arg Leu Asp Glu Val Gly Tyr Asp Asp Val Gly Gly Val Arg Lys Gln

atg gct cag att cgt gag ttg gtt gag ctt cca ttg agg cat cca cag 764
Met Ala Gln Ile Arg Glu Leu Val Glu Leu Pro Leu Arg His Pro Gln

ctt ttt aaa tca att ggt gtg aaa cca ccc aaa gga att tta ctt tat 812
Leu Phe Lys Ser Ile Gly Val Lys Pro Pro Lys Gly Ile Leu Leu Tyr

gga ccc cca ggt tct ggg aag aca tta ata gca aga gct gta gct aat 860
Gly Pro Pro Gly Ser Gly Lys Thr Leu Ile Ala Arg Ala Val Ala Asn

gaa act gga gct ttt ttc ttt tgt att aac gga cca gag att atg tcc 908
Glu Thr Gly Ala Phe Phe Phe Cys Ile Asn Gly Pro Glu Ile Met Ser

aaa ctt gct gga gag agt gaa agc aat ctc agg aaa gcg ttt gaa gaa 956
Lys Leu Ala Gly Glu Ser Glu Ser Asn Leu Arg Lys Ala Phe Glu Glu

gca gaa aag aat gca cca tcc att atc ttc att gat gaa att gat tcc 1004
Ala Glu Lys Asn Ala Pro Ser Ile Ile Phe Ile Asp Glu Ile Asp Ser

att gcc ccc aag cgg gag aag aca cat ggt gaa gtt gaa agg agg att 1052
Ile Ala Pro Lys Arg Glu Lys Thr His Gly Glu Val Glu Arg Arg Ile

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Val Ser Gln Leu Leu Thr Leu Met Asp Gly Leu Lys Ser Arg Ala His

gtt att gtt att gga gct act aat cgt cca aat agc att gac cca gca 1148
Val Ile Val Ile Gly Ala Thr Asn Arg Pro Asn Ser Ile Asp Pro Ala

ttg aga agg ttt ggt aga ttt gat agg gaa att gat att ggt gtt ccc 1196
Leu Arg Arg Phe Gly Arg Phe Asp Arg Glu Ile Asp Ile Gly Val Pro

gat gaa gtt ggg aga ctt gaa gtc ctt cgc ata cat act aaa aac atg 1244

PF59082SeqList_PF59082.txt

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Lys	Leu	Ser	Asp	Asp	Val	Asp	Leu	Glu	Arg	Ile	Ala	Lys	Asp	Thr	His	
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Gly	Tyr	Val	Gly	Ala	Asp	Leu	Ala	Ala	Leu	Cys	Thr	Glu	Ala	Ala	Leu	
caa	tgc	att	agg	gag	aag	atg	gat	gta	att	gac	ttg	gag	gat	gag	act	1388
Gln	Cys	Ile	Arg	Glu	Lys	Met	Asp	Val	Ile	Asp	Leu	Glu	Asp	Glu	Thr	
att	gat	gca	gaa	gta	ctg	aat	tcc	atg	gca	gtt	aca	aat	gag	cat	ttc	1436
Ile	Asp	Ala	Glu	Val	Leu	Asn	Ser	Met	Ala	Val	Thr	Asn	Glu	His	Phe	
cag	act	gcc	ctt	gga	aca	agc	aac	cca	tca	gct	tta	cgt	gaa	act	gtt	1484
Gln	Thr	Ala	Leu	Gly	Thr	Ser	Asn	Pro	Ser	Ala	Leu	Arg	Glu	Thr	Val	
gtt	gaa	gtg	cct	aat	gtc	agc	tgg	gaa	gac	att	gga	ggc	ctt	gaa	aat	1532
Val	Glu	Val	Pro	Asn	Val	Ser	Trp	Glu	Asp	Ile	Gly	Gly	Leu	Glu	Asn	
gtc	aag	cgt	gaa	ctg	caa	gag	act	gta	caa	tat	cca	ggt	gag	cac	cca	1580
Val	Lys	Arg	Glu	Leu	Gln	Glu	Thr	Val	Gln	Tyr	Pro	Val	Glu	His	Pro	
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Glu	Lys	Phe	Glu	Lys	Phe	Gly	Met	Ser	Pro	Ser	Lys	Gly	Val	Leu	Phe	
tat	ggt	cct	cca	gga	tgt	ggg	aaa	act	ttg	tta	gcc	aaa	gca	att	gct	1676
Tyr	Gly	Pro	Pro	Gly	Cys	Gly	Lys	Thr	Leu	Leu	Ala	Lys	Ala	Ile	Ala	
aat	gaa	tgt	caa	gct	aac	ttc	atc	agt	gtg	aaa	ggt	cca	gaa	ttg	ctt	1724
Asn	Glu	Cys	Gln	Ala	Asn	Phe	Ile	Ser	Val	Lys	Gly	Pro	Glu	Leu	Leu	
aca	atg	tgg	ttt	ggt	gaa	agt	gaa	gct	aat	gtt	aga	gaa	att	ttt	gac	1772
Thr	Met	Trp	Phe	Gly	Glu	Ser	Glu	Ala	Asn	Val	Arg	Glu	Ile	Phe	Asp	
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Lys	Ala	Arg	Gln	Ser	Ala	Pro	Cys	Val	Leu	Phe	Phe	Asp	Glu	Leu	Asp	
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Ser	Ile	Ala	Thr	Gln	Arg	Gly	Ser	Ser	Val	Gly	Asp	Ala	Gly	Gly	Ala	
gct	gat	aga	gtt	cta	aat	caa	ctt	ttg	act	gaa	atg	gat	ggc	atg	tct	1916
Ala	Asp	Arg	Val	Leu	Asn	Gln	Leu	Leu	Thr	Glu	Met	Asp	Gly	Met	Ser	
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Arg	His	Thr	Gln	Gly	Phe	Ser	Gly	Ala	Asp	Ile	Thr	Glu	Ile	Cys	Gln	
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Arg	Ala	Cys	Lys	Tyr	Ala	Ile	Arg	Glu	Asn	Ile	Glu	Lys	Asp	Ile	Glu	
cga	gag	agg	aag	agt	agg	gaa	aac	cct	gag	gcc	atg	gat	gaa	gat	acc	2252
Arg	Glu	Arg	Lys	Ser	Arg	Glu	Asn	Pro	Glu	Ala	Met	Glu	Glu	Asp	Thr	
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Val	Asp	Asp	Glu	Val	Ala	Glu	Ile	Lys	Ala	Ala	His	Phe	Glu	Glu	Ser	
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PF59082SeqList_PF59082.txt

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Phe	Arg	Phe	Pro	Glu	Ser	Gly	Asp	Arg	Thr	Thr	Thr	Gly	Ser	Asp	Pro	
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ttt	gca	gct	tct	gct	ggg	gct	gac	gaa	gat	gat	cta	tat	agt			2489
Phe	Ala	Ala	Ser	Ala	Gly	Gly	Ala	Asp	Glu	Asp	Asp	Leu	Tyr	Ser		
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taact	tttgaa	gcctgt	ctta	tatttt	gctt	ttctt	gtact	caattat	ctc	gaattg	ttac					2609
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Glu	Glu	Pro	Lys	Ile	Arg	Met	Asn	Lys	Val	Val	Arg	Ser	Asn	Leu	Arg	
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Val	Arg	Leu	Gly	Asp	Val	Val	Ser	Val	His	Gln	Cys	Pro	Asp	Val	Lys	
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PF59082SeqList_PF59082.txt

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 Asp Leu Glu Asp Glu Thr Ile Asp Ala Glu Val Leu Asn Ser Met Ala
 385 390 395 400
 Val Thr Asn Glu His Phe Gln Thr Ala Leu Gly Thr Ser Asn Pro Ser
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 420 425 430
 Ile Gly Gly Leu Glu Asn Val Lys Arg Glu Leu Gln Glu Thr Val Gln
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 Tyr Pro Val Glu His Pro Glu Lys Phe Glu Lys Phe Gly Met Ser Pro
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 Ser Lys Gly Val Leu Phe Tyr Gly Pro Pro Gly Cys Gly Lys Thr Leu
 465 470 475 480
 Leu Ala Lys Ala Ile Ala Asn Glu Cys Gln Ala Asn Phe Ile Ser Val
 485 490 495
 Lys Gly Pro Glu Leu Leu Thr Met Trp Phe Gly Glu Ser Glu Ala Asn
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 Val Arg Glu Ile Phe Asp Lys Ala Arg Gln Ser Ala Pro Cys Val Leu
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 Glu Met Asp Gly Met Ser Ala Lys Lys Thr Val Phe Ile Ile Gly Ala
 565 570 575
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 580 585 590
 Leu Asp Gln Leu Ile Tyr Ile Pro Leu Pro Asp Glu Asp Ser Arg His
 595 600 605
 Gln Ile Phe Lys Ala Cys Leu Arg Lys Ser Pro Ile Ala Lys Asn Val
 610 615 620
 Asp Leu Arg Ala Leu Ala Arg His Thr Gln Gly Phe Ser Gly Ala Asp
 625 630 635 640
 Ile Thr Glu Ile Cys Gln Arg Ala Cys Lys Tyr Ala Ile Arg Glu Asn
 645 650 655
 Ile Glu Lys Asp Ile Glu Arg Glu Arg Lys Ser Arg Glu Asn Pro Glu
 660 665 670
 Ala Met Asp Glu Asp Thr Val Asp Asp Glu Val Ala Glu Ile Lys Ala
 675 680 685
 Ala His Phe Glu Glu Ser Met Lys Phe Ala Arg Arg Ser Val Ser Asp
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48

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PF59082SeqList_PF59082.txt

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Asn	Asn	Thr	Met	Glu	Thr	Leu	Gln	Leu	Phe	Arg	Gly	Asp	Thr	Val	Leu
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Val	Lys	Gly	Lys	Lys	Arg	Lys	Asp	Thr	Val	Leu	Ile	Val	Leu	Ala	Asp
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Asn	Leu	Arg	Val	Lys	His	Gly	Asp	Ile	Ile	Thr	Val	His	Pro	Cys	Pro
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gat	atc	aaa	tat	gcc	aag	cgg	att	gcc	gtc	ctt	ccc	att	gca	gac	acc
Asp	Ile	Lys	Tyr	Ala	Lys	Arg	Ile	Ala	Val	Leu	Pro	Ile	Ala	Asp	Thr
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gta	gag	ggt	ctg	act	gga	tcc	ctt	ttc	gac	gtc	tac	ctc	gcc	cca	tac
Val	Glu	Gly	Leu	Thr	Gly	Ser	Leu	Phe	Asp	Val	Tyr	Leu	Ala	Pro	Tyr
	115						120					125			
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Phe	Arg	Glu	Ala	Tyr	Arg	Pro	Val	Lys	Gln	Gly	Asp	Leu	Phe	Thr	Val
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Arg	Gly	Gly	Met	Arg	Gln	Val	Glu	Phe	Lys	Val	Val	Glu	Val	Asp	Pro
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gag	ccc	atc	cag	cgg	gag	gat	gag	gag	ggc	aac	ctg	aac	gag	gtc	ggt
Glu	Pro	Ile	Gln	Arg	Glu	Asp	Glu	Glu	Gly	Asn	Leu	Asn	Glu	Val	Gly
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tat	gac	gat	atc	ggt	ggt	tgc	aga	aag	cag	atg	gca	cag	atc	cg	gaa
Tyr	Asp	Asp	Ile	Gly	Gly	Cys	Arg	Lys	Gln	Met	Ala	Gln	Ile	Arg	Glu
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Leu	Val	Glu	Leu	Pro	Leu	Arg	His	Pro	Gln	Leu	Phe	Lys	Ser	Ile	Gly
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Lys	Thr	Leu	Met	Ala	Arg	Ala	Val	Ala	Asn	Glu	Thr	Gly	Ala	Phe	Phe
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ttc	ctg	atc	aat	ggt	ccc	gaa	atc	atg	tcc	aag	atg	gcc	ggt	gaa	tcc
Phe	Leu	Ile	Asn	Gly	Pro	Glu	Ile	Met	Ser	Lys	Met	Ala	Gly	Glu	Ser
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gag	tcg	aat	ttg	cgc	aag	gcg	ttc	gag	gag	gct	gag	aaa	aac	tct	ccc
Glu	Ser	Asn	Leu	Arg	Lys	Ala	Phe	Glu	Glu	Ala	Glu	Lys	Asn	Ser	Pro
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gcc	att	atc	ttc	att	gac	gaa	atc	gac	tcc	atc	gcg	cct	aag	cgt	gag
Ala	Ile	Ile	Phe	Ile	Asp	Glu	Ile	Asp	Ser	Ile	Ala	Pro	Lys	Arg	Glu
	290					295					300				
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Lys	Thr	Asn	Gly	Glu	Val	Glu	Arg	Arg	Val	Val	Ser	Gln	Leu	Leu	Thr
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ctg	atg	gac	ggc	atg	aag	gct	cgt	tcc	aac	gtc	gtc	gtc	atg	gct	gct
Leu	Met	Asp	Gly	Met	Lys	Ala	Arg	Ser	Asn	Val	Val	Val	Met	Ala	Ala
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Thr	Asn	Arg	Pro	Asn	Ser	Ile	Asp	Pro	Ala	Leu	Arg	Arg	Phe	Gly	Arg
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Phe	Asp	Arg	Glu	Val	Asp	Ile	Gly	Ile	Pro	Asp	Pro	Thr	Gly	Arg	Leu
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Asp 385	Leu	Glu	Thr	Ile	Ala 390	Ala	Glu	Thr	His	Gly 395	Tyr	Val	Gly	Ser	Asp 400	
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Leu	Ala	Ser	Leu	Cys 405	Ser	Glu	Ala	Ala	Met 410	Gln	Gln	Ile	Arg	Glu 415	Lys	
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			420					425					430			
gac	tcc	ctt	ggg	gtt	aca	atg	gag	aac	ttc	cgt	tac	gcc	ctc	ggc	gtt	1344
Asp	Ser	Leu	Gly	Val	Thr	Met	Glu	Asn	Phe	Arg	Tyr	Ala	Leu	Gly	Val	
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tcc	aac	ccc	tct	gct	ctt	cgc	gag	gtt	gct	gtt	gtc	gag	gtt	ccc	aat	1392
Ser	Asn	Pro	Ser	Ala	Leu	Arg	Glu	Val	Ala	Val	Val	Glu	Val	Pro	Asn	
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Val	Arg	Trp	Glu	Asp	Ile	Gly	Gly	Leu	Glu	Glu	Val	Lys	Arg	Glu	Leu	
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Ile	Glu	Ser	Val	Gln	Tyr	Pro	Val	Asp	His	Pro	Glu	Lys	Phe	Gln	Lys	
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Phe	Gly	Leu	Ser	Pro	Ser	Arg	Gly	Val	Leu	Phe	Tyr	Gly	Pro	Pro	Gly	
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Thr	Gly	Lys	Thr	Met	Leu	Ala	Lys	Ala	Val	Ala	Asn	Glu	Cys	Ala	Ala	
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Asn	Phe	Ile	Ser	Val	Lys	Gly	Pro	Glu	Leu	Leu	Ser	Met	Trp	Phe	Gly	
	530					535					540					
gag	tct	gag	agc	aac	atc	cgg	gac	att	ttc	gac	aag	gcc	cgt	gct	gct	1680
Glu	Ser	Glu	Ser	Asn	Ile	Arg	Asp	Ile	Phe	Asp	Lys	Ala	Arg	Ala	Ala	
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gcg	cct	tgc	gtc	gtt	ttc	ctt	gac	gag	ttg	gat	tcg	atc	gcc	aag	tcc	1728
Ala	Pro	Cys	Val	Val	Phe	Leu	Asp	Glu	Leu	Asp	Ser	Ile	Ala	Lys	Ser	
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cgt	ggg	ggc	tcc	gtc	ggg	gac	gct	ggg	ggg	gca	tct	gac	cgt	gtg	gtc	1776
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Asn	Gln	Leu	Leu	Thr	Glu	Met	Asp	Gly	Met	Thr	Ser	Lys	Lys	Asn	Val	
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Phe	Val	Ile	Gly	Ala	Thr	Asn	Arg	Pro	Glu	Gln	Leu	Asp	Ala	Ala	Leu	
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Gln	Ala	Ser	Arg	Glu	Ser	Ile	Leu	Arg	Ala	Gln	Leu	Arg	Lys	Thr	Pro	
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Val	Ala	Pro	Asp	Val	Asp	Ile	Pro	Phe	Ile	Ala	Ser	Lys	Thr	His	Gly	
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Phe	Ser	Gly	Ala	Asp	Leu	Gly	Phe	Val	Thr	Gln	Arg	Ala	Val	Lys	Leu	
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Glu	Ala	Ala	Gly	Glu	Asp	Ile	Lys	Met	Asp	Asp	Glu	Gly	Glu	Glu	Glu	
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gac	ccg	gtg	ccc	cag	ctc	acc	cgt	gct	cac	ttc	gag	gag	gct	atg	aag	2208
Asp	Pro	Val	Pro	Gln	Leu	Thr	Arg	Ala	His	Phe	Glu	Glu	Ala	Met	Lys	
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Ser	Ala	Arg	Arg	Ser	Val	Ser	Asp	Val	Glu	Ile	Arg	Arg	Tyr	Glu	Ala	
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 Pro Ser Ser Gly Glu Ile Gln Asn Asn Asp Thr Phe Gly Asp Ala Gly
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 Asn Asp Asp Ser Leu Tyr Asp
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2352

2376

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 35 40 45
 Val Lys Gly Lys Lys Arg Lys Asp Thr Val Leu Ile Val Leu Ala Asp
 50 55 60
 Asp Asp Leu Asp Asp Gly Ser Ala Arg Ile Asn Arg Val Val Arg His
 65 70 75 80
 Asn Leu Arg Val Lys His Gly Asp Ile Ile Thr Val His Pro Cys Pro
 85 90 95
 Asp Ile Lys Tyr Ala Lys Arg Ile Ala Val Leu Pro Ile Ala Asp Thr
 100 105 110
 Val Glu Gly Leu Thr Gly Ser Leu Phe Asp Val Tyr Leu Ala Pro Tyr
 115 120 125
 Phe Arg Glu Ala Tyr Arg Pro Val Lys Gln Gly Asp Leu Phe Thr Val
 130 135 140
 Arg Gly Gly Met Arg Gln Val Glu Phe Lys Val Val Glu Val Asp Pro
 145 150 155 160
 Pro Glu Tyr Gly Ile Val Ala Gln Asp Thr Ile Ile His Cys Glu Gly
 165 170 175
 Glu Pro Ile Gln Arg Glu Asp Glu Glu Gly Asn Leu Asn Glu Val Gly
 180 185 190
 Tyr Asp Asp Ile Gly Gly Cys Arg Lys Gln Met Ala Gln Ile Arg Glu
 195 200 205
 Leu Val Glu Leu Pro Leu Arg His Pro Gln Leu Phe Lys Ser Ile Gly
 210 215 220
 Ile Lys Pro Pro Arg Gly Ile Leu Met Tyr Gly Pro Pro Gly Thr Gly
 225 230 235 240
 Lys Thr Leu Met Ala Arg Ala Val Ala Asn Glu Thr Gly Ala Phe Phe
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 Phe Leu Ile Asn Gly Pro Glu Ile Met Ser Lys Met Ala Gly Glu Ser
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 Glu Ser Asn Leu Arg Lys Ala Phe Glu Glu Ala Glu Lys Asn Ser Pro
 275 280 285
 Ala Ile Ile Phe Ile Asp Glu Ile Asp Ser Ile Ala Pro Lys Arg Glu
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 Lys Thr Asn Gly Glu Val Glu Arg Arg Val Val Ser Gln Leu Leu Thr
 305 310 315 320
 Leu Met Asp Gly Met Lys Ala Arg Ser Asn Val Val Val Met Ala Ala
 325 330 335
 Thr Asn Arg Pro Asn Ser Ile Asp Pro Ala Leu Arg Arg Phe Gly Arg
 340 345 350
 Phe Asp Arg Glu Val Asp Ile Gly Ile Pro Asp Pro Thr Gly Arg Leu
 355 360 365
 Glu Ile Leu Ser Ile His Thr Lys Asn Met Lys Leu Ala Glu Asp Val
 370 375 380
 Asp Leu Glu Thr Ile Ala Glu Thr His Gly Tyr Val Gly Ser Asp
 385 390 395 400
 Leu Ala Ser Leu Cys Ser Glu Ala Ala Met Gln Gln Ile Arg Glu Lys
 405 410 415
 Met Asp Leu Ile Asp Leu Asp Glu Asp Thr Ile Asp Ala Glu Val Leu
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 Ser Asn Pro Ser Ala Leu Arg Glu Val Ala Val Val Glu Val Pro Asn
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 485 490 495
 Phe Gly Leu Ser Pro Ser Arg Gly Val Leu Phe Tyr Gly Pro Pro Gly
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 Thr Gly Lys Thr Met Leu Ala Lys Ala Val Ala Asn Glu Cys Ala Ala
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 Asn Phe Ile Ser Val Lys Gly Pro Glu Leu Leu Ser Met Trp Phe Gly
 530 535 540
 Glu Ser Glu Ser Asn Ile Arg Asp Ile Phe Asp Lys Ala Arg Ala Ala
 545 550 555 560
 Ala Pro Cys Val Val Phe Leu Asp Glu Leu Asp Ser Ile Ala Lys Ser
 565 570 575
 Arg Gly Gly Ser Val Gly Asp Ala Gly Gly Ala Ser Asp Arg Val Val
 580 585 590
 Asn Gln Leu Leu Thr Glu Met Asp Gly Met Thr Ser Lys Lys Asn Val
 595 600 605
 Phe Val Ile Gly Ala Thr Asn Arg Pro Glu Gln Leu Asp Ala Ala Leu
 610 615 620
 Val Arg Pro Gly Arg Leu Asp Thr Leu Val Tyr Val Pro Leu Pro Asp
 625 630 635 640
 Gln Ala Ser Arg Glu Ser Ile Leu Arg Ala Gln Leu Arg Lys Thr Pro
 645 650 655
 Val Ala Pro Asp Val Asp Ile Pro Phe Ile Ala Ser Lys Thr His Gly
 660 665 670
 Phe Ser Gly Ala Asp Leu Gly Phe Val Thr Gln Arg Ala Val Lys Leu
 675 680 685
 Ala Ile Lys Glu Ser Ile Ala Ala Glu Ile Glu Arg Gln Lys Gln Arg
 690 695 700
 Glu Ala Ala Gly Glu Asp Ile Lys Met Asp Asp Glu Gly Glu Glu Glu
 705 710 715 720
 Asp Pro Val Pro Gln Leu Thr Arg Ala His Phe Glu Glu Ala Met Lys
 725 730 735
 Ser Ala Arg Arg Ser Val Ser Asp Val Glu Ile Arg Arg Tyr Glu Ala
 740 745 750
 Phe Ala Gln Ser Leu Lys Asn Ser Gly Gly Ser Ser Phe Phe Arg Phe
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 Lys Asp Tyr Ser Thr Ala Ile Leu Glu Arg Lys Lys Ser Pro Asn Arg
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 ctg gtg gtg gac gag gcc acc aat gac gac aac tcc gtc gtc gcg ctg 144
 Leu Val Val Asp Glu Ala Thr Asn Asp Asp Asn Ser Val Val Ala Leu
 35 40 45
 cac ccg gac acc atg gag agg ctg cag ctc ttc cgc ggc gac acc gtc 192
 His Pro Asp Thr Met Glu Arg Leu Gln Leu Phe Arg Gly Asp Thr Val
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Asp	Glu	Thr	Cys	Glu	Glu	Pro	Lys	Ile	Arg	Met	Asn	Lys	Val	Val	Arg	
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aag	aac	ctg	agg	gtg	cga	ctt	ggt	gat	gtt	gtt	tct	gtc	cac	cag	tgc	336
Lys	Asn	Leu	Arg	Val	Arg	Leu	Gly	Asp	Val	Val	Ser	Val	His	Gln	Cys	
		100						105					110			
cag	gat	gtg	aaa	tac	ggg	aaa	cgt	gtg	cac	att	ctt	ccg	att	gat	gat	384
Gln	Asp	Val	Lys	Tyr	Gly	Lys	Arg	Val	His	Ile	Leu	Pro	Ile	Asp	Asp	
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Val	Arg	Gly	Gly	Met	Arg	Ser	Val	Glu	Phe	Lys	Val	Ile	Glu	Thr	Asp	
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Pro	Thr	Glu	Tyr	Cys	Ile	Val	Ala	Pro	Asp	Thr	Glu	Ile	Phe	Cys	Asp	
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Gly	Glu	Pro	Ile	Lys	Arg	Glu	Asp	Glu	Glu	Arg	Leu	Asp	Glu	Val	Gly	
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Glu	Ser	Asn	Leu	Arg	Lys	Ala	Phe	Glu	Glu	Ala	Glu	Lys	Asn	Ala	Pro	
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Thr	Asn	Arg	Pro	Asn	Ser	Ile	Asp	Pro	Ala	Leu	Arg	Arg	Phe	Gly	Arg	
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Asp	Leu	Glu	Leu	Ile	Ala	Lys	Asp	Thr	His	Gly	Tyr	Val	Gly	Ala	Asp	
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Ile	Phe	Asp	Lys	Ala	Arg	Gln	Ser	Ala	Pro	Cys	Val	Leu	Phe	Phe	Asp	
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Glu	Leu	Asp	Ser	Ile	Ala	Thr	Gln	Arg	Gly	Ser	Ser	Val	Gly	Asp	Ala	
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Arg	Ser	Val	Ser	Asp	Ala	Asp	Ile	Arg	Lys	Tyr	Gln	Ala	Phe	Ala	Gln	
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 Leu Ile Tyr Ile Pro Leu Pro Asp Glu Gln Ser Arg Leu Gln Ile Phe
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 675 680 685
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 Met Ala Ser Gln

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 Gly Glu Pro Ser Ala Ser Ala Ser Asp Pro Lys Glu Lys Lys Asp Tyr
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Thr	Met	Glu	Arg	Leu	Gln	Leu	Phe	Arg	Gly	Asp	Thr	Val	Leu	Leu	Lys	
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Gly	Lys	Lys	Arg	Lys	Asp	Thr	Val	Cys	Ile	Val	Leu	Ala	Asp	Glu	Thr	
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Cys	Glu	Glu	Pro	Lys	Val	Arg	Met	Asn	Lys	Val	Val	Arg	Gln	Asn	Leu	
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Lys	Tyr	Gly	Lys	Arg	Val	His	Ile	Leu	Pro	Ile	Asp	Asp	Thr	Val	Glu	
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Gly	Ile	Thr	Gly	Asn	Leu	Phe	Asp	Ala	Phe	Leu	Lys	Pro	Tyr	Phe	Leu	
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Glu	Ala	Tyr	Arg	Pro	Val	Arg	Lys	Gly	Asp	Leu	Phe	Leu	Val	Arg	Gly	
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Tyr	Cys	Ile	Val	Ala	Pro	Asp	Thr	Glu	Ile	Phe	Cys	Asp	Gly	Glu	Pro	
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Ile	Lys	Arg	Glu	Asp	Glu	Glu	Arg	Leu	Asp	Glu	Val	Gly	Tyr	Asp	Asp	
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Pro	Lys	Gly	Ile	Leu	Leu	Tyr	Gly	Pro	Pro	Gly	Ser	Gly	Lys	Thr	Leu	
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Ile	Ala	Arg	Ala	Val	Ala	Asn	Glu	Thr	Gly	Ala	Phe	Phe	Phe	Leu	Ile	
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Asn	Gly	Pro	Glu	Ile	Met	Ser	Lys	Leu	Ala	Gly	Glu	Ser	Glu	Ser	Asn	
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Gly	Glu	Val	Glu	Arg	Arg	Ile	Val	Ser	Gln	Leu	Leu	Thr	Leu	Met	Asp	
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Arg	Gly	Phe 775	Gly	Ser	Glu	Phe	Arg 780	Phe	Ser	Glu	Gln	Ser 785	Ala	Thr	Ala	
ggt	gct	gct	gca	gcc	gat	ccg	ttt	gct	tcg	gct	ggt	gct	gcg	gct	gac	2515
Gly	Ala	Ala	Ala	Ala	Asp	Pro	Phe 795	Ala	Ser	Ala	Gly 800	Ala	Ala	Ala	Asp	
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Asp	Asp	Asp	Leu	Tyr	Ser 810											
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Arg	Leu	Val 35	Val	Asp	Glu	Ala	Thr 40	Asn	Asp	Asp	Asn	Ser 45	Val	Val	Ala	
Leu	His 50	Pro	Asp	Thr	Met	Glu 55	Arg	Leu	Gln	Leu	Phe 60	Arg	Gly	Asp	Thr	
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Cys	Gln	Asp 115	Val	Lys	Tyr	Gly	Lys 120	Arg	Val	His	Ile	Leu 125	Pro	Ile	Asp	
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PF59082SeqList_PF59082.txt

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Phe Gly Met Ser Pro Ser Lys Gly Val Leu Phe Tyr Gly Pro Pro Gly
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725 730 735
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740 745 750
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755 760 765
Leu Gln Gln Ser Arg Gly Phe Gly Ser Glu Phe Arg Phe Ser Glu Gln
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<212> DNA

<213> Oryza sativa (japonica cultivar-group)

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Lys Asp Tyr Ser Thr Ala Ile Leu Glu Arg Lys Lys Ser Pro Asn Arg
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ctg gtg gtg gac gag gcc acc aat gac gac aac tcc gtc gtc gcg ctg      144
Leu Val Val Asp Glu Ala Thr Asn Asp Asp Asn Ser Val Val Ala Leu
35 40 45
cac ccg gac acc atg gag agg ctg cag ctc ttc cgc ggc gac acc gtc      192
His Pro Asp Thr Met Glu Arg Leu Gln Leu Phe Arg Gly Asp Thr Val
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ctc ctc aag ggc aag aag agg aaa gat act att tgc att gtc ctt gcg      240
Leu Leu Lys Gly Lys Lys Arg Lys Asp Thr Ile Cys Ile Val Leu Ala
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Tyr Phe Leu Glu Ala Tyr Arg Pro Val Arg Lys Gly Asp Leu Phe Leu
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gtc agg ggt gga atg aga agt gtg gaa ttc aaa gtc ata gag act gac      528
Val Arg Gly Gly Met Arg Ser Val Glu Phe Lys Val Ile Glu Thr Asp
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Pro Thr Glu Tyr Cys Ile Val Ala Pro Asp Thr Glu Ile Phe Cys Asp
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Ser	Glu	Phe	Arg	Phe	Glu	Arg	Thr	Glu	Ala	Gly	Ala	Gly	Ala	Ala	Ala	
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<213> Oryza sativa (japonica cultivar-group)

<400> 692

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Ser	Ile	Ile	Phe	Ile	Asp	Glu	Ile	Asp	Ser	Ile	Ala	Pro	Lys	Arg	Glu	
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Lys	Thr	Asn	Gly	Glu	Val	Glu	Arg	Arg	Ile	Val	Ser	Gln	Leu	Leu	Thr	
			325					330					335			

PF59082SeqList_PF59082.txt

Leu Met Asp Gly Leu Lys Ala Arg Ser His Val Ile Val Met Gly Ala
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 Thr Asn Arg Pro Asn Ser Ile Asp Pro Ala Leu Arg Arg Phe Gly Arg
 355 360 365
 Phe Asp Arg Glu Ile Asp Ile Gly Val Pro Asp Glu Val Gly Arg Leu
 370 375 380
 Glu Val Leu Arg Ile His Thr Lys Asn Met Lys Leu Ala Glu Asp Val
 385 390 395 400
 Asp Leu Glu Leu Ile Ala Lys Asp Thr His Gly Tyr Val Gly Ala Asp
 405 410 415
 Leu Ala Ala Leu Cys Thr Glu Ala Ala Leu Gln Cys Ile Arg Glu Lys
 420 425 430
 Met Asp Ile Ile Asp Leu Glu Asp Glu Thr Ile Asp Ala Glu Ile Leu
 435 440 445
 Asn Ser Met Ala Val Thr Asn Asp His Phe Lys Thr Ala Leu Gly Thr
 450 455 460
 Ser Asn Pro Ser Ala Leu Arg Glu Thr Val Val Glu Val Pro Asn Val
 465 470 475 480
 Ser Trp Glu Asp Ile Gly Gly Leu Glu Asn Val Lys Arg Glu Leu Gln
 485 490 495
 Glu Pro Ile Tyr Val Leu Glu Phe Leu Gln Thr Val Gln Tyr Pro Val
 500 505 510
 Glu His Pro Glu Lys Phe Glu Lys Phe Gly Met Ser Pro Ser Lys Gly
 515 520 525
 Val Leu Phe Tyr Gly Pro Pro Gly Cys Gly Lys Thr Leu Leu Ala Lys
 530 535 540
 Ala Ile Ala Asn Glu Cys Gln Ala Asn Phe Ile Ser Val Lys Gly Pro
 545 550 555 560
 Glu Leu Leu Thr Met Trp Phe Gly Glu Ser Glu Ala Asn Val Arg Glu
 565 570 575
 Ile Phe Asp Lys Ala Arg Gln Ser Ala Pro Cys Val Leu Phe Phe Asp
 580 585 590
 Glu Leu Asp Ser Ile Ala Thr Gln Arg Gly Ser Ser Val Gly Asp Ala
 595 600 605
 Gly Gly Ala Ala Asp Arg Val Leu Asn Gln Leu Leu Thr Glu Met Asp
 610 615 620
 Gly Met Asn Ala Lys Lys Thr Val Phe Ile Ile Gly Ala Thr Asn Arg
 625 630 635 640
 Pro Asp Ile Ile Asp Pro Ala Leu Leu Arg Pro Gly Arg Leu Asp Gln
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 Leu Ile Tyr Ile Pro Leu Pro Asp Glu Gln Ser Arg Leu Gln Ile Phe
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 Lys Ala Cys Leu Arg Lys Ser Pro Val Ala Lys Asp Val Asp Leu Asn
 675 680 685
 Ala Leu Ala Lys Tyr Thr Gln Gly Phe Ser Gly Ala Asp Ile Thr Glu
 690 695 700
 Ile Cys Gln Arg Ala Cys Lys Tyr Ala Ile Arg Glu Asn Ile Glu Lys
 705 710 715 720
 Asp Ile Glu Arg Glu Arg Arg Ser Lys Glu Asn Pro Glu Ala Met Glu
 725 730 735
 Glu Asp Glu Val Asp Asp Ile Ala Glu Ile Lys Ala Ala His Phe Glu
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 Glu Ser Met Lys Tyr Ala Arg Arg Ser Val Ser Asp Ala Asp Ile Arg
 755 760 765
 Lys Tyr Gln Ala Phe Ala Gln Thr Leu Gln Gln Ser Arg Gly Phe Gly
 770 775 780
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<210> 693

<211> 1737

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

PF59082SeqList_PF59082.txt

<221> CDS

<222> (1)..(1737)

<400> 693

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Gly Gly Gly Gly Gly Asp Gly Asp Gly Glu Arg Thr Gly Arg Trp Arg	
20 25 30	
gcc gag gag gtc atc gct ggg aac cgc gcg gtt ctg gag gct ctc cgc	144
Ala Glu Glu Val Ile Ala Gly Asn Arg Ala Val Leu Glu Ala Leu Arg	
35 40 45	
gag ctc gtg atg tat cct gtc ctc tac gca cgg gag gcc cgc gtg ctc	192
Glu Leu Val Met Tyr Pro Val Leu Tyr Ala Arg Glu Ala Arg Val Leu	
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ggc ctc aat ttt ccc aga gga ttg ctg ctc cac ggc ccc tct ggc act	240
Gly Leu Asn Phe Pro Arg Gly Leu Leu Leu His Gly Pro Ser Gly Thr	
65 70 75 80	
gga aag aaa agc atg gtc cga gct gtt gtt gga tgt aat gcc cac	288
Gly Lys Lys Ser Met Val Arg Ala Val Val Arg Glu Cys Asn Ala His	
85 90 95	
ctc aca gtg att gat tca att tct gtg cat aaa ccc cac gct gga gag	336
Leu Thr Val Ile Asp Ser Ile Ser Val His Lys Pro His Ala Gly Glu	
100 105 110	
ggg gag aag ttc atg cga gag gct ttt act gaa gca tat tcc cag gca	384
Gly Glu Lys Phe Met Arg Glu Ala Phe Thr Glu Ala Tyr Ser Gln Ala	
115 120 125	
tca cag ggt aga cca gcc gtg ata ttc att gat gaa ctt gat gac ata	432
Ser Gln Gly Arg Pro Ala Val Ile Phe Ile Asp Glu Leu Asp Asp Ile	
130 135 140	
tgt cca ccg cgt ggc agt agg aga gag caa ggg tcc cgc att gtt ggt	480
Cys Pro Pro Arg Gly Ser Arg Arg Glu Gln Gly Ser Arg Ile Val Gly	
145 150 155 160	
cag ctg ttg act ctg atg gac ggg aag tca aag ctg ctt ccc cac	528
Gln Leu Leu Thr Leu Met Asp Gly Lys Ser Ser Lys Leu Leu Pro His	
165 170 175	
cta gtt gtt gtt gca tct gct acc agg gtg gat gct att gag tca gca	576
Leu Val Val Val Ala Ser Ala Thr Arg Val Asp Ala Ile Glu Ser Ala	
180 185 190	
ctg cga agg cct ggg cgt ttt gac tca gag ata gag gtt act gtt cct	624
Leu Arg Arg Pro Gly Arg Phe Asp Ser Glu Ile Glu Val Thr Val Pro	
195 200 205	
aca gca gaa gaa agg ttc gag att ctt aag ctt tat acc aag aat cta	672
Thr Ala Glu Glu Arg Phe Glu Ile Leu Lys Leu Thr Thr Lys Asn Leu	
210 215 220	
cat ctt ggt gaa tgt gtt gat ctt caa tct gtt gct gca tcc tgc aat	720
His Leu Gly Glu Cys Val Asp Leu Gln Ser Val Ala Ala Ser Cys Asn	
225 230 235 240	
ggg tat gtt gga gct gat tta caa gct tta tgt cga gaa gct gca aga	768
Gly Tyr Val Gly Ala Asp Leu Gln Ala Leu Cys Arg Glu Ala Ala Arg	
245 250 255	
cgt gct tat ggt aga tta tca agc tca tca gag agt gag aat gtg cta	816
Arg Ala Tyr Gly Arg Leu Ser Ser Ser Glu Ser Glu Asn Val Leu	
260 265 270	
acg cta atc atg gag gat tgg gag tct gct aaa tct gtg gcc aaa aat	864
Thr Leu Ile Met Glu Asp Trp Glu Ser Ala Lys Ser Val Ala Lys Asn	
275 280 285	
agt gtg aca aga ggg gta act aaa gaa att cca gct gtt tca tgg gat	912
Ser Val Thr Arg Gly Val Thr Lys Glu Ile Pro Ala Val Ser Trp Asp	
290 295 300	
gat ata gga ggt ttg aaa gct gtt aag aaa aaa ctt cag caa gct gtt	960
Asp Ile Gly Gly Leu Lys Ala Val Lys Lys Lys Leu Gln Gln Ala Val	
305 310 315 320	
gaa tgg ccc atc aag cat gct gct tca ttt gat gat aga ctt gga ata tca	1008
Glu Trp Pro Ile Lys His Ala Ala Ser Phe Asp Arg Leu Gly Ile Ser	
325 330 335	
cct atc cgt ggg gtg cta ttg cat ggt cca cca ggg tgc tca aag act	1056
Pro Ile Arg Gly Val Leu Leu His Gly Pro Pro Gly Cys Ser Lys Thr	

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Ser Gln Gly Arg Pro Ala Val Ile Phe Ile Asp Glu Leu Asp Asp Ile
130 135 140
Cys Pro Pro Arg Gly Ser Arg Arg Glu Gln Gly Ser Arg Ile Val Gly
145 150 155 160
Gln Leu Leu Thr Leu Met Asp Gly Lys Ser Ser Lys Leu Leu Pro His
165 170 175
Leu Val Val Val Ala Ser Ala Thr Arg Val Asp Ala Ile Glu Ser Ala
180 185 190
Leu Arg Arg Pro Gly Arg Phe Asp Ser Glu Ile Glu Val Thr Val Pro
195 200 205
Thr Ala Glu Glu Arg Phe Glu Ile Leu Lys Leu Tyr Thr Lys Asn Leu
210 215 220
His Leu Gly Glu Cys Val Asp Leu Gln Ser Val Ala Ala Ser Cys Asn
225 230 235 240
Gly Tyr Val Gly Ala Asp Leu Gln Ala Leu Cys Arg Glu Ala Ala Arg
245 250 255
Arg Ala Tyr Gly Arg Leu Ser Ser Ser Ser Glu Ser Glu Asn Val Leu
260 265 270
Thr Leu Ile Met Glu Asp Trp Glu Ser Ala Lys Ser Val Ala Lys Asn
275 280 285
Ser Val Thr Arg Gly Val Thr Lys Glu Ile Pro Ala Val Ser Trp Asp
290 295 300
Asp Ile Gly Gly Leu Lys Ala Val Lys Lys Lys Leu Gln Gln Ala Val
305 310 315 320
Glu Trp Pro Ile Lys His Ala Ala Ser Phe Asp Arg Leu Gly Ile Ser
325 330 335
Pro Ile Arg Gly Val Leu Leu His Gly Pro Pro Gly Cys Ser Lys Thr
340 345 350
Thr Leu Ala Lys Ala Ala Ala His Ala Ala Gln Ala Ser Phe Phe Ser
355 360 365
Leu Ser Gly Ala Glu Leu Tyr Ser Lys Tyr Val Gly Glu Gly Glu Ala
370 375 380
Leu Leu Arg Arg Thr Phe Gln Met Ala Arg Leu Ala Ser Pro Ser Ile
385 390 395 400
Ile Phe Phe Asp Glu Ala Asp Ala Ile Ala Pro Lys Arg Thr Gly Pro
405 410 415
Ser Gly Asn Ser Ser Gly Asn Ala Thr Val Gly Glu Arg Leu Leu Ser
420 425 430
Thr Leu Leu Thr Glu Met Asp Gly Leu Glu Leu Ala Thr Gly Ile Ile
435 440 445
Val Leu Ala Ala Thr Asn Arg Pro Asn Ala Ile Asp Ala Ala Leu Leu
450 455 460
Arg Pro Gly Arg Phe Asp Met Val Leu Tyr Val Pro Pro Pro Asp Ala
465 470 475 480
Glu Gly Arg Tyr Glu Ile Leu Arg Ile His Thr Arg Lys Met Pro Leu
485 490 495
Gly Asp Asp Val Asp Leu Trp Lys Val Ala Glu Arg Thr Glu Leu Phe
500 505 510
Thr Gly Ala Asp Leu Glu Gly Leu Cys Arg Glu Ala Gly Met Ala Ala
515 520 525
Leu Arg Glu Ser Leu Arg Ser Glu Arg Phe Val Cys Asp Asp Ile His
530 535 540
Phe Gln Ala Ala Leu Arg Ser Leu Arg Pro Ser Leu Thr Gln Ser Val
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Val Asp Glu Tyr Ser Asn Ala Ala Ile His Gly Pro Leu Thr Arg Arg
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Lys His

<210> 695

<211> 2547

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<221> CDS

<222> (1)..(2547)

<400> 695

PF59082SeqList_PF59082.txt

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tac	agc	acg	gcg	atc	ctg	gag	tgc	gcc	aag	aag	aag	tcc	ccg	aac	cgg	96
Tyr	Ser	Thr	Ala	Ile	Leu	Glu	Cys	Ala	Lys	Lys	Lys	Ser	Pro	Asn	Arg	
			20					25					30			
ctg	atg	gcg	gac	gac	gcc	gag	ggc	ggg	gtg	gcc	gtc	gac	aac	tcc	acg	144
Leu	Met	Ala	Asp	Asp	Ala	Glu	Gly	Gly	Val	Ala	Val	Asp	Asn	Ser	Thr	
		35				40						45				
gtg	acg	ctc	agc	gag	gag	acc	atg	gag	gag	ctc	ggc	atc	ttc	cgc	ggc	192
Val	Thr	Leu	Ser	Glu	Ala	Thr	Met	Glu	Glu	Leu	Gly	Ile	Phe	Arg	Gly	
	50					55					60					
gac	ctg	gtg	acc	ctc	cgc	ggg	agg	cgg	cgc	cgc	gag	gcc	gtc	tgc	tac	240
Asp	Leu	Val	Thr	Leu	Arg	Gly	Arg	Arg	Arg	Arg	Glu	Ala	Val	Cys	Tyr	
65					70					75					80	
gcg	cag	aag	gac	gag	tgc	tgc	ccc	gac	ggc	cgc	ctc	cgc	ctc	agc	cgc	288
Ala	Gln	Lys	Asp	Glu	Ser	Cys	Pro	Asp	Gly	Arg	Leu	Arg	Leu	Ser	Arg	
				85					90					95		
ggc	gtc	cgc	agc	aac	ctc	cac	gtc	cgc	ctc	ggc	gac	ctc	gtc	acc	gtc	336
Gly	Val	Arg	Ser	Asn	Leu	His	Val	Arg	Leu	Gly	Asp	Leu	Val	Thr	Val	
			100					105					110			
aag	ccg	tgc	ccc	acc	att	agg	aac	gcc	aag	agg	gtg	cag	ctc	cgc	ccc	384
Lys	Pro	Cys	Pro	Thr	Ile	Arg	Asn	Ala	Lys	Arg	Val	Gln	Leu	Arg	Pro	
		115					120					125				
ttc	gac	gac	tct	gtc	gag	ggc	atc	tcc	ggc	gat	ctg	ttc	gag	ccc	tac	432
Phe	Asp	Asp	Ser	Val	Glu	Gly	Ile	Ser	Gly	Asp	Leu	Phe	Glu	Pro	Tyr	
	130					135					140					
ctc	aaa	ccg	tac	ttc	atg	gat	gcg	ttg	cgg	ccg	gtg	aag	aag	ggc	gac	480
Leu	Lys	Pro	Tyr	Phe	Met	Asp	Ala	Leu	Arg	Pro	Val	Lys	Lys	Gly	Asp	
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Arg	Phe	Leu	Val	Arg	Gly	His	Met	His	Ala	Val	Glu	Phe	Lys	Val	Met	
				165					170					175		
gac	acg	gag	ccg	aac	aac	gag	ccc	gtg	atc	gtg	gcg	ggc	gac	acg	gag	576
Asp	Thr	Glu	Pro	Asn	Asn	Glu	Pro	Val	Ile	Val	Ala	Gly	Asp	Thr	Glu	
			180					185					190			
atc	ttc	tgc	gac	gag	ggc	gac	ccg	gtg	aag	cgc	gag	gac	gag	gag	cgg	624
Ile	Phe	Cys	Asp	Glu	Gly	Asp	Pro	Val	Lys	Arg	Glu	Asp	Glu	Glu	Arg	
		195					200					205				
ctc	gac	ggg	ccg	ggc	tac	gac	gac	gtc	ggc	ggc	gtc	aag	cag	ctg		672
Leu	Asp	Gly	Pro	Gly	Tyr	Asp	Asp	Val	Gly	Gly	Val	Arg	Lys	Gln	Leu	
	210					215					220					
gcg	cag	atc	agg	gag	ctc	gtc	gag	ctg	ccc	ctg	cgc	cac	ccc	aag	ctg	720
Ala	Gln	Ile	Arg	Glu	Leu	Val	Glu	Leu	Pro	Leu	Arg	His	Pro	Lys	Leu	
225					230					235					240	
ttc	cag	acg	ctc	ggc	gtg	cgc	ccg	ccc	aag	ggc	atc	ctc	ctc	tac	ggg	768
Phe	Gln	Thr	Leu	Gly	Val	Arg	Pro	Pro	Lys	Gly	Ile	Leu	Leu	Tyr	Gly	
				245					250					255		
ccc	ccc	ggc	acc	ggc	aag	acg	ctg	ctt	gcg	cgc	gcc	atc	gcc	gcc	gag	816
Pro	Pro	Gly	Thr	Gly	Lys	Thr	Leu	Leu	Ala	Arg	Ala	Ile	Ala	Ala	Glu	
			260					265					270			
tcc	ggc	gcc	cac	ttc	gtc	gtc	gtc	aac	ggg	ccg	gag	atc	atg	tcc	ggg	864
Ser	Gly	Ala	His	Phe	Val	Val	Val	Asn	Gly	Pro	Glu	Ile	Met	Ser	Gly	
		275					280					285				
atg	ccc	ggc	gag	agc	gag	gcc	aac	ctg	cgc	gcc	gtg	ttc	gcc	gag	gcg	912
Met	Pro	Gly	Glu	Ser	Glu	Ala	Asn	Leu	Arg	Ala	Val	Phe	Ala	Glu	Ala	
	290					295					300					
gac	gcc	gag	gag	ccg	tcc	atc	gtg	ttc	atg	gac	gag	atc	gac	tcc	atc	960
Asp	Ala	Ala	Ala	Pro	Ser	Ile	Val	Phe	Met	Asp	Glu	Ile	Asp	Ser	Ile	
305					310					315					320	
gcg	ccc	agc	cgc	gag	aag	gcg	cac	ggc	gag	gtg	gag	cgc	cgc	gtc	gtg	1008
Ala	Pro	Ser	Arg	Glu	Lys	Ala	His	Gly	Glu	Val	Glu	Arg	Arg	Val	Val	
				325					330					335		
tcg	cag	ctg	ctc	acg	ctc	atg	gac	ggc	ctc	cgc	ccg	cgg	gcc	cag	gtg	1056
Ser	Gln	Leu	Leu	Thr	Leu	Met	Asp	Gly	Leu	Arg	Pro	Arg	Ala	Gln	Val	
				340				345					350			
atc	gtc	atc	ggc	gcc	acc	aac	cgc	ccc	aac	agc	ctc	gac	ccg	gcg	ctc	1104
Ile	Val	Ile	Gly	Ala	Thr	Asn	Arg	Pro	Asn	Ser	Leu	Asp	Pro	Ala	Leu	
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PF59082SeqList_PF59082.txt																
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gag Glu 385	ctc Leu	ggc Gly	cgc Arg	ctc Leu	gag Glu 390	atc Ile	ctc Leu	cgc Arg	atc Ile	cac His 395	acc Thr	aag Lys	aac Asn	atg Met	ccg Pro 400	1200
ctc Leu	tcc Ser	gac Asp	gac Asp	gtc Val 405	gac Asp	ctc Leu	gag Glu	cgc Arg	gtc Val 410	ggc Gly	aag Lys	gac Asp	acc Thr	cac His 415	ggg Gly	1248
ttc Phe	gtc Val	ggc Gly	tcc Ser 420	gac Asp	ctc Leu	gcc Ala	tcg Ser	ctc Leu 425	tgc Cys	tcc Ser	gag Glu	gcc Ala	gcc Ala 430	atg Met	cag Gln	1296
tgc Cys	atc Ile	cgg Arg 435	gag Glu	aag Lys	ctg Leu	gac Asp	atc Ile 440	atc Ile	gac Asp	atc Ile	gag Glu	aac Asn 445	gac Asp	acc Thr	atc Ile	1344
gac Asp	gtg Val 450	gag Glu	atc Ile	ctc Leu	aac Asn	tcg Ser 455	ctg Leu	acc Thr	gtc Val	acc Thr 460	atg Met	gac Asp	cac His	ctc Leu	aag Lys	1392
ttc Phe 465	gcc Ala	atg Met	gag Glu	gtc Val 470	acc Thr	aag Lys	ccc Pro	tcc Ser	gcc Ala	ctg Leu 475	cgc Arg	gag Glu	acc Thr	ggg Gly	atc Ile 480	1440
gtc Val	gag Glu	gtg Val	ccc Pro	aag Lys 485	gtg Val	tcg Ser	tgg Trp	gac Asp	gac Asp 490	atc Ile	ggc Gly	ggc Gly	ctg Leu	ggc Gly 495	gag Glu	1488
gtc Val	aag Lys	cgc Arg	gag Glu 500	ctc Leu	cag Gln	gag Glu	acg Thr	gtg Val 505	cag Gln	tac Tyr	ccg Pro	gtg Val 510	gag Glu	cac His	ccg Pro	1536
gag Glu	atg Met	ttc Phe 515	gac Asp	ctg Leu	ttt Phe	ggc Gly	atg Met 520	tcg Ser	ccg Pro	tcg Ser	cgc Arg	ggc Gly 525	gtg Val	ctc Leu	ttc Phe	1584
tac Tyr	ggc Gly 530	ccg Pro	ccg Pro	ggg Gly	tgc Cys	ggc Gly 535	aag Lys	acg Thr	atg Met	atg Met	gcc Ala 540	aag Lys	gcc Ala	atc Ile	gcc Ala	1632
aag Lys 545	gag Glu	tgc Cys	aag Lys	gcc Ala	aac Asn 550	ttc Phe	atc Ile	agc Ser	atc Ile	aag Lys 555	ggg Gly	ccc Pro	gag Glu	ctg Leu	ctc Leu 560	1680
acc Thr	atg Met	tgg Trp	ttc Phe	ggc Gly 565	gag Glu	agc Ser	gag Glu	ggc Gly	aac Asn 570	gtc Val	cgc Arg	aac Asn	ctg Leu	ttc Phe 575	gac Asp	1728
aag Lys	gcg Ala	cgg Arg	cag Gln 580	tcg Ser	gcg Ala	ccg Pro	tgc Cys	atc Ile 585	ctc Leu	ttc Phe	ttc Phe	gac Asp 590	gag Glu	ctc Leu	gac Asp	1776
tcc Ser	atc Ile	gcc Ala 595	gtc Val	aag Lys	cgc Arg	ggc Gly	aac Asn 600	agc Ser	gtc Val	ggc Gly	gac Asp	gcc Ala 605	ggc Gly	ggc Gly	acg Thr	1824
ccg Pro 610	gac Asp	cgc Arg	gtg Val	ctc Leu	aac Asn	cag Gln 615	ctg Leu	ctc Leu	acc Thr	gag Glu	atg Met 620	gac Asp	ggc Gly	atc Ile	aac Asn	1872
gcc Ala 625	aag Lys	aag Lys	acg Thr	gtg Val	ttc Phe 630	gtc Val	atc Ile	ggc Gly	gcc Ala	acc Thr 635	aac Asn	cgg Arg	ccg Pro	gac Asp	atc Ile 640	1920
atc Ile	gac Asp	ccg Pro	gcg Ala	atg Met 645	ctc Leu	cgg Arg	ccg Pro	ggc Gly	cgc Arg 650	ctc Leu	gac Asp	cag Gln	ctc Leu	atc Ile 655	tac Tyr	1968
atc Ile	ccg Pro	ctc Leu	ccg Pro	gac Asp 660	gcc Ala	tcg Ser	tcg Ser	cgg Arg 665	ctg Leu	gag Glu	atc Ile	ttc Phe 670	agg Arg	gcg Ala	aac Asn	2016
ctc Leu	cgc Arg	aag Lys 675	gcg Ala	ccc Pro	atg Met	tcc Ser	cgc Arg 680	cac His	gtc Val	gac Asp	ctg Leu	ccg Pro 685	gcc Ala	atg Met	gcc Ala	2064
gcc Ala 690	tcc Ser	acc Thr	gac Asp	ggg Gly	ttc Phe 695	agc Ser	ggc Gly	gcc Ala	gac Asp	atc Ile 700	aag Lys	gag Glu	atc Ile	tgc Cys	cag Gln	2112
cgc Arg 705	gcg Ala	tgc Cys	aag Lys	ctc Leu	gcg Ala 710	gtg Val	cgc Arg	gag Glu	gtg Val 715	gtc Val	cag Gln	aag Lys	agc Ser	acc Thr	ctg Leu 720	2160
gtc Val	ggg Gly	aag Lys	gcc Ala	ctg Leu 725	gca Ala	atg Met	gcg Ala	ggc Gly	gcg Ala 730	gag Glu	ctc Leu	acc Thr	gtg Val	gac Asp 735	cac His	2208

PF59082SeqList_PF59082.txt

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Phe Lys Ser Ala Met Lys His Ala Arg Lys Ser Val Ser Glu Leu Asp	
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gtc atc aag tac gag tac ttc aag cac aag ttc agc ggc ggc atc ccc	2304
Val Ile Lys Tyr Glu Tyr Phe Lys His Lys Phe Ser Gly Gly Ile Pro	
	755
gac gag gag gag gcg ccg gcg acg gag ccg gag ctg ccg gtg gga cag	2352
Asp Glu Glu Glu Ala Pro Ala Thr Glu Pro Glu Leu Pro Val Gly Gln	
	770
ctg agg ttg gtg gcg aag ccg aag acg aag acg aag gcg gag cta gaa	2400
Leu Arg Leu Val Ala Lys Pro Lys Thr Lys Thr Lys Ala Glu Leu Glu	
	785
gca gag gcg gag gct gcg gca aaa gcg aag gcg gag gca gag gcg aag	2448
Ala Glu Ala Glu Ala Ala Lys Ala Lys Ala Glu Ala Glu Ala Lys	
	805
gcg aaa gca aag ctg aag ggg aag gcg gtg gcc gtg gat gac gac	2496
Ala Lys Ala Lys Leu Lys Gly Lys Ala Val Ala Val Asp Asp Asp	
	820
gac gac tct acg tac tcc atg gat tcg atg gac gag gac ttg ctg tat	2544
Asp Asp Ser Thr Tyr Ser Met Asp Ser Met Asp Glu Asp Leu Leu Tyr	
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tag	2547

<210> 696

<211> 848

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<400> 696

Met Ala Asp Ala Asp Val Ser Ser Ser Lys Thr Thr Thr Ala Arg Asp	1	5	10	15
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Val Thr Leu Ser Glu Ala Thr Met Glu Glu Leu Gly Ile Phe Arg Gly	50	55	60	
Asp Leu Val Thr Leu Arg Gly Arg Arg Arg Arg Glu Ala Val Cys Tyr	65	70	75	80
Ala Gln Lys Asp Glu Ser Cys Pro Asp Gly Arg Leu Arg Leu Ser Arg	85	90	95	
Gly Val Arg Ser Asn Leu His Val Arg Leu Gly Asp Leu Val Thr Val	100	105	110	
Lys Pro Cys Pro Thr Ile Arg Asn Ala Lys Arg Val Gln Leu Arg Pro	115	120	125	
Phe Asp Asp Ser Val Glu Gly Ile Ser Gly Asp Leu Phe Glu Pro Tyr	130	135	140	
Leu Lys Pro Tyr Phe Met Asp Ala Leu Arg Pro Val Lys Lys Gly Asp	145	150	155	160
Arg Phe Leu Val Arg Gly His Met His Ala Val Glu Phe Lys Val Met	165	170	175	
Asp Thr Glu Pro Asn Asn Glu Pro Val Ile Val Ala Gly Asp Thr Glu	180	185	190	
Ile Phe Cys Asp Glu Gly Asp Pro Val Lys Arg Glu Asp Glu Glu Arg	195	200	205	
Leu Asp Gly Pro Gly Tyr Asp Asp Val Gly Gly Val Arg Lys Gln Leu	210	215	220	
Ala Gln Ile Arg Glu Leu Val Glu Leu Pro Leu Arg His Pro Lys Leu	225	230	235	240
Phe Gln Thr Leu Gly Val Arg Pro Pro Lys Gly Ile Leu Leu Tyr Gly	245	250	255	
Pro Pro Gly Thr Gly Lys Thr Leu Leu Ala Arg Ala Ile Ala Ala Glu	260	265	270	
Ser Gly Ala His Phe Val Val Val Asn Gly Pro Glu Ile Met Ser Gly	275	280	285	
Met Pro Gly Glu Ser Glu Ala Asn Leu Arg Ala Val Phe Ala Glu Ala	290	295	300	

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Arg	Arg	Phe	Gly	Arg	Phe	Asp	Arg	Glu	Leu	Asp	Ile	Gly	Val	Pro	Asp
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Phe	Val	Gly	Ser	Asp	Leu	Ala	Ser	Leu	Cys	Ser	Glu	Ala	Ala	Met	Gln
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Cys	Ile	Arg	Glu	Lys	Leu	Asp	Ile	Ile	Asp	Ile	Glu	Asn	Asp	Thr	Ile
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Phe	Lys	Ser	Ala	Met	Lys	His	Ala	Arg	Lys	Ser	Val	Ser	Glu	Leu	Asp
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Val	Ile	Lys	Tyr	Glu	Tyr	Phe	Lys	His	Lys	Phe	Ser	Gly	Gly	Ile	Pro
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Ala	Lys	Ala	Lys	Leu	Lys	Gly	Lys	Ala	Val	Ala	Val	Asp	Asp	Asp	Asp
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Phe Ser Thr Ala Ile Leu Glu Lys Lys Lys Ala Ala Asn Arg Leu Val
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gtg gat gaa gcc att aac gat gat aac tcc gtc gtt tct ctt cac cct     144
Val Asp Glu Ala Ile Asn Asp Asp Asn Ser Val Val Ser Leu His Pro
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gat acc atg gag aag cta cag ctt ttt cgt ggt gat act atc tta atc     192
Asp Thr Met Glu Lys Leu Gln Leu Phe Arg Gly Asp Thr Ile Leu Ile
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aag gga aag aag agg aag gat act gtg tgt att gct tta gct gat gag     240
Lys Gly Lys Lys Arg Lys Asp Thr Val Cys Ile Ala Leu Ala Asp Glu
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aca tgt gat gaa cca aaa att aga atg aac aag gtt gtt agg tct aat     288
Thr Cys Asp Glu Pro Lys Ile Arg Met Asn Lys Val Val Arg Ser Asn
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Leu Arg Val Arg Leu Gly Asp Val Ile Ser Val His Gln Cys Pro Asp
      100      105      110
gtc aag tat ggg aac cgt gtt cac atc tta cct tta gat gat acc att     384
Val Lys Tyr Gly Asn Arg Val His Ile Leu Pro Leu Asp Asp Thr Ile
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Glu Gly Val Ser Gly Asn Ile Phe Asp Ala Tyr Leu Lys Pro Tyr Phe
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tta gag gca tat cgt ccg gtg agg aag ggc gat ctt ttc cta gtt aga     480
Leu Glu Ala Tyr Arg Pro Val Arg Lys Gly Asp Leu Phe Leu Val Arg
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Glu Tyr Cys Val Val Ala Pro Asp Thr Glu Ile Phe Cys Glu Gly Glu
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Glu Leu Pro Leu Arg His Pro Gln Leu Phe Lys Ser Ile Gly Val Lys
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cct ccc aaa gga atc ttg ctc tat ggc cct cct ggt tct ggg aag aca     768
Pro Pro Lys Gly Ile Leu Leu Tyr Gly Pro Pro Gly Ser Gly Lys Thr
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Ile Asn Gly Pro Glu Ile Met Ser Lys Leu Ala Gly Glu Ser Glu Ser
      275      280      285      290
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Asn Leu Arg Lys Ala Phe Glu Glu Ala Glu Lys Asn Ala Pro Ser Ile
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PF59082SeqList_PF59082.txt

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Glu	Arg	Val	Ser	Lys	Asp	Thr	His	Gly	Tyr	Val	Gly	Ala	Asp	Leu	Ala	1248
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Ala	Leu	Cys	Thr	Glu	Ala	Ala	Leu	Gln	Cys	Ile	Arg	Glu	Lys	Met	Asp	1296
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Val	Ile	Asp	Leu	Asp	Asp	Glu	Glu	Ile	Asp	Ala	Glu	Ile	Leu	Asn	Ser	1344
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Val	Ser	Trp	Glu	Asp	Ile	Gly	Gly	Leu	Glu	Asn	Val	Lys	Arg	Glu	Leu	
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Phe	Gly	Met	Ser	Pro	Ser	Lys	Gly	Val	Leu	Phe	Tyr	Gly	Pro	Pro	Gly	
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Cys	Gly	Lys	Thr	Leu	Leu	Ala	Lys	Ala	Ile	Ala	Asn	Glu	Cys	Gln	Ala	
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Val	Ala	Lys	Asp	Val	Asp	Leu	Asn	Ala	Leu	Ala	Lys	Tyr	Thr	Gln	Gly	
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<212> PRT

<213> Zea mays

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Pro	Ser	Ile	Ile	Phe	Ile	Asp	Glu	Ile	Asp	Ser	Ile	Ala	Pro	Lys	Arg
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 Asp Tyr Ser Thr Ala Ile Leu Glu Arg Lys Lys Ser Pro Asn Arg Leu
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 Asn Leu Arg Val Arg Leu Gly Asp Val Val Ser Val His Gln Cys Pro
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 Asp Val Lys Tyr Gly Lys Arg Val His Ile Leu Pro Ile Asp Asp Thr
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Asn	Pro	Glu	Ala	Met	Glu	Glu	Asp	Glu	Val	Asp	Asp	Ile	Ala	Glu	Ile	
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<400> 706

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Cys	Val	Leu	Phe	Phe	Asp	Glu	Leu	Asp	Ser	Ile	Ala	Thr	Gln	Arg	Gly
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Ile	Gly	Ala	Thr	Asn	Arg	Pro	Asp	Ile	Ile	Asp	Pro	Ala	Leu	Leu	Arg
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Asn	Pro	Glu	Ala	Met	Glu	Glu	Asp	Glu	Val	Asp	Asp	Ile	Ala	Glu	Ile
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Ser	Asp	Ala	Asp	Ile	Arg	Lys	Tyr	Gln	Ala	Phe	Ala	Gln	Thr	Leu	Gln
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Lys Lys Asp Phe Ser Thr Ala Ile Leu Glu Arg Lys Lys Ser Pro Asn	
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cgc ctt gtc gtc gac gag gcc acc aac gac gat aac tcc gtc gtc gct	144
Arg Leu Val Val Asp Glu Ala Asn Asp Asp Asn Ser Val Val Ala	
35 40 45	
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Leu His Pro Asp Thr Met Glu Arg Leu Gln Leu Phe Arg Gly Asp Thr	
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Val Leu Leu Lys Gly Lys Lys Arg Lys Asp Thr Ile Cys Ile Val Leu	
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Ala Asp Glu Thr Cys Glu Glu Pro Lys Val Arg Met Asn Lys Val Val	
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cgc cag aac cta agg gtg agg ctt ggt gat gtg gtt tct gtc cac cag	336
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Cys Gln Asp Val Lys Tyr Gly Lys Arg Val His Ile Leu Pro Ile Asp	
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Asp Thr Val Glu Gly Ile Thr Gly Asn Leu Phe Asp Ala Phe Leu Lys	
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Gly Val Lys Pro Pro Lys Gly Ile Leu Leu Tyr Gly Pro Pro Gly Ser	
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Gly Lys Thr Leu Ile Ala Arg Ala Val Ala Asn Glu Thr Gly Ala Phe	
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Phe Phe Leu Ile Asn Gly Pro Glu Ile Met Ser Lys Leu Ala Gly Glu	
275 280 285	
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Ser Glu Ser Asn Leu Arg Lys Ala Phe Glu Glu Ala Glu Lys Asn Ala	
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Pro Ser Ile Ile Phe Ile Asp Glu Ile Asp Ser Ile Ala Pro Lys Arg	
305 310 315 320	
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Ser	Val	Ser	Asp	Ala	Asp	Ile	Arg	Lys	Tyr	Gln	Ala	Phe	Ala	Gln	Thr	
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Trp Glu Asp Ile Gly Gly Leu Glu Asn Val Lys Arg Glu Leu Gln Glu
485 490 495
Thr Val Gln Tyr Pro Val Glu His Pro Asp Lys Phe Glu Lys Phe Gly
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Lys Thr Leu Leu Ala Lys Ala Ile Ala Asn Glu Cys Gln Ala Asn Phe
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Pro Gly Arg Leu Asp Gln Leu Ile Tyr Ile Pro Leu Pro Asp Glu Gln
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675 680 685
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Asn Pro Glu Ala Met Glu Glu Asp Glu Val Asp Asp Ile Ala Glu Ile
725 730 735
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755 760 765
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aac cgc ctc gtc gtc gac gag gcc acc aac gat gac aac tcc gtc gtc      144
Asn Arg Leu Val Val Asp Glu Ala Thr Asn Asp Asp Asn Ser Val Val
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Thr Val Leu Leu Lys Gly Lys Lys Arg Lys Asp Thr Ile Cys Ile Val
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Leu Ala Asp Asp Thr Cys Glu Glu Pro Lys Ile Arg Met Asn Lys Thr
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gtc agg aag aac ttg aga gtg cga ctt ggt gac gtg gtg tct gtt cac      336
Val Arg Lys Asn Leu Arg Val Arg Leu Gly Asp Val Val Ser Val His
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Gln Cys Pro Asp Val Lys Tyr Gln Lys Arg Val His Thr Leu Pro Ile
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gat gac aca gtt gaa ggc att act gga aac ttg ttt gac gcg ttc ttg      432
Asp Asp Thr Val Glu Gly Ile Thr Gly Asn Leu Phe Asp Ala Phe Leu
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<223> Xaa in position 57 is Ile or Val

<220>
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<222> (58)..(61)
<223> Xaa in position 58 to 61 is any amino acid

<220>
<221> Variant
<222> (62)..(62)
<223> Xaa in position 62 is Ala or Pro

<220>
<221> Variant
<222> (65)..(65)

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<223> Xaa in position 65 is Gly or Ser

<220>

<221> Variant

<222> (67)..(68)

<223> Xaa in position 67 to 68 is any amino acid

<220>

<221> Variant

<222> (69)..(69)

<223> Xaa in position 69 is Leu or Met

<220>

<221> Variant

<222> (71)..(71)

<223> Xaa in position 71 is any amino acid

<220>

<221> Variant

<222> (72)..(72)

<223> Xaa in position 72 is Ala or Val

<220>

<221> Variant

<222> (74)..(74)

<223> Xaa in position 74 is Ala, Glu or Thr

<400> 722

Glu	Leu	Xaa	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1				5			10				15				
Gly	Xaa	Xaa	Xaa	Pro	Xaa	Gly	Xaa	Leu	Xaa	Xaa	Gly	Pro	Xaa	Gly	Xaa
			20				25				30				
Gly	Lys	Xaa	Xaa	Xaa	Xaa	Arg	Ala	Xaa	Xaa	Xaa	Glu	Xaa	Xaa	Ala	Xaa
		35				40					45				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Glu
	50				55					60					
Xaa	Glu	Xaa	Xaa	Xaa	Arg	Xaa	Xaa	Phe	Xaa	Glu	Ala				
65				70						75					

<210> 723

<211> 37

<212> PRT

<213> Artificial sequence

<220>

<223> protein pattern

<220>

<221> Variant

<222> (2)..(2)

<223> Xaa in position 2 is any amino acid

<220>

<221> Variant

<222> (3)..(3)

<223> Xaa in position 3 is any or no amino acid

<220>

<221> Variant

<222> (5)..(5)

<223> Xaa in position 5 is any or no amino acid

<220>

<221> Variant

<222> (7)..(7)

<223> Xaa in position 7 is Ile or Met

<220>

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<221> Variant
<222> (10)..(10)
<223> Xaa in position 10 is Ile or Leu

<220>
<221> Variant
<222> (12)..(12)
<223> Xaa in position 12 is Asp, Ser or Val

<220>
<221> Variant
<222> (13)..(13)
<223> Xaa in position 13 is Ile or Leu

<220>
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<222> (14)..(14)
<223> Xaa in position 14 is Ala or Cys

<220>
<221> Variant
<222> (16)..(16)
<223> Xaa in position 16 is any amino acid

<220>
<221> Variant
<222> (18)..(21)
<223> Xaa in position 18 to 21 is any amino acid

<220>
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<222> (22)..(22)
<223> Xaa in position 22 is any or no amino acid

<220>
<221> Variant
<222> (24)..(24)
<223> Xaa in position 24 is any amino acid

<220>
<221> Variant
<222> (25)..(25)
<223> Xaa in position 25 is Asp, Glu or Gly

<220>
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<222> (26)..(26)
<223> Xaa in position 26 is any amino acid

<220>
<221> Variant
<222> (28)..(28)
<223> Xaa in position 28 is Ile or Val

<220>
<221> Variant
<222> (29)..(29)
<223> Xaa in position 29 is Ala or Val

<220>
<221> Variant
<222> (30)..(30)
<223> Xaa in position 30 is Gly or Ser

<220>
<221> Variant
<222> (33)..(33)
<223> Xaa in position 33 is Phe or Leu

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PF59082SeqList_PF59082.txt

<400> 723

Pro Xaa Xaa Ile Xaa Phe Xaa Asp Glu Xaa Asp Xaa Xaa Xaa Pro Xaa
 1 5 10 15
 Arg Xaa Xaa Xaa Xaa Xaa Glu Xaa Xaa Arg Xaa Xaa Xaa Gln Leu
 20 25 30
 Xaa Thr Leu Met Asp
 35

<210> 724

<211> 9

<212> PRT

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<220>

<223> protein pattern

<220>

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<222> (5)..(5)

<223> Xaa in position 5 is any amino acid

<400> 724

Ala Leu Arg Arg Xaa Gly Arg Phe Asp
 1 5

<210> 725

<211> 20

<212> PRT

<213> Artificial sequence

<220>

<223> protein pattern

<220>

<221> Variant

<222> (2)..(2)

<223> Xaa in position 2 is any amino acid

<220>

<221> Variant

<222> (3)..(3)

<223> Xaa in position 3 is Pro or Val

<220>

<221> Variant

<222> (4)..(4)

<223> Xaa in position 4 is any amino acid

<220>

<221> Variant

<222> (6)..(6)

<223> Xaa in position 6 is any amino acid

<220>

<221> Variant

<222> (8)..(8)

<223> Xaa in position 8 is Asp or Glu

<220>

<221> Variant

<222> (10)..(10)

<223> Xaa in position 10 is Ile or Val

<220>

<221> Variant

<222> (14)..(14)

<223> Xaa in position 14 is any amino acid

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<220>
<221> Variant
<222> (15)..(15)
<223> Xaa in position 15 is Ala, Asp, Glu or Asn

<220>
<221> Variant
<222> (16)..(16)
<223> Xaa in position 16 is Ile, Leu or Val

<220>
<221> Variant
<222> (18)..(18)
<223> Xaa in position 18 is Glu, Lys or Arg

<220>
<221> Variant
<222> (19)..(19)
<223> Xaa in position 19 is Glu or Lys

<400> 725
Glu Xaa Xaa Xaa Val Xaa Trp Xaa Asp Xaa Gly Gly Leu Xaa Xaa Xaa
1      5      10      15
Lys Xaa Xaa Leu
      20

<210> 726
<211> 26
<212> PRT
<213> Artificial sequence

<220>
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<220>
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<222> (2)..(2)
<223> Xaa in position 2 is Ile, Leu or Met

<220>
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<222> (5)..(5)
<223> Xaa in position 5 is any amino acid

<220>
<221> Variant
<222> (6)..(6)
<223> Xaa in position 6 is Lys or Arg

<220>
<221> Variant
<222> (8)..(8)
<223> Xaa in position 8 is Ile or Val

<220>
<221> Variant
<222> (10)..(10)
<223> Xaa in position 10 is Phe or Leu

<220>
<221> Variant
<222> (11)..(11)
<223> Xaa in position 11 is His or Tyr

<220>
<221> Variant
<222> (16)..(16)

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<223> Xaa in position 16 is Cys or Thr

<220>

<221> Variant

<222> (17)..(17)

<223> Xaa in position 17 is Gly or Ser

<220>

<221> Variant

<222> (20)..(20)

<223> Xaa in position 20 is any amino acid

<220>

<221> Variant

<222> (21)..(21)

<223> Xaa in position 21 is Leu or Met

<220>

<221> Variant

<222> (25)..(25)

<223> Xaa in position 25 is Ala, Ile or Val

<400> 726

Gly	Xaa	Ser	Pro	Xaa	Xaa	Gly	Xaa	Leu	Xaa	Xaa	Gly	Pro	Pro	Gly	Xaa
1				5			10							15	
Xaa	Lys	Thr	Xaa	Xaa	Ala	Lys	Ala	Xaa	Ala						
			20				25								

<210> 727

<211> 7

<212> PRT

<213> Artificial sequence

<220>

<223> protein pattern

<400> 727

Leu	Leu	Thr	Glu	Met	Asp	Gly
1				5		

<210> 728

<211> 29

<212> PRT

<213> Artificial sequence

<220>

<223> protein pattern

<220>

<221> Variant

<222> (6)..(7)

<223> Xaa in position 6 to 7 is any amino acid

<220>

<221> Variant

<222> (8)..(8)

<223> Xaa in position 8 is Ile or Leu

<220>

<221> Variant

<222> (10)..(10)

<223> Xaa in position 10 is Ala, Asn, Pro or Ser

<220>

<221> Variant

<222> (12)..(12)

<223> Xaa in position 12 is any or no amino acid

PF59082SeqList_PF59082.txt

<220>
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 <222> (14)..(14)
 <223> Xaa in position 14 is any or no amino acid

<220>
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 <222> (19)..(19)
 <223> Xaa in position 19 is Phe or Leu

<220>
 <221> Variant
 <222> (21)..(21)
 <223> Xaa in position 21 is any amino acid

<220>
 <221> Variant
 <222> (22)..(22)
 <223> Xaa in position 22 is any or no amino acid

<220>
 <221> Variant
 <222> (24)..(25)
 <223> Xaa in position 24 to 25 is any amino acid

<220>
 <221> Variant
 <222> (26)..(26)
 <223> Xaa in position 26 is Ile, Pro or Val

<220>
 <221> Variant
 <222> (28)..(28)
 <223> Xaa in position 28 is Leu or Pro

<220>
 <221> Variant
 <222> (29)..(29)
 <223> Xaa in position 29 is Asp or Pro

<400> 728
 Ala Thr Asn Arg Pro Xaa Xaa Xaa Asp Xaa Ala Xaa Leu Xaa Arg Pro
 1 5 10 15
 Gly Arg Xaa Asp Xaa Xaa Leu Xaa Xaa Xaa Pro Xaa Xaa
 20 25

<210> 729
 <211> 1140
 <212> DNA
 <213> Arabidopsis thaliana

<220>
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 <222> (1)..(1140)

<400> 729
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 Met Cys Gly Gly Ala Ile Ile Ser Asp Phe Ile Pro Pro Pro Arg Ser
 1 5 10 15
 ctc cgc gtc act aac gag ttt atc tgg ccg gat ctg aaa aac aaa gtg 96
 Leu Arg Val Thr Asn Glu Phe Ile Trp Pro Asp Leu Lys Asn Lys Val
 20 25 30
 aaa gct tca aag aag aga tcg aat aag cga tcc gat ttc ttc gat ctt 144
 Lys Ala Ser Lys Lys Arg Ser Asn Lys Arg Ser Asp Phe Phe Asp Leu
 35 40 45
 gac gat gat ttc gaa gct gat ttc caa ggg ttt aag gat gac tcg gct 192
 Asp Asp Asp Phe Glu Ala Asp Phe Gln Gly Phe Lys Asp Asp Ser Ala
 50 55 60

PF59082SeqList_PF59082.txt

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Phe	Asp	Cys	Glu	Asp	Asp	Asp	Asp	Val	Phe	Val	Asn	Val	Lys	Pro	Phe	
65					70				75						80	
gtc	ttc	acc	gca	act	act	aag	ccc	gta	gct	tcc	gct	ttc	gtc	tcc	act	288
Val	Phe	Thr	Ala	Thr	Lys	Pro	Val	Ala	Ser	Ala	Phe	Val	Ser	Thr		
			85					90						95		
ggt	ata	tat	ttg	gta	ggt	tca	gca	tat	gcc	aag	aaa	act	gta	gag	tcc	336
Gly	Ile	Tyr	Leu	Val	Gly	Ser	Ala	Tyr	Ala	Lys	Lys	Thr	Val	Glu	Ser	
			100					105					110			
gct	gag	caa	gct	gag	aaa	tct	tct	aag	agg	aag	agg	aag	aat	caa	tac	384
Ala	Glu	Gln	Ala	Glu	Lys	Ser	Ser	Lys	Arg	Lys	Arg	Lys	Asn	Gln	Tyr	
		115					120					125				
cga	ggg	att	agg	cag	cgt	cct	tgg	gga	aaa	tgg	gct	gcg	gag	atc	cgt	432
Arg	Gly	Ile	Arg	Gln	Arg	Pro	Trp	Gly	Lys	Trp	Ala	Ala	Glu	Ile	Arg	
			130			135					140					
gat	ccg	aga	aaa	ggc	tcc	cga	gaa	tgg	ctt	gga	aca	ttc	gac	act	gct	480
Asp	Pro	Arg	Lys	Gly	Ser	Arg	Glu	Trp	Leu	Gly	Thr	Phe	Asp	Thr	Ala	
145				150				155							160	
gag	gaa	gca	gca	aga	gct	tat	gat	gct	gca	gca	cgc	aga	atc	cgt	ggc	528
Glu	Glu	Ala	Ala	Arg	Ala	Tyr	Asp	Ala	Ala	Ala	Arg	Arg	Ile	Arg	Gly	
			165					170						175		
acg	aaa	gct	aag	gtg	aat	ttt	ccc	gag	gag	aag	aac	cct	agc	gtc	gta	576
Thr	Lys	Ala	Lys	Val	Asn	Phe	Pro	Glu	Glu	Lys	Asn	Pro	Ser	Val	Val	
			180				185						190			
tcc	cag	aaa	cgt	cct	agt	gct	aag	act	aat	aat	ctt	cag	aaa	tca	gtg	624
Ser	Gln	Lys	Arg	Pro	Ser	Ala	Lys	Thr	Asn	Asn	Leu	Gln	Lys	Ser	Val	
		195					200					205				
gct	aaa	cca	aac	aaa	agc	gta	act	ttg	ggt	cag	cag	cca	aca	cat	ctg	672
Ala	Lys	Pro	Asn	Lys	Ser	Val	Thr	Leu	Val	Gln	Gln	Pro	Thr	His	Leu	
	210				215					220						
agt	cag	cag	tac	tgc	aac	tcc	ttt	gac	aac	tct	ttt	ggt	gat	atg		720
Ser	Gln	Gln	Tyr	Cys	Asn	Asn	Ser	Phe	Asp	Asn	Ser	Phe	Gly	Asp	Met	
225				230				235						240		
agt	ttc	atg	gaa	gag	aag	cct	cag	atg	tac	aac	aat	cag	ttt	ggg	tta	768
Ser	Phe	Met	Glu	Glu	Lys	Pro	Gln	Met	Tyr	Asn	Asn	Gln	Phe	Gly	Leu	
			245					250						255		
aca	aac	tcg	ttc	gat	gct	gga	ggt	aac	aat	gga	tac	cag	tat	ttc	agt	816
Thr	Asn	Ser	Phe	Asp	Ala	Gly	Gly	Asn	Asn	Gly	Tyr	Gln	Tyr	Phe	Ser	
			260			265							270			
tcc	gat	cag	ggc	agt	aac	tcc	ttc	gac	tgt	tct	gag	ttc	ggg	tgg	agt	864
Ser	Asp	Gln	Gly	Ser	Asn	Ser	Phe	Asp	Cys	Ser	Glu	Phe	Gly	Trp	Ser	
		275				280					285					
gat	cac	ggc	cct	aaa	aca	ccc	gag	atc	tct	tca	atg	ctt	gtc	aat	aac	912
Asp	His	Gly	Pro	Lys	Thr	Pro	Glu	Ile	Ser	Ser	Met	Leu	Val	Asn	Asn	
	290					295					300					
aac	gaa	gca	tca	ttt	gtt	gaa	gaa	acc	aat	gca	gcc	aag	aag	ctc	aaa	960
Asn	Glu	Ala	Ser	Phe	Val	Glu	Glu	Thr	Asn	Ala	Ala	Lys	Lys	Leu	Lys	
305				310				315						320		
cca	aac	tct	gat	gag	tca	gac	gat	ctg	atg	gca	tac	ctt	gac	aac	gcc	1008
Pro	Asn	Ser	Asp	Glu	Ser	Asp	Asp	Leu	Met	Ala	Tyr	Leu	Asp	Asn	Ala	
			325					330						335		
ttg	tgg	gac	acc	cca	cta	gaa	gtg	gaa	gcc	atg	ctt	ggc	gca	gat	gct	1056
Leu	Trp	Asp	Thr	Pro	Leu	Glu	Val	Glu	Ala	Met	Leu	Gly	Ala	Asp	Ala	
			340				345						350			
ggt	gct	gtg	act	cag	gaa	gag	gaa	aac	cca	gtg	gag	cta	tgg	agc	tta	1104
Gly	Ala	Val	Thr	Gln	Glu	Glu	Glu	Asn	Pro	Val	Glu	Leu	Trp	Ser	Leu	
		355				360						365				
gat	gag	atc	aat	ttc	atg	ctg	gaa	gga	gac	ttt	tga					1140
Asp	Glu	Ile	Asn	Phe	Met	Leu	Glu	Gly	Asp	Phe						
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<210> 730

<211> 379

<212> PRT

<213> Arabidopsis thaliana

<400> 730

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 20 25 30
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 35 40 45
 Asp Asp Asp Phe Glu Ala Asp Phe Gln Gly Phe Lys Asp Asp Ser Ala
 50 55 60
 Phe Asp Cys Glu Asp Asp Asp Asp Val Phe Val Asn Val Lys Pro Phe
 65 70 75 80
 Val Phe Thr Ala Thr Lys Pro Val Ala Ser Ala Phe Val Ser Thr
 85 90 95
 Gly Ile Tyr Leu Val Gly Ser Ala Tyr Ala Lys Lys Thr Val Glu Ser
 100 105 110
 Ala Glu Gln Ala Glu Lys Ser Ser Lys Arg Lys Arg Lys Asn Gln Tyr
 115 120 125
 Arg Gly Ile Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg
 130 135 140
 Asp Pro Arg Lys Gly Ser Arg Glu Trp Leu Gly Thr Phe Asp Thr Ala
 145 150 155 160
 Glu Glu Ala Ala Arg Ala Tyr Asp Ala Ala Ala Arg Arg Ile Arg Gly
 165 170 175
 Thr Lys Ala Lys Val Asn Phe Pro Glu Glu Lys Asn Pro Ser Val Val
 180 185 190
 Ser Gln Lys Arg Pro Ser Ala Lys Thr Asn Asn Leu Gln Lys Ser Val
 195 200 205
 Ala Lys Pro Asn Lys Ser Val Thr Leu Val Gln Gln Pro Thr His Leu
 210 215 220
 Ser Gln Gln Tyr Cys Asn Asn Ser Phe Asp Asn Ser Phe Gly Asp Met
 225 230 235 240
 Ser Phe Met Glu Glu Lys Pro Gln Met Tyr Asn Asn Gln Phe Gly Leu
 245 250 255
 Thr Asn Ser Phe Asp Ala Gly Gly Asn Asn Gly Tyr Gln Tyr Phe Ser
 260 265 270
 Ser Asp Gln Gly Ser Asn Ser Phe Asp Cys Ser Glu Phe Gly Trp Ser
 275 280 285
 Asp His Gly Pro Lys Thr Pro Glu Ile Ser Ser Met Leu Val Asn Asn
 290 295 300
 Asn Glu Ala Ser Phe Val Glu Glu Thr Asn Ala Ala Lys Lys Leu Lys
 305 310 315 320
 Pro Asn Ser Asp Glu Ser Asp Asp Leu Met Ala Tyr Leu Asp Asn Ala
 325 330 335
 Leu Trp Asp Thr Pro Leu Glu Val Glu Ala Met Leu Gly Ala Asp Ala
 340 345 350
 Gly Ala Val Thr Gln Glu Glu Glu Asn Pro Val Glu Leu Trp Ser Leu
 355 360 365
 Asp Glu Ile Asn Phe Met Leu Glu Gly Asp Phe
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<210> 731

<211> 1889

<212> DNA

<213> Glycine max

<220>

<221> CDS

<222> (163)..(1341)

<400> 731

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gattgagcga aagctttgtt ttttctgcga tcattttcca ttgggtggaa gaaagtctca

120

accttagtc gaaagagcaa ggatctgagt gagtgagcga tc atg tgt ggt ggt
 Met Cys Gly Gly

174

gcg att atc tcc gac ttc att cca gcg ggt ccc gcc gcc ggc ggc ggc cag
 Ala Ile Ile Ser Asp Phe Ile Pro Ala Gly Pro Ala Gly Gly Ala Gln
 5 10 15 20

222

PF59082SeqList_PF59082.txt

cgc	gtg	acc	gcc	gac	atc	ctg	tgg	ccg	aat	ttg	agg	aag	cgg	ttc	tcg	270
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				25					30					35		
aag	tcg	ctg	ctg	gac	gat	gat	ttc	gag	gca	ggg	ttc	aga	gaa	ttc	gag	318
Lys	Ser	Leu	Leu	Asp	Asp	Asp	Phe	Glu	Ala	Gly	Phe	Arg	Glu	Phe	Glu	
			40					45					50			
gat	gac	tcg	gaa	atc	gag	gat	gtc	gat	gat	gag	gac	gat	gaa	gag	gag	366
Asp	Asp	Ser	Glu	Ile	Glu	Asp	Val	Asp	Asp	Glu	Asp	Asp	Glu	Glu	Glu	
		55					60					65				
gag	gag	ttg	aag	aag	aag	aag	ccc	ttt	ggg	ttc	tct	cgc	tcc	aac	aac	414
Glu	Glu	Leu	Lys	Lys	Lys	Lys	Pro	Phe	Gly	Phe	Ser	Arg	Ser	Asn	Asn	
	70						75				80					
aag	gct	gct	tct	aag	cct	ctc	tct	cgt	gga	gca	aca	act	gtg	aaa	tct	462
Lys	Ala	Ala	Ser	Lys	Pro	Leu	Ser	Arg	Gly	Ala	Thr	Thr	Val	Lys	Ser	
	85				90					95					100	
gtg	gaa	tca	aag	ggg	caa	gct	gag	aag	tgt	gcc	aag	aga	aag	agg	aag	510
Val	Glu	Ser	Lys	Gly	Gln	Ala	Glu	Lys	Cys	Ala	Lys	Arg	Lys	Arg	Lys	
			105					110						115		
aac	cag	tat	cgc	gga	atc	cgc	cag	cgt	cca	tgg	gga	aag	tgg	gct	gct	558
Asn	Gln	Tyr	Arg	Gly	Ile	Arg	Gln	Arg	Pro	Trp	Gly	Lys	Trp	Ala	Ala	
			120					125					130			
gag	att	cgc	gac	cca	aga	aag	ggg	gtt	cgt	gtt	tgg	ctt	gga	act	ttc	606
Glu	Ile	Arg	Asp	Pro	Arg	Lys	Gly	Val	Arg	Val	Trp	Leu	Gly	Thr	Phe	
		135					140					145				
agc	act	gct	gaa	gaa	gct	gca	aga	gct	tac	gat	gct	gaa	gca	agg	agg	654
Ser	Thr	Ala	Glu	Glu	Ala	Ala	Arg	Ala	Tyr	Asp	Ala	Glu	Ala	Arg	Arg	
	150				155						160					
atc	cgt	ggc	aag	aaa	gcc	aag	gtg	aat	ttc	cct	gat	gag	cct	tca	ggc	702
Ile	Arg	Gly	Lys	Lys	Ala	Lys	Val	Asn	Phe	Pro	Asp	Glu	Pro	Ser	Gly	
	165				170					175					180	
gct	gct	tcc	tca	aaa	cgt	ctc	aag	gcg	aat	cca	gag	gct	cag	cca	atg	750
Ala	Ala	Ser	Ser	Lys	Arg	Leu	Lys	Ala	Asn	Pro	Glu	Ala	Gln	Pro	Met	
			185					190						195		
aag	aaa	aat	ctg	aac	tct	gtg	aag	ccg	aaa	ata	aac	cag	atg	ttc	aat	798
Lys	Lys	Asn	Leu	Asn	Ser	Val	Lys	Pro	Lys	Ile	Asn	Gln	Met	Phe	Asn	
			200					205					210			
ttt	ggt	gac	aat	ctt	gag	ggc	tac	tac	agc	cct	ata	gat	cag	gtg	gaa	846
Phe	Gly	Asp	Asn	Leu	Glu	Gly	Tyr	Tyr	Ser	Pro	Ile	Asp	Gln	Val	Glu	
		215					220					225				
cag	aaa	cca	ctg	gtt	aac	cag	gtt	aac	cgt	gcc	cca	ttt	gct	gga		894
Gln	Lys	Pro	Leu	Val	Asn	Gln	Tyr	Val	Asn	Arg	Ala	Pro	Phe	Ala	Gly	
	230				235					240						
aat	gga	gtt	caa	gtc	tca	cct	gtt	act	cca	tct	gct	gat	gtt	act	gct	942
Asn	Gly	Val	Gln	Val	Ser	Pro	Val	Thr	Pro	Ser	Ala	Asp	Val	Thr	Ala	
	245				250					255					260	
tac	ttc	agc	tct	gag	cat	tcg	agc	agc	tcg	ttt	gat	tat	tct	gac	ctc	990
Tyr	Phe	Ser	Ser	Glu	His	Ser	Ser	Ser	Ser	Phe	Asp	Tyr	Ser	Asp	Leu	
			265					270						275		
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Gln	Leu	Lys	Phe	Phe	Glu	Thr	Pro	Ser	Phe	Leu	Asp	Glu	Ala	Trp	Ala	
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 Leu Thr Glu Arg Asp Ile Trp Gln Lys Lys Lys 30 Lys Arg Gly
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 Gly Gly Gly Gly Arg Arg Ser Phe Ala Ala Glu Asp Asp Glu Asp Phe
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 Thr Ala Lys Arg Thr Phe Ser Ser Asp Gly Leu Ser Thr Met Thr Ser
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Pro Phe Ala Phe Thr Ala Ala Ser Leu Pro Thr Asn Val Ala Ser Thr	
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 <213> Brassica napus

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 Phe Glu Ala Asp Phe Lys Gly Phe Lys Asp Asp Asp Ser Ser Phe Asp
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 Cys Glu Asp Gly Phe Asp Val Lys Pro Phe Ala Phe Thr Ala Ala Ser
 65 70 75 80
 Leu Pro Thr Asn Val Ala Ser Thr Gly Ser Val Ser Gly Lys Lys Thr
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 Ile Glu Ser Asp Glu Lys Ser Gly Lys Arg Lys Arg Lys Asn Gln Tyr
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 Arg Gly Ile Arg Leu Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg
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 Asp Pro Lys Lys Gly Ser Arg Glu Trp Leu Gly Thr Phe Glu Thr Ala
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 Glu Glu Ala Ala Arg Ala Tyr Asp Ala Ala Ala Arg Arg Ile Arg Gly
 145 150 155 160
 Gly Lys Ala Lys Val Asn Phe Pro Glu Glu Val Ile Ser Asn Leu Lys
 165 170 175
 Lys Pro Val Ala Lys Pro Asn His Thr Pro Ala Leu Val Gln Pro Pro
 180 185 190
 Thr His Val Gly Gln Tyr Cys Asn Asn Asn Ser Phe Asp Asn Met Gly
 195 200 205
 His Asp Ser Leu Ser Phe Ile Glu Glu Lys Pro Gln Met Tyr Asn Asn
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 Gln Phe Phe Asp Val Gly Gln Tyr Phe Ser Ser Asp Gln Gly Ser Asn
 225 230 235 240
 Ser Phe Asp Cys Ser Glu Phe Gly Trp Ser Asp His Ala Pro Lys Thr
 245 250 255
 Pro Pro Glu Ile Ser Ser Met Leu Val Asn Asn Asn Arg Ala Thr Phe
 260 265 270
 Asp Glu Glu Thr Asn Ala Ala Lys Lys Val Lys Leu Asn Ser Glu Asp
 275 280 285
 Glu Thr Ser Asp Asn Asp Asp Leu Met Ala Tyr Leu Asp Asn Ala Leu
 290 295 300
 Trp Glu Ser Pro Leu Glu Met Glu Ala Met Leu Gly Val Asp Val Ala
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 Met Cys Gly Gly Ala Ile Ile Ser Asp Phe
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113

ata cct ccg tcg agg tcc cgc cgc gtc acg agc gag tac ctc tgg ccg
 Seite 955

161

PF59082SeqList_PF59082.txt

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Asp	Leu	Lys	Asn	Lys	Val	Lys	Ala	Ser	Lys	Lys	Lys	Lys	Arg	Ser	Asp		
			30					35					40				
ttc	ctc	gat	ctg	gac	gac	gag	ttc	gag	gct	gac	ttt	caa	ggg	ttt	aag	257	
Phe	Leu	Asp	Leu	Asp	Asp	Glu	Phe	Glu	Ala	Asp	Phe	Gln	Gly	Phe	Lys		
		45				50					55						
gat	ggt	gca	tcg	ttc	gat	tgc	gaa	gat	gaa	ttc	gat	gtg	gat	gat	gaa	305	
Asp	Gly	Ala	Ser	Phe	Asp	Cys	Glu	Asp	Glu	Phe	Asp	Val	Asp	Asp	Glu		
	60					65				70							
gtc	ttc	gcc	gat	gtc	aaa	ccc	ttt	gtc	ttc	gcc	gca	ggg	gcc	aag	ccc	353	
Val	Phe	Ala	Asp	Val	Lys	Pro	Phe	Val	Phe	Ala	Ala	Gly	Ala	Lys	Pro		
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gta	gcg	tcc	cct	ccc	gcc	gcc	ttc	gcc	tcc	gct	ggg	tca	gtt	tct	ggc	401	
Val	Ala	Ser	Pro	Pro	Ala	Ala	Phe	Ala	Ser	Ala	Gly	Ser	Val	Ser	Gly		
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Lys	Lys	Thr	Ile	Glu	Ser	Gly	Gly	Gln	Ala	Glu	Lys	Ser	Ala	Lys	Arg		
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Lys	Arg	Lys	Asn	Gln	Tyr	Arg	Gly	Ile	Arg	Gln	Arg	Pro	Trp	Gly	Lys		
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Trp	Ala	Ala	Glu	Ile	Arg	Asp	Pro	Arg	Lys	Gly	Ser	Arg	Glu	Trp	Leu		
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Gly	Thr	Phe	Asp	Thr	Ala	Glu	Glu	Ala	Ala	Arg	Ala	Tyr	Asp	Ala	Ala		
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Met	Val	Pro	Ser	Val	Ser	Gln	Lys	Arg	Pro	Ala	Ala	Lys	Lys	Ala	Val		
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Ala	Lys	Pro	Asn	Gln	Ser	Pro	Ala	Ser	Val	Gln	Gln	Pro	Thr	His	Val		
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Ser	Glu	Tyr	Cys	Asn	Asn	Ser	Phe	Asp	Asn	Met	Gly	His	Asp	Pro	Ser		
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Phe	Gly	Asp	Val	Ser	Phe	Met	Glu	Glu	Lys	Pro	Gln	Met	Tyr	Asn	Asn		
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cag	ttc	ctt	gat	gtc	gga	ggc	aac	aat	gga	tac	cag	tat	ttc	agt	tct	881	
Gln	Phe	Leu	Asp	Val	Gly	Gly	Asn	Asn	Gly	Tyr	Gln	Tyr	Phe	Ser	Ser		
			255					260						265			
gac	cag	ggc	agt	aac	tca	ctg	gac	tgc	tct	gag	ttt	ggg	tgg	agt	gat	929	
Asp	Gln	Gly	Ser	Asn	Ser	Leu	Asp	Cys	Ser	Glu	Phe	Gly	Trp	Ser	Asp		
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cat	acc	ccc	aag	aca	cct	gag	atc	tct	tca	atg	ctg	gtc	aac	agt	aac	977	
His	Thr	Pro	Lys	Thr	Pro	Glu	Ile	Ser	Ser	Met	Leu	Val	Asn	Ser	Asn		
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Gln	Ala	Pro	Phe	Ile	Glu	Glu	Thr	Asn	Pro	Ala	Lys	Lys	Leu	Lys	Thr		
	300					305					310						
aac	tct	gag	gac	ggg	aca	agc	aac	aat	ggt	aat	tct	gat	gat	ctg	atg	1073	
Asn	Ser	Glu	Asp	Gly	Thr	Ser	Asn	Asn	Gly	Asn	Ser	Asp	Asp	Leu	Met		
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gca	tat	ttg	aac	aac	gcc	ttg	tgg	gag	tct	cca	ttg	gaa	gtg	gaa	gct	1121	
Ala	Tyr	Leu	Asn	Asn	Ala	Leu	Trp	Glu	Ser	Pro	Leu	Glu	Val	Glu	Ala		
			335					340						345			
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Met	Phe	Gly	Asp	Ala	Ala	Ala	Thr	Met	Thr	Gln	Glu	Glu	Gly	Thr	Pro		
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Met	Asp	Leu	Trp	Ser	Phe	Asp	Asp	Ile	Asn	Ser	Met	Leu	Asp	Gly	Gly		
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PF59082SeqList_PF59082.txt

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tatcttatat gagtctcttt ctcacggaga gcgtctctct tttaaattcc tgaaataaaa 1393

ggggtgatga agtaaataga gttataatth ctatctaatt agtctgtgag tttttttttt 1453

tttgtttact aatgttttaa actctctttt tgatctttct ttttatagcg tatcatcatc 1513

accctcgaaa gtgtttatgt tttgtacccc caacactaat ataaaaactg tctggaacca 1573

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<213> Brassica napus

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35 40 45
Glu Phe Glu Ala Asp Phe Gln Gly Phe Lys Asp Gly Ala Ser Phe Asp
50 55 60
Cys Glu Asp Glu Phe Asp Val Asp Asp Glu Val Phe Ala Asp Val Lys
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Pro Phe Val Phe Ala Ala Gly Ala Lys Pro Val Ala Ser Pro Pro Ala
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Ala Phe Ala Ser Ala Gly Ser Val Ser Gly Lys Lys Thr Ile Glu Ser
100 105 110
Gly Gly Gln Ala Glu Lys Ser Ala Lys Arg Lys Arg Lys Asn Gln Tyr
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Arg Gly Ile Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg
130 135 140
Asp Pro Arg Lys Gly Ser Arg Glu Trp Leu Gly Thr Phe Asp Thr Ala
145 150 155 160
Glu Glu Ala Ala Arg Ala Tyr Asp Ala Ala Arg Arg Ile Arg Gly
165 170 175
Asn Lys Ala Lys Val Asn Phe Pro Glu Met Val Pro Ser Val Ser
180 185 190
Gln Lys Arg Pro Ala Ala Lys Lys Ala Val Ala Lys Pro Asn Gln Ser
195 200 205
Pro Ala Ser Val Gln Gln Pro Thr His Val Ser Glu Tyr Cys Asn Asn
210 215 220
Ser Phe Asp Asn Met Gly His Asp Pro Ser Phe Gly Asp Val Ser Phe
225 230 235 240
Met Glu Glu Lys Pro Gln Met Tyr Asn Asn Gln Phe Leu Asp Val Gly
245 250 255
Gly Asn Asn Gly Tyr Gln Tyr Phe Ser Ser Asp Gln Gly Ser Asn Ser
260 265 270
Leu Asp Cys Ser Glu Phe Gly Trp Ser Asp His Thr Pro Lys Thr Pro
275 280 285
Glu Ile Ser Ser Met Leu Val Asn Ser Asn Gln Ala Pro Phe Ile Glu
290 295 300
Glu Thr Asn Pro Ala Lys Lys Leu Lys Thr Asn Ser Glu Asp Gly Thr
305 310 315 320
Ser Asn Asn Gly Asn Ser Asp Asp Leu Met Ala Tyr Leu Asn Asn Ala
325 330 335

PF59082SeqList_PF59082.txt

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 Ala Thr Met Thr Gln Glu Glu Gly Thr Pro Met Asp Leu Trp Ser Phe
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 aggatctgag ttgagttgag tgatc atg tgt ggt ggt gcg att atc tcc gac 172
 Met Cys Gly Gly Ala Ile Ile Ser Asp
 1 5
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 Phe Ile Pro Ala Gly Pro Ala Ser Gly Ala Arg Arg Val Thr Ala Asp
 10 15 20 25
 atc ctg tgg ccg agt ttg agg aag cgc ttc tcg aag ccg ctg ctg gac 268
 Ile Leu Trp Pro Ser Leu Arg Lys Arg Phe Ser Lys Pro Leu Leu Asp
 30 35 40
 gat gat ttc gag gct ggg ttc aga gaa ttc aag gat gat tcg gaa atc 316
 Asp Asp Phe Glu Ala Gly Phe Arg Glu Phe Lys Asp Asp Ser Glu Ile
 45 50 55
 gag gat gtt gat gac gag gac gat gaa gac gag gag gag ttg aag aag 364
 Glu Asp Val Asp Asp Glu Asp Asp Glu Asp Glu Glu Glu Leu Lys Lys
 60 65 70
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 Lys Pro Phe Gly Phe Ser Arg Ser Ser Asn Lys Ala Ala Ser Lys Pro
 75 80 85
 ctc tct cgt gga tca gca act gtg gaa tca aag ggg caa gct gag aag 460
 Leu Ser Arg Gly Ser Ala Thr Val Glu Ser Lys Gly Gln Ala Glu Lys
 90 95 100 105
 tgt gcc aag aga aag agg aag aac cag tat cgt gga atc cgt cag cgt 508
 Cys Ala Lys Arg Lys Arg Lys Asn Gln Tyr Arg Gly Ile Arg Gln Arg
 110 115 120
 cca tgg gga aag tgg gct gct gag atc cgt gac cca aga aag ggg gtt 556
 Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp Pro Arg Lys Gly Val
 125 130 135
 cgt gtt tgg ctt gga act ttc agc act gct gaa gaa gct gca aga gct 604
 Arg Val Trp Leu Gly Thr Phe Ser Thr Ala Glu Glu Ala Ala Arg Ala
 140 145 150
 tat gat gct gaa gca agg agg atc cgg ggc aag aaa gcc aag gtg aat 652
 Tyr Asp Ala Glu Ala Arg Arg Ile Arg Gly Lys Lys Ala Lys Val Asn
 155 160 165
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 Phe Pro Asp Glu Pro Ser Gly Ala Ala Ala Ser Ser Lys Arg Leu Lys
 170 175 180 185
 gtg aat cca gag gct cag cca atg aag gaa aat ctg aac acc gtg aag 748
 Val Asn Pro Glu Ala Gln Pro Met Lys Glu Asn Leu Asn Thr Val Lys
 190 195 200
 ccg aaa atg aac cag atg ttc aat ttt ggt cac aat ctg gag ggc tac 796
 Pro Lys Met Asn Gln Met Phe Asn Phe Gly His Asn Leu Glu Gly Tyr
 205 210 215
 tac agc cca ata gat cag gtg gaa cag aaa cca ctg gtt aac cag tat 844
 Tyr Ser Pro Ile Asp Gln Val Glu Gln Lys Pro Leu Val Asn Gln Tyr
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 gtt aac cct gcc ccg ttc cct gga aac gga gtt caa gtc tca cct gtt 892

PF59082SeqList_PF59082.txt

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Thr	Pro	Ser	Ala	Asp	Val	Thr	Ala	Tyr	Phe	Ser	Ser	Glu	His	Ser	Ser			
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Asn	Ser	Phe	Asp	Tyr	Ser	Asp	Leu	Gly	Trp	Gly	Glu	Gln	Val	Pro	Lys			
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Gln	Asp	Asp	Ser	Ala	Lys	Thr	Leu	Ser	Glu	Glu	Leu	Ala	Asp	Ile	Glu			
				315		320					325							
tcc	cag	ctc	aag	ttc	ttt	gag	acc	cct	tct	ttt	ctt	gat	gaa	gcc	tg	1180		
Ser	Gln	Leu	Lys	Phe	Phe	Glu	Thr	Pro	Ser	Phe	Leu	Asp	Glu	Ala	Trp			
330					335					340					345			
gct	gat	gct	aca	ttg	gcg	tct	ttg	ctc	ggc	gga	gac	gca	act	cat	gac	1228		
Ala	Asp	Ala	Thr	Leu	Ala	Ser	Leu	Leu	Gly	Gly	Asp	Ala	Thr	His	Asp			
				350					355					360				
gcc	gcc	gga	aac	cct	atg	aac	ctt	tg	agc	ttc	gac	gac	ctg	cct	tcc	1276		
Ala	Ala	Gly	Asn	Pro	Met	Asn	Leu	Trp	Ser	Phe	Asp	Asp	Leu	Pro	Ser			
				365			370							375				
atg	gca	gga	gtc	ttc	tga	acaccct	ttatctcccc	ttttatgtaa	ataaagctac							1331		
Met	Ala	Gly	Val	Phe														
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tc	ct	ta	agga	tt	at	ca	atta	tg	tt	at	atat	gg	t	ct	tg	gat	acagtcttga ctgctgatac	1571
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 35 40 45
 Arg Glu Phe Lys Asp Asp Ser Glu Ile Glu Asp Val Asp Asp Glu Asp
 50 55 60
 Asp Glu Asp Glu Glu Glu Leu Lys Lys Lys Pro Phe Gly Phe Ser Arg
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 Ser Ser Asn Lys Ala Ala Ser Lys Pro Leu Ser Arg Gly Ser Ala Thr
 85 90 95
 Val Glu Ser Lys Gly Gln Ala Glu Lys Cys Ala Lys Arg Lys Arg Lys
 100 105 110
 Asn Gln Tyr Arg Gly Ile Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala
 Seite 959

PF59082SeqList_PF59082.txt

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Ile	Arg	Gly	Lys	Lys	Ala	Lys	Val	Asn	Phe	Pro	Asp	Glu	Pro	Ser	Gly
Ala	Ala	Ala	Ser	Ser	Lys	Arg	Leu	Lys	Val	Asn	Pro	Glu	Ala	Gln	Pro
Met	Lys	Glu	Asn	Leu	Asn	Thr	Val	Lys	Pro	Lys	Met	Asn	Gln	Met	Phe
Asn	Phe	Gly	His	Asn	Leu	Glu	Gly	Tyr	Tyr	Ser	Pro	Ile	Asp	Gln	Val
Glu	Gln	Lys	Pro	Leu	Val	Asn	Gln	Tyr	Val	Asn	Pro	Ala	Pro	Phe	Pro
Gly	Asn	Gly	Val	Gln	Val	Ser	Pro	Val	Thr	Pro	Ser	Ala	Asp	Val	Thr
Ala	Tyr	Phe	Ser	Ser	Glu	His	Ser	Ser	Asn	Ser	Phe	Asp	Tyr	Ser	Asp
Leu	Gly	Trp	Gly	Glu	Gln	Val	Pro	Lys	Thr	Pro	Glu	Ile	Ser	Ser	Leu
Leu	Ser	Ala	Ala	Pro	Leu	Glu	Gly	Ala	Ala	Asp	Gln	Val	Gln	Lys	Thr
Asn	Asn	Ser	Gln	Asp	Val	Val	Ala	Ala	Gln	Asp	Asp	Ser	Ala	Lys	Thr
Leu	Ser	Glu	Glu	Leu	Ala	Asp	Ile	Glu	Ser	Gln	Leu	Lys	Phe	Phe	Glu
Thr	Pro	Ser	Phe	Leu	Asp	Glu	Ala	Trp	Ala	Asp	Ala	Thr	Leu	Ala	Ser
Leu	Leu	Gly	Gly	Asp	Ala	Thr	His	Asp	Ala	Ala	Gly	Asn	Pro	Met	Asn
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<213> Brassica napus

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<222> (168)..(1259)
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gtttgtgttt ctgaacattt aaccccctcg aatttgagtt atacgcc atg tgt gga 176
Met Cys Gly

gga gct ata atc tcc gat ttc atc cct ccg ccg agt tcc cgc cgc gtc 224
Gly Ala Ile Ile Ser Asp Phe Ile Pro Pro Pro Ser Ser Arg Arg Val
5 10 15

acg agc gag ttt ctc tgg ccg gat ctg aag aag aac aag ggg aaa gcc 272
Thr Ser Glu Phe Leu Trp Pro Asp Leu Lys Lys Asn Lys Gly Lys Ala
20 25 30 35

tcg aag aag cga tcc gat ttc ttc gat ctg gac gac gag ttc gag gct 320
Ser Lys Lys Arg Ser Asp Phe Phe Asp Leu Asp Asp Glu Phe Glu Ala
40 45 50

gat ttt caa ggg ttt gag gat gac gac gcg tct ttt gac tgc gaa gac 368
Asp Phe Gln Gly Phe Glu Asp Asp Asp Ala Ser Phe Asp Cys Glu Asp
55 60 65

gat gat gat gat gtc ttc gct aaa gtg aag ccc ttt gtc ttc acc gcg 416
Asp Asp Asp Asp Val Phe Ala Lys Val Lys Pro Phe Val Phe Thr Ala
70 75 80

acc acc aag ccc gta gct tcc cct ccc acc gcc act ggt tca gtg tct 464
Seite 960

PF59082SeqList_PF59082.txt

Thr	Thr	Lys	Pro	Val	Ala	Ser	Pro	Pro	Thr	Ala	Thr	Gly	Ser	Val	Ser	
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Gly	Lys	Lys	Ile	Ile	Glu	Ser	Gly	Gly	Gln	Ala	Glu	Lys	Ser	Ala	Lys	
100					105					110					115	
aga	aag	aga	aag	aat	cag	tac	agg	ggg	att	agg	cag	cga	cct	tgg	ggg	560
Arg	Lys	Arg	Lys	Asn	Gln	Tyr	Arg	Gly	Ile	Arg	Gln	Arg	Pro	Trp	Gly	
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aaa	tgg	gct	gct	gag	atc	cgt	gat	cct	aga	aaa	ggc	tcc	agg	gaa	tgg	608
Lys	Trp	Ala	Ala	Glu	Ile	Arg	Asp	Pro	Arg	Lys	Gly	Ser	Arg	Glu	Trp	
				135				140					145			
ctt	gga	aca	ttc	gac	acc	gcc	gag	gaa	gca	gca	aga	gcc	tat	gat	gca	656
Leu	Gly	Thr	Phe	Asp	Thr	Ala	Glu	Glu	Ala	Ala	Arg	Ala	Tyr	Asp	Ala	
				150			155					160				
gct	gca	cgc	agg	atc	cgt	ggt	agt	aaa	gct	aag	gtg	aat	ttc	cca	gag	704
Ala	Ala	Arg	Arg	Ile	Arg	Gly	Ser	Lys	Ala	Lys	Val	Asn	Phe	Pro	Glu	
	165				170						175					
gag	agc	aac	aac	aac	cgt	agc	gtc	tcc	cag	aaa	cga	cct	tct	gct	aag	752
Glu	Ser	Asn	Asn	Asn	Arg	Ser	Val	Ser	Gln	Lys	Arg	Pro	Ser	Ala	Lys	
180					185					190					195	
aag	ctg	gtg	gct	aaa	cca	aac	caa	agc	cca	gct	ttg	gtt	cag	cag	cca	800
Lys	Leu	Val	Ala	Lys	Pro	Asn	Gln	Ser	Pro	Ala	Leu	Val	Gln	Gln	Pro	
				200					205					210		
atg	agt	cag	tac	tgc	aac	aac	tcc	ttt	ggt	gat	gtg	agt	ttc	gtg	gaa	848
Met	Ser	Gln	Tyr	Cys	Asn	Asn	Ser	Phe	Gly	Asp	Val	Ser	Phe	Val	Glu	
				215				220					225			
gag	aag	cct	cag	atg	tac	aac	aac	cag	ttt	ggg	tta	gca	aac	tcg	tac	896
Glu	Lys	Pro	Gln	Met	Tyr	Asn	Asn	Gln	Phe	Gly	Leu	Ala	Asn	Ser	Tyr	
				230			235					240				
aac	aac	cac	tac	ttc	agt	tct	gat	cag	ggg	agt	aac	tca	ttt	gac	tgc	944
Asn	Asn	His	Tyr	Phe	Ser	Ser	Asp	Gln	Gly	Ser	Asn	Ser	Phe	Asp	Cys	
				245		250					255					
tct	gag	ttt	ggg	tgg	agc	gac	cac	ggc	ccc	aag	aca	cct	gag	atc	tct	992
Ser	Glu	Phe	Gly	Trp	Ser	Asp	His	Gly	Pro	Lys	Thr	Pro	Glu	Ile	Ser	
260					265					270					275	
tcg	atg	cta	gtc	ggt	aac	aac	caa	gct	ccg	ttc	act	gaa	gaa	acc	aat	1040
Ser	Met	Leu	Val	Gly	Asn	Asn	Gln	Ala	Pro	Phe	Thr	Glu	Glu	Thr	Asn	
				280				285						290		
gca	gcc	aag	aag	ctc	aaa	ccc	agc	tct	gat	gac	gga	aca	agc	aac	cag	1088
Ala	Ala	Lys	Lys	Leu	Lys	Pro	Ser	Ser	Asp	Asp	Gly	Thr	Ser	Asn	Gln	
				295				300					305			
tct	gat	gat	ctg	atg	gca	tac	ctt	gac	aat	gcc	ttg	tgg	gaa	tct	cca	1136
Ser	Asp	Asp	Leu	Met	Ala	Tyr	Leu	Asp	Asn	Ala	Leu	Trp	Glu	Ser	Pro	
				310			315					320				
tct	cca	tta	gaa	gtt	gaa	gcc	atg	ctt	ggt	gta	gat	gct	gtt	gct	gtg	1184
Ser	Pro	Leu	Glu	Val	Glu	Ala	Met	Leu	Gly	Val	Asp	Ala	Val	Ala	Val	
				325		330					335					
act	cag	gga	gag	gag	aac	ccg	atg	gac	cta	tgg	agc	tta	gat	gat	atc	1232
Thr	Gln	Gly	Glu	Glu	Asn	Pro	Met	Asp	Leu	Trp	Ser	Leu	Asp	Asp	Ile	
340					345					350					355	
aat	tac	atg	ctg	gaa	gga	gtc	ttc	tga	agt	gagt	gat	gggtttgc	cta	attt	gta	1286
Asn	Tyr	Met	Leu	Glu	Gly	Val	Phe									
				360												
aatagagcta tgtgtgtgtt ggatttcgct gttgaagagg gaacggtaca agtcacaacc																1346
tgagagcttat tgcacgtttt ttatcttata tatgagtctc ttttaaattc tctgaaataa																1406
atgggggtgg tgattagtaa atagaggat aatctatcta atgagtcctc ttccttcagt																1466
tttttctttc ttcttttcta agacagctta ttaaacttat taagctctgt ttttgatctt																1526
ggtatcatca ccctcgcaag tgttttgttt tgtcccatat ttatttaaca ttatataatg																1586
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PF59082SeqList_PF59082.txt

<210> 742
 <211> 363
 <212> PRT
 <213> Brassica napus

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Gly Lys Ala Ser Lys Lys Arg Ser Asp Phe Phe Asp Leu Asp Asp Glu
      35      40      45
Phe Glu Ala Asp Phe Gln Gly Phe Glu Asp Asp Asp Ala Ser Phe Asp
      50      55      60
Cys Glu Asp Asp Asp Asp Val Phe Ala Lys Val Lys Pro Phe Val
65      70      75      80
Phe Thr Ala Thr Thr Lys Pro Val Ala Ser Pro Pro Thr Ala Thr Gly
      85      90      95
Ser Val Ser Gly Lys Lys Ile Ile Glu Ser Gly Gly Gln Ala Glu Lys
      100      105      110
Ser Ala Lys Arg Lys Arg Lys Asn Gln Tyr Arg Gly Ile Arg Gln Arg
      115      120      125
Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp Pro Arg Lys Gly Ser
130      135      140
Arg Glu Trp Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala Ala Arg Ala
145      150      155      160
Tyr Asp Ala Ala Ala Arg Arg Ile Arg Gly Ser Lys Ala Lys Val Asn
      165      170      175
Phe Pro Glu Glu Ser Asn Asn Asn Arg Ser Val Ser Gln Lys Arg Pro
      180      185      190
Ser Ala Lys Lys Leu Val Ala Lys Pro Asn Gln Ser Pro Ala Leu Val
      195      200      205
Gln Gln Pro Met Ser Gln Tyr Cys Asn Asn Ser Phe Gly Asp Val Ser
210      215      220
Phe Val Glu Glu Lys Pro Gln Met Tyr Asn Asn Gln Phe Gly Leu Ala
225      230      235      240
Asn Ser Tyr Asn Asn His Tyr Phe Ser Ser Asp Gln Gly Ser Asn Ser
      245      250      255
Phe Asp Cys Ser Glu Phe Gly Trp Ser Asp His Gly Pro Lys Thr Pro
      260      265      270
Glu Ile Ser Ser Met Leu Val Gly Asn Asn Gln Ala Pro Phe Thr Glu
      275      280      285
Glu Thr Asn Ala Ala Lys Lys Leu Lys Pro Ser Ser Asp Asp Gly Thr
290      295      300
Ser Asn Gln Ser Asp Asp Leu Met Ala Tyr Leu Asp Asn Ala Leu Trp
305      310      315      320
Glu Ser Pro Ser Pro Leu Glu Val Glu Ala Met Leu Gly Val Asp Ala
      325      330      335
Val Ala Val Thr Gln Gly Glu Glu Asn Pro Met Asp Leu Trp Ser Leu
      340      345      350
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355      360
    
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<210> 743
 <211> 957
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (1)..(957)

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1      5      10      15
    
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PF59082SeqList_PF59082.txt

caa	ggt	ttc	aaa	gat	gat	tcg	tct	atc	gat	tgc	gat	gat	gat	ttc	gac	96
Gln	Gly	Phe	Lys	Asp	Asp	Ser	Ser	Ile	Asp	Cys	Asp	Asp	Asp	Phe	Asp	
			20					25					30			
gtc	ggt	gat	gtt	ttc	gcc	gat	gtg	aaa	cca	ttc	gtt	ttc	act	tcg	act	144
Val	Gly	Asp	Val	Phe	Ala	Asp	Val	Lys	Pro	Phe	Val	Phe	Thr	Ser	Thr	
			35				40					45				
cca	aaa	ccc	gcc	gtc	tcc	gcc	gct	gcg	gaa	ggt	tca	gtt	ttt	ggt	aag	192
Pro	Lys	Pro	Ala	Val	Ser	Ala	Ala	Ala	Glu	Gly	Ser	Val	Phe	Gly	Lys	
			50			55					60					
aaa	gtt	act	ggc	ttg	gat	ggg	gac	gct	gag	aaa	tct	gca	aat	agg	aag	240
Lys	Val	Thr	Gly	Leu	Asp	Gly	Asp	Ala	Glu	Lys	Ser	Ala	Asn	Arg	Lys	
			65		70					75					80	
agg	aag	aat	cag	tac	cga	ggg	att	agg	caa	cgt	cct	tgg	gga	aaa	tgg	288
Arg	Lys	Asn	Gln	Tyr	Arg	Gly	Ile	Arg	Gln	Arg	Pro	Trp	Gly	Lys	Trp	
			85					90						95		
gct	gct	gag	ata	cgt	gat	cca	agg	gaa	ggt	gct	aga	atc	tgg	ctt	gga	336
Ala	Ala	Glu	Ile	Arg	Asp	Pro	Arg	Glu	Gly	Ala	Arg	Ile	Trp	Leu	Gly	
			100				105						110			
acg	ttc	aag	aca	gct	gag	gaa	gct	gct	aga	gct	tac	gat	gct	gca	gcg	384
Thr	Phe	Lys	Thr	Ala	Glu	Glu	Ala	Ala	Arg	Ala	Tyr	Asp	Ala	Ala	Ala	
			115				120					125				
cgg	aga	atc	cgt	gga	tct	aaa	gct	aag	gtg	aat	ttc	cct	gaa	gaa	aac	432
Arg	Arg	Ile	Arg	Gly	Ser	Lys	Ala	Lys	Val	Asn	Phe	Pro	Glu	Glu	Asn	
			130		135					140						
atg	aag	gct	aat	tct	cag	aaa	cgc	tct	gtg	aag	gct	aat	ctt	cag	aaa	480
Met	Lys	Ala	Asn	Ser	Gln	Lys	Arg	Ser	Val	Lys	Ala	Asn	Leu	Gln	Lys	
					150					155					160	
cca	gtg	gct	aaa	cct	aac	cct	aac	cca	agt	cca	gct	ttg	gtt	cag	aac	528
Pro	Val	Ala	Lys	Pro	Asn	Pro	Asn	Pro	Ser	Pro	Ala	Leu	Val	Gln	Asn	
				165				170						175		
tcg	aac	atc	tcc	ttt	gaa	aat	atg	tgt	ttc	atg	gag	gag	aaa	cac	caa	576
Ser	Asn	Ile	Ser	Phe	Glu	Asn	Met	Cys	Phe	Met	Glu	Glu	Lys	His	Gln	
			180				185						190			
gtg	agc	aac	aac	aac	aac	aac	cag	ttt	ggg	atg	aca	aac	tcc	gtt	gat	624
Val	Ser	Asn	Asn	Asn	Asn	Asn	Gln	Phe	Gly	Met	Thr	Asn	Ser	Val	Asp	
			195				200					205				
gct	gga	tgt	aat	ggg	tat	cag	tat	ttc	agc	tct	gac	cag	ggt	agt	aat	672
Ala	Gly	Cys	Asn	Gly	Tyr	Gln	Tyr	Phe	Ser	Ser	Asp	Gln	Gly	Ser	Asn	
			210		215					220						
tct	ttc	gat	tgt	tcg	gag	ttt	ggg	tgg	agc	gat	caa	gct	ccg	ata	act	720
Ser	Phe	Asp	Cys	Ser	Glu	Phe	Gly	Trp	Ser	Asp	Gln	Ala	Pro	Ile	Thr	
					230					235					240	
ccc	gac	atc	tct	tct	gcg	gtt	atc	aac	aac	aac	aac	tca	gct	ctg	ttc	768
Pro	Asp	Ile	Ser	Ser	Ala	Val	Ile	Asn	Asn	Asn	Asn	Ser	Ala	Leu	Phe	
				245				250						255		
ttt	gag	gaa	gcc	aat	cca	gct	aag	aag	ctc	aag	tct	atg	gat	ttc	gag	816
Phe	Glu	Glu	Ala	Asn	Pro	Ala	Lys	Lys	Leu	Lys	Ser	Met	Asp	Phe	Glu	
			260				265					270				
aca	cct	tac	aac	aac	act	gaa	tgg	gac	gct	tca	ctg	gat	ttc	ctc	aac	864
Thr	Pro	Tyr	Asn	Asn	Thr	Glu	Trp	Asp	Ala	Ser	Leu	Asp	Phe	Leu	Asn	
			275			280						285				
gaa	gat	gct	gta	acg	act	cag	gac	aat	ggt	gca	aac	cct	atg	gac	cta	912
Glu	Asp	Ala	Val	Thr	Thr	Gln	Asp	Asn	Gly	Ala	Asn	Pro	Met	Asp	Leu	
			290			295				300						
tgg	agt	att	gat	gaa	att	cat	tcc	atg	att	gga	gga	gtc	ttc	tga		957
Trp	Ser	Ile	Asp	Glu	Ile	His	Ser	Met	Ile	Gly	Gly	Val	Phe			
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<211> 318

<212> PRT

<213> Arabidopsis thaliana

<400> 744

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Gln	Gly	Phe	Lys	Asp	Asp	Ser	Ser	Ile	Asp	Cys	Asp	Asp	Asp	Phe	Asp
			20					25				30			
Val	Gly	Asp	Val	Phe	Ala	Asp	Val	Lys	Pro	Phe	Val	Phe	Thr	Ser	Thr

PF59082SeqList_PF59082.txt

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      35      40      45
Pro Lys Pro Ala Val Ser Ala Ala Ala Glu Gly Ser Val Phe Gly Lys
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Lys Val Thr Gly Leu Asp Gly Asp Ala Glu Lys Ser Ala Asn Arg Lys
  65      70      75      80
Arg Lys Asn Gln Tyr Arg Gly Ile Arg Gln Arg Pro Trp Gly Lys Trp
      85      90      95
Ala Ala Glu Ile Arg Asp Pro Arg Glu Gly Ala Arg Ile Trp Leu Gly
      100      105      110
Thr Phe Lys Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Ala Ala Ala
      115      120      125
Arg Arg Ile Arg Gly Ser Lys Ala Lys Val Asn Phe Pro Glu Glu Asn
      130      135      140
Met Lys Ala Asn Ser Gln Lys Arg Ser Val Lys Ala Asn Leu Gln Lys
      145      150      155      160
Pro Val Ala Lys Pro Asn Pro Asn Pro Ser Pro Ala Leu Val Gln Asn
      165      170      175
Ser Asn Ile Ser Phe Glu Asn Met Cys Phe Met Glu Glu Lys His Gln
      180      185      190
Val Ser Asn Asn Asn Asn Gln Phe Gly Met Thr Asn Ser Val Asp
      195      200      205
Ala Gly Cys Asn Gly Tyr Gln Tyr Phe Ser Ser Asp Gln Gly Ser Asn
      210      215      220
Ser Phe Asp Cys Ser Glu Phe Gly Trp Ser Asp Gln Ala Pro Ile Thr
      225      230      235      240
Pro Asp Ile Ser Ser Ala Val Ile Asn Asn Asn Asn Ser Ala Leu Phe
      245      250      255
Phe Glu Glu Ala Asn Pro Ala Lys Lys Leu Lys Ser Met Asp Phe Glu
      260      265      270
Thr Pro Tyr Asn Asn Thr Glu Trp Asp Ala Ser Leu Asp Phe Leu Asn
      275      280      285
Glu Asp Ala Val Thr Thr Gln Asp Asn Gly Ala Asn Pro Met Asp Leu
      290      295      300
Trp Ser Ile Asp Glu Ile His Ser Met Ile Gly Gly Val Phe
      305      310      315

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<210> 745

<211> 1173

<212> DNA

<213> Gossypium hirsutum

<220>

<221> CDS

<222> (1)..(1173)

<400> 745

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  1      5      10      15
cga cga ttg acg gcc gat ttc ttg tgg ccc gat ctg aaa aaa tcc ggg      96
Arg Arg Leu Thr Ala Asp Phe Leu Trp Pro Asp Leu Lys Lys Ser Gly
      20      25      30
ttg aag aag ggg tcg ggt aag aga tac tcg aag ccc gtg atc gac ttg      144
Leu Lys Lys Gly Ser Gly Lys Arg Tyr Ser Lys Pro Val Ile Asp Leu
      35      40      45
ggc gat gat ttc gag act gac ttt cag gag ttc aaa gat gaa gaa tct      192
Gly Asp Asp Phe Glu Thr Asp Phe Gln Glu Phe Lys Asp Glu Glu Ser
      50      55      60
gat ata gat gat tat gat gtt gat gat gtt ttg gct gat gta aag ccc      240
Asp Ile Asp Asp Tyr Val Asp Asp Val Leu Ala Asp Val Lys Pro
      65      70      75      80
ttt gct ttt aac gct aca aag aaa cct gct tct gct gtc tct cat ggt      288
Phe Ala Phe Asn Ala Thr Lys Lys Pro Ala Ser Ala Val Ser His Gly
      85      90      95
tcg aac tct gaa aaa tcc atg caa ttc aat ggt caa gct gag aaa tgt      336
Ser Asn Ser Glu Lys Ser Met Gln Phe Asn Gly Gln Ala Glu Lys Cys
      100      105      110
gcg aaa aga aag agg aag aac cag tat cgt gga atc cgg cag cgc cca      384
Ala Lys Arg Lys Arg Lys Asn Gln Tyr Arg Gly Ile Arg Gln Arg Pro

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PF59082SeqList_PF59082.txt

115	120	125		
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130	135	140		
gtc tgg tta gga act ttc aat act gct gaa gaa gct gcg aga gct tat	Val Trp Leu Gly Thr Phe Asn Thr Ala Glu Glu Ala Ala Arg Ala Tyr			480
145	150	155		
gat gct gag gca cgg aga att cgt ggt aag aaa gct aag gtg aac ttc	Asp Ala Glu Ala Arg Arg Ile Arg Gly Lys Lys Ala Lys Val Asn Phe			528
165	170	175		
cct aac gag act ccg cgt acc tct cca aag cat gca gtc aag aca aat	Pro Asn Glu Thr Pro Arg Thr Ser Pro Lys His Ala Val Lys Thr Asn			576
180	185	190		
tct cag aaa cca ctt tcc aag tca aat tcg agc cct gtt cag cca aat	Ser Gln Lys Pro Leu Ser Lys Ser Asn Ser Ser Pro Val Gln Pro Asn			624
195	200	205		
ctc aac cag aat tac aat tac ttg aac cag cct gag cag gaa tac ttt	Leu Asn Gln Asn Tyr Asn Tyr Leu Asn Gln Pro Glu Gln Glu Tyr Phe			672
210	215	220		
gat acc atg ggt ttc gta gaa gag aag cca tcg gtc aat cag ttc gca	Asp Thr Met Gly Phe Val Glu Glu Lys Pro Ser Val Asn Gln Phe Ala			720
225	230	235		
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245	250	255		
gat aat gcc ccc ttg tac ttc aat tca gac cag gga agt aac tcg atc	Asp Asn Ala Pro Leu Tyr Phe Asn Ser Asp Gln Gly Ser Asn Ser Ile			816
260	265	270		
aat tgt tcc gac tat ggc tgg gga gaa cag ggt gcc aaa act cct gaa	Asn Cys Ser Asp Tyr Gly Trp Glu Gln Gly Ala Lys Thr Pro Glu			864
275	280	285		
ata tca tcc att ctg gaa gct tct gta gag ggt gat gag ttt ctt gag	Ile Ser Ser Ile Leu Glu Ala Ser Val Glu Gly Asp Glu Phe Leu Glu			912
290	295	300		
gat gct aac cct agc aag aag ctg aaa cca agt tcc gac aat gtt atg	Asp Ala Asn Pro Ser Lys Lys Leu Lys Pro Ser Ser Asp Asn Val Met			960
305	310	315		
cct gcc gaa gac aac tcc gcg aag acc ttg tcg gac gag ctg ttg gct	Pro Ala Glu Asp Asn Ser Ala Lys Thr Leu Ser Asp Glu Leu Leu Ala			1008
325	330	335		
ttg gac aac cag atg aaa tac ttc caa atg ccg cca ttt att gaa gga	Leu Asp Asn Gln Met Lys Tyr Phe Gln Met Pro Pro Phe Ile Glu Gly			1056
340	345	350		
aac tgg gac gcc act att gat gct ttc ctc aat gga gat gca aca cag	Asn Trp Asp Ala Thr Ile Asp Ala Phe Leu Asn Gly Asp Ala Thr Gln			1104
355	360	365		
gat ggt gga aac ccg atg gat ctt tgg aac ttt gat gat ttc cct acc	Asp Gly Gly Asn Pro Met Asp Leu Trp Asn Phe Asp Asp Phe Pro Thr			1152
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385	390			

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<211> 390

<212> PRT

<213> Gossypium hirsutum

<400> 746

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Leu Lys Lys Gly Ser Gly Lys Arg Tyr Ser Lys Pro Val Ile Asp Leu	40	45	50	55
Gly Asp Asp Phe Glu Thr Asp Phe Gln Glu Phe Lys Asp Glu Glu Ser	60	65	70	75
Asp Ile Asp Asp Tyr Asp Val Asp Asp Val Leu Ala Asp Val Lys Pro	80			

PF59082SeqList_PF59082.txt

Phe Ala Phe Asn Ala Thr Lys Lys Pro Ala Ser His Gly
 85 90 95
 Ser Asn Ser Glu Lys Ser Met Gln Phe Asn Gly Gln Ala Glu Lys Cys
 100 105 110
 Ala Lys Arg Lys Arg Lys Asn Gln Tyr Arg Gly Ile Arg Gln Arg Pro
 115 120 125
 Trp Gly Lys Trp Ala Ala Glu Ile Arg Gly Pro Arg Lys Gly Val Arg
 130 135 140
 Val Trp Leu Gly Thr Phe Asn Thr Ala Glu Glu Ala Ala Arg Ala Tyr
 145 150 155 160
 Asp Ala Glu Ala Arg Ile Arg Gly Lys Lys Ala Lys Val Asn Phe
 165 170 175
 Pro Asn Glu Thr Pro Arg Thr Ser Pro Lys His Ala Val Lys Thr Asn
 180 185 190
 Ser Gln Lys Pro Leu Ser Lys Ser Asn Ser Ser Pro Val Gln Pro Asn
 195 200 205
 Leu Asn Gln Asn Tyr Asn Tyr Leu Asn Gln Pro Glu Gln Glu Tyr Phe
 210 215 220
 Asp Thr Met Gly Phe Val Glu Glu Lys Pro Ser Val Asn Gln Phe Ala
 225 230 235 240
 Tyr Val Asp Pro Val Pro Thr Ser Ile Asp Ala Gly Phe Asn Gln Ser
 245 250 255
 Asp Asn Ala Pro Leu Tyr Phe Asn Ser Asp Gln Gly Ser Asn Ser Ile
 260 265 270
 Asn Cys Ser Asp Tyr Gly Trp Gly Gln Gly Ala Lys Thr Pro Glu
 275 280 285
 Ile Ser Ser Ile Leu Glu Ala Ser Val Glu Gly Asp Glu Phe Leu Glu
 290 295 300
 Asp Ala Asn Pro Ser Lys Lys Leu Lys Pro Ser Ser Asp Asn Val Met
 305 310 315 320
 Pro Ala Glu Asp Asn Ser Ala Lys Thr Leu Ser Asp Glu Leu Leu Ala
 325 330 335
 Leu Asp Asn Gln Met Lys Tyr Phe Gln Met Pro Pro Phe Ile Glu Gly
 340 345 350
 Asn Trp Asp Ala Thr Ile Asp Ala Phe Leu Asn Gly Asp Ala Thr Gln
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 370 375 380
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<210> 747

<211> 1077

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1077)

<400> 747

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Arg Arg Val Thr Ser Glu Phe Ile Trp Pro Asp Leu Lys Lys Asn Leu	
20 25 30	
aaa gga tcg aag aaa agc tcg aag aat cgt tcg aat ttc ttc gat ttt	144
Lys Gly Ser Lys Lys Ser Ser Lys Asn Arg Ser Asn Phe Phe Asp Phe	
35 40 45	
gac gct gag ttc gaa gct gat ttc caa ggt ttc aaa gat gat tcg tct	192
Asp Ala Glu Phe Glu Ala Asp Phe Gln Gly Phe Lys Asp Asp Ser Ser	
50 55 60	
atc gat tgc gat gat gat ttc gac gtc ggt gat gtt ttc gcc gat gtg	240
Ile Asp Cys Asp Asp Asp Phe Asp Val Gly Asp Val Phe Ala Asp Val	
65 70 75 80	
aaa cca ttc gtt ttc act tcg act cca aaa ccc gcc gtc tcc gcc gct	288
Lys Pro Phe Val Phe Thr Ser Thr Pro Lys Pro Ala Val Ser Ala Ala	
85 90 95	

PF59082SeqList_PF59082.txt

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			100					105					110			
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Ala	Glu	Lys	Ser	Ala	Asn	Arg	Lys	Arg	Lys	Asn	Gln	Tyr	Arg	Gly	Ile	
		115					120					125				
agg	caa	cgt	cct	tgg	gga	aaa	tgg	gct	gct	gag	ata	cgt	gat	cca	agg	432
Arg	Gln	Arg	Pro	Trp	Gly	Lys	Trp	Ala	Ala	Glu	Ile	Arg	Asp	Pro	Arg	
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gaa	ggt	gct	aga	atc	tgg	ctt	gga	acg	ttc	aag	aca	gct	gag	gaa	gct	480
Glu	Gly	Ala	Arg	Ile	Trp	Leu	Gly	Thr	Phe	Lys	Thr	Ala	Glu	Glu	Ala	
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gct	aga	gct	tac	gat	gct	gca	gcg	cgg	aga	atc	cgt	gga	tct	aaa	gct	528
Ala	Arg	Ala	Tyr	Asp	Ala	Ala	Ala	Arg	Arg	Ile	Arg	Gly	Ser	Lys	Ala	
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Lys	Val	Asn	Phe	Pro	Glu	Glu	Asn	Met	Lys	Ala	Asn	Ser	Gln	Lys	Arg	
		180						185					190			
tct	gtg	aag	gct	aat	ctt	cag	aaa	cca	gtg	gct	aaa	cct	aac	cct	aac	624
Ser	Val	Lys	Ala	Asn	Leu	Gln	Lys	Pro	Val	Ala	Lys	Pro	Asn	Pro	Asn	
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cca	agt	cca	gct	ttg	gtt	cag	aac	tcg	aac	atc	tcc	ttt	gaa	aat	atg	672
Pro	Ser	Pro	Ala	Leu	Val	Gln	Asn	Ser	Asn	Ile	Ser	Phe	Glu	Asn	Met	
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tgt	ttc	atg	gag	gag	aaa	cac	caa	gtg	agc	aac	aac	aac	aac	aac	cag	720
Cys	Phe	Met	Glu	Glu	Lys	His	Gln	Val	Ser	Asn	Asn	Asn	Asn	Asn	Gln	
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Phe	Gly	Met	Thr	Asn	Ser	Val	Asp	Ala	Gly	Cys	Asn	Gly	Tyr	Gln	Tyr	
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ttc	agc	tct	gac	cag	ggt	agt	aat	tct	ttc	gat	tgt	tcg	gag	ttt	ggt	816
Phe	Ser	Ser	Asp	Gln	Gly	Ser	Asn	Ser	Phe	Asp	Cys	Ser	Glu	Phe	Gly	
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Trp	Ser	Asp	Gln	Ala	Pro	Ile	Thr	Pro	Asp	Ile	Ser	Ser	Ala	Val	Ile	
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Asn	Asn	Asn	Asn	Ser	Ala	Leu	Phe	Phe	Glu	Glu	Ala	Asn	Pro	Ala	Lys	
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Lys	Leu	Lys	Ser	Met	Asp	Phe	Glu	Thr	Pro	Tyr	Asn	Asn	Thr	Glu	Trp	
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gac	gct	tca	ctg	gat	ttc	ctc	aac	gaa	gat	gct	gta	acg	act	cag	gac	1008
Asp	Ala	Ser	Leu	Asp	Phe	Leu	Asn	Glu	Asp	Ala	Val	Thr	Thr	Gln	Asp	
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aat	ggt	gca	aac	cct	atg	gac	cta	tgg	agt	att	gat	gaa	att	cat	tcc	1056
Asn	Gly	Ala	Asn	Pro	Met	Asp	Leu	Trp	Ser	Ile	Asp	Glu	Ile	His	Ser	
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atg	att	gga	gga	gtc	ttc	tga										1077
Met	Ile	Gly	Gly	Val	Phe											
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<211> 358

<212> PRT

<213> Arabidopsis thaliana

<400> 748

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Lys	Gly	Ser	Lys	Lys	Ser	Ser	Lys	Asn	Arg	Ser	Asn	Phe	Phe	Asp	Phe
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Asp	Ala	Glu	Phe	Glu	Ala	Asp	Phe	Gln	Gly	Phe	Lys	Asp	Asp	Ser	Ser
	50					55				60					
Ile	Asp	Cys	Asp	Asp	Asp	Phe	Asp	Val	Gly	Asp	Val	Phe	Ala	Asp	Val
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PF59082SeqList_PF59082.txt

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gct gaa att cgt gat ccg agg aaa ggg att cga gtt tgg ctt gga act	500			
Ala Glu Ile Arg Asp Pro Arg Lys Gly Ile Arg Val Trp Leu Gly Thr				
ttc aat tct gcg gaa gaa gca gct aga gct tat gat gtt gag gca cga	548			
Phe Asn Ser Ala Glu Glu Ala Ala Arg Ala Tyr Asp Val Glu Ala Arg				
agg atc aga ggc aag aag gct aag gtg aac ttt cct gat gga tct cca	596			
Arg Ile Arg Gly Lys Lys Ala Lys Val Asn Phe Pro Asp Gly Ser Pro				
gct tct gct tca aga cgt gct gtt aag cca aat cct cag gag gca ctt	644			
Ala Ser Ala Ser Arg Ala Val Lys Pro Asn Pro Gln Glu Ala Leu				
cgc gag gaa atc ttg aac aca gtt cag ccg aac aca act tat atc aac	692			
Arg Glu Glu Ile Leu Asn Thr Val Gln Pro Asn Thr Thr Tyr Ile Asn				
aac ttg gac ggc gga tct gat gat tcg ttt ggc ttt ttc gaa gag aaa	740			
Asn Leu Asp Gly Gly Ser Asp Asp Ser Phe Gly Phe Phe Glu Glu Lys				
cca gca gca aag cag tat ggc tat gag aat gtt tct ttt act gct gga	788			
Pro Ala Ala Lys Gln Tyr Gly Tyr Glu Asn Val Ser Phe Thr Ala Gly				
gat atg gga ctg ggt tca att tcc cct tca act ggt aca aca aat gtt	836			
Asp Met Gly Leu Gly Ser Ile Ser Pro Ser Thr Gly Thr Thr Asn Val				
tac ttc agt tct gat gaa gga agc aac acc ttt gac tgc tct gat ttc	884			
Tyr Phe Ser Ser Asp Glu Gly Ser Asn Thr Phe Asp Cys Ser Asp Phe				
ggg tgg ggt gaa cca tgt ccg agg act cca gag atc tca tct gtt ctg	932			
Gly Trp Gly Glu Pro Cys Pro Arg Thr Pro Glu Ile Ser Ser Val Leu				
tca gaa gtt cta gaa tgt aat ggt act caa tct gat gaa gat gct aga	980			
Ser Glu Val Leu Glu Cys Asn Gly Thr Gln Ser Asp Glu Asp Ala Arg				
cca gag aaa aaa ctg aag tcg tgt tcc aac gct tcc ttg cca gat gag	1028			
Pro Glu Lys Lys Leu Lys Ser Cys Ser Asn Ala Ser Leu Pro Asp Glu				
gat aac act gtg cac acg cta tct gaa gag cta tcg gct ttt gaa tcc	1076			
Asp Asn Thr Val His Thr Leu Ser Glu Glu Leu Ser Ala Phe Glu Ser				
cag atg aag ttc ttg cag atc cca tat ctt gag gga aat tgg gat gca	1124			
Gln Met Lys Phe Leu Gln Ile Pro Tyr Leu Glu Gly Asn Trp Asp Ala				
tca gtt gat gcc ttt gtc aac aca ggc gca att cag gat ggc gga aat	1172			
Ser Val Asp Ala Phe Val Asn Thr Gly Ala Ile Gln Asp Gly Gly Asn				
gcg atg gat ctc tgg acc ttc gat gat gtt cct tct tta atg gga ggt	1220			
Ala Met Asp Leu Trp Thr Phe Asp Asp Val Pro Ser Leu Met Gly Gly				
gtc tac taagccaaca cgcaccttcc cttactaagt tttgtaaata aagcttcatt	1276			
Val Tyr				
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<210> 750

<211> 375

<212> PRT

<213> Capsicum annuum

<400> 750

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PF59082SeqList_PF59082.txt

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Ser Lys Phe Ile Asp Leu Asp Glu Glu Phe Glu Ala Asp Phe Gln Asp
Phe Lys Asp Tyr Ala Asp Asp Asp Val Asp Asp Val Lys Pro Phe Gly
65 Ser Lys Ser Val Lys Ser Gly Asp Ser Ser Ser Cys Asp Thr Glu Lys Ser
Ser Lys Arg Lys Arg Lys Asn Gln Tyr Arg Gly Ile Arg Gln Arg Pro
Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp Pro Arg Lys Gly Ile Arg
Val Trp Lys Glu Thr Phe Asn Ser Ala Glu Glu Ala Ala Arg Ala Tyr
130 Asp Val Glu Ala Arg Arg Ile Arg Gly Lys Lys Ala Lys Val Asn Phe
145 Pro Asp Gly Ser Pro Ala Ser Ala Ser Arg Ala Val Lys Pro Asn
Pro Gln Glu Ala Leu Arg Glu Glu Ile Leu Asn Thr Val Gln Pro Asn
Thr Thr Tyr Ile Asn Asn Leu Asp Gly Gly Ser Asp Asp Ser Phe Gly
195 Phe Phe Glu Glu Lys Pro Ala Lys Gln Tyr Gly Tyr Glu Asn Val
210 Ser Phe Thr Ala Gly Asp Met Gly Leu Gly Ser Ile Ser Pro Ser Thr
225 Gly Thr Thr Asn Val Tyr Phe Ser Ser Asp Glu Gly Ser Asn Thr Phe
245 Asp Cys Ser Asp Phe Gly Trp Gly Glu Pro Cys Pro Arg Thr Pro Glu
260 Ile Ser Ser Val Leu Ser Glu Val Leu Glu Cys Asn Gly Thr Gln Ser
275 Asp Glu Asp Ala Arg Pro Glu Lys Lys Leu Lys Ser Cys Ser Asn Ala
290 Ser Leu Pro Asp Glu Asp Asn Thr Val His Thr Leu Ser Glu Glu Leu
305 Ser Ala Phe Glu Ser Gln Met Lys Phe Leu Gln Ile Pro Tyr Leu Glu
325 Gly Asn Trp Asp Ala Ser Val Asp Ala Phe Val Asn Thr Gly Ala Ile
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<210> 751

<211> 1191

<212> DNA

<213> Gossypium hirsutum

<220>

<221> CDS

<222> (1)..(1191)

<400> 751

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cga	ctg	gtg	acg	gcg	aat	tat	ttg	tgg	ccg	gat	ctg	aaa	aaa	tcc	ggc	96
Arg	Leu	Val	Thr	Ala	Asn	Tyr	Leu	Trp	Pro	Asp	Leu	Lys	Lys	Ser	Gly	
			20					25					30			
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Ser	Lys	Lys	Arg	Ser	Gly	Arg	Lys	His	Ser	Lys	Lys	Pro	Ala	Val	Gly	
		35				40						45				
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Phe	Glu	Asp	Asp	Phe	Glu	Ala	Asp	Phe	Gln	Val	Phe	Lys	Asp	Glu	Asp	

PF59082SeqList_PF59082.txt

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Val Lys Ser Phe Ala Phe Ser Ala Thr Lys Lys Pro Ser Pro Ala Val				
85 90 95				
tct cat ggt tca aac tcc ata aaa tct gtg gaa ttc agt ggt caa gct	336			
Ser His Gly Ser Asn Ser Ile Lys Ser Val Glu Phe Ser Gly Gln Ala				
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gag aaa tct gca aaa aga aag agg aac cag tat cgc gga att cgc	384			
Glu Lys Ser Ala Lys Arg Lys Arg Lys Asn Gln Tyr Arg Gly Ile Arg				
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cag cgt ccg tgg ggt aaa tgg gct gct gag atc cgt gat cct agg aaa	432			
Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp Pro Arg Lys				
130 135 140				
ggg gtt agg gtg tgg ctt gga act ttt aat act gct gag gaa gct gca	480			
Gly Val Arg Val Trp Leu Gly Thr Phe Asn Thr Ala Glu Glu Ala Ala				
145 150 155 160				
cga gct tat gat gct gag gca ctg aga att cgg ggt aag aaa gca aag	528			
Arg Ala Tyr Asp Ala Glu Ala Leu Arg Ile Arg Gly Lys Lys Ala Lys				
165 170 175				
gtg aac ttc cct gat gag act cca cgt acc act cca aag cat gct gtt	576			
Val Asn Phe Pro Asp Glu Thr Pro Arg Thr Thr Pro Lys His Ala Val				
180 185 190				
aaa atg aat tct cag aaa cct ctt tcc ggg tca aat ttg agt tct gtt	624			
Lys Met Asn Ser Gln Lys Pro Leu Ser Gly Ser Asn Leu Ser Ser Val				
195 200 205				
caa tca agt ctc aac cca gat ttc agt tac tcg aac aaa ctt gag cag	672			
Gln Ser Leu Asn Pro Asp Phe Ser Tyr Ser Asn Lys Leu Glu Gln				
210 215 220				
ggc tac tat gat acc gtg ggt ttc att gaa gag aag tca cta atg gat	720			
Gly Tyr Tyr Asp Thr Val Gly Phe Ile Glu Glu Lys Ser Leu Met Asp				
225 230 235 240				
cag ttt gca tat gca gac cct gtt aga gct gta gat gat ggg tta	768			
Gln Phe Ala Tyr Ala Asp Pro Val Arg Ala Ala Val Asp Asp Gly Leu				
245 250 255				
aaa ccc ttt gct gac cct gag aat acc gct tcg ttt ttt atc tca gat	816			
Lys Pro Phe Ala Asp Pro Glu Asn Thr Ala Ser Phe Phe Ile Ser Asp				
260 265 270				
cca ggg agt aac aac ttt gac agt tcc gac ctt gtc tgg ggc gac cag	864			
Pro Gly Ser Asn Asn Phe Asp Ser Ser Asp Leu Val Trp Gly Asp Gln				
275 280 285				
ggt gcc aag act cct gaa ata tca tcc tct ctt gaa cct act cta gag	912			
Gly Ala Lys Thr Pro Glu Ile Ser Ser Ser Leu Glu Pro Thr Leu Glu				
290 295 300				
gtc aac gag ttt ctg gac aac gca aac cct acg aag aag ttg aaa ctg	960			
Val Asn Glu Phe Leu Asp Asn Ala Asn Pro Thr Lys Lys Leu Lys Leu				
305 310 315 320				
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Ser Leu Asn Asn Val Met Pro Thr Gly Gly Asp Asn Ser Val Lys Ser				
325 330 335				
tta tcc gat gag cta tta gct atg gac aat caa gtg aac tac ttt cag	1056			
Leu Ser Asp Glu Leu Leu Ala Met Asp Asn Gln Val Asn Tyr Phe Gln				
340 345 350				
aca cca ttt att gac gag aac tgg aat gtt tcg atg gat gac ttc ctt	1104			
Thr Pro Phe Ile Asp Glu Asn Trp Asn Val Ser Met Asp Asp Phe Leu				
355 360 365				
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Asn Gly Asp Ala Thr Gln Val Gly Gly Asn Glu Met Gly Phe Trp Ser				
370 375 380				
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<211> 396

<212> PRT

<213> Gossypium hirsutum

PF59082SeqList_PF59082.txt

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35      40      45
Phe Glu Asp Asp Phe Glu Ala Asp Phe Gln Val Phe Lys Asp Glu Asp
50      55      60
Ser Asp Val Asp Asp Phe Asn Asp Asp Val Asp Val Leu Ala Asp
65      70      75      80
Val Lys Ser Phe Ala Phe Ser Ala Thr Lys Lys Pro Ser Pro Ala Val
85      90      95
Ser His Gly Ser Asn Ser Ile Lys Ser Val Glu Phe Ser Gly Gln Ala
100     105     110
Glu Lys Ser Ala Lys Arg Lys Arg Lys Asn Gln Tyr Arg Gly Ile Arg
115     120     125
Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp Pro Arg Lys
130     135     140
Gly Val Arg Val Trp Leu Gly Thr Phe Asn Thr Ala Glu Glu Ala Ala
145     150     155     160
Arg Ala Tyr Asp Ala Glu Ala Leu Arg Ile Arg Gly Lys Lys Ala Lys
165     170     175
Val Asn Phe Pro Asp Glu Thr Pro Arg Thr Thr Pro Lys His Ala Val
180     185     190
Lys Met Asn Ser Gln Lys Pro Leu Ser Gly Ser Asn Leu Ser Ser Val
195     200     205
Gln Ser Ser Leu Asn Pro Asp Phe Ser Tyr Ser Asn Lys Leu Glu Gln
210     215     220
Gly Tyr Tyr Asp Thr Val Gly Phe Ile Glu Glu Lys Ser Leu Met Asp
225     230     235     240
Gln Phe Ala Tyr Ala Asp Pro Val Arg Ala Ala Val Asp Asp Gly Leu
245     250     255
Lys Pro Phe Ala Asp Pro Glu Asn Thr Ala Ser Phe Phe Ile Ser Asp
260     265     270
Pro Gly Ser Asn Asn Phe Asp Ser Ser Asp Leu Val Trp Gly Asp Gln
275     280     285
Gly Ala Lys Thr Pro Glu Ile Ser Ser Ser Leu Glu Pro Thr Leu Glu
290     295     300
Val Asn Glu Phe Leu Asp Asn Ala Asn Pro Thr Lys Lys Leu Lys Leu
305     310     315     320
Ser Leu Asn Asn Val Met Pro Thr Gly Gly Asp Asn Ser Val Lys Ser
325     330     335
Leu Ser Asp Glu Leu Leu Ala Met Asp Asn Gln Val Asn Tyr Phe Gln
340     345     350
Thr Pro Phe Ile Asp Glu Asn Trp Asn Val Ser Met Asp Asp Phe Leu
355     360     365
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<211> 1173
<212> DNA
<213> Gossypium hirsutum

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<220>
<221> CDS
<222> (1)..(1173)

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cga cga ttg acg gcc gat ttc ttg tgg ccc gat ctg aaa aaa tcc ggg      96
Arg Arg Leu Thr Ala Asp Phe Leu Trp Pro Asp Leu Lys Lys Ser Gly
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Gly	Asp	Asp	Phe	Glu	Thr	Asp	Phe	Gln	Glu	Phe	Lys	Asp	Glu	Glu	Ser	
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Asp	Ile	Asp	Asp	Tyr	Asp	Val	Asp	Asp	Val	Leu	Ala	Asp	Val	Lys	Pro	
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Phe	Ala	Phe	Asn	Ala	Thr	Lys	Lys	Pro	Ala	Ser	Ala	Val	Ser	His	Gly	
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tcg	aac	tct	gaa	aaa	tcc	atg	caa	ttc	aat	ggg	caa	gct	gag	aaa	tgt	336
Ser	Asn	Ser	Glu	Lys	Ser	Met	Gln	Phe	Asn	Gly	Gln	Ala	Glu	Lys	Cys	
			100					105					110			
gcg	aaa	aga	aag	agg	aag	aac	cag	tat	cgt	gga	atc	cgg	cag	cgc	cca	384
Ala	Lys	Arg	Lys	Arg	Lys	Asn	Gln	Tyr	Arg	Gly	Ile	Arg	Gln	Arg	Pro	
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Trp	Gly	Lys	Trp	Ala	Ala	Glu	Ile	Arg	Asp	Pro	Arg	Lys	Gly	Val	Arg	
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gtc	tggt	tta	gga	act	ttc	aat	act	gct	gaa	gaa	gct	gcg	aga	gct	tat	480
Val	Trp	Leu	Gly	Thr	Phe	Asn	Thr	Ala	Glu	Glu	Ala	Ala	Arg	Ala	Tyr	
145					150				155						160	
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Asp	Ala	Glu	Ala	Arg	Arg	Ile	Arg	Gly	Lys	Lys	Ala	Lys	Val	Asn	Phe	
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Pro	Asn	Glu	Thr	Pro	Arg	Thr	Ser	Pro	Lys	His	Ala	Val	Lys	Thr	Asn	
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Ser	Gln	Lys	Pro	Leu	Ser	Lys	Ser	Asn	Ser	Ser	Pro	Val	Gln	Pro	Asn	
		195					200					205				
ctc	aac	cag	aat	tac	aat	tac	ttg	aac	cag	cct	gag	cag	gaa	tac	ttt	672
Leu	Asn	Gln	Asn	Tyr	Asn	Tyr	Leu	Asn	Gln	Pro	Glu	Gln	Glu	Tyr	Phe	
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Tyr	Val	Asp	Pro	Val	Pro	Thr	Ser	Ile	Asp	Ala	Gly	Phe	Asn	Gln	Ser	
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gat	aat	gcc	ccc	ttg	tac	ttc	aat	tca	gac	cag	gga	agt	aac	tcg	atc	816
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aat	tgt	tcc	gac	tat	ggc	tggt	gga	gaa	cag	ggg	gcc	aaa	act	cct	gaa	864
Asn	Cys	Ser	Asp	Tyr	Gly	Trp	Gly	Glu	Gln	Gly	Ala	Lys	Thr	Pro	Glu	
		275				280					285					
ata	tca	tcc	att	ctg	gaa	gct	tct	gta	gag	ggg	gat	gag	ttt	ctt	gag	912
Ile	Ser	Ser	Ile	Leu	Glu	Ala	Ser	Val	Glu	Gly	Asp	Glu	Phe	Leu	Glu	
	290					295					300					
gat	gct	aac	cct	agc	aag	aag	ctg	aaa	cca	agt	tcc	gac	aat	gtt	atg	960
Asp	Ala	Asn	Pro	Ser	Lys	Lys	Leu	Lys	Pro	Ser	Ser	Asp	Asn	Val	Met	
305					310					315					320	
cct	gcc	gaa	gac	aac	tcc	gcg	aag	acc	ttg	tcg	gac	gag	ctg	ttg	gct	1008
Pro	Ala	Glu	Asp	Asn	Ser	Ala	Lys	Thr	Leu	Ser	Asp	Glu	Leu	Leu	Ala	
				325					330					335		
ttg	gac	aac	cag	atg	aaa	tac	ttc	caa	atg	ccg	cca	ttt	att	gaa	gga	1056
Leu	Asp	Asn	Gln	Met	Lys	Tyr	Phe	Gln	Met	Pro	Pro	Phe	Ile	Glu	Gly	
			340					345					350			
aac	tggt	gac	gcc	act	att	gat	gct	ttc	ctc	aat	gga	gat	gca	aca	cag	1104
Asn	Trp	Asp	Ala	Thr	Ile	Asp	Ala	Phe	Leu	Asn	Gly	Asp	Ala	Thr	Gln	
		355					360					365				
gat	ggg	gga	aac	ccg	atg	gat	ctt	tggt	aac	ttt	gat	gat	ttc	cct	acc	1152
Asp	Gly	Gly	Asn	Pro	Met	Asp	Leu	Trp	Asn	Phe	Asp	Asp	Phe	Pro	Thr	
	370					375					380					
atg	gcg	gag	ggg	gtt	ttc	tga										1173
Met	Ala	Glu	Gly	Val	Phe											
385					390											

PF59082SeqList_PF59082.txt

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 <211> 390
 <212> PRT
 <213> Gossypium hirsutum

<400> 754
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 Leu Lys Lys Gly Ser Gly Lys Arg Tyr Ser Lys Pro Val Ile Asp Leu
 35 40 45
 Gly Asp Asp Phe Glu Thr Asp Phe Gln Glu Phe Lys Asp Glu Glu Ser
 50 55 60
 Asp Ile Asp Asp Tyr Asp Val Asp Asp Val Leu Ala Asp Val Lys Pro
 65 70 75 80
 Phe Ala Phe Asn Ala Thr Lys Lys Pro Ala Ser Ala Val Ser His Gly
 85 90 95
 Ser Asn Ser Glu Lys Ser Met Gln Phe Asn Gly Gln Ala Glu Lys Cys
 100 105 110
 Ala Lys Arg Lys Arg Lys Asn Gln Tyr Arg Gly Ile Arg Gln Arg Pro
 115 120 125
 Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp Pro Arg Lys Gly Val Arg
 130 135 140
 Val Trp Leu Gly Thr Phe Asn Thr Ala Glu Glu Ala Ala Arg Ala Tyr
 145 150 155 160
 Asp Ala Glu Ala Arg Arg Ile Arg Gly Lys Lys Ala Lys Val Asn Phe
 165 170 175
 Pro Asn Glu Thr Pro Arg Thr Ser Pro Lys His Ala Val Lys Thr Asn
 180 185 190
 Ser Gln Lys Pro Leu Ser Lys Ser Asn Ser Ser Pro Val Gln Pro Asn
 195 200 205
 Leu Asn Gln Asn Tyr Asn Tyr Leu Asn Gln Pro Glu Gln Glu Tyr Phe
 210 215 220
 Asp Thr Met Gly Phe Val Glu Glu Lys Pro Ser Val Asn Gln Phe Ala
 225 230 235 240
 Tyr Val Asp Pro Val Pro Thr Ser Ile Asp Ala Gly Phe Asn Gln Ser
 245 250 255
 Asp Asn Ala Pro Leu Tyr Phe Asn Ser Asp Gln Gly Ser Asn Ser Ile
 260 265 270
 Asn Cys Ser Asp Tyr Gly Trp Gly Glu Gln Gly Ala Lys Thr Pro Glu
 275 280 285
 Ile Ser Ser Ile Leu Glu Ala Ser Val Glu Gly Asp Glu Phe Leu Glu
 290 295 300
 Asp Ala Asn Pro Ser Lys Lys Leu Lys Pro Ser Ser Asp Asn Val Met
 305 310 315 320
 Pro Ala Glu Asp Asn Ser Ala Lys Thr Leu Ser Asp Glu Leu Leu Ala
 325 330 335
 Leu Asp Asn Gln Met Lys Tyr Phe Gln Met Pro Pro Phe Ile Glu Gly
 340 345 350
 Asn Trp Asp Ala Thr Ile Asp Ala Phe Leu Asn Gly Asp Ala Thr Gln
 355 360 365
 Asp Gly Gly Asn Pro Met Asp Leu Trp Asn Phe Asp Asp Phe Pro Thr
 370 375 380
 Met Ala Glu Gly Val Phe
 385 390

<210> 755
 <211> 1460
 <212> DNA
 <213> Manihot esculenta

<220>
 <221> CDS
 <222> (18)..(1163)

<400> 755
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 Seite 974

PF59082SeqList_PF59082.txt

	Met	Cys	Gly	Gly	Ala	Ile	Ile	Ser	Asp	Phe	Ile						
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ctc tgg cct gat cta aag aag ccc att ggg aaa atc gtt ggt gac ctt	Leu	Trp	Pro	Asp	Leu	Lys	Lys	Pro	Ile	Gly	Lys	Ile	Val	Gly	Asp	Leu	146
gac gat gat ttc gag gct gat ttc cag gag ttt aag gat gag tct gat	Asp	Asp	Asp	Phe	Glu	Ala	Asp	Phe	Gln	Glu	Phe	Lys	Asp	Glu	Ser	Asp	194
gtc gat gag gaa gat gac gtt ttg ttt gat gtc aag cct ttc tct ttc	Val	Asp	Glu	Glu	Asp	Asp	Val	Leu	Phe	Asp	Val	Lys	Pro	Phe	Ser	Phe	242
tct gct act gct tct cct cct cct cgc aat cgc agt cct tca cgt ggt	Ser	Ala	Thr	Ala	Ser	Pro	Pro	Pro	Arg	Asn	Arg	Ser	Pro	Ser	Arg	Gly	290
tct aca gct gta aag tct gtg gaa ttt aat ggg cta gct gaa aaa tct	Ser	Thr	Ala	Val	Lys	Ser	Val	Glu	Phe	Asn	Gly	Leu	Ala	Glu	Lys	Ser	338
gca aag aga aag aga aaa aac cag tac aga gga atc cgg cag cgc cca	Ala	Lys	Arg	Lys	Arg	Lys	Asn	Gln	Tyr	Arg	Gly	Ile	Arg	Gln	Arg	Pro	386
tgg gga aaa tgg gct gct gag att cgt gac ccc agg aaa ggg gtg cgt	Trp	Gly	Lys	Trp	Ala	Ala	Glu	Ile	Arg	Asp	Pro	Arg	Lys	Gly	Val	Arg	434
gtc tgg cta gga aca ttc aat act gct gaa gaa gct gca aga gcg tat	Val	Trp	Leu	Gly	Thr	Phe	Asn	Thr	Ala	Glu	Glu	Ala	Ala	Arg	Ala	Tyr	482
gat gct gag gca cgt aga att cgt ggc aag aaa gct aaa gtg aac ttt	Asp	Ala	Glu	Ala	Arg	Arg	Ile	Arg	Gly	Lys	Lys	Ala	Lys	Val	Asn	Phe	530
cct gat gaa gct cca cgt gct tcc cca aag cgg aca atg aag gca aac	Pro	Asp	Glu	Ala	Pro	Arg	Ala	Ser	Pro	Lys	Arg	Thr	Met	Lys	Ala	Asn	578
cct cag aaa cca ctt cct aag aga aat gct act gag agt atg agt tac	Pro	Gln	Lys	Pro	Leu	Pro	Lys	Arg	Asn	Ala	Thr	Glu	Ser	Met	Ser	Tyr	626
ttg aac aat cca gat cag gac tac ttc aat act ttg ggc tct gtt gat	Leu	Asn	Asn	Pro	Asp	Gln	Gac	Tyr	Phe	Asn	Thr	Leu	Gly	Ser	Val	Asp	674
gag aaa cca cta gtg agc cag ttt gat ttg atg gac tct ttt cct gcc	Glu	Lys	Pro	Leu	Val	Ser	Gln	Phe	Asp	Leu	Met	Asp	Ser	Phe	Pro	Ala	722
aat gga gat gct aca gtc aaa tct att cct cca tgt gat aat gtt ccc	Asn	Gly	Asp	Ala	Thr	Val	Lys	Ser	Ile	Pro	Pro	Cys	Asp	Asn	Val	Pro	770
acg ttt ttc aat tct gat cag gga agc aac tca ttt gaa tgt tcc gac	Thr	Phe	Phe	Asn	Ser	Asp	Gln	Gly	Ser	Asn	Ser	Phe	Glu	Cys	Ser	Asp	818
ttt gga tgg ggg gag cag gcc tca aag act cct gaa atc tca tct gtt	Phe	Gly	Trp	Gly	Glu	Gln	Ala	Ser	Lys	Thr	Pro	Glu	Ile	Ser	Ser	Val	866
ctt tca gct act cca gaa att gat gaa tca ctt ttc atg gat gat gct	Leu	Ser	Ala	Thr	Pro	Glu	Ile	Asp	Glu	Ser	Leu	Phe	Met	Asp	Asp	Ala	914
aac cct aaa aag aag atg aag tct gac tct gaa aat gca gtt cct ata	Asn	Pro	Lys	Lys	Lys	Met	Lys	Ser	Asp	Ser	Glu	Asn	Ala	Val	Pro	Ile	962
gaa gaa agc aat gga aaa tct cta tca gag gag ttg ttg gct ttt gac	Glu	Glu	Ser	Asn	Gly	Lys	Ser	Leu	Ser	Glu	Glu	Leu	Leu	Ala	Phe	Asp	1010
aac cag atg aac ttt cag atg cct tat ctt gag gga agt tgg gag gct	Asn	Gln	Met	Asn	Phe	Gln	Met	Pro	Tyr	Leu	Glu	Gly	Ser	Trp	Glu	Ala	1058
tca ctt gat ggc ttc ctt aat gga gac gtg act cag gat ggt gga aat	Ser	Leu	Asp	Gly	Phe	Leu	Asn	Gly	Asp	Val	Thr	Gln	Asp	Gly	Gly	Asn	1106
cca atg gac ctg tgg agc ttt gat gac ctc cct aat atg gtt ggg gga																	1154

PF59082SeqList_PF59082.txt

Pro Met Asp Leu Trp Ser Phe Asp Asp Leu Pro Asn Met Val Gly Gly
 365 370 375
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 Val Tyr
 380
 tggttttctc tctgaaatgt attacaagca catctgaaca tgcttaatcc tttgaggaga 1270

 gtgtcctagg gagcttttgg tacaagagtt gtagtaaata ggaatattta gtttcccttt 1330

 tacattttga gacactggac ttgggttggt caatttaata actgtaattg acaatgtgcg 1390

 tgtgatttgt gtttaaaact gatataaatt ttatctctac tgttgTTTTT aaaaaaaaaa 1450

 aaaaaaaaaa 1460

<210> 756
 <211> 381
 <212> PRT
 <213> Manihot esculenta

<400> 756
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 Lys Lys Pro Ile Gly Lys Ile Val Gly Asp Leu Asp Asp Asp Phe Glu
 35 40 45
 Ala Asp Phe Gln Glu Phe Lys Asp Glu Ser Asp Val Asp Glu Glu Asp
 50 55 60
 Asp Val Leu Phe Asp Val Lys Pro Phe Ser Phe Ser Ala Thr Ala Ser
 65 70 75 80
 Pro Pro Pro Arg Asn Arg Ser Pro Ser Arg Gly Ser Thr Ala Val Lys
 85 90 95
 Ser Val Glu Phe Asn Gly Leu Ala Glu Lys Ser Ala Lys Arg Lys Arg
 100 105 110
 Lys Asn Gln Tyr Arg Gly Ile Arg Gln Arg Pro Trp Gly Lys Trp Ala
 115 120 125
 Ala Glu Ile Arg Asp Pro Arg Lys Gly Val Arg Val Trp Leu Gly Thr
 130 135 140
 Phe Asn Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Ala Glu Ala Arg
 145 150 155 160
 Arg Ile Arg Gly Lys Lys Ala Lys Val Asn Phe Pro Asp Glu Ala Pro
 165 170 175
 Arg Ala Ser Pro Lys Arg Thr Met Lys Ala Asn Pro Gln Lys Pro Leu
 180 185 190
 Pro Lys Arg Asn Ala Thr Glu Ser Met Ser Tyr Leu Asn Asn Pro Asp
 195 200 205
 Gln Asp Tyr Phe Asn Thr Leu Gly Ser Val Asp Glu Lys Pro Leu Val
 210 215 220
 Ser Gln Phe Asp Leu Met Asp Ser Phe Pro Ala Asn Gly Asp Ala Thr
 225 230 235 240
 Val Lys Ser Ile Pro Pro Cys Asp Asn Val Pro Thr Phe Phe Asn Ser
 245 250 255
 Asp Gln Gly Ser Asn Ser Phe Glu Cys Ser Asp Phe Gly Trp Gly Glu
 260 265 270
 Gln Ala Ser Lys Thr Pro Glu Ile Ser Ser Val Leu Ser Ala Thr Pro
 275 280 285
 Glu Ile Asp Glu Ser Leu Phe Met Asp Asp Ala Asn Pro Lys Lys Lys
 290 295 300
 Met Lys Ser Asp Ser Glu Asn Ala Val Pro Ile Glu Glu Ser Asn Gly
 305 310 315 320
 Lys Ser Leu Ser Glu Glu Leu Leu Ala Phe Asp Asn Gln Met Asn Phe
 325 330 335

PF59082SeqList_PF59082.txt

Gln Met Pro Tyr Leu Glu Gly Ser Trp Glu Ala Ser Leu Asp Gly Phe
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 Leu Asn Gly Asp Val Thr Gln Asp Gly Gly Asn Pro Met Asp Leu Trp
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 Ser Phe Asp Asp Leu Pro Asn Met Val Gly Gly Val Tyr
 370 375 380

<210> 757
 <211> 1409
 <212> DNA
 <213> Populus alba x Populus tremula

<220>
 <221> CDS
 <222> (20)..(1162)

<400> 757
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 gct ccg aca acc acc gct cga tct tct cgg cgg ttg acc tcg ggc ttt 100
 Ala Pro Thr Thr Thr Ala Arg Ser Ser Arg Arg Leu Thr Ser Gly Phe 15 20 25
 gag tgg ctt gag ccg aag aaa ccc ttc aac aac aag cac ttg aag cca 148
 Glu Trp Leu Glu Pro Lys Lys Pro Phe Asn Asn Lys His Leu Lys Pro 30 35 40
 gtt gtt gct gat ccc gaa gat gat ttt gag gct gat ctt caa gag ttt 196
 Val Val Ala Asp Pro Glu Asp Asp Phe Glu Ala Asp Leu Gln Glu Phe 45 50 55
 aag gac gag tct gat gtc gac gag gat tat gat gtc ttt gct gat gcc 244
 Lys Asp Glu Ser Asp Val Asp Glu Asp Tyr Asp Val Phe Ala Asp Ala 60 65 70 75
 aag cct ttt gct ttc tct gcc agt gct tct gaa cct gct aaa aaa cgt 292
 Lys Pro Phe Ala Phe Ser Ala Ser Ala Ser Glu Pro Ala Lys Lys Arg 80 85 90
 ggg ctc cct cgt ggt tct act gct gtt aaa tct gct gga ttc agt gga 340
 Gly Leu Pro Arg Gly Ser Thr Ala Val Lys Ser Ala Gly Phe Ser Gly 95 100 105
 ctt gct aaa aac tca gca aag agg aag aga aag aac cag ttt aga gga 388
 Leu Ala Lys Asn Ser Ala Lys Arg Lys Arg Lys Asn Gln Phe Arg Gly 110 115 120
 att agg cag cgt cca tgg gga aaa tgg gct gct gag att cgt gat ccc 436
 Ile Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp Pro 125 130 135
 agg aaa ggg gta cgt gtc tgg gga aca ttc aat act gca gaa gaa 484
 Arg Lys Gly Val Arg Val Trp Leu Gly Thr Phe Asn Thr Ala Glu Glu 140 145 150 155
 gct gct aga gca tat gat tct gag gca cgt aga att cgt ggc aag aaa 532
 Ala Ala Arg Ala Tyr Asp Ser Glu Ala Arg Ile Arg Gly Lys Lys 160 165 170
 gcg aag gtg aac ttc cct gat gaa gct cca tgt gct tca gca agg cat 580
 Ala Lys Val Asn Phe Pro Asp Glu Ala Pro Cys Ala Ser Ala Arg His 175 180 185
 cca att aag gaa aac tca cag aaa cga ctt aca aag gca aat tta agc 628
 Pro Ile Lys Glu Asn Ser Gln Lys Arg Leu Thr Lys Ala Asn Leu Ser 190 195 200
 cag gat ttt agt tac ttg agc aac cca gaa acg gat tat aat aat atg 676
 Gln Asp Phe Ser Tyr Leu Ser Asn Pro Glu Thr Asp Tyr Asn Asn Met 205 210 215
 ggc ttt gtg gaa gag aaa cca caa gtg agc cag ttt gga ata atg aat 724
 Gly Phe Val Glu Glu Lys Pro Gln Val Ser Gln Phe Gly Ile Met Asn 220 225 230 235
 tct atc ccg gtc aat gga gat tct ggg gtg acg ccc tta act cct tct 772
 Ser Ile Pro Val Asn Gly Asp Ser Gly Val Thr Pro Leu Thr Pro Ser 240 245 250
 gac aat gct tct atg tat ttc aat tct gac aag ggg agc aac tca ttt 820
 Asp Asn Ala Ser Met Tyr Phe Asn Ser Asp Lys Gly Ser Asn Ser Phe 255 260 265
 gat tgt gac ttt ggg tgg gga gaa caa ggc gct gaa atc ttg tct gtt 868

PF59082SeqList_PF59082.txt

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Leu	Ala	Ala	Thr	Pro	Glu	Val	Asp	Glu	Ser	Val	Phe	Val	Glu	Ala	Asn		
	285					290					295						
cct	aag	aag	ttg	aaa	tca	tac	act	gag	tat	gca	gtg	cct	gtt	gaa	gag	964	
Pro	Lys	Lys	Leu	Lys	Ser	Tyr	Thr	Glu	Tyr	Ala	Val	Pro	Val	Glu	Glu		
300					305					310					315		
agg	aat	gga	aaa	tct	ctg	tcc	gaa	gag	ttg	ctg	gct	ttt	gac	aat	cag	1012	
Arg	Asn	Gly	Lys	Ser	Leu	Ser	Glu	Glu	Leu	Leu	Ala	Phe	Asp	Asn	Gln		
				320					325					330			
ttg	atg	aac	ctt	cag	atg	cca	gat	ctt	gtg	ggc	aac	tgg	gag	gct	tct	1060	
Leu	Met	Asn	Leu	Gln	Met	Pro	Asp	Leu	Val	Gly	Asn	Trp	Glu	Ala	Ser		
			335				340						345				
ctt	gat	agc	ttc	ctt	aat	gga	gac	aca	act	cag	gat	ggc	aca	aac	gca	1108	
Leu	Asp	Ser	Phe	Leu	Asn	Gly	Asp	Thr	Thr	Gln	Asp	Gly	Thr	Asn	Ala		
		350					355					360					
gtg	gac	ttg	tgg	agc	ttc	gaa	gac	ttc	ccc	tcc	atg	gtt	ggg	gga	gtt	1156	
Val	Asp	Leu	Trp	Ser	Phe	Glu	Asp	Phe	Pro	Ser	Met	Val	Gly	Gly	Val		
	365					370					375						
tat	tgagccaact	tttctgtgct	tgccagggttt	tgtaaataat	aaggctacat											1209	
Tyr	380																
gaatggttgt	ttatctgaga	tgggaaatgga	gtgcaacaca	gatgaacatg	cttagccttg											1269	
gtgtgggaga	agcatttctca	ggagcatttt	ccatataaaa	gtagtacatc	ggtttcccgt											1329	
ttcattacat	ttggagtcac	tggactttgg	aagttggatt	cgatgactgt	aatttgacaa											1389	
tgtggtgtga	cttattttaga															1409	

<210> 758
 <211> 380
 <212> PRT
 <213> Populus alba x Populus tremula

<400> 758

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			20					25					30				
Lys	Lys	Pro	Phe	Asn	Asn	Lys	His	Leu	Lys	Pro	Val	Val	Ala	Asp	Pro		
		35				40						45					
Glu	Asp	Asp	Phe	Glu	Ala	Asp	Leu	Gln	Glu	Phe	Lys	Asp	Glu	Ser	Asp		
	50					55					60						
Val	Asp	Glu	Asp	Tyr	Asp	Val	Phe	Ala	Asp	Ala	Lys	Pro	Phe	Ala	Phe		
65					70				75					80			
Ser	Ala	Ser	Ala	Ser	Glu	Pro	Ala	Lys	Lys	Arg	Gly	Leu	Pro	Arg	Gly		
			85					90					95				
Ser	Thr	Ala	Val	Lys	Ser	Ala	Gly	Phe	Ser	Gly	Leu	Ala	Lys	Asn	Ser		
			100					105					110				
Ala	Lys	Arg	Lys	Arg	Lys	Asn	Gln	Phe	Arg	Gly	Ile	Arg	Gln	Arg	Pro		
		115				120						125					
Trp	Gly	Lys	Trp	Ala	Ala	Glu	Ile	Arg	Asp	Pro	Arg	Lys	Gly	Val	Arg		
	130					135						140					
Val	Trp	Leu	Gly	Thr	Phe	Asn	Thr	Ala	Glu	Glu	Ala	Ala	Arg	Ala	Tyr		
145					150				155						160		
Asp	Ser	Glu	Ala	Arg	Arg	Ile	Arg	Gly	Lys	Lys	Ala	Lys	Val	Asn	Phe		
			165					170					175				
Pro	Asp	Glu	Ala	Pro	Cys	Ala	Ser	Ala	Arg	His	Pro	Ile	Lys	Glu	Asn		
			180					185					190				
Ser	Gln	Lys	Arg	Leu	Thr	Lys	Ala	Asn	Leu	Ser	Gln	Asp	Phe	Ser	Tyr		
		195				200						205					
Leu	Ser	Asn	Pro	Glu	Thr	Asp	Tyr	Asn	Asn	Met	Gly	Phe	Val	Glu	Glu		

PF59082SeqList_PF59082.txt

210 215 220
 Lys Pro Gln Val Ser Gln Phe Gly Ile Met Asn Ser Ile Pro Val Asn
 225 230 235 240
 Gly Asp Ser Gly Val Thr Pro Leu Thr Pro Ser Asp Asn Ala Ser Met
 245 250 255
 Tyr Phe Asn Ser Asp Lys Gly Ser Asn Ser Phe Asp Cys Asp Phe Gly
 260 265 270
 Trp Gly Glu Gln Gly Ala Glu Ile Leu Ser Val Leu Ala Ala Thr Pro
 275 280 285
 Glu Val Asp Glu Ser Val Phe Val Glu Ala Asn Pro Lys Lys Leu Lys
 290 295 300
 Ser Tyr Thr Glu Tyr Ala Val Pro Val Glu Glu Arg Asn Gly Lys Ser
 305 310 315 320
 Leu Ser Glu Glu Leu Leu Ala Phe Asp Asn Gln Leu Met Asn Leu Gln
 325 330 335
 Met Pro Asp Leu Val Gly Asn Trp Glu Ala Ser Leu Asp Ser Phe Leu
 340 345 350
 Asn Gly Asp Thr Thr Gln Asp Gly Thr Asn Ala Val Asp Leu Trp Ser
 355 360 365
 Phe Glu Asp Phe Pro Ser Met Val Gly Gly Val Tyr
 370 375 380

<210> 759
 <211> 1110
 <212> DNA
 <213> Capsicum annuum

<220>
 <221> CDS
 <222> (1)..(1110)

<400> 759
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 tcc cgc cgg cta acc gcc gag ttg cta tgg ggt aac tct gat ctg agc 96
 Ser Arg Arg Leu Thr Ala Glu Leu Leu Trp Gly Asn Ser Asp Leu Ser
 20 25 30
 aaa aag aag aaa aat cca ggg aat tat tac tca aag cct ttg aac agg 144
 Lys Lys Lys Lys Asn Pro Gly Asn Tyr Tyr Ser Lys Pro Leu Asn Arg
 35 40 45
 tct aag ttt att gac ctt gat gag gaa ttt gaa gct gac ttt cag gac 192
 Ser Lys Phe Ile Asp Leu Asp Glu Glu Phe Glu Ala Asp Phe Gln Asp
 50 55 60
 ttc aag gac tat gcc gat gat gtt gat gat aag ccc ttc ggt 240
 Phe Lys Asp Tyr Ala Asp Asp Val Asp Asp Val Lys Pro Phe Gly
 65 70 75 80
 tcc aaa tct gtg aaa tct ggc gat tca agc tgc gat act gaa aaa tct 288
 Ser Lys Ser Val Lys Ser Gly Asp Ser Ser Cys Asp Thr Glu Lys Ser
 85 90 95
 tcc aag aga aag agg aag aat cag tac cgg ggg atc aga cag cgt cct 336
 Ser Lys Arg Lys Arg Lys Asn Gln Tyr Arg Gly Ile Arg Gln Arg Pro
 100 105 110
 tgg ggt aag tgg gca gct gaa att cgt gat ccg agg aaa ggg att cga 384
 Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp Pro Arg Lys Gly Ile Arg
 115 120 125
 gtt tgg ctt gga act ttc aat tct gcg gaa gaa gca gct aga gct tat 432
 Val Trp Leu Gly Thr Phe Asn Ser Ala Glu Glu Ala Ala Arg Ala Tyr
 130 135 140
 gat gtt gag gca cga agg atc aga ggc aag aag gct aag gtg aac ttt 480
 Asp Val Glu Ala Arg Arg Ile Arg Gly Lys Lys Ala Lys Val Asn Phe
 145 150 155 160
 cct gat gga tct cca gct tct gct tca aga cgt gct gtt aag cca aat 528
 Pro Asp Gly Ser Pro Ala Ser Ala Ser Arg Ala Val Lys Pro Asn
 165 170 175
 cct cag gag gca ctt cgc gag gaa atc ttg aac aca gtt cag ccg aac 576
 Pro Gln Glu Ala Leu Arg Glu Glu Ile Leu Asn Thr Val Gln Pro Asn
 180 185 190
 aca act tat atc aac aac ttg gac ggc tct gat gat tcg ttt ggc 624
 195

PF59082SeqList_PF59082.txt

Thr	Thr	Tyr	Ile	Asn	Asn	Leu	Asp	Gly	Gly	Ser	Asp	Ser	Phe	Gly	
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Phe	Phe	Glu	Glu	Lys	Pro	Ala	Ala	Lys	Gln	Tyr	Gly	Tyr	Glu	Asn	Val
210	215	220													
tct	ttt	act	gct	gga	gat	atg	gga	ctg	ggg	tca	att	tcc	cct	tca	act
Ser	Phe	Thr	Ala	Gly	Asp	Met	Gly	Leu	Gly	Ser	Ile	Ser	Pro	Ser	Thr
225	230	235													
ggg	aca	aca	aat	gtt	tac	ttc	agt	tct	gat	gaa	gga	agc	aac	acc	ttt
Gly	Thr	Thr	Asn	Val	Tyr	Phe	Ser	Ser	Asp	Glu	Gly	Ser	Asn	Thr	Phe
245	250	255													
gac	tgc	tct	gat	ttc	ggg	tgg	ggg	gaa	cca	tgt	ccg	agg	act	cca	gag
Asp	Cys	Ser	Asp	Phe	Gly	Trp	Gly	Glu	Pro	Cys	Pro	Arg	Thr	Pro	Glu
260	265	270													
atc	tca	tct	gtt	ctg	tca	gaa	gtt	cta	gaa	tgt	aat	ggg	act	caa	tct
Ile	Ser	Val	Leu	Ser	Glu	Val	Val	Leu	Glu	Cys	Asn	Gly	Thr	Gln	Ser
275	280	285													
gat	gaa	gat	gct	aga	cca	gag	aaa	aaa	ctg	aag	tcg	tgt	tcc	aac	gct
Asp	Glu	Asp	Ala	Arg	Pro	Glu	Lys	Lys	Leu	Lys	Ser	Cys	Ser	Asn	Ala
290	295	300													
tcc	ttg	cca	gat	gag	gat	aac	act	gtg	cac	acg	cta	tct	gaa	gag	cta
Ser	Leu	Pro	Asp	Glu	Asp	Asn	Thr	Val	His	Thr	Leu	Ser	Glu	Glu	Leu
305	310	315													
tcg	gct	ttt	gaa	tcc	cag	atg	aag	ttc	ttg	cag	atc	cca	tat	ctt	gag
Ser	Ala	Phe	Glu	Ser	Gln	Met	Lys	Phe	Leu	Gln	Ile	Pro	Tyr	Leu	Glu
325	330	335													
gga	aat	tgg	gat	gca	tca	gtt	gat	gcc	ttt	gtc	aac	aca	ggc	gca	att
Gly	Asn	Trp	Asp	Ala	Ser	Val	Asp	Ala	Phe	Val	Asn	Thr	Gly	Ala	Ile
340	345	350													
cag	gat	ggc	gga	aat	gcg	atg	gat	ctc	tgg	cct	tcg	atg	atg	ttc	ctt
Gln	Asp	Gly	Gly	Asn	Ala	Met	Asp	Leu	Trp	Pro	Ser	Met	Met	Phe	Leu
355	360	365													
ctt	taa														
Leu															

<210> 760
 <211> 369
 <212> PRT
 <213> Capsicum annuum

<400> 760
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 Ser Arg Arg Leu Thr Ala Glu Leu Leu Trp Gly Asn Ser Asp Leu Ser
 20 25 30
 Lys Lys Lys Lys Asn Pro Gly Asn Tyr Tyr Ser Lys Pro Leu Asn Arg
 35 40 45
 Ser Lys Phe Ile Asp Leu Asp Glu Glu Phe Glu Ala Asp Phe Gln Asp
 50 55 60
 Phe Lys Asp Tyr Ala Asp Asp Asp Val Asp Asp Val Lys Pro Phe Gly
 65 70 75 80
 Ser Lys Ser Val Lys Ser Gly Asp Ser Ser Cys Asp Thr Glu Lys Ser
 85 90 95
 Ser Lys Arg Lys Arg Lys Asn Gln Tyr Arg Gly Ile Arg Gln Arg Pro
 100 105 110
 Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp Pro Arg Lys Gly Ile Arg
 115 120 125
 Val Trp Leu Gly Thr Phe Asn Ser Ala Glu Glu Ala Ala Arg Ala Tyr
 130 135 140
 Asp Val Glu Ala Arg Arg Ile Arg Gly Lys Lys Ala Lys Val Asn Phe
 145 150 155 160
 Pro Asp Gly Ser Pro Ala Ser Ala Ser Arg Arg Ala Val Lys Pro Asn
 165 170 175
 Pro Gln Glu Ala Leu Arg Glu Glu Ile Leu Asn Thr Val Gln Pro Asn
 180 185 190
 Thr Thr Tyr Ile Asn Asn Leu Asp Gly Gly Ser Asp Asp Ser Phe Gly
 195 200 205
 Phe Phe Glu Glu Lys Pro Ala Ala Lys Gln Tyr Gly Tyr Glu Asn Val
 Seite 980

PF59082SeqList_PF59082.txt

210 215 220
 Ser Phe Thr Ala Gly Asp Met Gly Leu Gly Ser Ile Ser Pro Ser Thr
 225 230 235 240
 Gly Thr Thr Asn Val Tyr Phe Ser Ser Asp Glu Gly Ser Asn Thr Phe
 245 250 255
 Asp Cys Ser Asp Phe Gly Trp Gly Glu Pro Cys Pro Arg Thr Pro Glu
 260 265 270
 Ile Ser Ser Val Leu Ser Glu Val Leu Glu Cys Asn Gly Thr Gln Ser
 275 280 285
 Asp Glu Asp Ala Arg Pro Glu Lys Lys Leu Lys Ser Cys Ser Asn Ala
 290 295 300
 Ser Leu Pro Asp Glu Asp Asn Thr Val His Thr Leu Ser Glu Glu Leu
 305 310 315 320
 Ser Ala Phe Glu Ser Gln Met Lys Phe Leu Gln Ile Pro Tyr Leu Glu
 325 330 335
 Gly Asn Trp Asp Ala Ser Val Asp Ala Phe Val Asn Thr Gly Ala Ile
 340 345 350
 Gln Asp Gly Gly Asn Ala Met Asp Leu Trp Pro Ser Met Met Phe Leu
 355 360 365
 Leu

<210> 761

<211> 984

<212> DNA

<213> Lycopersicon esculentum

<220>

<221> CDS

<222> (1)..(984)

<400> 761

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1 5 10 15	
tct cgc cgg ctc acc gcc gag ttt cta tgg ggt cgt ttc gat ctc ggt	96
Ser Arg Arg Leu Thr Ala Glu Phe Leu Trp Gly Arg Phe Asp Leu Gly	
20 25 30	
aag aag caa aaa aat ccc aac aat tat cac tct aaa gct aag cat ttg	144
Lys Lys Lys Asn Pro Asn Asn Tyr His Ser Lys Ala Lys His Leu	
35 40 45	
cga tct gaa gtt gtt gac gac ttt gaa gcc gat ttt cag gac ttc aaa	192
Arg Ser Glu Val Val Asp Asp Phe Glu Ala Asp Phe Gln Asp Phe Lys	
50 55 60	
gag tta tcc gat gat gag gat gtt caa gtc gat gtc aag cca ttt gcc	240
Glu Leu Ser Asp Asp Glu Asp Val Gln Val Asp Val Lys Pro Phe Ala	
65 70 75 80	
ttc tct gct tcc aaa cac tct act ggt tcc aaa tct ttg aaa act gtt	288
Phe Ser Ala Ser Lys His Ser Thr Gly Ser Lys Ser Leu Lys Thr Val	
85 90 95	
gat tca gac aag gat gct gct gct gat aaa tcc tct aag aga aag agg	336
Asp Ser Asp Lys Asp Ala Ala Ala Asp Lys Ser Ser Lys Arg Lys Arg	
100 105 110	
aag aat caa tat aga ggg atc aga cag aga cct tgg ggt aag tgg gca	384
Lys Asn Gln Tyr Arg Gly Ile Arg Gln Arg Pro Trp Gly Lys Trp Ala	
115 120 125	
gct gaa ata cgt gac cca agg aaa ggg gtt cgg gtc tgg ctg gga acc	432
Ala Glu Ile Arg Asp Pro Arg Lys Gly Val Arg Val Trp Leu Gly Thr	
130 135 140	
ttc aat act gca gaa gaa gct gcc aaa gct tat gat att gag gcg agg	480
Phe Asn Thr Ala Glu Glu Ala Ala Lys Ala Tyr Asp Ile Glu Ala Arg	
145 150 155 160	
agg atc aga ggc aag aag gct aag gta aac ttt cct gat gaa gct ccc	528
Arg Ile Arg Gly Lys Lys Ala Lys Val Asn Phe Pro Asp Glu Ala Pro	
165 170 175	
gcc cct gca tca aga cac act gtt aag gtg aat cct cag aag gtc ctt	576
Ala Pro Ala Ser Arg His Thr Val Lys Val Asn Pro Gln Lys Val Leu	
180 185 190	
cct gag gag agc ctg tat tca ctt cag tcc gac tca gca atc atg aac	624

PF59082SeqList_PF59082.txt

Pro	Glu	Glu	Ser	Leu	Tyr	Ser	Leu	Gln	Ser	Asp	Ser	Ala	Ile	Met	Asn	
		195					200					205				
agc	gtg	gag	gat	gac	cat	tat	gat	tct	ttt	gga	ttt	ttt	gaa	gag	aaa	672
Ser	Val	Glu	Asp	Asp	His	Tyr	Asp	Ser	Phe	Gly	Phe	Phe	Glu	Glu	Lys	
	210					215					220					
ccc	atg	aca	aaa	cag	tat	gga	tat	gag	aat	ggg	agc	agt	gct	tct	gca	720
Pro	Met	Thr	Lys	Gln	Tyr	Gly	Tyr	Glu	Asn	Gly	Ser	Ser	Ala	Ser	Ala	
225					230					235					240	
gat	acg	gga	ttt	ggt	tcg	ttc	gtc	cct	tca	gct	ggc	ggg	gat	atc	tac	768
Asp	Thr	Gly	Phe	Gly	Ser	Phe	Val	Pro	Ser	Ala	Gly	Gly	Asp	Ile	Tyr	
				245					250					255		
ttc	aac	tct	gat	gta	gga	agc	aac	tct	ttt	gaa	tgc	tct	gat	ttt	ggt	816
Phe	Asn	Ser	Asp	Val	Gly	Ser	Asn	Ser	Phe	Glu	Cys	Ser	Asp	Phe	Gly	
			260				265						270			
tgg	gga	gag	cca	tgc	tcc	agg	act	cca	gag	ata	tca	tct	gtt	ctg	tca	864
Trp	Gly	Glu	Pro	Cys	Ser	Arg	Thr	Pro	Glu	Ile	Ser	Ser	Val	Leu	Ser	
		275					280						285			
gct	gct	att	gaa	tgt	aat	gaa	gct	caa	ttt	gtt	gaa	gat	gcc	aat	tct	912
Ala	Ala	Ile	Glu	Cys	Asn	Glu	Ala	Gln	Phe	Val	Glu	Asp	Ala	Asn	Ser	
	290					295					300					
cag	aaa	aag	ttg	aaa	tca	acc	aac	aac	ccc	gta	gct	gat	gat	gga		960
Gln	Lys	Lys	Leu	Lys	Ser	Cys	Thr	Asn	Asn	Pro	Val	Ala	Asp	Asp	Gly	
305					310					315					320	
aac	ccc	cgt	tac	tat	ggt	acc	tga									984
Asn	Pro	Arg	Tyr	Tyr	Gly	Thr										
				325												

<210> 762

<211> 327

<212> PRT

<213> Lycopersicon esculentum

<400> 762

Met	Cys	Gly	Gly	Ser	Ile	Ile	Ser	Asp	Tyr	Ile	Asp	Pro	Ser	Arg	Thr	
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Ser	Arg	Arg	Leu	Thr	Ala	Glu	Phe	Leu	Trp	Gly	Arg	Phe	Asp	Leu	Gly	
			20					25					30			
Lys	Lys	Gln	Lys	Asn	Pro	Asn	Asn	Tyr	His	Ser	Lys	Ala	Lys	His	Leu	
		35				40						45				
Arg	Ser	Glu	Val	Val	Asp	Asp	Phe	Glu	Ala	Asp	Phe	Gln	Asp	Phe	Lys	
	50					55				60						
Glu	Leu	Ser	Asp	Asp	Glu	Asp	Val	Gln	Val	Asp	Val	Lys	Pro	Phe	Ala	
65					70				75						80	
Phe	Ser	Ala	Ser	Lys	His	Ser	Thr	Gly	Ser	Lys	Ser	Leu	Lys	Thr	Val	
				85				90						95		
Asp	Ser	Asp	Lys	Asp	Ala	Ala	Ala	Asp	Lys	Ser	Ser	Lys	Arg	Lys	Arg	
			100					105					110			
Lys	Asn	Gln	Tyr	Arg	Gly	Ile	Arg	Gln	Arg	Pro	Trp	Gly	Lys	Trp	Ala	
	115					120						125				
Ala	Glu	Ile	Arg	Asp	Pro	Arg	Lys	Gly	Val	Arg	Val	Trp	Leu	Gly	Thr	
	130					135					140					
Phe	Asn	Thr	Ala	Glu	Glu	Ala	Ala	Lys	Ala	Tyr	Asp	Ile	Glu	Ala	Arg	
145					150				155						160	
Arg	Ile	Arg	Gly	Lys	Lys	Ala	Lys	Val	Asn	Phe	Pro	Asp	Glu	Ala	Pro	
			165					170						175		
Ala	Pro	Ala	Ser	Arg	His	Thr	Val	Lys	Val	Asn	Pro	Gln	Lys	Val	Leu	
			180					185					190			
Pro	Glu	Glu	Ser	Leu	Tyr	Ser	Leu	Gln	Ser	Asp	Ser	Ala	Ile	Met	Asn	
	195					200						205				
Ser	Val	Glu	Asp	Asp	His	Tyr	Asp	Ser	Phe	Gly	Phe	Phe	Glu	Glu	Lys	
	210					215					220					
Pro	Met	Thr	Lys	Gln	Tyr	Gly	Tyr	Glu	Asn	Gly	Ser	Ser	Ala	Ser	Ala	
225					230					235					240	
Asp	Thr	Gly	Phe	Gly	Ser	Phe	Val	Pro	Ser	Ala	Gly	Gly	Asp	Ile	Tyr	
			245						250					255		
Phe	Asn	Ser	Asp	Val	Gly	Ser	Asn	Ser	Phe	Glu	Cys	Ser	Asp	Phe	Gly	
			260					265					270			
Trp	Gly	Glu	Pro	Cys	Ser	Arg	Thr	Pro	Glu	Ile	Ser	Ser	Val	Leu	Ser	
	275						280						285			

PF59082SeqList_PF59082.txt

Ala Ala Ile Glu Cys Asn Glu Ala Gln Phe Val Glu Asp Ala Asn Ser
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 Gln Lys Lys Leu Lys Ser Cys Thr Asn Asn Pro Val Ala Asp Asp Gly
 305 310 315 320
 Asn Pro Arg Tyr Tyr Gly Thr
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<210> 763
 <211> 1137
 <212> DNA
 <213> Fagus sylvatica

<220>
 <221> CDS
 <222> (1)..(1137)

<400> 763
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 1 5 10 15
 cgg cgg ttg acg gcg gat tat ctc tgg ggc gat cgg aaa aaa ccc att 96
 Arg Arg Leu Thr Ala Asp Tyr Leu Trp Gly Asp Arg Lys Lys Pro Ile
 20 25 30
 tca gga aag cga ttc tcg aag cct gta gtc gat ttg gac gac gaa ttc 144
 Ser Gly Lys Arg Phe Ser Lys Val Val Asp Leu Asp Asp Glu Phe
 35 40 45
 gag ctc gat ttt cag ggc ttt aag gac gag gag gag tct gat atc gac 192
 Glu Leu Asp Phe Gln Gly Phe Lys Asp Glu Glu Glu Ser Asp Ile Asp
 50 55 60
 gag gaa gag gtc ctt gtg caa gat gtc aag ccc ttc act ttt tct gct 240
 Glu Glu Glu Val Leu Val Gln Asp Val Lys Pro Phe Thr Phe Ser Ala
 65 70 75 80
 cct cct agc tct gga tct aag cct gta aaa tcc gtg gaa ttc aat ggg 288
 Pro Pro Ser Ser Gly Ser Lys Pro Val Lys Ser Val Glu Phe Asn Gly
 85 90 95
 caa gct gag aaa tct gca aag aga aag agg aag aat cag tat cgg ggg 336
 Gln Ala Glu Lys Ser Ala Lys Arg Lys Arg Lys Asn Gln Tyr Arg Gly
 100 105 110
 atc cgg cag cgc cca tgg ggt aag tgg gct gct gag att cga gac cca 384
 Ile Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp Pro
 115 120 125
 agg aaa ggg gtc cgt gtc tgg ctt gga act ttt aac act gca gaa aaa 432
 Arg Lys Gly Val Arg Val Trp Leu Gly Thr Phe Asn Thr Ala Glu Lys
 130 135 140
 gct gca aga gct tat gat gca gag gca cgg aga att cgt ggc aag aag 480
 Ala Ala Arg Ala Tyr Asp Ala Glu Ala Arg Arg Ile Arg Gly Lys Lys
 145 150 155 160
 gct aag gtg aat ttt ccc gat gag act ccc cgt gct tct cca aag cgt 528
 Ala Lys Val Asn Phe Pro Asp Glu Thr Pro Arg Ala Ser Pro Lys Arg
 165 170 175
 tca gtt aag gca aat ctg cag aag cca ctt gcc aag gca aac ctg aac 576
 Ser Val Lys Ala Asn Leu Gln Lys Pro Leu Ala Lys Ala Asn Leu Asn
 180 185 190
 tct gtc cag ccc aac ctg aac caa aat ttc aat ttt atg aac aac tct 624
 Ser Val Gln Pro Asn Leu Asn Gln Asn Phe Asn Phe Met Asn Asn Ser
 195 200 205
 gat cag gac tat acc atg ggt ttg atg gaa gag aaa cct ttc aca aac 672
 Asp Gln Asp Tyr Thr Met Gly Leu Met Glu Glu Lys Pro Phe Thr Asn
 210 215 220
 cag tat ggg tat atg gat tcc atc cct gcc aat gca gat gtt gga cta 720
 Gln Tyr Gly Tyr Met Asp Ser Ile Pro Ala Asn Ala Asp Val Gly Leu
 225 230 235 240
 aaa ccc ttt gct tcc aat aat act acc ccg tac ttt aac tca gat cag 768
 Lys Pro Phe Ala Ser Asn Asn Thr Thr Pro Tyr Phe Asn Ser Asp Gln
 245 250 255
 ggg agt aac tcg ttt gat tgt tct gac tat gga tgg gga gaa cag ggc 816
 Gly Ser Asn Ser Phe Asp Cys Ser Asp Tyr Gly Trp Gly Glu Gln Gly
 260 265 270
 tct aag act cca gaa atc tca tct gtt ctt tca gct act tta gaa ggg 864

PF59082SeqList_PF59082.txt

Ser	Lys	Thr	Pro	Glu	Ile	Ser	Ser	Val	Leu	Ser	Ala	Thr	Leu	Glu	Gly	
		275					280					285				
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Asp	Glu	Ser	Gln	Phe	Val	Glu	Asp	Ala	Met	Pro	Thr	Lys	Lys	Leu	Lys	
	290					295				300						
tca	gac	tct	ggg	aat	gca	gtg	ttc	att	gaa	aat	aac	act	gca	aag	aca	960
Ser	Asp	Ser	Gly	Asn	Ala	Val	Phe	Ile	Glu	Asn	Asn	Thr	Ala	Lys	Thr	
305					310					315					320	
ctg	tca	gag	gag	ctc	tca	gct	ttt	gag	tcc	cag	atg	aac	ttt	cag	atg	1008
Leu	Ser	Glu	Glu	Leu	Ser	Ala	Phe	Glu	Ser	Gln	Met	Asn	Phe	Gln	Met	
				325					330					335		
cca	ttt	ctt	gag	gga	agc	tgg	gaa	tcc	aac	atg	gag	gca	ctg	ttc	agt	1056
Pro	Phe	Leu	Glu	Gly	Ser	Trp	Glu	Ser	Asn	Met	Glu	Ala	Leu	Phe	Ser	
				340				345					350			
ggg	gac	aca	act	cag	gat	ggt	aac	tcg	atg	gat	ctt	tgg	agc	ttc	gat	1104
Gly	Asp	Thr	Thr	Gln	Asp	Gly	Asn	Ser	Met	Asp	Leu	Trp	Ser	Phe	Asp	
		355					360					365				
gac	ctc	ccc	ggt	atg	gct	ggg	gga	gtt	ctg	tga						1137
Asp	Leu	Pro	Val	Met	Ala	Gly	Gly	Val	Leu							
	370					375										

<210> 764

<211> 378

<212> PRT

<213> Fagus sylvatica

<400> 764

Met	Cys	Gly	Gly	Ala	Ile	Ile	Ser	Asp	Phe	Ile	Ala	Pro	Thr	Gly	Ser	
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Arg	Arg	Leu	Thr	Ala	Asp	Tyr	Leu	Trp	Gly	Asp	Arg	Lys	Lys	Pro	Ile	
			20					25					30			
Ser	Gly	Lys	Arg	Phe	Ser	Lys	Pro	Val	Val	Asp	Leu	Asp	Asp	Glu	Phe	
		35					40					45				
Glu	Leu	Asp	Phe	Gln	Gly	Phe	Lys	Asp	Glu	Glu	Glu	Ser	Asp	Ile	Asp	
	50					55					60					
Glu	Glu	Glu	Val	Leu	Val	Gln	Asp	Val	Lys	Pro	Phe	Thr	Phe	Ser	Ala	
65					70					75					80	
Pro	Pro	Ser	Ser	Gly	Ser	Lys	Pro	Val	Lys	Ser	Val	Glu	Phe	Asn	Gly	
				85					90					95		
Gln	Ala	Glu	Lys	Ser	Ala	Lys	Arg	Lys	Arg	Lys	Asn	Gln	Tyr	Arg	Gly	
			100					105					110			
Ile	Arg	Gln	Arg	Pro	Trp	Gly	Lys	Trp	Ala	Ala	Glu	Ile	Arg	Asp	Pro	
		115					120					125				
Arg	Lys	Gly	Val	Arg	Val	Trp	Leu	Gly	Thr	Phe	Asn	Thr	Ala	Glu	Lys	
	130					135					140					
Ala	Ala	Arg	Ala	Tyr	Asp	Ala	Glu	Ala	Arg	Arg	Ile	Arg	Gly	Lys	Lys	
145					150				155						160	
Ala	Lys	Val	Asn	Phe	Pro	Asp	Glu	Thr	Pro	Arg	Ala	Ser	Pro	Lys	Arg	
			165						170					175		
Ser	Val	Lys	Ala	Asn	Leu	Gln	Lys	Pro	Leu	Ala	Lys	Ala	Asn	Leu	Asn	
			180					185					190			
Ser	Val	Gln	Pro	Asn	Leu	Asn	Gln	Asn	Phe	Asn	Phe	Met	Asn	Asn	Ser	
		195					200					205				
Asp	Gln	Asp	Tyr	Thr	Met	Gly	Leu	Met	Glu	Glu	Lys	Pro	Phe	Thr	Asn	
	210					215					220					
Gln	Tyr	Gly	Tyr	Met	Asp	Ser	Ile	Pro	Ala	Asn	Ala	Asp	Val	Gly	Leu	
225					230					235					240	
Lys	Pro	Phe	Ala	Ser	Asn	Asn	Thr	Thr	Pro	Tyr	Phe	Asn	Ser	Asp	Gln	
			245						250					255		
Gly	Ser	Asn	Ser	Phe	Asp	Cys	Ser	Asp	Tyr	Gly	Trp	Gly	Glu	Gln	Gly	
			260					265					270			
Ser	Lys	Thr	Pro	Glu	Ile	Ser	Ser	Val	Leu	Ser	Ala	Thr	Leu	Glu	Gly	
		275					280					285				
Asp	Glu	Ser	Gln	Phe	Val	Glu	Asp	Ala	Met	Pro	Thr	Lys	Lys	Leu	Lys	
	290					295					300					
Ser	Asp	Ser	Gly	Asn	Ala	Val	Phe	Ile	Glu	Asn	Asn	Thr	Ala	Lys	Thr	
305					310					315					320	
Leu	Ser	Glu	Glu	Leu	Ser	Ala	Phe	Glu	Ser	Gln	Met	Asn	Phe	Gln	Met	
				325					330					335		

PF59082SeqList_PF59082.txt

Pro Phe Leu Glu Gly Ser Trp Glu Ser Asn Met Glu Ala Leu Phe Ser
 340 345 350
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 355 360 365
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 370 375

<210> 765
 <211> 1155
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (1)..(1155)

<400> 765
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 agc ggg gcg cgg cgc gtg acc gcc gac atc ctg tgg ccg agt ttg agg 96
 Ser Gly Ala Arg Arg Val Thr Ala Asp Ile Leu Trp Pro Ser Leu Arg
 20 25 30
 aag cgc ttc tcg aag ccg ctg ctg gac gat gat ttc gag gct ggg ttc 144
 Lys Arg Phe Ser Lys Pro Leu Leu Asp Asp Asp Phe Glu Ala Gly Phe
 35 40 45
 aga gaa ttc aag gat gat tcg gaa atc gag gat gtt gat gac gag gac 192
 Arg Glu Phe Lys Asp Asp Ser Glu Ile Glu Asp Val Asp Asp Glu Asp
 50 55 60
 gat gaa gac gag gag gag ttg aag aag aag ccc ttt ggg ttc tct cgc 240
 Asp Glu Asp Glu Glu Glu Leu Lys Lys Lys Pro Phe Gly Phe Ser Arg
 65 70 75 80
 tcc agc aac aag gct gct tct aag cct ctc tct cgt gga gca aca act 288
 Ser Ser Asn Lys Ala Ala Ser Lys Pro Leu Ser Arg Gly Ala Thr Thr
 85 90 95
 gtg aaa tct gtg gaa tca aag ggg caa gct gag aag tgt gcc aag aga 336
 Val Lys Ser Val Glu Ser Lys Gly Gln Ala Glu Lys Cys Ala Lys Arg
 100 105 110
 aag agg aag aac cag tat cgc gga atc cgc cag cgt cca tgg gga aag 384
 Lys Arg Lys Asn Gln Tyr Arg Gly Ile Arg Gln Arg Pro Trp Gly Lys
 115 120 125
 tgg gct gct gag att cgc gac cca aga aag ggg gtt cgt gtt tgg ctt 432
 Trp Ala Ala Glu Ile Arg Asp Pro Arg Lys Gly Val Arg Val Trp Leu
 130 135 140
 gga act ttc agc act gct gaa gaa gct gca aga gct tac gat gct gaa 480
 Gly Thr Phe Ser Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Ala Glu
 145 150 155 160
 gca agg agg atc cgt ggc aag aaa gcc aag gtg aat ttc cct gat gag 528
 Ala Arg Arg Ile Arg Gly Lys Lys Ala Val Asn Phe Pro Asp Glu
 165 170 175
 cct tca ggc gct gct tcc tca aaa cgt ctc aag gcg aat cca gag gct 576
 Pro Ser Gly Ala Ala Ser Ser Lys Arg Leu Lys Ala Asn Pro Glu Ala
 180 185 190
 cag cca atg aag aaa aat ctg aac tct gtg aag ccg aaa ata aac cag 624
 Gln Pro Met Lys Lys Asn Leu Asn Ser Val Lys Pro Lys Ile Asn Gln
 195 200 205
 atg ttc aat ttt ggt gac aat ctt gag ggc tac tac agc cct ata gat 672
 Met Phe Asn Phe Gly Asp Asn Leu Glu Gly Tyr Tyr Ser Pro Ile Asp
 210 215 220
 cag gtg gaa cag aaa cca ctg gtt aac cag tat gtt aac cgt gcc ccg 720
 Gln Val Glu Gln Lys Pro Leu Val Asn Gln Tyr Val Asn Arg Ala Pro
 225 230 235 240
 ttt gct gga aat gga gtt caa gtc tca cct gtt act cca tct gct gat 768
 Phe Ala Gly Asn Gly Val Gln Val Ser Pro Val Thr Pro Ser Ala Asp
 245 250 255
 gtt act gct tac ttc agc tct gag cat tcg agc aac tcg ttt gat tat 816
 Val Thr Ala Tyr Phe Ser Ser Glu His Ser Ser Asn Ser Phe Asp Tyr
 260 265 270
 tct gac ctt gga tgg ggt gaa caa gtc ccc aag acc ccc gag atc tca 864

PF59082SeqList_PF59082.txt

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Ser	Leu	Leu	Ser	Ala	Ala	Pro	Leu	Glu	Gly	Ala	Ala	Asp	Gln	Val	Gln	
		290				295					300					
aag	acc	aac	aac	tcg	cag	gat	gtg	gtg	gct	gca	caa	gat	gat	tct	gca	960
Lys	Thr	Asn	Asn	Ser	Gln	Asp	Val	Val	Ala	Ala	Gln	Asp	Asp	Ser	Ala	
		305			310					315					320	
aaa	acc	ctt	tcc	gaa	gag	ctt	gca	gac	att	gaa	tcc	cag	ctc	aag	ttc	1008
Lys	Thr	Leu	Ser	Glu	Glu	Leu	Ala	Asp	Ile	Glu	Ser	Gln	Leu	Lys	Phe	
				325					330					335		
ttt	gag	acc	cct	tct	ttt	ctt	gat	gaa	gcc	tgg	gct	gat	gct	aca	ttg	1056
Phe	Glu	Thr	Pro	Ser	Phe	Leu	Asp	Glu	Ala	Trp	Ala	Asp	Ala	Thr	Leu	
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gcg	tct	ttg	ctc	ggc	gga	gac	gca	act	cat	gac	gcc	gcc	gga	aac	cct	1104
Ala	Ser	Leu	Leu	Gly	Gly	Asp	Ala	Thr	His	Asp	Ala	Ala	Gly	Asn	Pro	
		355					360					365				
atg	aac	ctt	tgg	agc	ttc	gac	gac	ctg	cct	tcc	atg	gca	gga	gtc	ttc	1152
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			20					25					30			
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Arg	Glu	Phe	Lys	Asp	Asp	Ser	Glu	Ile	Glu	Asp	Val	Asp	Asp	Glu	Asp	
	50					55					60					
Asp	Glu	Asp	Glu	Glu	Glu	Leu	Lys	Lys	Lys	Pro	Phe	Gly	Phe	Ser	Arg	
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Ser	Ser	Asn	Lys	Ala	Ala	Ser	Lys	Pro	Leu	Ser	Arg	Gly	Ala	Thr	Thr	
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Val	Lys	Ser	Val	Glu	Ser	Lys	Gly	Gln	Ala	Glu	Lys	Cys	Ala	Lys	Arg	
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Lys	Arg	Lys	Asn	Gln	Tyr	Arg	Gly	Ile	Arg	Gln	Arg	Pro	Trp	Gly	Lys	
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Trp	Ala	Ala	Glu	Ile	Arg	Asp	Pro	Arg	Lys	Gly	Val	Arg	Val	Trp	Leu	
	130					135					140					
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145					150					155					160	
Ala	Arg	Arg	Ile	Arg	Gly	Lys	Lys	Ala	Lys	Val	Asn	Phe	Pro	Asp	Glu	
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Pro	Ser	Gly	Ala	Ala	Ser	Ser	Lys	Arg	Leu	Lys	Ala	Asn	Pro	Glu	Ala	
			180					185					190			
Gln	Pro	Met	Lys	Lys	Asn	Leu	Asn	Ser	Val	Lys	Pro	Lys	Ile	Asn	Gln	
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Met	Phe	Asn	Phe	Gly	Asp	Asn	Leu	Glu	Gly	Tyr	Tyr	Ser	Pro	Ile	Asp	
	210					215					220					
Gln	Val	Glu	Gln	Lys	Pro	Leu	Val	Asn	Gln	Tyr	Val	Asn	Arg	Ala	Pro	
225					230					235					240	
Phe	Ala	Gly	Asn	Gly	Val	Gln	Val	Ser	Pro	Val	Thr	Pro	Ser	Ala	Asp	
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Val	Thr	Ala	Tyr	Phe	Ser	Ser	Glu	His	Ser	Ser	Asn	Ser	Phe	Asp	Tyr	
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Ser	Asp	Leu	Gly	Trp	Gly	Glu	Gln	Val	Pro	Lys	Thr	Pro	Glu	Ile	Ser	
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Ser	Leu	Leu	Ser	Ala	Ala	Pro	Leu	Glu	Gly	Ala	Ala	Asp	Gln	Val	Gln	
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Lys	Thr	Asn	Asn	Ser	Gln	Asp	Val	Val	Ala	Ala	Gln	Asp	Asp	Ser	Ala	

PF59082SeqList_PF59082.txt

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 Phe Glu Thr Pro Ser Phe Leu Asp Glu Ala Trp Ala Asp Ala Thr Leu
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 Met Asn Leu Trp Ser Phe Asp Asp Leu Pro Ser Met Ala Gly Val Phe
 370 375 380

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 Ser Arg Arg Leu Thr Ala Glu Leu Trp Gly Arg Ser Asp Leu Ser
 20 25 30
 aat aag caa aaa aat cct aac aat tat cac tcc aag ccg ttg aga tcc 144
 Asn Lys Gln Lys Asn Pro Asn Asn Tyr His Ser Lys Pro Leu Arg Ser
 35 40 45
 caa gta gtt gac cta gac gat gac ttc gag gct gat ttt cag gac ttt 192
 Gln Val Val Asp Leu Asp Asp Phe Glu Ala Asp Phe Gln Asp Phe
 50 55 60
 aaa gat ttc tcc gat gac gag gat gtt caa gtc gat gtc aag cca ttt 240
 Lys Asp Phe Ser Asp Asp Glu Asp Val Gln Val Asp Val Lys Pro Phe
 65 70 75 80
 gcc ttc tct gct tcg aaa aac tct aat gtt gaa ggc tcc aaa tct gtg 288
 Ala Phe Ser Ala Ser Lys Asn Ser Asn Val Glu Gly Ser Lys Ser Val
 85 90 95
 aaa act gat gat tca gac aag gat gct gat aga tcc tct aag aga aag 336
 Lys Thr Asp Asp Ser Asp Lys Asp Ala Asp Arg Ser Ser Lys Arg Lys
 100 105 110
 agg aag aat cag tat agg ggg atc aga cag cga cct tgg ggt aag tgg 384
 Arg Lys Asn Gln Tyr Arg Gly Ile Arg Gln Arg Pro Trp Gly Lys Trp
 115 120 125
 gca gct gaa ata cgt gac cca aga aaa ggg gtt cgg gtg tgg ctg gga 432
 Ala Ala Glu Ile Arg Asp Pro Arg Lys Gly Val Arg Val Trp Leu Gly
 130 135 140
 act ttc aat act gca gaa gaa gct gcc aga gct tat gat gtt gag gct 480
 Thr Phe Asn Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Val Glu Ala
 145 150 155 160
 agg agg atc aga ggc aat aaa gct aag gta aac ttt ccc gat gaa gct 528
 Arg Arg Ile Arg Gly Asn Lys Ala Lys Val Asn Phe Pro Asp Glu Ala
 165 170 175
 cca gtg cct gcc tcg aga cgt act gtt aag gtg aat cct caa aag gtc 576
 Pro Val Pro Ala Ser Arg Arg Thr Val Lys Val Asn Pro Gln Lys Val
 180 185 190
 ctt cct aag gag atc ctg gac tcg gtt cag ccc gac tcg act atc ata 624
 Leu Pro Lys Glu Ile Leu Asp Ser Val Gln Pro Asp Ser Thr Ile Ile
 195 200 205
 aac aac atg gag gat tgc tgt tat gat tct ttg gga ttt ctt gaa gag 672
 Asn Asn Met Glu Asp Cys Cys Tyr Asp Ser Leu Gly Phe Leu Glu Glu
 210 215 220
 aaa ccc atg acg aag cag ttt gga tgt gag gat ggg agc agt gct tct 720
 Lys Pro Met Thr Lys Gln Phe Gly Cys Glu Asp Gly Ser Ser Ala Ser
 225 230 235 240
 gga gat acg gga ttt ggc tca ttt gcc cct tca gct ggt acc gat atc 768
 Gly Asp Thr Gly Phe Gly Ser Phe Ala Pro Ser Ala Gly Thr Asp Ile
 245 250 255
 tac ttc aac tct gat gtt gga agt aac tct ttt gac tgc tct gat ttt 816

PF59082SeqList_PF59082.txt

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Gly	Trp	Gly	Glu	Pro	Cys	Ala	Arg	Thr	Pro	Glu	Ile	Ser	Ser	Val	Leu	
275							280					285				
tca	gct	gtt	att	gaa	agc	aat	gaa	tct	caa	ctt	gtt	gaa	gat	gat	acc	912
Ser	Ala	Val	Ile	Glu	Ser	Asn	Glu	Ser	Gln	Leu	Val	Glu	Asp	Asp	Thr	
290						295					300					
agt	cca	atg	aaa	aaa	ctg	aaa	tca	agc	ccc	att	aat	cca	gta	gct	gat	960
Ser	Pro	Met	Lys	Lys	Leu	Lys	Ser	Ser	Pro	Ile	Asn	Pro	Val	Ala	Asp	
305					310					315					320	
gat	gga	aat	acc	gca	aac	aag	cta	tct	gaa	gag	ctt	tca	gct	ttt	gaa	1008
Asp	Gly	Asn	Thr	Ala	Asn	Lys	Leu	Ser	Glu	Glu	Leu	Ser	Ala	Phe	Glu	
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acc	cag	atg	aag	ttc	ctt	cag	atc	ccc	tat	ctg	gag	gga	aat	tgg	gat	1056
Thr	Gln	Met	Lys	Phe	Leu	Gln	Ile	Pro	Tyr	Leu	Glu	Gly	Asn	Trp	Asp	
				340				345					350			
gca	tca	gtt	gat	act	ttc	ctc	aac	tca	agt	gca	act	cag	gat	ggg	gat	1104
Ala	Ser	Val	Asp	Thr	Phe	Leu	Asn	Ser	Ser	Ala	Thr	Gln	Asp	Gly	Asp	
		355					360					365				
aat	gct	atg	gac	tta	tgg	tcc	ttt	gat	gat	gtt	cct	tct	tta	ttg	gga	1152
Asn	Ala	Met	Asp	Leu	Trp	Ser	Phe	Asp	Asp	Val	Pro	Ser	Leu	Leu	Gly	
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Gly	Val	Phe														
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<211> 387

<212> PRT

<213> Nicotiana tabacum

<400> 768

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			20					25					30			
Asn	Lys	Gln	Lys	Asn	Pro	Asn	Asn	Tyr	His	Ser	Lys	Pro	Leu	Arg	Ser	
		35				40						45				
Gln	Val	Val	Asp	Leu	Asp	Asp	Asp	Phe	Glu	Ala	Asp	Phe	Gln	Asp	Phe	
	50					55				60						
Lys	Asp	Phe	Ser	Asp	Asp	Glu	Asp	Val	Gln	Val	Asp	Val	Lys	Pro	Phe	
65					70				75						80	
Ala	Phe	Ser	Ala	Ser	Lys	Asn	Ser	Asn	Val	Glu	Gly	Ser	Lys	Ser	Val	
				85				90						95		
Lys	Thr	Asp	Asp	Ser	Asp	Lys	Asp	Ala	Asp	Arg	Ser	Ser	Lys	Arg	Lys	
			100					105					110			
Arg	Lys	Asn	Gln	Tyr	Arg	Gly	Ile	Arg	Gln	Arg	Pro	Trp	Gly	Lys	Trp	
		115				120						125				
Ala	Ala	Glu	Ile	Arg	Asp	Pro	Arg	Lys	Gly	Val	Arg	Val	Trp	Leu	Gly	
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Thr	Phe	Asn	Thr	Ala	Glu	Glu	Ala	Ala	Arg	Ala	Tyr	Asp	Val	Glu	Ala	
145					150				155					160		
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Pro	Val	Pro	Ala	Ser	Arg	Arg	Thr	Val	Lys	Val	Asn	Pro	Gln	Lys	Val	
			180					185					190			
Leu	Pro	Lys	Glu	Ile	Leu	Asp	Ser	Val	Gln	Pro	Asp	Ser	Thr	Ile	Ile	
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	210					215					220					
Lys	Pro	Met	Thr	Lys	Gln	Phe	Gly	Cys	Glu	Asp	Gly	Ser	Ser	Ala	Ser	
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Gly	Asp	Thr	Gly	Phe	Gly	Ser	Phe	Ala	Pro	Ser	Ala	Gly	Thr	Asp	Ile	
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Tyr	Phe	Asn	Ser	Asp	Val	Gly	Ser	Asn	Ser	Phe	Asp	Cys	Ser	Asp	Phe	
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Gly	Trp	Gly	Glu	Pro	Cys	Ala	Arg	Thr	Pro	Glu	Ile	Ser	Ser	Val	Leu	
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PF59082SeqList_PF59082.txt

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 290 295 300
 Ser Pro Met Lys Lys Leu Lys Ser Ser Pro Ile Asn Pro Val Ala Asp
 305 310 315 320
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 325 330 335
 Thr Gln Met Lys Phe Leu Gln Ile Pro Tyr Leu Glu Gly Asn Trp Asp
 340 345 350
 Ala Ser Val Asp Thr Phe Leu Asn Ser Ser Ala Thr Gln Asp Gly Asp
 355 360 365
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 Gly Val Phe
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aatcgccgcc atg tgt gga gga gct ata ata tcc gat ttc att cca ccg 169

Met Cys Gly Gly Ala Ile Ile Ser Asp Phe Ile Pro Pro
 1 5 10

ccg agg tct cgc cgt gtt act agc gag ttt att tgg ccg gat ctg aag 217

Pro Arg Ser Arg Arg Val Thr Ser Glu Phe Ile Trp Pro Asp Leu Lys
 15 20 25

aag aat ttg aaa gga tcg aag aaa agc tcg aag aat cgt tcg aat ttc 265

Lys Asn Leu Lys Gly Ser Lys Lys Ser Ser Lys Asn Arg Ser Asn Phe
 30 35 40 45

ttc gat ttt gac gct gag ttc gaa gct gat ttc caa ggt ttc aaa gat 313

Phe Asp Phe Asp Ala Glu Phe Glu Ala Asp Phe Gln Gly Phe Lys Asp
 50 55 60

gat tcg tct atc gat tgc gat gat gat ttc gac gtc ggt gat gtt ttc 361

Asp Ser Ser Ile Asp Cys Asp Asp Asp Phe Asp Val Gly Asp Val Phe
 65 70 75

gcc gat gtg aaa cca ttc gtt ttc act tcg act cca aaa ccc gcc gtc 409

Ala Asp Val Lys Pro Phe Val Phe Thr Ser Thr Pro Lys Pro Ala Val
 80 85 90

tcc gcc gct gcg gaa ggt tca gtt ttt ggt aag aaa gtt act ggc ttg 457

Ser Ala Ala Ala Glu Gly Ser Val Phe Gly Lys Lys Val Thr Gly Leu
 95 100 105

gat ggg gaa gct gag aaa tct gca aat agg aag agg aag aat cag tac 505

Asp Gly Glu Ala Glu Lys Ser Ala Asn Arg Lys Arg Lys Asn Gln Tyr
 110 115 120 125

cga ggg att agg caa cgt cct tgg gga aaa tgg gct gct gag ata cgt 553

Arg Gly Ile Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg
 130 135 140

gat cca agg gaa ggt gct aga atc tgg ctt gga acg ttc aag aca gct 601

Asp Pro Arg Glu Gly Ala Arg Ile Trp Leu Gly Thr Phe Lys Thr Ala
 145 150 155

gag gaa gct gct aga gct tac gat gct gca gcg cgg aga atc cgt gga 649

Glu Glu Ala Ala Arg Ala Tyr Asp Ala Ala Ala Arg Arg Ile Arg Gly
 160 165 170

tct aaa gct aag gtg aat ttc cct gaa gaa aac ctg aag gct aat tct 697

Ser Lys Ala Lys Val Asn Phe Pro Glu Glu Asn Leu Lys Ala Asn Ser
 175 180 185

cag aaa cgc tct gtg aag gct aat ctt cag aaa cca gtg gct aaa cct 745

Gln Lys Arg Ser Val Lys Ala Asn Leu Gln Lys Pro Val Ala Lys Pro

PF59082SeqList_PF59082.txt

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		210		215		220	
gaa aat atg tgt ttc atg gag gag aaa cac caa gtg agc aac aac aac	841						
Glu Asn Met Cys Phe Met Glu Glu Lys His Gln Val Ser Asn Asn Asn							
		225		230		235	
aac aac cag ttt ggg atg aca aac tcc gtt gat gct gga tgt aat ggg	889						
Asn Asn Gln Phe Gly Met Thr Asn Ser Val Asp Ala Gly Cys Asn Gly							
		240		245		250	
tat cag tat ttc agc tct gac cag ggt agt aat tct ttc gat tgt tcg	937						
Tyr Gln Tyr Phe Ser Ser Asp Gln Gly Ser Asn Ser Phe Asp Cys Ser							
		255		260		265	
gag ttt ggt tgg agc gat caa gct ccg ata act ccc gac atc tct tct	985						
Glu Phe Gly Trp Ser Asp Gln Ala Pro Ile Thr Pro Asp Ile Ser Ser							
		270		275		280	
gcg gtt atc aac aac aac aac tca gct ctg ttc ttt gag gaa gcc aat	1033						
Ala Val Ile Asn Asn Asn Asn Ser Ala Leu Phe Phe Glu Glu Ala Asn							
		290		295		300	
cca gct aag aag ctc aag tct atg gat ttc gag aca cct tac aac aac	1081						
Pro Ala Lys Lys Leu Lys Ser Met Asp Phe Glu Thr Pro Tyr Asn Asn							
		305		310		315	
act gaa tgg gac gct tca ctg gat ttc ctc aac gaa gat gct gta acg	1129						
Thr Glu Trp Asp Ala Ser Leu Asp Phe Leu Asn Glu Asp Ala Val Thr							
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act cag gac aat ggt gca aac cct atg gac cta tgg agt att gat gaa	1177						
Thr Gln Asp Asn Gly Ala Asn Pro Met Asp Leu Trp Ser Ile Asp Glu							
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		350		355			
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gtgttttggt tttgttactt tatgccccaa aactccttta acatttgtca taatgtgttt	1524						
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 35 40 45
 Asp Ala Glu Phe Glu Ala Asp Phe Gln Gly Phe Lys Asp Asp Ser Ser
 50 55 60
 Ile Asp Cys Asp Asp Asp Phe Asp Val Gly Asp Val Phe Ala Asp Val
 65 70 75 80
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 85 90 95
 Ala Glu Gly Ser Val Phe Gly Lys Lys Val Thr Gly Leu Asp Gly Glu
 Seite 990

PF59082SeqList_PF59082.txt

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Arg	Lys	Gly	Ile	Arg	Val	Trp	Leu	Gly	Thr	Phe	Asn	Ser	Ala	Glu	Glu		
		125						130					135				
gca	gcc	aga	gct	tat	gat	gct	gag	gcg	cga	agg	atc	aga	ggc	aag	aaa	545	
Ala	Ala	Arg	Ala	Tyr	Asp	Ala	Glu	Ala	Arg	Arg	Ile	Arg	Gly	Lys	Lys		
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Ala	Lys	Val	Asn	Phe	Pro	Asp	Glu	Ala	Pro	Val	Ser	Val	Ser	Arg	Arg		
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gct	att	aag	caa	aat	ccc	caa	aag	gca	ctt	cgt	gag	gaa	acc	ctg	aac	641	
Ala	Ile	Lys	Gln	Asn	Pro	Gln	Lys	Ala	Leu	Arg	Glu	Glu	Thr	Leu	Asn		
170				175				180						185			
aca	gtt	cag	ccc	aac	atg	act	tat	att	agt	aac	ttg	gat	ggt	gga	tct	689	
Thr	Val	Gln	Pro	Asn	Met	Thr	Tyr	Ile	Ser	Asn	Leu	Asp	Gly	Gly	Ser		
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gat	gat	tcg	ttc	agt	ttt	ttc	gaa	gag	aaa	cca	gca	acc	aag	cag	tac	737	
Asp	Asp	Ser	Phe	Ser	Phe	Phe	Glu	Glu	Lys	Pro	Ala	Thr	Lys	Gln	Tyr		
			205				210					215					
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Gly	Phe	Glu	Asn	Val	Ser	Phe	Thr	Ala	Val	Asp	Met	Gly	Leu	Gly	Ser		
		220				225					230						
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Val	Ser	Pro	Ser	Ala	Gly	Asn	Val	Tyr	Phe	Ser	Ser	Asp	Glu	Ala			
		235			240					245							
agt	aac	act	ttt	gac	tgc	tct	gat	ttc	ggt	tgg	gct	gaa	ccg	tgt	gca	881	
Ser	Asn	Thr	Phe	Asp	Cys	Ser	Asp	Phe	Gly	Trp	Ala	Glu	Pro	Cys	Ala		
250				255				260						265			
agg	act	cca	gag	atc	tca	tct	gtt	ctg	tcg	gaa	gtt	ctg	gaa	acc	aat	929	
Arg	Thr	Pro	Glu	Ile	Ser	Ser	Val	Leu	Ser	Glu	Val	Leu	Glu	Thr	Asn		
			270					275					280				
gag	act	cat	ttt	gat	gat	gat	tcc	aga	cca	gag	aaa	aaa	ctg	aag	tcc	977	
Glu	Thr	His	Phe	Asp	Asp	Asp	Ser	Arg	Pro	Glu	Lys	Lys	Leu	Lys	Ser		
			285				290					295					
tgt	tcc	agc	act	tca	ttg	aca	gtt	gac	ggt	aac	act	gtg	aac	acg	cta	1025	
Cys	Ser	Ser	Thr	Ser	Leu	Thr	Val	Asp	Gly	Asn	Thr	Val	Asn	Thr	Leu		
		300				305					310						
tct	gaa	gag	cta	tcg	gct	ttt	gaa	tcc	cag	atg	aag	ttc	ttg	cag	atc	1073	
Ser	Glu	Glu	Leu	Ser	Ala	Phe	Glu	Ser	Gln	Met	Lys	Phe	Leu	Gln	Ile		
		315			320					325							
cca	tat	ctc	gag	gga	aat	tgg	gat	gca	tcg	gtt	gat	gcc	ttc	ctc	aat	1121	
Pro	Tyr	Leu	Glu	Gly	Asn	Trp	Asp	Ala	Ser	Val	Asp	Ala	Phe	Leu	Asn		
330				335				340						345			
aca	agt	gca	att	cag	gat	ggt	gga	aac	gcc	atg	gac	ctt	tgg	tcc	ttc	1169	
Thr	Ser	Ala	Ile	Gln	Asp	Gly	Gly	Asn	Ala	Met	Asp	Leu	Trp	Ser	Phe		
			350				355						360				
gat	gat	gta	cct	tct	tta	atg	gga	ggt	gcc	tac	taagctgcat	acacatcttc				1222	
Asp	Asp	Val	Pro	Ser	Leu	Met	Gly	Gly	Ala	Tyr							
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<211> 372

<212> PRT

<213> Lycopersicon esculentum

<400> 772

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PF59082SeqList_PF59082.txt

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 Lys Asp Asn Ser Asp Asp Asp Asp Val Lys Ala Phe Gly Pro Lys
 65 70 75 80
 Ser Val Arg Ser Gly Asp Ser Asn Cys Glu Ala Asp Arg Ser Ser Lys
 85 90 95
 Arg Lys Arg Lys Asn Gln Tyr Arg Gly Ile Arg Gln Arg Pro Trp Gly
 100 105 110
 Lys Trp Ala Ala Glu Ile Arg Asp Pro Arg Lys Gly Ile Arg Val Trp
 115 120 125
 Leu Gly Thr Phe Asn Ser Ala Glu Glu Ala Ala Arg Ala Tyr Asp Ala
 130 135 140
 Glu Ala Arg Arg Ile Arg Gly Lys Lys Ala Lys Val Asn Phe Pro Asp
 145 150 155 160
 Glu Ala Pro Val Ser Val Ser Arg Arg Ala Ile Lys Gln Asn Pro Gln
 165 170 175
 Lys Ala Leu Arg Glu Glu Thr Leu Asn Thr Val Gln Pro Asn Met Thr
 180 185 190
 Tyr Ile Ser Asn Leu Asp Gly Gly Ser Asp Asp Ser Phe Ser Phe Phe
 195 200 205
 Glu Glu Lys Pro Ala Thr Lys Gln Tyr Gly Phe Glu Asn Val Ser Phe
 210 215 220
 Thr Ala Val Asp Met Gly Leu Gly Ser Val Ser Pro Ser Ala Gly Thr
 225 230 235 240
 Asn Val Tyr Phe Ser Ser Asp Glu Ala Ser Asn Thr Phe Asp Cys Ser
 245 250 255
 Asp Phe Gly Trp Ala Glu Pro Cys Ala Arg Thr Pro Glu Ile Ser Ser
 260 265 270
 Val Leu Ser Glu Val Leu Glu Thr Asn Glu Thr His Phe Asp Asp Asp
 275 280 285
 Ser Arg Pro Glu Lys Lys Leu Lys Ser Cys Ser Ser Thr Ser Leu Thr
 290 295 300
 Val Asp Gly Asn Thr Val Asn Thr Leu Ser Glu Glu Leu Ser Ala Phe
 305 310 315 320
 Glu Ser Gln Met Lys Phe Leu Gln Ile Pro Tyr Leu Glu Gly Asn Trp
 325 330 335
 Asp Ala Ser Val Asp Ala Phe Leu Asn Thr Ser Ala Ile Gln Asp Gly
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 Gly Gly Ala Tyr
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 <212> DNA
 <213> Fagus sylvatica

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 Arg Arg Leu Thr Ala Asp Tyr Leu Trp Gly Asp Arg Lys Lys Pro Ile
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 Ser Gly Lys Arg Phe Ser Lys Pro Val Val Asp Leu Asp Asp Glu Phe
 35 40 45
 gag ctc gat ttt cag ggc ttc aag gac gag gag gag tct gat atc gac 192
 Glu Leu Asp Phe Gln Gly Phe Lys Asp Glu Glu Glu Ser Asp Ile Asp
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PF59082SeqList_PF59082.txt

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Pro	Pro	Ser	Ser	Gly 85	Ser	Lys	Pro	Val	Lys 90	Ser	Val	Glu	Phe	Asn 95	Gly	
caa	gct	gag	aaa	tct	gca	aag	aga	aag	agg	aag	aat	cag	tat	cgg	ggg	336
Gln	Ala	Glu	Lys	Ser	Ala	Lys	Arg	Lys	Arg	Lys	Asn	Gln	Tyr	Arg	Gly	
atc	cgg	cag	cgc	cca	tgg	ggt	aag	tgg	gct	gct	gag	att	cga	gac	cca	384
Ile	Arg	Gln 115	Arg	Pro	Trp	Gly	Lys 120	Trp	Ala	Ala	Glu	Ile	Arg	Asp	Pro	
agg	aaa	ggg	gtc	cgt	gtc	tgg	ctc	gga	act	ttt	aac	act	gca	gaa	gaa	432
Arg	Lys 130	Gly	Val	Arg	Val	Trp 135	Leu	Gly	Thr	Phe	Asn 140	Thr	Ala	Glu	Glu	
gct	gca	aga	gct	tat	gat	gca	gaa	gca	cgg	aga	att	cgt	ggc	aag	aaa	480
Ala 145	Ala	Arg	Ala	Tyr	Asp 150	Ala	Glu	Ala	Arg	Arg 155	Ile	Arg	Gly	Lys	Lys 160	
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Ser	Lys	Gly	Asn	Phe 165	Pro	Met	Arg	Leu	Pro 170	Val	Pro	Lys	Arg	Ser	Val	
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Lys	Ala	Asn	Leu	Gln 180	Lys	Pro	Leu	Ala 185	Lys	Ala	Asn	Leu	Asn	Ser	Val	
cag	ccc	aac	ctg	aac	caa	aat	ttc	aat	ttt	atg	aac	tct	gat	cag	gac	624
Gln	Pro	Asn 195	Leu	Asn	Gln	Asn	Phe 200	Asn	Phe	Met	Asn	Ser 205	Asp	Gln	Asp	
tat	acc	atg	ggt	ttg	atg	gaa	gag	aaa	cct	ttc	acg	aac	cag	tat	ggg	672
Tyr	Thr 210	Met	Gly	Leu	Met	Glu 215	Glu	Lys	Pro	Phe	Thr 220	Asn	Gln	Tyr	Gly	
tat	atg	gat	tcc	atc	cct	gtc	aat	gca	gat	gtt	gga	cta	aaa	tcc	ttt	720
Tyr 225	Met	Asp	Ser	Ile	Pro 230	Val	Asn	Ala	Asp	Val 235	Gly	Leu	Lys	Ser	Phe 240	
gct	tcc	aat	aat	act	gcc	cca	tac	ttt	aac	tca	gat	cag	ggg	agt	aac	768
Ala	Ser	Asn	Asn	Thr 245	Ala	Pro	Tyr	Phe	Asn 250	Ser	Asp	Gln	Gly	Ser	Asn 255	
tcg	ttt	gat	tgt	tct	gac	tat	gga	tgg	gga	gaa	cag	ggc	tct	aag	act	816
Ser	Phe	Asp	Cys	Ser	Asp	Tyr	Gly 260	Trp	Gly 265	Glu	Gln	Gly	Ser	Lys	Thr	
cca	gaa	atc	tca	tct	gtt	ctt	tca	gcc	act	tta	gaa	ggg	gat	gaa	tct	864
Pro	Glu	Ile 275	Ser	Ser	Val	Leu	Ser 280	Ala	Thr	Leu	Glu	Gly 285	Asp	Glu	Ser	
cag	ttt	gtg	gag	gat	gct	gtg	ccc	acg	aag	aaa	ttg	aag	tca	gac	tct	912
Gln	Phe 290	Val	Glu	Asp	Ala	Val 295	Pro	Thr	Lys	Lys	Leu 300	Lys	Ser	Asp	Ser	
ggg	aat	gca	gtg	ttc	att	gaa	aat	aac	act	gca	aag	aca	ctg	tca	gag	960
Gly 305	Asn	Ala	Val	Phe	Ile 310	Glu	Asn	Asn	Thr	Ala 315	Lys	Thr	Leu	Ser	Glu 320	
gag	ctc	tca	gct	ttt	gag	tcc	cag	atg	aac	ttt	cag	atg	cca	ttt	ctt	1008
Glu	Leu	Ser	Ala	Phe 325	Glu	Ser	Gln	Met	Asn 330	Phe	Gln	Met	Pro	Phe 335	Leu	
gag	gga	agc	tgg	gaa	tcc	aac	atg	gag	gca	ctg	ttc	agt	ggg	gac	aca	1056
Glu	Gly	Ser	Trp	Glu	Ser	Asn	Met	Glu 340	Ala 345	Leu	Phe	Ser	Gly 350	Asp	Thr	
act	cag	gat	ggt	aac	tcg	atg	gat	ctt	tgg	agc	ttc	gat	gac	ctc	ccc	1104
Thr	Gln	Asp 355	Gly	Asn	Ser	Met	Asp 360	Leu	Trp	Ser	Phe	Asp 365	Asp	Leu	Pro	
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<212> PRT

<213> Fagus sylvatica

<400> 774

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Arg	Arg	Leu	Thr	Ala	Asp	Tyr	Leu	Trp	Gly	Asp	Arg	Lys	Lys	Pro	Ile	

PF59082SeqList_PF59082.txt

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 65 70 75 80
 Pro Pro Ser Ser Gly Ser Lys Pro Val Lys Ser Val Glu Phe Asn Gly
 85 90 95
 Gln Ala Glu Lys Ser Ala Lys Arg Lys Arg Lys Asn Gln Tyr Arg Gly
 100 105 110
 Ile Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp Pro
 115 120 125
 Arg Lys Gly Val Arg Val Trp Leu Gly Thr Phe Asn Thr Ala Glu Glu
 130 135 140
 Ala Ala Arg Ala Tyr Asp Ala Glu Ala Arg Arg Ile Arg Gly Lys Lys
 145 150 155 160
 Ser Lys Gly Asn Phe Pro Met Arg Leu Pro Val Pro Lys Arg Ser Val
 165 170 175
 Lys Ala Asn Leu Gln Lys Pro Leu Ala Lys Ala Asn Leu Asn Ser Val
 180 185 190
 Gln Pro Asn Leu Asn Gln Asn Phe Asn Phe Met Asn Ser Asp Gln Asp
 195 200 205
 Tyr Thr Met Gly Leu Met Glu Glu Lys Pro Phe Thr Asn Gln Tyr Gly
 210 215 220
 Tyr Met Asp Ser Ile Pro Val Asn Ala Asp Val Gly Leu Lys Ser Phe
 225 230 235 240
 Ala Ser Asn Asn Thr Ala Pro Tyr Phe Asn Ser Asp Gln Gly Ser Asn
 245 250 255
 Ser Phe Asp Cys Ser Asp Tyr Gly Trp Gly Glu Gln Gly Ser Lys Thr
 260 265 270
 Pro Glu Ile Ser Ser Val Leu Ser Ala Thr Leu Glu Gly Asp Glu Ser
 275 280 285
 Gln Phe Val Glu Asp Ala Val Pro Thr Lys Lys Leu Lys Ser Asp Ser
 290 295 300
 Gly Asn Ala Val Phe Ile Glu Asn Asn Thr Ala Lys Thr Leu Ser Glu
 305 310 315 320
 Glu Leu Ser Ala Phe Glu Ser Gln Met Asn Phe Gln Met Pro Phe Leu
 325 330 335
 Glu Gly Ser Trp Glu Ser Asn Met Glu Ala Leu Phe Ser Gly Asp Thr
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gagttatacg cc atg tgt gga gga gct ata atc tcc gat ttc atc cct ccg 171
 Met Cys Gly Gly Ala Ile Ile Ser Asp Phe Ile Pro Pro

ccg agt ttc cgc cgc gtc acg agc gag ttt ctc tgg ccg gat ctg aag 219
 Pro Ser Phe Arg Arg Val Thr Ser Glu Phe Leu Trp Pro Asp Leu Lys

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 Seite 995

PF59082SeqList_PF59082.txt

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Asp	Asp	Glu	Phe	Glu 50	Ala	Asp	Phe	Gln	Gly 55	Phe	Glu	Asp	Asp	Asp	Ala 60	
tct	ttt	gac	tgc	gaa	gac	gat	gat	gat	gaa	gtc	ttc	gct	aaa	gtg	aag	363
Ser	Phe	Asp	Cys 65	Glu	Asp	Asp	Asp	Asp	Glu 70	Val	Phe	Ala	Lys 75	Val	Lys	
ccc	ttt	gtc	ttc	acc	gcg	acc	acc	aag	ccc	gta	gct	tcc	cct	ccc	act	411
Pro	Phe	Val 80	Phe	Thr	Ala	Thr	Thr 85	Lys	Pro	Val	Ala	Ser 90	Pro	Pro	Thr	
ggg	tca	gtg	tct	ggc	aag	aag	atc	ata	gag	tcc	ggg	ggg	caa	gct	gag	459
Gly	Ser 95	Val	Ser	Gly	Lys	Lys 100	Ile	Ile	Glu	Ser	Gly 105	Gly	Gln	Ala	Glu	
aag	tct	gct	aag	aga	aag	aga	aag	aat	cag	tac	agg	ggg	att	agg	cag	507
Lys 110	Ser	Ala	Lys	Arg	Lys 115	Arg	Lys	Asn	Gln	Tyr 120	Arg	Gly	Ile	Arg	Gln 125	
cga	cct	tgg	ggg	aaa	tgg	gct	gct	gag	atc	cgt	gat	cca	aga	aaa	ggc	555
Arg	Pro	Trp	Gly 130	Lys	Trp	Ala	Ala	Glu	Ile 135	Arg	Asp	Pro	Arg	Lys 140	Gly	
tcc	agg	gaa	tgg	ctt	gga	acg	ttt	gac	acc	gcc	gag	gaa	gct	gca	aga	603
Ser	Arg	Glu 145	Trp	Leu	Gly	Thr	Phe 150	Asp	Thr	Ala	Glu	Glu 155	Ala	Ala	Arg	
gcc	tat	gat	gca	act	gca	cgc	aga	atc	cgc	ggc	agt	aaa	gcc	aag	gtg	651
Ala	Tyr 160	Asp	Ala	Thr	Ala	Arg	Arg 165	Ile	Arg	Gly	Ser 170	Lys	Ala	Lys	Val	
aat	ttc	cca	gag	gag	agc	aac	aac	aac	cgt	agc	gtc	tcc	cag	aaa	cga	699
Asn	Phe 175	Pro	Glu	Glu	Ser	Asn 180	Asn	Asn	Arg	Ser	Val 185	Ser	Gln	Lys	Arg	
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Pro 190	Ser	Ala	Lys	Lys	Leu 195	Val	Ala	Lys	Pro	Asn 200	Gln	Ser	Pro	Ala	Leu 205	
gtt	cag	cag	cca	atg	agt	cag	tac	tac	aac	aac	gcc	ttt	ggg	gat	gtg	795
Val	Gln	Gln	Pro	Met 210	Ser	Gln	Tyr	Tyr	Asn 215	Asn	Ala	Phe	Gly	Asp 220	Val	
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Ser	Phe 225	Met	Glu	Glu	Lys	Pro	Gln	Met	Tyr 230	Asn	Asn	Gln	Phe 235	Gly	Leu	
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Ala	Asn 240	Ser	Tyr	Asn	Asn	Gln	Tyr 245	Phe	Ser	Ser	Asp	Gln 250	Gly	Ser	Asn	
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Ser	Phe 255	Asp	Cys	Ser	Glu 260	Phe	Gly	Arg	Ser	Asp	His 265	Gly	Pro	Lys	Thr	
cct	gag	atc	tct	tca	atg	ctg	gtt	aat	aat	aac	caa	act	ccg	ttc	att	987
Pro 270	Glu	Ile	Ser	Ser	Met 275	Leu	Val	Asn	Asn	Asn 280	Gln	Thr	Pro	Phe 285	Ile	
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Glu	Val	Thr	Asn	Ala 290	Ala	Lys	Lys	Leu	Lys 295	Pro	Ser	Ser	Asp	Asp	Leu	
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Met	Ala 305	Tyr	Leu	Asp	Asn	Ala	Leu	Trp	Glu 310	Ser	Pro	Ser	Pro	Leu	Glu	
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Val	Glu	Ala 320	Met	Leu	Gly	Val	Asp 325	Ala	Ala	Ala	Val	Thr 330	Gln	Gly	Glu	
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Glu	Asn 335	Pro	Met	Asp	Leu 340	Trp	Ser	Leu	Asp	Asp	Ile 345	Asn	Tyr	Met	Leu	
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Glu 350	Gly	Val	Phe													
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gc	atc	g	ttt	t	at	g	at	g	t	c	t	t	at	t	at	1354
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PF59082SeqList_PF59082.txt

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35 40 45
Phe Glu Ala Asp Phe Gln Gly Phe Glu Asp Asp Ala Ser Phe Asp
50 55 60
Cys Glu Asp Asp Asp Glu Val Phe Ala Lys Val Lys Pro Phe Val
65 70 75 80
Phe Thr Ala Thr Lys Pro Val Ala Ser Pro Pro Thr Gly Ser Val
85 90 95
Ser Gly Lys Lys Ile Ile Glu Ser Gly Gly Gln Ala Glu Lys Ser Ala
100 105 110
Lys Arg Lys Arg Lys Asn Gln Tyr Arg Gly Ile Arg Gln Arg Pro Trp
115 120 125
Gly Lys Trp Ala Ala Glu Ile Arg Asp Pro Arg Lys Gly Ser Arg Glu
130 135 140
Trp Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp
145 150 155 160
Ala Thr Ala Arg Arg Ile Arg Gly Ser Lys Ala Lys Val Asn Phe Pro
165 170 175
Glu Glu Ser Asn Asn Asn Arg Ser Val Ser Gln Lys Arg Pro Ser Ala
180 185 190
Lys Lys Leu Val Ala Lys Pro Asn Gln Ser Pro Ala Leu Val Gln Gln
195 200 205
Pro Met Ser Gln Tyr Tyr Asn Asn Ala Phe Gly Asp Val Ser Phe Met
210 215 220
Glu Glu Lys Pro Gln Met Tyr Asn Asn Gln Phe Gly Leu Ala Asn Ser
225 230 235 240
Tyr Asn Asn Gln Tyr Phe Ser Ser Asp Gln Gly Ser Asn Ser Phe Asp
245 250 255
Cys Ser Glu Phe Gly Arg Ser Asp His Gly Pro Lys Thr Pro Glu Ile
260 265 270
Ser Ser Met Leu Val Asn Asn Asn Gln Thr Pro Phe Ile Glu Val Thr
275 280 285
Asn Ala Lys Lys Leu Lys Pro Ser Ser Asp Asp Leu Met Ala Tyr
290 295 300
Leu Asp Asn Ala Leu Trp Glu Ser Pro Ser Pro Leu Glu Val Glu Ala
305 310 315 320
Met Leu Gly Val Asp Ala Ala Ala Val Thr Gln Gly Glu Glu Asn Pro
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Phe

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Arg	Arg	Val	Thr	Ser	Glu	Tyr	Leu	Trp	Pro	Asp	Leu	Lys	Asn	Lys	Val	
			20					25					30			
aaa	gct	tcg	aag	aag	aag	aag	cga	tcc	gat	ttc	ctc	gat	ctg	gac	gac	144
Lys	Ala	Ser	Lys	Lys	Lys	Lys	Arg	Ser	Asp	Phe	Leu	Asp	Leu	Asp	Asp	
		35					40					45				
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Glu	Phe	Glu	Ala	Asp	Phe	Gln	Gly	Phe	Lys	Asp	Gly	Ala	Ser	Phe	Asp	
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tgc	gaa	gat	gaa	ttc	gat	gtg	gat	gat	gaa	gtc	ttc	gcc	gat	gtc	aaa	240
Cys	Glu	Asp	Glu	Phe	Asp	Val	Asp	Asp	Glu	Val	Phe	Ala	Asp	Val	Lys	
	65				70					75					80	
ccc	ttt	gtc	ttc	gcc	gca	ggt	gcc	aag	ccc	gta	gcg	tcc	cct	ccc	gcc	288
Pro	Phe	Val	Phe	Ala	Ala	Gly	Ala	Lys	Pro	Val	Ala	Ser	Pro	Pro	Ala	
				85					90					95		
gcc	ttc	gcc	tcc	gct	ggt	tca	gtt	tct	ggc	aag	aaa	acc	ata	gag	tct	336
Ala	Phe	Ala	Ser	Ala	Gly	Ser	Val	Ser	Gly	Lys	Lys	Thr	Ile	Glu	Ser	
			100					105					110			
ggt	gga	caa	gct	gag	aaa	tct	gcc	aag	aga	aag	agg	aag	aat	cag	tac	384
Gly	Gly	Gln	Ala	Glu	Lys	Ser	Ala	Lys	Arg	Lys	Arg	Lys	Asn	Gln	Tyr	
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Arg	Gly	Ile	Arg	Gln	Arg	Pro	Trp	Gly	Lys	Trp	Ala	Ala	Glu	Ile	Arg	
	130					135					140					
gat	ccc	aga	aaa	ggc	tcc	cgg	gag	tgg	ctt	gga	aca	ttc	gac	acc	gcc	480
Asp	Pro	Arg	Lys	Gly	Ser	Arg	Glu	Trp	Leu	Gly	Thr	Phe	Asp	Thr	Ala	
	145				150					155					160	
gag	gaa	gca	gca	aga	gct	tat	gat	gca	gct	gca	cgc	agg	atc	cgc	ggt	528
Glu	Glu	Ala	Ala	Arg	Ala	Tyr	Asp	Ala	Ala	Ala	Arg	Arg	Ile	Arg	Gly	
				165				170						175		
aat	aaa	gct	aag	gtg	aac	ttc	cca	gag	gag	atg	gtc	cct	agc	gtc	tcc	576
Asn	Lys	Ala	Lys	Val	Asn	Phe	Pro	Glu	Glu	Met	Val	Pro	Ser	Val	Ser	
			180					185					190			
cag	aaa	cgc	cct	gct	gct	aag	aag	gca	gtg	gct	aaa	cca	aac	caa	agc	624
Gln	Lys	Arg	Pro	Ala	Ala	Lys	Lys	Ala	Val	Ala	Lys	Pro	Asn	Gln	Ser	
		195					200					205				
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Pro	Ala	Ser	Val	Gln	Gln	Pro	Thr	His	Val	Ser	Glu	Tyr	Cys	Asn	Asn	
		210				215					220					
tcc	ttt	gac	aac	atg	gga	cat	gac	ccc	tct	ttt	ggg	gat	gtg	agt	ttc	720
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atg	gaa	gag	aag	cct	cag	atg	tac	aac	aat	cag	ttc	ctt	gat	gtc	gga	768
Met	Glu	Glu	Lys	Pro	Gln	Met	Tyr	Asn	Asn	Gln	Phe	Leu	Asp	Val	Gly	
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Gly	Asn	Asn	Gly	Tyr	Gln	Tyr	Phe	Ser	Ser	Asp	Gln	Gly	Ser	Asn	Ser	
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ctg	gac	tgc	tct	gag	ttt	ggg	tgg	agt	gat	cat	acc	ccc	aag	aca	cct	864
Leu	Asp	Cys	Ser	Glu	Phe	Gly	Trp	Ser	Asp	His	Thr	Pro	Lys	Thr	Pro	
		275					280					285				
gag	atc	tct	tca	atg	ctg	gtc	aac	agt	aac	caa	gct	cct	ttc	att	gaa	912
Glu	Ile	Ser	Ser	Met	Leu	Val	Asn	Ser	Asn	Gln	Ala	Pro	Phe	Ile	Glu	
		290				295					300					
gaa	acc	aat	cca	gcc	aag	ctc	aaa	acc	aac	tct	gag	gac	ggg	aca		960
Glu	Thr	Asn	Pro	Ala	Lys	Lys	Leu	Lys	Thr	Asn	Ser	Glu	Asp	Gly	Thr	
				310						315					320	
agc	aac	aat	ggt	aat	tct	gat	gat	ctg	atg	gca	tat	ttg	aac	aac	gcc	1008
Ser	Asn	Asn	Gly	Asn	Ser	Asp	Asp	Leu	Met	Ala	Tyr	Leu	Asn	Asn	Ala	
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PF59082SeqList_PF59082.txt

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gct	act	atg	act	cag	gaa	gag	gga	acc	cca	atg	gac	cta	tgg	agc	ttc	1104
Ala	Thr	Met	Thr	Gln	Glu	Glu	Gly	Thr	Pro	Met	Asp	Leu	Trp	Ser	Phe	
		355					360					365				
gat	gat	atc	aac	tcc	atg	ctg	gat	ggg	gga	gtc	ttc	tga				1143
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 <212> PRT
 <213> Brassica napus

<400> 778

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			20					25					30		
Lys	Ala	Ser	Lys	Lys	Lys	Arg	Ser	Asp	Phe	Leu	Asp	Leu	Asp	Asp	
		35				40					45				
Glu	Phe	Glu	Ala	Asp	Phe	Gln	Gly	Phe	Lys	Asp	Gly	Ala	Ser	Phe	Asp
	50					55					60				
Cys	Glu	Asp	Glu	Phe	Asp	Val	Asp	Asp	Glu	Val	Phe	Ala	Asp	Val	Lys
65					70				75						80
Pro	Phe	Val	Phe	Ala	Ala	Gly	Ala	Lys	Pro	Val	Ala	Ser	Pro	Pro	Ala
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Ala	Phe	Ala	Ser	Ala	Gly	Ser	Val	Ser	Gly	Lys	Lys	Thr	Ile	Glu	Ser
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Gly	Gly	Gln	Ala	Glu	Lys	Ser	Ala	Lys	Arg	Lys	Arg	Lys	Asn	Gln	Tyr
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Arg	Gly	Ile	Arg	Gln	Arg	Pro	Trp	Gly	Lys	Trp	Ala	Ala	Glu	Ile	Arg
	130					135					140				
Asp	Pro	Arg	Lys	Gly	Ser	Arg	Glu	Trp	Leu	Gly	Thr	Phe	Asp	Thr	Ala
145					150					155					160
Glu	Glu	Ala	Ala	Arg	Ala	Tyr	Asp	Ala	Ala	Ala	Arg	Arg	Ile	Arg	Gly
				165				170						175	
Asn	Lys	Ala	Lys	Val	Asn	Phe	Pro	Glu	Met	Val	Pro	Ser	Val	Ser	
			180					185				190			
Gln	Lys	Arg	Pro	Ala	Ala	Lys	Lys	Ala	Val	Ala	Lys	Pro	Asn	Gln	Ser
		195					200					205			
Pro	Ala	Ser	Val	Gln	Gln	Pro	Thr	His	Val	Ser	Glu	Tyr	Cys	Asn	Asn
	210					215					220				
Ser	Phe	Asp	Asn	Met	Gly	His	Asp	Pro	Ser	Phe	Gly	Asp	Val	Ser	Phe
225					230					235					240
Met	Glu	Glu	Lys	Pro	Gln	Met	Tyr	Asn	Asn	Gln	Phe	Leu	Asp	Val	Gly
				245					250					255	
Gly	Asn	Asn	Gly	Tyr	Gln	Tyr	Phe	Ser	Ser	Asp	Gln	Gly	Ser	Asn	Ser
			260					265					270		
Leu	Asp	Cys	Ser	Glu	Phe	Gly	Trp	Ser	Asp	His	Thr	Pro	Lys	Thr	Pro
		275					280					285			
Glu	Ile	Ser	Ser	Met	Leu	Val	Asn	Ser	Asn	Gln	Ala	Pro	Phe	Ile	Glu
	290					295					300				
Glu	Thr	Asn	Pro	Ala	Lys	Lys	Leu	Lys	Thr	Asn	Ser	Glu	Asp	Gly	Thr
305					310					315					320
Ser	Asn	Asn	Gly	Asn	Ser	Asp	Asp	Leu	Met	Ala	Tyr	Leu	Asn	Asn	Ala
				325					330					335	
Leu	Trp	Glu	Ser	Pro	Leu	Glu	Val	Glu	Ala	Met	Phe	Gly	Gly	Asp	Ala
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Ala	Thr	Met	Thr	Gln	Glu	Glu	Gly	Thr	Pro	Met	Asp	Leu	Trp	Ser	Phe
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PF59082SeqList_PF59082.txt

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<222> (1)..(1086)

<400> 779

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cgc	cgc	gtc	acg	agc	gag	ttt	ctc	tgg	ccg	gat	ctg	aag	aag	agc	aag	96
Arg	Arg	Val	Thr	Ser	Glu	Phe	Leu	Trp	Pro	Asp	Leu	Lys	Lys	Ser	Lys	
			20					25					30			
ggg	aaa	gcc	tcg	aag	aag	cga	tcc	gat	ttc	ttc	gat	ctg	gac	gac	gag	144
Gly	Lys	Ala	Ser	Lys	Lys	Arg	Ser	Asp	Phe	Phe	Asp	Leu	Asp	Asp	Glu	
		35					40					45				
ttc	gag	gct	gat	ttt	caa	ggg	ttt	gag	gat	gac	gac	gag	tct	ttt	gac	192
Phe	Glu	Ala	Asp	Phe	Gln	Gly	Phe	Glu	Asp	Asp	Asp	Ala	Ser	Phe	Asp	
	50					55				60						
tgc	gaa	gac	gat	gat	gat	gaa	gtc	ttc	gct	aaa	gtg	aag	ccc	ttt	gtc	240
Cys	Glu	Asp	Asp	Asp	Asp	Glu	Val	Phe	Ala	Lys	Val	Lys	Pro	Phe	Val	
	65				70					75					80	
ttc	acc	gcg	acc	acc	aag	ccc	gta	gct	tcc	cct	ccc	act	ggg	tca	gtg	288
Phe	Thr	Ala	Thr	Thr	Lys	Pro	Val	Ala	Ser	Pro	Pro	Thr	Gly	Ser	Val	
			85					90					95			
tct	ggc	aag	aag	atc	ata	gag	tcc	ggg	ggg	caa	gct	gag	aag	tct	gct	336
Ser	Gly	Lys	Lys	Ile	Ile	Glu	Ser	Gly	Gly	Gln	Ala	Glu	Lys	Ser	Ala	
			100					105					110			
aag	aga	aag	aga	aag	aat	cag	tac	agg	ggg	att	agg	cag	cga	cct	tgg	384
Lys	Arg	Lys	Arg	Lys	Asn	Gln	Tyr	Arg	Gly	Ile	Arg	Gln	Arg	Pro	Trp	
		115					120					125				
ggg	aaa	tgg	gct	gct	gag	atc	cgt	gat	cca	aga	aaa	ggc	tcc	agg	gaa	432
Gly	Lys	Trp	Ala	Ala	Glu	Ile	Arg	Asp	Pro	Arg	Lys	Gly	Ser	Arg	Glu	
	130					135					140					
tgg	ctt	gga	acg	ttt	gac	acc	gcc	gag	gaa	gct	gca	aga	gcc	tat	gat	480
Trp	Leu	Gly	Thr	Phe	Asp	Thr	Ala	Glu	Glu	Ala	Ala	Arg	Ala	Tyr	Asp	
	145				150				155						160	
gca	gct	gca	cgc	aga	atc	cgc	ggc	agt	aaa	gcc	aag	gtg	aat	ttc	cca	528
Ala	Ala	Ala	Arg	Arg	Ile	Arg	Gly	Ser	Lys	Ala	Lys	Val	Asn	Phe	Pro	
			165				170						175			
gag	gag	agc	aac	aac	aac	cgt	agc	gtc	tcc	cag	aaa	cga	cct	tct	gct	576
Glu	Glu	Ser	Asn	Asn	Asn	Arg	Ser	Val	Ser	Gln	Lys	Arg	Pro	Ser	Ala	
			180				185					190				
aag	aag	ctg	gtg	gct	aaa	cca	aac	caa	agc	cca	gct	ttg	ggt	cag	cag	624
Lys	Lys	Leu	Val	Ala	Lys	Pro	Asn	Gln	Ser	Pro	Ala	Leu	Val	Gln	Gln	
		195					200					205				
cca	atg	agt	cag	tac	tac	aac	aac	gcc	ttt	ggg	gat	gtg	agt	ttc	atg	672
Pro	Met	Ser	Gln	Tyr	Tyr	Asn	Asn	Ala	Phe	Gly	Asp	Val	Ser	Phe	Met	
	210					215				220						
gaa	gag	aag	cct	cag	atg	tac	aac	aat	cag	ttt	ggg	tta	gca	aac	tcg	720
Glu	Glu	Lys	Pro	Gln	Met	Tyr	Asn	Asn	Gln	Phe	Gly	Leu	Ala	Asn	Ser	
	225				230				235						240	
tac	aac	aac	cac	tac	ttc	agt	tct	gat	cag	ggg	agt	aac	tca	ttt	gac	768
Tyr	Asn	Asn	His	Tyr	Phe	Ser	Ser	Asp	Gln	Gly	Ser	Asn	Ser	Phe	Asp	
			245					250					255			
tgc	tct	gag	ttt	ggg	tgg	agc	gac	cac	ggc	ccc	aag	aca	cct	gag	atc	816
Cys	Ser	Glu	Phe	Gly	Trp	Ser	Asp	His	Gly	Pro	Lys	Thr	Pro	Glu	Ile	
		260					265						270			
tct	tcg	atg	cta	gtc	ggg	aac	aac	caa	gct	ccg	ttc	act	gaa	gaa	acc	864
Ser	Ser	Met	Leu	Val	Gly	Asn	Asn	Gln	Ala	Pro	Phe	Thr	Glu	Glu	Thr	
		275				280						285				
aat	gca	gcc	aag	aag	ctc	aaa	ccc	agc	tct	gat	gac	gga	aca	agc	aac	912
Asn	Ala	Ala	Lys	Lys	Leu	Lys	Pro	Ser	Ser	Asp	Asp	Gly	Thr	Ser	Asn	
	290					295				300						
cag	tct	gat	gat	ctg	atg	gca	tac	ctt	gac	aat	gcc	ttg	tgg	gaa	tct	960
Gln	Ser	Asp	Asp	Leu	Met	Ala	Tyr	Leu	Asp	Asn	Ala	Leu	Trp	Glu	Ser	
	305				310				315						320	
cca	tct	cca	ttg	gaa	gtt	gaa	gcc	atg	ctg	ggg	gta	gat	gct	gcc	gct	1008
Pro	Ser	Pro	Leu	Glu	Val	Glu	Ala	Met	Leu	Gly	Val	Asp	Ala	Ala	Ala	
				325					330					335		

PF59082SeqList_PF59082.txt

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Val Thr Gln Gly Glu Glu Asn Pro Met Asp Leu Trp Ser Leu Asp Asp
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<210> 780

<211> 361

<212> PRT

<213> Brassica napus

<400> 780

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20 25 30
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35 40 45
Phe Glu Ala Asp Phe Gln Gly Phe Glu Asp Asp Ala Ser Phe Asp
50 55 60
Cys Glu Asp Asp Asp Asp Glu Val Phe Ala Lys Val Lys Pro Phe Val
65 70 75 80
Phe Thr Ala Thr Thr Lys Pro Val Ala Ser Pro Pro Thr Gly Ser Val
85 90 95
Ser Gly Lys Lys Ile Ile Glu Ser Gly Gly Gln Ala Glu Lys Ser Ala
100 105 110
Lys Arg Lys Arg Lys Asn Gln Tyr Arg Gly Ile Arg Gln Arg Pro Trp
115 120 125
Gly Lys Trp Ala Ala Glu Ile Arg Asp Pro Arg Lys Gly Ser Arg Glu
130 135 140
Trp Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp
145 150 155 160
Ala Ala Ala Arg Arg Ile Arg Gly Ser Lys Ala Lys Val Asn Phe Pro
165 170 175
Glu Glu Ser Asn Asn Asn Arg Ser Val Ser Gln Lys Arg Pro Ser Ala
180 185 190
Lys Lys Leu Val Ala Lys Pro Asn Gln Ser Pro Ala Leu Val Gln Gln
195 200 205
Pro Met Ser Gln Tyr Tyr Asn Asn Ala Phe Gly Asp Val Ser Phe Met
210 215 220
Glu Glu Lys Pro Gln Met Tyr Asn Asn Gln Phe Gly Leu Ala Asn Ser
225 230 235 240
Tyr Asn Asn His Tyr Phe Ser Ser Asp Gln Gly Ser Asn Ser Phe Asp
245 250 255
Cys Ser Glu Phe Gly Trp Ser Asp His Gly Pro Lys Thr Pro Glu Ile
260 265 270
Ser Ser Met Leu Val Gly Asn Asn Gln Ala Pro Phe Thr Glu Glu Thr
275 280 285
Asn Ala Ala Lys Lys Leu Lys Pro Ser Ser Asp Asp Gly Thr Ser Asn
290 295 300
Gln Ser Asp Asp Leu Met Ala Tyr Leu Asp Asn Ala Leu Trp Glu Ser
305 310 315 320
Pro Ser Pro Leu Glu Val Glu Ala Met Leu Gly Val Asp Ala Ala Ala
325 330 335
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Ile Asn Tyr Met Leu Glu Gly Val Phe
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cgc cgc gtc acc agc gag ttt ctc tgg ccg gat ctg aag aag agc tcg      96
Arg Arg Val Thr Ser Glu Phe Leu Trp Pro Asp Leu Lys Lys Ser Ser
20      25      30
aag aaa cgc tcg agt ttc ttc gat ctt gac gat gag ttc gag gct gac      144
Lys Lys Arg Ser Ser Phe Phe Asp Leu Asp Asp Glu Phe Glu Ala Asp
35      40      45
ttc cag ggc ttc aag gat gat tcc tct atc gat tgc gat gat gcg aag      192
Phe Gln Gly Phe Lys Asp Asp Ser Ser Ile Asp Cys Asp Asp Ala Lys
50      55      60
ccg ttc gtt ttc gcc ggg gct cgt aaa ccc gcc gtc tcc gcc gcc act      240
Pro Phe Val Phe Ala Gly Ala Arg Lys Pro Ala Val Ser Ala Ala Thr
65      70      75
gcc gat tca gtt att ggc aag aaa gtt gct gac gga gaa ggt gag agg      288
Ala Asp Ser Val Ile Gly Lys Lys Val Ala Asp Gly Glu Gly Glu Arg
85      90      95
tct gca aag agg aag agg aag agc cag tac cga ggg ata agg caa cgt      336
Ser Ala Lys Arg Lys Arg Lys Ser Gln Tyr Arg Gly Ile Arg Gln Arg
100      105      110
cct tgg gga aaa tgg gct gct gag att cgt gat cca agg gaa ggt tca      384
Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp Pro Arg Glu Gly Ser
115      120      125
aga gtt tgg ctt gga act ttt aaa aca gcc gag gaa gct gca aga gct      432
Arg Val Trp Leu Gly Thr Phe Lys Thr Ala Glu Glu Ala Ala Arg Ala
130      135      140
tac gac gct gca gct cgt aga atc cgt ggt tcc aaa gct aag gtg aat      480
Tyr Asp Ala Ala Ala Arg Ile Arg Gly Lys Lys Ala Lys Val Asn
145      150      155
ttc cct gag gag aag gag aac cca cct gcc aag aag gtg gct cca aac      528
Phe Pro Glu Glu Lys Glu Asn Pro Pro Ala Lys Lys Val Ala Pro Asn
165      170      175
cca agt cca gtt ttg gct cag aac ttg gag aac tcc ttt gac aac atg      576
Pro Ser Pro Val Leu Ala Gln Asn Leu Asp Asn Ser Phe Asp Asn Met
180      185      190
tgt ttc atg gag gag aag cac caa gtt aac aac aac aac aat cag ttt      624
Cys Phe Met Glu Glu Lys His Gln Val Asn Asn Asn Asn Asn Gln Phe
195      200      205
ggg ggt aat gga tat cat cag tat ttc agc tca gac cag ggt agt aac      672
Gly Gly Asn Gly Tyr His Gln Tyr Phe Ser Ser Asp Gln Gly Ser Asn
210      215      220
tca ttc ggt tgt tct gag ttt ggt tgg aac gat caa gct cct ata act      720
Ser Phe Gly Cys Ser Glu Phe Gly Trp Asn Asp Gln Ala Pro Ile Thr
225      230      235
cct gag atc tcc tct gct ttt atc aac aac aac tct gcc aca ttc gcc      768
Pro Glu Ile Ser Ser Ala Phe Ile Asn Asn Asn Ser Ala Thr Phe Ala
245      250      255
gag gaa gct gat cca gct aag cag ctc aag gtc atg gat ttt gag aca      816
Glu Glu Ala Asp Pro Ala Lys Gln Leu Lys Val Met Asp Phe Glu Thr
260      265      270
act tac aac agc act gaa tgg gat tct tca ctt gat ttc ttc agt gga      864
Thr Tyr Asn Ser Thr Glu Trp Asp Ser Ser Leu Asp Phe Phe Ser Gly
275      280      285
gac gct gtg gcg act cag gac aat ggt gca aat cct atg gag cta tgg      912
Asp Ala Val Ala Thr Gln Asp Asn Gly Ala Asn Pro Met Glu Leu Trp
290      295      300
agc att gat gag atc aat tcc atg atg gga gga gtc ttc taa      954
Ser Ile Asp Glu Ile Asn Ser Met Met Gly Val Phe
305      310      315

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<210> 782
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 <213> Brassica napus

<400> 782
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65      70
Ala Asp Ser Val Ile Gly Lys Lys Val Ala Asp Gly Glu Gly Glu Arg
      85
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      100
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Arg Val Trp Leu Gly Thr Phe Lys Thr Ala Glu Glu Ala Ala Arg Ala
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Tyr Asp Ala Ala Ala Arg Arg Ile Arg Gly Ser Lys Ala Lys Val Asn
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      165
Pro Ser Pro Val Leu Ala Gln Asn Leu Asp Asn Ser Phe Asp Asn Met
      180
Cys Phe Met Glu Glu Lys His Gln Val Asn Asn Asn Asn Gln Phe
      195
Gly Gly Asn Gly Tyr His Gln Tyr Phe Ser Ser Asp Gln Gly Ser Asn
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225      230
Pro Glu Ile Ser Ser Ala Phe Ile Asn Asn Asn Ser Ala Thr Phe Ala
      245
Glu Glu Ala Asp Pro Ala Lys Gln Leu Lys Val Met Asp Phe Glu Thr
      260
Thr Tyr Asn Ser Thr Glu Trp Asp Ser Ser Leu Asp Phe Phe Ser Gly
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 <222> (1)..(954)

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cgc cgc gtc acc agc gag ttt ctc tgg ccg gat ctg aag aag agc tcg      96
Arg Arg Val Thr Ser Glu Phe Leu Trp Pro Asp Leu Lys Lys Ser Ser
      20
aag aaa cgc tcg agt ttc ttc gat ctt gac gat gag ttc gag gct gac      144
Lys Lys Arg Ser Ser Phe Phe Asp Leu Asp Asp Glu Phe Glu Ala Asp
      35
ttc cag ggc ttc aag gat gat tcc tct atc gat tgc gat gat gcg aag      192
Phe Gln Gly Phe Lys Asp Asp Ser Ser Ile Asp Cys Asp Asp Ala Lys
      50
ccg ttc gtt ttc gcc ggg gct cgt aag ccc gcc gta tcc gcc gcc act      240
Pro Phe Val Phe Ala Gly Ala Arg Lys Pro Ala Val Ser Ala Ala Thr
      65
gcc gat tca gtg ttt ggc aag aaa gtt gtt gat gga gaa ggt gag agg      288
Ala Asp Ser Val Phe Gly Lys Lys Val Val Asp Gly Glu Gly Glu Arg
      85
tct gca aag agg aag agg aag agc cag tac cga ggg ata agg caa cgt      336
      90

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PF59082SeqList_PF59082.txt

Ser	Ala	Lys	Arg	Lys	Arg	Lys	Ser	Gln	Tyr	Arg	Gly	Ile	Arg	Gln	Arg		
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Pro	Trp	Gly	Lys	Trp	Ala	Ala	Glu	Ile	Arg	Asp	Pro	Arg	Glu	Gly	Ser		
		115					120					125					
aga	gtt	tgg	ctt	gga	act	ttt	aaa	aca	gcc	gag	gaa	gct	gca	aga	gct	432	
Arg	Val	Trp	Leu	Gly	Thr	Phe	Lys	Thr	Ala	Glu	Glu	Ala	Ala	Arg	Ala		
	130					135					140						
tat	gat	gct	gca	gct	cgt	aga	atc	cgt	ggt	tcc	aaa	gct	aag	gtg	aat	480	
Tyr	Asp	Ala	Ala	Ala	Arg	Arg	Ile	Arg	Gly	Ser	Lys	Ala	Lys	Val	Asn		
	145				150					155					160		
ttc	cct	gag	gag	aag	gag	aac	cca	cct	gcc	aag	aag	gtg	gct	cca	aac	528	
Phe	Pro	Glu	Glu	Lys	Glu	Asn	Pro	Pro	Ala	Lys	Lys	Val	Ala	Pro	Asn		
				165					170					175			
cca	agt	cca	gtt	ttg	gct	cag	aac	ttg	gac	aac	tcc	ttt	gac	aac	atg	576	
Pro	Ser	Pro	Val	Leu	Ala	Gln	Asn	Leu	Asp	Asn	Ser	Phe	Asp	Asn	Met		
			180					185					190				
tgt	ttc	atg	gag	gag	aag	cac	caa	gtt	aac	aac	aac	agc	aat	cag	ttt	624	
Cys	Phe	Met	Glu	Glu	Lys	His	Gln	Val	Asn	Asn	Asn	Ser	Asn	Gln	Phe		
		195					200					205					
ggt	ggt	aat	gga	tat	cat	cag	tat	ttc	agc	tca	gac	cag	ggt	agt	aac	672	
Gly	Gly	Asn	Gly	Tyr	His	Gln	Tyr	Phe	Ser	Ser	Asp	Gln	Gly	Ser	Asn		
	210					215					220						
tca	ttc	ggt	tgt	tct	gag	ttc	ggt	tgg	aac	gat	caa	gct	cct	ata	act	720	
Ser	Phe	Gly	Cys	Ser	Glu	Phe	Gly	Trp	Asn	Asp	Gln	Ala	Pro	Ile	Thr		
	225				230					235					240		
cct	gag	atc	tcc	tct	gct	ttt	atc	aac	aac	aac	tct	gtc	aca	ttc	gcc	768	
Pro	Glu	Ile	Ser	Ser	Ala	Phe	Ile	Asn	Asn	Asn	Ser	Val	Thr	Phe	Ala		
				245					250					255			
gag	gaa	gct	gat	cca	gct	aag	cag	ctc	aag	gtc	atg	gat	ttt	gag	aca	816	
Glu	Glu	Ala	Asp	Pro	Ala	Lys	Gln	Leu	Lys	Val	Met	Asp	Phe	Glu	Thr		
			260					265					270				
act	tac	aac	agc	act	gaa	tgg	gat	tct	tca	ctt	gat	ttc	ttc	agt	gga	864	
Thr	Tyr	Asn	Ser	Thr	Glu	Trp	Asp	Ser	Ser	Leu	Asp	Phe	Phe	Ser	Gly		
		275					280					285					
gac	gct	gtg	gcg	act	cag	gac	aat	ggt	gca	aat	cct	atg	gag	cta	tgg	912	
Asp	Ala	Val	Ala	Thr	Gln	Asp	Asn	Gly	Ala	Asn	Pro	Met	Glu	Leu	Trp		
	290				295					300							
agc	att	gat	gag	atc	aat	tcc	atg	att	gga	gga	gtc	ttc	taa			954	
Ser	Ile	Asp	Glu	Ile	Asn	Ser	Met	Ile	Gly	Gly	Val	Phe					
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<211> 317

<212> PRT

<213> Brassica napus

<400> 784

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Arg	Arg	Val	Thr	Ser	Glu	Phe	Leu	Trp	Pro	Asp	Leu	Lys	Lys	Ser	Ser		
			20					25					30				
Lys	Lys	Arg	Ser	Ser	Phe	Phe	Asp	Leu	Asp	Asp	Glu	Phe	Glu	Ala	Asp		
		35					40					45					
Phe	Gln	Gly	Phe	Lys	Asp	Asp	Ser	Ser	Ile	Asp	Cys	Asp	Asp	Ala	Lys		
	50					55					60						
Pro	Phe	Val	Phe	Ala	Gly	Ala	Arg	Lys	Pro	Ala	Val	Ser	Ala	Ala	Thr		
	65				70					75					80		
Ala	Asp	Ser	Val	Phe	Gly	Lys	Lys	Val	Val	Asp	Gly	Glu	Gly	Glu	Arg		
				85					90					95			
Ser	Ala	Lys	Arg	Lys	Arg	Lys	Ser	Gln	Tyr	Arg	Gly	Ile	Arg	Gln	Arg		
			100					105					110				
Pro	Trp	Gly	Lys	Trp	Ala	Ala	Glu	Ile	Arg	Asp	Pro	Arg	Glu	Gly	Ser		
		115					120					125					
Arg	Val	Trp	Leu	Gly	Thr	Phe	Lys	Thr	Ala	Glu	Glu	Ala	Ala	Arg	Ala		
	130					135					140						
Tyr	Asp	Ala	Ala	Ala	Arg	Arg	Ile	Arg	Gly	Ser	Lys	Ala	Lys	Val	Asn		
	145				150					155					160		
Phe	Pro	Glu	Glu	Lys	Glu	Asn	Pro	Pro	Ala	Lys	Lys	Val	Ala	Pro	Asn		

PF59082SeqList_PF59082.txt

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165      170      175
Pro Ser Pro Val Leu Ala Gln Asn Leu Asp Asn Ser Phe Asp Asn Met
Cys Phe Met Glu Glu Lys His Gln Val Asn Asn Asn Ser Asn Gln Phe
Gly Gly Asn Gly Tyr His Gln Tyr Phe Ser Ser Asp Gln Gly Ser Asn
Ser Phe Gly Cys Ser Glu Phe Gly Trp Asn Asp Gln Ala Pro Ile Thr
225 225 230 235 240
Pro Glu Ile Ser Ser Ala Phe Ile Asn Asn Ser Val Thr Phe Ala
Glu Glu Ala Asp Pro Ala Lys Gln Leu Lys Val Met Asp Phe Glu Thr
Thr Tyr Asn Ser Thr Glu Trp Asp Ser Ser Leu Asp Phe Phe Ser Gly
Asp Ala Val Ala Thr Gln Asp Asn Gly Ala Asn Pro Met Glu Leu Trp
Ser Ile Asp Glu Ile Asn Ser Met Ile Gly Gly Val Phe
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 <212> DNA
 <213> Brassica napus

<220>
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 <222> (1)..(1092)

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1      5      10      15
cgc cgc gtc acg agc gag ttt ctc tgg ccg gat ctg aag aag agc aag      96
Arg Arg Val Thr Ser Glu Phe Leu Trp Pro Asp Leu Lys Lys Ser Lys
20      25      30
ggg aaa gcc tcg aag aag cga tcc gat ttc ttc gat ctg gac gac gag      144
Gly Lys Ala Ser Lys Lys Arg Ser Asp Phe Phe Asp Leu Asp Asp Glu
35      40      45
ttc gag gct gat ttt caa ggg ttt gag gat gac gac gcg tct ttt gac      192
Phe Glu Ala Asp Phe Gln Gly Phe Glu Asp Asp Asp Ala Ser Phe Asp
50      55      60
tgc gaa gac gat gat gat gat gtc ttc gct aaa gtg aag ccc ttt gtc      240
Cys Glu Asp Asp Asp Asp Val Phe Ala Lys Val Lys Pro Phe Val
65      70      75
ttc acc gcg acc acc aag ccc gta gct tcc cct ccc acc gcc act ggt      288
Phe Thr Ala Thr Thr Lys Pro Val Ala Ser Pro Pro Thr Ala Thr Gly
85      90      95
tca gtg tct ggc aag aag atc ata gag tcc ggt ggt caa gct gag aag      336
Ser Val Ser Gly Lys Lys Ile Ile Glu Ser Gly Gly Gln Ala Glu Lys
100      105      110
tct gct aag aga aag aga aag aat cag tac agg ggg att agg cag cga      384
Ser Ala Lys Arg Lys Arg Lys Asn Gln Tyr Arg Gly Ile Arg Gln Arg
115      120      125
cct tgg gga aaa tgg gct gct gag atc cgt gat cct aga aaa ggc tcc      432
Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp Pro Arg Lys Gly Ser
130      135      140
agg gaa tgg ctt gga aca ttc gac acc gcc gag gaa gca gca aga gcc      480
Arg Glu Trp Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala Ala Arg Ala
145      150      155
tat gat gca gct gca cgc agg atc cgt ggt agt aaa gct aag gtg aat      528
Tyr Asp Ala Ala Ala Arg Arg Ile Arg Gly Ser Lys Ala Lys Val Asn
165      170      175
ttc cca gag gag agc aac aac aac cgt agc gtc tcc cag aaa cga cct      576
Phe Pro Glu Ser Asn Asn Asn Arg Ser Val Ser Gln Lys Arg Pro
180      185      190
tct gct aag aag ctg gtg gct aaa cca aac caa agc cca gct ttg gtt      624
Ser Ala Lys Lys Leu Val Ala Lys Pro Asn Gln Ser Pro Ala Leu Val
195      200      205

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PF59082SeqList_PF59082.txt

cag	cag	cca	atg	agt	cag	tac	tgc	aac	aac	tcc	ttt	ggg	gat	gtg	agt	672
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ttc	gtg	gaa	gag	aag	cct	cag	atg	tac	aac	aat	cag	ttt	ggg	tta	gca	720
Phe	Val	Glu	Glu	Lys	Pro	Gln	Met	Tyr	Asn	Asn	Gln	Phe	Gly	Leu	Ala	
225					230					235					240	
aac	tcg	tac	aac	aac	cac	tac	ttc	agt	tct	gat	cag	ggg	agt	aac	tca	768
Asn	Ser	Tyr	Asn	Asn	His	Tyr	Phe	Ser	Ser	Asp	Gln	Gly	Ser	Asn	Ser	
				245					250					255		
ttt	gac	tgc	tct	gag	ttt	ggg	tgg	agc	gac	cac	ggc	ccc	aag	aca	cct	816
Phe	Asp	Cys	Ser	Glu	Phe	Gly	Trp	Ser	Asp	His	Gly	Pro	Lys	Thr	Pro	
				260				265					270			
gag	atc	tct	tcg	atg	cta	gtc	ggg	aat	aac	caa	gct	ccg	ttc	act	gaa	864
Glu	Ile	Ser	Ser	Met	Leu	Val	Gly	Asn	Asn	Gln	Ala	Pro	Phe	Thr	Glu	
				275			280					285				
gaa	acc	aat	gca	gcc	aag	aag	ctc	aaa	ccc	agc	tct	gat	gac	gga	aca	912
Glu	Thr	Asn	Ala	Ala	Lys	Lys	Leu	Lys	Pro	Ser	Ser	Asp	Asp	Gly	Thr	
				290		295					300					
agc	aac	cag	tct	gat	gat	ctg	atg	gca	tac	ctt	gac	aat	gcc	ttg	tgg	960
Ser	Asn	Gln	Ser	Asp	Asp	Leu	Met	Ala	Tyr	Leu	Asp	Asn	Ala	Leu	Trp	
305					310					315					320	
gaa	tct	cca	tct	cca	tta	gaa	gtt	gaa	gcc	atg	ctt	ggg	gta	gat	gct	1008
Glu	Ser	Pro	Ser	Pro	Leu	Glu	Val	Glu	Ala	Met	Leu	Gly	Val	Asp	Ala	
				325				330						335		
gtt	gct	gtg	act	cag	gga	gag	gag	aac	ccg	atg	gac	cta	tgg	agc	tta	1056
Val	Ala	Val	Thr	Gln	Gly	Glu	Glu	Asn	Pro	Met	Asp	Leu	Trp	Ser	Leu	
				340				345					350			
gat	gat	atc	aat	tac	atg	ctg	gaa	gga	gtc	ttc	tga					1092
Asp	Asp	Ile	Asn	Tyr	Met	Leu	Glu	Gly	Val	Phe						
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 35 40 45
 Phe Glu Ala Asp Phe Gln Gly Phe Glu Asp Asp Ala Ser Phe Asp
 50 55 60
 Cys Glu Asp Asp Asp Asp Val Phe Ala Lys Val Lys Pro Phe Val
 65 70 75 80
 Phe Thr Ala Thr Thr Lys Pro Val Ala Ser Pro Pro Thr Ala Thr Gly
 85 90 95
 Ser Val Ser Gly Lys Lys Ile Ile Glu Ser Gly Gly Gln Ala Glu Lys
 100 105 110
 Ser Ala Lys Arg Lys Arg Lys Asn Gln Tyr Arg Gly Ile Arg Gln Arg
 115 120 125
 Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp Pro Arg Lys Gly Ser
 130 135 140
 Arg Glu Trp Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala Ala Arg Ala
 145 150 155 160
 Tyr Asp Ala Ala Arg Arg Ile Arg Gly Ser Lys Ala Lys Val Asn
 165 170 175
 Phe Pro Glu Glu Ser Asn Asn Asn Arg Ser Val Ser Gln Lys Arg Pro
 180 185 190
 Ser Ala Lys Lys Leu Val Ala Lys Pro Asn Gln Ser Pro Ala Leu Val
 195 200 205
 Gln Gln Pro Met Ser Gln Tyr Cys Asn Asn Ser Phe Gly Asp Val Ser
 210 215 220
 Phe Val Glu Glu Lys Pro Gln Met Tyr Asn Asn Gln Phe Gly Leu Ala
 225 230 235 240
 Asn Ser Tyr Asn Asn His Tyr Phe Ser Ser Asp Gln Gly Ser Asn Ser
 245 250 255

PF59082SeqList_PF59082.txt

Phe Asp Cys Ser Glu Phe Gly Trp Ser Asp His Gly Pro Lys Thr Pro
 260 265 270
 Glu Ile Ser Ser Met Leu Val Gly Asn Asn Gln Ala Pro Phe Thr Glu
 275 280 285
 Glu Thr Asn Ala Ala Lys Lys Leu Lys Pro Ser Ser Asp Asp Gly Thr
 290 295 300
 Ser Asn Gln Ser Asp Asp Leu Met Ala Tyr Leu Asp Asn Ala Leu Trp
 305 310 315 320
 Glu Ser Pro Ser Pro Leu Glu Val Glu Ala Met Leu Gly Val Asp Ala
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<210> 787
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 <212> DNA
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<220>
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 Arg Arg Val Thr Ser Glu Phe Leu Trp Pro Asp Leu Lys Lys Ser Lys
 20 25 30
 ggg aaa gcc tcg aag aag cga tcc gat ttc ttc gat ctg gac gac gag 144
 Gly Lys Ala Ser Lys Lys Arg Ser Asp Phe Phe Asp Leu Asp Asp Glu
 35 40 45
 ttc gag gct gat ttt caa ggg ttt gag gat gac gac gac tct ttt gac 192
 Phe Glu Ala Asp Phe Gln Gly Phe Glu Asp Asp Asp Ala Ser Phe Asp
 50 55 60
 tgc gaa gac gat gat gat gaa gtc ttc gct aaa gtg aag ccc ttt gtc 240
 Cys Glu Asp Asp Asp Asp Glu Val Phe Ala Lys Val Lys Pro Phe Val
 65 70 75 80
 ttc acc gcg acc acc aag ccc gta gct tcc cct ccc act ggt tca gtg 288
 Phe Thr Ala Thr Thr Lys Pro Val Ala Ser Pro Pro Thr Gly Ser Val
 85 90 95
 tct ggc aag aag atc ata gag tcc ggt ggt caa gct gag aag tct gct 336
 Ser Gly Lys Lys Ile Ile Glu Ser Gly Gln Ala Glu Lys Ser Ala
 100 105 110
 aag aga aag aga aag aat cag tac agg ggg att agg cag cga cct tgg 384
 Lys Arg Lys Arg Lys Asn Gln Tyr Arg Gly Ile Arg Gln Arg Pro Trp
 115 120 125
 ggg aaa tgg gct gct gag atc cgt gat cca aga aaa ggc tcc agg gaa 432
 Gly Lys Trp Ala Ala Glu Ile Arg Asp Pro Arg Lys Gly Ser Arg Glu
 130 135 140
 tgg ctt gga acg ttt gac acc gcc gag gaa gct gca aga gcc tat gat 480
 Trp Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp
 145 150 155 160
 gca act gca cgc aga atc cgc ggc agt aaa gcc aag gtg aat ttc cca 528
 Ala Thr Ala Arg Arg Ile Arg Gly Ser Lys Ala Lys Val Asn Phe Pro
 165 170 175
 gag gag agc aac aac cgt agc gtc tcc cag aaa cga cct tct gct 576
 Glu Glu Ser Asn Asn Arg Ser Val Ser Gln Lys Arg Pro Ser Ala
 180 185 190
 aag aag ctg gtg gct aaa cca aac caa agc cca gct ttg gtt cag cag 624
 Lys Lys Leu Val Ala Lys Pro Asn Gln Ser Pro Ala Leu Val Gln Gln
 195 200 205
 cca atg agt cag tac tac aac gcc ttt ggt gat gtg agt ttc atg 672
 Pro Met Ser Gln Tyr Tyr Asn Asn Ala Phe Gly Asp Val Ser Phe Met
 210 215 220
 gaa gag aag cct cag atg tac aac aat cag ttt ggt tta gca aac tcg 720
 Glu Glu Lys Pro Gln Met Tyr Asn Asn Gln Phe Gly Leu Ala Asn Ser

PF59082SeqList_PF59082.txt

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Tyr	Asn	Asn	Gln	Tyr	Phe	Ser	Ser	Asp	Gln	Gly	Ser	Asn	Ser	Phe	Asp		
				245					250					255			
tgc	tct	gag	ttt	ggg	cgg	agc	gat	cac	ggg	ccc	aag	aca	cct	gag	atc		816
Cys	Ser	Glu	Phe	Gly	Arg	Ser	Asp	His	Gly	Pro	Lys	Thr	Pro	Glu	Ile		
			260					265					270				
tct	tca	atg	ctg	gtt	aat	aat	aac	caa	act	ccg	ttc	att	gaa	gta	acc		864
Ser	Ser	Met	Leu	Val	Asn	Asn	Asn	Gln	Thr	Pro	Phe	Ile	Glu	Val	Thr		
		275					280					285					
aat	gca	gcc	aag	aag	ctc	aaa	ccc	agc	tct	gat	gat	ctg	atg	gca	tac		912
Asn	Ala	Ala	Lys	Lys	Leu	Lys	Pro	Ser	Ser	Asp	Asp	Leu	Met	Ala	Tyr		
	290					295					300						
ctt	gac	aat	gcc	ttg	tg	gaa	tct	cca	tct	cca	ttg	gaa	gtt	gaa	gcc		960
Leu	Asp	Asn	Ala	Leu	Trp	Glu	Ser	Pro	Ser	Pro	Leu	Glu	Val	Glu	Ala		
305					310					315					320		
atg	ctg	ggg	gta	gat	gct	gcc	gct	gtg	act	cag	gga	gag	gag	aac	cct		1008
Met	Leu	Gly	Val	Asp	Ala	Ala	Ala	Val	Thr	Gln	Gly	Glu	Glu	Asn	Pro		
				325					330					335			
atg	gac	cta	tg	agc	tta	gat	gat	att	aat	tac	atg	ctg	gaa	gga	gtc		1056
Met	Asp	Leu	Trp	Ser	Leu	Asp	Asp	Ile	Asn	Tyr	Met	Leu	Glu	Gly	Val		
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Phe																	

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 <212> PRT
 <213> Brassica napus

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 35 40 45
 Phe Glu Ala Asp Phe Gln Gly Phe Glu Asp Asp Ala Ser Phe Asp
 50 55 60
 Cys Glu Asp Asp Asp Asp Glu Val Phe Ala Lys Val Lys Pro Phe Val
 65 70 75 80
 Phe Thr Ala Thr Thr Lys Pro Val Ala Ser Pro Pro Thr Gly Ser Val
 85 90 95
 Ser Gly Lys Lys Ile Ile Glu Ser Gly Gly Gln Ala Glu Lys Ser Ala
 100 105 110
 Lys Arg Lys Arg Lys Asn Gln Tyr Arg Gly Ile Arg Gln Arg Pro Trp
 115 120 125
 Gly Lys Trp Ala Ala Glu Ile Arg Asp Pro Arg Lys Gly Ser Arg Glu
 130 135 140
 Trp Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp
 145 150 155 160
 Ala Thr Ala Arg Arg Ile Arg Gly Ser Lys Ala Lys Val Asn Phe Pro
 165 170 175
 Glu Glu Ser Asn Asn Arg Ser Val Ser Gln Lys Arg Pro Ser Ala
 180 185 190
 Lys Lys Leu Val Ala Lys Pro Asn Gln Ser Pro Ala Leu Val Gln Gln
 195 200 205
 Pro Met Ser Gln Tyr Tyr Asn Asn Ala Phe Gly Asp Val Ser Phe Met
 210 215 220
 Glu Glu Lys Pro Gln Met Tyr Asn Asn Gln Phe Gly Leu Ala Asn Ser
 225 230 235 240
 Tyr Asn Asn Gln Tyr Phe Ser Ser Asp Gln Gly Ser Asn Ser Phe Asp
 245 250 255
 Cys Ser Glu Phe Gly Arg Ser Asp His Gly Pro Lys Thr Pro Glu Ile
 260 265 270
 Ser Ser Met Leu Val Asn Asn Asn Gln Thr Pro Phe Ile Glu Val Thr
 275 280 285
 Asn Ala Ala Lys Lys Leu Lys Pro Ser Ser Asp Asp Leu Met Ala Tyr

PF59082SeqList_PF59082.txt

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<220>
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 Arg Arg Val Thr 20 Ser Glu Phe Leu Trp 25 Pro Asp Leu Lys Lys Asn Lys
 30
 ggg aaa gcc tcg aag aag cga tcc gat ttc ttc gat ctg gac gac gag 144
 Gly Lys Ala Ser Lys Lys Arg Ser Asp Phe Phe Asp Leu Asp Asp Glu
 35 40 45
 ttc gag gct gat ttt caa ggg ttt gag gat gac gac gac tct ttt gac 192
 Phe Glu Ala Asp Phe Gln Gly Phe Glu Asp Asp Asp Ala Ser Phe Asp
 50 55 60
 tgc gaa gac gat gat gat gat gtc ttc gct aaa gtg aag ccc ttt gtc 240
 Cys Glu Asp Asp Asp Asp Val Phe Ala Lys Val Lys Pro Phe Val
 65 70 75 80
 ttc acc gcg acc acc aag ccc gta gct tcc cct ccc acc gcc act ggt 288
 Phe Thr Ala Thr Thr Lys Pro Val Ala Ser Pro Pro Thr Ala Thr Gly
 85 90 95
 tca gtg tct ggc aag aag atc ata gag tcc ggt ggt caa gct gag aag 336
 Ser Val Ser Gly Lys Lys Ile Ile Glu Ser Gly Gly Gln Ala Glu Lys
 100 105 110
 tct gct aag aga aag aga aag aat cag tac agg ggg att agg cag cga 384
 Ser Ala Lys Arg Lys Arg Lys Asn Gln Tyr Arg Gly Ile Arg Gln Arg
 115 120 125
 cct tgg ggg aaa tgg gct gct gag atc cgt gat cct aga aaa ggc tcc 432
 Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp Pro Arg Lys Gly Ser
 130 135 140
 agg gaa tgg ctt gga aca ttc gac acc gcc gag gaa gca gca aga gcc 480
 Arg Glu Trp Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala Ala Arg Ala
 145 150 155 160
 tat gat gca gct gca cgc agg atc cgt ggt agt aaa gct aag gtg aat 528
 Tyr Asp Ala Ala Ala Arg Arg Ile Arg Gly Ser Lys Ala Lys Val Asn
 165 170 175
 ttc cca gag gag agc aac aac aac cgt agc gtc tcc cag aaa cga cct 576
 Phe Pro Glu Glu Ser Asn Asn Asn Arg Ser Val Ser Gln Lys Arg Pro
 180 185 190
 tct gct aag aag ctg gtg gct aaa cca aac caa agc cca gct ttg gtt 624
 Ser Ala Lys Lys Leu Val Ala Lys Pro Asn Gln Ser Pro Ala Leu Val
 195 200 205
 cag cag cca atg agt cag tac tgc aac aac tcc ttt ggt gat gtg agt 672
 Gln Gln Pro Met Ser Gln Tyr Cys Asn Asn Ser Phe Gly Asp Val Ser
 210 215 220
 ttc gtg gaa gag aag cct cag atg tac aac aat cag ttt ggg tta gca 720
 Phe Val Glu Glu Lys Pro Gln Met Tyr Asn Asn Gln Phe Gly Leu Ala
 225 230 235 240
 aac tcg tac aac aac cac tac ttc agt tct gat cag ggg agt aac tca 768
 Asn Ser Tyr Asn Asn His Tyr Phe Ser Ser Asp Gln Gly Ser Asn Ser
 245 250 255
 ttt gac tgc tct gag ttt ggg tgg agc gac cac ggc ccc aag aca cct 816

PF59082SeqList_PF59082.txt

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Glu	Ile	Ser	Ser	Met	Leu	Val	Gly	Asn	Asn	Gln	Ala	Pro	Phe	Thr	Glu	
		275					280					285				
gaa	acc	aat	gca	gcc	aag	aag	ctc	aaa	ccc	agc	tct	gat	gac	gga	aca	912
Glu	Thr	Asn	Ala	Ala	Lys	Lys	Leu	Lys	Pro	Ser	Ser	Asp	Asp	Gly	Thr	
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agc	aac	cag	tct	gat	gat	ctg	atg	gca	tac	ctt	gac	aat	gcc	ttg	tgg	960
Ser	Asn	Gln	Ser	Asp	Asp	Leu	Met	Ala	Tyr	Leu	Asp	Asn	Ala	Leu	Trp	
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gaa	tct	cca	tct	cca	tta	gaa	gtt	gaa	gcc	atg	ctt	ggc	gta	gat	gct	1008
Glu	Ser	Pro	Ser	Pro	Leu	Glu	Val	Glu	Ala	Met	Leu	Gly	Val	Asp	Ala	
				325					330					335		
gtt	gct	gtg	act	cag	gga	gag	gag	aac	ccg	atg	gac	cta	tgg	agc	tta	1056
Val	Ala	Val	Thr	Gln	Gly	Glu	Glu	Asn	Pro	Met	Asp	Leu	Trp	Ser	Leu	
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gat	gat	atc	aat	tac	atg	ctg	gaa	gga	gtc	ttc	tga					1092
Asp	Asp	Ile	Asn	Tyr	Met	Leu	Glu	Gly	Val	Phe						
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<211> 363

<212> PRT

<213> Brassica napus

<400> 790

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Gly	Lys	Ala	Ser	Lys	Lys	Arg	Ser	Asp	Phe	Phe	Asp	Leu	Asp	Asp	Glu	
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Phe	Glu	Ala	Asp	Phe	Gln	Gly	Phe	Glu	Asp	Asp	Asp	Ala	Ser	Phe	Asp	
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Cys	Glu	Asp	Asp	Asp	Asp	Asp	Val	Phe	Ala	Lys	Val	Lys	Pro	Phe	Val	
65					70					75					80	
Phe	Thr	Ala	Thr	Thr	Lys	Pro	Val	Ala	Ser	Pro	Pro	Thr	Ala	Thr	Gly	
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Ser	Val	Ser	Gly	Lys	Lys	Ile	Ile	Glu	Ser	Gly	Gly	Gln	Ala	Glu	Lys	
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Ser	Ala	Lys	Arg	Lys	Arg	Lys	Asn	Gln	Tyr	Arg	Gly	Ile	Arg	Gln	Arg	
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Pro	Trp	Gly	Lys	Trp	Ala	Ala	Glu	Ile	Arg	Asp	Pro	Arg	Lys	Gly	Ser	
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Arg	Glu	Trp	Leu	Gly	Thr	Phe	Asp	Thr	Ala	Glu	Glu	Ala	Ala	Arg	Ala	
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Tyr	Asp	Ala	Ala	Ala	Arg	Arg	Ile	Arg	Gly	Ser	Lys	Ala	Lys	Val	Asn	
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Phe	Pro	Glu	Glu	Ser	Asn	Asn	Asn	Arg	Ser	Val	Ser	Gln	Lys	Arg	Pro	
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Ser	Ala	Lys	Lys	Leu	Val	Ala	Lys	Pro	Asn	Gln	Ser	Pro	Ala	Leu	Val	
		195					200					205				
Gln	Gln	Pro	Met	Ser	Gln	Tyr	Cys	Asn	Asn	Ser	Phe	Gly	Asp	Val	Ser	
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Asn	Ser	Tyr	Asn	Asn	His	Tyr	Phe	Ser	Ser	Asp	Gln	Gly	Ser	Asn	Ser	
				245					250					255		
Phe	Asp	Cys	Ser	Glu	Phe	Gly	Trp	Ser	Asp	His	Gly	Pro	Lys	Thr	Pro	
			260					265					270			
Glu	Ile	Ser	Ser	Met	Leu	Val	Gly	Asn	Asn	Gln	Ala	Pro	Phe	Thr	Glu	
		275					280					285				
Glu	Thr	Asn	Ala	Ala	Lys	Lys	Leu	Lys	Pro	Ser	Ser	Asp	Asp	Gly	Thr	
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Ser	Asn	Gln	Ser	Asp	Asp	Leu	Met	Ala	Tyr	Leu	Asp	Asn	Ala	Leu	Trp	
305					310					315					320	
Glu	Ser	Pro	Ser	Pro	Leu	Glu	Val	Glu	Ala	Met	Leu	Gly	Val	Asp	Ala	
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 Asp Asp Ile Asn Tyr Met Leu Glu Gly Val Phe
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 gcc ggg tct cgc cgc ctg acc gcc gat tac ctg tgg ccg gat ttg aag 96
 Ala Gly Ser Arg Arg Leu Thr Ala Asp Tyr Leu Trp Pro Asp Leu Lys
 20 25 30
 aag cgg aag tct gac ttg gac gtt gac ttc gag gct gat ttc agg gat 144
 Lys Arg Lys Ser Asp Leu Asp Val Asp Phe Glu Ala Asp Phe Arg Asp
 35 40 45
 ttt aaa gac gat tct gat atc gac gac gac gat gat cac caa gtc 192
 Phe Lys Asp Asp Ser Asp Ile Asp Asp Asp Asp Asp His Gln Val
 50 55 60
 aag ccc ttt gct ttc gcc gcc tct tct cgt ctg tct acg gca gcg aaa 240
 Lys Pro Phe Ala Phe Ala Ala Ser Ser Arg Leu Ser Thr Ala Ala Lys
 65 70 75 80
 tct gtg gca ttc caa ggt cgg gct gag ata tct gca aat aga aag agg 288
 Ser Val Ala Phe Gln Gly Arg Ala Glu Ile Ser Ala Asn Arg Lys Arg
 85 90 95
 aag aat cag tat agg gga atc cgt caa cgc cct tgg gga aaa tgg gca 336
 Lys Asn Gln Tyr Arg Gly Ile Arg Gln Arg Pro Trp Gly Lys Trp Ala
 100 105 110
 gct gag att cgg gat cca aga aag ggg gtt cgt gtc tgg ctt gga acc 384
 Ala Glu Ile Arg Asp Pro Arg Lys Gly Val Arg Val Trp Leu Gly Thr
 115 120 125
 ttc aac act gct gaa gaa gct gca aga gct tat gat gct gaa gca cgg 432
 Phe Asn Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Ala Glu Ala Arg
 130 135 140
 agg att cgt ggc aag aaa gcc aag gtg aat ttt cct gag gca cca ggt 480
 Arg Ile Arg Gly Lys Lys Ala Lys Val Asn Phe Pro Glu Ala Pro Gly
 145 150 155 160
 act tct tct gta aaa cgt tcc aag gta aat cca cag gaa aat ctt aag 528
 Thr Ser Ser Val Lys Arg Ser Lys Val Asn Pro Gln Glu Asn Leu Lys
 165 170 175
 act gtt cag ccc aat ctg ggt cac aag ttc agt gct ggc aac aat cac 576
 Thr Val Gln Pro Asn Leu Gly His Lys Phe Ser Ala Gly Asn Asn His
 180 185 190
 atg gat ctg gtg gaa cag aaa ccc cta gtt agc cag tat gct aac atg 624
 Met Asp Leu Val Glu Gln Lys Pro Leu Val Ser Gln Tyr Ala Asn Met
 195 200 205
 gct tcc ttc cct ggc agt gga aat ggg cta aga tcc ctt tcg tct 672
 Ala Ser Phe Pro Gly Ser Gly Asn Gly Leu Arg Ser Leu Pro Ser Ser
 210 215 220
 gat gat gca acc ctt tac ttc agt tca gat caa ggg agt aat tca ttt 720
 Asp Asp Ala Thr Leu Tyr Phe Ser Ser Asp Gln Gly Ser Asn Ser Phe
 225 230 235 240
 gat tat gct cct gag atc tca tcc atg ctt tct gct cct ttg gat tgt 768
 Asp Tyr Ala Pro Glu Ile Ser Ser Met Leu Ser Ala Pro Leu Asp Cys
 245 250 255
 gaa tct cat ttt gtg caa aat gcc aac cag cag cct aac tct cag 816
 Glu Ser His Phe Val Gln Asn Ala Asn Gln Gln Gln Pro Asn Ser Gln
 260 265 270
 aat gtg gta tct att gaa gat gat tct gca aag aca ctc tct gag gag 864
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PF59082SeqList_PF59082.txt

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Glu	Gly	Ser	Trp	Gly	Asp	Thr	Ser	Leu	Glu	Ser	Leu	Leu	Ser	Gly	Asp	
305					310					315					320	
aca	act	cag	gat	ggt	gga	aac	ctc	atg	aac	ctt	tgg	tgc	ttt	gat	gac	1008
Thr	Thr	Gln	Asp	Gly	Gly	Asn	Leu	Met	Asn	Leu	Trp	Cys	Phe	Asp	Asp	
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			20					25					30			
Lys	Arg	Lys	Ser	Asp	Leu	Asp	Val	Asp	Phe	Glu	Ala	Asp	Phe	Arg	Asp	
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Phe	Lys	Asp	Asp	Ser	Asp	Ile	Asp	Asp	Asp	Asp	Asp	Asp	His	Gln	Val	
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Lys	Pro	Phe	Ala	Phe	Ala	Ala	Ser	Ser	Arg	Leu	Ser	Thr	Ala	Ala	Lys	
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Ser	Val	Ala	Phe	Gln	Gly	Arg	Ala	Glu	Ile	Ser	Ala	Asn	Arg	Lys	Arg	
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Lys	Asn	Gln	Tyr	Arg	Gly	Ile	Arg	Gln	Arg	Pro	Trp	Gly	Lys	Trp	Ala	
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Ala	Glu	Ile	Arg	Asp	Pro	Arg	Lys	Gly	Val	Arg	Val	Trp	Leu	Gly	Thr	
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Phe	Asn	Thr	Ala	Glu	Glu	Ala	Ala	Arg	Ala	Tyr	Asp	Ala	Glu	Ala	Arg	
	130					135					140					
Arg	Ile	Arg	Gly	Lys	Lys	Ala	Lys	Val	Asn	Phe	Pro	Glu	Ala	Pro	Gly	
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Thr	Ser	Ser	Val	Lys	Arg	Ser	Lys	Val	Asn	Pro	Gln	Glu	Asn	Leu	Lys	
				165					170					175		
Thr	Val	Gln	Pro	Asn	Leu	Gly	His	Lys	Phe	Ser	Ala	Gly	Asn	Asn	His	
			180					185					190			
Met	Asp	Leu	Val	Glu	Gln	Lys	Pro	Leu	Val	Ser	Gln	Tyr	Ala	Asn	Met	
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Ala	Ser	Phe	Pro	Gly	Ser	Gly	Asn	Gly	Leu	Arg	Ser	Leu	Pro	Ser	Ser	
	210					215					220					
Asp	Asp	Ala	Thr	Leu	Tyr	Phe	Ser	Ser	Asp	Gln	Gly	Ser	Asn	Ser	Phe	
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Asp	Tyr	Ala	Pro	Glu	Ile	Ser	Ser	Met	Leu	Ser	Ala	Pro	Leu	Asp	Cys	
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Glu	Ser	His	Phe	Val	Gln	Asn	Ala	Asn	Gln	Gln	Gln	Pro	Asn	Ser	Gln	
			260					265					270			
Asn	Val	Val	Ser	Ile	Glu	Asp	Asp	Ser	Ala	Lys	Thr	Leu	Ser	Glu	Glu	
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Leu	Val	Asp	Ile	Glu	Ser	Glu	Leu	Lys	Phe	Phe	Gln	Met	Pro	Tyr	Leu	
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Glu	Gly	Ser	Trp	Gly	Asp	Thr	Ser	Leu	Glu	Ser	Leu	Leu	Ser	Gly	Asp	
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Thr	Thr	Gln	Asp	Gly	Gly	Asn	Leu	Met	Asn	Leu	Trp	Cys	Phe	Asp	Asp	
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<222> (1)..(1149)

<400> 793

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Arg	Glu	Phe	Lys	Asp	Asp	Ser	Glu	Ile	Glu	Asp	Val	Asp	Asp	Glu	Asp	
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Asp	Glu	Asp	Glu	Glu	Glu	Leu	Lys	Lys	Lys	Pro	Phe	Gly	Phe	Ser	Arg	
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tcc	agc	aac	aag	gct	gct	tct	aag	cct	ctc	tct	cgt	gga	tca	gca	act	288
Ser	Ser	Asn	Lys	Ala	Ala	Ser	Lys	Pro	Leu	Ser	Arg	Gly	Ser	Ala	Thr	
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gtg	gaa	tca	aag	ggg	caa	gct	gag	aag	tgt	gcc	aag	aga	aag	agg	aag	336
Val	Glu	Ser	Lys	Gly	Gln	Ala	Glu	Lys	Cys	Ala	Lys	Arg	Lys	Arg	Lys	
			100				105						110			
aac	cag	tat	cgt	gga	atc	cgt	cag	cgt	cca	tgg	gga	aag	tgg	gct	gct	384
Asn	Gln	Tyr	Arg	Gly	Ile	Arg	Gln	Arg	Pro	Trp	Gly	Lys	Trp	Ala	Ala	
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Ser	Thr	Ala	Glu	Glu	Ala	Ala	Arg	Ala	Tyr	Asp	Ala	Glu	Ala	Arg	Arg	
	145				150			155							160	
atc	cgg	ggc	aag	aaa	gcc	aag	gtg	aat	ttc	ccg	gat	gag	cct	tca	ggc	528
Ile	Arg	Gly	Lys	Lys	Ala	Lys	Val	Asn	Phe	Pro	Asp	Glu	Pro	Ser	Gly	
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gct	gct	gct	tcc	tca	aaa	cgc	ctc	aag	gtg	aat	cca	gag	gct	cag	cca	576
Ala	Ala	Ala	Ser	Ser	Lys	Arg	Leu	Lys	Val	Asn	Pro	Glu	Ala	Gln	Pro	
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Met	Lys	Glu	Asn	Leu	Asn	Thr	Val	Lys	Pro	Lys	Met	Asn	Gln	Met	Phe	
		195				200					205					
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Asn	Phe	Gly	His	Asn	Leu	Glu	Gly	Tyr	Tyr	Ser	Pro	Ile	Asp	Gln	Val	
	210				215						220					
gaa	cag	aaa	cca	ctg	gtt	aac	cag	tat	gtt	aac	cct	gcc	ccg	ttc	cct	720
Glu	Gln	Lys	Pro	Leu	Val	Asn	Gln	Tyr	Val	Asn	Pro	Ala	Pro	Phe	Pro	
	225				230					235				240		
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Gly	Asn	Gly	Val	Gln	Val	Ser	Pro	Val	Thr	Pro	Ser	Ala	Asp	Val	Thr	
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gct	tac	ttc	agc	tct	gag	cat	tcg	agc	aac	tcg	ttt	gat	tat	tct	gac	816
Ala	Tyr	Phe	Ser	Ser	Glu	His	Ser	Ser	Asn	Ser	Phe	Asp	Tyr	Ser	Asp	
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aac	aac	tcg	cag	gat	gtg	gtg	gct	gca	caa	gat	gat	tct	gca	aaa	acc	960
Asn	Asn	Ser	Gln	Asp	Val	Val	Ala	Ala	Gln	Asp	Asp	Ser	Ala	Lys	Thr	
	305				310					315				320		
ctt	tcc	gag	gag	ctt	gca	gac	att	gaa	tcc	cag	ctc	aag	ttc	ttt	gag	1008
Leu	Ser	Glu	Glu	Leu	Ala	Asp	Ile	Glu	Ser	Gln	Leu	Lys	Phe	Phe	Glu	
			325					330						335		
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PF59082SeqList_PF59082.txt

Thr	Pro	Ser	Phe	Leu	Asp	Glu	Ala	Trp	Ala	Asp	Ala	Thr	Leu	Ala	Ser		
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Leu	Leu	Gly	Gly	Asp	Ala	Thr	His	Asp	Ala	Ala	Gly	Asn	Pro	Met	Asn		
		355					360					365					
ctt	tgg	agc	ttc	gac	gac	ctg	cct	tcc	atg	gca	gga	gtc	ttc	tga			1149
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			20					25					30				
Lys	Arg	Phe	Ser	Lys	Pro	Leu	Leu	Asp	Asp	Asp	Phe	Glu	Ala	Gly	Phe		
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Arg	Glu	Phe	Lys	Asp	Asp	Ser	Glu	Ile	Glu	Asp	Val	Asp	Asp	Glu	Asp		
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Ser	Ser	Asn	Lys	Ala	Ala	Ser	Lys	Pro	Leu	Ser	Arg	Gly	Ser	Ala	Thr		
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Glu	Ile	Arg	Asp	Pro	Arg	Lys	Gly	Val	Arg	Val	Trp	Leu	Gly	Thr	Phe		
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			165						170					175			
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Asn	Phe	Gly	His	Asn	Leu	Glu	Gly	Tyr	Tyr	Ser	Pro	Ile	Asp	Gln	Val		
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Glu	Gln	Lys	Pro	Leu	Val	Asn	Gln	Tyr	Val	Asn	Pro	Ala	Pro	Phe	Pro		
225					230					235					240		
Gly	Asn	Gly	Val	Gln	Val	Ser	Pro	Val	Thr	Pro	Ser	Ala	Asp	Val	Thr		
			245						250					255			
Ala	Tyr	Phe	Ser	Ser	Glu	His	Ser	Ser	Asn	Ser	Phe	Asp	Tyr	Ser	Asp		
			260					265					270				
Leu	Gly	Trp	Gly	Glu	Gln	Val	Pro	Lys	Thr	Pro	Glu	Ile	Ser	Ser	Leu		
		275					280					285					
Leu	Ser	Ala	Ala	Pro	Leu	Glu	Gly	Ala	Ala	Asp	Gln	Val	Gln	Lys	Thr		
	290					295					300						
Asn	Asn	Ser	Gln	Asp	Val	Val	Ala	Ala	Gln	Asp	Asp	Ser	Ala	Lys	Thr		
305					310					315					320		
Leu	Ser	Glu	Glu	Leu	Ala	Asp	Ile	Glu	Ser	Gln	Leu	Lys	Phe	Phe	Glu		
			325						330					335			
Thr	Pro	Ser	Phe	Leu	Asp	Glu	Ala	Trp	Ala	Asp	Ala	Thr	Leu	Ala	Ser		
			340					345					350				
Leu	Leu	Gly	Gly	Asp	Ala	Thr	His	Asp	Ala	Ala	Gly	Asn	Pro	Met	Asn		
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<222> (1)..(1149)

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Ser	Gly	Ala	Arg	Arg	Val	Thr	Ala	Asp	Ile	Leu	Trp	Pro	Ser	Leu	Arg	
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aag	cgc	ttc	tcg	aag	ccg	ctg	ctg	gac	gat	gat	ttc	gag	gct	ggg	ttc	144
Lys	Arg	Phe	Ser	Lys	Pro	Leu	Leu	Asp	Asp	Asp	Phe	Glu	Ala	Gly	Phe	
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aga	gaa	ttc	aag	gat	gat	tcg	gaa	atc	gag	gat	gtt	gat	gac	gag	gac	192
Arg	Glu	Phe	Lys	Asp	Asp	Ser	Glu	Ile	Glu	Asp	Val	Asp	Asp	Glu	Asp	
	50					55					60					
gat	gaa	gac	gag	gag	gag	ttg	aag	aag	aag	ccc	ttt	ggg	ttc	tct	cgc	240
Asp	Glu	Asp	Glu	Glu	Glu	Leu	Lys	Lys	Lys	Pro	Phe	Gly	Phe	Ser	Arg	
	65				70					75					80	
tcc	agc	aac	aag	gct	gct	tct	aag	cct	ctc	tct	cgt	gga	tca	gca	act	288
Ser	Ser	Asn	Lys	Ala	Ala	Ser	Lys	Pro	Leu	Ser	Arg	Gly	Ser	Ala	Thr	
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gtg	gaa	tca	aag	ggg	caa	gct	gag	aag	tgt	gcc	aag	aga	aag	agg	aag	336
Val	Glu	Ser	Lys	Gly	Gln	Ala	Glu	Lys	Cys	Ala	Lys	Arg	Lys	Arg	Lys	
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aac	cag	tat	cgt	gga	atc	cgt	cag	cgt	cca	tgg	gga	aag	tgg	gct	gct	384
Asn	Gln	Tyr	Arg	Gly	Ile	Arg	Gln	Arg	Pro	Trp	Gly	Lys	Trp	Ala	Ala	
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Glu	Ile	Arg	Asp	Pro	Arg	Lys	Gly	Val	Arg	Val	Trp	Leu	Gly	Thr	Phe	
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Ser	Thr	Ala	Glu	Glu	Ala	Ala	Arg	Ala	Tyr	Asp	Ala	Glu	Ala	Arg	Arg	
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Ile	Arg	Gly	Lys	Lys	Ala	Lys	Val	Asn	Phe	Pro	Asp	Glu	Pro	Ser	Gly	
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Ala	Ala	Ala	Ser	Ser	Lys	Arg	Leu	Lys	Val	Asn	Pro	Glu	Ala	Gln	Pro	
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Met	Lys	Glu	Asn	Leu	Asn	Thr	Val	Lys	Pro	Lys	Met	Asn	Gln	Met	Phe	
		195				200					205					
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Asn	Phe	Gly	His	Asn	Leu	Glu	Gly	Tyr	Tyr	Ser	Pro	Ile	Asp	Gln	Val	
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gga	aac	gga	gtt	caa	gtc	tca	cct	gtt	act	cca	tct	gct	gat	gtt	act	768
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gct	tac	ttc	agc	tct	gag	cat	tcg	agc	aac	tcg	ttt	gat	tat	tct	gac	816
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Leu	Ser	Ala	Ala	Pro	Leu	Glu	Gly	Ala	Ala	Asp	Gln	Val	Gln	Lys	Thr	
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aac	aac	tcg	cag	gat	gtg	gtg	gct	gca	caa	gat	gat	tct	gca	aaa	acc	960
Asn	Asn	Ser	Gln	Asp	Val	Val	Ala	Ala	Gln	Asp	Asp	Ser	Ala	Lys	Thr	
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ctt	tcc	gaa	gag	ctt	gca	gac	att	gaa	tcc	cag	ctc	aag	ttc	ttt	gag	1008
Leu	Ser	Glu	Glu	Leu	Ala	Asp	Ile	Glu	Ser	Gln	Leu	Lys	Phe	Phe	Glu	
				325					330					335		
acc	cct	tct	ttt	ctt	gat	gaa	gcc	tgg	gct	gat	gct	aca	ttg	gcg	tct	1056

PF59082SeqList_PF59082.txt

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Lys	Arg	Phe	Ser	Lys	Pro	Leu	Leu	Asp	Asp	Asp	Phe	Glu	Ala	Gly	Phe		
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Arg	Glu	Phe	Lys	Asp	Asp	Ser	Glu	Ile	Glu	Asp	Val	Asp	Asp	Glu	Asp		
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Asp	Glu	Asp	Glu	Glu	Glu	Leu	Lys	Lys	Lys	Pro	Phe	Gly	Phe	Ser	Arg		
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Ser	Ser	Asn	Lys	Ala	Ala	Ser	Lys	Pro	Leu	Ser	Arg	Gly	Ser	Ala	Thr		
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Ser	Thr	Ala	Glu	Glu	Ala	Ala	Arg	Ala	Tyr	Asp	Ala	Glu	Ala	Arg	Arg		
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Ala	Ala	Ala	Ser	Ser	Lys	Arg	Leu	Lys	Val	Asn	Pro	Glu	Ala	Gln	Pro		
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Met	Lys	Glu	Asn	Leu	Asn	Thr	Val	Lys	Pro	Lys	Met	Asn	Gln	Met	Phe		
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Glu	Gln	Lys	Pro	Leu	Val	Asn	Gln	Tyr	Val	Asn	Pro	Ala	Pro	Phe	Pro		
225					230					235					240		
Gly	Asn	Gly	Val	Gln	Val	Ser	Pro	Val	Thr	Pro	Ser	Ala	Asp	Val	Thr		
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Ala	Tyr	Phe	Ser	Ser	Glu	His	Ser	Ser	Asn	Ser	Phe	Asp	Tyr	Ser	Asp		
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Leu	Gly	Trp	Gly	Glu	Gln	Val	Pro	Lys	Thr	Pro	Glu	Ile	Ser	Ser	Leu		
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Leu	Ser	Ala	Ala	Pro	Leu	Glu	Gly	Ala	Ala	Asp	Gln	Val	Gln	Lys	Thr		
	290					295					300						
Asn	Asn	Ser	Gln	Asp	Val	Val	Ala	Ala	Gln	Asp	Asp	Ser	Ala	Lys	Thr		
305					310					315					320		
Leu	Ser	Glu	Glu	Leu	Ala	Asp	Ile	Glu	Ser	Gln	Leu	Lys	Phe	Phe	Glu		
			325						330					335			
Thr	Pro	Ser	Phe	Leu	Asp	Glu	Ala	Trp	Ala	Asp	Ala	Thr	Leu	Ala	Ser		
			340					345					350				
Leu	Leu	Gly	Gly	Asp	Ala	Thr	His	Asp	Ala	Ala	Gly	Asn	Pro	Met	Asn		
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Leu	Trp	Ser	Phe	Asp	Asp	Leu	Pro	Ser	Met	Ala	Gly	Val	Phe				
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Gly Gly Ala Gln Arg Val Thr Ala Asp Ile Leu Trp Pro Asn Leu Arg	
20 25 30	
aag cgg ttc tcg aag tcg ctg ctg gac gat gat ttc gag gca ggg ttc	144
Lys Arg Phe Ser Lys Ser Leu Leu Asp Asp Asp Phe Glu Ala Gly Phe	
35 40 45	
aga gaa ttc gag gat gac tcg gaa atc gag gat gtc gat gat gag gac	192
Arg Glu Phe Glu Asp Asp Ser Glu Ile Glu Asp Val Asp Asp Glu Asp	
50 55 60	
gat gaa gag gag gag gag ttg aag aag aag aag ccc ttt ggg ttc tct	240
Asp Glu Glu Glu Glu Glu Leu Lys Lys Lys Lys Pro Phe Gly Phe Ser	
65 70 75 80	
cgc tcc aac aac aag gct gct tct aag cct ctg tct cgt gga gca aca	288
Arg Ser Asn Asn Lys Ala Ala Ser Lys Pro Leu Ser Arg Gly Ala Thr	
85 90 95	
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Thr Val Lys Ser Val Glu Ser Lys Gly Gln Ala Glu Lys Cys Ala Lys	
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aga aag agg aag aac cag tat cgc gga atc cgc cag cgt cca tgg gga	384
Arg Lys Arg Lys Asn Gln Tyr Arg Gly Ile Arg Gln Arg Pro Trp Gly	
115 120 125	
aag tgg gct gct gag att cgc gac cca aga aag ggg gtt cgt gtt tgg	432
Lys Trp Ala Ala Glu Ile Arg Asp Pro Arg Lys Gly Val Arg Val Trp	
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Leu Gly Thr Phe Ser Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Ala	
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Glu Ala Arg Arg Ile Arg Gly Lys Lys Ala Lys Val Asn Phe Pro Asp	
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Glu Pro Ser Gly Ala Ala Ser Ser Lys Arg Leu Lys Ala Asn Pro Glu	
180 185 190	
gct cag cca atg aag aaa aat ctg aac tct gtg aag ccg aaa ata aac	624
Ala Gln Pro Met Lys Lys Asn Leu Asn Ser Val Lys Pro Lys Ile Asn	
195 200 205	
cag atg ttc aat ttt ggt gac aat ctt gag ggc tac tac agc cct ata	672
Gln Met Phe Asn Phe Gly Asp Asn Leu Glu Gly Tyr Tyr Ser Pro Ile	
210 215 220	
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225 230 235 240	
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Pro Phe Ala Gly Asn Gly Val Gln Val Ser Pro Val Thr Pro Ser Ala	
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gat gtt act gct tac ttc agc tct gag cat tcg agc agc tcg ttt gat	816
Asp Val Thr Ala Tyr Phe Ser Ser Glu His Ser Ser Ser Phe Asp	
260 265 270	
tat tct gac ctg gga tgg ggt gaa caa gtc ccc aag aca ccc gag atc	864
Tyr Ser Asp Leu Gly Trp Gly Glu Gln Val Pro Lys Thr Pro Glu Ile	
275 280 285 290	
tca tcc atg ctt tct gct gct cct ttg gac ggt gaa tct cag ttt gtg	912
Ser Ser Met Leu Ser Ala Ala Pro Leu Asp Gly Glu Ser Gln Phe Val	
295 300 305	
cag ggt gct gct gat cag aat cag aag aag aac aac ctg ctg gat atg	960
Gln Gly Ala Ala Asp Gln Asn Gln Lys Lys Asn Asn Leu Leu Asp Met	
310 315 320	
gca tct gtg caa gat gat tct gca aaa act ctt tct gag gag ctt gca	1008
Ala Ser Val Gln Asp Asp Ser Ala Lys Thr Leu Ser Glu Glu Leu Ala	
325 330 335	
gac att gaa tcc cag ctg aag ttc ttt gag acc cct tct ttt ctt gat	1056

PF59082SeqList_PF59082.txt

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Glu	Ala	Trp	Ala	Asp	Ala	Ala	Leu	Ala	Ser	Leu	Leu	Ser	Glu	Asp	Ala
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tct	cag	gat	gct	gct	gga	aac	cct	atg	aac	ctt	tgg	agc	ttc	gac	gac
Ser	Gln	Asp	Ala	Ala	Gly	Asn	Pro	Met	Asn	Leu	Trp	Ser	Phe	Asp	Asp
	370					375					380				
ctg	cct	tcc	atg	gca	gga	gtc	ttc	tga							
Leu	Pro	Ser	Met	Ala	Gly	Val	Phe								
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1104

1152

1179

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			20					25					30		
Lys	Arg	Phe	Ser	Lys	Ser	Leu	Leu	Asp	Asp	Asp	Phe	Glu	Ala	Gly	Phe
		35					40					45			
Arg	Glu	Phe	Glu	Asp	Asp	Ser	Glu	Ile	Glu	Asp	Val	Asp	Asp	Glu	Asp
	50					55					60				
Asp	Glu	Glu	Glu	Glu	Glu	Leu	Lys	Lys	Lys	Lys	Pro	Phe	Gly	Phe	Ser
65					70				75						80
Arg	Ser	Asn	Asn	Lys	Ala	Ala	Ser	Lys	Pro	Leu	Ser	Arg	Gly	Ala	Thr
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Thr	Val	Lys	Ser	Val	Glu	Ser	Lys	Gly	Gln	Ala	Glu	Lys	Cys	Ala	Lys
			100					105					110		
Arg	Lys	Arg	Lys	Asn	Gln	Tyr	Arg	Gly	Ile	Arg	Gln	Arg	Pro	Trp	Gly
		115					120					125			
Lys	Trp	Ala	Ala	Glu	Ile	Arg	Asp	Pro	Arg	Lys	Gly	Val	Arg	Val	Trp
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Leu	Gly	Thr	Phe	Ser	Thr	Ala	Glu	Glu	Ala	Ala	Arg	Ala	Tyr	Asp	Ala
145					150				155						160
Glu	Ala	Arg	Arg	Ile	Arg	Gly	Lys	Lys	Ala	Lys	Val	Asn	Phe	Pro	Asp
				165					170					175	
Glu	Pro	Ser	Gly	Ala	Ala	Ser	Ser	Lys	Arg	Leu	Lys	Ala	Asn	Pro	Glu
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Asp	Val	Thr	Ala	Tyr	Phe	Ser	Ser	Glu	His	Ser	Ser	Ser	Ser	Phe	Asp
			260					265					270		
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Ser	Ser	Met	Leu	Ser	Ala	Ala	Pro	Leu	Asp	Gly	Glu	Ser	Gln	Phe	Val
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Ala	Ser	Val	Gln	Asp	Ser	Ala	Lys	Thr	Leu	Ser	Glu	Glu	Leu	Ala	
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Asp	Ile	Glu	Ser	Gln	Leu	Lys	Phe	Phe	Glu	Thr	Pro	Ser	Phe	Leu	Asp
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Glu	Ala	Trp	Ala	Asp	Ala	Ala	Leu	Ala	Ser	Leu	Leu	Ser	Glu	Asp	Ala
		355					360					365			
Ser	Gln	Asp	Ala	Ala	Gly	Asn	Pro	Met	Asn	Leu	Trp	Ser	Phe	Asp	Asp
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29

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<223> Xaa in position 16 to 20 is any or no amino acid

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<221> Variant

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<223> Xaa in position 25 to 27 is any amino acid

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<222> (30)..(30)

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			20					25					30		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		35					40					45			
Xaa	Xaa	Xaa	Arg	Xaa	Xaa	Xaa	Xaa	Xaa	Leu	Asp	Xaa	Xaa	Phe	Glu	Ala
	50					55				60					
Asp	Phe	Xaa	Xaa	Phe	Xaa	Asp	Xaa	Xaa	Xaa	Xaa	Xaa	Asp	Xaa	Xaa	Xaa
65					70				75						80
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Lys	Pro	Phe	Xaa
				85				90						95	
Phe	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			100					105					110		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Lys	Xaa	Xaa	Xaa	Xaa	Xaa
		115						120				125			
Xaa	Xaa	Xaa	Xaa	Ala	Glu	Lys	Xaa	Ala	Lys	Arg	Lys	Arg	Lys	Asn	Gln
	130					135					140				
Tyr	Arg	Gly	Ile	Arg	Gln	Arg	Pro	Trp	Gly	Lys	Trp	Ala	Ala	Glu	Ile
145					150					155					160
Arg	Asp	Pro	Arg	Lys	Gly	Xaa	Arg	Xaa	Trp	Leu	Gly	Thr	Phe	Xaa	Thr
				165					170					175	
Ala	Glu	Glu	Ala	Ala	Arg	Ala	Tyr	Asp	Ala	Xaa	Ala	Arg	Arg	Ile	Arg
			180					185					190		
Gly	Xaa	Lys	Ala	Lys	Val	Asn	Phe	Pro	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		195					200						205		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
	210					215						220			
Xaa	Xaa	Lys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
225						230				235					240
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				245					250					255	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Glu	Xaa	Lys	Pro	Xaa	Xaa	Xaa	Xaa
				260				265					270		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		275						280					285		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Tyr	Phe	Xaa	Ser	Asp
	290					295					300				
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305					310					315					320
Xaa	Xaa	Xaa	Thr	Pro	Xaa	Glu	Ile	Ser	Ser	Xaa	Leu	Xaa	Xaa	Xaa	Xaa

PF59082SeqList_PF59082.txt

				325					330					335			
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				340					345					350			
Xaa	Xaa	Lys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		355						360					365				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		370					375					380					
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		385				390					395						400
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				405					410							415	
Asn	Xaa	Met	Xaa	Leu	Trp	Ser	Xaa	Asp	Xaa	Xaa	Xaa	Xaa	Met	Xaa	Xaa	Xaa	Xaa
			420					425					430				
Xaa	Xaa	Val															
		435															

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<211> 60

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<220>

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<220>

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<223> Xaa in position 27 is any amino acid

<220>

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<223> Xaa in position 29 is any amino acid

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<221> Variant

<222> (35)..(35)

<223> Xaa in position 35 is any amino acid

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<222> (36)..(36)

<223> Xaa in position 36 is Ser or Thr

<220>

<221> Variant

<222> (42)..(42)

<223> Xaa in position 42 is Lys or Arg

<220>

<221> Variant

<222> (46)..(46)

<223> Xaa in position 46 is Ala, Ile or Val

<220>

<221> Variant

<222> (47)..(47)

<223> Xaa in position 47 is Ala, Glu or Thr

<220>

<221> Variant

<222> (49)..(49)

<223> Xaa in position 49 is any amino acid

PF59082SeqList_PF59082.txt

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<223> Xaa in position 56 is Ala or Ser

<220>
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Ala Ala Glu Ile Arg Asp Pro Arg Xaa Gly Xaa Arg Xaa Trp Leu Gly
      20      25      30
Thr Phe Xaa Xaa Ala Glu Glu Ala Ala Xaa Ala Tyr Asp Xaa Xaa Ala
      35      40      45
Xaa Arg Ile Arg Gly Xaa Lys Xaa Lys Xaa Asn Phe
      50      55      60

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<220>
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<223> Xaa in position 12 is any or no amino acid

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Met Cys Gly Gly Ala Ile Ile Ser Asp Xaa Xaa Xaa Pro Xaa
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<210> 810
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<223> Xaa in position 10 is Phe, Ile or Leu

<220>
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<222> (11)..(11)
<223> Xaa in position 11 is Asp, Glu, Gly or Asn

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<220>
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<400> 810
Phe Xaa Ser Xaa Xaa Xaa Ser Asn Xaa Xaa Xaa Xaa Ser Xaa
1          5          10

<210> 811
<211> 21
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<220>
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<220>
<221> Variant

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$\langle 222 \rangle$ (14) .. (14)

$\langle 220 \rangle$

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 $\langle 220 \rangle$ $\langle 222 \rangle$ (20) .. (20)

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$\langle 210 \rangle$	01
$\langle 211 \rangle$	11

<213> Artificial sequence

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$\langle 220 \rangle$

$\langle 222 \rangle \quad (4) \dots (4)$

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$\langle 222 \rangle$ (5) . . (5)

$\langle 220 \rangle$

 $\langle 222 \rangle \quad (6) \dots (6)$

$\langle 220 \rangle$

$\langle 222 \rangle \quad (7) \dots (7)$

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PF59082SeqList_PF59082.txt

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1 5 10 15
ttc aca ctc ctc tcc gcc act aaa ccc cta aat ctc act ctc cct cac      96
Phe Thr Leu Leu Ser Ala Thr Lys Pro Leu Asn Leu Thr Leu Pro His
20 25 30
caa cac cct tcc cct gat tcc gtc gct ctc cat gtc atc agg agt gta      144
Gln His Pro Ser Pro Asp Ser Val Ala Leu His Val Ile Arg Ser Val
35 40 45
aat gaa tct ctt gca aga aga caa cta agc tca cca tca tca tcc tca      192
Asn Glu Ser Leu Ala Arg Arg Gln Leu Ser Ser Pro Ser Ser Ser Ser
50 55 60
tca tca tca tcc tcc tca tca tca tcc tct tgc cgt acc gga aac cca      240
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Cys Arg Thr Gly Asn Pro
65 70 75 80
atc gac gat tgc tgg aga tgc agc gac gca gac tgg tca aca aac cga      288
Ile Asp Asp Cys Trp Arg Cys Ser Asp Ala Asp Trp Ser Thr Asn Arg
85 90 95
caa aga cta gca gac tgt tca atc ggc ttc gga cac ggc aca ctc gga      336
Gln Arg Leu Ala Asp Cys Ser Ile Gly Phe Gly His Gly Thr Leu Gly
100 105 110
ggc aaa aac ggc aag atc tac gtc gta act gac tca tcc gac aac aac      384
Gly Lys Asn Gly Lys Ile Tyr Val Val Thr Asp Ser Ser Asp Asn Asn
115 120 125
cca aca aac cca aca cca gga aca ctc cgt tac ggc gta atc caa gaa      432
Pro Thr Asn Pro Thr Pro Gly Thr Leu Arg Tyr Gly Val Ile Gln Glu
130 135 140
gag cca ctc tgg atc gtc ttc tct tca aac atg ctc atc aga cta aaa      480
Glu Pro Leu Trp Ile Val Phe Ser Ser Asn Met Leu Ile Arg Leu Lys
145 150 155 160
caa gaa ctc atc atc aac agc tac aaa acc tta gat ggt cgt ggc tca      528
Gln Glu Leu Ile Ile Asn Ser Tyr Lys Thr Leu Asp Gly Arg Gly Ser
165 170 175
gcc gtt cac att acc gga aac ggt tgc tta act ctc caa tac gtt caa      576
Ala Val His Ile Thr Gly Asn Gly Cys Leu Thr Leu Gln Tyr Val Gln
180 185 190
cac atc atc atc cac aac ctc cat atc tat gac tgt aaa cct tca gct      624
His Ile Ile Ile His Asn Leu His Ile Tyr Asp Cys Lys Pro Ser Ala
195 200 205
gga ttc gag aaa cgt ggt aga tcc gat gga gat ggg atc tcg atc ttc      672
Gly Phe Glu Lys Arg Gly Arg Ser Asp Gly Asp Gly Ile Ser Ile Phe
210 215 220
gga tct cag aag atc tgg gtt gat cat tgt tca atg agt cat tgc acc      720
Gly Ser Gln Lys Ile Trp Val Asp His Cys Ser Met Ser His Cys Thr
225 230 235 240
gac ggg cta att gat gct gtg atg ggt tct aca gct ata act ata tct      768
Asp Gly Leu Ile Asp Ala Val Met Gly Ser Thr Ala Ile Thr Ile Ser
245 250 255
aac aat tac ttc acc cac cac gac gag gtt atg ttg ttg ggt cat gat      816
Asn Asn Tyr Phe Thr His His Asp Glu Val Met Leu Leu Gly His Asp
260 265 270
gat aac tat gct cct gat acg ggg atg caa gtg acg ata gcg ttt aat      864
Asp Asn Tyr Ala Pro Asp Thr Gly Met Gln Val Thr Ile Ala Phe Asn
275 280 285
cat ttc gga caa ggg ctt gtt cag agg atg cct agg tgt cgg aga ggt      912
His Phe Gly Gln Gly Leu Val Gln Arg Met Pro Arg Cys Arg Arg Gly

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305	310	315	320
att ggt ggt agt ggt aat ccc acc att aac agt caa gga aat cgt tac			1008
Ile Gly Gly Ser Gly Asn Pro Thr Ile Asn Ser Gln Gly Asn Arg Tyr			
	325	330	335
tct gct cct tct gat cct agc gcc aaa gag gtg acg aag cga gtg gac			1056
Ser Ala Pro Ser Asp Pro Ser Ala Lys Glu Val Thr Lys Arg Val Asp			
	340	345	350
tcg aag gac gat ggt gaa tgg tcg aat tgg aga aca gaa ggg			1104
Ser Lys Asp Asp Gly Glu Trp Ser Asn Trp Asn Trp Arg Thr Glu Gly			
	355	360	365
gat ttg atg gag aat gga gct ttc ttt gtg gcc tct ggt gaa gga atg			1152
Asp Leu Met Glu Asn Gly Ala Phe Phe Val Ala Ser Gly Glu Gly Met			
	370	375	380
agc tca atg tac tct aaa gct tct agt gtt gac cct aaa gct gct tct			1200
Ser Ser Met Tyr Ser Lys Ala Ser Ser Val Asp Pro Lys Ala Ala Ser			
	385	390	400
ctc gta gac cag ctc act cga aac gct ggc gtt ttt ggc ggt ccc agg			1248
Leu Val Asp Gln Leu Thr Arg Asn Ala Gly Val Phe Gly Gly Pro Arg			
	405	410	415
gat gat caa ggt cag agt ggc aat tct tac tct cct tat gga ggc gac			1296
Asp Asp Gln Gly Gln Ser Gly Asn Ser Tyr Ser Pro Tyr Gly Gly Asp			
	420	425	430
ggc ggt ggc ggt ggg agc agc ggt ggg agc agc ggt gga ggg atg gac			1344
Gly Gly Gly Gly Gly Ser Ser Gly Gly Ser Ser Gly Gly Gly Met Asp			
	435	440	445
gtt atg gga ggt acg acg aga gga agc agc agc agc agc ggc gat gac			1392
Val Met Gly Gly Thr Thr Arg Gly Ser Ser Ser Ser Ser Gly Asp Asp			
	450	455	460
agc aat gtc ttc cag atg ata ttt gga agc gat gca ccg tct cgg ccg			1440
Ser Asn Val Phe Gln Met Ile Phe Gly Ser Asp Ala Pro Ser Arg Pro			
	465	470	480
cgt tta acg tta ttg ttt tct ttg tta atg att tcg gtt ttg tcg tta			1488
Arg Leu Thr Leu Leu Phe Ser Leu Leu Met Ile Ser Val Leu Ser Leu			
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Ser Thr Leu Leu Leu			
	500		

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 <212> PRT
 <213> Arabidopsis thaliana

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 20 25 30
 Gln His Pro Ser Pro Asp Ser Val Ala Leu His Val Ile Arg Ser Val
 35 40 45
 Asn Glu Ser Leu Ala Arg Arg Gln Leu Ser Ser Pro Ser Ser Ser Ser
 50 55 60
 Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Cys Arg Thr Gly Asn Pro
 65 70 75 80
 Ile Asp Asp Cys Trp Arg Cys Ser Asp Ala Asp Trp Ser Thr Asn Arg
 85 90 95
 Gln Arg Leu Ala Asp Cys Ser Ile Gly Phe Gly His Gly Thr Leu Gly
 100 105 110
 Gly Lys Asn Gly Lys Ile Tyr Val Val Thr Asp Ser Ser Asp Asn Asn
 115 120 125
 Pro Thr Asn Pro Thr Pro Gly Thr Leu Arg Tyr Gly Val Ile Gln Glu
 130 135 140
 Glu Pro Leu Trp Ile Val Phe Ser Ser Asn Met Leu Ile Arg Leu Lys
 145 150 155 160
 Gln Glu Leu Ile Ile Asn Ser Tyr Lys Thr Leu Asp Gly Arg Gly Ser
 165 170 175

PF59082SeqList_PF59082.txt

Ala Val His Ile Thr Gly Asn Gly Cys Leu Thr Leu Gln Tyr Val Gln
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 His Ile Ile Ile His Asn Leu His Ile Tyr Asp Cys Lys Pro Ser Ala
 195 200 205
 Gly Phe Glu Lys Arg Gly Arg Ser Asp Gly Asp Gly Ile Ser Ile Phe
 210 215 220
 Gly Ser Gln Lys Ile Trp Val Asp His Cys Ser Met Ser His Cys Thr
 225 230 235 240
 Asp Gly Leu Ile Asp Ala Val Met Gly Ser Thr Ala Ile Thr Ile Ser
 245 250 255
 Asn Asn Tyr Phe Thr His His Asp Glu Val Met Leu Leu Gly His Asp
 260 265 270
 Asp Asn Tyr Ala Pro Asp Thr Gly Met Gln Val Thr Ile Ala Phe Asn
 275 280 285
 His Phe Gly Gln Gly Leu Val Gln Arg Met Pro Arg Cys Arg Arg Gly
 290 295 300
 Tyr Ile His Val Val Asn Asn Asp Phe Thr Glu Trp Lys Met Tyr Ala
 305 310 315 320
 Ile Gly Gly Ser Gly Asn Pro Thr Ile Asn Ser Gln Gly Asn Arg Tyr
 325 330 335
 Ser Ala Pro Ser Asp Pro Ser Ala Lys Glu Val Thr Lys Arg Val Asp
 340 345 350
 Ser Lys Asp Asp Gly Glu Trp Ser Asn Trp Asn Trp Arg Thr Glu Gly
 355 360 365
 Asp Leu Met Glu Asn Gly Ala Phe Phe Val Ala Ser Gly Glu Gly Met
 370 375 380
 Ser Ser Met Tyr Ser Lys Ala Ser Ser Val Asp Pro Lys Ala Ala Ser
 385 390 395 400
 Leu Val Asp Gln Leu Thr Arg Asn Ala Gly Val Phe Gly Gly Pro Arg
 405 410 415
 Asp Asp Gln Gly Gln Ser Gly Asn Ser Tyr Ser Pro Tyr Gly Gly Asp
 420 425 430
 Gly Gly Gly Gly Gly Ser Ser Gly Gly Ser Ser Gly Gly Met Asp
 435 440 445
 Val Met Gly Gly Thr Thr Arg Gly Ser Ser Ser Ser Gly Asp Asp
 450 455 460
 Ser Asn Val Phe Gln Met Ile Phe Gly Ser Asp Ala Pro Ser Arg Pro
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 Ser Thr Leu Leu Leu
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 ctt gtc cta gct ccg acc ttc act gac tcc aac cat gtc tcc gac cct 96
 Leu Val Leu Ala Pro Thr Phe Thr Asp Ser Asn His Val Ser Asp Pro
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 gaa ctc gta gtt caa gaa gta aac gag aag att aat gcg tct agg agg 144
 Glu Leu Val Val Gln Glu Val Asn Glu Lys Ile Asn Ala Ser Arg Arg
 35 40 45
 aat ctt ggt gtc ctc tca tgt ggg aca gga aac cct atc gac gat tgt 192
 Asn Leu Gly Val Leu Ser Cys Gly Thr Gly Asn Pro Ile Asp Asp Cys
 50 55 60
 tgg aga tgc gac ccg aaa tgg gag aaa aac cga caa cga cta gct gat 240
 Trp Arg Cys Asp Pro Lys Trp Glu Lys Asn Arg Gln Arg Leu Ala Asp
 65 70 75 80
 tgc gcc att gga ttt ggc aaa cac gca ata ggc ggc cgt gac ggc aaa 288
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PF59082SeqList_PF59082.txt

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Ile	Tyr	Val	Val	Thr	Asp	Pro	Ser	Asp	Lys	Asp	Val	Val	Asn	Pro	Lys	
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ccg	gga	acc	cta	aga	cac	gca	gtg	atc	caa	gac	gag	ccg	cta	tgg	atc	384
Pro	Gly	Thr	Leu	Arg	His	Ala	Val	Ile	Gln	Asp	Glu	Pro	Leu	Trp	Ile	
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Ile	Phe	Ala	Arg	Asp	Met	Val	Ile	Lys	Leu	Lys	Glu	Glu	Leu	Leu	Met	
	130					135					140					
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Gly	Gly	Ala	Cys	Ile	Thr	Ala	Gln	Tyr	Val	Thr	Asn	Ile	Ile	Ile	His	
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Asp	Ser	Pro	Ser	His	Tyr	Gly	Trp	Arg	Thr	Ala	Ser	Asp	Gly	Asp	Ala	
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225				230			235			235					240	
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Ile	Thr	Ile	Ser	Asn	Asn	Tyr	Leu	Thr	His	His	Asn	Lys	Val	Met	Leu	
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Leu	Gly	His	Ser	Asp	Ser	Tyr	Thr	Arg	Asp	Lys	Asn	Met	Gln	Val	Thr	
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Cys	Arg	His	Gly	Tyr	Phe	His	Val	Val	Asn	Asn	Asp	Tyr	Thr	His	Trp	
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Gln	Met	Tyr	Ala	Ile	Gly	Gly	Ser	Ala	Ala	Pro	Thr	Ile	Asn	Ser	Gln	
305					310					315					320	
ggc	aat	agg	ttt	ctt	gct	ccc	aat	gac	cat	gtc	ttc	aaa	gag	gtg	act	1008
Gly	Asn	Arg	Phe	Leu	Ala	Pro	Asn	Asp	His	Val	Phe	Lys	Glu	Val	Thr	
			325				330							335		
aaa	tac	gaa	gat	gca	cca	caa	agc	aaa	tgg	aag	aag	tgg	aac	tgg	aga	1056
Lys	Tyr	Glu	Asp	Ala	Pro	Gln	Ser	Lys	Trp	Lys	Lys	Trp	Asn	Trp	Arg	
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		355					360					365				
gga	aga	gcc	tct	tca	agc	tat	gca	aaa	gct	tca	agt	ctg	tcg	gct	aga	1152
Gly	Arg	Ala	Ser	Ser	Ser	Tyr	Ala	Lys	Ala	Ser	Ser	Leu	Ser	Ala	Arg	
	370					375					380					
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<211> 407

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Glu Leu Val Val Gln Glu Val Asn Glu Lys Ile Asn Ala Ser Arg Arg
35 40 45
Asn Leu Gly Val Leu Ser Cys Gly Thr Gly Asn Pro Ile Asp Asp Cys
50 55 60
Trp Arg Cys Asp Pro Lys Trp Glu Lys Asn Arg Gln Arg Leu Ala Asp
65 70 75 80
Cys Ala Ile Gly Phe Gly Lys His Ala Ile Gly Gly Arg Asp Gly Lys
85 90 95
Ile Tyr Val Val Thr Asp Pro Ser Asp Lys Asp Val Val Asn Pro Lys
100 105 110
Pro Gly Thr Leu Arg His Ala Val Ile Gln Asp Glu Pro Leu Trp Ile
115 120 125
Ile Phe Ala Arg Asp Met Val Ile Lys Leu Lys Glu Glu Leu Leu Met
130 135 140
Asn Ser Phe Lys Thr Ile Asp Gly Arg Gly Ala Asn Val His Ile Ala
145 150 155 160
Gly Gly Ala Cys Ile Thr Ala Gln Tyr Val Thr Asn Ile Ile Ile His
165 170 175
Gly Ile Asn Ile His Asp Cys Lys Lys Arg Gly Asn Ala Tyr Val Arg
180 185 190
Asp Ser Pro Ser His Tyr Gly Trp Arg Thr Ala Ser Asp Gly Asp Ala
195 200 205
Val Ser Ile Phe Gly Gly Ser His Val Trp Val Asp His Cys Ser Leu
210 215 220
Ser Asn Cys Glu Asp Gly Leu Val Asp Pro Ile Arg Gly Ser Thr Ala
225 230 235 240
Ile Thr Ile Ser Asn Asn Tyr Leu Thr His His Asn Lys Val Met Leu
245 250 255
Leu Gly His Ser Asp Ser Tyr Thr Arg Asp Lys Asn Met Gln Val Thr
260 265 270
Ile Ala Phe Asn His Phe Gly Glu Gly Leu Val Gln Arg Met Pro Arg
275 280 285
Cys Arg His Gly Tyr Phe His Val Val Asn Asn Asp Tyr Thr His Trp
290 295 300
Gln Met Tyr Ala Ile Gly Ser Ala Ala Pro Thr Ile Asn Ser Gln
305 310 315 320
Gly Asn Arg Phe Leu Ala Pro Asn Asp His Val Phe Lys Glu Val Thr
325 330 335
Lys Tyr Glu Asp Ala Pro Gln Ser Lys Trp Lys Lys Trp Asn Trp Arg
340 345 350
Ser Glu Gly Asp Leu Phe Leu Asn Gly Ala Phe Phe Thr Pro Ser Gly
355 360 365
Gly Arg Ala Ser Ser Ser Tyr Ala Lys Ala Ser Ser Leu Ser Ala Arg
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Cys Lys Lys Gly Ser Arg Cys
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ttc gtc gga gca ata gag aac agt aca cac gac aag ata tca tct ctc 96
Phe Val Gly Ala Ile Glu Asn Ser Thr His Asp Lys Ile Ser Ser Leu 20 25 30

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Asp	Glu	Val	Ala	Asp	Glu	Val	Ile	Thr	Leu	Ala	Glu	Met	Ser	Val	Arg	
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Asp	Pro	Val	Asn	Pro	Arg	Pro	Gly	Thr	Leu	Arg	His	Ala	Val	Ile	Gln	
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Lys	Gln	Glu	Leu	Ile	Val	Asn	Ser	Phe	Lys	Thr	Ile	Asp	Gly	Arg	Gly	
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Thr	Asn	Val	Ile	Val	His	Gly	Leu	His	Ile	His	Asp	Cys	Arg	Pro	Thr	
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Val	Met	Gly	Ser	Thr	Ala	Ile	Thr	Ile	Ser	Asn	Asn	His	Met	Thr	His	
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Ile	Gln	Arg	Met	Pro	Arg	Cys	Arg	His	Gly	Tyr	Phe	His	Val	Val	Asn	
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aat	gac	tac	act	cac	tgg	gaa	atg	tac	gcg	att	ggg	gga	agc	gca	aac	1008
Asn	Asp	Tyr	Thr	His	Trp	Glu	Met	Tyr	Ala	Ile	Gly	Gly	Ser	Ala	Asn	
				325					330					335		
ccg	aca	atc	aac	agt	caa	gga	aac	cgc	tac	gcc	gcc	ccg	aaa	aat	ccc	1056
Pro	Thr	Ile	Asn	Ser	Gln	Gly	Asn	Arg	Tyr	Ala	Ala	Pro	Lys	Asn	Pro	
			340					345						350		
ttt	gct	aaa	gag	gtg	act	aag	aga	gtg	gac	aca	ccg	gcg	agt	cat	tgg	1104
Phe	Ala	Lys	Glu	Val	Thr	Lys	Arg	Val	Asp	Thr	Pro	Ala	Ser	His	Trp	
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aaa	gga	tgg	aac	tgg	aga	acg	gaa	gga	gat	ttg	ctt	cag	aac	gga	gct	1152
Lys	Gly	Trp	Asn	Trp	Arg	Thr	Glu	Gly	Asp	Leu	Leu	Gln	Asn	Gly	Ala	
	370					375					380					
tac	ttc	act	gct	tca	gga	gcc	gct	gca	tct	ggg	agc	tac	gca	cga	gcc	1200
Tyr	Phe	Thr	Ala	Ser	Gly	Ala	Ala	Ala	Ser	Gly	Ser	Tyr	Ala	Arg	Ala	
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gac	gct	gga	gct	cta	cct	tgt	cgt	aga	gga	cgt	caa	tgt	acc	tca		1293
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Ser	Arg	Ser	Asn	Glu	Asn	Glu	Trp	Asn	Thr	His	Ala	Val	Thr	Asn	Pro	
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Asn	His	Thr	Glu	Arg	Arg	Lys	Leu	Gly	Tyr	Phe	Ala	Cys	Gly	Thr	Gly	
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Asn	Pro	Ile	Asp	Asp	Cys	Trp	Arg	Cys	Asp	Ala	Asn	Trp	His	Lys	Asn	
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Gly	Gly	Arg	Asp	Gly	Arg	Phe	Tyr	Val	Val	Thr	Asp	Pro	Asn	Asp	His	
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Asp	Pro	Val	Asn	Pro	Arg	Pro	Gly	Thr	Leu	Arg	His	Ala	Val	Ile	Gln	
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Asp	Arg	Pro	Leu	Trp	Ile	Val	Phe	Lys	Arg	Asp	Met	Val	Ile	Gln	Leu	
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Lys	Gln	Glu	Leu	Ile	Val	Asn	Ser	Phe	Lys	Thr	Ile	Asp	Gly	Arg	Gly	
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Ala	Asn	Val	His	Ile	Ala	Asn	Gly	Gly	Cys	Ile	Thr	Ile	Gln	Tyr	Val	
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Thr	Asn	Val	Ile	Val	His	Gly	Leu	His	Ile	His	Asp	Cys	Arg	Pro	Thr	
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Val	Met	Gly	Ser	Thr	Ala	Ile	Thr	Ile	Ser	Asn	Asn	His	Met	Thr	His	
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His	Asn	Glu	Val	Met	Leu	Leu	Gly	His	Ser	Asp	Ser	Tyr	Thr	Lys	Asp	
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Lys	Ala	Met	Gln	Val	Thr	Ile	Ala	Tyr	Asn	His	Phe	Gly	Val	Gly	Leu	
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			325						330					335		
Pro	Thr	Ile	Asn	Ser	Gln	Gly	Asn	Arg	Tyr	Ala	Ala	Pro	Lys	Asn	Pro	
			340					345					350			
Phe	Ala	Lys	Glu	Val	Thr	Lys	Arg	Val	Asp	Thr	Pro	Ala	Ser	His	Trp	
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Lys	Gly	Trp	Asn	Trp	Arg	Thr	Glu	Gly	Asp	Leu	Leu	Gln	Asn	Gly	Ala	
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Tyr	Phe	Thr	Ala	Ser	Gly	Ala	Ala	Ala	Ser	Gly	Ser	Tyr	Ala	Arg	Ala	
385				390						395					400	
Ser	Ser	Leu	Ala	Ala	Lys	Ser	Ser	Ser	Leu	Val	Ala	Thr	Ile	Thr	Asn	
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<220>
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Phe Val Gly Ala Met Asp Asn Ser Thr His Asp Lys Ile Ser Ser Leu
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tcc aga tcg gac gaa atc gaa tgg aac aag cat gca gtg acg aat ccg      144
Ser Arg Ser Asp Glu Ile Glu Trp Asn Lys His Ala Val Thr Asn Pro
35 40 45
gat gaa gta gct gac gaa gtt atc gcc ttg gct gaa atg agt gta aga      192
Asp Glu Val Ala Asp Glu Val Ile Ala Leu Ala Glu Met Ser Val Arg
50 55 60
aac cat acc gag agg agg aag cta ggt tac ttt act tgc gga aca ggc      240
Asn His Thr Glu Arg Arg Lys Leu Gly Tyr Phe Thr Cys Gly Thr Gly
65 70 75 80
aac cca atc gac gat tgt tgg cga tgc gat cgc aac tgg cac aag aac      288
Asn Pro Ile Asp Asp Cys Trp Arg Cys Asp Arg Asn Trp His Lys Asn
85 90 95
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Arg Lys Arg Leu Ala Asp Cys Gly Ile Gly Phe Gly Arg Asn Ala Ile
100 105 110
ggc ggt cgc gac ggg cgt ttc tac gta gtc act gac cca aga gac gac      384
Gly Gly Arg Asp Gly Arg Phe Tyr Val Val Thr Asp Pro Arg Asp Asp
115 120 125
aac ccg gtt aac cct aga ccg ggg aca tta cgt cac gcc gtg atc caa      432
Asn Pro Val Asn Pro Arg Pro Gly Thr Leu Arg His Ala Val Ile Gln
130 135 140
gac cga cca cta tgg atc gtt ttc aaa cgt gac atg gtg att cag tta      480
Asp Arg Pro Leu Trp Ile Val Phe Lys Arg Asp Met Val Ile Gln Leu
145 150 155 160
aaa caa gag ctg atc gta aac agc ttc aaa acg atc gac gga cgc ggc      528
Lys Gln Glu Leu Ile Val Asn Ser Phe Lys Thr Ile Asp Gly Arg Gly
165 170 175
gca aac gtt cac atc gct aac ggc ggt tgc atc acg att cag tac gtg      576
Ala Asn Val His Ile Ala Asn Gly Gly Cys Ile Thr Ile Gln Tyr Val
180 185 190
acg aac gtc atc gtg cat gga ttg cat att cat gac tgt aga ccg acg      624
Thr Asn Val Ile Val His Gly Leu His Ile His Asp Cys Arg Pro Thr
195 200 205
ggt aac gct atg gtg aga agc tca gag acg cac ttt ggg tgg agg acg      672
Gly Asn Ala Met Val Arg Ser Ser Glu Thr His Phe Gly Trp Arg Thr
210 215 220
atg gcg gat ggt gac gcg att tcg atc ttt gga tcg agt cat gtt tgg      720
Met Ala Asp Gly Asp Ala Ile Ser Ile Phe Gly Ser Ser His Val Trp
225 230 235 240
att gat cac aac tcg ttg tct cat tgc gct gat ggg ctt gtg gat gca      768
Ile Asp His Asn Ser Leu Ser His Cys Ala Asp Gly Leu Val Asp Ala
245 250 255
gtc atg ggc tcg acg gcc att acc atc tct aac aac cac atg act cat      816
Val Met Gly Ser Thr Ala Ile Thr Ile Ser Asn Asn His Met Thr His
260 265 270
cac aac gag gtt atg ttg ctc gga cat agt gat tct tac acg agg gat      864
His Asn Glu Val Met Leu Leu Gly His Ser Asp Ser Tyr Thr Arg Asp
275 280 285
aaa gct atg caa gtt act att gct tat aac cat ttt ggt gtc gga ctt      912
Lys Ala Met Gln Val Thr Ile Ala Tyr Asn His Phe Gly Val Gly Leu
290 295 300

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PF59082SeqList_PF59082.txt

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305					310				315						320	
aat	gac	tac	act	cac	tgg	gaa	atg	tac	gcg	att	ggt	gga	agc	gca	aac	1008
Asn	Asp	Tyr	Thr	His	Trp	Glu	Met	Tyr	Ala	Ile	Gly	Gly	Ser	Ala	Asn	
				325					330					335		
ccg	aca	atc	aac	agt	caa	gga	aac	cgc	tac	gcc	gct	cct	aaa	aat	cct	1056
Pro	Thr	Ile	Asn	Ser	Gln	Gly	Asn	Arg	Tyr	Ala	Ala	Pro	Lys	Asn	Pro	
			340			345							350			
ttt	gct	aaa	gag	gtg	act	aag	aga	gtg	gac	aca	ccg	gcg	agt	cat	tgg	1104
Phe	Ala	Lys	Glu	Val	Thr	Lys	Arg	Val	Asp	Thr	Pro	Ala	Ser	His	Trp	
		355				360						365				
aaa	gga	tgg	aac	tgg	aga	tcg	gaa	gga	gat	ttg	ctt	cag	aac	gga	gct	1152
Lys	Gly	Trp	Asn	Trp	Arg	Ser	Glu	Gly	Asp	Leu	Leu	Gln	Asn	Gly	Ala	
	370					375					380					
tac	ttc	act	tct	tca	gga	gcc	gct	gca	tct	ggt	agc	tac	gca	cg	gcc	1200
Tyr	Phe	Thr	Ser	Ser	Gly	Ala	Ala	Ala	Ser	Gly	Ser	Tyr	Ala	Arg	Ala	
385					390					395					400	
tct	agc	ctc	gcc	gct	aaa	tct	tct	tca	ttg	ggt	gca	acc	att	act	tct	1248
Ser	Ser	Leu	Ala	Ala	Lys	Ser	Ser	Ser	Leu	Val	Ala	Thr	Ile	Thr	Ser	
				405					410					415		
gac	gct	gga	gct	cta	cct	tgt	cgt	aga	gga	cgt	caa	tgt	acc	tca		1293
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tag																1296

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 <212> PRT
 <213> Brassica napus

<400> 820

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Ser	Arg	Ser	Asp	Glu	Ile	Glu	Trp	Asn	Lys	His	Ala	Val	Thr	Asn	Pro
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Asp	Glu	Val	Ala	Asp	Glu	Val	Ile	Ala	Leu	Ala	Glu	Met	Ser	Val	Arg
	50					55					60				
Asn	His	Thr	Glu	Arg	Arg	Lys	Leu	Gly	Tyr	Phe	Thr	Cys	Gly	Thr	Gly
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Asn	Pro	Ile	Asp	Asp	Cys	Trp	Arg	Cys	Asp	Arg	Asn	Trp	His	Lys	Asn
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Arg	Lys	Arg	Leu	Ala	Asp	Cys	Gly	Ile	Gly	Phe	Gly	Arg	Asn	Ala	Ile
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Gly	Gly	Arg	Asp	Gly	Arg	Phe	Tyr	Val	Val	Thr	Asp	Pro	Arg	Asp	Asp
		115					120					125			
Asn	Pro	Val	Asn	Pro	Arg	Pro	Gly	Thr	Leu	Arg	His	Ala	Val	Ile	Gln
	130					135					140				
Asp	Arg	Pro	Leu	Trp	Ile	Val	Phe	Lys	Arg	Asp	Met	Val	Ile	Gln	Leu
145					150					155					160
Lys	Gln	Glu	Leu	Ile	Val	Asn	Ser	Phe	Lys	Thr	Ile	Asp	Gly	Arg	Gly
				165					170					175	
Ala	Asn	Val	His	Ile	Ala	Asn	Gly	Gly	Cys	Ile	Thr	Ile	Gln	Tyr	Val
			180					185					190		
Thr	Asn	Val	Ile	Val	His	Gly	Leu	His	Ile	His	Asp	Cys	Arg	Pro	Thr
		195					200					205			
Gly	Asn	Ala	Met	Val	Arg	Ser	Ser	Glu	Thr	His	Phe	Gly	Trp	Arg	Thr
	210					215					220				
Met	Ala	Asp	Gly	Asp	Ala	Ile	Ser	Ile	Phe	Gly	Ser	Ser	His	Val	Trp
225					230					235					240
Ile	Asp	His	Asn	Ser	Leu	Ser	His	Cys	Ala	Asp	Gly	Leu	Val	Asp	Ala
				245					250					255	
Val	Met	Gly	Ser	Thr	Ala	Ile	Thr	Ile	Ser	Asn	Asn	His	Met	Thr	His
			260					265					270		
His	Asn	Glu	Val	Met	Leu	Leu	Gly	His	Ser	Asp	Ser	Tyr	Thr	Arg	Asp

Lys	Ala	Met	Gln	Val	Thr	Ile	Ala	Tyr	Asn	His	Phe	Gly	Val	Gly	Leu
Ile	290	Gln	Arg	Met	Pro	Arg	295	Cys	Arg	His	Gly	Tyr	300	Phe	His
305	Asn	Asp	Tyr	Thr	His	Trp	Glu	Met	Tyr	Ala	Ile	Gly	Gly	Ser	Ala
Pro	Thr	Ile	Asn	Ser	Gln	Gly	Asn	Arg	Tyr	Ala	Ala	Pro	Lys	Asn	Pro
Phe	Ala	Lys	Glu	Val	Thr	Lys	Arg	Val	Asp	Thr	Pro	Ala	Ser	His	Trp
Lys	Gly	Trp	Asn	Trp	Arg	Ser	Glu	Gly	Asp	Leu	Leu	Gln	Asn	Gly	Ala
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385	Ser	Ser	Leu	Ala	Lys	Ser	Ser	Ser	Leu	Val	Ala	Thr	Ile	Thr	Ser
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					Met	Ala	Pro	Leu									
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tca	tgc	atc	att	gtt	ctt	ttt	gct	ctt	tct	ctt	ctg	aca	ccc	tgt	ttt		105
Ser	Cys	Ile	Ile	Val	Leu	Phe	Ala	Leu	Ser	Leu	Leu	Thr	Pro	Cys	Phe		
5					10					15					20		
gtt	tcc	tcc	tcc	gca	gtg	aga	gac	cct	gag	tta	gta	gta	caa	gaa	gta		153
Val	Ser	Ser	Ser	Ala	Val	Arg	Asp	Pro	Glu	Leu	Val	Val	Gln	Glu	Val		
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caa	aga	agc	atc	aat	gcc	tct	aga	aga	aac	ttg	ggt	tat	tta	tca	tgc		201
Gln	Arg	Ser	Ile	Asn	Ala	Ser	Arg	Arg	Asn	Leu	Gly	Tyr	Leu	Ser	Cys		
			40				45						50				
gga	aca	ggc	aac	cct	att	gac	gat	tgc	tgg	cgt	tgt	gaa	tcc	aac	tgg		249
Gly	Thr	Gly	Asn	Pro	Ile	Asp	Asp	Cys	Trp	Arg	Cys	Glu	Ser	Asn	Trp		
		55				60						65					
gag	aac	aac	cgg	caa	aga	cta	gct	gat	tgt	gca	att	ggg	ttt	ggc	aag		297
Glu	Asn	Asn	Arg	Gln	Arg	Leu	Ala	Asp	Cys	Ala	Ile	Gly	Phe	Gly	Lys		
			70			75				80							
gac	gca	ata	gga	gga	aaa	aat	ggg	cga	atc	tat	gtg	gtc	acc	gac	tcc		345
Asp	Ala	Ile	Gly	Gly	Lys	Asn	Gly	Arg	Ile	Tyr	Val	Val	Thr	Asp	Ser		
85					90					95					100		
ggc	gac	gac	gat	gcc	gtg	aac	cct	agg	cca	gga	acc	cta	agg	tac	gca		393
Gly	Asp	Asp	Asp	Ala	Val	Asn	Pro	Arg	Pro	Gly	Thr	Leu	Arg	Tyr	Ala		
				105					110					115			
gcc	ata	caa	gac	gag	cca	ttg	tgg	atc	att	ttc	aag	agg	gac	atg	gtg		441
Ala	Ile	Gln	Asp	Glu	Pro	Leu	Trp	Ile	Ile	Phe	Lys	Arg	Asp	Met	Val		
			120				125					130					
atc	acc	cta	aaa	gaa	gag	ctt	ttg	gtg	aat	tcc	ttc	aag	aca	att	gat		489
Ile	Thr	Leu	Lys	Glu	Glu	Leu	Leu	Val	Asn	Ser	Phe	Lys	Thr	Ile	Asp		
		135				140						145					
gga	agg	ggt	gct	agt	gtt	cac	att	gct	aat	ggg	gga	tgc	att	act	ata		537
Gly	Arg	Gly	Ala	Ser	Val	His	Ile	Ala	Asn	Gly	Gly	Cys	Ile	Thr	Ile		
		150				155				160							
cac	tat	gtt	agt	aac	att	att	atc	cat	ggt	att	cac	att	cat	gat	tgc		585
His	Tyr	Val	Ser	Asn	Ile	Ile	Ile	His	Gly	Ile	His	Ile	His	Asp	Cys		
165					170				175						180		
aag	ccc	acg	ggg	aat	acc	aat	att	aga	gac	tct	cca	cat					

PF59082SeqList_PF59082.txt

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Phe Trp Thr Gln Ser Asp Gly Asp Gly Val Ser Ile Phe Asn Ser Lys	
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cat att tgg gtt gat cat tgc tct ttg tct aat tgt cgt gat ggt ctc	729
His Ile Trp Val Asp His Cys Ser Leu Ser Asn Cys Arg Asp Gly Leu	
	215
att gat gcc att cat gga tcc acg gcc atc acc atc tcc aac aat tac	777
Ile Asp Ala Ile His Gly Ser Thr Ala Ile Thr Ile Ser Asn Asn Tyr	
	230
atg acc cat cat gac aag gtt atg ctt ttg ggg cac agt gat tcg tac	825
Met Thr His His Asp Lys Val Met Leu Leu Gly His Ser Asp Ser Tyr	
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act caa gac aag gac atg cag gtc act ata gca ttc aat cat ttt gga	873
Thr Gln Asp Lys Asp Met Gln Val Thr Ile Ala Phe Asn His Phe Gly	
	265
gaa ggc ctt gtc caa aga atg cca agg tgt aga cac ggg tat ttc cat	921
Glu Gly Leu Val Gln Arg Met Pro Arg Cys Arg His Gly Tyr Phe His	
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gtg gtg aac aac gac tac acc cac tgg gaa atg tat gca att ggt ggg	969
Val Val Asn Asn Asp Tyr Thr His Trp Glu Met Tyr Ala Ile Gly Gly	
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agt gca aac cct acc atc aac agc caa ggg aac agg ttc ctt gcc cca	1017
Ser Ala Asn Pro Thr Ile Asn Ser Gln Gly Asn Arg Phe Leu Ala Pro	
	310
aac atc agg ttc agc aaa gag gta acc aag cat gag gat gct cca cag	1065
Asn Ile Arg Phe Ser Lys Glu Val Thr Lys His Glu Asp Ala Pro Gln	
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agt gag tgg atg ggg tgg aat tgg agg tca gag ggt gac atg ttc ttg	1113
Ser Glu Trp Met Gly Trp Asn Trp Arg Ser Glu Gly Asp Met Phe Leu	
	345
aat gga gca tac ttc agg caa tct ggt gct ggt gcc tct tcc agc tat	1161
Asn Gly Ala Tyr Phe Arg Gln Ser Gly Ala Gly Ala Ser Ser Ser Tyr	
	360
gct agg gct tca agt ctc agt gca aga cct tct tct ctt gtt ggc tcc	1209
Ala Arg Ala Ser Ser Leu Ser Ala Arg Pro Ser Ser Leu Val Gly Ser	
	375
atg acc acc act gct ggt gca ctt acc tgt aga aag ggc aac cgt tgc	1257
Met Thr Thr Thr Ala Gly Ala Leu Thr Cys Arg Lys Gly Asn Arg Cys	
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tgatgattga tgaattaatg atgatcactt taattattat tagctaagaa atgaaatata	1317
	395
	400
tatacagctg cagggttgca aaaagaaaaa ttaatatgta tgatttatat gaattaattc	1377
accttatgct taatttgctt cccttgcagt ttactatata taatatatca ttagcctttt	1437
gctcttc	1444

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 <212> PRT
 <213> Glycine max

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 35 40 45
 Tyr Leu Ser Cys Gly Thr Gly Asn Pro Ile Asp Asp Cys Trp Arg Cys
 50 55 60
 Glu Ser Asn Trp Glu Asn Asn Arg Gln Arg Leu Ala Asp Cys Ala Ile
 65 70 75 80
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seite 1039

[illegible]

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<212> DNA
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ttcagca atg gcg gtt tct tct tct gca aca aaa tgg gtc ctc ttc ttg 169

ctt ctg g¹cg ctg ctc a⁹tt cga g¹⁰aa g¹⁰aa g¹⁰cc atg g¹⁰cc atg g¹⁰ct a¹⁰ct a¹⁰ca 217

cca cag atc tct gac ctc agg aat ctt gaa gtt gaa aga cac agg ttg 265

ccg agc ttg a⁹⁹cg aac tcg tca atg gtg g¹⁰ag agg gca aaa g¹⁰ag gct gac 313

PF59082SeqList_PF59082.txt

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atg gtt gag atg agc atc cag aac agc aca gag agg agg aag ttg gga	409			
Met Val Glu Met Ser Ile Gln Asn Ser Thr Glu Arg Arg Lys Leu Gly				
tat ttc tct tgt gga act ggc aac ccc att gat gat tgc tgg cgt tgc	457			
Tyr Phe Ser Cys Gly Thr Gln Asn Pro Ile Asp Asp Cys Trp Arg Cys				
gac ccc aac tgg caa cgc aat cgg aag cgt ctt gcg gat tgt ggc att	505			
Asp Pro Asn Trp Gln Arg Asn Arg Lys Arg Leu Ala Asp Cys Gly Ile				
ggg ttt ggc cga aac gcc atc ggt ggc cgt gat gga aaa ttc tat gtg	553			
Gly Phe Gly Arg Asn Ala Ile Gly Arg Asp Gly Lys Phe Tyr Val				
gtg act gac ccc agg gat gat gac cct gtg aac ccg aaa ccc ggc act	601			
Val Thr Asp Pro Arg Asp Asp Pro Val Asn Pro Lys Pro Gly Thr				
ctt cgc cat gct gtg atc cag gat agg ccc ttg tgg att gtg ttc aag	649			
Leu Arg His Ala Val Ile Gln Asp Arg Pro Leu Trp Ile Val Phe Lys				
agg gac atg gtt att cag ctg aaa caa gag ctg atc atg aac agc ttc	697			
Arg Asp Met Val Ile Gln Leu Lys Gln Glu Leu Ile Met Asn Ser Phe				
aag aca att gat ggt aga gga gtc aat gtg cac att gct aat gga gca	745			
Lys Thr Ile Asp Gly Arg Gly Val Asn Val His Ile Ala Asn Gly Ala				
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Cys Ile Thr Gln Phe Val Thr Asn Val Ile Ile His Gly Leu His				
att cat gat tgc aaa cct act gga aat gct atg gtg aga agc tcc cca	841			
Ile His Asp Cys Lys Pro Thr Gly Asn Ala Met Val Arg Ser Ser Pro				
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Thr His Phe Gly Trp Arg Thr Met Ala Asp Gly Asp Ala Ile Ser Ile				
ttt ggc tca agc cac att tgg gtt gac cac aac tcc ttg tca cac tgt	937			
Phe Gly Ser Ser His Ile Trp Val Asp His Asn Ser Leu Ser His Cys				
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Ala Asp Gly Leu Val Asp Ala Val Met Gly Ser Thr Ala Ile Thr Ile				
tcc aac aac cac ttc acc cac cac aat gag gtg att cta cta ggc cac	1033			
Ser Asn Asn His Phe Thr His His Asn Glu Val Ile Leu Leu Gly His				
agt gac tct tac aca aga gac aag ctg atg caa gtg acc atc gca tac	1081			
Ser Asp Ser Tyr Thr Arg Asp Lys Leu Met Gln Val Thr Ile Ala Tyr				
aac cat ttc gga gag gga ctt atc cag aga atg cca cgt tgt aga cat	1129			
Asn His Phe Gly Glu Gly Leu Ile Gln Arg Met Pro Arg Cys Arg His				
gga tat ttc cac gtg gtg aac aat gac tac act cac tgg gag atg tat	1177			
Gly Tyr Phe His Val Val Asn Asn Asp Tyr Thr His Trp Glu Met Tyr				
gct att ggt gga agt gct aac ccc acc atc aac agc cag ggc aac aga	1225			
Ala Ile Gly Gly Ser Ala Asn Pro Thr Ile Asn Ser Gln Gly Asn Arg				
tac aat gct cct act aac cct ttt gcc aag gag gtg act aag aga gtg	1273			
Tyr Asn Ala Pro Thr Asn Pro Phe Ala Lys Glu Val Thr Lys Arg Val				
gaa aca gca gaa acc caa tgg aag ggt tgg aat tgg agg tca gag gga	1321			
Glu Thr Ala Glu Thr Gln Trp Lys Gly Trp Asn Trp Arg Ser Glu Gly				
gat ttg tta ctg aat ggg gcc tat ttc act cca tct ggt gct gga gcc	1369			
Asp Leu Leu Leu Asn Gly Ala Tyr Phe Thr Pro Ser Gly Ala Gly Ala				
tca gcc agc tat gct aga gcc tct agc tta gga gca aaa tct tct tcc	1417			
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PF59082SeqList_PF59082.txt

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Gly Arg Gln Cys
          450
ccatccatta tttttctttt gtgtttgatt ctcaagtttt taccatatta tagtagaaaa      1577

tcatcatcat cgtatccatt gctttctttc ctcacacctc gattaccata tcctgcattt      1637

ttcttgacaa gtgtacatta aattacacat gtcaatatgg ttttatgttg ttaccccatt      1697

gccacattgt gtgttttggt gttggtcaac cttagctgct cgacttgctc caactgaaac      1757

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aagcttttta gccttttttt tctttttgcc cttgtcaatg caagtaatct ttgatttttt      2237

tatgcaatta tggttgtaaa tcattaaaca tatctgcttg tgtttgtttc tcttaatcaa      2297

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Ile Ser Asp Leu Arg Asn Leu Glu Val Glu Arg His Arg Leu Pro Ser
          35          40          45
Leu Thr Asn Ser Ser Met Val Glu Arg Ala Lys Glu Ala Asp Lys Leu
          50          55          60
Asn Glu Gln Ala Ala Val Ala Asn Pro Glu Glu Val Val Ser Met Val
65          70          75          80

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PF59082SeqList_PF59082.txt

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 Ser Cys Gly Thr Gly Asn Pro Ile Asp Asp Cys Trp Arg Cys Asp Pro
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 Asn Trp Gln Arg Asn Arg Lys Arg Leu Ala Asp Cys Gly Ile Gly Phe
 115 120 125
 Gly Arg Asn Ala Ile Gly Gly Arg Asp Gly Lys Phe Tyr Val Val Thr
 130 135 140
 Asp Pro Arg Asp Asp Asp Pro Val Asn Pro Lys Pro Gly Thr Leu Arg
 145 150 155 160
 His Ala Val Ile Gln Asp Arg Pro Leu Trp Ile Val Phe Lys Arg Asp
 165 170 175
 Met Val Ile Gln Leu Lys Gln Glu Leu Ile Met Asn Ser Phe Lys Thr
 180 185 190
 Ile Asp Gly Arg Gly Val Asn Val His Ile Ala Asn Gly Ala Cys Ile
 195 200 205
 Thr Ile Gln Phe Val Thr Asn Val Ile Ile His Gly Leu His Ile His
 210 215 220
 Asp Cys Lys Pro Thr Gly Asn Ala Met Val Arg Ser Ser Pro Thr His
 225 230 235 240
 Phe Gly Trp Arg Thr Met Ala Asp Gly Asp Ala Ile Ser Ile Phe Gly
 245 250 255
 Ser Ser His Ile Trp Val Asp His Asn Ser Leu Ser His Cys Ala Asp
 260 265 270
 Gly Leu Val Asp Ala Val Met Gly Ser Thr Ala Ile Thr Ile Ser Asn
 275 280 285
 Asn His Phe Thr His His Asn Glu Val Ile Leu Leu Gly His Ser Asp
 290 295 300
 Ser Tyr Thr Arg Asp Lys Leu Met Gln Val Thr Ile Ala Tyr Asn His
 305 310 315 320
 Phe Gly Glu Gly Leu Ile Gln Arg Met Pro Arg Cys Arg His Gly Tyr
 325 330 335
 Phe His Val Val Asn Asn Asp Tyr Thr His Trp Glu Met Tyr Ala Ile
 340 345 350
 Gly Gly Ser Ala Asn Pro Thr Ile Asn Ser Gln Gly Asn Arg Tyr Asn
 355 360 365
 Ala Pro Thr Asn Pro Phe Ala Lys Glu Val Thr Lys Arg Val Glu Thr
 370 375 380
 Ala Glu Thr Gln Trp Lys Gly Trp Asn Trp Arg Ser Glu Gly Asp Leu
 385 390 395 400
 Leu Leu Asn Gly Ala Tyr Phe Thr Pro Ser Gly Ala Gly Ala Ser Ala
 405 410 415
 Ser Tyr Ala Arg Ala Ser Ser Leu Gly Ala Lys Ser Ser Ser Met Val
 420 425 430
 Asp Ser Met Thr Ser Asn Ala Gly Ala Leu Gly Cys Lys Arg Gly Arg
 435 440 445
 Gln Cys
 450

<210> 825
 <211> 1577
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (19)..(1326)

<220>
 <221> misc_feature
 <222> (982)..(982)
 <223> n is a, g, c or t

<400> 825
 cggctcgcgc caatagtc atg gaa act agc aag ttc agt ttg cta ttc ttt 51
 Met Glu Thr Ser Lys Phe Ser Leu Leu Phe Phe 10
 1
 5
 10
 tac gta att tgt ctt gct ata ttc cct acc ctt aac gct aac ata ggt 99
 Tyr Val Ile Cys Leu Ala Ile Phe Pro Thr Leu Asn Ala Asn Ile Gly
 1043

PF59082SeqList_PF59082.txt

	15	20	25	
cac ttc gat cat gtc tgg cat agg cga tta aaa gaa gca aga gaa gcc	147			
His Phe Asp His Val Trp His Arg Arg Leu Lys Glu Ala Arg Glu Ala				
gca aaa caa gct tac aag ccg aac ccc atg aaa gtt acc gct gag ttc	195			
Ala Lys 30 Gln Ala Tyr Lys 35 Pro 40 Met Lys 45 Val Thr Ala Glu Phe				
aat aca cat gtc atc agg gca atg aga ggc tcc aac aac tca aga agg	243			
Asn Thr His Val Ile Arg 65 Ala Met Arg Gly Ser 70 Asn Asn Ser Arg Arg				
ggc tta tca aac caa tac gat ggt cca tgc aag gcg aca aac ccc att	291			
Gly Leu Ser Asn Gln Tyr Asp Gly Pro Cys Lys Ala Thr Asn Pro Ile				
gac aaa tgt tgg aga tgt gac ccc aat tgg gag aaa aac cgc aag agg	339			
Asp Lys Cys Trp Arg Cys Asp Pro Asn Trp Glu Lys Asn Arg Lys Arg				
cta gca gat tgt gcc cta ggc ttt ggc cat ggc aca aca ggg ggc aaa	387			
Leu Ala Asp Cys Ala Leu Gly Phe Gly His Gly Thr Thr Gly Gly Lys				
gat ggc aaa att tac gtg gtt aac gac tct tcc gac aat gac ctc gta	435			
Asp Gly 125 Lys Ile Tyr Val 130 Asn Asp Ser Ser 135 Asn Asp Leu Val				
aac cct aaa cca ggg aca ttg aga cat gct gca att caa aga gag cca	483			
Asn Pro Lys Pro Gly Thr 145 Leu Arg His Ala Ala Ile Gln Arg Glu Pro				
ctg tgg atc att ttt gat cga aac atg aac att aaa ctt cac gcg gag	531			
Leu Trp Ile Ile Phe Asp Arg Asn Met Asn Ile Lys Leu His Ala Glu				
ctc atg cta acg gat aat aag acc ata gat gca cgt ggt gcc aat gtg	579			
Leu Met Leu Thr 175 Asp Asn Lys Thr 180 Asp Ala Arg Gly Ala Asn Val				
cac att agt gag ggt gcc caa ata acg ttg caa tat gtg aaa aac atc	627			
His Ile Ser Glu Gly Ala Gln Ile Thr Leu Gln Tyr Val 200 Lys Asn Ile				
atc att cac ggt ctg cac att cat gac att aag aaa tgt agt ggt ggc	675			
Ile Ile 205 His Gly Leu His Ile 210 His Asp Ile Lys 215 Cys Ser Gly Gly				
ctc atc aga gac tcc atg gat cac tat gga gtc cgt gcc atg agt gat	723			
Leu Ile Arg Asp Ser Met 225 Asp His Tyr Gly Val 230 Arg Ala Met Ser Asp				
ggg gat gcc att tcg gtg ttt gga tcc aca tat gtt tgg ata gat cat	771			
Gly Asp Ala Ile Ser Val Phe Gly Ser Thr Tyr Val Trp Ile Asp His				
gtt tcc ttt acc aac tgc gat gac ggc ctc atc gat gtc gtt agc gct	819			
Val Ser Phe 255 Asn Cys Asp Asp Gly Leu Ile Asp Val Val Ser Ala				
tca act gct gtt acc atc tcc aac tgc cat ctt acc aaa cat aac gat	867			
Ser Thr 270 Ala Val Thr Ile Ser Asn Cys His Leu Thr 280 Lys His Asn Asp				
gta tta tta ttt ggt gcg agt gat agc tac tcg ggg gat aaa atc atg	915			
Val Leu Leu Phe Gly Ala Ser Asp Ser Tyr Ser Gly Asp Lys Ile Met				
caa gtg act ttg gct ttc aac cat ttc ggg aaa gga ttg att cag agg	963			
Gln Val Thr Leu Ala Phe 305 Asn His Phe Gly Lys 310 Gly Leu Ile Gln Arg				
atg cca agg tgc aga tgg ngc ttc ttt cat att gtt aac aat gac tac	1011			
Met Pro Arg Cys Arg Trp Xaa Phe Phe His Ile Val Asn Asn Asp Tyr				
acg cat tgg cta atg tac gcc ata ggt ggt agc caa caa ccc acc atc	1059			
Thr His Trp 335 Met Tyr Ala Ile 340 Gly Ser Gln Gln 345 Pro Thr Ile				
atc agc cag ggc aac ggg ttt atc gcc cca aat gac cga aat gcc aaa	1107			
Ile Ser 350 Gln Gly Asn Gly Phe 355 Ile Ala Pro Asn Asp 360 Arg Asn Ala Lys				
gaa gtg aca aaa agg gac tat gca cca gaa agt gtg tgg aag aac tgg	1155			
Glu Val Thr Lys Arg Asp Tyr 370 Ala Pro Glu Ser Val Trp Lys Asn Trp				
aat tgg aga tca gag ggt gat tta ttg atg aat gga gcc ttc ttt gtt	1203			
Asn Trp Arg Ser Glu Gly Asp Leu Leu Met Asn Gly Ala Phe Phe Val				

PF59082SeqList_PF59082.txt

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380          385          390          395
cag tct ggg aaa aac gta gca aaa aat ccc aag gca gaa atc ata gca      1251
Gln Ser Gly Lys Asn Val Ala Lys Asn Pro Lys Ala Glu Ile Ile Ala
          400          405          410
aag cct ggg aaa gcc gta tcg agt ctc act cgc ttt gca ggt cct cta      1299
Lys Pro Gly Lys Ala Val Ser Ser Leu Thr Arg Phe Ala Gly Pro Leu
          415          420          425
aaa tgt gaa gta aac aag tcg tgt tgaaccaaataaagagcttc gtttgtggtt      1353
Lys Cys Glu Val Asn Lys Ser Cys
          430          435
gtaacataaaa taagtcgtgt acatatcaaaa cccgaagtga atgcttccgt ggttttttaa      1413

ttccttttcc tcgctttggt cttccttttc ccttggatta tatgatttga gggatctgag      1473

gcaaagaaaa tagtagaact aagatgtact ccactgtct ttaattataa gacttaattt      1533

attaatttaa catttattaa aaaaaaaaaa aaaaaaaaaa atag      1577

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<210> 826
<211> 435
<212> PRT
<213> Glycine max

<220>
<221> misc_feature
<222> (322)..(322)
<223> The Xaa at location 322 stands for Arg, Cys, Gly, or Ser.

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<400> 826
Met Glu Thr Ser Lys Phe Ser Leu Leu Phe Phe Tyr Val Ile Cys Leu
1          5          10          15
Ala Ile Phe Pro Thr Leu Asn Ala Asn Ile Gly His Phe Asp His Val
          20          25          30
Trp His Arg Arg Leu Lys Glu Ala Arg Glu Ala Ala Lys Gln Ala Tyr
          35          40          45
Lys Pro Asn Pro Met Lys Val Thr Ala Glu Phe Asn Thr His Val Ile
          50          55          60
Arg Ala Met Arg Gly Ser Asn Asn Ser Arg Arg Gly Leu Ser Asn Gln
65          70          75          80
Tyr Asp Gly Pro Cys Lys Ala Thr Asn Pro Ile Asp Lys Cys Trp Arg
          85          90          95
Cys Asp Pro Asn Trp Glu Lys Asn Arg Lys Arg Leu Ala Asp Cys Ala
          100          105          110
Leu Gly Phe Gly His Gly Thr Thr Gly Gly Lys Asp Gly Lys Ile Tyr
          115          120          125
Val Val Asn Asp Ser Ser Asp Asn Asp Leu Val Asn Pro Lys Pro Gly
          130          135          140
Thr Leu Arg His Ala Ala Ile Gln Arg Glu Pro Leu Trp Ile Ile Phe
145          150          155          160
Asp Arg Asn Met Asn Ile Lys Leu His Ala Glu Leu Met Leu Thr Asp
          165          170          175
Asn Lys Thr Ile Asp Ala Arg Gly Ala Asn Val His Ile Ser Glu Gly
          180          185          190
Ala Gln Ile Thr Leu Gln Tyr Val Lys Asn Ile Ile Ile His Gly Leu
          195          200          205
His Ile His Asp Ile Lys Lys Cys Ser Gly Gly Leu Ile Arg Asp Ser
          210          215          220
Met Asp His Tyr Gly Val Arg Ala Met Ser Asp Gly Asp Ala Ile Ser
225          230          235          240
Val Phe Gly Ser Thr Tyr Val Trp Ile Asp His Val Ser Phe Thr Asn
          245          250          255
Cys Asp Asp Gly Leu Ile Asp Val Val Ser Ala Ser Thr Ala Val Thr
          260          265          270
Ile Ser Asn Cys His Leu Thr Lys His Asn Asp Val Leu Leu Phe Gly

```

PF59082SeqList_PF59082.txt

275 280 285
 Ala Ser Asp Ser Tyr Ser Gly Asp Lys Ile Met Gln Val Thr Leu Ala
 290 295 300
 Phe Asn His Phe Gly Lys Gly Leu Ile Gln Arg Met Pro Arg Cys Arg
 305 310 315
 Trp Xaa Phe Phe His Ile Val Asn Asn Asp Tyr Thr His Trp Leu Met
 325 330 335
 Tyr Ala Ile Gly Gly Ser Gln Gln Pro Thr Ile Ile Ser Gln Gly Asn
 340 345 350
 Gly Phe Ile Ala Pro Asn Asp Arg Asn Ala Lys Glu Val Thr Lys Arg
 355 360 365
 Asp Tyr Ala Pro Glu Ser Val Trp Lys Asn Trp Asn Trp Arg Ser Glu
 370 375 380
 Gly Asp Leu Leu Met Asn Gly Ala Phe Phe Val Gln Ser Gly Lys Asn
 385 390 395
 Val Ala Lys Asn Pro Lys Ala Glu Ile Ile Ala Lys Pro Gly Lys Ala
 400 405 410 415
 Val Ser Ser Leu Thr Arg Phe Ala Gly Pro Leu Lys Cys Glu Val Asn
 420 425 430
 Lys Ser Cys
 435

<210> 827
 <211> 1847
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (73)..(1272)

<400> 827
 gctcctctct tcctttctct ctcgccgcag gcgggcagtt cgagagggcg tgcgttgctc

60

gaggggcggt aa atg gca gcg gcg acg acg agg ggc agg gcc gac ggt gac
 Met Ala Ala Ala Thr Thr Arg Gly Arg Ala Asp Gly Asp

111

1 5 10
 gcc ggc gcc ggc gcg gtg gta gat ccg gaa gcc gtg gcc aac gac gtc
 Ala Gly Ala Gly Ala Val Val Asp Pro Glu Ala Val Ala Asn Asp Val

159

15 20 25
 cac gcg tcc atc aac aac atc acg gcc cgg cga aat ctc ggg tac ctg
 His Ala Ser Ile Asn Asn Ile Thr Ala Arg Arg Asn Leu Gly Tyr Leu

207

30 35 40
 tcg tgc ggg aca ggc aac ccc atc gac gac tgc tgg cgc tgc gac tcg
 Ser Cys Gly Thr Gly Asn Pro Ile Asp Asp Cys Trp Arg Cys Asp Ser

255

50 55 60
 gac tgg cac aac aac cgg aag cgc ctc gcc gac tgt ggc acg gcc ggc
 Asp Trp His Asn Asn Arg Lys Arg Leu Ala Asp Cys Gly Thr Ala Gly

303

65 70 75
 gtg ggc aag ccg gag tgg tta tcg gac ggc aag gtg tac gtg gtg acc
 Val Gly Lys Pro Glu Trp Leu Ser Asp Gly Lys Val Tyr Val Val Thr

351

80 85 90
 gac ccg agc gac gac gac ccc gtg aac ccg cgc gag ggc acc ctc cgc
 Asp Pro Ser Asp Asp Asp Pro Val Asn Pro Arg Glu Gly Thr Leu Arg

399

95 100 105
 cac gcc gtc atc cag gag gag ccg ctg tgg atc atc ttc aag cgg gac
 His Ala Val Ile Gln Glu Glu Pro Leu Trp Ile Ile Phe Lys Arg Asp

447

110 115 120
 atg gtg atc acg ctc agg gag gag ctc atc atg aac agc ttc aag acc
 Met Val Ile Thr Leu Arg Glu Glu Leu Ile Met Asn Ser Phe Lys Thr

495

130 135 140
 atc gac gga cgc ggc gcc aac gtg cac atc gcc aat ggt gcc tgc atc
 Ile Asp Gly Arg Gly Ala Asn Val His Ile Ala Asn Gly Ala Cys Ile

543

145 150 155
 acc atc cag tac atc acc aac gtc atc atc cac ggg ctc cac atc cac
 Thr Ile Gln Tyr Ile Thr Asn Val Ile Ile His Gly Leu His Ile His

591

160 165 170
 gac tgc agg ccc acg ggg aac gcc atg gtg cgc agc tcc ccg agc cac

639

PF59082SeqList_PF59082.txt

Asp	Cys	Arg	Pro	Thr	Gly	Asn	Ala	Met	Val	Arg	Ser	Ser	Pro	Ser	His	
175	185					180				185						
tac	ggc	tgg	cgc	acc	atg	gcc	gac	ggg	gac	ggc	gtg	tcc	atc	ttc	ggt	687
Tyr	Gly	Trp	Arg	Thr	Met	Ala	Asp	Gly	Asp	Gly	Val	Ser	Ile	Phe	Gly	
190					195					200					205	
tcc	agc	cac	gtc	tgg	gtg	gac	cac	tgc	tcg	ctc	tcc	aac	tgc	gcc	gac	735
Ser	Ser	His	Val	Trp	Val	Asp	His	Cys	Ser	Leu	Ser	Asn	Cys	Ala	Asp	
				210					215					220		
ggc	ctc	atc	gac	gcc	atc	atg	gga	tcc	acg	gcc	atc	act	ctg	tcc	aac	783
Gly	Leu	Ile	Asp	Ala	Ile	Met	Gly	Ser	Thr	Ala	Ile	Thr	Leu	Ser	Asn	
			225					230					235			
aac	tac	ttc	acc	cac	cac	aac	gag	gtg	atg	ctc	ctg	ggc	cac	agt	gac	831
Asn	Tyr	Phe	Thr	His	His	Asn	Glu	Val	Met	Leu	Leu	Gly	His	Ser	Asp	
		240					245					250				
tcc	tat	gtg	aag	gac	aag	gcg	atg	cag	gtc	acg	ata	gcc	ttc	aac	cat	879
Ser	Tyr	Val	Lys	Asp	Lys	Met	Met	Gln	Val	Thr	Ile	Ala	Phe	Asn	His	
	255					260					265					
ttc	ggc	gaa	ggc	ctc	att	cag	aga	atg	cca	agg	tgc	cgg	cac	ggc	tac	927
Phe	Gly	Glu	Gly	Leu	Ile	Gln	Arg	Met	Pro	Arg	Cys	Arg	His	Gly	Tyr	
270					275					280					285	
ttc	cac	gtt	gtg	aac	aac	gac	tac	acc	cac	tgg	gag	atg	tac	gcc	att	975
Phe	His	Val	Val	Asn	Asn	Asp	Tyr	Thr	His	Trp	Glu	Met	Tyr	Ala	Ile	
				290					295					300		
ggg	ggc	agc	gcg	gag	cca	acc	atc	aac	agc	cag	ggc	aac	cgc	tac	ctt	1023
Gly	Gly	Ser	Ala	Glu	Pro	Thr	Ile	Asn	Ser	Gln	Gly	Asn	Arg	Tyr	Leu	
			305					310					315			
gct	ccg	acg	aac	ccg	ttc	gcc	aag	gag	gtg	acc	aag	agg	gtg	gag	act	1071
Ala	Pro	Thr	Asn	Pro	Phe	Ala	Lys	Glu	Val	Thr	Lys	Arg	Val	Glu	Thr	
			320				325					330				
gcc	cag	acc	gtg	tgg	aag	agc	tgg	aac	tgg	agg	tca	gag	ggc	gac	ctg	1119
Ala	Gln	Thr	Val	Trp	Lys	Ser	Trp	Asn	Trp	Arg	Ser	Glu	Gly	Asp	Leu	
	335					340					345					
ctg	ctg	aac	ggc	gcc	tac	ttc	acc	ccg	tcc	ggc	gag	ggc	ggc	tcg	gcc	1167
Leu	Leu	Asn	Gly	Ala	Tyr	Phe	Thr	Pro	Ser	Gly	Ala	Gly	Ala	Ser	Ala	
350					355					360					365	
agc	tac	tcg	cgc	gcg	tcc	agc	ctc	ggc	gcc	aag	tcg	tcg	tcc	atg	gtc	1215
Ser	Tyr	Ser	Arg	Ala	Ser	Ser	Leu	Gly	Ala	Lys	Ser	Ser	Ser	Met	Val	
				370					375					380		
ggc	acc	atc	acc	tcg	gac	gcc	ggc	gca	ctg	tcg	tgc	cgc	aag	ggc	gcg	1263
Gly	Thr	Ile	Thr	Ser	Asp	Ala	Gly	Ala	Leu	Ser	Cys	Arg	Lys	Gly	Ala	
			385				390						395			
gcc	tgc	tagcgcgat	cgcgctccct	ctccagcaac	aggaaaagaa	acaggacaac										1319
Ala	Cys															
aggaaactaa	gccacctcaa	caccaccacc	accatgggta	cagtttcttc	ttcccttctt											1379
tttaggggtc	gcttttgaca	agggttatat	tatatatata	tatgatgggc	ctccttgata											1439
ttttcaccat	ttgctcaacc	tccccctgc	tcccgacatg	gaaagctacc	tggagcagca											1499
ggcgtgaagc	gttgctgatt	ggtcgctcgg	tctctctatt	agtcgtctga	tctgagtgtt											1559
gcgtgttggt	ccctctgcct	acaagcaagt	ggtgtatggt	gagggcaggg	ggtgcgtgcg											1619
tgcggtgtgt	gtgtgatact	tactcacttg	gttggtgtgt	tgagaaaaaa	agggtcagat											1679
tgtagtagt	ggtagtacta	catgttacgc	ctggacagac	tgggatggaa	tggatgtaca											1739
agacatggag	gaatacccat	gttcttaact	cttcttcttc	ttcagtgaag	aaagctaaaa											1799
cgttacagtt	tagctgaata	ttttgatcta	aaaaaaaaaa	aaaaaaaa												1847

PF59082SeqList_PF59082.txt

<210> 828
 <211> 399
 <212> PRT
 <213> Zea mays

<400> 828
 Met Ala Ala Ala Thr Thr Arg Gly Arg Ala Asp Gly Asp Ala Gly Ala
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 Gly Ala Val Val Asp Pro Glu Ala Val Ala Asn Asp Val His Ala Ser
 20 25 30
 Ile Asn Asn Ile Thr Ala Arg Arg Asn Leu Gly Tyr Leu Ser Cys Gly
 35 40 45
 Thr Gly Asn Pro Ile Asp Asp Cys Trp Arg Cys Asp Ser Asp Trp His
 50 55 60
 Asn Asn Arg Lys Arg Leu Ala Asp Cys Gly Thr Ala Gly Val Gly Lys
 65 70 75 80
 Pro Glu Trp Leu Ser Asp Gly Lys Val Tyr Val Val Thr Asp Pro Ser
 85 90 95
 Asp Asp Asp Pro Val Asn Pro Arg Glu Gly Thr Leu Arg His Ala Val
 100 105 110
 Ile Gln Glu Glu Pro Leu Trp Ile Ile Phe Lys Arg Asp Met Val Ile
 115 120 125
 Thr Leu Arg Glu Glu Leu Ile Met Asn Ser Phe Lys Thr Ile Asp Gly
 130 135 140
 Arg Gly Ala Asn Val His Ile Ala Asn Gly Ala Cys Ile Thr Ile Gln
 145 150 155 160
 Tyr Ile Thr Asn Val Ile Ile His Gly Leu His Ile His Asp Cys Arg
 165 170 175
 Pro Thr Gly Asn Ala Met Val Arg Ser Ser Pro Ser His Tyr Gly Trp
 180 185 190
 Arg Thr Met Ala Asp Gly Asp Gly Val Ser Ile Phe Gly Ser Ser His
 195 200 205
 Val Trp Val Asp His Cys Ser Leu Ser Asn Cys Ala Asp Gly Leu Ile
 210 215 220
 Asp Ala Ile Met Gly Ser Thr Ala Ile Thr Leu Ser Asn Asn Tyr Phe
 225 230 235 240
 Thr His His Asn Glu Val Met Leu Leu Gly His Ser Asp Ser Tyr Val
 245 250 255
 Lys Asp Lys Ala Met Gln Val Thr Ile Ala Phe Asn His Phe Gly Glu
 260 265 270
 Gly Leu Ile Gln Arg Met Pro Arg Cys Arg His Gly Tyr Phe His Val
 275 280 285
 Val Asn Asn Asp Tyr Thr His Trp Glu Met Tyr Ala Ile Gly Gly Ser
 290 295 300
 Ala Glu Pro Thr Ile Asn Ser Gln Gly Asn Arg Tyr Leu Ala Pro Thr
 305 310 315 320
 Asn Pro Phe Ala Lys Glu Val Thr Lys Arg Val Glu Thr Ala Gln Thr
 325 330 335
 Val Trp Lys Ser Trp Asn Trp Arg Ser Glu Gly Asp Leu Leu Leu Asn
 340 345 350
 Gly Ala Tyr Phe Thr Pro Ser Gly Ala Gly Ala Ser Ala Ser Tyr Ser
 355 360 365
 Arg Ala Ser Ser Leu Gly Ala Lys Ser Ser Ser Met Val Gly Thr Ile
 370 375 380
 Thr Ser Asp Ala Gly Ala Leu Ser Cys Arg Lys Gly Ala Ala Cys
 385 390 395

<210> 829
 <211> 1401
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (1)..(1401)

PF59082SeqList_PF59082.txt

<400> 829

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Met Ala Ala Ala Gly Ser Ser Ala Ala Arg Ala Arg Arg Ala Gly Leu	
1 5 10 15	
gca gcc gcc gcc gcc gcg gcg ctc ctc gtc ctc gtg gtg gtc gcc gtc	96
Ala Ala Ala Ala Ala Ala Leu Leu Val Leu Val Val Val Ala Val	
20 25 30	
agc gcg gcg ctc cct ggc ggg cgg gtg agg gtc ctc gac ggc ctt cgg	144
Ser Ala Ala Leu Pro Gly Gly Arg Val Arg Val Leu Asp Gly Leu Arg	
35 40 45	
caa agg agc acg tcc gtg gtg gcg gga ggc gcg agg cgg tgg ctg cgg	192
Gln Arg Ser Thr Ser Val Val Ala Gly Gly Ala Arg Arg Trp Leu Arg	
50 55 60	
gac tcc tcc ttg ccg gcg gcg acg acg agg ggc agg gcc gac ggt gac	240
Asp Ser Ser Leu Pro Ala Ala Thr Thr Arg Gly Arg Ala Asp Gly Asp	
65 70 75 80	
gcc ggc gcc ggc gcg gtg gag gat ccg gaa gcc gtg gcc aac gac gtc	288
Ala Gly Ala Gly Ala Val Glu Asp Pro Glu Ala Val Ala Asn Asp Val	
85 90 95	
cac gcg tcc atc aac aac atc acg gcc cgg cga aat ctc ggg tac ctg	336
His Ala Ser Ile Asn Asn Ile Thr Ala Arg Arg Asn Leu Gly Tyr Leu	
100 105 110	
tcg tgc ggg aca ggc aac ccc atc gac gac tgc tgg cgc tgc gac tcg	384
Ser Cys Gly Thr Gly Asn Pro Ile Asp Asp Cys Trp Arg Cys Asp Ser	
115 120 125	
gac tgg cac aac aac ccg aag gcg ctc gcc gac tgt ggc atc ggc ttt	432
Asp Trp His Asn Asn Arg Lys Arg Leu Ala Asp Cys Gly Ile Gly Phe	
130 135 140	
ggc cgc aac gcc atc ggc ggc cgt gac ggc aag atc tac gtg gtc acc	480
Gly Arg Asn Ala Ile Gly Gly Arg Asp Gly Ile Tyr Val Val Thr	
145 150 155 160	
gac ccg agc gat gac gac cct gtc aac ccg cgc aag ggc acc ctc cgc	528
Asp Pro Ser Asp Asp Asp Pro Val Asn Pro Arg Lys Gly Thr Leu Arg	
165 170 175	
tac gcc gtc atc cag gaa gag ccg ctc ttg atc atc ttc aag cgg gac	576
Tyr Ala Val Ile Gln Glu Glu Pro Leu Trp Ile Ile Phe Lys Arg Asp	
180 185 190	
atg gtc atc acg ctc aag gag gag ctc atc atg aac agc ttc aag acc	624
Met Val Ile Thr Leu Lys Glu Glu Leu Ile Met Asn Ser Phe Lys Thr	
195 200 205	
atc gac gga cgc ggc gcc aac gtg cac atc gcc aat ggt gcc tgc atc	672
Ile Asp Gly Arg Gly Ala Asn Val His Ile Ala Asn Gly Ala Cys Ile	
210 215 220	
acc atc cag tac atc acc aac gtc atc atc cac ggg ctc cac atc cac	720
Thr Ile Gln Tyr Ile Thr Asn Val Ile Ile His Gly Leu His Ile His	
225 230 235 240	
gac tgc aag ccc acg ggc aac gcc atg gtg cgc agc tcg ccc agc cac	768
Asp Cys Lys Pro Thr Gly Asn Ala Met Val Arg Ser Ser Pro Ser His	
245 250 255	
tat ggg tgg cgc acc atg gcc gac gga gat ggt gtg tcc atc ttc ggt	816
Tyr Gly Trp Arg Thr Met Ala Asp Gly Asp Gly Val Ser Ile Phe Gly	
260 265 270	
tcc agc cac gtc tgg gtg gac cac tgc tcg ctc tcc aac tgc gcc gac	864
Ser Ser His Val Trp Val Asp His Cys Ser Leu Ser Asn Cys Ala Asp	
275 280 285	
ggc ctg atc gat gct atc atg gga tcc acg gct atc aca gtg tcc aac	912
Gly Leu Ile Asp Ala Ile Met Gly Ser Thr Ala Ile Thr Val Ser Asn	
290 295 300	
aac tac ttc acc cac cac aac gag gtg atg ctc ctg ggc cac agt gac	960
Asn Tyr Phe Thr His Asn Glu Val Met Leu Leu Gly His Ser Asp	
305 310 315 320	
tcc tat gtg aag gac aag gca atg cag gtg acg ata gcc ttc aac cat	1008
Ser Tyr Val Lys Asp Lys Ala Met Gln Val Thr Ile Ala Phe Asn His	
325 330 335	
ttc ggt gaa ggt ctc atc cag aga atg cca agg tgc cgg cat ggc tac	1056
Phe Gly Glu Gly Leu Ile Gln Arg Met Pro Arg Cys Arg His Gly Tyr	
340 345 350	
ttc cat gtt gtg aac aac gac tac acc cac tgg gaa atg tac gcc att	1104
Phe His Val Val Asn Asn Asp Tyr Thr His Trp Glu Met Tyr Ala Ile	

PF59082SeqList_PF59082.txt

ggc	ggg	agc	gct	gag	cca	acc	atc	aac	agc	cag	ggc	aac	cgc	tac	ctt	1152
Gly	Gly	Ser	Ala	Glu	Pro	Thr	Ile	Asn	Ser	Gln	Gly	Asn	Arg	Tyr	Leu	
	370					375				380						
gct	ccc	aca	aac	ccg	ttc	gcc	aag	gag	gtg	acc	aag	agg	gtc	gaa	act	1200
Ala	Pro	Thr	Asn	Pro	Phe	Ala	Lys	Glu	Val	Thr	Lys	Arg	Val	Glu	Thr	
385					390					395					400	
gct	cac	act	gtc	tgg	aag	agg	tgg	aac	tgg	aga	tca	gag	ggg	gac	ctc	1248
Ala	His	Thr	Val	Trp	Lys	Arg	Trp	Asn	Trp	Arg	Ser	Glu	Gly	Asp	Leu	
				405					410					415		
ctg	ctg	aac	ggc	gcc	tac	ttc	acc	ccc	tcc	ggc	gcg	ggc	gcc	tca	gcc	1296
Leu	Leu	Asn	Gly	Ala	Tyr	Phe	Thr	Pro	Ser	Gly	Ala	Gly	Ala	Ser	Ala	
			420					425					430			
agc	tac	tgc	cgc	gcg	tcc	agc	ctt	ggc	gcc	aag	tca	tca	tct	atg	gtc	1344
Ser	Tyr		Ser	Arg	Ala	Ser	Ser	Leu	Gly	Ala	Lys	Ser	Ser	Met	Val	
		435					440					445				
ggc	acc	atc	acc	ctg	gat	gcc	ggg	gcc	ctg	tcg	tgc	cac	aag	ggc	gcg	1392
Gly	Thr	Ile	Thr	Leu	Asp	Ala	Gly	Ala	Leu	Ser	Cys	His	Lys	Gly	Ala	
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ccc	tgc	tag														1401
Pro	Cys															
465																

<210> 830
 <211> 466
 <212> PRT
 <213> Zea mays

<400> 830

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Ala	Ala	Ala	Ala	Ala	Ala	Ala	Leu	Leu	Val	Leu	Val	Val	Val	Ala	Val
			20					25					30		
Ser	Ala	Ala	Leu	Pro	Gly	Gly	Arg	Val	Arg	Val	Leu	Asp	Gly	Leu	Arg
		35					40					45			
Gln	Arg	Ser	Thr	Ser	Val	Val	Ala	Gly	Gly	Ala	Arg	Arg	Trp	Leu	Arg
	50					55				60					
Asp	Ser	Ser	Leu	Pro	Ala	Ala	Thr	Thr	Arg	Gly	Arg	Ala	Asp	Gly	Asp
65					70				75					80	
Ala	Gly	Ala	Gly	Ala	Val	Glu	Asp	Pro	Glu	Ala	Val	Ala	Asn	Asp	Val
			85						90				95		
His	Ala	Ser	Ile	Asn	Asn	Ile	Thr	Ala	Arg	Arg	Asn	Leu	Gly	Tyr	Leu
			100					105					110		
Ser	Cys	Gly	Thr	Gly	Asn	Pro	Ile	Asp	Asp	Cys	Trp	Arg	Cys	Asp	Ser
		115					120					125			
Asp	Trp	His	Asn	Asn	Arg	Lys	Arg	Leu	Ala	Asp	Cys	Gly	Ile	Gly	Phe
	130					135					140				
Gly	Arg	Asn	Ala	Ile	Gly	Gly	Arg	Asp	Gly	Lys	Ile	Tyr	Val	Val	Thr
145					150				155						160
Asp	Pro	Ser	Asp	Asp	Asp	Pro	Val	Asn	Pro	Arg	Lys	Gly	Thr	Leu	Arg
			165						170					175	
Tyr	Ala	Val	Ile	Gln	Glu	Glu	Pro	Leu	Trp	Ile	Ile	Phe	Lys	Arg	Asp
			180					185					190		
Met	Val	Ile	Thr	Leu	Lys	Glu	Glu	Leu	Ile	Met	Asn	Ser	Phe	Lys	Thr
		195					200					205			
Ile	Asp	Gly	Arg	Gly	Ala	Asn	Val	His	Ile	Ala	Asn	Gly	Ala	Cys	Ile
	210					215					220				
Thr	Ile	Gln	Tyr	Ile	Thr	Asn	Val	Ile	Ile	His	Gly	Leu	His	Ile	His
225					230				235						240
Asp	Cys	Lys	Pro	Thr	Gly	Asn	Ala	Met	Val	Arg	Ser	Ser	Pro	Ser	His
			245						250					255	
Tyr	Gly	Trp	Arg	Thr	Met	Ala	Asp	Gly	Asp	Gly	Val	Ser	Ile	Phe	Gly
			260					265					270		
Ser	Ser	His	Val	Trp	Val	Asp	His	Cys	Ser	Leu	Ser	Asn	Cys	Ala	Asp
		275					280					285			
Gly	Leu	Ile	Asp	Ala	Ile	Met	Gly	Ser	Thr	Ala	Ile	Thr	Val	Ser	Asn
	290					295					300				
Asn	Tyr	Phe	Thr	His	His	Asn	Glu	Val	Met	Leu	Gly	His	Ser	Asp	
305					310				315					320	

PF59082SeqList_PF59082.txt

Ser Tyr Val Lys Asp Lys Ala Met Gln Val Thr Ile Ala Phe Asn His
 325 330 335
 Phe Gly Glu Gly Leu Ile Gln Arg Met Pro Arg Cys Arg His Gly Tyr
 340 345 350
 Phe His Val Val Asn Asn Asp Tyr Thr His Trp Glu Met Tyr Ala Ile
 355 360 365
 Gly Gly Ser Ala Glu Pro Thr Ile Asn Ser Gln Gly Asn Arg Tyr Leu
 370 375 380
 Ala Pro Thr Asn Pro Phe Ala Lys Glu Val Thr Lys Arg Val Glu Thr
 385 390 400
 Ala His Thr Val Trp Lys Arg Trp Asn Trp Arg Ser Glu Gly Asp Leu
 405 410 415
 Leu Leu Asn Gly Ala Tyr Phe Thr Pro Ser Gly Ala Gly Ala Ser Ala
 420 425 430
 Ser Tyr Ser Arg Ala Ser Ser Leu Gly Ala Lys Ser Ser Met Val
 435 440 445
 Gly Thr Ile Thr Leu Asp Ala Gly Ala Leu Ser Cys His Lys Gly Ala
 450 455 460
 Pro Cys
 465

<210> 831
 <211> 1440
 <212> DNA
 <213> Zinnia elegans

<220>
 <221> CDS
 <222> (28)..(1233)

<400> 831
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 Met Ala Thr Thr Ile Leu Pro Leu Ile

54

ctc ttt ata tct tca cta gcc att gct tct tca tca cca agt aga acc
 1 5
 Leu Phe Ile Ser Ser Leu Ala Ile Ala Ser Ser Ser Pro Ser Arg Thr
 10 15 20 25
 cca cat gcc ata gtc aat gaa gtc cac aag agc atc aat gct tcc cgt
 Pro His Ala Ile Val Asn Glu Val His Lys Ser Ile Asn Ala Ser Arg
 30 35 40
 aga aac ttg ggt tac ctg tct tgt ggg aca ggt aac cca att gat gat
 Arg Asn Leu Gly Tyr Leu Ser Cys Gly Thr Gly Asn Pro Ile Asp Asp
 45 50 55
 tgc tgg cgg tgt gac cct aac tgg gcc aat aac cgc cag cgt ctt gct
 Cys Trp Arg Cys Asp Pro Asn Trp Ala Asn Asn Arg Gln Arg Leu Ala
 60 65 70
 gac tgt gcc att ggg ttt gga aag aac gcg atg ggt ggg cga aat gga
 Asp Cys Ala Ile Gly Phe Gly Lys Asn Ala Met Gly Gly Arg Asn Gly
 75 80 85
 agg ata tat gtt gtc act gat ccc ggg aat gat cca gtg aac cct
 Arg Ile Tyr Val Val Thr Asp Pro Gly Asn Asp Asp Pro Val Asn Pro
 90 95 100 105
 gtt ccc ggg acc ctg aga tat gcg gtt att caa gat gaa ccg ttg tgg
 Val Pro Gly Thr Leu Arg Tyr Ala Val Ile Gln Asp Glu Pro Leu Trp
 110 115 120
 atc atc ttt aaa cgc gac atg gta att caa cta cgg caa gaa ctt gtg
 Ile Ile Phe Lys Arg Asp Met Val Ile Gln Leu Arg Gln Glu Leu Val
 125 130 135
 atg aat tct cac aag acc ata gat ggt agg ggt gtg aat gtg cat att
 Met Asn Ser His Lys Thr Ile Asp Gly Arg Gly Val Asn Val His Ile
 140 145 150
 ggt aat ggc cca tgc att act ata cat tat gct agt aat att att ata
 Gly Asn Gly Pro Cys Ile Thr Ile His Tyr Ala Ser Asn Ile Ile Ile
 155 160 165
 cat ggt att cat ata cat gat tgt aag cag gct aat ggt aac att
 His Gly Ile His Ile His Asp Cys Lys Gln Ala Gly Asn Gly Asn Ile
 170 175 180 185
 aga aac tca cca cat cat agt gga tgg tgg aca caa tct gat ggt gat
 Arg Asn Ser Pro His His Ser Gly Trp Trp Thr Ser Asp Gly Asp

102

150

198

246

294

342

390

438

486

534

582

630

PF59082SeqList_PF59082.txt

190	195	200	
ggg ata tcc att ttt gct agc aaa gat ata tgg att gat cat aat tct			678
Gly Ile Ser Ile Phe Ala Ser Lys Asp Ile Trp Ile Asp His Asn Ser			
205	210	215	
ttg tct aat tgt cat gat ggg ctc att gat gcc ata cat gga tct act			726
Leu Ser Asn Cys His Asp Gly Leu Ile Asp Ala Ile His Gly Ser Thr			
220	225	230	
gcc atc act att tct aac aat tac atg act cat cat gat aaa gtt atg			774
Ala Ile Thr Ile Ser Asn Asn Tyr Met Thr His His Asp Lys Val Met			
235	240	245	
ttg tta gga cat agt gat agt tat act caa gat aag aac atg caa gtt			822
Leu Leu Gly His Ser Asp Ser Tyr Thr Gln Asp Lys Asn Met Gln Val			
250	255	260	
act att gca ttt aac cat ttt ggt gaa ggt ctt gtt caa aga atg cca			870
Thr Ile Ala Phe Asn His Phe Gly Glu Gly Leu Val Gln Arg Met Pro			
270	275	280	
aga tgt aga cat ggg tat ttc cat gtg gtg aac aat gac tat aca cat			918
Arg Cys Arg His Gly Tyr Phe His Val Val Asn Asn Asp Tyr Thr His			
285	290	295	
tggt gag atg tat gct att gga gga agt gca tct cct acc atc tat agc			966
Trp Glu Met Tyr Ala Ile Gly Gly Ser Ala Ser Pro Thr Ile Tyr Ser			
300	305	310	
caa ggc aat aga ttt ttg gct ccc aat aca aga ttt gac aag gag gtg			1014
Gln Gly Asn Arg Phe Leu Ala Pro Asn Thr Arg Phe Asp Lys Glu Val			
315	320	325	
aca aaa cat gag aat gca ccc gaa agt gaa tgg aag aac tgg aat tgg			1062
Thr Lys His Glu Asn Ala Pro Glu Ser Glu Trp Lys Asn Trp Asn Trp			
330	335	340	
aga tca gaa gga gat ttg atg tta aac ggt gct tat ttt aga gaa tca			1110
Arg Ser Glu Gly Asp Leu Met Leu Asn Gly Ala Tyr Phe Arg Glu Ser			
350	355	360	
ggt gga cgt gct gct tca tct ttt gca agg gcg tcg agt ttg agt ggc			1158
Gly Gly Arg Ala Ala Ser Ser Phe Ala Arg Ala Ser Ser Leu Ser Gly			
365	370	375	
aga cca tct aca ctt gtg gcg tca atg act cga tca gcc gga gcg ctc			1206
Arg Pro Ser Thr Leu Val Ala Ser Met Thr Arg Ser Ala Gly Ala Leu			
380	385	390	
gtt tgc cga aaa ggg tct cgt tgt tga ttatggacta gagacatata			1253
Val Cys Arg Lys Gly Ser Arg Cys			
395	400		
ttaaagttatt gcattttgtg tttcttttctt gtattttctat gttttttgtta cttgctttta			1313
ctaatatgtc atgtcaacct ttgtgcttgg ttggatatga atcaagatga gtctttcata			1373
tggaaccaaca aattaaatgc aaaagagttg accaaatgaa tatttatata ttatatattaa			1433
tttctct			1440

<210> 832
 <211> 401
 <212> PRT
 <213> Zinnia elegans

<400> 832
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 Val His Lys Ser Ile Asn Ala Ser Arg Arg Asn Leu Gly Tyr Leu Ser
 35 40 45
 Cys Gly Thr Gly Asn Pro Ile Asp Asp Cys Trp Arg Cys Asp Pro Asn
 50 55 60
 Trp Ala Asn Asn Arg Gln Arg Leu Ala Asp Cys Ala Ile Gly Phe Gly
 65 70 75 80

PF59082SeqList_PF59082.txt

Lys Asn Ala Met Gly Gly Arg Asn Gly Arg Ile Tyr Val Val Thr Asp
 85 90 95
 Pro Gly Asn Asp Asp Pro Val Asn Pro Val Pro Gly Thr Leu Arg Tyr
 100 105 110
 Ala Val Ile Gln Asp Glu Pro Leu Trp Ile Ile Phe Lys Arg Asp Met
 115 120 125
 Val Ile Gln Leu Arg Gln Glu Leu Val Met Asn Ser His Lys Thr Ile
 130 135 140
 Asp Gly Arg Gly Val Asn Val His Ile Gly Asn Gly Pro Cys Ile Thr
 145 150 155 160
 Ile His Tyr Ala Ser Asn Ile Ile Ile His Gly Ile His Ile His Asp
 165 170 175
 Cys Lys Gln Ala Gly Asn Gly Asn Ile Arg Asn Ser Pro His His Ser
 180 185 190
 Gly Trp Trp Thr Gln Ser Asp Gly Asp Gly Ile Ser Ile Phe Ala Ser
 195 200 205
 Lys Asp Ile Trp Ile Asp His Asn Ser Leu Ser Asn Cys His Asp Gly
 210 215 220
 Leu Ile Asp Ala Ile His Gly Ser Thr Ala Ile Thr Ile Ser Asn Asn
 225 230 235 240
 Tyr Met Thr His His Asp Lys Val Met Leu Leu Gly His Ser Asp Ser
 245 250 255
 Tyr Thr Gln Asp Lys Asn Met Gln Val Thr Ile Ala Phe Asn His Phe
 260 265 270
 Gly Glu Gly Leu Val Gln Arg Met Pro Arg Cys Arg His Gly Tyr Phe
 275 280 285
 His Val Val Asn Asn Asp Tyr Thr His Trp Glu Met Tyr Ala Ile Gly
 290 295 300
 Gly Ser Ala Ser Pro Thr Ile Tyr Ser Gln Gly Asn Arg Phe Leu Ala
 305 310 315 320
 Pro Asn Thr Arg Phe Asp Lys Glu Val Thr Lys His Glu Asn Ala Pro
 325 330 335
 Glu Ser Glu Trp Lys Asn Trp Asn Trp Arg Ser Glu Gly Asp Leu Met
 340 345 350
 Leu Asn Gly Ala Tyr Phe Arg Glu Ser Gly Gly Arg Ala Ala Ser Ser
 355 360 365
 Phe Ala Arg Ala Ser Ser Leu Ser Gly Arg Pro Ser Thr Leu Val Ala
 370 375 380
 Ser Met Thr Arg Ser Ala Gly Ala Leu Val Cys Arg Lys Gly Ser Arg
 385 390 395 400
 Cys

<210> 833
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 <212> DNA
 <213> Glycine max

<220>
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 ctg gcg ctg ctt att cga gaa gaa gct atg gct aca cca cag atc tct 96
 Leu Ala Leu Leu Ile Arg Glu Glu Ala Met Ala Thr Pro Gln 30 Ile Ser
 20 25
 gac ctc agg aat ctt gaa gtt gaa aga cac agg ttg ccg agc ttg acg 144
 Asp Leu Arg Asn Leu Glu Val Glu Arg His Arg Leu Pro Ser Leu Thr
 35 40 45
 aac tcg tca atg gcg gag agg gca aaa gag gct gac aaa tta aat gaa 192
 Asn Ser Ser Met Ala Glu 55 Ala Lys Glu Ala Asp 60 Lys Leu Asn Glu
 50 60
 caa gct gct gtg gct aac cca gag gaa gtg gtt tca atg gtt gag atg 240
 Gln Ala Ala Val Ala Asn 70 Pro Glu Glu Val Val Ser Met Val Glu Met
 65 70 75 80
 agc atc caa aac agc aca gag agg agg aag ttg gga ttt ttc tct tgt 288
 85 90 95

PF59082SeqList_PF59082.txt

Ser	Ile	Gln	Asn	Ser	Thr	Glu	Arg	Arg	Lys	Leu	Gly	Phe	Phe	Ser	Cys	
gga	act	ggc	aac	ccc	att	gat	gat	tgc	tgg	cgt	tgc	gac	ccc	aac	tgg	336
Gly	Thr	Gly	Asn	Pro	Ile	Asp	Asp	Cys	Trp	Arg	Cys	Asp	Pro	Asn	Trp	
caa	cgc	aat	cgg	aag	cgt	ctt	gca	gat	tgt	ggc	att	ggt	ttt	ggc	cga	384
Gln	Arg	Asn	Arg	Lys	Arg	Leu	Ala	Asp	Cys	Gly	Ile	Gly	Phe	Gly	Arg	
aac	gcc	atc	ggt	ggc	cgt	gat	gga	aaa	ttc	tat	gtg	gtg	act	gac	ccc	432
Asn	Ala	Ile	Gly	Gly	Arg	Asp	Gly	Lys	Phe	Tyr	Val	Val	Thr	Asp	Pro	
agg	gat	gat	gac	cct	gtg	aac	ccg	aaa	ccc	ggc	act	ctt	cgc	cat	gct	480
Arg	Asp	Asp	Asp	Pro	Val	Asn	Pro	Lys	Pro	Gly	Thr	Leu	Arg	His	Ala	
gtg	atc	cag	gat	aag	cca	ttg	tgg	att	gtg	ttc	aag	agg	gac	atg	gtt	528
Val	Ile	Gln	Asp	Lys	Pro	Leu	Trp	Ile	Val	Phe	Lys	Arg	Asp	Met	Val	
att	cag	ctg	aaa	caa	gag	ctg	atc	atg	aac	agc	ttc	aag	aca	att	gat	576
Ile	Gln	Leu	Lys	Gln	Glu	Leu	Ile	Met	Asn	Ser	Phe	Lys	Thr	Ile	Asp	
ggt	aga	gga	gtc	aat	gtg	cac	att	gct	aat	gga	gca	tgc	atc	aca	att	624
Gly	Arg	Gly	Val	Asn	Val	His	Ile	Ala	Asn	Gly	Ala	Cys	Ile	Thr	Ile	
cag	ttt	gta	acc	aat	gtt	atc	att	cat	ggc	ttg	cac	att	cat	gat	tgc	672
Gln	Phe	Val	Thr	Asn	Val	Ile	Ile	His	Gly	Leu	His	Ile	His	Asp	Cys	
aaa	cct	act	gga	aat	gct	atg	gtg	aga	agc	tcc	cca	aca	cat	ttt	ggt	720
Lys	Pro	Thr	Gly	Asn	Ala	Met	Val	Arg	Ser	Ser	Pro	Thr	His	Phe	Gly	
tgg	agg	aca	atg	gct	gat	gga	gat	gct	atc	tcc	ata	ttt	ggc	tca	agc	768
Trp	Arg	Thr	Met	Ala	Asp	Gly	Asp	Ala	Ile	Ser	Ile	Phe	Gly	Ser	Ser	
cac	att	tgg	gtt	gac	cac	aac	tcc	ttg	tca	cac	tgt	gcg	gat	ggc	ctt	816
His	Ile	Trp	Val	Asp	His	Asn	Ser	Leu	Ser	His	Cys	Ala	Asp	Gly	Leu	
gtg	gat	gct	gtc	atg	ggc	tca	aca	gcc	att	act	att	tcc	aac	aac	cac	864
Val	Asp	Ala	Val	Met	Gly	Ser	Thr	Ala	Ile	Thr	Ile	Ser	Asn	Asn	His	
ttc	acc	cac	cac	aat	gag	gtg	att	cta	cta	ggc	cac	agt	gac	tct	tac	912
Phe	Thr	His	His	Asn	Glu	Val	Ile	Leu	Leu	Gly	His	Ser	Asp	Ser	Tyr	
aca	aga	gac	aag	ctg	atg	caa	gtg	acc	atc	gca	tac	aac	cat	ttc	gga	960
Thr	Arg	Asp	Lys	Leu	Met	Gln	Val	Thr	Ile	Ala	Tyr	Asn	His	Phe	Gly	
gag	gga	ctt	atc	cag	aga	atg	cca	cgt	tgt	aga	cat	gga	tat	ttc	cac	1008
Glu	Gly	Leu	Ile	Gln	Arg	Met	Pro	Arg	Cys	Arg	His	Gly	Tyr	Phe	His	
gtg	gtg	aac	aat	gac	tac	act	cac	tgg	gag	atg	tat	gct	att	ggt	gga	1056
Val	Val	Asn	Asn	Asp	Tyr	Thr	His	Trp	Glu	Met	Tyr	Ala	Ile	Gly	Gly	
agt	gct	aac	ccc	acc	atc	aac	agc	cag	ggc	aac	aga	tac	aat	gct	cct	1104
Ser	Ala	Asn	Pro	Thr	Ile	Asn	Ser	Gln	Gly	Asn	Arg	Tyr	Asn	Ala	Pro	
act	aac	cct	ttt	gcc	aag	gag	gtg	act	aag	aga	gtg	gaa	aca	gca	gaa	1152
Thr	Asn	Pro	Phe	Ala	Lys	Glu	Val	Thr	Lys	Arg	Val	Glu	Thr	Ala	Glu	
acc	caa	tgg	aag	ggt	tgg	aat	tgg	agg	tca	gag	gga	gat	ttg	tta	ctg	1200
Thr	Gln	Trp	Lys	Gly	Trp	Asn	Trp	Arg	Ser	Glu	Gly	Asp	Leu	Leu	Leu	
aat	ggg	gcc	tat	ttc	act	cca	tct	ggt	gct	gga	gcc	tca	gcc	agc	tat	1248
Asn	Gly	Ala	Tyr	Phe	Thr	Pro	Ser	Gly	Ala	Gly	Ala	Ser	Ala	Ser	Tyr	
gct	aga	gcc	tct	agc	tta	gga	gca	aaa	tct	tct	tcc	atg	gtt	gat	tcc	1296
Ala	Arg	Ala	Ser	Ser	Leu	Gly	Ala	Lys	Ser	Ser	Ser	Met	Val	Asp	Ser	
atg	act	tcc	aat	gct	ggt	gca	cta	ggt	tgc	aaa	aga	ggc	cgt	cag	tgc	1344
Met	Thr	Ser	Asn	Ala	Gly	Ala	Leu	Gly	Cys	Lys	Arg	Gly	Arg	Gln	Cys	
tag		435				440						445				1347

PF59082SeqList_PF59082.txt

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 <212> PRT
 <213> Glycine max

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 Asp Leu Arg Asn Leu Glu Val Glu Arg His Arg Leu Pro Ser Leu Thr
 35 40 45
 Asn Ser Ser Met Ala Glu Arg Ala Lys Glu Ala Asp Lys Leu Asn Glu
 50 55 60
 Gln Ala Ala Val Ala Asn Pro Glu Glu Val Val Ser Met Val Glu Met
 65 70 75 80
 Ser Ile Gln Asn Ser Thr Glu Arg Arg Lys Leu Gly Phe Phe Ser Cys
 85 90 95
 Gly Thr Gly Asn Pro Ile Asp Asp Cys Trp Arg Cys Asp Pro Asn Trp
 100 105 110
 Gln Arg Asn Arg Lys Arg Leu Ala Asp Cys Gly Ile Gly Phe Gly Arg
 115 120 125
 Asn Ala Ile Gly Gly Arg Asp Gly Lys Phe Tyr Val Val Thr Asp Pro
 130 135 140
 Arg Asp Asp Asp Pro Val Asn Pro Lys Pro Gly Thr Leu Arg His Ala
 145 150 155 160
 Val Ile Gln Asp Lys Pro Leu Trp Ile Val Phe Lys Arg Asp Met Val
 165 170 175
 Ile Gln Leu Lys Gln Glu Leu Ile Met Asn Ser Phe Lys Thr Ile Asp
 180 185 190
 Gly Arg Gly Val Asn Val His Ile Ala Asn Gly Ala Cys Ile Thr Ile
 195 200 205
 Gln Phe Val Thr Asn Val Ile Ile His Gly Leu His Ile His Asp Cys
 210 215 220
 Lys Pro Thr Gly Asn Ala Met Val Arg Ser Ser Pro Thr His Phe Gly
 225 230 235 240
 Trp Arg Thr Met Ala Asp Gly Asp Ala Ile Ser Ile Phe Gly Ser Ser
 245 250 255
 His Ile Trp Val Asp His Asn Ser Leu Ser His Cys Ala Asp Gly Leu
 260 265 270
 Val Asp Ala Val Met Gly Ser Thr Ala Ile Thr Ile Ser Asn Asn His
 275 280 285
 Phe Thr His His Asn Glu Val Ile Leu Leu Gly His Ser Asp Ser Tyr
 290 295 300
 Thr Arg Asp Lys Leu Met Gln Val Thr Ile Ala Tyr Asn His Phe Gly
 305 310 315 320
 Glu Gly Leu Ile Gln Arg Met Pro Arg Cys Arg His Gly Tyr Phe His
 325 330 335
 Val Val Asn Asn Asp Tyr Thr His Trp Glu Met Tyr Ala Ile Gly Gly
 340 345 350
 Ser Ala Asn Pro Thr Ile Asn Ser Gln Gly Asn Arg Tyr Asn Ala Pro
 355 360 365
 Thr Asn Pro Phe Ala Lys Glu Val Thr Lys Arg Val Glu Thr Ala Glu
 370 375 380
 Thr Gln Trp Lys Gly Trp Asn Trp Arg Ser Glu Gly Asp Leu Leu Leu
 385 390 395 400
 Asn Gly Ala Tyr Phe Thr Pro Ser Gly Ala Gly Ala Ser Ala Ser Tyr
 405 410 415
 Ala Arg Ala Ser Ser Leu Gly Ala Lys Ser Ser Ser Met Val Asp Ser
 420 425 430
 Met Thr Ser Asn Ala Gly Ala Leu Gly Cys Lys Arg Gly Arg Gln Cys
 435 440 445

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 <211> 1356
 <212> DNA

PF59082SeqList_PF59082.txt

<213> Glycine max

<220>

<221> CDS

<222> (1)..(1356)

<400> 835

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1 5 10 15	
gcg gcg ctg gtt tta gct tcc gcc gac gca gtc agt gac aat gag atg	96
Ala Ala Leu Val Leu Ala Ser Ala Asp Ala Val Ser Asp Asn Glu Met	
20 25 30	
cag aaa cat gaa gcc acg gaa tca agg gac gtg gtt gaa gag aag ttg	144
Gln Lys His Glu Ala Thr Glu Ser Arg Asp Val Val Glu Glu Lys Leu	
35 40 45	
cga gtg cag agc ttg aag aat tcg tca atg gca gaa agg tca ggg ggt	192
Arg Val Gln Ser Leu Lys Asn Ser Ser Met Ala Glu Arg Ser Gly Gly	
50 55 60	
gct tta aat gaa cat gca gtt gat aat cca gag gag att gct tcc atg	240
Ala Leu Asn Glu His Ala Val Asp Asn Pro Glu Glu Ile Ala Ser Met	
65 70 75 80	
gtt gat gag agc ata cgc aat tac aca gct cga agg aac ctg aac ttc	288
Val Asp Glu Ser Ile Arg Asn Tyr Thr Ala Arg Arg Asn Leu Asn Phe	
85 90 95	
ttc tca tgc ggg acc ggg aac cca atc gac gac tgc tgg cgg tgc gac	336
Phe Ser Cys Gly Thr Gly Asn Pro Ile Asp Asp Cys Trp Arg Cys Asp	
100 105 110	
aag cgg tgg tac gcc cgc cgc aag cgc cta gcc aac tgc ggc atc ggc	384
Lys Arg Trp Tyr Ala Arg Arg Lys Arg Leu Ala Asn Cys Gly Ile Gly	
115 120 125	
ttc ggc cgc aac gcc atc ggc ggc cgc gac ggg cgc tac tac gtc gtg	432
Phe Gly Arg Asn Ala Ile Gly Gly Arg Asp Gly Arg Tyr Tyr Val Val	
130 135 140	
tcg gac ccc aac gac gac gac cca gta aac ccc aaa ccc ggc acc ctc	480
Ser Asp Pro Asn Asp Asp Asp Pro Val Asn Pro Lys Pro Gly Thr Leu	
145 150 155 160	
cgg cac gcc gtg atc cag gac cgc ccc ctc tgg atc gtg ttc aag cgc	528
Arg His Ala Val Ile Gln Asp Arg Pro Leu Trp Ile Val Phe Lys Arg	
165 170 175	
gac atg gtc ata acc cta aag caa gaa ctc atc atg aac agc ttc aag	576
Asp Met Val Ile Thr Leu Lys Gln Glu Leu Ile Met Asn Ser Phe Lys	
180 185 190	
acc atc gac ggc cgc ggc gtg aac gtc cac atc gct tat ggt gcg tgc	624
Thr Ile Asp Gly Arg Gly Val Asn Val His Ile Ala Tyr Gly Ala Cys	
195 200 205	
atc acc ata cag ttc gtc acc aac gtg atc atc cat ggg ttg cat att	672
Ile Thr Ile Gln Phe Val Thr Asn Val Ile Ile His Gly Leu His Ile	
210 215 220	
cat gac tgc aag gtg act ggg aac gcc atg gtt cgg agc tct cct tcg	720
His Asp Cys Lys Val Thr Gly Asn Ala Met Val Arg Ser Ser Pro Ser	
225 230 235 240	
cat tat ggt tgg agg acc ctt gct gat gga gat ggg atc tcc atc ttt	768
His Tyr Gly Trp Arg Thr Leu Ala Asp Gly Asp Gly Ile Ser Ile Phe	
245 250 255	
ggc tcg agt cat att tgg att gat cat aac tcg ctg tcg aat tgc gct	816
Gly Ser Ser His Ile Trp Ile Asp His Asn Ser Leu Ser Asn Cys Ala	
260 265 270	
gat ggg ctt gtg gat gct gtt atg ggg tcc act gct att act att tcc	864
Asp Gly Leu Val Asp Ala Val Met Gly Ser Thr Ala Ile Thr Ile Ser	
275 280 285	
aac aac tac ttc acc cac cac aac gag gtt atg cta ctg ggt cac agt	912
Asn Asn Tyr Phe Thr His His Asn Glu Val Met Leu Leu Gly His Ser	
290 295 300	
gac tct tat gtc cgc gac aag caa atg caa gta acc att gct tac aac	960
Asp Ser Tyr Val Arg Asp Lys Gln Met Gln Val Thr Ile Ala Tyr Asn	
305 310 315 320	
cat ttt ggg gag gga ctt atc caa aga atg ccc agg tgc aga cat ggg	1008
His Phe Gly Glu Gly Leu Ile Gln Arg Met Pro Arg Cys Arg His Gly	

PF59082SeqList_PF59082.txt

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Tyr	Phe	His	Val	Val	Asn	Asn	Asp	Tyr	Thr	His	Trp	Val	Met	Tyr	Ala		
			340				345					350					
att	gga	ggc	agt	gct	aac	ccc	aca	att	aat	agc	cag	ggc	aac	aga	tac		1104
Ile	Gly	Gly	Ser	Ala	Asn	Pro	Thr	Ile	Asn	Ser	Gln	Gly	Asn	Arg	Tyr		
		355					360					365					
ctc	gcc	cct	ctg	aac	cct	ttt	gct	aaa	gag	gtg	aca	aag	aga	gtg	gat		1152
Leu	Ala	Pro	Leu	Asn	Pro	Phe	Ala	Lys	Glu	Val	Thr	Lys	Arg	Val	Asp		
	370					375					380						
aca	ggg	tca	tcc	gta	tggt	aaa	agt	tggt	aat	tggt	aga	tct	gaa	gga	gac		1200
Thr	Gly	Ser	Ser	Val	Trp	Lys	Ser	Trp	Asn	Trp	Arg	Ser	Glu	Gly	Asp		
	385				390					395					400		
ctt	ttg	ctc	aat	gga	gcc	ttt	ttt	act	tca	tca	gga	gca	gga	gct	gca		1248
Leu	Leu	Leu	Asn	Gly	Ala	Phe	Phe	Thr	Ser	Ser	Gly	Ala	Gly	Ala	Ala		
			405					410					415				
gca	agc	tat	gcc	aga	gcc	tca	agt	ttg	ggg	gca	aaa	tca	tct	tct	ttg		1296
Ala	Ser	Tyr	Ala	Arg	Ala	Ser	Ser	Leu	Gly	Ala	Lys	Ser	Ser	Ser	Leu		
			420				425					430					
gtt	ggt	acc	atc	aca	tct	gga	gct	ggt	gtt	ctt	aaa	tgc	cgc	agg	ggt		1344
Val	Gly	Thr	Ile	Thr	Ser	Gly	Ala	Gly	Val	Leu	Lys	Cys	Arg	Arg	Gly		
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gtc	atg	tgt	taa														1356
Val	Met	Cys															
	450																

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 <212> PRT
 <213> Glycine max

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 Gln Lys His Glu Ala Thr Glu Ser Arg Asp Val Val Glu Glu Lys Leu
 35 40 45
 Arg Val Gln Ser Leu Lys Asn Ser Ser Met Ala Glu Arg Ser Gly Gly
 50 55 60
 Ala Leu Asn Glu His Ala Val Asp Asn Pro Glu Glu Ile Ala Ser Met
 65 70 75 80
 Val Asp Glu Ser Ile Arg Asn Tyr Thr Ala Arg Arg Asn Leu Asn Phe
 85 90 95
 Phe Ser Cys Gly Thr Gly Asn Pro Ile Asp Asp Cys Trp Arg Cys Asp
 100 105 110
 Lys Arg Trp Tyr Ala Arg Arg Lys Arg Leu Ala Asn Cys Gly Ile Gly
 115 120 125
 Phe Gly Arg Asn Ala Ile Gly Gly Arg Asp Gly Arg Tyr Tyr Val Val
 130 135 140
 Ser Asp Pro Asn Asp Asp Asp Pro Val Asn Pro Lys Pro Gly Thr Leu
 145 150 155 160
 Arg His Ala Val Ile Gln Asp Arg Pro Leu Trp Ile Val Phe Lys Arg
 165 170 175
 Asp Met Val Ile Thr Leu Lys Gln Glu Leu Ile Met Asn Ser Phe Lys
 180 185 190
 Thr Ile Asp Gly Arg Gly Val Asn Val His Ile Ala Tyr Gly Ala Cys
 195 200 205
 Ile Thr Ile Gln Phe Val Thr Asn Val Ile Ile His Gly Leu His Ile
 210 215 220
 His Asp Cys Lys Val Thr Gly Asn Ala Met Val Arg Ser Ser Pro Ser
 225 230 235 240
 His Tyr Gly Trp Arg Thr Leu Ala Asp Gly Asp Gly Ile Ser Ile Phe
 245 250 255
 Gly Ser Ser His Ile Trp Ile Asp His Asn Ser Leu Ser Asn Cys Ala
 260 265 270
 Asp Gly Leu Val Asp Ala Val Met Gly Ser Thr Ala Ile Thr Ile Ser
 275 280 285
 Asn Asn Tyr Phe Thr His His Asn Glu Val Met Leu Leu Gly His Ser

PF59082SeqList_PF59082.txt

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290          295          300
Asp Ser Tyr Val Arg Asp Lys Gln Met Gln Val Thr Ile Ala Tyr Asn
305 His Phe Gly Glu Gly 310 Leu Ile Gln Arg Met Pro Arg Cys Arg His Gly
325
Tyr Phe His Val Asn Asn Asp Tyr Thr His Trp Val Met Tyr Ala
340
Ile Gly Gly Ser Ala Asn Pro Thr Ile Asn Ser Gln Gly Asn Arg Tyr
355
Leu Ala Pro Leu Asn Pro Phe Ala Lys Glu Val Thr Lys Arg Val Asp
370
Thr Gly Ser Ser Val Trp Lys Ser Trp Asn Trp Arg Ser Glu Gly Asp
385 390
Leu Leu Leu Asn Gly Ala Phe Phe Thr Ser Ser Gly Ala Gly Ala Ala
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Ala Ser Tyr Ala Arg Ala Ser Ser Leu Gly Ala Lys Ser Ser Ser Leu
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Val Met Cys
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 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (1)..(1434)

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ttg cct cat gga aca gca atg ctc aac ctc act ctc cca gga caa cac      96
Leu Pro His Gly Thr 20 Ala Met Leu Asn Leu Thr Leu Pro Gly Gln His
25
cca gac cct gaa gcc gtt gct cga gaa gtt cat agg aaa gtg aat gct      144
Pro Asp Pro Glu Ala Val Ala Arg Glu Val His Arg Lys Val Asn Ala
35
tca atg gca aga agg gaa atg ctg gga gtg tca gag aaa gag gtg gca      192
Ser Met Ala Arg Arg Glu Met Leu Gly Val Ser Glu Lys Glu Val Ala
50
tca tgt cta aca ggg aat ccc ata gat gat tgt tgg aaa tgt gac cca      240
Ser Cys Leu Thr Gly Asn Pro Ile Asp Asp Cys Trp Lys Cys Asp Pro
65
gat tgg gcc aac aac agg cag agg cta gca gat tgt gca ata ggg ttc      288
Asp Trp Ala Asn Asn Arg Gln Arg Leu Ala Asp Cys Ala Ile Gly Phe
85
ggg cag aac gca aag gga gga aaa ggt ggc caa ttt tac ata gtc act      336
Gly Gln Asn Ala Lys Gly Gly Lys Gly Gly Gln Phe Tyr Ile Val Thr
100
gat tcc tca gat gag gac cct gtg aac cca aaa cct gga aca ctt aga      384
Asp Ser Ser Asp Glu Asp Pro Val Asn Pro Lys Pro Gly Thr Leu Arg
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Tyr Ala Val Ile Gln Asn Glu Pro Leu Trp Ile Val Phe Pro Ser Asn
130
atg atg att aag ctg tct caa gaa ctc att ttt aat agc tac aag acc      480
Met Met Ile Lys Leu Ser Gln Glu Leu Ile Phe Asn Ser Tyr Lys Thr
145
att gat ggg cgt gga gct gac gtg cac att gtg ggt gga ggc tgc att      528
Ile Asp Gly Arg Gly Ala Asp Val His Ile Val Gly Gly Gly Cys Ile
165
act ctt cag tat att agc aat gtc att att cac aac att cac atc cac      576
Thr Leu Gln Tyr Ile Ser Asn Val Ile Ile His Asn Ile His Ile His
180
cat tgc cat ccc tct ggc aac gct aac gtg cgg tcg agc ccc gaa cat      624
185

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PF59082SeqList_PF59082.txt

His	Cys	His	Pro	Ser	Gly	Asn	Ala	Asn	Val	Arg	Ser	Pro	Glu	His	
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Tyr	Gly	Tyr	Arg	Thr	Glu	Ser	Asp	Gly	Asp	Gly	Ile	Ser	Ile	Phe	Gly
210						215					220				
tcg	cgt	gac	att	tgg	atc	gac	cac	tgc	acc	ctc	tcc	cgg	tgc	aag	gac
Ser	Arg	Asp	Ile	Trp	Ile	Asp	His	Cys	Thr	Leu	Ser	Arg	Cys	Lys	Asp
225					230					235					240
ggc	ctg	atc	gat	gca	gtg	atg	ggg	tcc	agc	gct	atc	acg	atc	tcc	aac
Gly	Leu	Ile	Asp	Ala	Val	Met	Gly	Ser	Ser	Ala	Ile	Thr	Ile	Ser	Asn
				245				250						255	
aac	cac	ttc	tcc	cac	cac	aat	gac	gtg	atg	ctc	ctg	tgc	cac	agc	gac
Asn	His	Phe	Ser	His	His	Asn	Asp	Val	Met	Leu	Leu	Cys	His	Ser	Asp
			260				265					270			
cac	tac	ctc	cca	gac	tcc	agc	atg	cag	gtg	acc	att	ggc	ttc	aac	cac
His	Tyr	Leu	Pro	Asp	Ser	Ser	Met	Gln	Val	Thr	Ile	Gly	Phe	Asn	His
		275				280						285			
ttt	cgg	gag	ggc	ctc	gtc	cag	cgc	atg	ccg	cgt	tgc	cga	cga	ggt	tac
Phe	Arg	Glu	Gly	Leu	Val	Gln	Arg	Met	Pro	Arg	Cys	Arg	Arg	Gly	Tyr
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att	cac	gtg	gag	aac	aat	gac	ttc	aca	cga	tgg	gag	atg	tac	gcc	atc
Ile	His	Val	Glu	Asn	Asn	Asp	Phe	Thr	Arg	Trp	Glu	Met	Tyr	Ala	Ile
305					310					315					320
ggc	ggc	agt	gcg	gga	ccc	acc	att	aac	agc	cag	gga	aac	cgc	tac	acc
Gly	Gly	Ser	Ala	Gly	Pro	Thr	Ile	Asn	Ser	Gln	Gly	Asn	Arg	Tyr	Thr
				325				330						335	
gcg	ccg	gag	gat	ccg	tac	gcg	aag	cag	gtt	acg	aag	agg	ctg	gat	gcc
Ala	Pro	Glu	Asp	Pro	Tyr	Ala	Lys	Gln	Val	Thr	Lys	Arg	Leu	Asp	Ala
			340				345						350		
gaa	aaa	ggg	gag	tgg	agc	ggg	tgg	aat	tgg	cgg	tcc	gaa	ggg	gat	gtt
Glu	Lys	Gly	Glu	Trp	Ser	Gly	Trp	Asn	Trp	Arg	Ser	Glu	Gly	Asp	Val
		355				360						365			
ttg	ttg	aat	ggc	gcg	ttc	ttc	gtt	gct	tcg	gga	gca	gtt	gct	gaa	cct
Leu	Leu	Asn	Gly	Ala	Phe	Phe	Val	Ala	Ser	Gly	Ala	Val	Ala	Glu	Pro
370					375						380				
aac	tat	cag	aac	gcc	tac	agc	acc	caa	cct	aag	aac	gtg	gat	cgc	att
Asn	Tyr	Gln	Asn	Ala	Tyr	Ser	Thr	Gln	Pro	Lys	Asn	Val	Asp	Arg	Ile
385					390					395					400
tcg	ctt	ctc	act	atg	tcc	gcc	ggg	gtt	ctc	ggc	gtt	gct	agg	gac	aat
Ser	Leu	Leu	Thr	Met	Ser	Ala	Gly	Val	Leu	Gly	Val	Ala	Arg	Asp	Asn
				405				410						415	
aat	ctg	gga	atg	tgg	atc	aga	gga	ccc	aac	gat	ggc	act	gta	tat	ttt
Asn	Leu	Gly	Met	Trp	Ile	Arg	Gly	Pro	Asn	Asp	Gly	Thr	Val	Tyr	Phe
			420				425						430		
tca	gat	tct	ggc	cca	gaa	tac	aca	gac	gaa	atg	tcc	cgg	agt	aca	atg
Ser	Asp	Ser	Gly	Pro	Glu	Tyr	Thr	Asp	Glu	Met	Ser	Arg	Ser	Thr	Met
			435			440						445			
ccg	ttg	cta	cct	tca	cgt	att	ttg	att	ctt	gta	tct	gca	ctc	tta	tgc
Pro	Leu	Leu	Pro	Ser	Arg	Ile	Leu	Ile	Leu	Val	Ser	Ala	Leu	Leu	Cys
		450				455					460				
ttc	tta	ggt	cat	aca	aca	acc	tta	aca	aca	cta	ccc	aat	tag		
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<210> 838

<211> 477

<212> PRT

<213> Glycine max

<400> 838

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			20					25					30		
Pro	Asp	Pro	Glu	Ala	Val	Ala	Arg	Glu	Val	His	Arg	Lys	Val	Asn	Ala
		35					40					45			
Ser	Met	Ala	Arg	Arg	Glu	Met	Leu	Gly	Val	Ser	Glu	Lys	Glu	Val	Ala
	50					55				60					
Ser	Cys	Leu	Thr	Gly	Asn	Pro	Ile	Asp	Asp	Cys	Trp	Lys	Cys	Asp	Pro

PF59082SeqList_PF59082.txt

65 70 75 80
 Asp Trp Ala Asn Asn Arg Gln Arg Leu Ala Asp Cys Ala Ile Gly Phe
 Gly Gln Asn Ala Lys Gly Gly Lys Gly Gly Gln Phe Tyr Ile Val Thr
 Asp Ser Ser Asp Glu Asp Pro Val Asn Pro Lys Pro Gly Thr Leu Arg
 Tyr Ala Val Ile Gln Asn Glu Pro Leu Trp Ile Val Phe Pro Ser Asn
 Met Met Ile Lys Leu Ser Gln Glu Leu Ile Phe Asn Ser Tyr Lys Thr
 Ile Asp Gly Arg Gly Ala Asp Val His Ile Val Gly Gly Gly Cys Ile
 Thr Leu Gln Tyr Ile Ser Asn Val Ile Ile His Asn Ile His Ile His
 His Cys His Pro Ser Gly Asn Ala Asn Val Arg Ser Ser Pro Glu His
 Tyr Gly Tyr Arg Thr Glu Ser Asp Gly Asp Gly Ile Ser Ile Phe Gly
 Ser Arg Asp Ile Trp Ile Asp His Cys Thr Leu Ser Arg Cys Lys Asp
 Gly Leu Ile Asp Ala Val Met Gly Ser Ser Ala Ile Thr Ile Ser Asn
 Asn His Phe Ser His His Asn Asp Val Met Leu Leu Cys His Ser Asp
 His Tyr Leu Pro Asp Ser Ser Met Gln Val Thr Ile Gly Phe Asn His
 Phe Arg Glu Gly Leu Val Gln Arg Met Pro Arg Cys Arg Arg Gly Tyr
 Ile His Val Glu Asn Asn Asp Phe Thr Arg Trp Glu Met Tyr Ala Ile
 Gly Gly Ser Ala Gly Pro Thr Ile Asn Ser Gln Gly Asn Arg Tyr Thr
 Ala Pro Glu Asp Pro Tyr Ala Lys Gln Val Thr Lys Arg Leu Asp Ala
 Glu Lys Gly Glu Trp Ser Gly Trp Asn Trp Arg Ser Glu Gly Asp Val
 Leu Leu Asn Gly Ala Phe Phe Val Ala Ser Gly Ala Val Ala Glu Pro
 Asn Tyr Gln Asn Ala Tyr Ser Thr Gln Pro Lys Asn Val Asp Arg Ile
 Ser Leu Leu Thr Met Ser Ala Gly Val Leu Gly Val Ala Arg Asp Asn
 Asn Leu Gly Met Trp Ile Arg Gly Pro Asn Asp Gly Thr Val Tyr Phe
 Ser Asp Ser Gly Pro Glu Tyr Thr Asp Glu Met Ser Arg Ser Thr Met
 Pro Leu Leu Pro Ser Arg Ile Leu Ile Leu Val Ser Ala Leu Leu Cys
 Phe Leu Gly His Thr Thr Thr Leu Thr Thr Leu Pro Asn

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 <211> 1227
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (1)..(1227)

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 1 5 10 15
 act cca act cta att tcc tct tca cca gtt cta aac cct caa gag gtc 96
 Thr Pro Thr Leu Ile Ser Ser Ser Pro Val Leu Asn Pro Gln Glu Val
 20 25 30
 gta caa gag gtc aac aag aaa atc aat ggc tct ata gca aga ccc aga 144
 40 45 50
 Seite 1060

PF59082SeqList_PF59082.txt

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Arg	Asn	Leu	Gly	Tyr	Leu	Ser	Cys	Gly	Ser	Gly	Asn	Pro	Ile	Asp	Asp	
	50					55					60					
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Cys	Trp	Arg	Cys	Asp	Pro	Asn	Trp	Glu	Gln	Asn	Arg	Gln	Arg	Leu	Ala	
	65				70					75					80	
gac	tgc	gca	atc	ggg	ttc	ggc	aag	aac	gcc	att	ggc	ggc	aga	gac	ggc	288
Asp	Cys	Ala	Ile	Gly	Phe	Gly	Lys	Asn	Ala	Ile	Gly	Gly	Arg	Asp	Gly	
				85					90					95		
aag	atc	tat	gtg	gtg	gag	gac	gac	ggc	gac	gac	gac	gag	gtg	aac	ccg	336
Lys	Ile	Tyr	Val	Val	Glu	Asp	Asp	Gly	Asp	Asp	Asp	Ala	Val	Asn	Pro	
			100					105					110			
aag	ccg	gga	acc	ctc	cgg	cac	gcc	gtg	atc	caa	gac	gag	ccc	tta	tgg	384
Lys	Pro	Gly	Thr	Leu	Arg	His	Ala	Val	Ile	Gln	Asp	Glu	Pro	Leu	Trp	
		115					120					125				
ata	atc	ttc	gcc	aga	gac	atg	gtg	atc	caa	ctt	aaa	gaa	gag	ctt	ctc	432
Ile	Ile	Phe	Ala	Arg	Asp	Met	Val	Ile	Gln	Leu	Lys	Glu	Glu	Leu	Leu	
						135					140					
atg	aac	tcc	ttc	aag	acc	atc	gac	gga	aga	ggg	ggc	agc	gtg	cac	gtt	480
Met	Asn	Ser	Phe	Lys	Thr	Ile	Asp	Gly	Arg	Gly	Ala	Ser	Val	His	Val	
	145				150					155					160	
gct	ggg	ggg	cca	tgc	ata	acg	ata	cag	tac	gtg	acc	aac	gtc	atc	atc	528
Ala	Gly	Gly	Pro	Cys	Ile	Thr	Ile	Gln	Tyr	Val	Thr	Asn	Val	Ile	Ile	
				165						170				175		
cat	ggg	att	cac	ata	cac	gat	tgc	aag	cag	gga	ggg	aac	gct	atg	gtg	576
His	Gly	Ile	His	Ile	His	Asp	Cys	Lys	Gln	Gly	Gly	Asn	Ala	Met	Val	
			180					185					190			
cgg	gac	tcc	cca	cgg	cac	tac	ggc	tgg	aga	acc	gta	tcg	gac	ggg	gac	624
Arg	Asp	Ser	Pro	Arg	His	Tyr	Gly	Trp	Arg	Thr	Val	Ser	Asp	Gly	Asp	
		195					200					205				
ggc	gtg	tcc	atc	ttc	gga	ggg	agc	cac	gtg	tgg	gtt	gac	cat	tgc	tcg	672
Gly	Val	Ser	Ile	Phe	Gly	Gly	Ser	His	Val	Trp	Val	Asp	His	Cys	Ser	
		210				215					220					
ctg	tct	aac	tgc	aac	gac	ggg	ttg	atc	gac	gcc	atc	cat	ggc	tcc	acc	720
Leu	Ser	Asn	Cys	Asn	Asp	Gly	Leu	Ile	Asp	Ala	Ile	His	Gly	Ser	Thr	
					230					235					240	
gct	att	acc	att	tct	aat	aac	tac	atg	acc	cat	cat	gat	aag	gtc	atg	768
Ala	Ile	Thr	Ile	Ser	Asn	Asn	Tyr	Met	Thr	His	His	Asp	Lys	Val	Met	
				245						250				255		
ttg	ttg	ggg	cac	agc	gat	tct	tac	acc	cag	gac	aag	gac	atg	caa	gtc	816
Leu	Leu	Gly	His	Ser	Asp	Ser	Tyr	Thr	Gln	Asp	Lys	Asp	Met	Gln	Val	
			260					265					270			
act	att	gct	ttc	aac	cac	ttt	ggg	gaa	ggc	ctt	gtt	caa	agg	atg	cca	864
Thr	Ile	Ala	Phe	Asn	His	Phe	Gly	Glu	Gly	Leu	Val	Gln	Arg	Met	Pro	
			275				280					285				
agg	tgt	agg	ctt	ggg	tat	ttc	cat	gtg	gtg	aac	aat	gat	tat	act	cac	912
Arg	Cys	Arg	Leu	Gly	Tyr	Phe	His	Val	Val	Asn	Asn	Asp	Tyr	Thr	His	
		290				295					300					
tgg	gaa	atg	tat	gcc	att	ggg	gga	agt	gct	aat	cca	acc	atc	aac	tgc	960
Trp	Glu	Met	Tyr	Ala	Ile	Gly	Gly	Ser	Ala	Asn	Pro	Thr	Ile	Asn	Cys	
					310					315					320	
caa	ggc	aac	aga	ttt	gtt	gca	ccc	gat	gac	aga	ttc	agc	aaa	gag	gtg	1008
Gln	Gly	Asn	Arg	Phe	Val	Ala	Pro	Asp	Asp	Arg	Phe	Ser	Lys	Glu	Val	
				325						330				335		
aca	aag	cat	gag	gat	gca	cca	gag	agt	gaa	tgg	aaa	gga	tgg	aat	tgg	1056
Thr	Lys	His	Glu	Asp	Ala	Pro	Glu	Ser	Glu	Trp	Lys	Gly	Trp	Asn	Trp	
			340					345					350			
agg	tca	gaa	ggg	gac	ttg	ttg	gta	aac	ggg	gag	ttt	ttc	acg	gca	tcg	1104
Arg	Ser	Glu	Gly	Asp	Leu	Leu	Val	Asn	Gly	Ala	Phe	Phe	Thr	Ala	Ser	
			355				360					365				
ggg	gct	gga	gcc	tcc	tct	agc	tat	gca	aga	gca	tct	agc	ttg	agt	gca	1152
Gly	Ala	Gly	Ala	Ser	Ser	Ser	Tyr	Ala	Arg	Ala	Ser	Ser	Leu	Ser	Ala	
						375					380					
agg	cca	tct	tca	ttg	gtg	ggg	tcc	ata	acc	act	ggg	gag	ggg	gca	ctc	1200
Arg	Pro	Ser	Ser	Leu	Val	Gly	Ser	Ile	Thr	Thr	Gly	Ala	Gly	Ala	Leu	
					390					395					400	
agc	tgt	agg	aag	ggg	tcc	cgc	tgc	tga								1227

PF59082SeqList_PF59082.txt

Ser Cys Arg Lys Gly Ser Arg Cys
405

<210> 840
<211> 408
<212> PRT
<213> Glycine max

<400> 840

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Thr	Pro	Thr	Leu	Ile	Ser	Ser	Ser	Pro	Val	Leu	Asn	Pro	Gln	Glu	Val
			20					25					30		
Val	Gln	Glu	Val	Asn	Lys	Lys	Ile	Asn	Gly	Ser	Ile	Ala	Arg	Pro	Arg
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Arg	Asn	Leu	Gly	Tyr	Leu	Ser	Cys	Gly	Ser	Gly	Asn	Pro	Ile	Asp	Asp
	50					55					60				
Cys	Trp	Arg	Cys	Asp	Pro	Asn	Trp	Glu	Gln	Asn	Arg	Gln	Arg	Leu	Ala
65					70					75					80
Asp	Cys	Ala	Ile	Gly	Phe	Gly	Lys	Asn	Ala	Ile	Gly	Gly	Arg	Asp	Gly
				85					90					95	
Lys	Ile	Tyr	Val	Val	Glu	Asp	Asp	Gly	Asp	Asp	Asp	Ala	Val	Asn	Pro
			100					105					110		
Lys	Pro	Gly	Thr	Leu	Arg	His	Ala	Val	Ile	Gln	Asp	Glu	Pro	Leu	Trp
		115					120					125			
Ile	Ile	Phe	Ala	Arg	Asp	Met	Val	Ile	Gln	Leu	Lys	Glu	Glu	Leu	Leu
	130					135					140				
Met	Asn	Ser	Phe	Lys	Thr	Ile	Asp	Gly	Arg	Gly	Ala	Ser	Val	His	Val
145					150					155					160
Ala	Gly	Gly	Pro	Cys	Ile	Thr	Ile	Gln	Tyr	Val	Thr	Asn	Val	Ile	Ile
				165					170					175	
His	Gly	Ile	His	Ile	His	Asp	Cys	Lys	Gln	Gly	Gly	Asn	Ala	Met	Val
			180					185					190		
Arg	Asp	Ser	Pro	Arg	His	Tyr	Gly	Trp	Arg	Thr	Val	Ser	Asp	Gly	Asp
		195					200					205			
Gly	Val	Ser	Ile	Phe	Gly	Gly	Ser	His	Val	Trp	Val	Asp	His	Cys	Ser
	210					215					220				
Leu	Ser	Asn	Cys	Asn	Asp	Gly	Leu	Ile	Asp	Ala	Ile	His	Gly	Ser	Thr
225					230					235					240
Ala	Ile	Thr	Ile	Ser	Asn	Asn	Tyr	Met	Thr	His	His	Asp	Lys	Val	Met
				245					250					255	
Leu	Leu	Gly	His	Ser	Asp	Ser	Tyr	Thr	Gln	Asp	Lys	Asp	Met	Gln	Val
			260					265					270		
Thr	Ile	Ala	Phe	Asn	His	Phe	Gly	Glu	Gly	Leu	Val	Gln	Arg	Met	Pro
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Arg	Cys	Arg	Leu	Gly	Tyr	Phe	His	Val	Val	Asn	Asn	Asp	Tyr	Thr	His
	290					295					300				
Trp	Glu	Met	Tyr	Ala	Ile	Gly	Gly	Ser	Ala	Asn	Pro	Thr	Ile	Asn	Cys
305					310					315					320
Gln	Gly	Asn	Arg	Phe	Val	Ala	Pro	Asp	Asp	Arg	Phe	Ser	Lys	Glu	Val
				325					330					335	
Thr	Lys	His	Glu	Asp	Ala	Pro	Glu	Ser	Glu	Trp	Lys	Gly	Trp	Asn	Trp
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		355					360					365			
Gly	Ala	Gly	Ala	Ser	Ser	Ser	Tyr	Ala	Arg	Ala	Ser	Ser	Leu	Ser	Ala
	370					375					380				
Arg	Pro	Ser	Ser	Leu	Val	Gly	Ser	Ile	Thr	Thr	Gly	Ala	Gly	Ala	Leu
385					390					395					400
Ser	Cys	Arg	Lys	Gly	Ser	Arg	Cys								
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<210> 841
<211> 1110
<212> DNA
<213> Fragaria ananassa

<220>
<221> CDS

<222> (1)..(1110)

<400> 841

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tgt	gga	act	gga	aat	ccc	att	gat	gat	tgc	tgg	cgt	tgt	gat	ccc	aac	96
Cys	Gly	Thr	Gly	Asn	Pro	Ile	Asp	Asp	Cys	Trp	Arg	Cys	Asp	Pro	Asn	
		20					25					30				
tgg	caa	aag	aac	cgc	aag	cgt	ctt	gca	gac	tgt	gga	att	ggt	ttt	ggc	144
Trp	Gln	Lys	Asn	Arg	Lys	Arg	Leu	Ala	Asp	Cys	Gly	Ile	Gly	Phe	Gly	
		35					40				45					
aga	aat	gcc	att	ggt	ggt	cgt	gat	gga	cgc	ttc	tat	ggt	gtc	act	gat	192
Arg	Asn	Ala	Ile	Gly	Gly	Arg	Asp	Gly	Arg	Phe	Tyr	Val	Val	Thr	Asp	
	50					55				60						
cct	aat	gat	gat	gat	ccc	ggt	aac	ccc	aga	ccc	ggc	act	ctg	cgc	cat	240
Pro	Asn	Asp	Asp	Asp	Pro	Val	Asn	Pro	Arg	Pro	Gly	Thr	Leu	Arg	His	
	65				70			75							80	
gct	gtc	atc	cag	gat	gag	cct	ctc	tgg	att	gtg	ttc	aaa	cgt	gac	atg	288
Ala	Val	Ile	Gln	Asp	Glu	Pro	Leu	Trp	Ile	Val	Phe	Lys	Arg	Asp	Met	
			85					90						95		
gtg	atc	caa	ttg	aag	cag	gag	ctt	atc	atg	aat	agc	ttc	aag	acc	att	336
Val	Ile	Gln	Leu	Lys	Gln	Glu	Leu	Ile	Met	Asn	Ser	Phe	Lys	Thr	Ile	
		100					105					110				
gat	ggc	cgt	gga	gtc	aat	gtc	cac	att	gct	aat	gga	gca	tgc	att	aca	384
Asp	Gly	Arg	Gly	Val	Asn	Val	His	Ile	Ala	Asn	Gly	Ala	Cys	Ile	Thr	
		115				120					125					
atc	cag	ttt	ggt	aca	aat	ggt	ata	ggt	cat	ggt	ctg	cat	atc	cat	gac	432
Ile	Gln	Phe	Val	Thr	Asn	Val	Ile	Val	His	Gly	Leu	His	Ile	His	Asp	
	130					135					140					
tgc	aag	ccc	aca	gga	aat	gct	atg	gtg	agg	agc	tcc	cca	tct	cac	ttt	480
Cys	Lys	Pro	Thr	Gly	Asn	Ala	Met	Val	Arg	Ser	Ser	Pro	Ser	His	Phe	
	145				150				155						160	
gga	tgg	agg	aca	atg	gct	gat	ggg	gat	gct	atc	tcc	atc	ttc	ggg	tca	528
Gly	Trp	Arg	Thr	Met	Ala	Asp	Gly	Asp	Ala	Ile	Ser	Ile	Phe	Gly	Ser	
			165				170						175			
agc	cat	atc	tgg	ggt	gat	cac	aat	tcc	ctc	tcc	aat	tgt	gct	gat	ggt	576
Ser	His	Ile	Trp	Val	Asp	His	Asn	Ser	Leu	Ser	Asn	Cys	Ala	Asp	Gly	
		180					185					190				
ctt	ggt	gat	gct	gtc	atg	ggg	tca	act	gct	att	acc	atc	tcc	aac	aac	624
Leu	Val	Asp	Ala	Val	Met	Gly	Ser	Thr	Ala	Ile	Thr	Ile	Ser	Asn	Asn	
		195				200					205					
cac	cta	acc	cac	cac	aat	gaa	gta	atg	ctg	ttg	ggc	cac	agc	gat	tct	672
His	Leu	Thr	His	His	Asn	Glu	Val	Met	Leu	Leu	Gly	His	Ser	Asp	Ser	
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Tyr	Thr	Arg	Asp	Lys	Gln	Met	Gln	Val	Thr	Ile	Ala	Tyr	Asn	His	Phe	
	225			230				235							240	
gga	gag	gga	ctt	atc	cag	aga	atg	cca	agg	tgc	aga	cat	gga	tat	ttc	768
Gly	Glu	Gly	Leu	Ile	Gln	Arg	Met	Pro	Arg	Cys	Arg	His	Gly	Tyr	Phe	
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cat	gtg	gtg	aac	aac	gac	tac	act	cac	tgg	gaa	atg	tat	gcc	atc	ggt	816
His	Val	Val	Asn	Asn	Asp	Tyr	Thr	His	Trp	Glu	Met	Tyr	Ala	Ile	Gly	
		260				265						270				
gga	agt	gca	gac	ccc	act	atc	aac	agc	caa	ggc	aac	aga	tat	gca	gct	864
Gly	Ser	Ala	Asp	Pro	Thr	Ile	Asn	Ser	Gln	Gly	Asn	Arg	Tyr	Ala	Ala	
		275				280					285					
cca	acc	aac	ccc	ttt	gca	aag	gag	gtt	acc	aag	aga	gtg	gag	aca	tcg	912
Pro	Thr	Asn	Pro	Phe	Ala	Lys	Glu	Val	Thr	Lys	Val	Glu	Glu	Thr	Ser	
	290					295					300					
caa	act	cag	tgg	agg	ggc	tgg	aac	tgg	agg	tca	gaa	ggt	gat	ctt	cta	960
Gln	Thr	Gln	Trp	Arg	Gly	Trp	Asn	Trp	Arg	Ser	Glu	Gly	Asp	Leu	Leu	
	305				310				315						320	
ctc	aat	ggt	gcc	ttc	ttc	act	cca	tct	gga	gct	gga	gct	tca	gct	gtc	1008
Leu	Asn	Gly	Ala	Phe	Phe	Thr	Pro	Ser	Gly	Ala	Gly	Ala	Ser	Ala	Val	
			325					330					335			
tat	gcc	agg	gcc	tca	agc	ttg	gga	gcc	aag	tca	tct	gcc	atg	gtg	gga	1056
Tyr	Ala	Arg	Ala	Ser	Ser	Leu	Gly	Ala	Lys	Ser	Ser	Ala	Met	Val	Gly	
			340				345						350			

PF59082SeqList_PF59082.txt

acc ata act gct agt gct ggt gca ctt gga tgc cgc aga gga cgt acc 1104
 Thr Ile Thr Ala Ser Ala Gly Ala Leu Gly Cys Arg Arg Gly Arg Thr
 355 360 365
 tgc tag 1110
 Cys

<210> 842
 <211> 369
 <212> PRT
 <213> Fragaria ananassa

<400> 842
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 Cys Gly Thr Gly Asn Pro Ile Asp Asp Cys Trp Arg Cys Asp Pro Asn
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 Trp Gln Lys Asn Arg Lys Arg Leu Ala Asp Cys Gly Ile Gly Phe Gly
 35 40 45
 Arg Asn Ala Ile Gly Gly Arg Asp Gly Arg Phe Tyr Val Val Thr Asp
 50 55 60
 Pro Asn Asp Asp Asp Pro Val Asn Pro Arg Pro Gly Thr Leu Arg His
 65 70 75 80
 Ala Val Ile Gln Asp Glu Pro Leu Trp Ile Val Phe Lys Arg Asp Met
 85 90 95
 Val Ile Gln Leu Lys Gln Glu Leu Ile Met Asn Ser Phe Lys Thr Ile
 100 105 110
 Asp Gly Arg Gly Val Asn Val His Ile Ala Asn Gly Ala Cys Ile Thr
 115 120 125
 Ile Gln Phe Val Thr Asn Val Ile Val His Gly Leu His Ile His Asp
 130 135 140
 Cys Lys Pro Thr Gly Asn Ala Met Val Arg Ser Ser Pro Ser His Phe
 145 150 155 160
 Gly Trp Arg Thr Met Ala Asp Gly Asp Ala Ile Ser Ile Phe Gly Ser
 165 170 175
 Ser His Ile Trp Val Asp His Asn Ser Leu Ser Asn Cys Ala Asp Gly
 180 185 190
 Leu Val Asp Ala Val Met Gly Ser Thr Ala Ile Thr Ile Ser Asn Asn
 195 200 205
 His Leu Thr His His Asn Glu Val Met Leu Leu Gly His Ser Asp Ser
 210 215 220
 Tyr Thr Arg Asp Lys Gln Met Gln Val Thr Ile Ala Tyr Asn His Phe
 225 230 235 240
 Gly Glu Gly Leu Ile Gln Arg Met Pro Arg Cys Arg His Gly Tyr Phe
 245 250 255
 His Val Val Asn Asn Asp Tyr Thr His Trp Glu Met Tyr Ala Ile Gly
 260 265 270
 Gly Ser Ala Asp Pro Thr Ile Asn Ser Gln Gly Asn Arg Tyr Ala Ala
 275 280 285
 Pro Thr Asn Pro Phe Ala Lys Glu Val Thr Lys Arg Val Glu Thr Ser
 290 295 300
 Gln Thr Gln Trp Arg Gly Trp Asn Trp Arg Ser Glu Gly Asp Leu Leu
 305 310 315 320
 Leu Asn Gly Ala Phe Thr Pro Ser Gly Ala Gly Ala Ser Ala Val
 325 330 335
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 Thr Ile Thr Ala Ser Ala Gly Ala Leu Gly Cys Arg Arg Gly Arg Thr
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 <212> DNA
 <213> Musa acuminata

<220>
 <221> CDS

PF59082SeqList_PF59082.txt

<222> (1)..(1200)

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Ser 20 Ala Ala Val Arg Asp Pro Glu Leu Val Val Gln Glu Val Gln Arg 25 30	
agc ttg aac gtg tcg cgg cgg cga ctg ggc tac ttg tca tgc ggc acc	144
Ser 35 Leu Asn Val Ser Arg Arg Arg Leu Gly Tyr Leu Ser 45 Cys Gly Thr 50	
ggc aat ccg atc gac gac tgc tgg cgg tgc gac cct gac tgg gct gac	192
Gly 55 Asn Pro Ile Asp Asp Cys Trp Arg Cys Asp Pro Asp Trp Ala Asp 60	
aac cgg cag cgg ctc gcg gac tgc gcc atc ggg ttc ggg aag aac gcg	240
Asn 65 Arg Gln Arg Leu Ala Asp Cys Ala Ile Gly Phe Gly Lys Asn Ala 70 80	
att ggg ggc agg gac ggc gag ata tac gtg gtg acc gac agt ggc gac	288
Ile 85 Gly Gly Arg Asp Gly Glu Ile Tyr Val Val Thr Asp Ser Gly Asp 90 95	
gac gac ccc gtc aat ccg aag ccg ggc acg ctc cgg tac gcc gtc atc	336
Asp 100 Asp Pro Val Asn Pro Lys Pro Gly Thr Leu Arg Tyr Ala Val Ile 105 110	
cag gag gag ccg ctg tgg atc atc ttc aag cgc gac att gtc atc cag	384
Gln 115 Glu Glu Pro Leu Trp Ile Ile Phe Lys Arg Asp Ile Val Ile Gln 120 125	
ctg aag gag gag ctc atc atg aac tcc cac aag acc atc gac ggc cgg	432
Leu 130 Lys Glu Glu Leu Ile Met Asn Ser His Lys Thr Ile Asp Gly Arg 135 140	
ggc gcc agc gtc cac atc tcc ggc ggg ccg tgc acc atc cag tac	480
Gly 145 Ala Ser Val His Ile Ser Gly Gly Pro Cys Ile Thr Ile Gln Tyr 150 155 160	
gtc acc aac atc atc atc cac ggc gtc cac atc cac gac tgc aag cag	528
Val 165 Thr Asn Ile Ile Ile His Gly Val His Ile His Asp Cys Lys Gln 170 175	
ggc ggg aac gcg tac gtg cgc gac tcc cca ggg cac tac ggg tgg cgc	576
Gly 180 Gly Asn Ala Tyr Val Arg Asp Ser Pro Gly His Tyr Gly Trp Arg 185 190	
acg gtg tcg gac ggc gac ggg gtg tcc atc ttc ggc ggg cag cca ccg	624
Thr 195 Val Ser Asp Gly Asp Gly Val Ser Ile Phe Gly Gly Gln Pro Pro 200 205	
tct tgg gtc gac cac tgc acg ctg ttc aac tgc cac gac ggg ctc att	672
Ser 210 Trp Val Asp His Cys Thr Leu Phe Asn Cys His Asp Gly Leu Ile 215 220	
gac gca att cat ggg tcc acc gcg atc acc att tcc aac aac tac ttg	720
Asp 225 Ala Ile His Gly Ser Thr Ala Ile Thr Ile Ser Asn Asn Tyr Leu 230 235 240	
agg cac cat gac aag gtc atg ctg ctg ggt cac agc gac gag ttg acg	768
Arg 245 His His Asp Lys Val Met Leu Leu Gly His Ser Asp Glu Leu Thr 250 255	
tcc gac aag agc atg cag gtc acc ata gcc ttc aac cac ttc ggg gaa	816
Ser 260 Asp Lys Ser Met Gln Val Thr Ile Ala Phe Asn His Phe Gly Glu 265 270	
gac ctg gtt cag agg atg cca agg tgt cgg cat ggc tat ttc cac gtg	864
Asp 275 Leu Val Gln Arg Met Pro Arg Cys Arg His Gly Tyr Phe His Val 280 285	
gtg aac aat gac tac acc cac tgg gag atg tac gca att ggt ggg agt	912
Val 290 Asn Asn Asp Tyr Thr His Trp Glu Met Tyr Ala Ile Gly Gly Ser 295 300	
gct gct ccc act ata aac agc caa ggc aac aga ttt ctt gcg ccc aat	960
Ala 305 Ala Pro Thr Ile Asn Ser Gln Gly Asn Arg Phe Leu Ala Pro Asn 310 315 320	
gat cgg ttt gca aaa gag gtg act aaa cgc gag gac gca cag gag agc	1008
Asp 325 Arg Phe Ala Lys Glu Val Thr Lys Arg Glu Asp Ala Gln Glu Ser 330 335	
gag tgg aag aag tgg aac tgg agg tcg gaa ggg gac cag atg ctg aat	1056
Glu 340 Trp Lys Lys Trp Asn Trp Arg Ser Glu Gly Asp Gln Met Leu Asn 345 350	

PF59082SeqList_PF59082.txt

gga	gcc	ttc	ttc	acg	ccg	tcc	ggg	gcc	gga	gct	tcg	tcg	agt	cac	gcg	1104
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		355					360				365					
aag	gcg	tcg	agc	ttg	ggg	ccc	agg	tcg	tcg	tct	ctc	gtc	ggg	acc	atc	1152
Lys	Ala	Ser	Ser	Leu	Gly	Pro	Arg	Ser	Ser	Ser	Leu	Val	Gly	Thr	Ile	
	370					375					380					
acc	gtc	tct	gcc	ggc	gtt	ctc	tcg	tgc	aag	aag	gga	tcc	cgc	tgt		1197
Thr	Val	Ser	Ala	Gly	Val	Leu	Ser	Cys	Lys	Lys	Gly	Ser	Arg	Cys		
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tga																1200

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 <212> PRT
 <213> Musa acuminata

<400> 844

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			20				25						30		
Ser	Leu	Asn	Val	Ser	Arg	Arg	Arg	Leu	Gly	Tyr	Leu	Ser	Cys	Gly	Thr
		35					40					45			
Gly	Asn	Pro	Ile	Asp	Asp	Cys	Trp	Arg	Cys	Asp	Pro	Asp	Trp	Ala	Asp
	50					55					60				
Asn	Arg	Gln	Arg	Leu	Ala	Asp	Cys	Ala	Ile	Gly	Phe	Gly	Lys	Asn	Ala
65					70					75				80	
Ile	Gly	Gly	Arg	Asp	Gly	Glu	Ile	Tyr	Val	Val	Thr	Asp	Ser	Gly	Asp
			85						90					95	
Asp	Asp	Pro	Val	Asn	Pro	Lys	Pro	Gly	Thr	Leu	Arg	Tyr	Ala	Val	Ile
			100					105					110		
Gln	Glu	Glu	Pro	Leu	Trp	Ile	Ile	Phe	Lys	Arg	Asp	Ile	Val	Ile	Gln
		115					120					125			
Leu	Lys	Glu	Glu	Leu	Ile	Met	Asn	Ser	His	Lys	Thr	Ile	Asp	Gly	Arg
	130					135					140				
Gly	Ala	Ser	Val	His	Ile	Ser	Gly	Gly	Pro	Cys	Ile	Thr	Ile	Gln	Tyr
145					150					155				160	
Val	Thr	Asn	Ile	Ile	Ile	His	Gly	Val	His	Ile	His	Asp	Cys	Lys	Gln
			165						170					175	
Gly	Gly	Asn	Ala	Tyr	Val	Arg	Asp	Ser	Pro	Gly	His	Tyr	Gly	Trp	Arg
			180					185					190		
Thr	Val	Ser	Asp	Gly	Asp	Gly	Val	Ser	Ile	Phe	Gly	Gly	Gln	Pro	Pro
		195					200					205			
Ser	Trp	Val	Asp	His	Cys	Thr	Leu	Phe	Asn	Cys	His	Asp	Gly	Leu	Ile
	210					215					220				
Asp	Ala	Ile	His	Gly	Ser	Thr	Ala	Ile	Thr	Ile	Ser	Asn	Asn	Tyr	Leu
225					230					235				240	
Arg	His	His	Asp	Lys	Val	Met	Leu	Leu	Gly	His	Ser	Asp	Glu	Leu	Thr
				245					250					255	
Ser	Asp	Lys	Ser	Met	Gln	Val	Thr	Ile	Ala	Phe	Asn	His	Phe	Gly	Glu
			260					265					270		
Asp	Leu	Val	Gln	Arg	Met	Pro	Arg	Cys	Arg	His	Gly	Tyr	Phe	His	Val
		275					280					285			
Val	Asn	Asn	Asp	Tyr	Thr	His	Trp	Glu	Met	Tyr	Ala	Ile	Gly	Gly	Ser
	290					295					300				
Ala	Ala	Pro	Thr	Ile	Asn	Ser	Gln	Gly	Asn	Arg	Phe	Leu	Ala	Pro	Asn
305					310					315				320	
Asp	Arg	Phe	Ala	Lys	Glu	Val	Thr	Lys	Arg	Glu	Asp	Ala	Gln	Glu	Ser
				325					330					335	
Glu	Trp	Lys	Lys	Trp	Asn	Trp	Arg	Ser	Glu	Gly	Asp	Gln	Met	Leu	Asn
			340					345					350		
Gly	Ala	Phe	Thr	Pro	Ser	Gly	Ala	Gly	Ala	Ser	Ser	Ser	His	Ala	
		355				360					365				
Lys	Ala	Ser	Ser	Leu	Gly	Pro	Arg	Ser	Ser	Ser	Leu	Val	Gly	Thr	Ile
	370					375					380				
Thr	Val	Ser	Ala	Gly	Val	Leu	Ser	Cys	Lys	Lys	Gly	Ser	Arg	Cys	
385					390					395					

PF59082SeqList_PF59082.txt

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 <211> 1239
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (1)..(1239)

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cta aca atc ggt aac acg ctt gca ttt tct tcg agt ttg ccg gat cat      96
Leu Thr Ile Gly Asn Thr Leu Ala Phe Ser Ser Leu Pro Asp His
20      25      30
gtt caa gat cca aat cta gtc gtt gac gac gtt aac aga agt gta ttc      144
Val Gln Asp Pro Asn Leu Val Val Asp Asp Val Asn Arg Ser Val Phe
35      40      45
aat gcg tca agg agg agc ttg gcc tac cta tct tgt aga acc gga aat      192
Asn Ala Ser Arg Arg Ser Leu Ala Tyr Leu Ser Cys Arg Thr Gly Asn
50      55      60
cct att gac gat tgt tgg cgg tgt gac cct aat tgg gaa aca aac cgc      240
Pro Ile Asp Asp Cys Trp Arg Cys Asp Pro Asn Trp Glu Thr Asn Arg
65      70      75
caa cgg tta gca gat tgt gcc att gga ttt ggc aaa aat gct atc gga      288
Gln Arg Leu Ala Asp Cys Ala Ile Gly Phe Gly Lys Asn Ala Ile Gly
85      90      95
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Gly Arg Lys Gly Arg Ile Tyr Val Val Thr Asp Pro Ala Asn Asp Asp
100      105      110
ccc gta aac cct aga cct ggg act cta aga tat gca gtg aca caa gaa      384
Pro Val Asn Pro Arg Pro Gly Thr Leu Arg Tyr Ala Val Thr Gln Glu
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gaa cca tta tgg atc att ttc aag aga gat atg gtc att agg ctc aaa      432
Glu Pro Leu Trp Ile Ile Phe Lys Arg Asp Met Val Ile Arg Leu Lys
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Ser Val His Ile Thr Asp Gly Pro Cys Leu Lys Ile His Tyr Ala Thr
165      170      175
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Asn Ile Ile Ile His Gly Ile Asn Ile His Asp Cys Lys Pro Gly Ser
180      185      190
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Gly Gly Met Ile Lys Asp Gly Pro His His Thr Gly Trp Trp Met Gln
195      200      205
tcc gat gga gac gcg gtg gcg ata ttt gga ggg aaa cac gtg tgg att      672
Ser Asp Gly Asp Ala Val Ala Ile Phe Gly Gly Lys His Val Trp Ile
210      215      220
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Asp His Cys Ser Leu Ser Asn Cys Asp Asp Gly Leu Ile Asp Ala Ile
225      230      235
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His Gly Ser Thr Ala Ile Thr Ile Ser Asn Asn His Met Thr His His
245      250      255
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Asp Lys Val Met Leu Leu Gly His Ser Asp Ser Tyr Thr Gln Asp Lys
260      265      270
aac atg caa gtc aca att gcg ttt aac cat ttc gga gaa gga ctc gtt      864
Asn Met Gln Val Thr Ile Ala Phe Asn His Phe Gly Glu Gly Leu Val
275      280      285
caa aga atg cca cgg tgc agg cat gga tat ttc cat gta gtg aac aat      912
Gln Arg Met Pro Arg Cys Arg His Gly Tyr Phe His Val Val Asn Asn
290      295      300
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PF59082SeqList_PF59082.txt

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Asp	Trp	Asn 355	Trp	Arg	Ser	Glu 360	Gly	Asp	Met	Leu	Leu	Asn 365	Gly	Ala	Tyr	
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Phe	Arg	Glu	Ser	Gly 370	Ala	Glu 375	Ala	Pro	Ser	Thr	Tyr 380	Ala	Arg	Ala	Ser	
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Ser 385	Leu	Ser	Ala	Arg	Pro 390	Ser	Ser	Leu	Val 395	Gly	Ser	Ile	Thr	Thr	Thr 400	
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<400> 846

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Val	Gln	Asp 35	Pro	Asn	Leu	Val	Val 40	Asp	Asp	Val	Asn	Arg 45	Ser	Val	Phe	
Asn	Ala	Ser	Arg	Arg	Ser	Leu 55	Ala	Tyr	Leu	Ser	Cys 60	Arg	Thr	Gly	Asn	
Pro 65	Ile	Asp	Asp	Cys	Trp 70	Arg	Cys	Asp	Pro	Asn 75	Trp	Glu	Thr	Asn	Arg 80	
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Ser	Val	His	Ile	Thr 165	Asp	Gly	Pro	Cys	Leu 170	Lys	Ile	His	Tyr	Ala 175	Thr	
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PF59082SeqList_PF59082.txt

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 Ile Cys Ile Ile Trp Phe Cys Leu Leu Val Ser Leu Ser His His Gly
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 Arg Ala Ser Ser Thr Ser Ala Ser Ile Phe Asn Leu Ser Leu Pro His
 35 40 45
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 Gln His Pro Phe Pro Glu His Val Val Leu Asn Val Gln Arg Lys Leu
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 Gly Thr Thr Ala Ser Ser Pro Ile Pro Ser Cys Ile Thr Gly Asn Pro
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 Ile Asp Asp Cys Trp Arg Cys Asp Pro Asn Trp Ser Ala Asn Arg Gln
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 Arg Leu Ala Asp Cys Ser Ile Gly Phe Gly Gln Gly Thr Leu Gly Gly
 115 120 125
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 Lys Gly Gly Gln Phe Tyr Leu Val Thr Asp Ser Ser Asp Asn Asp Ala
 130 135 140
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 Ala Asn Pro Ile Pro Gly Thr Leu Arg His Ala Val Ile Gln Pro Glu
 145 150 155 160
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 Ile Gln Ile Thr Gly His Gly Cys Leu Thr Ile Gln Gln Val Ser His
 195 200 205
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 225 230 235 240
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Ala	Ser	Thr	Ala	Val	Thr	Ile	Ser	Asn	Asn	Tyr	Phe	Ser	His	His	Asp	
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Val	Gln	Pro	Lys	Ala	Ala	Ala	Ile	Ile	Asp	Gln	Leu	Thr	Val	Asn	Ala	
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Gly	Val	Phe	Gly	Asp	Pro	Ser	Gly	Arg	Asn	Gly	Gln	Gly	Gly	Ser	Phe	
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Phe	Thr	Leu	Ile	Phe	Gly	Asn	Asn	Ser	Gly	Ala	Val	Ala	Leu	Arg	Pro	
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Gly	Gln	Val	Trp	Ser	Ile	Leu	Leu	Ile	Ile	Ile	Leu	Tyr	Trp	Tyr	Ile	
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Gln	His	Pro	Phe	Pro	Glu	His	Val	Val	Leu	Asn	Val	Gln	Arg	Lys	Leu
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Asn	Asp	Ser	Leu	Ser	Arg	Arg	Gln	Leu	Leu	Thr	Tyr	Gln	Gln	Asp	Asp
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<213> *Oryza sativa* (japonica cultivar-group)

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Ser	Leu	Pro	Asp	Pro	Ala	Ala	Val	Val	Ala	Asp	Phe	His	Ser	Lys	Val	
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Gly	Ile	Gly	Phe	Gly	Arg	Asn	Ala	Met	Gly	Gly	Lys	Gly	Gly	Pro	Val	
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tcg	cgc	tgc	gcc	gac	ggc	ctc	atc	gac	gcc	atc	atg	ggg	tcc	acg	gcg	768
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Leu	Gly	His	Ser	Asp	Gly	Tyr	Leu	Pro	Asp	Ser	Ala	Met	Gln	Val	Thr	
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Glu	Met	Tyr	Ala	Ile	Gly	Gly	Ser	Ala	Ser	Pro	Thr	Ile	Asn	Gln		
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Lys	Arg	Val	Asp	Thr	Glu	Glu	Gly	Gln	Trp	Ala	Gly	Trp	Asn	Trp	Arg	
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Glu	Gly	Leu	Glu	Ala	Ile	Tyr	Asp	Lys	Ala	Ser	Ser	Thr	Asp	Pro	Lys	
385					390					395					400	
tcg	tcg	gcg	ctc	gtc	gac	cag	ctc	acc	gcc	ggc	gcc	ggc	gtc	ctc	ggc	1248
Ser	Ser	Ala	Leu	Val	Asp	Gln	Leu	Thr	Ala	Gly	Ala	Gly	Val	Leu	Gly	
				405					410					415		
ggc	ccc	aga	gga	gtt	ggg	tct	gga	gtg	gat	cta	att	cat	ttt	gtg	aga	1296
Gly	Pro	Arg	Gly	Val	Gly	Ser	Gly	Val	Asp	Leu	Ile	His	Phe	Val	Arg	
			420		425								430			
gct	cca	tcc	aac	tcc	act	ccc	agt	tct	agt	gga	gct	gaa	act	gtt	tgg	1344
Ala	Pro	Ser	Asn	Ser	Thr	Pro	Ser	Ser	Ser	Gly	Ala	Glu	Thr	Val	Trp	
			435				440					445				
cca	agc	tcc	agc	tct	aga	agg	ggg	gga	gct	gga	gct	gtg	cca	aac	agg	1392
Pro	Ser	Ser	Ser	Ser	Arg	Arg	Gly	Gly	Ala	Gly	Ala	Val	Pro	Asn	Arg	
	450					455					460					
ccc	gta	cta	tag													1404
Pro	Val	Leu														
465																

<210> 850

<211> 467

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<400> 850

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Ala	Thr	Leu	Leu	Leu	Leu	Pro	Pro	Pro	Leu	Ala	Ala	Ser	Leu	Asn	Ser	
			20					25					30			
Ser	Leu	Pro	Asp	Pro	Ala	Ala	Val	Val	Ala	Asp	Phe	His	Ser	Lys	Val	
		35					40					45				
Ala	Thr	Ser	Arg	Arg	Arg	Met	Gln	Lys	Ala	Asp	Gly	Gly	Gly	Gly	Gly	
	50					55				60						
Gly	Gly	Gly	Gly	Cys	Leu	Thr	Gly	Asn	Pro	Ile	Asp	His	Cys	Trp	Arg	
65				70					75						80	
Cys	Ala	Gly	Thr	Asp	Trp	Arg	Gln	Asp	Arg	Gln	Arg	Leu	Ala	Asp	Cys	
			85					90						95		
Gly	Ile	Gly	Phe	Gly	Arg	Asn	Ala	Met	Gly	Gly	Lys	Gly	Gly	Pro	Val	
			100					105					110			
Tyr	Val	Val	Thr	Asp	Pro	Ser	Asp	Gly	Asp	Pro	Val	Asn	Pro	Ala	Pro	
		115					120					125				
Gly	Thr	Leu	Arg	Tyr	Gly	Ala	Ile	Gln	Glu	Gly	Pro	Leu	Trp	Ile	Val	
	130					135				140						
Phe	Ala	Gly	Asp	Met	Thr	Ile	Arg	Leu	Asn	Glu	Glu	Leu	Leu	Val	Asn	
145				150					155						160	
Ser	Tyr	Lys	Thr	Ile	Asp	Gly	Arg	Gly	Ala	Asn	Val	His	Val	Gly	Ala	
			165					170						175		
Gly	Gly	Ala	Cys	Ile	Thr	Leu	Gln	Tyr	Val	Ser	Asn	Val	Ile	Ile	His	
			180					185					190			
Asn	Ile	His	Val	His	Asp	Cys	Val	Pro	Ala	Gly	Asn	Ala	Asn	Val	Arg	
		195					200					205				
Ala	Ser	Pro	Thr	His	Tyr	Gly	Trp	Arg	Thr	Arg	Ser	Asp	Gly	Asp	Gly	
	210					215					220					
Ile	Ser	Leu	Tyr	Ser	Ala	Arg	Asp	Val	Trp	Val	Asp	His	Cys	Ala	Leu	
225					230					235					240	
Ser	Arg	Cys	Ala	Asp	Gly	Leu	Ile	Asp	Ala	Ile	Met	Gly	Ser	Thr	Ala	
			245						250					255		
Ile	Thr	Val	Ser	Asn	Ser	Tyr	Phe	Ser	His	His	Asn	Glu	Val	Met	Leu	
			260					265					270			
Leu	Gly	His	Ser	Asp	Gly	Tyr	Leu	Pro	Asp	Ser	Ala	Met	Gln	Val	Thr	
		275					280					285				
Ile	Ala	Phe	Asn	His	Phe	Gly	Ile	Gln	Leu	Val	Gln	Arg	Met	Pro	Arg	
	290					295					300					
Cys	Arg	Arg	Gly	Tyr	Phe	His	Ile	Val	Asn	Asn	Asp	Tyr	Thr	Ala	Trp	
305					310					315					320	
Glu	Met	Tyr	Ala	Ile	Gly	Gly	Ser	Ala	Ser	Pro	Thr	Ile	Asn	Ser	Gln	
			325						330					335		
Gly	Asn	Arg	Tyr	Ile	Ala	Pro	Ala	Asp	Pro	Asn	Ala	Lys	Glu	Val	Thr	
			340					345					350			

PF59082SeqList_PF59082.txt

Lys Arg Val Asp Thr Glu Glu Gly Gln Trp Ala Gly Trp Asn Trp Arg
 355 360 365
 Thr Glu Gly Asp Met Met Val Asn Gly Ala Phe Phe Val Pro Ser Gly
 370 375 380
 Glu Gly Leu Glu Ala Ile Tyr Asp Lys Ala Ser Ser Thr Asp Pro Lys
 385 390 395 400
 Ser Ser Ala Leu Val Asp Gln Leu Thr Ala Gly Ala Gly Val Leu Gly
 405 410 415
 Gly Pro Arg Gly Val Gly Ser Gly Val Asp Leu Ile His Phe Val Arg
 420 425 430
 Ala Pro Ser Asn Ser Thr Pro Ser Ser Gly Ala Glu Thr Val Trp
 435 440 445
 Pro Ser Ser Ser Ser Arg Arg Gly Gly Ala Gly Ala Val Pro Asn Arg
 450 455 460
 Pro Val Leu
 465

<210> 851

<211> 1419

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<221> CDS

<222> (1)..(1419)

<400> 851

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Met	Ala	Glu	Ala	Ala	Ala	Arg	Arg	Trp	Ala	Ala	Ala	Leu	Val	Leu	Leu	
1				5					10					15		
gtg	ctt	ctc	acc	ggc	acc	gtc	gag	ctc	atc	ggc	ggc	gga	ggc	ggg	agg	96
Val	Leu	Leu	Thr	Gly	Thr	Val	Glu	Leu	Ile	Gly	Gly	Gly	Gly	Gly	Ser	
			20				25						30			
ggc	ggg	cgg	cgg	ctt	ctc	gct	ggc	ctc	cgg	gcc	ggg	agc	acg	gcg	gcg	144
Gly	Gly	Arg	Arg	Leu	Leu	Ala	Gly	Leu	Arg	Ala	Gly	Ser	Thr	Ala	Ala	
		35					40					45				
gcg	agc	ggc	acg	cgg	cgg	tgg	ctg	cgc	gac	tcg	tcc	tgg	ccg	gcg	acg	192
Ala	Ser	Gly	Thr	Arg	Arg	Trp	Leu	Arg	Asp	Ser	Ser	Trp	Pro	Ala	Thr	
	50					55				60						
gcg	gcg	gcc	gcg	gcg	gcg	gcg	aga	gga	gat	gac	ggt	gat	ggc	gat	gag	240
Ala	Ala	Ala	Ala	Ala	Ala	Ala	Arg	Gly	Asp	Asp	Gly	Asp	Gly	Asp	Glu	
	65				70				75						80	
gcg	tcg	tcg	gcg	gcg	atg	acg	gtg	ccc	ggc	gcg	gtg	gac	gac	ccg	gag	288
Ala	Ser	Ser	Ala	Ala	Met	Thr	Val	Pro	Gly	Ala	Val	Asp	Asp	Pro	Glu	
				85					90					95		
gag	gtg	gtc	tcg	caa	gtg	cac	atg	tcg	atc	agg	aac	agc	acg	gcg	agg	336
Glu	Val	Val	Ser	Gln	Val	His	Met	Ser	Ile	Arg	Asn	Ser	Thr	Ala	Arg	
			100				105					110				
agg	aag	ctg	ggc	tac	ctg	tcg	tgc	ggc	acc	ggc	aat	ccg	atc	gac	gac	384
Arg	Lys	Leu	Gly	Tyr	Leu	Ser	Cys	Gly	Thr	Gly	Asn	Pro	Ile	Asp	Asp	
		115					120					125				
tgc	tgg	agg	tgc	gac	ccg	gac	tgg	cac	aag	aat	cgc	cag	cgg	ctc	gcc	432
Cys	Trp	Arg	Cys	Asp	Pro	Asp	Trp	His	Lys	Asn	Arg	Gln	Arg	Leu	Ala	
	130					135					140					
gac	tgc	ggc	atc	ggc	ttc	ggc	cgc	aac	gcc	atc	ggc	ggc	cgc	gac	ggc	480
Asp	Cys	Gly	Ile	Gly	Phe	Gly	Arg	Asn	Ala	Ile	Gly	Gly	Arg	Asp	Gly	
	145				150					155					160	
aag	atc	tac	gtg	gtc	acc	gac	ccc	agc	gac	gac	gac	gcg	gtg	aac	ccc	528
Lys	Ile	Tyr	Val	Val	Thr	Asp	Pro	Ser	Asp	Asp	Asp	Ala	Val	Asn	Pro	
				165					170					175		
aag	aag	ggc	acg	ctc	cgg	tac	gcc	gtc	atc	cgc	gac	gag	ccg	ctg	tgg	576
Lys	Lys	Gly	Thr	Leu	Arg	Tyr	Ala	Val	Ile	Arg	Asp	Glu	Pro	Leu	Trp	
			180				185					190				
atc	gtc	ttc	aag	cgc	gac	atg	gtg	atc	acg	ctc	aag	cag	gag	ctg	atc	624
Ile	Val	Phe	Lys	Arg	Asp	Met	Val	Ile	Thr	Leu	Lys	Gln	Glu	Leu	Ile	
		195				200						205				
atg	aac	agc	ttc	aag	acc	atc	gac	ggc	cgt	ggc	gcc	aac	gtg	cac	atc	672
Met	Asn	Ser	Phe	Lys	Thr	Ile	Asp	Gly	Arg	Gly	Ala	Asn	Val	His	Ile	
	210					215					220					

PF59082SeqList_PF59082.txt

gcc	aat	ggc	gcc	tgc	atc	acc	atc	cag	tac	gtc	acc	aac	gtc	atc	atc	720
Ala	Asn	Gly	Ala	Cys	Ile	Thr	Ile	Gln	Tyr	Val	Thr	Asn	Val	Ile	Ile	
225				230				235		235				240		
cat	ggc	ctg	cac	atc	cat	gac	tgc	agg	ccc	acc	ggc	aat	gcc	atg	gtc	768
His	Gly	Leu	His	Ile	His	Asp	Cys	Arg	Pro	Thr	Gly	Asn	Ala	Met	Val	
				245				250						255		
cgg	agc	tcg	ccc	agc	cac	tac	ggg	tgg	cgc	acc	atg	gcc	gac	ggc	gac	816
Arg	Ser	Ser	Pro	Ser	His	Tyr	Gly	Trp	Arg	Thr	Met	Ala	Asp	Gly	Asp	
			260					265					270			
gcc	gtc	tcc	atc	ttc	ggc	gcc	agc	cac	atc	tgg	gtt	gac	cat	tgc	tcg	864
Ala	Val	Ser	Ile	Phe	Gly	Ala	Ser	His	Ile	Trp	Val	Asp	His	Cys	Ser	
			275					280					285			
ctc	tcc	aac	tgc	gcc	gac	ggc	ctc	atc	gac	gcc	atc	atg	ggt	tcc	act	912
Leu	Ser	Asn	Cys	Ala	Asp	Gly	Leu	Ile	Asp	Ala	Ile	Met	Gly	Ser	Thr	
			290			295					300					
gca	atc	aca	gtg	tcc	aac	aac	tac	ttc	acc	cac	cac	aat	gag	gtg	atg	960
Ala	Ile	Thr	Val	Ser	Asn	Asn	Tyr	Phe	Thr	His	His	Asn	Glu	Val	Met	
305					310					315					320	
ctc	ctg	ggt	cac	agc	gat	tcc	tat	gtc	aag	gac	aag	gca	atg	cag	gtc	1008
Leu	Leu	Gly	His	Ser	Asp	Ser	Tyr	Val	Lys	Asp	Lys	Ala	Met	Gln	Val	
				325				330						335		
acg	ata	gca	ttc	aac	cat	ttc	gga	gaa	ggt	ctt	att	cag	aga	atg	cca	1056
Thr	Ile	Ala	Phe	Asn	His	Phe	Gly	Glu	Gly	Leu	Ile	Gln	Arg	Met	Pro	
			340					345					350			
agg	tgc	agg	cat	ggt	tac	ttc	cat	gtg	gtg	aac	aat	gac	tac	acc	cac	1104
Arg	Cys	Arg	His	Gly	Tyr	Phe	His	Val	Val	Asn	Asn	Asp	Tyr	Thr	His	
			355				360						365			
tgg	gag	atg	tac	gca	att	ggt	gga	agt	gct	gag	cca	acc	atc	aac	agc	1152
Trp	Glu	Met	Tyr	Ala	Ile	Gly	Gly	Ser	Ala	Glu	Pro	Thr	Ile	Asn	Ser	
			370			375					380					
cag	ggc	aac	cgc	tac	ctt	gct	ccg	aca	aat	ccc	ttt	gcc	aag	gag	gtt	1200
Gln	Gly	Asn	Arg	Tyr	Leu	Ala	Pro	Thr	Asn	Pro	Phe	Ala	Lys	Glu	Val	
385					390					395					400	
aca	aag	agg	gtt	gag	act	gct	cag	acc	atc	tgg	aag	ggc	tgg	aac	tgg	1248
Thr	Lys	Arg	Val	Glu	Thr	Ala	Gln	Thr	Ile	Trp	Lys	Gly	Trp	Asn	Trp	
				405				410						415		
aga	tca	gag	ggg	gat	ctc	ctc	ctg	aac	ggc	gcc	ttc	ttc	acc	cca	tca	1296
Arg	Ser	Glu	Gly	Asp	Leu	Leu	Leu	Asn	Gly	Ala	Phe	Phe	Thr	Pro	Ser	
			420					425					430			
ggt	gca	ggc	gcc	tcg	gcc	agc	tac	tcg	cgc	gcc	tca	agc	ctc	ggt	gcc	1344
Gly	Ala	Gly	Ala	Ser	Ala	Ser	Tyr	Ser	Arg	Ala	Ser	Ser	Leu	Gly	Ala	
			435				440					445				
aag	tca	tca	tcc	atg	gtt	ggc	acc	atc	aca	tcc	ggt	gcg	ggc	gcc	ttg	1392
Lys	Ser	Ser	Ser	Met	Val	Gly	Thr	Ile	Thr	Ser	Gly	Ala	Gly	Ala	Leu	
			450			455					460					
tcg	tgc	cgc	ggg	ggc	tca	gcc	tgc	tag								1419
Ser	Cys	Arg	Gly	Gly	Ser	Ala	Cys									
465					470											

<210> 852

<211> 472

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<400> 852

Met	Ala	Glu	Ala	Ala	Ala	Arg	Arg	Trp	Ala	Ala	Ala	Leu	Val	Leu	Leu	
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Val	Leu	Leu	Thr	Gly	Thr	Val	Glu	Leu	Ile	Gly	Gly	Gly	Gly	Gly	Ser	
			20				25						30			
Gly	Gly	Arg	Leu	Leu	Ala	Gly	Leu	Arg	Ala	Gly	Ser	Thr	Ala	Ala		
			35			40						45				
Ala	Ser	Gly	Thr	Arg	Arg	Trp	Leu	Arg	Asp	Ser	Ser	Trp	Pro	Ala	Thr	
			50			55					60					
Ala	Ala	Ala	Ala	Ala	Ala	Ala	Arg	Gly	Asp	Asp	Gly	Asp	Gly	Asp	Glu	
65				70						75					80	
Ala	Ser	Ser	Ala	Ala	Met	Thr	Val	Pro	Gly	Ala	Val	Asp	Asp	Pro	Glu	
			85					90						95		
Glu	Val	Val	Ser	Gln	Val	His	Met	Ser	Ile	Arg	Asn	Ser	Thr	Ala	Arg	
			100					105					110			

PF59082SeqList_PF59082.txt

Arg Lys Leu Gly Tyr Leu Ser Cys Gly Thr Gly Asn Pro Ile Asp Asp
 115 120 125
 Cys Trp Arg Cys Asp Pro Asp Trp His Lys Asn Arg Gln Arg Leu Ala
 130 135 140
 Asp Cys Gly Ile Gly Phe Gly Arg Asn Ala Ile Gly Gly Arg Asp Gly
 145 150 155 160
 Lys Ile Tyr Val Val Thr Asp Pro Ser Asp Asp Ala Val Asn Pro
 165 170 175
 Lys Lys Gly Thr Leu Arg Tyr Ala Val Ile Arg Asp Glu Pro Leu Trp
 180 185 190
 Ile Val Phe Lys Arg Asp Met Val Ile Thr Leu Lys Gln Glu Leu Ile
 195 200 205
 Met Asn Ser Phe Lys Thr Ile Asp Gly Arg Gly Ala Asn Val His Ile
 210 215 220
 Ala Asn Gly Ala Cys Ile Thr Ile Gln Tyr Val Thr Asn Val Ile Ile
 225 230 235 240
 His Gly Leu His Ile His Asp Cys Arg Pro Thr Gly Asn Ala Met Val
 245 250 255
 Arg Ser Ser Pro Ser His Tyr Gly Trp Arg Thr Met Ala Asp Gly Asp
 260 265 270
 Ala Val Ser Ile Phe Gly Ala Ser His Ile Trp Val Asp His Cys Ser
 275 280 285
 Leu Ser Asn Cys Ala Asp Gly Leu Ile Asp Ala Ile Met Gly Ser Thr
 290 295 300
 Ala Ile Thr Val Ser Asn Asn Tyr Phe Thr His His Asn Glu Val Met
 305 310 315 320
 Leu Leu Gly His Ser Asp Ser Tyr Val Lys Asp Lys Ala Met Gln Val
 325 330 335
 Thr Ile Ala Phe Asn His Phe Gly Glu Gly Leu Ile Gln Arg Met Pro
 340 345 350
 Arg Cys Arg His Gly Tyr Phe His Val Val Asn Asn Asp Tyr Thr His
 355 360 365
 Trp Glu Met Tyr Ala Ile Gly Gly Ser Ala Glu Pro Thr Ile Asn Ser
 370 375 380
 Gln Gly Asn Arg Tyr Leu Ala Pro Thr Asn Pro Phe Ala Lys Glu Val
 385 390 395 400
 Thr Lys Arg Val Glu Thr Ala Gln Thr Ile Trp Lys Gly Trp Asn Trp
 405 410 415
 Arg Ser Glu Gly Asp Leu Leu Leu Asn Gly Ala Phe Phe Thr Pro Ser
 420 425 430
 Gly Ala Gly Ala Ser Ala Ser Tyr Ser Arg Ala Ser Ser Leu Gly Ala
 435 440 445
 Lys Ser Ser Ser Met Val Gly Thr Ile Thr Ser Gly Ala Gly Ala Leu
 450 455 460
 Ser Cys Arg Gly Gly Ser Ala Cys
 465 470

<210> 853
 <211> 1242
 <212> DNA
 <213> Prunus mume

<220>
 <221> CDS
 <222> (1)..(1242)

<400> 853	
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Met 1 Ala Arg Pro Ser 5 Ser Gly Pro Ser 10 Leu Ser Leu Leu 15 Phe	
ctc ctc ttc tct ctc ctc acc cca acc ctc att gcc tcc aga cca ttg	96
Leu Leu Phe Ser 20 Leu Leu Thr Pro Thr 25 Leu Ile Ala Ser Arg 30 Pro Leu	
cag caa aac cct gaa ttg gtt gta caa gat gta caa cgg agc atc aat	144
Gln Gln 35 Asn Pro Glu Leu Val 40 Gln Asp Val Gln Arg 45 Ser Ile Asn	
gac tct gtt tct agg agg aac ttg ggc tac ttg tca tgt ggg act gga	192
Asp Ser 50 Val Ser Arg Arg Asn 55 Leu Gly Tyr Leu Ser 60 Cys Gly Thr Gly	

PF59082SeqList_PF59082.txt

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Asn	Pro	Ile	Asp	Asp	Cys	Trp	Arg	Cys	Asp	Pro	Asn	Trp	Glu	Gln	Asn	
65					70				75						80	
agg	gag	agg	ctg	gca	gat	tgc	gca	att	ggg	ttt	ggg	aaa	aat	gcc	gtt	288
Arg	Glu	Arg	Leu	Ala	Asp	Cys	Ala	Ile	Gly	Phe	Gly	Lys	Asn	Ala	Val	
				85					90					95		
ggg	gga	aga	gat	ggc	aag	att	tac	gtg	gtc	acg	gat	tca	ggg	gat	agc	336
Gly	Gly	Arg	Asp	Gly	Lys	Ile	Tyr	Val	Val	Thr	Asp	Ser	Gly	Asp	Ser	
			100				105					110				
gac	cct	gta	aac	cca	aag	cca	ggg	act	cta	cga	cat	gcc	ggt	att	cag	384
Asp	Pro	Val	Asn	Pro	Lys	Pro	Gly	Thr	Leu	Arg	His	Ala	Val	Ile	Gln	
		115					120					125				
gac	gag	cca	ctg	tgg	atc	atc	ttc	cag	cgt	gac	atg	aca	atc	caa	ctg	432
Asp	Glu	Pro	Leu	Trp	Ile	Ile	Phe	Gln	Arg	Asp	Met	Thr	Ile	Gln	Leu	
	130					135					140					
aag	gaa	gag	ctg	atc	atg	aac	tct	ttc	aag	acc	atc	gac	ggg	cga	gga	480
Lys	Glu	Glu	Leu	Ile	Met	Asn	Ser	Phe	Lys	Thr	Ile	Asp	Gly	Arg	Gly	
145				150					155					160		
gcc	agc	gtg	cac	att	gct	ggg	cca	tgc	atc	acc	atc	caa	ttt	gtg		528
Ala	Ser	Val	His	Ile	Ala	Gly	Gly	Pro	Cys	Ile	Thr	Ile	Gln	Phe	Val	
				165				170					175			
acc	aac	att	atc	att	cat	ggg	ctg	cac	ata	cac	gat	tgc	aag	cag	gga	576
Thr	Asn	Ile	Ile	Ile	His	Gly	Leu	His	Ile	His	Asp	Cys	Lys	Gln	Gly	
		180					185					190				
ggg	aat	gct	atg	gtg	cgg	tcc	tcc	cga	gag	cac	tac	ggg	tgg	agg	act	624
Gly	Asn	Ala	Met	Val	Arg	Ser	Ser	Pro	Glu	His	Tyr	Gly	Trp	Arg	Thr	
		195				200						205				
ata	tcc	gac	ggg	gat	ggc	gtg	tcc	atc	ttc	ggg	ggg	agc	cac	gtg	tgg	672
Ile	Ser	Asp	Gly	Asp	Gly	Val	Ser	Ile	Phe	Gly	Gly	Ser	His	Val	Trp	
	210					215					220					
gtg	gat	cat	tgc	tct	ttg	tca	aat	tgc	aaa	gat	ggg	ttg	ggt	gat	gca	720
Val	Asp	His	Cys	Ser	Leu	Ser	Asn	Cys	Lys	Asp	Gly	Leu	Val	Asp	Ala	
225				230				235						240		
att	cat	ggg	tcc	act	gcc	ata	aca	att	tct	aac	aat	tac	atg	act	cac	768
Ile	His	Gly	Ser	Thr	Ala	Ile	Thr	Ile	Ser	Asn	Asn	Tyr	Met	Thr	His	
				245				250					255			
cat	gac	aaa	gtg	atg	ttg	ctt	ggg	cat	agc	gat	tct	tat	acc	gaa	gat	816
His	Asp	Lys	Val	Met	Leu	Leu	Gly	His	Ser	Asp	Ser	Tyr	Thr	Glu	Asp	
		260					265					270				
aag	aac	atg	caa	gtc	acc	att	gcc	ttc	aat	cac	ttt	gga	gaa	ggg	ttg	864
Lys	Asn	Met	Gln	Val	Thr	Ile	Ala	Phe	Asn	His	Phe	Gly	Glu	Gly	Leu	
		275					280					285				
gtc	cag	cga	atg	cca	aga	tgt	agg	cat	gga	tat	ttc	cat	gtg	gtg	aac	912
Val	Gln	Arg	Met	Pro	Arg	Cys	Arg	His	Gly	Tyr	Phe	His	Val	Val	Asn	
	290					295					300					
aat	gac	tac	acc	cat	tgg	gag	atg	tat	gcc	att	gga	ggc	agt	gcc	aac	960
Asn	Asp	Tyr	Thr	His	Trp	Glu	Met	Tyr	Ala	Ile	Gly	Gly	Ser	Ala	Asn	
305				310					315					320		
cct	aca	atc	aat	agc	caa	ggg	aat	aga	ttt	gct	gca	cca	gat	atc	aga	1008
Pro	Thr	Ile	Asn	Ser	Gln	Gly	Asn	Arg	Phe	Ala	Ala	Pro	Asp	Ile	Arg	
				325				330						335		
ttt	agc	aaa	gag	gtg	aca	aaa	cat	gag	gat	gca	cca	gaa	agt	gag	tgg	1056
Phe	Ser	Lys	Glu	Val	Thr	Lys	His	Glu	Asp	Ala	Pro	Glu	Ser	Glu	Trp	
		340					345					350				
agg	aat	tgg	aat	tgg	agg	tct	gaa	gga	gac	ttg	atg	ata	aat	ggg	gca	1104
Arg	Asn	Trp	Asn	Trp	Arg	Ser	Glu	Gly	Asp	Leu	Met	Ile	Asn	Gly	Ala	
		355				360					365					
ttt	ttt	aca	gca	tca	gga	gct	gga	gct	tcc	tca	agc	tat	gca	agg	gct	1152
Phe	Phe	Thr	Ala	Ser	Gly	Ala	Gly	Ala	Ser	Ser	Ser	Tyr	Ala	Arg	Ala	
	370				375						380					
tca	agc	ttg	ggg	gca	aag	cca	tct	tct	cta	gtg	ggg	tca	ata	acc	aca	1200
Ser	Ser	Leu	Gly	Ala	Lys	Pro	Ser	Ser	Leu	Val	Gly	Ser	Ile	Thr	Thr	
385				390					395						400	
gct	tct	ggg	gca	ctt	agc	tgc	aga	aag	ggg	tct	cgt	tgc	tga			1242
Ala	Ser	Gly	Ala	Leu	Ser	Cys	Arg	Lys	Gly	Ser	Arg	Cys				
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<210> 854

<211> 413

PF59082SeqList_PF59082.txt

<212> PRT

<213> Prunus mume

<400> 854

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Leu Leu Phe Ser Leu Leu Thr Pro Thr Leu Ile Ala Ser Arg Pro Leu
      20      25      30
Gln Gln Asn Pro Glu Leu Val Val Gln Asp Val Gln Arg Ser Ile Asn
      35      40      45
Asp Ser Val Ser Arg Arg Asn Leu Gly Tyr Leu Ser Cys Gly Thr Gly
      50      55      60
Asn Pro Ile Asp Asp Cys Trp Arg Cys Asp Pro Asn Trp Glu Gln Asn
      65      70      75      80
Arg Glu Arg Leu Ala Asp Cys Ala Ile Gly Phe Gly Lys Asn Ala Val
      85      90      95
Gly Gly Arg Asp Gly Lys Ile Tyr Val Val Thr Asp Ser Gly Asp Ser
      100      105      110
Asp Pro Val Asn Pro Lys Pro Gly Thr Leu Arg His Ala Val Ile Gln
      115      120      125
Asp Glu Pro Leu Trp Ile Ile Phe Gln Arg Asp Met Thr Ile Gln Leu
      130      135      140
Lys Glu Glu Leu Ile Met Asn Ser Phe Lys Thr Ile Asp Gly Arg Gly
      145      150      155      160
Ala Ser Val His Ile Ala Gly Gly Pro Cys Ile Thr Ile Gln Phe Val
      165      170      175
Thr Asn Ile Ile Ile His Gly Leu His Ile His Asp Cys Lys Gln Gly
      180      185      190
Gly Asn Ala Met Val Arg Ser Ser Pro Glu His Tyr Gly Trp Arg Thr
      195      200      205
Ile Ser Asp Gly Asp Gly Val Ser Ile Phe Gly Gly Ser His Val Trp
      210      215      220
Val Asp His Cys Ser Leu Ser Asn Cys Lys Asp Gly Leu Val Asp Ala
      225      230      235      240
Ile His Gly Ser Thr Ala Ile Thr Ile Ser Asn Asn Tyr Met Thr His
      245      250      255
His Asp Lys Val Met Leu Leu Gly His Ser Asp Ser Tyr Thr Glu Asp
      260      265      270
Lys Asn Met Gln Val Thr Ile Ala Phe Asn His Phe Gly Glu Gly Leu
      275      280      285
Val Gln Arg Met Pro Arg Cys Arg His Gly Tyr Phe His Val Val Asn
      290      295      300
Asn Asp Tyr Thr His Trp Glu Met Tyr Ala Ile Gly Gly Ser Ala Asn
      305      310      315      320
Pro Thr Ile Asn Ser Gln Gly Asn Arg Phe Ala Ala Pro Asp Ile Arg
      325      330      335
Phe Ser Lys Glu Val Thr Lys His Glu Asp Ala Pro Glu Ser Glu Trp
      340      345      350
Arg Asn Trp Asn Trp Arg Ser Glu Gly Asp Leu Met Ile Asn Gly Ala
      355      360      365
Phe Phe Thr Ala Ser Gly Ala Gly Ala Ser Ser Ser Tyr Ala Arg Ala
      370      375      380
Ser Ser Leu Gly Ala Lys Pro Ser Ser Leu Val Gly Ser Ile Thr Thr
      385      390      395      400
Ala Ser Gly Ala Leu Ser Cys Arg Lys Gly Ser Arg Cys
      405      410

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<210> 855

<211> 1539

<212> DNA

<213> Gossypium hirsutum

<220>

<221> CDS

<222> (36)..(1271)

<400> 855

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Met Ala Arg Thr Met Ala

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PF59082SeqList_PF59082.txt

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Met	Ala	Ile	Pro	Ser	Leu	Pro	Leu	Leu	Phe	Leu	Phe	Thr	Phe	Leu	Leu	
			10					15					20			
cta	ctc	cca	ctt	ctc	att	tcc	tct	tcc	cct	gtt	caa	gac	cct	gag	ctt	149
Leu	Leu	Pro	Leu	Leu	Ile	Ser	Ser	Ser	Pro	Val	Gln	Asp	Pro	Glu	Leu	
			25				30					35				
gtt	gtc	caa	gat	gtt	cac	agg	gct	atc	aat	gcg	tcc	aag	agg	aac	cta	197
Val	Val	Gln	Asp	Val	His	Arg	Ala	Ile	Asn	Ala	Ser	Lys	Arg	Asn	Leu	
			40			45					50					
ggg	tat	ctc	tcc	tgt	gga	acc	gga	aac	ccc	att	gat	gac	tgc	tgg	aga	245
Gly	Tyr	Leu	Ser	Cys	Gly	Thr	Gly	Asn	Pro	Ile	Asp	Asp	Cys	Trp	Arg	
					60				65						70	
tgt	gac	ccc	aac	tgg	gag	act	aat	cgc	cag	aag	cta	gct	gat	tgt	gcc	293
Cys	Asp	Pro	Asn	Trp	Glu	Thr	Asn	Arg	Gln	Lys	Leu	Ala	Asp	Cys	Ala	
				75				80						85		
att	gga	ttc	ggc	aag	aac	gcc	att	ggg	gga	aga	gat	ggg	aag	att	tat	341
Ile	Gly	Phe	Gly	Lys	Asn	Ala	Ile	Gly	Gly	Arg	Asp	Gly	Lys	Ile	Tyr	
			90				95						100			
gtg	gtc	act	gac	tcc	ggc	gat	gat	gac	ccc	gtt	aac	ccc	aaa	cca	ggg	389
Val	Val	Thr	Asp	Ser	Gly	Asp	Asp	Asp	Pro	Val	Asn	Pro	Lys	Pro	Gly	
			105			110						115				
aca	tta	cgg	cat	gcg	gtg	att	caa	ggc	gaa	ccg	ttg	tgg	atc	att	ttc	437
Thr	Leu	Arg	His	Ala	Val	Ile	Gln	Gly	Glu	Pro	Leu	Trp	Ile	Ile	Phe	
			120			125					130					
gct	cgt	gac	atg	acc	att	cag	ctg	aaa	gaa	gag	ctg	ata	atg	aac	tca	485
Ala	Arg	Asp	Met	Thr	Ile	Gln	Leu	Lys	Glu	Glu	Leu	Ile	Met	Asn	Ser	
					140				145						150	
ttc	aag	acc	atc	gac	ggg	agg	ggc	gcc	agc	ggt	cat	att	gca	ggg	ggg	533
Phe	Lys	Thr	Ile	Asp	Gly	Arg	Gly	Ala	Ser	Val	His	Ile	Ala	Gly	Gly	
				155				160						165		
cca	tgc	att	acc	gtt	cag	tat	gtg	acc	aac	att	atc	att	cat	gga	ctc	581
Pro	Cys	Ile	Thr	Val	Gln	Tyr	Val	Thr	Asn	Ile	Ile	Ile	His	Gly	Leu	
				170			175						180			
aac	ata	cac	gat	tgt	aaa	caa	gga	ggg	aat	gct	atg	gtg	agg	gac	tcc	629
Asn	Ile	His	Asp	Cys	Lys	Gln	Gly	Gly	Asn	Ala	Met	Val	Arg	Asp	Ser	
				185			190					195				
cca	cgt	cac	tat	ggg	tgg	agg	acg	ata	tca	gac	ggg	gat	ggg	gtt	tcc	677
Pro	Arg	His	Tyr	Gly	Trp	Arg	Thr	Ile	Ser	Asp	Gly	Asp	Gly	Val	Ser	
						205					210					
atc	ttc	ggg	ggg	agc	cat	gtt	tgg	gtt	gac	cat	aac	tcc	tta	tca	aac	725
Ile	Phe	Gly	Gly	Ser	His	Val	Trp	Val	Asp	His	Asn	Ser	Leu	Ser	Asn	
					220				225						230	
tgc	aaa	gac	ggc	ttg	att	gac	gct	atc	cat	ggc	tcc	acc	gct	atc	acc	773
Cys	Lys	Asp	Gly	Leu	Ile	Asp	Ala	Ile	His	Gly	Ser	Thr	Ala	Ile	Thr	
				235				240						245		
att	tcc	aac	aat	tac	atg	act	cac	cat	gat	aaa	gtc	atg	tta	ttg	gga	821
Ile	Ser	Asn	Asn	Tyr	Met	Thr	His	His	Asp	Lys	Val	Met	Leu	Leu	Gly	
				250			255						260			
cac	agt	gat	tcc	tat	act	caa	gac	aag	aac	atg	caa	gtc	act	att	gcc	869
His	Ser	Asp	Ser	Tyr	Thr	Gln	Asp	Lys	Asn	Met	Gln	Val	Thr	Ile	Ala	
							270					275				
ttt	aat	cac	ttt	ggg	gaa	ggc	ctt	gtc	caa	aga	atg	cca	cga	tgt	aga	917
Phe	Asn	His	Phe	Gly	Glu	Gly	Leu	Val	Gln	Arg	Met	Pro	Arg	Cys	Arg	
						285					290					
cat	ggg	tat	ttc	cac	gtg	gtg	aac	aat	gac	tat	act	cat	tgg	gaa	atg	965
His	Gly	Tyr	Phe	His	Val	Val	Asn	Asn	Asp	Tyr	Thr	His	Trp	Glu	Met	
					300				305						310	
tat	gcc	att	gga	gga	agt	gct	aac	cca	aca	ata	aac	agc	caa	ggg	aat	1013
Tyr	Ala	Ile	Gly	Gly	Ser	Ala	Asn	Pro	Thr	Ile	Asn	Ser	Gln	Gly	Asn	
				315				320						325		
aga	ttt	act	gca	cct	gac	aac	aga	ttc	agc	aaa	gag	gtg	acc	aag	cat	1061
Arg	Phe	Thr	Ala	Pro	Asp	Asn	Arg	Phe	Ser	Lys	Glu	Val	Thr	Lys	His	
				330			335						340			
gag	gat	gca	ccg	gag	agt	gaa	tgg	aag	agc	tgg	aat	tgg	aga	tcg	gaa	1109
Glu	Asp	Ala	Pro	Glu	Ser	Glu	Trp	Lys	Ser	Trp	Asn	Trp	Arg	Ser	Glu	
				345			350					355				
ggg	gac	cta	atg	gtg	aac	ggg	gca	ttc	ttt	atc	tcg	tcg	ggg	gct	ggc	1157
Gly	Asp	Leu	Met	Val	Asn	Gly	Ala	Phe	Ile	Ser	Ser	Gly	Ala	Gly		

PF59082SeqList_PF59082.txt

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360          365          370
gcc tcg tcg agc tat gcc aag gct tca agc ttg ggt gtt agg cca tct      1205
Ala Ser Ser Ser Tyr Ala Lys Ala Ser Ser Leu Gly Val Arg Pro Ser
375          380          385          390
tca ctg gtg gca acg ata acg acc aat gct ggt gca ctt aat tgc aag      1253
Ser Leu Val Ala Thr Ile Thr Thr Asn Ala Gly Ala Leu Asn Cys Lys
          395          400          405
aaa ggt tca cgt tgt tgatgataat gatggcgaca catgtgagtg aaacaagaca      1308
Lys Gly Ser Arg Cys
          410
gtttattaca agtgattgaa gtgatttaat gttgggttct tgtgcaatta catttagtta      1368

gagaaatcag aaatgatttt taaaaagaag gaaggataaa gaaaaagtct agagttaaaa      1428

ggacttctgt gttcccttcc attatttttt ttttcttggt ttattttattc atgtatgacg      1488

attacaacct cggcctgttg caaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a      1539

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<210> 856
 <211> 411
 <212> PRT
 <213> Gossypium hirsutum

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Leu Phe Thr Phe Leu Leu Leu Leu Pro Leu Leu Ile Ser Ser Ser Pro
          20          25          30
Val Gln Asp Pro Glu Leu Val Val Gln Asp Val His Arg Ala Ile Asn
          35          40          45
Ala Ser Lys Arg Asn Leu Gly Tyr Leu Ser Cys Gly Thr Gly Asn Pro
          50          55          60
Ile Asp Asp Cys Trp Arg Cys Asp Pro Asn Trp Glu Thr Asn Arg Gln
65          70          75          80
Lys Leu Ala Asp Cys Ala Ile Gly Phe Gly Lys Asn Ala Ile Gly Gly
          85          90          95
Arg Asp Gly Lys Ile Tyr Val Val Thr Asp Ser Gly Asp Asp Asp Pro
          100          105          110
Val Asn Pro Lys Pro Gly Thr Leu Arg His Ala Val Ile Gln Gly Glu
          115          120          125
Pro Leu Trp Ile Ile Phe Ala Arg Asp Met Thr Ile Gln Leu Lys Glu
          130          135          140
Glu Leu Ile Met Asn Ser Phe Lys Thr Ile Asp Gly Arg Gly Ala Ser
145          150          155          160
Val His Ile Ala Gly Pro Cys Ile Thr Val Gln Tyr Val Thr Asn
          165          170          175
Ile Ile Ile His Gly Leu Asn Ile His Asp Cys Lys Gln Gly Gly Asn
          180          185          190
Ala Met Val Arg Asp Ser Pro Arg His Tyr Gly Trp Arg Thr Ile Ser
          195          200          205
Asp Gly Asp Gly Val Ser Ile Phe Gly Gly Ser His Val Trp Val Asp
          210          215          220
His Asn Ser Leu Ser Asn Cys Lys Asp Gly Leu Ile Asp Ala Ile His
225          230          235          240
Gly Ser Thr Ala Ile Thr Ile Ser Asn Asn Tyr Met Thr His His Asp
          245          250          255
Lys Val Met Leu Leu Gly His Ser Asp Ser Tyr Thr Gln Asp Lys Asn
          260          265          270
Met Gln Val Thr Ile Ala Phe Asn His Phe Gly Glu Gly Leu Val Gln
          275          280          285
Arg Met Pro Arg Cys Arg His Gly Tyr Phe His Val Val Asn Asn Asp
          290          295          300
Tyr Thr His Trp Glu Met Tyr Ala Ile Gly Gly Ser Ala Asn Pro Thr
305          310          315          320

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PF59082SeqList_PF59082.txt

Ile Asn Ser Gln Gly Asn Arg Phe Thr Ala Pro Asp Asn Arg Phe Ser
 325 330 335
 Lys Glu Val Thr Lys His Glu Asp Ala Pro Glu Ser Glu Trp Lys Ser
 340 345 350
 Trp Asn Trp Arg Ser Glu Gly Asp Leu Met Val Asn Gly Ala Phe Phe
 355 360 365
 Ile Ser Ser Gly Ala Gly Ala Ser Ser Ser Tyr Ala Lys Ala Ser Ser
 370 375 380
 Leu Gly Val Arg Pro Ser Ser Leu Val Ala Thr Ile Thr Thr Asn Ala
 385 390 400
 Gly Ala Leu Asn Cys Lys Lys Gly Ser Arg Cys
 405 410

<210> 857

<211> 1314

<212> DNA

<213> Mangifera indica

<220>

<221> CDS

<222> (1)..(1314)

<400> 857

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cta tgt cta ttt ctc ggc gtt aaa gca tcg aca gtg aag cac gag cta	96
Leu Cys Leu Phe Leu Gly Val Lys Ala Ser Thr Val Lys His Glu Leu	
20 25 30	
aac tat agg ttg ttg aac tcc aaa aat aca tcc ata gcg gac agt tcg	144
Asn Tyr Arg Leu Leu Asn Ser Lys Asn Thr Ser Ile Ala Asp Ser Ser	
35 40 45	
gat gat tca tgg agc cag cac gct gtt gat aat cca gag gag gta gct	192
Asp Asp Ser Trp Ser Gln His Ala Val Asp Asn Pro Glu Glu Val Ala	
50 55 60	
gct atg gtc gac ata tca att cgt aat agt act gaa aga aga agg tta	240
Ala Met Val Asp Ile Ser Ile Arg Asn Ser Thr Glu Arg Arg Arg Leu	
65 70 75 80	
gga tat ttc tca tgt gaa act gga aac cca atc gat gat tgt tgg cgt	288
Gly Tyr Phe Ser Cys Glu Thr Gly Asn Pro Ile Asp Asp Cys Trp Arg	
85 90 95	
tgt gac cct aaa tgg cat ttg cac cga aaa cat ctt gct gat tgt gcc	336
Cys Asp Pro Lys Trp His Leu His Arg Lys His Leu Ala Asp Cys Ala	
100 105 110	
att ggt ttt ggg cgc aat gcc att ggt ggc cgt gat ggc aag ttc tat	384
Ile Gly Phe Gly Arg Asn Ala Ile Gly Gly Arg Asp Gly Lys Phe Tyr	
115 120 125	
gtt gta agt gac tct agc gat gat aat cct gtt gat cct aaa cca ggc	432
Val Val Ser Asp Ser Ser Asp Asp Asn Pro Val Asp Pro Lys Pro Gly	
130 135 140	
aca ctt cgt cat gct gtc atc caa gac agg cct ttg tgg att gtg ttc	480
Thr Leu Arg His Ala Val Ile Gln Asp Arg Pro Leu Trp Ile Val Phe	
145 150 155 160	
aaa cag gac atg gcg atc aca ctc aag caa gag ctt ata atg aat agc	528
Lys Gln Asp Met Ala Ile Thr Leu Lys Gln Glu Leu Ile Met Asn Ser	
165 170 175	
ttc aag aca att gat ggt cgt ggt gtc aat gtc cat att gct aat ggg	576
Phe Lys Thr Ile Asp Gly Arg Gly Val Asn Val His Ile Ala Asn Gly	
180 185 190	
gct tgc atc acc att caa tac att acc aat gtc att att cac ggt ata	624
Ala Cys Ile Thr Ile Gln Tyr Ile Thr Asn Val Ile Ile His Gly Ile	
195 200 205	
cat atc cat gat tgt aaa cca act ggc aat gcc atg gtg aga agc tcc	672
His Ile His Asp Cys Lys Pro Thr Gly Asn Ala Met Val Arg Ser Ser	
210 215 220	
cca agc cat tac ggg tgg agg aca atg gct gat ggt gat ggc att tca	720
Pro Ser His Tyr Gly Trp Arg Thr Met Ala Asp Gly Asp Gly Ile Ser	
225 230 235 240	
att ttt gga gca agc cat att tgg att gac cac aat tct cta tct aat	768

PF59082SeqList_PF59082.txt

Ile	Phe	Gly	Ala	Ser	His	Ile	Trp	Ile	Asp	His	Asn	Ser	Leu	Ser	Asn		
245				245				250					255				
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Cys	Ala	Asp	Gly	Leu	Ile	Asp	Ala	Ile	Met	Ala	Ser	Thr	Ala	Ile	Thr		
260							265						270				
att	tcc	aat	aac	tac	ttc	acc	cac	cat	aac	gag	gtt	atg	cta	ttg	gga	864	
Ile	Ser	Asn	Asn	Tyr	Phe	Thr	His	His	Asn	Glu	Val	Met	Leu	Leu	Gly		
275							280					285					
cac	agt	gac	tcg	tat	aca	aga	gac	aag	cag	atg	caa	gtg	acc	atc	gcc	912	
His	Ser	Asp	Ser	Tyr	Thr	Arg	Asp	Lys	Gln	Met	Gln	Val	Thr	Ile	Ala		
290						295					300						
tac	aac	cat	ttc	ggt	gaa	ggt	ctt	atc	cag	aga	atg	cca	cgg	tgc	agg	960	
Tyr	Asn	His	Phe	Gly	Glu	Gly	Leu	Ile	Gln	Arg	Met	Pro	Arg	Cys	Arg		
305				310					315						320		
cat	ggg	tat	ttc	cac	gtg	gtg	aac	aat	gac	tat	aca	cac	tgg	gaa	atg	1008	
His	Gly	Tyr	Phe	His	Val	Val	Asn	Asn	Asp	Tyr	Thr	His	Trp	Glu	Met		
				325					330					335			
ttt	gct	att	ggt	gga	agt	gct	gat	ccc	acc	att	aac	agc	cag	ggc	aac	1056	
Phe	Ala	Ile	Gly	Gly	Ser	Ala	Asp	Pro	Thr	Ile	Asn	Ser	Gln	Gly	Asn		
			340					345					350				
aga	tac	ctt	gcc	ccc	tca	aat	ccc	ttt	gcc	aag	gag	gta	aca	aag	agg	1104	
Arg	Tyr	Leu	Ala	Pro	Ser	Asn	Pro	Phe	Ala	Lys	Glu	Val	Thr	Lys	Arg		
			355				360					365					
gtg	gat	aca	tca	gac	ggt	gta	tgg	aag	agt	tgg	aat	tgg	cga	tca	gag	1152	
Val	Asp	Thr	Ser	Asp	Gly	Val	Trp	Lys	Ser	Trp	Asn	Trp	Arg	Ser	Glu		
			370			375					380						
gga	gat	ctg	ttg	ctg	aat	gga	gcc	tac	ttc	att	tca	tcg	gga	gct	cga	1200	
Gly	Asp	Leu	Leu	Leu	Asn	Gly	Ala	Tyr	Phe	Ile	Ser	Ser	Gly	Ala	Arg		
385					390				395						400		
tct	gct	gcc	agc	tat	gca	agg	gca	tca	agc	tta	ggg	gca	aaa	tcc	tct	1248	
Ser	Ala	Ala	Ser	Tyr	Ala	Arg	Ala	Ser	Ser	Leu	Gly	Ala	Lys	Ser	Ser		
				405					410					415			
tcc	ttg	gtt	ggc	gct	ctt	acc	tct	agc	gct	ggt	gct	atg	tcc	tgc	cgc	1296	
Ser	Leu	Val	Gly	Ala	Leu	Thr	Ser	Ser	Ala	Gly	Ala	Met	Ser	Cys	Arg		
			420					425					430				
ggt	ggt	aga	caa	tgt	taa											1314	
Val	Gly	Arg	Gln	Cys													
			435														

<210> 858

<211> 437

<212> PRT

<213> Mangifera indica

<400> 858

Met	Ala	Val	Ser	Pro	Arg	Trp	Ile	Ser	Ser	Val	Cys	Ala	Leu	Leu	Ile		
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			20					25					30				
Asn	Tyr	Arg	Leu	Leu	Asn	Ser	Lys	Asn	Thr	Ser	Ile	Ala	Asp	Ser	Ser		
		35					40					45					
Asp	Asp	Ser	Trp	Ser	Gln	His	Ala	Val	Asp	Asn	Pro	Glu	Glu	Val	Ala		
		50				55					60						
Ala	Met	Val	Asp	Ile	Ser	Ile	Arg	Asn	Ser	Thr	Glu	Arg	Arg	Arg	Leu		
65					70				75						80		
Gly	Tyr	Phe	Ser	Cys	Glu	Thr	Gly	Asn	Pro	Ile	Asp	Asp	Cys	Trp	Arg		
				85				90						95			
Cys	Asp	Pro	Lys	Trp	His	Leu	His	Arg	Lys	His	Leu	Ala	Asp	Cys	Ala		
			100					105					110				
Ile	Gly	Phe	Gly	Arg	Asn	Ala	Ile	Gly	Gly	Arg	Asp	Gly	Lys	Phe	Tyr		
			115				120					125					
Val	Val	Ser	Asp	Ser	Ser	Asp	Asp	Asn	Pro	Val	Asp	Pro	Lys	Pro	Gly		
			130			135					140						
Thr	Leu	Arg	His	Ala	Val	Ile	Gln	Asp	Arg	Pro	Leu	Trp	Ile	Val	Phe		
145					150				155						160		
Lys	Gln	Asp	Met	Ala	Ile	Thr	Leu	Lys	Gln	Glu	Leu	Ile	Met	Asn	Ser		
				165					170					175			
Phe	Lys	Thr	Ile	Asp	Gly	Arg	Gly	Val	Asn	Val	His	Ile	Ala	Asn	Gly		
			180					185					190				

PF59082SeqList_PF59082.txt

Ala Cys Ile Thr Ile Gln Tyr Ile Thr Asn Val Ile Ile His Gly Ile
 195 200 205
 His Ile His Asp Cys Lys Pro Thr Gly Asn Ala Met Val Arg Ser Ser
 210 215 220
 Pro Ser His Tyr Gly Trp Arg Thr Met Ala Asp Gly Asp Gly Ile Ser
 225 230 235 240
 Ile Phe Gly Ala Ser His Ile Trp Ile Asp His Asn Ser Leu Ser Asn
 245 250 255
 Cys Ala Asp Gly Leu Ile Asp Ala Ile Met Ala Ser Thr Ala Ile Thr
 260 265 270
 Ile Ser Asn Asp Tyr Phe Thr His Asn Glu Val Met Leu Leu Gly
 275 280 285
 His Ser Asp Ser Tyr Thr Arg Asp Lys Gln Met Gln Val Thr Ile Ala
 290 295 300
 Tyr Asn His Phe Gly Glu Gly Leu Ile Gln Arg Met Pro Arg Cys Arg
 305 310 315 320
 His Gly Tyr Phe His Val Val Asn Asn Asp Tyr Thr His Trp Glu Met
 325 330 335
 Phe Ala Ile Gly Gly Ser Ala Asp Pro Thr Ile Asn Ser Gln Gly Asn
 340 345 350
 Arg Tyr Leu Ala Pro Ser Asn Pro Phe Ala Lys Glu Val Thr Lys Arg
 355 360 365
 Val Asp Thr Ser Asp Gly Val Trp Lys Ser Trp Asn Trp Arg Ser Glu
 370 375 380
 Gly Asp Leu Leu Leu Asn Gly Ala Tyr Phe Ile Ser Ser Gly Ala Arg
 385 390 395 400
 Ser Ala Ala Ser Tyr Ala Arg Ala Ser Ser Leu Gly Ala Lys Ser Ser
 405 410 415
 Ser Leu Val Gly Ala Leu Thr Ser Ser Ala Gly Ala Met Ser Cys Arg
 420 425 430
 Val Gly Arg Gln Cys
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 <211> 1787
 <212> DNA
 <213> Brassica napus

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tggattccaa atccttctct gcttctcctt cctcacattt ctcaaccagc attcttcttc 180

ttttgacact ttcaacacac tgcaagtact gctcaatgag caattaacg atg ctg ctt 238
 Met Leu Leu
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cct cac ttc tcc acc gcc att ttc ctc ctc tgc ctc ttc ttc aca ctc 286
 Pro His Phe Ser Thr Ala Ile Phe Leu Leu Cys Leu Phe Phe Thr Leu
 5 10 15

ctc caa gcc act aat ctc act ctc cct cac cag cat cat tcc cct gac 334
 Leu Gln Ala Thr Asn Leu Thr Leu Pro His Gln His His Ser Pro Asp
 20 25 30 35

tcc gtc gct ctc cac gtc tta agt tca atc aat gca tcc ctc tca cgg 382
 Ser Val Ala Leu His Val Leu Ser Ser Ile Asn Ala Ser Leu Ser Arg
 40 45 50

aga caa ctc tcc tcc tcc agt tgc cgc acc ggc aac cca atc gac gac 430
 Arg Gln Leu Ser Ser Ser Ser Cys Arg Thr Gly Asn Pro Ile Asp Asp
 55 60 65

tgc tgg cgc tgc acc tcc tcg gac tgg tcc tcc aac cgc caa cgc ctc 478
 Cys Trp Arg Cys Thr Ser Ser Asp Trp Ser Ser Ser Arg Gln Arg Leu

PF59082SeqList_PF59082.txt

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Ala	Asp	Cys	Ser	Ile	Gly	Phe	Gly	Arg	Gly	Thr	Leu	Gly	Gly	Lys	Asn		
	85					90					95						
ggc	aag	atc	tac	gtc	gtc	aca	gac	tcc	tcc	gac	aac	agc	cca	tca	aac		574
Gly	Lys	Ile	Tyr	Val	Val	Thr	Asp	Ser	Ser	Asp	Asn	Ser	Pro	Ser	Asn		
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cca	acc	ccc	gga	aca	ctc	cgc	tac	gcc	gtc	atc	caa	gaa	gag	ccc	ctc		622
Pro	Thr	Pro	Gly	Thr	Leu	Arg	Tyr	Ala	Val	Ile	Gln	Glu	Glu	Pro	Leu		
			120						125					130			
tgg	atc	gtc	ttc	tcc	aac	atg	ctc	atc	cgc	ctc	aaa	cac	gaa	ctc			670
Trp	Ile	Val	Phe	Ser	Ser	Asn	Met	Leu	Ile	Arg	Leu	Lys	His	Glu	Leu		
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atc	atc	aac	agc	tac	aaa	acc	atc	gac	ggc	cgg	ggc	tcc	gcc	gtc	cac		718
Ile	Ile	Asn	Ser	Tyr	Lys	Thr	Ile	Asp	Gly	Arg	Gly	Ser	Ala	Val	His		
		150					155					160					
atc	acc	ggc	aac	ggc	tgc	ctg	acc	atc	cag	tac	gtg	caa	cac	gtc	atc		766
Ile	Thr	Gly	Asn	Gly	Cys	Leu	Thr	Ile	Gln	Tyr	Val	Gln	His	Val	Ile		
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atc	cac	aac	gtc	cac	atc	tac	gac	tgc	aaa	ccc	tcg	ggg	ggc	gcc	gtg		814
Ile	His	Asn	Val	His	Ile	Tyr	Asp	Cys	Lys	Pro	Ser	Gly	Gly	Ala	Val		
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Val	Ala	Ala	Thr	Pro	Thr	Lys	Ser	Gly	Arg	Arg	Gly	Arg	Ser	Asp	Gly		
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Asp	Gly	Ile	Ser	Ile	Phe	Gly	Ala	Gln	Lys	Ile	Trp	Ile	Asp	His	Cys		
		215						220					225				
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Ser	Met	Ser	His	Cys	Thr	Asp	Gly	Leu	Ile	Asp	Ala	Val	Met	Gly	Ser		
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Thr	Ala	Ile	Thr	Ile	Ser	Asn	Asn	Tyr	Phe	Ala	His	His	Asp	Glu	Val		
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Met	Leu	Leu	Gly	His	Asp	Asp	Ser	Tyr	Gly	Pro	Asp	Thr	Gly	Met	Gln		
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gtg	acg	att	gcg	ttt	aac	cat	ttc	gga	cag	ggg	ctt	ggt	cag	agg	atg		1102
Val	Thr	Ile	Ala	Phe	Asn	His	Phe	Gly	Gln	Gly	Leu	Val	Gln	Arg	Met		
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ccg	agg	tgt	cgg	aga	ggg	tat	ata	cac	gtg	gtg	aat	aat	gat	ttc	acg		1150
Pro	Arg	Cys	Arg	Arg	Gly	Tyr	Ile	His	Val	Val	Asn	Asn	Asp	Phe	Thr		
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Ser	Trp	Lys	Met	Tyr	Ala	Ile	Gly	Gly	Ser	Gly	Asn	Pro	Thr	Ile	Asn		
		310					315					320					
agt	cag	ggg	aat	cgt	tac	att	gct	cct	tct	gat	cct	agc	gcc	aaa	gag		1246
Ser	Gln	Gly	Asn	Arg	Tyr	Ile	Ala	Pro	Ser	Asp	Pro	Ser	Ala	Lys	Glu		
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Val	Thr	Lys	Arg	Val	Asp	Ser	Lys	Asp	Asp	Gly	Glu	Trp	Ser	Asn	Trp		
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Asn	Trp	Arg	Thr	Glu	Gly	Asp	Leu	Met	Glu	Asn	Gly	Ala	Phe	Phe	Val		
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Glu	Pro	Lys	Ala	Ser	Ala	Leu	Val	Asp	Gln	Leu	Thr	Arg	Asn	Ala	Gly		
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Val	Phe	Gly	Gly	Pro	Arg	Asp	Asp	Gln	Gly	Gln	Thr	Gly	Asp	Ser	Tyr		
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Ser	Gly	Tyr	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly		
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ggt	gga	agc	agc	ggc	agc	gat	gga	gga	act	agt	gct	att	ggc	ggt	act		1582
Gly	Gly	Ser	Ser	Gly	Ser	Asp	Gly	Gly	Thr	Ser	Ala	Ile	Gly	Gly	Thr		

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Met	Ile	Phe	Gly	Ser	Asn	Ala	Pro	Pro	Arg	Pro	Arg	Leu	Thr	Leu	Leu	
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Phe	Cys	Leu	Ile	Met	Ile	Cys	Val	Met	Ser	Ile	Ser	Ser	Leu	Leu	Leu	
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Leu																
500																
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			20					25					30			
Ser	Pro	Asp	Ser	Val	Ala	Leu	His	Val	Leu	Ser	Ser	Ile	Asn	Ala	Ser	
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Leu	Ser	Arg	Arg	Gln	Leu	Ser	Ser	Ser	Cys	Arg	Thr	Gly	Asn	Pro		
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Ile	Asp	Asp	Cys	Trp	Arg	Cys	Thr	Ser	Ser	Asp	Trp	Ser	Ser	Asn	Arg	
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Gln	Arg	Leu	Ala	Asp	Cys	Ser	Ile	Gly	Phe	Gly	Arg	Gly	Thr	Leu	Gly	
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Pro	Ser	Asn	Pro	Thr	Pro	Gly	Thr	Leu	Arg	Tyr	Ala	Val	Ile	Gln	Glu	
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Glu	Pro	Leu	Trp	Ile	Val	Phe	Ser	Ser	Asn	Met	Leu	Ile	Arg	Leu	Lys	
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His	Glu	Leu	Ile	Ile	Asn	Ser	Tyr	Lys	Thr	Ile	Asp	Gly	Arg	Gly	Ser	
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Ala	Val	His	Ile	Thr	Gly	Asn	Gly	Cys	Leu	Thr	Ile	Gln	Tyr	Val	Gln	
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His	Val	Ile	Ile	His	Asn	Val	His	Ile	Tyr	Asp	Cys	Lys	Pro	Ser	Gly	
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Gly	Ala	Val	Val	Ala	Ala	Thr	Pro	Thr	Lys	Ser	Gly	Arg	Arg	Gly	Arg	
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Ser	Asp	Gly	Asp	Gly	Ile	Ser	Ile	Phe	Gly	Ala	Gln	Lys	Ile	Trp	Ile	
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Asp	Glu	Val	Met	Leu	Leu	Gly	His	Asp	Asp	Ser	Tyr	Gly	Pro	Asp	Thr	
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Gln	Arg	Met	Pro	Arg	Cys	Arg	Arg	Gly	Tyr	Ile	His	Val	Val	Asn	Asn	
	290					295					300					
Asp	Phe	Thr	Ser	Trp	Lys	Met	Tyr	Ala	Ile	Gly	Gly	Ser	Gly	Asn	Pro	
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Thr	Ile	Asn	Ser	Gln	Gly	Asn	Arg	Tyr	Ile	Ala	Pro	Ser	Asp	Pro	Ser	
				325					330					335		
Ala	Lys	Glu	Val	Thr	Lys	Arg	Val	Asp	Ser	Lys	Asp	Asp	Gly	Glu	Trp	
			340					345					350			
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 405 410 415
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 420 425 430
 Gly Gly Gly Gly Gly Ser Ser Gly Ser Asp Gly Gly Thr Ser Ala Ile
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 Gly Gly Thr Thr Arg Gly Ser Thr Ser Ser Ser Asp Asp Ser Asn
 450 455 460
 Phe Phe Gly Met Ile Phe Gly Ser Asn Ala Pro Pro Arg Pro Arg Leu
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 Thr Leu Ile Ser Ser Arg Pro Leu His Leu Gln Asp Pro Glu Leu Val
 30 35 40
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 Val Gln Glu Val Gln Arg Asn Ile Ser Asp Ser Val Ser Arg Arg Asn
 45 50 55 60
 ttg ggc tac ttg tca tgc ggc acc ggc aac cct atc gac gac tgc tgg 301
 Leu Gly Tyr Leu Ser Cys Gly Thr Gly Asn Pro Ile Asp Asp Cys Trp
 65 70 75
 cgg tgc gac ccg aac tgg gag aag aac agg cag agc tta gct gat tgt 349
 Arg Cys Asp Pro Asn Trp Glu Lys Asn Arg Gln Ser Leu Ala Asp Cys
 80 85 90
 gcg ata ggg ttc gga aag aac gcc ata ggt gga aga gac ggg aag att 397
 Ala Ile Gly Phe Gly Lys Asn Ala Ile Gly Gly Arg Asp Gly Lys Ile
 95 100 105
 tac gtg gtc aca gat tcc ggc gat gac gac ccc gtg aac ccc aag cca 445
 Tyr Val Val Thr Asp Ser Gly Asp Asp Asp Pro Val Asn Pro Lys Pro
 110 115 120
 gga acc cta cga cac gcc gtc atc caa gac gag cca tta tgg atc att 493
 Gly Thr Leu Arg His Ala Val Ile Gln Asp Glu Pro Leu Trp Ile Ile
 125 130 135 140
 ttc cag cgt gac atg acc atc cag ctg aag gag ctg atc atg aac 541
 Phe Gln Arg Asp Met Thr Ile Gln Leu Lys Glu Glu Leu Ile Met Asn
 145 150 155
 tcc ttc aag aca atc gac ggc cgg gga gcg tcc gta cac att gcc ggc 589
 Ser Phe Lys Thr Ile Asp Gly Arg Gly Ala Ser Val His Ile Ala Gly
 160 165 170
 ggg cca tgc atc acc atc cag ttc gtg acc aac att att atc cac gga 637
 Gly Pro Cys Ile Thr Ile Gln Phe Val Thr Asn Ile Ile Ile His Gly
 175 180 185
 ctg cac ata cac gat tgc aag cag ggt ggg aac gct atg gtg agg agc 685

PF59082SeqList_PF59082.txt

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Ser	Pro	Arg	His	Phe	Gly	Trp	Arg	Thr	Val	Ser	Asp	Gly	Asp	Gly	Val	
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Ser	Ile	Phe	Gly	Gly	Ser	His	Val	Trp	Val	Asp	His	Cys	Ser	Leu	Ser	
			225						230					235		
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Asn	Cys	Lys	Asp	Gly	Leu	Val	Asp	Ala	Ile	Tyr	Gly	Ser	Thr	Ala	Ile	
			240					245					250			
acg	att	tcg	aac	aat	tac	atg	acg	cac	cat	gat	aag	gtg	atg	ctt	ttg	877
Thr	Ile	Ser	Asn	Asn	Tyr	Met	Thr	His	His	Asp	Lys	Val	Met	Leu	Leu	
			255			260						265				
ggg	cat	agc	gat	tcg	tat	acc	aac	gac	aag	aac	atg	caa	atc	acc	att	925
Gly	His	Ser	Asp	Ser	Tyr	Thr	Asn	Asp	Lys	Asn	Met	Gln	Ile	Thr	Ile	
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Ala	Phe	Asn	His	Phe	Gly	Glu	Gly	Leu	Val	Gln	Arg	Met	Pro	Arg	Cys	
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Arg	His	Gly	Tyr	Phe	His	Val	Val	Asn	Asn	Asp	Tyr	Thr	His	Trp	Glu	
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Met	Tyr	Ala	Ile	Gly	Gly	Ser	Ala	Asp	Pro	Thr	Ile	Asn	Ser	Gln	Gly	
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Asn	Arg	Phe	Ala	Ala	Pro	Asp	Ile	Arg	Ser	Ser	Lys	Glu	Val	Thr	Lys	
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His	Glu	Asp	Ala	Pro	Glu	Ser	Glu	Trp	Lys	Asn	Trp	Asn	Trp	Arg	Ser	
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gaa	ggc	gac	ttg	atg	ctc	aac	ggg	gca	ttt	ttt	act	gca	tca	ggg	gcc	1213
Glu	Gly	Asp	Leu	Met	Leu	Asn	Gly	Ala	Phe	Phe	Thr	Ala	Ser	Gly	Ala	
365					370					375					380	
gga	gct	tcc	tct	agc	tac	gcc	agg	gct	tcg	agc	ttg	ggg	gca	aag	cca	1261
Gly	Ala	Ser	Ser	Ser	Tyr	Ala	Arg	Ala	Ser	Ser	Leu	Gly	Ala	Lys	Pro	
			385					390						395		
tct	tct	cta	gtg	ggg	gca	att	acc	acg	gct	tcc	ggc	gca	ctt	agt	tgc	1309
Ser	Ser	Leu	Val	Gly	Ala	Ile	Thr	Thr	Ala	Ser	Gly	Ala	Leu	Ser	Cys	
			400				405						410			
cga	aag	ggc	tct	cgt	tgc	tgattgcata	tcgagcttgt	ggcctattga								1357
Arg	Lys	Gly	Ser	Arg	Cys											
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PF59082SeqList_PF59082.txt

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 Gln Arg Asn Ile Ser Asp Ser Val Ser Arg Arg Asn Leu Gly Tyr Leu
 50 55 60
 Ser Cys Gly Thr Gly Asn Pro Ile Asp Asp Cys Trp Arg Cys Asp Pro
 65 70 75 80
 Asn Trp Glu Lys Asn Arg Gln Ser Leu Ala Asp Cys Ala Ile Gly Phe
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 Gly Lys Asn Ala Ile Gly Gly Arg Asp Gly Lys Ile Tyr Val Val Thr
 100 105 110
 Asp Ser Gly Asp Asp Asp Pro Val Asn Pro Lys Pro Gly Thr Leu Arg
 115 120 125
 His Ala Val Ile Gln Asp Glu Pro Leu Trp Ile Ile Phe Gln Arg Asp
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 Met Thr Ile Gln Leu Lys Glu Glu Leu Ile Met Asn Ser Phe Lys Thr
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 Ile Asp Gly Arg Gly Ala Ser Val His Ile Ala Gly Gly Pro Cys Ile
 165 170 175
 Thr Ile Gln Phe Val Thr Asn Ile Ile Ile His Gly Leu His Ile His
 180 185 190
 Asp Cys Lys Gln Gly Gly Asn Ala Met Val Arg Ser Ser Pro Arg His
 195 200 205
 Phe Gly Trp Arg Thr Val Ser Asp Gly Asp Gly Val Ser Ile Phe Gly
 210 215 220
 Gly Ser His Val Trp Val Asp His Cys Ser Leu Ser Asn Cys Lys Asp
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 245 250 255
 Asn Tyr Met Thr His His Asp Lys Val Met Leu Leu Gly His Ser Asp
 260 265 270
 Ser Tyr Thr Asn Asp Lys Asn Met Gln Ile Thr Ile Ala Phe Asn His
 275 280 285
 Phe Gly Glu Gly Leu Val Gln Arg Met Pro Arg Cys Arg His Gly Tyr
 290 295 300
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 305 310 315 320
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 325 330 335
 Ala Pro Asp Ile Arg Ser Ser Lys Glu Val Thr Lys His Glu Asp Ala
 340 345 350
 Pro Glu Ser Glu Trp Lys Asn Trp Asn Trp Arg Ser Glu Gly Asp Leu
 355 360 365
 Met Leu Asn Gly Ala Phe Phe Thr Ala Ser Gly Ala Gly Ala Ser Ser
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PF59082SeqList_PF59082.txt

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ctt Leu	ctt Leu	ctt Leu	ctt Leu	atg Met	ggc Gly	ttc Phe	ctg Leu	ctg Leu	gtt Val	ttg Leu	aac Asn	gga Gly	ggt Gly	cgg Arg	ggg Gly	159
tgg Trp	att Ile	gga Gly	agc Ser	gag Glu	agg Arg	tcc Ser	tct Ser	ggc Gly	tcg Ser	agg Arg	aat Asn	ggc Gly	gga Gly	gca Ala	tcg Ser	207
cgg Arg	agg Arg	agc Ser	ttg Leu	aga Arg	gag Glu	gcc Ala	tcc Ser	gcg Ala	aac Asn	gcg Ala	acc Thr	agc Ser	gcc Ala	gat Asp	gct Ala	255
tcc Ser	ttg Leu	gaa Glu	gac Asp	agg Arg	gct Ala	gta Val	acc Thr	agg Arg	gca Ala	gca Ala	gaa Glu	gcc Ala	gca Ala	gtc Val	gat Asp	303
gac Asp	ccc Pro	gag Glu	gag Glu	ggt Val	gct Ala	tcg Ser	acg Thr	gtc Val	ctg Leu	acg Thr	acc Thr	ata Ile	atc Ile	aac Asn	agc Ser	351
acg Thr	gct Ala	cga Arg	aga Arg	tct Ser	ctt Leu	ggt Gly	tat Tyr	ctg Leu	tcg Ser	tgc Cys	ggt Gly	tca Ser	ggc Gly	aac Asn	ccg Pro	399
atc Ile	gac Asp	gac Asp	tgc Cys	tgg Trp	cgg Arg	tgc Cys	gac Asp	ccc Pro	gat Asp	tgg Trp	cat His	gtc Val	aac Asn	aga Arg	aaa Lys	447
aag Lys	ctc Leu	gct Ala	gac Asp	tgt Cys	ggc Gly	att Ile	ggc Gly	ttt Phe	ggc Gly	cgc Arg	aac Asn	gcg Ala	ata Ile	ggt Gly	ggc Gly	495
cgc Arg	gac Asp	ggg Gly	gag Glu	ttg Leu	tac Tyr	gtt Val	gtg Val	aca Thr	gac Asp	tcc Ser	ggg Gly	gac Asp	gat Asp	gat Asp	ccc Pro	543
gtg Val	aat Asn	cct Pro	cgc Arg	ccg Pro	gga Gly	aca Thr	ctt Leu	aga Arg	tac Tyr	gcc Ala	gtc Val	atc Ile	cag Gln	gac Asp	gtg Val	591
ccc Pro	ctc Leu	tgg Trp	atc Ile	acc Thr	ttt Phe	aaa Lys	cac His	gac Asp	atg Met	gag Glu	atc Ile	acg Thr	ctc Leu	aag Lys	gag Glu	639
gaa Glu	ctc Leu	att Ile	atg Met	aac Asn	agc Ser	ttt Phe	aag Lys	acg Thr	atc Ile	gat Asp	gga Gly	cgc Arg	ggt Gly	gtc Val	aac Asn	687
gtc Val	cac His	att Ile	gcc Ala	aat Asn	ggc Gly	gcc Ala	tgc Cys	atc Ile	acc Thr	atc Ile	cag Gln	tac Tyr	atc Ile	acc Thr	aac Asn	735
gtc Val	atc Ile	atc Ile	cat His	ggc Gly	ctc Leu	cac His	atc Ile	cac His	gac Asp	tgc Cys	aag Lys	ccc Pro	acc Thr	ggg Gly	aat Asn	783
gcc Ala	atg Met	gtc Val	cgc Arg	agc Ser	tct Ser	cct Pro	tct Ser	cac His	tat Tyr	gga Gly	tgg Trp	aga Arg	acc Thr	atg Met	gct Ala	831
gat Asp	ggg Gly	gat Asp	gcc Ala	ggt Val	tcc Ser	att Ile	ttc Phe	ggc Gly	tcc Ser	agc Ser	cac His	att Ile	tgg Trp	gtg Val	gac Asp	879
cac His	tgc Cys	tct Ser	ctg Leu	tcc Ser	aac Asn	tgc Cys	gcc Ala	gat Asp	gga Gly	ctt Leu	gtc Val	gat Asp	gcc Ala	gtc Val	atg Met	927
ggc Gly	tcc Ser	act Thr	gcc Ala	att Ile	acg Thr	gtc Val	tcc Ser	aac Asn	aat Asn	tac Tyr	ttc Phe	acc Thr	cac His	cac His	aat Asn	975
gag Glu	gtc Val	atg Met	ctt Leu	ttg Leu	gga Gly	cac His	act Thr	gat Asp	tct Ser	tat Tyr	gca Ala	agg Arg	gac Asp	agc Ser	atc Ile	1023
atg Met	caa Gln	gta Val	acg Thr	atc Ile	gca Ala	ttt Phe	aac Asn	cat His	ttt Phe	ggt Gly	gaa Glu	ggt Gly	ctg Leu	att Ile	cag Gln	1071
aga Arg	atg Met	ccc Pro	agg Arg	tgc Cys	agg Arg	cat His	ggc Gly	tac Tyr	ttc Phe	cac His	gtg Val	gta Val	aac Asn	aat Asn	gac Asp	1119
tac Tyr	acg Thr	cac His	tgg Trp	gag Glu	atg Met	tac Tyr	gcc Ala	att Ile	ggc Gly	ggg Gly	agc Ser	gcg Ala	aat Asn	cca Pro	acg Thr	1167
atc	aac	agt	caa	ggc	aac	ccg	ata	cct	tgc	gcc	gac	caa	tcc	att	tgc	1215

PF59082SeqList_PF59082.txt

Ile	Asn	Ser	Gln	Gly	Asn	Pro	Ile	Pro	Cys	Ala	Asp	Gln	Ser	Ile	Cys	
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aaa	gga	ggt	aac	aaa	aag	ggt	gga	cac	aga	tca	aac	acg	tgg	aag	aac	1263
Lys	Gly	Gly	Asn	Lys	Lys	Gly	Gly	His	Arg	Ser	Asn	Thr	Trp	Lys	Asn	
380					385					390					395	
tgg	aat	tgg	agg	tcg	gag	ggt	gac	ctg	ctt	ctg	aat	ggt	gct	ttt	ttc	1311
Trp	Asn	Trp	Arg	Ser	Glu	Gly	Asp	Leu	Leu	Leu	Asn	Gly	Ala	Phe	Phe	
				400				405						410		
acc	cct	tcc	ggt	gca	ggg	gct	tca	gcc	agc	tac	gca	cgg	gcc	tcc	agc	1359
Thr	Pro	Ser	Gly	Ala	Gly	Ala	Ser	Ala	Ser	Tyr	Ala	Arg	Ala	Ser	Ser	
			415					420					425			
ttt	ggg	gcc	aag	ccc	tct	tcc	ttg	gtt	gac	aca	ctg	act	tct	gat	gct	1407
Phe	Gly	Ala	Lys	Pro	Ser	Ser	Leu	Val	Asp	Thr	Leu	Thr	Ser	Asp	Ala	
		430					435					440				
ggg	gtc	ctg	tct	tgc	caa	gtc	ggc	act	cga	tgt	taacgtaatg	ccaagtagca				1460
Gly	Val	Leu	Ser	Cys	Gln	Val	Gly	Thr	Arg	Cys						
445						450										
gaacgccaca	acccgaagga	tgggaaatcg	tacttgacgg	tgttacaaat	ttcttctatg											1520
ttacaccgtc	agaaatgtca	tttctccaa	ttgcccaacc	tccgcctggc	tccatatgtg											1580
gagcgcacatgc	ggaagcggtg	tcagtttctt	ttattctact	ttgctgtttt	agctctgtta											1640
caccgtccat	ctagcaataa	gtgggtttat	agatagactt	catcctgggtg	gcgtgtcgtc											1700
acagttgaat	ttactacaat	gcagcagaat	tttatatagt	tgcaatttaa	tcttttgccc											1760
gttatccttg	tacctttcgc	ttggtcattg	tattggtagg	aatggatttt	gtcatcttaa											1820
aaaaaaaaaa																1830

<210> 864
 <211> 454
 <212> PRT
 <213> Musa acuminata

<400> 864
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 Arg Ser Ser Gly Ser Arg Asn Gly Gly Ala Ser Arg Arg Ser Leu Arg
 35 40 45
 Glu Ala Ser Ala Asn Ala Thr Ser Ala Asp Ala Ser Leu Glu Asp Arg
 50 55 60
 Ala Val Thr Arg Ala Ala Glu Ala Ala Val Asp Asp Pro Glu Glu Val
 65 70 75 80
 Ala Ser Thr Val Leu Thr Thr Ile Ile Asn Ser Thr Ala Arg Arg Ser
 85 90 95
 Leu Gly Tyr Leu Ser Cys Gly Ser Gly Asn Pro Ile Asp Asp Cys Trp
 100 105 110
 Arg Cys Asp Pro Asp Trp His Val Asn Arg Lys Lys Leu Ala Asp Cys
 115 120 125
 Gly Ile Gly Phe Gly Arg Asn Ala Ile Gly Gly Arg Asp Gly Glu Leu
 130 135 140
 Tyr Val Val Thr Asp Ser Gly Asp Asp Asp Pro Val Asn Pro Arg Pro
 145 150 155 160
 Gly Thr Leu Arg Tyr Ala Val Ile Gln Asp Val Pro Leu Trp Ile Thr
 165 170 175
 Phe Lys His Asp Met Glu Ile Thr Leu Lys Glu Glu Leu Ile Met Asn
 180 185 190

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Ser Phe Lys Thr Ile Asp Gly Arg Gly Val Asn Val His Ile Ala Asn
 195 200 205
 Gly Ala Cys Ile Thr Ile Gln Tyr Ile Thr Asn Val Ile Ile His Gly
 210 215 220
 Leu His Ile His Asp Cys Lys Pro Thr Gly Asn Ala Met Val Arg Ser
 225 230 235 240
 Ser Pro Ser His Tyr Gly Trp Arg Thr Met Ala Asp Gly Asp Ala Val
 245 250 255
 Ser Ile Phe Gly Ser Ser His Ile Trp Val Asp His Cys Ser Leu Ser
 260 265 270
 Asn Cys Ala Asp Gly Leu Val Asp Ala Val Met Gly Ser Thr Ala Ile
 275 280 285
 Thr Val Ser Asn Asn Tyr Phe Thr His His Asn Glu Val Met Leu Leu
 290 295 300
 Gly His Thr Asp Ser Tyr Ala Arg Asp Ser Ile Met Gln Val Thr Ile
 305 310 315 320
 Ala Phe Asn His Phe Gly Glu Gly Leu Ile Gln Arg Met Pro Arg Cys
 325 330 335
 Arg His Gly Tyr Phe His Val Val Asn Asn Asp Tyr Thr His Trp Glu
 340 345 350
 Met Tyr Ala Ile Gly Gly Ser Ala Asn Pro Thr Ile Asn Ser Gln Gly
 355 360 365
 Asn Pro Ile Pro Cys Ala Asp Gln Ser Ile Cys Lys Gly Gly Asn Lys
 370 375 380
 Lys Gly Gly His Arg Ser Asn Thr Trp Lys Asn Trp Asn Trp Arg Ser
 385 390 395 400
 Glu Gly Asp Leu Leu Leu Asn Gly Ala Phe Phe Thr Pro Ser Gly Ala
 405 410 415
 Gly Ala Ser Ala Ser Tyr Ala Arg Ala Ser Ser Phe Gly Ala Lys Pro
 420 425 430
 Ser Ser Leu Val Asp Thr Leu Thr Ser Asp Ala Gly Val Leu Ser Cys
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 Gln Val Gly Thr Arg Cys
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<210> 865
 <211> 1230
 <212> DNA
 <213> Salix gilgiana

<220>
 <221> CDS
 <222> (1)..(1230)

<400> 865
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 ctg ctg ctt att tta gct cca aat ttc att tcc tgt tcg cca gtt caa 96
 Leu Leu Leu Ile Leu Ala Pro Asn Phe Ile Ser Cys Ser Pro Val Gln
 20 25 30
 gat cct gaa gtg gta gtg gaa gaa gta cac agg agc atc aat gcc tcc 144
 Asp Pro Glu Val Val Val Glu Glu Val His Arg Ser Ile Asn Ala Ser
 35 40 45
 aga aga aaa ctg ggt ttc ctt tca tgt gga acc ggc aat ccg ata gac 192
 Arg Arg Lys Leu Gly Phe Leu Ser Cys Gly Thr Gly Asn Pro Ile Asp
 50 55 60
 gat tgc tgg aga tgt gac ccc aaa tgg ggg gag aat cgg cag aga tta 240
 Asp Cys Trp Arg Cys Asp Pro Lys Trp Gly Glu Asn Arg Gln Arg Leu
 65 70 75 80
 gca gat tgt gca atc ggg ttc ggc aag cac gct atc ggc ggc agg gat 288
 Ala Asp Cys Ala Ile Gly Phe Gly Lys His Ala Ile Gly Gly Arg Asp
 85 90 95
 ggc aag ata tat gca gtg aca gac tcc ggc gac gat gac cct gtg aat 336
 Gly Lys Ile Tyr Ala Val Thr Asp Ser Gly Asp Asp Asp Pro Val Asn
 100 105 110
 ccc aag cca ggc act ctt agg tat gct gtt ata cag gac gag cct ctg 384
 Pro Lys Pro Gly Thr Leu Arg Tyr Ala Val Ile Gln Asp Glu Pro Leu
 115 120 125

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tgg	atc	gtt	ttc	gct	cgg	gac	atg	gtg	atc	aag	ctc	agg	gaa	gag	ctg	432
Trp	Ile	Val	Phe	Ala	Arg	Asp	Met	Val	Ile	Lys	Leu	Arg	Glu	Glu	Leu	
130						135					140					
atc	atg	aac	tct	ttc	aag	acg	atc	gat	gga	aga	gga	gcc	agc	gtg	cac	480
Ile	Met	Asn	Ser	Phe	Lys	Thr	Ile	Asp	Gly	Arg	Gly	Ala	Ser	Val	His	
145					150					155					160	
att	gct	ggg	ggg	cca	tgc	atc	act	ata	cag	tat	gtg	acc	aac	att	ata	528
Ile	Ala	Gly	Gly	Pro	Cys	Ile	Thr	Ile	Gln	Tyr	Val	Thr	Asn	Ile	Ile	
				165					170					175		
atc	cat	ggg	gta	aat	att	cat	gac	tgc	aag	cga	gga	ggg	aat	gct	cat	576
Ile	His	Gly	Val	Asn	Ile	His	Asp	Cys	Lys	Arg	Gly	Gly	Asn	Ala	His	
			180					185					190			
gtg	agg	gat	tcg	ccg	agt	cat	tat	gga	tgg	cgg	act	gtt	tcg	gac	gga	624
Val	Arg	Asp	Ser	Pro	Ser	His	Tyr	Gly	Trp	Arg	Thr	Val	Ser	Asp	Gly	
		195					200					205				
gat	ggg	gtg	tcg	ata	ttc	gga	ggc	agc	cat	gtt	tgg	gtg	gat	cat	tgc	672
Asp	Gly	Val	Ser	Ile	Phe	Gly	Gly	Ser	His	Val	Trp	Val	Asp	His	Cys	
	210					215					220					
tct	cta	tcc	aac	tgc	aat	gat	ggg	ttg	atc	gac	gcg	att	cat	gga	tcc	720
Ser	Leu	Ser	Asn	Cys	Asn	Asp	Gly	Leu	Ile	Asp	Ala	Ile	His	Gly	Ser	
225					230					235					240	
acg	gcg	ata	aca	atc	tca	aac	aat	tac	ctg	acc	cat	cac	aac	aag	gtc	768
Thr	Ala	Ile	Thr	Ile	Ser	Asn	Asn	Tyr	Leu	Thr	His	His	Asn	Lys	Val	
				245					250					255		
atg	ctc	ctg	ggg	cac	agt	gat	agc	tat	aaa	cag	gac	aag	aac	atg	caa	816
Met	Leu	Leu	Gly	His	Ser	Asp	Ser	Tyr	Lys	Gln	Asp	Lys	Asn	Met	Gln	
			260					265					270			
gtc	acc	att	gcc	ttc	aac	cac	ttt	ggg	gaa	gga	ctt	gtg	cag	aga	atg	864
Val	Thr	Ile	Ala	Phe	Asn	His	Phe	Gly	Glu	Gly	Leu	Val	Gln	Arg	Met	
		275					280					285				
cca	agg	tgc	aga	cat	gga	tat	ttt	cac	gtg	gtg	aat	aat	gac	tac	acg	912
Pro	Arg	Cys	Arg	His	Gly	Tyr	Phe	His	Val	Val	Asn	Asn	Asp	Tyr	Thr	
	290					295					300					
cat	tgg	aaa	atg	tat	gca	att	ggc	ggc	agt	gct	gac	cct	aca	att	aat	960
His	Trp	Lys	Met	Tyr	Ala	Ile	Gly	Gly	Ser	Ala	Asp	Pro	Thr	Ile	Asn	
305					310					315					320	
agc	caa	ggc	aat	aga	ttt	ctt	gct	ccc	aat	gat	agg	ttt	aat	aaa	gag	1008
Ser	Gln	Gly	Asn	Arg	Phe	Leu	Ala	Pro	Asn	Asp	Arg	Phe	Asn	Lys	Glu	
				325					330					335		
gtg	act	aaa	cac	gag	gat	gca	ccg	cag	agt	gct	tgg	aag	ggg	tgg	aac	1056
Val	Thr	Lys	His	Glu	Asp	Ala	Pro	Gln	Ser	Ala	Trp	Lys	Gly	Trp	Asn	
			340					345					350			
tgg	agg	tct	gaa	ggg	gat	ttg	ctg	ctg	aac	gga	gca	ttc	ttc	acg	gca	1104
Trp	Arg	Ser	Glu	Gly	Asp	Leu	Leu	Leu	Asn	Gly	Ala	Phe	Phe	Thr	Ala	
		355					360					365				
tcc	ggg	gcc	gga	gct	tct	tct	agc	tac	gcc	aag	gcg	tca	agc	tta	ggg	1152
Ser	Gly	Ala	Gly	Ala	Ser	Ser	Ser	Tyr	Ala	Lys	Ala	Ser	Ser	Leu	Gly	
	370					375					380					
gca	aga	tcg	tct	tcc	ttg	gtt	agc	tcc	atc	acg	gca	gga	gca	ggc	tca	1200
Ala	Arg	Ser	Ser	Ser	Leu	Val	Ser	Ser	Ile	Thr	Ala	Gly	Ala	Gly	Ser	
385					390					395					400	
ctc	gtt	tgc	aag	aag	ggg	tcc	cgg	tgc	tga							1230
Leu	Val	Cys	Lys	Lys	Gly	Ser	Arg	Cys								
				405												

<210> 866
 <211> 409
 <212> PRT
 <213> Salix gilgiana

<400> 866
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 Leu Leu Leu Ile Leu Ala Pro Asn Phe Ile Ser Cys Ser Pro Val Gln
 20 25 30
 Asp Pro Glu Val Val Val Glu Glu Val His Arg Ser Ile Asn Ala Ser
 35 40 45
 Arg Arg Lys Leu Gly Phe Leu Ser Cys Gly Thr Gly Asn Pro Ile Asp
 50 55 60

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Asp Cys Trp Arg Cys Asp Pro Lys Trp Gly Glu Asn Arg Gln Arg Leu
65 70 75 80
Ala Asp Cys Ala Ile Gly Phe Gly Lys His Ala Ile Gly Gly Arg Asp
85 90 95
Gly Lys Ile Tyr Ala Val Thr Asp Ser Gly Asp Asp Asp Pro Val Asn
100 105 110
Pro Lys Pro Gly Thr Leu Arg Tyr Ala Val Ile Gln Asp Glu Pro Leu
115 120 125
Trp Ile Val Phe Ala Arg Asp Met Val Ile Lys Leu Arg Glu Glu Leu
130 135 140
Ile Met Asn Ser Phe Lys Thr Ile Asp Gly Arg Gly Ala Ser Val His
145 150 155 160
Ile Ala Gly Gly Pro Cys Ile Thr Ile Gln Tyr Val Thr Asn Ile Ile
165 170 175
Ile His Gly Val Asn Ile His Asp Cys Lys Arg Gly Gly Asn Ala His
180 185 190
Val Arg Asp Ser Pro Ser His Tyr Gly Trp Arg Thr Val Ser Asp Gly
195 200 205
Asp Gly Val Ser Ile Phe Gly Gly Ser His Val Trp Val Asp His Cys
210 215 220
Ser Leu Ser Asn Cys Asn Asp Gly Leu Ile Asp Ala Ile His Gly Ser
225 230 235 240
Thr Ala Ile Thr Ile Ser Asn Asn Tyr Leu Thr His His Asn Lys Val
245 250 255
Met Leu Leu Gly His Ser Asp Ser Tyr Lys Gln Asp Lys Asn Met Gln
260 265 270
Val Thr Ile Ala Phe Asn His Phe Gly Glu Gly Leu Val Gln Arg Met
275 280 285
Pro Arg Cys Arg His Gly Tyr Phe His Val Val Asn Asn Asp Tyr Thr
290 295 300
His Trp Lys Met Tyr Ala Ile Gly Gly Ser Ala Asp Pro Thr Ile Asn
305 310 315 320
Ser Gln Gly Asn Arg Phe Leu Ala Pro Asn Asp Arg Phe Asn Lys Glu
325 330 335
Val Thr Lys His Glu Asp Ala Pro Gln Ser Ala Trp Lys Gly Trp Asn
340 345 350
Trp Arg Ser Glu Gly Asp Leu Leu Leu Asn Gly Ala Phe Phe Thr Ala
355 360 365
Ser Gly Ala Gly Ala Ser Ser Ser Tyr Ala Lys Ala Ser Ser Leu Gly
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385 390 395 400
Leu Val Cys Lys Lys Gly Ser Arg Cys
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<211> 1362
<212> DNA
<213> Oryza sativa

<220>
<221> CDS
<222> (1)..(1362)

<400> 867
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gcc acc ctc ctc ctc ccg ccg ccg ctc gcc gcc tcc ctc aac tcc 96
Ala Thr Leu Leu Leu Pro Pro Leu Ala Ala Ser Leu Asn Ser
20 25 30
tcc ctc ccc gac ccc gcc gcc gtc gtc gcc gac ttc cac agc aag gtg 144
Ser Leu Pro Asp Pro Ala Ala Val Val Ala Asp Phe His Ser Lys Val
35 40 45
gcg acg tcg cgg cgg cgg atg cag gag gcc ggc ggc ggc ggc ggt 192
Ala Thr Ser Arg Arg Arg Met Gln Glu Ala Gly Gly Gly Gly Gly Gly
50 55 60
ggc ggc ggg ggg tgt ttg acg ggg aac ccc atc gac gac tgc tgg cgg 240
Gly Gly Gly Gly Cys Leu Thr Gly Asn Pro Ile Asp Asp Cys Trp Arg
seite 1093

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Cys	Ala	Gly	Thr	Asp	Trp	Arg	Gln	Asp	Arg	Gln	Arg	Leu	Ala	Asp	Cys																			
				85					90					95																				
ggc	atc	ggg	ttc	ggg	cgc	aac	gcc	atg	ggc	ggc	aag	ggc	ggg	ccg	gtg	336																		
Gly	Ile	Gly	Phe	Gly	Arg	Asn	Ala	Met	Gly	Gly	Lys	Gly	Gly	Pro	Val																			
			100					105					110																					
tac	gtc	gtc	acc	gac	ccc	tcc	gac	ggc	gac	ccg	gtg	aac	ccc	gcg	ccg	384																		
Tyr	Val	Val	Thr	Asp	Pro	Ser	Asp	Gly	Asp	Pro	Val	Asn	Pro	Ala	Pro																			
		115					120					125																						
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Gly	Thr	Leu	Arg	Tyr	Gly	Ala	Ile	Gln	Glu	Gly	Pro	Leu	Trp	Ile	Val																			
	130				135					140																								
ttc	gcc	ggc	gac	atg	acc	atc	cgc	ctc	aac	gag	gag	ctc	ctc	gtg	aac	480																		
Phe	Ala	Gly	Asp	Met	Thr	Ile	Arg	Leu	Asn	Glu	Glu	Leu	Leu	Val	Asn																			
145					150					155					160																			
agc	tac	aag	acc	atc	gac	ggc	cgc	ggc	gcc	aac	gtc	cac	gtc	ggc	gcc	528																		
Ser	Tyr	Lys	Thr	Ile	Asp	Gly	Arg	Gly	Ala	Asn	Val	His	Val	Gly	Ala																			
			165					170						175																				
ggc	ggc	gcg	tgc	atc	acg	ctc	cag	tac	gtc	tcc	aac	gtc	atc	atc	cac	576																		
Gly	Gly	Ala	Cys	Ile	Thr	Leu	Gln	Tyr	Val	Ser	Asn	Val	Ile	Ile	His																			
			180					185					190																					
aac	atc	cac	gtc	cac	gac	tgc	gtc	ccc	gcc	ggc	aac	gcc	aac	gtg	cg	624																		
Asn	Ile	His	Val	His	Asp	Cys	Val	Pro	Ala	Gly	Asn	Ala	Asn	Val	Arg																			
		195				200				205																								
gcc	tcg	ccg	acg	cac	tac	ggg	tgg	cgc	acc	cgc	tcc	gac	ggc	gac	ggc	672																		
Ala	Ser	Pro	Thr	His	Tyr	Gly	Trp	Arg	Thr	Arg	Ser	Asp	Gly	Asp	Gly																			
	210				215					220																								
atc	tcg	ctc	tac	tcg	gcg	cgc	gac	gtg	tgg	gtg	gac	cac	tgc	gcg	ctg	720																		
Ile	Ser	Leu	Tyr	Ser	Ala	Arg	Asp	Val	Trp	Val	Asp	His	Cys	Ala	Leu																			
225					230					235					240																			
tcg	cgc	tgc	gcc	gac	ggc	ctc	atc	gac	gcc	atc	atg	ggg	tcc	acg	gcg	768																		
Ser	Arg	Cys	Ala	Asp	Gly	Leu	Ile	Asp	Ala	Ile	Met	Gly	Ser	Thr	Ala																			
			245						250					255																				
atc	acc	gtg	tcg	aac	agc	tac	ttc	tcg	cac	cac	aac	gag	gtg	atg	ctg	816																		
Ile	Thr	Val	Ser	Asn	Ser	Tyr	Phe	Ser	His	His	Asn	Glu	Val	Met	Leu																			
			260					265					270																					
ctg	ggg	cac	agc	gac	ggg	tac	ctg	ccg	gac	tcg	gcg	atg	cag	gtg	acc	864																		
Leu	Gly	His	Ser	Asp	Gly	Tyr	Leu	Pro	Asp	Ser	Ala	Met	Gln	Val	Thr																			
		275					280					285																						
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Ile	Ala	Phe	Asn	His	Phe	Gly	Ile	Gln	Leu	Val	Gln	Arg	Met	Pro	Arg																			
	290				295					300																								
tgc	agg	agg	ggg	tac	ttc	cac	atc	gtc	aac	aac	gac	tac	acg	gcg	tgg	960																		
Cys	Arg	Arg	Gly	Tyr	Phe	His	Ile	Val	Asn	Asn	Asp	Tyr	Thr	Ala	Trp																			
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gag	atg	tac	gcc	att	gga	ggg	agc	gcg	agc	ccc	acc	atc	aac	agc	cag	1008																		
Glu	Met	Tyr	Ala	Ile	Gly	Gly	Ser	Ala	Ser	Pro	Thr	Ile	Asn	Ser	Gln																			
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ggc	aac	cgc	tac	atc	gcc	ccc	gcc	gat	ccc	aac	gcc	aag	gag	gtg	acg	1056																		
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			340					345					350																					
aag	cgg	gtg	gac	acg	gag	gag	ggg	cag	tgg	gcg	ggg	tgg	aac	tgg	agg	1104																		
Lys	Arg	Val	Asp	Thr	Glu	Glu	Gly	Gln	Trp	Ala	Gly	Trp	Asn	Trp	Arg																			
		355					360					365																						
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Thr	Glu	Gly	Asp	Met	Met	Val	Asn	Gly	Ala	Phe	Phe	Val	Pro	Ser	Gly																			
	370				375					380																								
gag	ggc	ctc	gag	gcc	atc	tac	gac	aag	gcc	tcc	agc	acc	gac	ccc	aag	1200																		
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Ser	Ser	Ala	Leu	Val	Asp	Gln	Leu	Thr	Ala	Gly	Ala	Gly	Val	Leu	Gly																			
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ggc	ccc	agc	ggc	gtc	ttt	aaa	ctg	cca	cct	ccg	gtc	gcc	gga	ggg	gcg	1296																		
Gly	Pro	Ser	Gly	Ala	Phe	Lys	Leu	Pro	Pro	Pro	Val	Ala	Gly	Gly	Ala																			
			420					425					430																					
ccg	ctt	gtc	gag	ttg	ttg	tcg	gcg	cca	ttg	ccg	cga	cct	gga	tgg	gta	1344																		
Pro	Leu	Val	Glu	Leu	Leu	Ser	Ala	Pro	Leu	Pro	Arg	Pro	Gly	Trp	Val																			

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Glu Arg Asp Leu Arg
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440 445

1362

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<211> 453
<212> PRT
<213> Oryza sativa

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35 40 45
Ala Thr Ser Arg Arg Arg Met Gln Glu Ala Gly Gly Gly Gly Gly
50 55 60
Gly Gly Gly Gly Cys Leu Thr Gly Asn Pro Ile Asp Asp Cys Trp Arg
65 70 75 80
Cys Ala Gly Thr Asp Trp Arg Gln Asp Arg Gln Arg Leu Ala Asp Cys
85 90 95
Gly Ile Gly Phe Gly Arg Asn Ala Met Gly Gly Lys Gly Gly Pro Val
100 105 110
Tyr Val Val Thr Asp Pro Ser Asp Gly Asp Pro Val Asn Pro Ala Pro
115 120 125
Gly Thr Leu Arg Tyr Gly Ala Ile Gln Glu Gly Pro Leu Trp Ile Val
130 135 140
Phe Ala Gly Asp Met Thr Ile Arg Leu Asn Glu Glu Leu Leu Val Asn
145 150 155 160
Ser Tyr Lys Thr Ile Asp Gly Arg Gly Ala Asn Val His Val Gly Ala
165 170 175
Gly Gly Ala Cys Ile Thr Leu Gln Tyr Val Ser Asn Val Ile Ile His
180 185 190
Asn Ile His Val His Asp Cys Val Pro Ala Gly Asn Ala Asn Val Arg
195 200 205
Ala Ser Pro Thr His Tyr Gly Trp Arg Thr Arg Ser Asp Gly Asp Gly
210 215 220
Ile Ser Leu Tyr Ser Ala Arg Asp Val Trp Val Asp His Cys Ala Leu
225 230 235 240
Ser Arg Cys Ala Asp Gly Leu Ile Asp Ala Ile Met Gly Ser Thr Ala
245 250 255
Ile Thr Val Ser Asn Ser Tyr Phe Ser His His Asn Glu Val Met Leu
260 265 270
Leu Gly His Ser Asp Gly Tyr Leu Pro Asp Ser Ala Met Gln Val Thr
275 280 285
Ile Ala Phe Asn His Phe Gly Ile Gln Leu Val Gln Arg Met Pro Arg
290 295 300
Cys Arg Arg Gly Tyr Phe His Ile Val Asn Asn Asp Tyr Thr Ala Trp
305 310 315 320
Glu Met Tyr Ala Ile Gly Gly Ser Ala Ser Pro Thr Ile Asn Ser Gln
325 330 335
Gly Asn Arg Tyr Ile Ala Pro Ala Asp Pro Asn Ala Lys Glu Val Thr
340 345 350
Lys Arg Val Asp Thr Glu Glu Gly Gln Trp Ala Gly Trp Asn Trp Arg
355 360 365
Thr Glu Gly Asp Met Met Val Asn Gly Ala Phe Phe Val Pro Ser Gly
370 375 380
Glu Gly Leu Glu Ala Ile Tyr Asp Lys Ala Ser Thr Asp Pro Lys
385 390 395 400
Ser Ser Ala Leu Val Asp Gln Leu Thr Ala Gly Ala Gly Val Leu Gly
405 410 415
Gly Pro Ser Gly Ala Phe Lys Leu Pro Pro Val Ala Gly Gly Ala
420 425 430
Pro Leu Val Glu Leu Leu Ser Ala Pro Leu Pro Arg Pro Gly Trp Val
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Glu Arg Asp Leu Arg
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PF59082SeqList_PF59082.txt

<210> 869
 <211> 1437
 <212> DNA
 <213> Vitis vinifera

<220>
 <221> CDS
 <222> (20)..(1216)

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cca att ctt ggt tcc ccc gca cca gtc caa gac cct gaa gta gtt gtg      100
Pro Ile Leu Gly Ser Pro Ala Pro Val Gln Asp Pro Glu Val Val Val
                        15           20           25
caa gag gtg cac agg agc atc aat gcc tct agg agg aac ttg ggc tat      148
Gln Glu Val His Arg Ser Ile Asn Ala Ser Arg Arg Asn Leu Gly Tyr
                        30           35           40
ttc tct tgt gga aca ggc aac cct atc gac gat tgc tgg agg tgc gac      196
Phe Ser Cys Gly Thr Gly Asn Pro Ile Asp Asp Cys Trp Arg Cys Asp
                        45           50           55
gcc aac tgg gac aag aac cgc cag cga tta gcc gac tgc gct att ggg      244
Ala Asn Trp Asp Lys Asn Arg Gln Arg Leu Ala Asp Cys Ala Ile Gly
                        60           65           70
ttt ggc aag gat gca atg ggc gga aag aat ggt aga att tac gtg gtc      292
Phe Gly Lys Asp Ala Met Gly Gly Lys Asn Gly Arg Ile Tyr Val Val
                        75           80           85
acc gac tcc gag gat gat gac cct gtc aat cca agg cca ggg act ctc      340
Thr Asp Ser Glu Asp Asp Asp Pro Val Asn Pro Arg Pro Gly Thr Leu
                        90           95           100
cgt cat gct gtg atc caa gat gag cca ttg tgg atc atc ttc aag cgt      388
Arg His Ala Val Ile Gln Asp Glu Pro Leu Trp Ile Ile Phe Lys Arg
                        105           110           115
gac atg gtc atc aag ctg aag caa gag ctg gtg atg aac tcg ttc aag      436
Asp Met Val Ile Lys Leu Lys Gln Glu Leu Val Met Asn Ser Phe Lys
                        120           125           130
aca att gat ggt agg ggt gct agc gtt cac att gct gga ggg cca tgc      484
Thr Ile Asp Gly Arg Gly Ala Ser Val His Ile Ala Gly Gly Pro Cys
                        135           140           145
att acc atc cat tac gcc agt aac atc atc ata cat ggt ctc cat atc      532
Ile Thr Ile His Tyr Ala Ser Asn Ile Ile Ile His Gly Leu His Ile
                        150           155           160
cat gac tgt aag caa gga ggg aat gcc aac atc aga aac tct cct cac      580
His Asp Cys Lys Gln Gly Gly Asn Ala Asn Ile Arg Asn Ser Pro His
                        165           170           175
cac tcc ggc tgg tgg act gta tct gat ggt gat ggg gtg tcc atc ttc      628
His Ser Gly Trp Trp Thr Val Ser Asp Gly Asp Gly Val Ser Ile Phe
                        180           185           190
ggg ggg agg cat ata tgg gtt gac cat tgc tct ttg tcc aac tgc cat      676
Gly Gly Arg His Ile Trp Val Asp His Cys Ser Leu Ser Asn Cys His
                        195           200           205
gac ggc ctc att gat gcc atc cat gga tcc acc gcc ata acc atc tct      724
Asp Gly Leu Ile Asp Ala Ile His Gly Ser Thr Ala Ile Thr Ile Ser
                        210           215           220
aac aat ttc atg act cac cat gac aag gtc atg ctc ctg ggc cac agc      772
Asn Asn Phe Met Thr His His Asp Lys Val Met Leu Leu Gly His Ser
                        225           230           235
gat tct tat aca gaa gac aag aac atg caa gtc acc att gcc ttc aac      820
Asp Ser Tyr Thr Glu Asp Lys Asn Met Gln Val Thr Ile Ala Phe Asn
                        240           245           250
cat ttc gga gag ggg ctc gtg cag aga atg ccc aga tgt agg cat ggg      868
His Phe Gly Glu Gly Leu Val Gln Arg Met Pro Arg Cys Arg His Gly
                        255           260           265
tat ttt cat gtg gtg aac aac gac tac acc cac tgg gaa atg tat gcc      916
Tyr Phe His Val Val Asn Asn Asp Tyr Thr His Trp Glu Met Tyr Ala
                        270           275           280
att ggt gga agt gct gac cct acc atc aac agc cag ggc aac aga ttc      964
                        285           290           295

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PF59082SeqList_PF59082.txt

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Leu	Ala	Pro	Asn	Asp	Arg	Phe	Lys	Lys	Ala	Val	Thr	Lys	His	Glu	Asp	
				320					325					330		
gca	cca	gaa	agt	gag	tg	agg	cat	tg	aac	tg	aga	tct	gaa	ggg	gac	1060
Ala	Pro	Glu	Ser	Glu	Trp	Arg	His	Trp	Asn	Trp	Arg	Ser	Glu	Gly	Asp	
			335					340					345			
ctg	atg	ttg	aat	gg	gcc	ttc	ttc	ctg	cag	tcg	ggg	gca	ggc	gct	tct	1108
Leu	Met	Leu	Asn	Gly	Ala	Phe	Phe	Leu	Gln	Ser	Gly	Ala	Gly	Ala	Ser	
		350				355					360					
tcc	tcg	tac	gcc	aga	cgt	tcc	agc	ttg	agt	gcc	aga	cca	tct	tct	ctg	1156
Ser	Ser	Tyr	Ala	Arg	Arg	Ser	Ser	Leu	Ser	Ala	Arg	Pro	Ser	Ser	Leu	
	365				370					375						
gtg	ggt	tca	atc	acc	ttg	ggt	tct	ggc	gca	ctc	ggc	tgc	agg	aag	ggg	1204
Val	Gly	Ser	Ile	Thr	Leu	Gly	Ser	Gly	Ala	Leu	Gly	Cys	Arg	Lys	Gly	
380					385					390					395	
tct	cgt	tgc	taattaa	aatg	aagg	gatg	ta	ccata	acaa	gtatt	actat	tatcatt	atc			1263
Ser	Arg	Cys														
caaaaattat aggttcgatt aggggtttatc tttctttcta gtgctcactt aactgattat																1323
ccacctgggt ctgatgcttg gagaagcatg ttgagttccc tgggaggcag ttaagttgca																1383
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<210> 870

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<213> vitis vinifera

<400> 870

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Ser	Ile	Asn	Ala	Ser	Arg	Arg	Asn	Leu	Gly	Tyr	Phe	Ser	Cys	Gly	Thr	
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Gly	Asn	Pro	Ile	Asp	Asp	Cys	Trp	Arg	Cys	Asp	Ala	Asn	Trp	Asp	Lys	
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65				70				75						80		
Met	Gly	Gly	Lys	Asn	Gly	Arg	Ile	Tyr	Val	Val	Thr	Asp	Ser	Glu	Asp	
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Asp	Asp	Pro	Val	Asn	Pro	Arg	Pro	Gly	Thr	Leu	Arg	His	Ala	Val	Ile	
		100						105					110			
Gln	Asp	Glu	Pro	Leu	Trp	Ile	Ile	Phe	Lys	Arg	Asp	Met	Val	Ile	Lys	
	115					120						125				
Leu	Lys	Gln	Glu	Leu	Val	Met	Asn	Ser	Phe	Lys	Thr	Ile	Asp	Gly	Arg	
	130				135						140					
Gly	Ala	Ser	Val	His	Ile	Ala	Gly	Gly	Pro	Cys	Ile	Thr	Ile	His	Tyr	
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Gly	Gly	Asn	Ala	Asn	Ile	Arg	Asn	Ser	Pro	His	His	Ser	Gly	Trp	Trp	
		180						185					190			
Thr	Val	Ser	Asp	Gly	Asp	Gly	Val	Ser	Ile	Phe	Gly	Gly	Arg	His	Ile	
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Trp	Val	Asp	His	Cys	Ser	Leu	Ser	Asn	Cys	His	Asp	Gly	Leu	Ile	Asp	
	210				215						220					
Ala	Ile	His	Gly	Ser	Thr	Ala	Ile	Thr	Ile	Ser	Asn	Asn	Phe	Met	Thr	
225				230					235					240		
His	His	Asp	Lys	Val	Met	Leu	Leu	Gly	His	Ser	Asp	Ser	Tyr	Thr	Glu	
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Asp	Lys	Asn	Met	Gln	Val	Thr	Ile	Ala	Phe	Asn	His	Phe	Gly	Glu	Gly	

PF59082SeqList_PF59082.txt

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 275
 Asn Asn Asp Tyr Thr His Trp Glu Met Tyr Ala Ile Gly Gly Ser Ala
 290
 Asp Pro Thr Ile Asn Ser Trp Gln Gly Asn Arg Phe Leu Ala Pro Asn Asp
 305
 Arg Phe Lys Lys Ala Val Thr Lys His Glu Asp Ala Pro Glu Ser Glu
 325
 Trp Arg His Trp Asn Trp Arg Ser Glu Gly Asp Leu Met Leu Asn Gly
 340
 Ala Phe Phe Leu Gln Ser Gly Ala Gly Ala Ser Ser Ser Tyr Ala Arg
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<211> 1788

<212> DNA

<213> Musa acuminata

<220>

<221> CDS

<222> (78)..(1442)

<400> 871

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Met Thr Ala Gly Leu Arg Trp Ile Pro Pro Leu

ctt ctt ctt ctt ctg ggc ttc ctg ctg gtt ttg aac gga agt cgg ggg 158

Leu Leu Leu Leu Leu Gly Phe Leu Leu Val Leu Asn Gly Ser Arg Gly

tgg att gga agc gag cgg tcc tct ggc tcg agg aat ggc gga gca tcg 206

Trp Ile Gly Ser Glu Arg Ser Ser Gly Ser Arg Asn Gly Gly Ala Ser

cgg agg agc ttg aga gag gcc tcc gcg aac gcg acc agc gcc gat gct 254

Arg Arg Ser Leu Arg Glu Ala Ser Ala Asn Ala Thr Ser Ala Asp Ala

tcc ttg gaa gag agg gct gta acc agg gca gca gaa gcc gca gtc gac 302

Ser Leu Glu Glu Arg Val Thr Arg Ala Ala Glu Ala Ala Val Asp

gac ccc gag gag gtt gct tcg acg gtc ctg acg acc ata atc aac agc 350

Asp Pro Glu Glu Val Ala Ser Thr Val Leu Thr Thr Ile Ile Asn Ser

acg gct cgc aga tct ctt ggt tat ctg tcg tgc ggt tca ggc aac ccg 398

Thr Ala Arg Arg Ser Leu Gly Tyr Leu Ser Cys Gly Ser Gly Asn Pro

atc gac gac tgc tgg cgg tgc gac ccc gat tgg cat gtc aac aga aaa 446

Ile Asp Asp Cys Trp Arg Cys Asp Pro Asp Trp His Val Asn Arg Lys

aag ctc gct gac tgc ggc att ggc ttt ggc cgc aac gcg ata ggt ggc 494

Lys Leu Ala Asp Cys Gly Ile Gly Phe Gly Arg Asn Ala Ile Gly Gly

cgc gac ggg gag ttg tac gtt gtg aca gac tcc ggg gac gat gat ccc 542

Arg Asp Gly Glu Leu Tyr Val Val Thr Asp Ser Gly Asp Asp Asp Pro

gtg aat cct cgc ccg gga aca ctt aga tac gcc gtc atc cag gac gtg 590

Val Asn Pro Arg Pro Gly Thr Leu Arg Tyr Ala Val Ile Gln Asp Val

ccc ctc tgg atc acc ttt aaa cac gac atg gag atc acg ctc aag gag 638

Pro Leu Trp Ile Thr Phe Lys His Asp Met Glu Ile Thr Leu Lys Glu

gaa ctc att atg aac agc ttt aag acg atc gat gga cgc ggt gtc aac 686

Glu Leu Ile Met Asn Ser Phe Lys Thr Ile Asp Gly Arg Gly Val Asn

PF59082SeqList_PF59082.txt

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Val	Ile	Ile	His	Gly	Leu	His	Ile	His	Asp	Cys	Lys	Pro	Thr	Gly	Asn	
	220				225					230					235	
gcc	atg	gtc	cgc	agc	tct	cct	tct	cac	tat	gga	tgg	aga	acc	atg	gct	830
Ala	Met	Val	Arg	Ser	Ser	Pro	Ser	His	Tyr	Gly	Trp	Arg	Thr	Met	Ala	
				240					245					250		
gat	ggg	gat	gcc	ggt	tcc	att	ttc	ggc	tcc	agc	cac	att	tgg	gtg	gac	878
Asp	Gly	Asp	Ala	Val	Ser	Ile	Phe	Gly	Ser	Ser	His	Ile	Trp	Val	Asp	
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cac	tgc	tct	ctg	tcc	aac	tgc	gcc	gat	gga	ctt	gtc	gat	gcc	gtc	atg	926
His	Cys	Ser	Leu	Ser	Asn	Cys	Ala	Asp	Gly	Leu	Val	Asp	Ala	Val	Met	
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ggc	tcc	act	gcc	att	acg	gtc	tcc	aac	aat	tac	ttc	acc	cac	cac	aat	974
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Glu	Val	Met	Leu	Leu	Gly	His	Thr	Asp	Ser	Tyr	Ala	Arg	Asp	Ser	Ile	
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Met	Gln	Val	Thr	Ile	Ala	Phe	Asn	His	Phe	Gly	Glu	Gly	Leu	Ile	Gln	
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Arg	Met	Pro	Arg	Cys	Arg	His	Gly	Tyr	Phe	His	Val	Val	Asn	Asn	Asp	
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Tyr	Thr	His	Trp	Glu	Met	Tyr	Ala	Ile	Gly	Gly	Ser	Ala	Asn	Pro	Thr	
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Ile	Asn	Ser	Gln	Gly	Asn	Arg	Tyr	Leu	Ala	Pro	Thr	Asn	Pro	Phe	Ala	
	365				370					375						
aag	gag	gta	aca	aaa	agg	gtg	gac	aca	gat	caa	agc	acg	tgg	aag	aac	1262
Lys	Glu	Val	Thr	Lys	Arg	Val	Asp	Thr	Asp	Gln	Ser	Thr	Trp	Lys	Asn	
	380				385					390					395	
tgg	aat	tgg	agg	tcg	gag	ggt	gac	ctg	ctt	ctg	aat	ggt	gct	ttt	ttc	1310
Trp	Asn	Trp	Arg	Ser	Glu	Gly	Asp	Leu	Leu	Leu	Asn	Gly	Ala	Phe	Phe	
				400				405					410			
acc	cct	tcc	ggt	gca	ggg	gct	tca	gcc	agc	tac	gca	cgg	gcc	tcc	agc	1358
Thr	Pro	Ser	Gly	Ala	Gly	Ala	Ser	Ala	Ser	Tyr	Ala	Arg	Ala	Ser	Ser	
			415			420						425				
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Phe	Gly	Ala	Lys	Pro	Ser	Ser	Leu	Val	Asp	Thr	Leu	Thr	Ser	Asp	Ala	
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ggg	gtc	ctg	tct	tgc	caa	gtc	ggc	act	cga	tgt	taacgtaatg	ccaagtagca				1459
Gly	Val	Leu	Ser	Cys	Gln	Val	Gly	Thr	Arg	Cys						
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PF59082SeqList_PF59082.txt

<211> 454

<212> PRT

<213> Musa acuminata

<400> 872

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Arg Ser Ser Gly Ser Arg Asn Gly Ala Ser Arg Arg Ser Leu Arg
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Glu Ala Ser Ala Asn Ala Thr Ser Ala Asp Ala Ser Leu Glu Glu Arg
      50      55      60
Ala Val Thr Arg Ala Ala Glu Ala Ala Val Asp Asp Pro Glu Glu Val
65      70      75      80
Ala Ser Thr Val Leu Thr Thr Ile Ile Asn Ser Thr Ala Arg Arg Ser
      85      90      95
Leu Gly Tyr Leu Ser Cys Gly Ser Gly Asn Pro Ile Asp Asp Cys Trp
      100      105      110
Arg Cys Asp Pro Asp Trp His Val Asn Arg Lys Lys Leu Ala Asp Cys
      115      120      125
Gly Ile Gly Phe Gly Arg Asn Ala Ile Gly Gly Arg Asp Gly Glu Leu
      130      135      140
Tyr Val Val Thr Asp Ser Gly Asp Asp Asp Pro Val Asn Pro Arg Pro
145      150      155      160
Gly Thr Leu Arg Tyr Ala Val Ile Gln Asp Val Pro Leu Trp Ile Thr
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Phe Lys His Asp Met Glu Ile Thr Leu Lys Glu Glu Leu Ile Met Asn
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Ser Phe Lys Thr Ile Asp Gly Arg Gly Val Asn Val His Ile Ala Asn
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Gly Ala Cys Ile Thr Ile Gln Tyr Ile Thr Asn Val Ile Ile His Gly
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Leu His Ile His Asp Cys Lys Pro Thr Gly Asn Ala Met Val Arg Ser
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Ser Pro Ser His Tyr Gly Trp Arg Thr Met Ala Asp Gly Asp Ala Val
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Gly His Thr Asp Ser Tyr Ala Arg Asp Ser Ile Met Gln Val Thr Ile
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Ala Phe Asn His Phe Gly Glu Gly Leu Ile Gln Arg Met Pro Arg Cys
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Arg His Gly Tyr Phe His Val Val Asn Asn Asp Tyr Thr His Trp Glu
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Ser Ala Ala Val Arg Asp Pro Glu Leu Val Val Gln Glu Val Gln Arg
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Ser Leu Asn Val Ser Arg Arg Arg Leu Gly Tyr Leu Ser Cys Gly Thr
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Gly Asn Pro Ile Asp Asp Cys Trp Arg Cys Asp Pro Asp Trp Ala Asp
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Ile Gly Gly Arg Asp Gly Glu Ile Tyr Val Val Thr Asp Ser Gly Asp
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Asp Asp Pro Val Asn Pro Lys Thr Gly Thr Leu Arg Tyr Ala Val Ile
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Thr Val Ser Asp Gly Asp Gly Val Ser Ile Phe Gly Gly Ser His Val
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Trp Val Asp His Cys Thr Leu Ser Asn Cys His Asp Gly Leu Ile Asp
220 225 230

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	Trp	Arg	Cys	Asp	Pro	Asp	Trp	Ala	Asp	Asn	Arg	Gln	Arg	Leu	Ala
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	Ile	Tyr	Val	Val	Thr	Asp	Ser	Gly	Asp	Asp	Asp	Pro	Val	Asn	Pro
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	Gly	Val	His	Ile	His	Asp	Cys	Lys	Gln	Gly	Gly	Asn	Ala	Tyr	Val
	Asp	Ser	Pro	Gly	His	Tyr	Gly	Trp	Arg	Thr	Val	Ser	Asp	Gly	Asp
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PF59082SeqList_PF59082.txt

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Ala	Gly	Gly	Ala	Cys	Ile	Thr	Ile	Gln	Tyr	Val	Thr	Asn	Ile	Ile	Ile	
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Ile	His	Asn	Ile	His	Ile	His	His	Cys	Tyr	Gln	Ser	Gly	Asn	Thr	Asn	
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Val	Arg	Ser	Ser	Pro	Thr	His	Tyr	Gly	Phe	Arg	Thr	Lys	Ser	Asp	Gly	
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Asp	Gly	Ile	Ser	Ile	Phe	Gly	Ser	Lys	Asp	Ile	Trp	Ile	Asp	His	Cys	
			225					230					235			
tct	cta	tcg	aga	tgc	aag	gac	ggt	ctg	ata	gat	gcg	gta	atg	ggt	tcc	889
Ser	Leu	Ser	Arg	Cys	Lys	Asp	Gly	Leu	Ile	Asp	Ala	Val	Met	Gly	Ser	
		240					245					250				
aca	gga	ata	act	ata	tcg	aac	aac	ttc	ttc	tct	cac	cat	aat	gaa	gtc	937
Thr	Gly	Ile	Thr	Ile	Ser	Asn	Asn	Phe	Phe	Ser	His	His	Asn	Glu	Val	
	255					260					265					
atg	ctt	ctt	ggt	cac	agc	gac	cac	tat	gaa	cca	gac	agt	ggc	atg	cag	985
Met	Leu	Leu	Gly	His	Ser	Asp	His	Tyr	Glu	Pro	Asp	Ser	Gly	Met	Gln	
270					275					280				285		
gta	aca	att	gcg	ttt	aat	cac	ttt	gga	gag	aaa	ttg	ata	caa	agg	atg	1033
Val	Thr	Ile	Ala	Phe	Asn	His	Phe	Gly	Glu	Lys	Leu	Ile	Gln	Arg	Met	
				290					295					300		
ccg	agg	tgt	cga	cgt	gga	tat	atc	cat	gtg	gtt	aat	aac	gat	ttt	act	1081
Pro	Arg	Cys	Arg	Arg	Gly	Tyr	Ile	His	Val	Val	Asn	Asn	Asp	Phe	Thr	
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caa	tgg	gaa	atg	tat	gcc	att	ggc	ggt	agc	ggt	aac	ccg	act	att	aac	1129
Gln	Trp	Glu	Met	Tyr	Ala	Ile	Gly	Gly	Ser	Gly	Asn	Pro	Thr	Ile	Asn	
		320					325					330				
agt	cag	ggt	aac	cgc	tac	acc	gcc	cca	acc	aac	ccg	ttt	gcc	aag	gag	1177
Ser	Gln	Gly	Asn	Arg	Tyr	Thr	Ala	Pro	Thr	Asn	Pro	Phe	Ala	Lys	Glu	
	335					340					345					
gtg	aca	aag	aga	gtg	gaa	aca	ccg	gat	ggt	gat	tgg	aaa	ggg	tgg	aat	1225
Val	Thr	Lys	Arg	Val	Glu	Thr	Pro	Asp	Gly	Asp	Trp	Lys	Gly	Trp	Asn	
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tgg	aga	tcg	gag	ggg	gac	att	ttg	gtg	aat	gga	gcc	ttc	ttc	gtg	gca	1273
Trp	Arg	Ser	Glu	Gly	Asp	Ile	Leu	Val	Asn	Gly	Ala	Phe	Phe	Val	Ala	
				370					375					380		
tcc	ggg	gaa	ggt	gcg	gaa	atg	agg	tat	gag	aag	gca	tat	agc	gtc	gag	1321
Ser	Gly	Glu	Gly	Ala	Glu	Met	Arg	Tyr	Glu	Lys	Ala	Tyr	Ser	Val	Glu	
			385					390					395			
cct	aaa	tcc	gcc	tca	ttc	atc	acc	caa	atc	aca	ttt	cac	tct	ggt	gtt	1369
Pro	Lys	Ser	Ala	Ser	Phe	Ile	Thr	Gln	Ile	Thr	Phe	His	Ser	Gly	Val	
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ctt	ggc	gtt	ggt	ggc	agg	aat	aac	aat	ctg	ggg	atg	tgg	act	act	act	1417
Leu	Gly	Val	Gly	Gly	Arg	Asn	Asn	Asn	Leu	Gly	Met	Trp	Thr	Thr	Thr	
	415					420				425						
gga	tcg	gaa	ggt	act	agc	ggt	tta	gat	tct	tat	aat	gac	tat	acc	gat	1465
Gly	Ser	Glu	Gly	Thr	Ser	Gly	Leu	Asp	Ser	Tyr	Asn	Asp	Tyr	Thr	Asp	
430					435					440					445	
gaa	atg	tct	ggc	gct	ggt	tca	acc	aac	cgg	tta	tct	ttt	tca	gtt	ctt	1513

PF59082SeqList_PF59082.txt

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Val Phe Leu Leu Ser Ser Ile Ser Tyr Leu Val Val Phe Thr Ser Ser	
465 470 475	
acc caa atg ttt atg ttg taacatgaat tgaatttacc tattttatca	1609
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<400> 878

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Val Asn Ala Ser Ile Thr Arg Gln Ala Leu Asp Thr Thr Asp Gln	
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Ala Gly Ser Thr Pro Cys Ile Thr Gly Asn Pro Ile Asp Asp Cys Trp	
65 70 75 80	
Lys Cys Asp Pro Asn Trp Pro Asn Asn Arg Gln Gly Leu Ala Asp Cys	
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Gly Ile Gly Phe Gly Gln Tyr Ala Leu Gly Gly Lys Gly Gly Gln Phe	
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Tyr Phe Val Thr Asp Ser Ser Asp Asp Asp Ala Val Asn Pro Lys Pro	
115 120 125	
Gly Thr Leu Arg Tyr Gly Val Ile Gln Glu Glu Pro Leu Trp Ile Val	
130 135 140	
Phe Pro Ser Asn Met Met Ile Lys Leu Lys Gln Glu Leu Ile Phe Asn	
145 150 155 160	
Ser Tyr Lys Thr Leu Asp Gly Arg Gly Ala Asn Val His Ile Val Gly	
165 170 175	
Gly Gly Cys Ile Thr Leu Gln Tyr Val Ser Asn Ile Ile Ile His Asn	
180 185 190	
Ile His Ile His His Cys Tyr Gln Ser Gly Asn Thr Asn Val Arg Ser	
195 200 205	
Ser Pro Thr His Tyr Gly Phe Arg Thr Lys Ser Asp Gly Asp Gly Ile	
210 215 220	
Ser Ile Phe Gly Ser Lys Asp Ile Trp Ile Asp His Cys Ser Leu Ser	
225 230 235 240	
Arg Cys Lys Asp Gly Leu Ile Asp Ala Val Met Gly Ser Thr Gly Ile	
245 250 255	
Thr Ile Ser Asn Asn Phe Phe Ser His His Asn Glu Val Met Leu Leu	
260 265 270	
Gly His Ser Asp His Tyr Glu Pro Asp Ser Gly Met Gln Val Thr Ile	
275 280 285	
Ala Phe Asn His Phe Gly Glu Lys Leu Ile Gln Arg Met Pro Arg Cys	
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Arg Arg Gly Tyr Ile His Val Val Asn Asn Asp Phe Thr Gln Trp Glu	
305 310 315 320	
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325 330 335	
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340 345 350	
Arg Val Glu Thr Pro Asp Gly Asp Trp Lys Gly Trp Asn Trp Arg Ser	
355 360 365	
Glu Gly Asp Ile Leu Val Asn Gly Ala Phe Phe Val Ala Ser Gly Glu	
370 375 380	
Gly Ala Glu Met Arg Tyr Glu Lys Ala Tyr Ser Val Glu Pro Lys Ser	
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Ala Ser Phe Ile Thr Gln Ile Thr Phe His Ser Gly Val Leu Gly Val	

PF59082SeqList_PF59082.txt

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 420 425 430
 Gly Thr Ser Gly Leu Asp Ser Tyr Asn Asp Tyr Thr Asp Glu Met Ser
 435 440 445
 Gly Ala Gly Ser Thr Asn Arg Leu Ser Phe Ser Val Leu Val Phe Leu
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 Leu Ser Ser Ile Ser Tyr Leu Val Val Phe Thr Ser Ser Thr Gln Met
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 Phe Met Leu

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 Phe Leu Ala Leu Phe Leu His Val Asn Ala Leu Ser Asp Gly Glu Trp
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 cat gaa cac gcc gtt aaa gac cca gaa gaa ata gca gca atg gtc gat 144
 His Glu His Ala Val Lys Asp Pro Glu Glu Ile Ala Ala Met Val Asp
 35 40 45
 atg agc ata cgt aac agt acg tat cgt aga aag cta ggg ttc ttc tcc 192
 Met Ser Ile Arg Asn Ser Thr Tyr Arg Arg Lys Leu Gly Phe Phe Ser
 50 55 60
 tca tgc tca aca gga aac cca ata gat gat tgt tgg cga tgc gat aaa 240
 Ser Cys Ser Thr Gly Asn Pro Ile Asp Asp Cys Trp Arg Cys Asp Lys
 65 70 75 80
 aaa tgg cat cgc cga aga aag cga tta gcg gat tgc gcg atc ggt ttc 288
 Lys Trp His Arg Arg Arg Lys Arg Leu Ala Asp Cys Ala Ile Gly Phe
 85 90 95
 gga cgt aac gca gtc gga ggc cgt gat gga cgt tac tac att gtt act 336
 Gly Arg Asn Ala Val Gly Gly Arg Asp Gly Arg Tyr Tyr Ile Val Thr
 100 105 110
 gat cca tct gat cat gat ccg gtt aca cca aaa ccc ggt aca ctc cgg 384
 Asp Pro Ser Asp His Asp Pro Val Thr Pro Lys Pro Gly Thr Leu Arg
 115 120 125
 tac gct gtt ata caa gac gaa ccg cta tgg atc gtc ttt aaa cgt gac 432
 Tyr Ala Val Ile Gln Asp Glu Pro Leu Trp Ile Val Phe Lys Arg Asp
 130 135 140
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 Met Val Ile Thr Leu Ser Gln Glu Leu Ile Met Asn Ser Phe Lys Thr
 145 150 155 160
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 Ile Asp Gly Arg Gly Val Asn Val His Ile Ala Gly Gly Ala Cys Leu
 165 170 175
 acg gtt cag tac gtt acg aat att atc atc cat ggg ata aat att cat 576
 Thr Val Gln Tyr Val Thr Asn Ile Ile Ile His Gly Ile Asn Ile His
 180 185 190
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 Asp Cys Lys Arg Thr Gly Asn Ala Met Val Arg Ser Ser Glu Ser His
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 Tyr Gly Trp Arg Thr Met Ala Asp Gly Asp Gly Ile Ser Ile Phe Gly
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 Ser Ser His Ile Trp Ile Asp His Asn Ser Leu Ser Ser Cys Ala Asp
 225 230 235 240
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PF59082SeqList_PF59082.txt

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Ser	Tyr	Thr	Arg	Asp	Lys	Met	Met	Gln	Val	Thr	Ile	Ala	Tyr	Asn	His	
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ttt	gga	gaa	ggt	ctt	ata	cag	aga	atg	cca	agg	tgc	agg	cat	gga	tac	912
Phe	Gly	Glu	Gly	Leu	Ile	Gln	Arg	Met	Pro	Arg	Cys	Arg	His	Gly	Tyr	
	290					295					300					
ttt	cac	gta	gta	aac	aat	gat	tac	act	cac	tgg	gaa	atg	tat	gca	att	960
Phe	His	Val	Val	Asn	Asn	Asp	Tyr	Thr	His	Trp	Glu	Met	Tyr	Ala	Ile	
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ggt	gga	agt	gct	aac	cct	acc	atc	aat	agt	caa	gga	aac	cgg	ttc	ctt	1008
Gly	Gly	Ser	Ala	Asn	Pro	Thr	Ile	Asn	Ser	Gln	Gly	Asn	Arg	Phe	Leu	
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Ala	Pro	Gly	Asn	Arg	Phe	Ala	Lys	Glu	Val	Thr	Lys	Arg	Val	Gly	Ala	
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ggg	aaa	gga	gaa	tgg	aac	aat	tgg	aat	tgg	aga	tcc	caa	gga	gac	tta	1104
Gly	Lys	Gly	Glu	Trp	Asn	Asn	Trp	Asn	Trp	Arg	Ser	Gln	Gly	Asp	Leu	
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Asn	Tyr	Ala	Arg	Ala	Ser	Ser	Leu	Ala	Ala	Lys	Ser	Ser	Ser	Leu	Val	
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ggt	atg	ctt	acc	tct	agc	tcg	ggt	gct	ttg	aaa	tgc	agg	atc	ggt	aca	1248
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<211> 418

<212> PRT

<213> Arabidopsis thaliana

<400> 880

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His	Glu	His	Ala	Val	Lys	Asp	Pro	Glu	Glu	Ile	Ala	Ala	Met	Val	Asp	
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Met	Ser	Ile	Arg	Asn	Ser	Thr	Tyr	Arg	Arg	Lys	Leu	Gly	Phe	Phe	Ser	
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Ser	Cys	Ser	Thr	Gly	Asn	Pro	Ile	Asp	Asp	Cys	Trp	Arg	Cys	Asp	Lys	
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Lys	Trp	His	Arg	Arg	Arg	Lys	Arg	Leu	Ala	Asp	Cys	Ala	Ile	Gly	Phe	
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Asp	Pro	Ser	Asp	His	Asp	Pro	Val	Thr	Pro	Lys	Pro	Gly	Thr	Leu	Arg	
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Tyr	Ala	Val	Ile	Gln	Asp	Glu	Pro	Leu	Trp	Ile	Val	Phe	Lys	Arg	Asp	
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Met	Val	Ile	Thr	Leu	Ser	Gln	Glu	Leu	Ile	Met	Asn	Ser	Phe	Lys	Thr	
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Thr	Val	Gln	Tyr	Val	Thr	Asn	Ile	Ile	Ile	His	Gly	Ile	Asn	Ile	His	
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Asp	Cys	Lys	Arg	Thr	Gly	Asn	Ala	Met	Val	Arg	Ser	Ser	Glu	Ser	His	
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PF59082SeqList_PF59082.txt

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 260 265 270
 Ser Tyr Thr Arg Asp Lys Met Met Gln Val Thr Ile Ala Tyr Asn His
 275 280 285
 Phe Gly Glu Gly Leu Ile Gln Arg Met Pro Arg Cys Arg His Gly Tyr
 290 300
 Phe His Val Val Asn Asn Asp Tyr Thr His Trp Glu Met Tyr Ala Ile
 305 310 315 320
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 340 345 350
 Gly Lys Gly Glu Trp Asn Asn Trp Asn Trp Arg Ser Gln Gly Asp Leu
 355 360 365
 Met Leu Asn Gly Ala Tyr Phe Thr Ser Ser Gly Ala Gly Ala Ser Ala
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<211> 1413

<212> DNA

<213> Arabidopsis thaliana

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<400> 881

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Val Val Leu Ala Leu Thr Ala Met Ile Phe Arg Asn Ser Glu Ile Ser	
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ctc tct agg aag ctg aaa aca gag gtg att cag agc tca aat agc tca	144
Leu Ser Arg Lys Leu Lys Thr Glu Val Ile Gln Ser Ser Asn Ser Ser	
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aca atg gcg gcg ata agg aag ctg aaa aca gag gag ttt cag agc tta	192
Thr Met Ala Ala Ile Arg Lys Leu Lys Thr Glu Glu Phe Gln Ser Leu	
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caa caa cac gcc gtt gct gat gat cca gat atg gtt gct gat gaa gtc	288
Gln Gln His Ala Val Ala Asp Asp Pro Asp Met Val Ala Asp Glu Val	
85 90 95	
gct aag ctt gtt caa atg agt gaa cag aac agg aca gca aga agg aag	336
Ala Lys Leu Val Gln Met Ser Glu Gln Asn Arg Thr Ala Arg Arg Lys	
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cta gga ttc ttc tca tgt gga act ggt aat cca att gat gac tgt tgg	384
Leu Gly Phe Ser Cys Gly Thr Gly Asn Pro Ile Asp Asp Cys Trp	
115 120 125	
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Arg Cys Asp Arg Asn Trp His Lys Asn Arg Lys Arg Leu Ala Asp Cys	
130 135 140	
ggc att ggt ttt gga aga aac gca att ggt ggt gat gga cgc ttc	480
Gly Ile Gly Phe Gly Arg Asn Ala Ile Gly Gly Arg Asp Gly Arg Phe	
145 150 155 160	
tac att gtt act gac ccg act gat gaa gac gtt gtt aat ccc aaa cct	528
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PF59082SeqList_PF59082.txt

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<212> PRT
<213> Arabidopsis thaliana
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 35 40 45
 Thr Met Ala Ala Ile Arg Lys Leu Lys Thr Glu Glu Phe Gln Ser Leu
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 Asn Ser Ser Thr Met Ala Thr Arg Leu Asp Gly Glu Pro Gln Gln
 65 70 75 80
 Gln Gln His Ala Val Ala Asp Asp Pro Asp Met Val Ala Asp Glu Val
 85 90 95
 Ala Lys Leu Val Gln Met Ser Glu Gln Asn Arg Thr Ala Arg Arg Lys
 100 105 110
 Leu Gly Phe Phe Ser Cys Gly Thr Gly Asn Pro Ile Asp Asp Cys Trp
 115 120 125
 Arg Cys Asp Arg Asn Trp His Lys Asn Arg Lys Arg Leu Ala Asp Cys
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 Gly Ile Gly Phe Gly Arg Asn Ala Ile Gly Gly Arg Asp Gly Arg Phe
 145 150 155 160
 Tyr Ile Val Thr Asp Pro Thr Asp Glu Asp Val Val Asn Pro Lys Pro
 165 170 175
 Gly Thr Leu Arg His Ala Val Ile Gln Glu Glu Pro Leu Trp Ile Val
 180 185 190
 Phe Lys Arg Asp Met Val Ile Glu Leu Lys Gln Glu Leu Ile Met Asn
 195 200 205
 Ser Phe Lys Thr Ile Asp Ala Arg Gly Ser Asn Val His Ile Ala Asn
 210 215 220
 Gly Ala Cys Ile Thr Ile Gln Phe Ile Thr Asn Val Ile Ile His Gly
 225 230 235 240
 Leu His Ile His Asp Cys Lys Pro Thr Gly Asn Ala Met Val Arg Ser
 245 250 255
 Ser Pro Ser His Phe Gly Trp Arg Thr Met Ala Asp Gly Asp Ala Val
 260 265 270
 Ser Ile Phe Gly Ser Ser His Ile Trp Ile Asp His Asn Ser Leu Ser
 275 280 285
 His Cys Ala Asp Gly Leu Val Asp Ala Val Met Gly Ser Thr Ala Ile
 290 295 300
 Thr Val Ser Asn Asn His Phe Thr His His Asn Glu Val Met Leu Leu
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 Gly His Ser Asp Ser Tyr Thr Lys Asp Lys Leu Met Gln Val Thr Ile
 325 330 335
 Ala Tyr Asn His Phe Gly Glu Gly Leu Val Gln Arg Met Pro Arg Cys
 340 345 350
 Arg His Gly Tyr Phe His Val Val Asn Asn Asp Tyr Thr His Trp Glu
 355 360 365
 Met Tyr Ala Ile Gly Gly Ser Ala Glu Pro Thr Ile Asn Ser Gln Gly
 370 375 380
 Asn Arg Tyr Ala Ala Pro Met Asp Arg Phe Ala Lys Glu Val Thr Lys
 385 390 395 400
 Arg Val Glu Thr Asp Ala Ser Glu Trp Lys Lys Trp Asn Trp Arg Ser
 405 410 415
 Glu Gly Asp Leu Leu Asn Gly Ala Phe Phe Arg Pro Ser Gly Ala
 420 425 430
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<400> 883

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Val	Ser	Phe	Leu	Leu	Tyr	Ala	Pro	Leu	Phe	Leu	Ser	Ser	Pro	Val
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gac	cct	gaa	tct	gtc	gtt	gaa	gaa	gtt	cac	aag	agc	att	aat	gcg
Asp	Pro	Glu	Ser	Val	Val	Glu	Glu	Val	His	Lys	Ser	Ile	Asn	Ala
	30					35					40			Ser
gtt	gca	gga	aga	agg	aag	tta	ggt	tac	ctc	tca	tgt	acg	acc	ggt
Val	Ala	Gly	Arg	Arg	Lys	Leu	Gly	Tyr	Leu	Ser	Cys	Thr	Thr	Gly
	45				50					55				Asn
cca	atc	gac	gac	tgt	tgg	cgt	tgt	gac	cct	cac	tgg	gag	caa	cac
Pro	Ile	Asp	Asp	Cys	Trp	Arg	Cys	Asp	Pro	His	Trp	Glu	Gln	His
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caa	cgt	ctc	gct	gac	tgc	gcc	att	gga	ttc	ggc	aaa	aac	gcc	atc
Gln	Arg	Leu	Ala	Asp	Cys	Ala	Ile	Gly	Phe	Gly	Lys	Asn	Ala	Ile
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ggc	cgt	gac	ggt	cgg	atc	tac	gtg	gtc	acc	gac	tca	gga	aac	gac
Gly	Arg	Asp	Gly	Arg	Ile	Tyr	Val	Val	Thr	Asp	Ser	Gly	Asn	Asp
		95					100					105		Asn
cca	gtt	agc	ccc	aag	ccc	gga	act	tta	aga	cac	gcc	gtg	gtc	caa
Pro	Val	Ser	Pro	Lys	Pro	Gly	Thr	Leu	Arg	His	Ala	Val	Val	Gln
	110					115					120			Asp
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Glu	Pro	Leu	Trp	Ile	Ile	Phe	Gln	Arg	Asp	Met	Thr	Ile	Gln	Leu
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Asn	Ile	Ile	Ile	His	Gly	Ile	His	Ile	His	Asp	Cys	Lys	Gln	Gly
		175					180					185		Gly
aac	gct	atg	gtg	cgg	agc	tct	cca	cgg	cat	ttc	ggg	tgg	aga	acg
Asn	Ala	Met	Val	Arg	Ser	Ser	Pro	Arg	His	Phe	Gly	Trp	Arg	Thr
	190					195					200			Ile
tcg	gac	ggt	gat	ggt	gtc	tct	atc	ttt	gga	gga	agt	cat	ggt	tgg
Ser	Asp	Gly	Asp	Gly	Val	Ser	Ile	Phe	Gly	Gly	Ser	His	Val	Trp
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gac	cat	tgt	tcg	ttc	tct	aac	tgt	gaa	gat	gga	ctt	att	gat	gct
Asp	His	Cys	Ser	Phe	Ser	Asn	Cys	Glu	Asp	Gly	Leu	Ile	Asp	Ala
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atg	ggc	tcg	acg	gct	atc	act	ttg	tct	aac	aat	cat	atg	aca	cat
Met	Gly	Ser	Thr	Ala	Ile	Thr	Leu	Ser	Asn	Asn	His	Met	Thr	His
				240				245				250		His
gat	aag	gtc	atg	ttg	ctt	ggt	cat	agt	gat	act	tac	agt	cgt	gac
Asp	Lys	Val	Met	Leu	Leu	Gly	His	Ser	Asp	Thr	Tyr	Ser	Arg	Asp
		255					260					265		Lys
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Gln	Arg	Met	Pro	Arg	Cys	Arg	His	Gly	Tyr	Phe	His	Val	Val	Asn
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gac	tac	aca	cat	tgg	gag	atg	tat	gcg	att	ggt	gga	agt	gct	aat
Asp	Tyr	Thr	His	Trp	Glu	Met	Tyr	Ala	Ile	Gly	Gly	Ser	Ala	Asn
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aca	atc	aat	agt	caa	ggg	aac	aga	ttt	ttg	gca	ccc	aat	atc	aga
Thr	Ile	Asn	Ser	Gln	Gly	Asn	Arg	Phe	Leu	Ala	Pro	Asn	Ile	Arg
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Ser	Lys	Glu	Val	Thr	Lys	His	Glu	Asp	Ala	Pro	Glu	Ser	Glu	Trp
		335					340				345			Lys
aga	tgg	aat	tgg	aga	tct	tcc	gga	gat	ttg	ttg	cta	aac	ggt	gcg
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PF59082SeqList_PF59082.txt

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365      370      375      380
agc ctt ggg gct aaa ccg tct tct cta gtt gga cca ttg acg tct act      1262
Ser Leu Gly Ala Lys Pro Ser Ser Leu Val Gly Pro Leu Thr Ser Thr
      385      390      395
tct ggt gca ctg aat tgc cgt aaa ggt tcc cgt tgc tgattgtggc      1308
Ser Gly Ala Leu Asn Cys Arg Lys Gly Ser Arg Cys
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      35      40      45
Arg Lys Leu Gly Tyr Leu Ser Cys Thr Thr Gly Asn Pro Ile Asp Asp
      50      55      60
Cys Trp Arg Cys Asp Pro His Trp Glu Gln His Arg Gln Arg Leu Ala
      65      70      75      80
Asp Cys Ala Ile Gly Phe Gly Lys Asn Ala Ile Gly Gly Arg Asp Gly
      85      90      95
Arg Ile Tyr Val Val Thr Asp Ser Gly Asn Asp Asn Pro Val Ser Pro
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Lys Pro Gly Thr Leu Arg His Ala Val Val Gln Asp Glu Pro Leu Trp
      115      120      125
Ile Ile Phe Gln Arg Asp Met Thr Ile Gln Leu Lys Glu Glu Leu Ile
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Met Asn Ser Phe Lys Thr Ile Asp Gly Arg Gly Ala Ser Val His Ile
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      165      170      175
His Gly Ile His Ile His Asp Cys Lys Gln Gly Gly Asn Ala Met Val
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      195      200      205
Gly Val Ser Ile Phe Gly Gly Ser His Val Trp Val Asp His Cys Ser
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Phe Ser Asn Cys Glu Asp Gly Leu Ile Asp Ala Ile Met Gly Ser Thr
      225      230      235      240
Ala Ile Thr Leu Ser Asn Asn His Met Thr His His Asp Lys Val Met
      245      250      255
Leu Leu Gly His Ser Asp Thr Tyr Ser Arg Asp Lys Asn Met Gln Val
      260      265      270
Thr Ile Ala Phe Asn His Phe Gly Glu Gly Leu Val Gln Arg Met Pro
      275      280      285
Arg Cys Arg His Gly Tyr Phe His Val Val Asn Asn Asp Tyr Thr His
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Trp Glu Met Tyr Ala Ile Gly Gly Ser Ala Asn Pro Thr Ile Asn Ser
      305      310      315      320
Gln Gly Asn Arg Phe Leu Ala Pro Asn Ile Arg Phe Ser Lys Glu Val
      325      330      335
Thr Lys His Glu Asp Ala Pro Glu Ser Glu Trp Lys Arg Trp Asn Trp
      340      345      350
Arg Ser Ser Gly Asp Leu Leu Leu Asn Gly Ala Phe Phe Thr Pro Ser
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PF59082SeqList_PF59082.txt

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 Ile Ser Ser Ile Gln Asp Pro Glu Leu Val Val Gln Asp Val His Arg
 20 25 30
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 Ser Ile Asn Ala Ser Leu Thr Arg Arg Asn Leu Gly Tyr Leu Ser Cys
 35 40 45 50
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 Gly Ser Gly Asn Pro Ile Asp Arg Leu Leu Ala Met Gln Pro Gln Leu
 55 60 65
 gga aaa aaa tcg cca gcg ttt agc tat tgc gcc att ggg ttt gga aag 298
 Gly Lys Lys Ser Pro Ala Phe Ser Tyr Cys Ala Ile Gly Phe Gly Lys
 70 75 80
 aat gct atc gga gga aaa aat ggc cga att tac gtg gtt act gat tca 346
 Asn Ala Ile Gly Gly Lys Asn Gly Arg Ile Tyr Val Val Thr Asp Ser
 85 90 95
 ggg aac gat gac ccc gtg aac cct aaa ccc gga acc ctg aga cat gct 394
 Gly Asn Asp Asp Pro Val Asn Pro Lys Pro Gly Thr Leu Arg His Ala
 100 105 110
 gtt ata caa gac gag cct tta tgg att att ttc aaa aga gat atg gtc 442
 Val Ile Gln Asp Glu Pro Leu Trp Ile Ile Phe Lys Arg Asp Met Val
 115 120 125 130
 att cag ctc aaa caa gag ctt gtc atg aac tct tat aag acc ata gat 490
 Ile Gln Leu Lys Gln Glu Leu Val Met Asn Ser Tyr Lys Thr Ile Asp
 135 140 145
 ggt cgt ggt gcg agt gtt cac att tca ggt ggt ccg tgc att aca atc 538
 Gly Arg Gly Ala Ser Val His Ile Ser Gly Gly Pro Cys Ile Thr Ile
 150 155 160
 cac cat acc agc aac att ata ata cac ggg att aat ata cac gat tgt 586
 His His Thr Ser Asn Ile Ile Ile His Gly Ile Asn Ile His Asp Cys
 165 170 175
 aaa cag agt ggt aac ggc aac att agg gac tca cca aac cat tcc gga 634
 Lys Gln Ser Gly Asn Gly Asn Ile Arg Asp Ser Pro Asn His Ser Gly
 180 185 190
 tgg tgg gat gtt tct gat ggt gat ggt att tca att ttt gga ggg aaa 682
 Trp Trp Asp Val Ser Asp Gly Asp Gly Ile Ser Ile Phe Gly Gly Lys
 195 200 205 210
 aac att tgg gtg gac cat tgt tcg ttg tct aat tgc cac gac ggt tta 730
 Asn Ile Trp Val Asp His Cys Ser Leu Ser Asn Cys His Asp Gly Leu
 215 220 225
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 Ile Asp Ala Ile His Gly Ser Thr Ala Ile Thr Ile Ser Asn Asn Tyr
 230 235 240
 ttc act cat cat gac aag gtg atg ttg ttg gga cat agt gat tct ttt 826
 Phe Thr His His Asp Lys Val Met Leu Leu Gly His Ser Asp Ser Phe
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PF59082SeqList_PF59082.txt

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Glu	Gly	Leu	Val	Gln	Arg	Met	Pro	Arg	Cys	Arg	His	Gly	Tyr	Phe	His		
275					280					285					290		
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Val	Val	Asn	Asn	Asp	Tyr	Thr	His	Trp	Glu	Met	Tyr	Ala	Ile	Gly	Gly		
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Ser	Ala	Ala	Pro	Thr	Ile	Asn	Ser	Gln	Gly	Asn	Arg	Phe	Leu	Ala	Pro		
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Ser	Gln	Trp	Arg	Ser	Trp	Asn	Trp	Arg	Ser	Glu	Gly	Asp	Leu	Met	Leu		
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Thr	Tyr	Ala	Arg	Ala	Ser	Ser	Leu	Ser	Ala	Arg	Pro	Ser	Ser	Leu	Val		
			375					380						385			
gga	tca	att	acc	aca	aat	gcc	ggt	cct	gtt	aac	tgc	aaa	aaa	ggc	tct	1258	
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<213> Lycopersicon esculentum

<400> 886

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			20					25					30				
His	Arg	Ser	Ile	Asn	Ala	Ser	Leu	Thr	Arg	Arg	Asn	Leu	Gly	Tyr	Leu		
		35				40					45						
Ser	Cys	Gly	Ser	Gly	Asn	Pro	Ile	Asp	Arg	Leu	Leu	Ala	Met	Gln	Pro		
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Gln	Leu	Gly	Lys	Lys	Ser	Pro	Ala	Phe	Ser	Tyr	Cys	Ala	Ile	Gly	Phe		
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Gly	Lys	Asn	Ala	Ile	Gly	Gly	Lys	Asn	Gly	Arg	Ile	Tyr	Val	Val	Thr		
			85					90					95				
Asp	Ser	Gly	Asn	Asp	Asp	Pro	Val	Asn	Pro	Lys	Pro	Gly	Thr	Leu	Arg		
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His	Ala	Val	Ile	Gln	Asp	Glu	Pro	Leu	Trp	Ile	Ile	Phe	Lys	Arg	Asp		
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Met	Val	Ile	Gln	Leu	Lys	Gln	Glu	Leu	Val	Met	Asn	Ser	Tyr	Lys	Thr		
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Asp	Cys	Lys	Gln	Ser	Gly	Asn	Gly	Asn	Ile	Arg	Asp	Ser	Pro	Asn	His		
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Ser	Gly	Trp	Trp	Asp	Val	Ser	Asp	Gly	Asp	Gly	Ile	Ser	Ile	Phe	Gly		
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PF59082SeqList_PF59082.txt

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Phe Gly Glu Gly Leu Val Gln Arg Met Pro Arg Cys Arg His Gly Tyr
275      280      285
Phe His Val Val Asn Asn Asp Tyr Thr His Trp Glu Met Tyr Ala Ile
290      295      300
Gly Gly Ser Ala Ala Pro Thr Ile Asn Ser Gln Gly Asn Arg Phe Leu
305      310      315
Ala Pro Asn Glu Lys Tyr Arg Lys Glu Val Thr Lys His Glu Asp Ala
325      330      335
Pro Glu Ser Gln Trp Arg Ser Trp Asn Trp Arg Ser Glu Gly Asp Leu
340      345      350
Met Leu Asn Gly Ala Tyr Phe Arg Gln Thr Gly Ala Gly Ala Ser Ser
355      360      365
Ser Ser Thr Tyr Ala Arg Ala Ser Ser Leu Ser Ala Arg Pro Ser Ser
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 Met Ala Val Leu Pro Thr Trp Leu Leu Ala 10

atg atg tgt tta ctc ttc ttc gtc gga gct atg gag aac act aca cac 161
 Met Met Cys Leu Leu Phe Phe Val Gly Ala Met Glu Asn Thr Thr His 25

gac aac atc tct tct ctc cct aga tcc gac gaa acc gaa tgg aac caa 209
 Asp Asn Ile Ser Ser Leu Pro Arg Ser Asp Glu Thr Glu Trp Asn Gln 30 35 40

cac gca gtg acg aat cca gat gaa gta gcg gac gaa gtt ctc gcc ttg 257
 His Ala Val Thr Asn Pro Asp Glu Val Ala Asp Glu Val Leu Ala Leu 45 50 55

aca gaa atg agt gtg aga aac cat acc gag agg agg aaa cta ggt tac 305
 Thr Glu Met Ser Val Arg Asn His Thr Glu Arg Arg Lys Leu Gly Tyr 60 65 70

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 Phe Thr Cys Gly Thr Gly Asn Pro Ile Asp Asp Cys Trp Arg Cys Asp 75 80 85 90

ccc aat tgg cac aag aac cgt aaa cgc cta gcg gat tgc ggt atc gga 401
 Pro Asn Trp His Lys Asn Arg Lys Arg Leu Ala Asp Cys Gly Ile Gly 95 100 105

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 Phe Gly Arg Asn Ala Ile Gly Gly Arg Asp Gly Arg Phe Tyr Val Val 110 115 120

act gac cca aga gac gac aat ccg gtt aac cct aga ccg ggg act tta 497
 Thr Asp Pro Arg Asp Asp Asn Pro Val Asn Pro Arg Pro Gly Thr Leu 125 130 135

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PF59082SeqList_PF59082.txt

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acg atc gat gga cgt ggc gca aac gtt cac att gct aac ggt ggt tgc	641
Thr Ile Asp Gly Arg Gly Ala Asn Val His Ile Ala Asn Gly Gly Cys	
175 180 185	
atc acg att cag ttt gtg acg aat gtg atc gtt cac gga ttg cat att	689
Ile Thr Ile Gln Phe Val Thr Asn Val Ile Val His Gly Leu His Ile	
190 195 200	
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His Asp Cys Lys Pro Thr Gly Asn Ala Met Val Arg Ser Ser Glu Thr	
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His Phe Gly Trp Arg Thr Met Ala Asp Gly Asp Ala Ile Ser Ile Phe	
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gga tcg agt cat gta tgg att gat cat aac tcg ttg tcc cat tgc gct	833
Gly Ser Ser His Val Trp Ile Asp His Asn Ser Leu Ser His Cys Ala	
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Asp Gly Leu Val Asp Ala Val Met Gly Ser Thr Ala Ile Thr Ile Ser	
255 260 265	
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Asn Asn His Leu Thr His His Asn Glu Val Met Leu Leu Gly His Ser	
270 275 280	
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Asp Ser Tyr Met Arg Asp Lys Ala Met Gln Val Thr Ile Ala Tyr Asn	
285 290 295	
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His Phe Gly Val Gly Leu Ile Gln Arg Met Pro Arg Cys Arg His Gly	
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Tyr Phe His Val Val Asn Asn Asp Tyr Thr His Trp Glu Met Tyr Ala	
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Ile Gly Gly Ser Ala Asn Pro Thr Ile Asn Ser Gln Gly Asn Arg Tyr	
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gcc gcc cca aaa aac ccc ttt gct aaa gag gtg acg aag aga gtg gac	1169
Ala Ala Pro Lys Asn Pro Phe Ala Lys Glu Val Thr Lys Arg Val Asp	
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Thr Pro Ala Ser His Trp Lys Gly Trp Asn Trp Arg Ser Glu Gly Asp	
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Leu Leu Gln Asn Gly Ala Tyr Phe Thr Ser Ser Gly Ala Ala Ala Ser	
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Gly Ser Tyr Ala Arg Ala Ser Ser Leu Ser Ala Lys Ser Ser Ser Leu	
395 400 405 410	
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Val Gly His Ile Thr Ser Asp Ala Gly Ala Leu Pro Cys Arg Arg Gly	
415 420 425	
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 Arg Lys Arg Leu Ala Asp Cys Gly Ile Gly Phe Gly Arg Asn Ala Ile
 100 105 110
 Gly Gly Arg Asp Gly Arg Phe Tyr Val Val Thr Asp Pro Arg Asp Asp
 115 120 125
 Asn Pro Val Asn Pro Arg Pro Gly Thr Leu Arg His Ala Val Ile Gln
 130 135 140
 Asp Arg Pro Leu Trp Ile Val Phe Lys Arg Asp Met Val Ile Gln Leu
 145 150 155 160
 Lys Gln Glu Leu Ile Val Asn Ser Phe Lys Thr Ile Asp Gly Arg Gly
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 Ala Asn Val His Ile Ala Asn Gly Gly Cys Ile Thr Ile Gln Phe Val
 180 185 190
 Thr Asn Val Ile Val His Gly Leu His Ile His Asp Cys Lys Pro Thr
 195 200 205
 Gly Asn Ala Met Val Arg Ser Ser Glu Thr His Phe Gly Trp Arg Thr
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 225 230 235 240
 Ile Asp His Asn Ser Leu Ser His Cys Ala Asp Gly Leu Val Asp Ala
 245 250 255
 Val Met Gly Ser Thr Ala Ile Thr Ile Ser Asn Asn His Leu Thr His
 260 265 270
 His Asn Glu Val Met Leu Leu Gly His Ser Asp Ser Tyr Met Arg Asp
 275 280 285
 Lys Ala Met Gln Val Thr Ile Ala Tyr Asn His Phe Gly Val Gly Leu
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 Ile Gln Arg Met Pro Arg Cys Arg His Gly Tyr Phe His Val Val Asn
 305 310 315 320
 Asn Asp Tyr Thr His Trp Glu Met Tyr Ala Ile Gly Gly Ser Ala Asn
 325 330 335
 Pro Thr Ile Asn Ser Gln Gly Asn Arg Tyr Ala Ala Pro Lys Asn Pro
 340 345 350
 Phe Ala Lys Glu Val Thr Lys Arg Val Asp Thr Pro Ala Ser His Trp
 355 360 365
 Lys Gly Trp Asn Trp Arg Ser Glu Gly Asp Leu Leu Gln Asn Gly Ala
 370 375 380
 Tyr Phe Thr Ser Ser Gly Ala Ala Ala Ser Gly Ser Tyr Ala Arg Ala
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Met Ala Val Thr

115

caa ata ctt gtc gtc ttt gct tct gca tta ctc cta tca atg ttc ttc
Gln Ile Leu Val Val Phe Ala Ser Ala Leu Leu Leu Ser Met Phe Phe
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163

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ggt	gag	aat	cca	gag	gaa	gta	gct	gcc	atg	gtg	gac	atg	agc	att	cga	259
Val	Glu	Asn	Pro	Glu	Glu	Val	Ala	Ala	Met	Val	Asp	Met	Ser	Ile	Arg	
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Asn	Ser	Thr	Ala	Arg	Arg	Arg	Leu	Gly	Tyr	Phe	Ser	Cys	Ser	Thr	Gly	
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aat	cca	atc	gat	gat	tgt	tgg	cgt	tgt	gac	cgg	aga	tgg	caa	tcc	cgg	355
Asn	Pro	Ile	Asp	Asp	Cys	Trp	Arg	Cys	Asp	Arg	Arg	Trp	Gln	Ser	Arg	
	70					75					80					
cga	aaa	cat	cta	gcc	aat	tgc	gca	atc	ggg	ttc	ggt	cgc	aat	gca	atc	403
Arg	Lys	His	Leu	Ala	Asn	Cys	Ala	Ile	Gly	Phe	Gly	Arg	Asn	Ala	Ile	
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ggc	ggt	aga	gac	ggt	cgt	tac	tac	gta	gtg	agt	gat	cca	aac	gac	gat	451
Gly	Gly	Arg	Asp	Gly	Arg	Tyr	Tyr	Val	Val	Ser	Asp	Pro	Asn	Asp	Asp	
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Asn	Pro	Val	Asn	Pro	Lys	Pro	Gly	Thr	Leu	Arg	His	Ala	Val	Ile	Gln	
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gaa	gaa	cca	tta	tgg	atc	gtc	ttt	aaa	cgt	gac	atg	gtc	ata	aca	tta	547
Glu	Glu	Pro	Leu	Trp	Ile	Val	Phe	Lys	Arg	Asp	Met	Val	Ile	Thr	Leu	
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Lys	Glu	Glu	Leu	Ile	Met	Asn	Ser	Phe	Lys	Thr	Ile	Asp	Gly	Arg	Gly	
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Thr	Asn	Ile	Ile	Ile	His	Gly	Ile	His	Ile	His	Asp	Cys	Arg	Pro	Thr	
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ggg	aac	gct	atg	ggt	aga	agc	tct	cct	tcg	cat	tat	ggg	tgg	aga	act	739
Gly	Asn	Ala	Met	Val	Arg	Ser	Ser	Pro	Ser	His	Tyr	Gly	Trp	Arg	Thr	
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Met	Ala	Asp	Gly	Asp	Gly	Ile	Ser	Ile	Phe	Gly	Ser	Ser	His	Ile	Trp	
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Ile	Asp	His	Asn	Ser	Leu	Ser	Asn	Cys	Ala	Asp	Gly	Leu	Ile	Asp	Ala	
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Val	Met	Ala	Ser	Thr	Ala	Ile	Thr	Ile	Ser	Asn	Asn	Tyr	Phe	Thr	His	
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Ile	Gln	Arg	Met	Pro	Arg	Cys	Arg	His	Gly	Tyr	Phe	His	Val	Val	Asn	
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Asn	Asp	Tyr	Thr	His	Trp	Glu	Met	Tyr	Ala	Ile	Gly	Gly	Ser	Ala	Ser	
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cct	acc	att	aac	agc	caa	gga	aat	aga	tat	ctc	gcc	cca	aga	aac	cgg	1123
Pro	Thr	Ile	Asn	Ser	Gln	Gly	Asn	Arg	Tyr	Leu	Ala	Pro	Arg	Asn	Arg	
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Phe	Ala	Lys	Glu	Val	Thr	Lys	Arg	Asp	Tyr	Ala	Gly	Gln	Trp	Gln	Trp	
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Arg	His	Trp	Asn	Trp	Arg	Ser	Glu	Gly	Asp	Leu	Phe	Leu	Asn	Gly	Ala	
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Asn Ala Gly Ala Leu Asn Cys Arg Gly Gly Arg Arg Cys	
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Cys Ser Thr Gly Asn Pro Ile Asp Asp Cys Trp Arg Cys Asp Arg Arg	
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Trp Gln Ser Arg Arg Lys His Leu Ala Asn Cys Ala Ile Gly Phe Gly	
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Arg Asn Ala Ile Gly Gly Arg Asp Gly Arg Tyr Tyr Val Val Ser Asp	
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Pro Asn Asp Asp Asn Pro Val Asn Pro Lys Pro Gly Thr Leu Arg His	
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Leu Ile Asp Ala Val Met Ala Ser Thr Ala Ile Thr Ile Ser Asn Asn	
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Tyr Phe Thr His Asn Glu Val Met Leu Leu Gly His Ser Asp Thr	
260 265 270	
Tyr Thr Arg Asp Lys Val Met Gln Val Thr Ile Ala Tyr Asn His Phe	
275 280 285	
Gly Glu Gly Leu Ile Gln Arg Met Pro Arg Cys Arg His Gly Tyr Phe	
290 295 300	
His Val Val Asn Asn Asp Tyr Thr His Trp Glu Met Tyr Ala Ile Gly	
305 310 315 320	
Gly Ser Ala Ser Pro Thr Ile Asn Ser Gln Gly Asn Arg Tyr Leu Ala	
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PF59082SeqList_PF59082.txt

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Thr Thr Val Thr Ser Asn Ser Thr Ala Ser Ser Cys Ser Ala Asn Gly
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Asn Pro Ile Asp Glu Cys Trp Arg Cys Asp Glu Asn Trp Lys Asp Asn
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Gly Gly Arg Ala Gly Glu Phe Tyr Thr Val Thr Asp Ser Gly Asp Asp
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Asn Pro Leu Asn Pro Thr Pro Gly Thr Leu Arg Tyr Ala Ala Thr Gln
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Asp Gln Pro Leu Trp Ile Ile Phe Asp Arg Asp Met Val Ile Gln Leu
115 120 125
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Lys Gln Asp Leu Gln Val Ala Ser Tyr Lys Thr Ile Asp Gly Arg Gly
130 135 140
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Asn Asn Val Gln Ile Ala Tyr Gly Pro Cys Leu Thr Leu Tyr Lys Val
145 150 155 160
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Ser Asn Ile Ile Asn Asn Leu Tyr Ile His Asp Cys Val Pro Val
165 170 175
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Lys Arg Asn Ala Leu Ser Ser Leu Gly Gly Tyr Ser Asp Gly Asp Gly
180 185 190
ata tcg ata ttc gag tct cga gat att tgg att gat cat tgt acg tta 624
Ile Ser Ile Phe Glu Ser Arg Asp Ile Trp Ile Asp His Cys Thr Leu
195 200 205
gag aaa tgt tac gat ggg ctt att gat gcg gtg aat gga tcc acg gat 672
Glu Lys Cys Tyr Asp Gly Leu Ile Asp Ala Val Asn Gly Ser Thr Asp
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ttg ggc cat agt gat gag tat tcc ggt gat cgg gat atg cga gtt acg 768
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245 250 255
atc gcg ttt aac tat ttt ggt gaa gga ctt gtc caa aga atg cca agg 816
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PF59082SeqList_PF59082.txt

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Gly	Lys	Glu	Asp	Ser	Pro	Ser	Tyr	Ala	Lys	Phe	Ser	Ser	Met	Val	Ala	
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cga	cca	gct	tca	ctt	ctc	aag	acc	aca	cat	cca	tca	gta	ggt	gtt	ctt	1152
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agt	tgc	gaa	att	gac	caa	gct	tgt	taa								1179
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Lys	Gln	Asp	Leu	Gln	Val	Ala	Ser	Tyr	Lys	Thr	Ile	Asp	Gly	Arg	Gly	
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Asn	Asn	Val	Gln	Ile	Ala	Tyr	Gly	Pro	Cys	Leu	Thr	Leu	Tyr	Lys	Val	
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Ser	Asn	Ile	Ile	Ile	Asn	Asn	Leu	Tyr	Ile	His	Asp	Cys	Val	Pro	Val	
			165					170					175			
Lys	Arg	Asn	Ala	Leu	Ser	Ser	Leu	Gly	Tyr	Ser	Asp	Gly	Asp	Gly		
		180					185					190				
Ile	Ser	Ile	Phe	Glu	Ser	Arg	Asp	Ile	Trp	Ile	Asp	His	Cys	Thr	Leu	
		195				200					205					
Glu	Lys	Cys	Tyr	Asp	Gly	Leu	Ile	Asp	Ala	Val	Asn	Gly	Ser	Thr	Asp	
	210					215					220					
Ile	Thr	Ile	Ser	Asn	Ser	Tyr	Met	Leu	Asn	His	Asn	Glu	Val	Met	Leu	
	225				230					235					240	
Leu	Gly	His	Ser	Asp	Glu	Tyr	Ser	Gly	Asp	Arg	Asp	Met	Arg	Val	Thr	
			245					250					255			
Ile	Ala	Phe	Asn	Tyr	Phe	Gly	Glu	Gly	Leu	Val	Gln	Arg	Met	Pro	Arg	
		260					265						270			
Cys	Arg	His	Gly	Tyr	Phe	His	Ile	Val	Asn	Asn	Ile	Tyr	Arg	Asp	Trp	
		275					280					285				
Lys	Met	Tyr	Ala	Ile	Gly	Gly	Ser	Ala	Asn	Pro	Thr	Ile	Phe	Ser	Gln	
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PF59082SeqList_PF59082.txt

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 Lys Arg Glu Ser Ala Asp Gly Asp Glu Glu Trp Lys Glu Trp Asn Trp
 325 330 335
 Lys Ser Glu Gly Asp Glu Met Val Asn Gly Ala Phe Phe Thr Pro Ser
 340 345 350
 Gly Lys Glu Asp Ser Pro Ser Tyr Ala Lys Phe Ser Ser Met Val Ala
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 Ser Cys Glu Ile Asp Gln Ala Cys
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<212> DNA

<213> Arabidopsis thaliana

<220>

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<400> 893

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Lys Ser Gln Arg Asn Thr Met Leu Asn Ser Ser Tyr Leu Ser Phe Ala	
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ctt atc ttt ttc tgc tgc att ttg ttc tcc gct ctc gct tcg tct ttg	144
Leu Ile Phe Phe Cys Cys Ile Leu Phe Ser Ala Leu Ala Ser Ser Leu	
35 40 45	
ccc gtt tcc gac cct gag ctt gtt gtc gag gaa gta cac aga aaa ata	192
Pro Val Ser Asp Pro Glu Leu Val Val Glu Glu Val His Arg Lys Ile	
50 55 60	
aac gag tcc ata tca aga agg aag cta ggg ttc ttc tgc ggc agt	240
Asn Glu Ser Ile Ser Arg Arg Lys Leu Gly Phe Phe Ser Cys Gly Ser	
65 70 75 80	
ggg aat cca atc gat gat tgt tgg cga tgc gac aag gat tgg gag aaa	288
Gly Asn Pro Ile Asp Asp Cys Trp Arg Cys Asp Lys Asp Trp Glu Lys	
85 90 95	
aac cga aaa cgg tta gca gac tgt ggt atc ggt ttt ggc aag aac gct	336
Asn Arg Lys Arg Leu Ala Asp Cys Gly Ile Gly Phe Gly Lys Asn Ala	
100 105 110	
att ggc ggt cgt gat ggt gaa atc tat gtg gtc acg gat cca gga aac	384
Ile Gly Gly Arg Asp Gly Glu Ile Tyr Val Val Thr Asp Pro Gly Asn	
115 120 125	
gat gat cca gta aac cct aga ccg gga aca cta aga tac gca gtc att	432
Asp Asp Pro Val Asn Pro Arg Pro Gly Thr Leu Arg Tyr Ala Val Ile	
130 135 140	
caa gat gaa ccg cta tgg atc att ttt aag cga gac atg acg atc caa	480
Gln Asp Glu Pro Leu Trp Ile Ile Phe Lys Arg Asp Met Thr Ile Gln	
145 150 155 160	
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Leu Lys Glu Glu Leu Ile Met Asn Ser Phe Lys Thr Leu Asp Gly Arg	
165 170 175	
gga gcc tcc gta cac atc tcc ggt ggg cca tgt ata acc ata caa tat	576
Gly Ala Ser Val His Ile Ser Gly Gly Pro Cys Ile Thr Ile Gln Tyr	
180 185 190	
gta acc aac atc atc atc cat ggt tta cac ata cat gac tgc aag caa	624
Val Thr Asn Ile Ile Ile His Gly Leu His Ile His Asp Cys Lys Gln	
195 200 205	
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Gly Gly Asn Thr Tyr Val Arg Asp Ser Pro Glu His Tyr Gly Tyr Arg	
210 215 220	
acg gta tcc gac ggt gac ggt gtg tca ata ttc ggt gga agc cac gtg	720
Thr Val Ser Asp Gly Asp Gly Val Ser Ile Phe Gly Gly Ser His Val	
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PF59082SeqList_PF59082.txt

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Ala	Ile	Arg	Gly	Ser	Thr	Ala	Ile	Thr	Ile	Ser	Asn	Asn	Tyr	Leu	Thr	
			260					265					270			
cat	cat	aat	aag	gtt	atg	tta	ttg	gga	cac	agt	gat	acg	tac	gaa	caa	864
His	His	Asn	Lys	Val	Met	Leu	Leu	Gly	His	Ser	Asp	Thr	Tyr	Glu	Gln	
			275				280					285				
gac	aag	aac	atg	caa	gtc	act	atc	gct	ttt	aac	cat	ttt	gga	gaa	ggc	912
Asp	Lys	Asn	Met	Gln	Val	Thr	Ile	Ala	Phe	Asn	His	Phe	Gly	Glu	Gly	
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Leu	Val	Gln	Arg	Met	Pro	Arg	Cys	Arg	His	Gly	Tyr	Phe	His	Val	Val	
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aac	aat	gac	tat	aca	cat	tgg	gaa	atg	tat	gca	att	gga	gga	agt	gct	1008
Asn	Asn	Asp	Tyr	Thr	His	Trp	Glu	Met	Tyr	Ala	Ile	Gly	Gly	Ser	Ala	
					325				330					335		
aat	cct	acc	atc	aac	tct	caa	ggc	aac	cgt	ttt	ctt	gct	cct	gat	gac	1056
Asn	Pro	Thr	Ile	Asn	Ser	Gln	Gly	Asn	Arg	Phe	Leu	Ala	Pro	Asp	Asp	
			340					345					350			
tca	tct	agc	aaa	gag	gta	aca	aag	cac	gag	gat	gcg	ccg	gaa	gac	gaa	1104
Ser	Ser	Ser	Lys	Glu	Val	Thr	Lys	His	Glu	Asp	Ala	Pro	Glu	Asp	Glu	
			355				360					365				
tgg	aga	aat	tgg	aat	tgg	aga	tct	gaa	gga	gat	cta	ctg	ctt	aat	ggt	1152
Trp	Arg	Asn	Trp	Asn	Trp	Arg	Ser	Glu	Gly	Asp	Leu	Leu	Leu	Asn	Gly	
			370			375					380					
gca	ttc	ttc	acc	tat	tct	ggt	gct	gga	cca	gct	aaa	tca	tca	agc	tat	1200
Ala	Phe	Phe	Thr	Tyr	Ser	Gly	Ala	Gly	Pro	Ala	Lys	Ser	Ser	Ser	Tyr	
385					390					395					400	
tca	aaa	gct	tcg	agt	cta	gcc	gcg	aga	ccg	tcc	tct	cat	gtt	ggt	gag	1248
Ser	Lys	Ala	Ser	Ser	Leu	Ala	Ala	Arg	Pro	Ser	Ser	His	Val	Gly	Glu	
					405				410					415		
ata	act	ata	gcc	tcg	ggt	gca	ctc	agc	tgc	aaa	agg	ggt	tct	cat	tgt	1296
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			20					25					30			
Leu	Ile	Phe	Phe	Cys	Cys	Ile	Leu	Phe	Ser	Ala	Leu	Ala	Ser	Ser	Leu	
		35					40					45				
Pro	Val	Ser	Asp	Pro	Glu	Leu	Val	Val	Glu	Glu	Val	His	Arg	Lys	Ile	
	50				55				60							
Asn	Glu	Ser	Ile	Ser	Arg	Arg	Lys	Leu	Gly	Phe	Phe	Ser	Cys	Gly	Ser	
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Gly	Asn	Pro	Ile	Asp	Asp	Cys	Trp	Arg	Cys	Asp	Lys	Asp	Trp	Glu	Lys	
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Asn	Arg	Lys	Arg	Leu	Ala	Asp	Cys	Gly	Ile	Gly	Phe	Gly	Lys	Asn	Ala	
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Gln	Asp	Glu	Pro	Leu	Trp	Ile	Ile	Phe	Lys	Arg	Asp	Met	Thr	Ile	Gln	
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Leu	Lys	Glu	Glu	Leu	Ile	Met	Asn	Ser	Phe	Lys	Thr	Leu	Asp	Gly	Arg	
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PF59082SeqList_PF59082.txt

Val Thr Asn Ile Ile Ile His Gly Leu His Ile His Asp Cys Lys Gln
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 225 230 235 240
 Trp Val Asp His Cys Ser Leu Ser Asn Cys Asn Asp Gly Leu Ile Asp
 245 250 255
 Ala Ile Arg Gly Ser Thr Ala Ile Thr Ile Ser Asn Asn Tyr Leu Thr
 260 265 270
 His His Asn Lys Val Met Leu Leu Gly His Ser Asp Thr Tyr Glu Gln
 275 280 285
 Asp Lys Asn Met Gln Val Thr Ile Ala Phe Asn His Phe Gly Glu Gly
 290 295 300
 Leu Val Gln Arg Met Pro Arg Cys Arg His Gly Tyr Phe His Val Val
 305 310 315 320
 Asn Asn Asp Tyr Thr His Trp Glu Met Tyr Ala Ile Gly Gly Ser Ala
 325 330 335
 Asn Pro Thr Ile Asn Ser Gln Gly Asn Arg Phe Leu Ala Pro Asp Asp
 340 345 350
 Ser Ser Ser Lys Glu Val Thr Lys His Glu Asp Ala Pro Glu Asp Glu
 355 360 365
 Trp Arg Asn Trp Asn Trp Arg Ser Glu Gly Asp Leu Leu Leu Asn Gly
 370 375 380
 Ala Phe Phe Thr Tyr Ser Gly Ala Gly Pro Ala Lys Ser Ser Ser Tyr
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Leu	Leu	Val	Leu	Ser	Pro	Thr	Phe	Ile	Ala	Ser	Thr	Pro	Val	Ser	Glu	
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ccc	gaa	ctc	gta	gtt	caa	gaa	gtt	aac	gaa	aag	att	aat	gcg	tct	agg	144
Pro	Glu	Leu	Val	Val	Gln	Glu	Val	Asn	Glu	Lys	Ile	Asn	Ala	Ser	Arg	
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Arg	Asn	Leu	Gly	Val	Leu	Ser	Cys	Gly	Thr	Gly	Asn	Pro	Ile	Asp	Asp	
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Cys	Trp	Arg	Cys	Asp	Pro	Lys	Trp	Glu	Lys	Asn	Arg	Gln	Arg	Leu	Ala	
	65				70				75					80		
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Lys	Ile	Tyr	Val	Val	Thr	Asp	Ser	Ser	Asp	Lys	Asp	Val	Val	Asn	Pro	
			100				105					110				
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Ile	Ile	Phe	Ala	Arg	Asp	Met	Val	Ile	Lys	Leu	Lys	Glu	Glu	Leu	Ile	
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PF59082SeqList_PF59082.txt

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Ala	Gly	Gly	Ala	Cys 165	Ile	Thr	Val	Gln	Tyr 170	Val	Thr	Asn	Ile	Ile	Ile	
cac	ggt	gtt	aac	atc	cat	gac	tgt	aaa	aga	aag	ggg	aat	gct	tac	gtt	576
His	Gly	Val	Asn 180	Ile	His	Asp	Cys	Lys 185	Arg	Lys	Gly	Asn	Ala 190	Tyr	Val	
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Arg	Asp	Ser 195	Pro	Ser	His	Tyr	Gly 200	Trp	Arg	Thr	Ala	Ser 205	Asp	Gly	Asp	
gcc	gtc	tcg	att	ttt	ggt	ggc	tcc	cac	gtg	tgg	gta	gac	cat	tgc	tcg	672
Ala	Val	Ser	Ile	Phe	Gly	Gly 215	Ser	His	Val	Trp	Val 220	Asp	His	Cys	Ser	
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Thr	Ile	Ala 275	Phe	Asn	His	Phe	Gly 280	Glu	Gly	Leu	Val 285	Gln	Arg	Met	Pro	
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Trp	Gln	Met	Tyr	Ala 310	Ile	Gly	Gly	Ser	Ala 315	Ala	Pro	Thr	Ile	Asn	Ser 320	
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Gln	Gly	Asn	Arg	Phe 325	Leu	Ala	Pro	Asn	Asp 330	His	Val	Phe	Lys	Glu 335	Val	
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Thr	Lys	Tyr	Glu 340	Asp	Ala	Pro	Arg	Ser 345	Lys	Trp	Lys	Lys	Trp 350	Asn	Trp	
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Arg	Ser	Glu 355	Gly	Asp	Leu	Phe	Leu 360	Asn	Gly	Ala	Phe 365	Thr	Pro	Ser		
ggt	gga	gga	gcc	tct	tca	agc	tat	gct	aag	gct	tcg	agt	ttg	tcg	gct	1152
Gly	Gly	Gly	Ala	Ser	Ser 375	Ser	Tyr	Ala	Lys	Ala 380	Ser	Ser	Leu	Ser	Ala	
aga	ccg	tcc	tca	ttg	gtg	gct	tca	gtc	acg	tcc	aat	gct	ggt	gca	ctc	1200
Arg	Pro	Ser	Ser	Leu 390	Val	Ala	Ser	Val	Thr 395	Ser	Asn	Ala	Gly	Ala	Leu 400	
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Pro	Glu	Leu	Val	Val 35	Gln	Glu	Val 40	Asn	Glu	Lys	Ile	Asn 45	Ala	Ser	Arg	
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Cys	Trp	Arg	Cys	Asp 65	Pro 70	Lys	Trp	Glu	Lys	Asn 75	Arg	Gln	Arg	Leu	Ala 80	
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PF59082SeqList_PF59082.txt

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 130 135 140
 Met Asn Ser Phe Lys Thr Ile Asp Gly Arg Gly Ala Ser Val His Ile
 145 150 155 160
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 165 170 175
 His Gly Val Asn Ile His Asp Cys Lys Arg Lys Gly Asn Ala Tyr Val
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 Arg Asp Ser Pro Ser His Tyr Gly Trp Arg Thr Ala Ser Asp Gly Asp
 195 200 205
 Ala Val Ser Ile Phe Gly Gly Ser His Val Trp Val Asp His Cys Ser
 210 215 220
 Leu Ser Asn Cys Ala Asp Gly Leu Ile Asp Ala Ile His Gly Ser Thr
 225 230 235 240
 Ala Ile Thr Ile Ser Asn Asn Tyr Leu Ser His His Asn Lys Val Met
 245 250 255
 Leu Leu Gly His Ser Asp Ser Tyr Thr Arg Asp Lys Asn Met Gln Val
 260 265 270
 Thr Ile Ala Phe Asn His Phe Gly Glu Gly Leu Val Gln Arg Met Pro
 275 280 285
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 Trp Gln Met Tyr Ala Ile Gly Gly Ser Ala Ala Pro Thr Ile Asn Ser
 305 310 315 320
 Gln Gly Asn Arg Phe Leu Ala Pro Asn Asp His Val Phe Lys Glu Val
 325 330 335
 Thr Lys Tyr Glu Asp Ala Pro Arg Ser Lys Trp Lys Lys Trp Asn Trp
 340 345 350
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 355 360 365
 Gly Gly Gly Ala Ser Ser Ser Tyr Ala Lys Ala Ser Ser Leu Ser Ala
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tctgcctcat atagagataa ctaaacagaa cagagcaaga actatacagc cataaca 177

atg gct gtc aca aaa ctt att ctc ttt gct tct gca tta ctt cta aca 225

Met Ala Val Thr Lys Leu Ile Leu Phe Ala Ser Ala Leu Leu Leu Thr 15
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Ala Leu Phe Ile Gly Val Asn Ala Ser Arg Ser Asn Glu Thr Trp His 20 25 30
 20 25 30
 gaa cat gca gtt gag aac cca gat gaa gtc gct gcc atg gtg gac atg 321

Glu His Ala Val Glu Asn Pro Asp Glu Val Ala Ala Met Val Asp Met 35 40 45
 35 40 45

PF59082SeqList_PF59082.txt

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Ala	Thr	Gly	Asn	Pro	Ile	Asp	Asp	Cys	Trp	Arg	Cys	Asp	Arg	Lys	Trp	
	65				70					75					80	
cag	ctc	cgt	cgc	aaa	cgt	tta	gcc	gat	tgc	tca	atc	gga	ttt	ggc	cgc	465
Gln	Leu	Arg	Arg	Lys	Arg	Leu	Ala	Asp	Cys	Ser	Ile	Gly	Phe	Gly	Arg	
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aac	gca	atc	gga	ggc	cgc	gac	ggt	cgt	ttc	tac	gtc	gta	acc	gac	cct	513
Asn	Ala	Ile	Gly	Gly	Arg	Asp	Gly	Arg	Phe	Tyr	Val	Val	Thr	Asp	Pro	
			100					105					110			
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Gly	Asp	Asp	Asp	Pro	Val	Asn	Pro	Ile	Pro	Gly	Thr	Leu	Arg	His	Ala	
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Val	Ile	Gln	Asp	Glu	Pro	Leu	Trp	Ile	Ile	Phe	Lys	Arg	Asp	Met	Val	
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Ile	Thr	Leu	Lys	Gln	Glu	Leu	Ile	Met	Asn	Ser	Phe	Lys	Thr	Ile	Asp	
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Gly	Arg	Gly	Val	Asn	Val	His	Ile	Ala	Asn	Gly	Ala	Cys	Leu	Thr	Ile	
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Gln	Tyr	Val	Thr	Asn	Ile	Ile	Val	His	Gly	Ile	His	Val	His	Asp	Cys	
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Lys	Pro	Thr	Gly	Asn	Ala	Met	Val	Arg	Ser	Ser	Pro	Ser	His	Tyr	Gly	
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Phe	Arg	Ser	Met	Ala	Asp	Gly	Asp	Ala	Ile	Ser	Ile	Phe	Gly	Ser	Ser	
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His	Ile	Trp	Ile	Asp	His	Asn	Ser	Leu	Ser	Asn	Cys	Ala	Asp	Gly	Leu	
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ggt	gac	gct	ggt	atg	agc	tcc	acc	gcc	att	act	gtc	tca	aac	aat	ttc	945
Val	Asp	Ala	Val	Met	Ser	Ser	Thr	Ala	Ile	Thr	Val	Ser	Asn	Asn	Phe	
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Phe	Thr	His	His	Asn	Glu	Val	Met	Leu	Leu	Gly	His	Ser	Asp	Ser	Tyr	
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Thr	Arg	Asp	Lys	Val	Met	Gln	Val	Thr	Ile	Ala	Tyr	Asn	His	Phe	Gly	
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gaa	ggt	tta	atc	cag	aga	atg	cca	aga	tgt	agg	cat	gga	tat	ttc	cat	1089
Glu	Gly	Leu	Ile	Gln	Arg	Met	Pro	Arg	Cys	Arg	His	Gly	Tyr	Phe	His	
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Val	Val	Asn	Asn	Asp	Tyr	Thr	His	Trp	Glu	Met	Tyr	Ala	Ile	Gly	Gly	
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agt	gct	ggt	cca	acc	atc	aac	agt	cag	ggc	aat	cga	ttt	ctt	gct	cca	1185
Ser	Ala	Gly	Pro	Thr	Ile	Asn	Ser	Gln	Gly	Asn	Arg	Phe	Leu	Ala	Pro	
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Val	Asn	Pro	Phe	Ala	Lys	Glu	Val	Thr	Lys	Arg	Glu	Tyr	Thr	Gly	Glu	
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Ser	Lys	Trp	Lys	His	Trp	Asn	Trp	Arg	Ser	Glu	Gly	Asp	Leu	Phe	Leu	
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aac	gga	gca	ttt	ttc	aca	cgt	tct	gga	gct	gga	gct	gga	gcc	aac	tat	1329
Asn	Gly	Ala	Phe	Phe	Thr	Arg	Ser	Gly	Ala	Gly	Ala	Gly	Ala	Asn	Tyr	
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gcc	aga	gct	tcg	agt	tta	tca	gcc	aaa	tca	tcc	tca	ctc	gtc	ggc	acc	1377
Ala	Arg	Ala	Ser	Ser	Leu	Ser	Ala	Lys	Ser	Ser	Ser	Leu	Val	Gly	Thr	
	385				390					395					400	
atg	acc	tct	tac	tca	ggt	gct	ctt	aac	tgc	aga	gcc	ggt	cgt	cga	tgt	1425
Met	Thr	Ser	Tyr	Ser	Gly	Ala	Leu	Asn	Cys	Arg	Ala	Gly	Arg	Arg	Cys	
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PF59082SeqList_PF59082.txt

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35 40 45
Ser Ile Arg Asn Ser Thr Glu Arg Arg Arg Leu Gly Tyr Phe Ser Cys
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Ala Thr Gly Asn Pro Ile Asp Asp Cys Trp Arg Cys Asp Arg Lys Trp
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Gln Leu Arg Arg Lys Arg Leu Ala Asp Cys Ser Ile Gly Phe Gly Arg
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Asn Ala Ile Gly Arg Asp Gly Arg Phe Tyr Val Val Thr Asp Pro
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Gly Asp Asp Asp Pro Val Asn Pro Ile Pro Gly Thr Leu Arg His Ala
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Val Ile Gln Asp Glu Pro Leu Trp Ile Ile Phe Lys Arg Asp Met Val
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Ile Thr Leu Lys Gln Glu Leu Ile Met Asn Ser Phe Lys Thr Ile Asp
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Gly Arg Gly Val Asn Val His Ile Ala Asn Gly Ala Cys Leu Thr Ile
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Gln Tyr Val Thr Asn Ile Ile Val His Gly Ile His Val His Asp Cys
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Phe Arg Ser Met Ala Asp Gly Asp Ala Ile Ser Ile Phe Gly Ser Ser
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Asn Gly Ala Phe Phe Thr Arg Ser Gly Ala Gly Ala Asn Tyr

PF59082SeqList_PF59082.txt

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Ala Cys Phe Val Leu Phe Ile Phe Val Gly Cys Val Leu Thr Ala
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Thr Asn Leu Arg Asn Asn Glu Ile Ser Arg Ser Arg Lys Leu Lys Thr
30 35 40
gag gat tca aag agc ttt aac agt tca cca atg acg act agg ctt gat 195
Glu Asp Ser Lys Ser Phe Asn Ser Ser Pro Met Thr Thr Arg Leu Asp
45 50 55
ggg gta gta gag ttg aat gaa cac gca gtt act gat cca gac aaa gtt 243
Gly Val Val Glu Leu Asn Glu His Ala Val Thr Asp Pro Asp Lys Val
60 65 70
gcc cat gaa gtc tct aac ctt att cac atg agt gaa cag aac atc act 291
Ala His Glu Val Ser Asn Leu Ile His Met Ser Glu Gln Asn Ile Thr
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gca agg agg aag ctt ggc ttc ttt tca tgt gga aat ggc aat cta ata 339
Ala Arg Arg Lys Leu Gly Phe Phe Ser Cys Gly Asn Gly Asn Leu Ile
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Asp Asp Cys Trp Arg Cys Asp Arg Asn Trp Asn Lys Asn Arg Lys His
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Leu Ala Asp Cys Gly Met Gly Phe Gly Ser Lys Ala Phe Gly Gly Arg
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Asn Gly Ser Tyr Tyr Val Val Thr Asp His Ser Asp Asp Val Val
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Asn Pro Lys Pro Gly Thr Leu Arg His Ala Val Ile Gln Val Glu Pro
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Leu Ile Met Asn Ser Phe Lys Thr Ile Asp Ala Arg Gly Ala Asn Val
190 195 200
cac att gcc aat ggt gct tgc ata aca atc caa aat ata acc aat gtt 675
His Ile Ala Asn Gly Ala Cys Ile Thr Ile Gln Asn Ile Thr Asn Val
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Ile Val His Gly Leu His Ile His Asp Cys Lys Arg Thr Gly Asn Val
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Thr Val Arg Ser Ser Pro Ser Gln Ala Gly Phe Arg Gly Thr Ala Asp
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Gly Asp Ala Ile Asn Ile Phe Gly Ser Ser His Ile Trp Ile Asp His
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PF59082SeqList_PF59082.txt

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Val	Met	Leu	Leu	Gly	His	Asn	Asp	Ser	Tyr	Thr	Arg	Asp	Lys	Met	Met	
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Gln	Val	Thr	Val	Ala	Tyr	Asn	His	Phe	Gly	Glu	Gly	Leu	Ile	Gln	Arg	
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Thr	His	Trp	Lys	Met	Tyr	Ala	Ile	Gly	Gly	Ser	Ala	Asn	Pro	Thr	Ile	
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Asn	Ser	Gln	Gly	Asn	Arg	Phe	Ala	Ala	Pro	Lys	Asn	His	Ser	Ala	Lys	
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Glu	Val	Thr	Lys	Arg	Leu	Asp	Thr	Lys	Gly	Asn	Glu	Trp	Met	Glu	Trp	
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aat	tgg	aga	tca	gaa	aaa	gac	ctt	cta	gtg	aat	gga	gcg	ttt	ttt	aca	1251
Asn	Trp	Arg	Ser	Glu	Lys	Asp	Leu	Leu	Val	Asn	Gly	Ala	Phe	Phe	Thr	
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Pro	Ser	Gly	Glu	Gly	Ala	Ser	Gly	Asp	Ser	Gln	Thr	Leu	Ser	Leu	Pro	
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Ala	Lys	Pro	Ala	Ser	Met	Val	Asp	Ala	Ile	Thr	Ala	Ser	Ala	Gly	Ala	
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ctt	agt	tgc	cgt	aga	ggc	aaa	cct	tgc	tac	tagtaaaaca	ttactctctc					1397
Leu	Ser	Cys	Arg	Arg	Gly	Lys	Pro	Cys	Tyr							
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 Leu Ile His Met Ser Glu Gln Asn Ile Thr Ala Arg Arg Lys Leu Gly
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 Leu Arg His Ala Val Ile Gln Val Glu Pro Leu Trp Ile Ile Phe Lys
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PF59082SeqList_PF59082.txt

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 245 250 255
 Phe Gly Ser Ser His Ile Trp Ile Asp His Asn Ser Leu Ser Asn Cys
 260 265 270
 Thr Asp Gly Leu Val Asp Val Val Asn Gly Ser Thr Ala Ile Thr Ile
 275 280 285
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 Asn Asp Ser Tyr Thr Arg Asp Lys Met Met Gln Val Thr Val Ala Tyr
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 Asp Leu Leu Val Asn Gly Ala Phe Phe Thr Pro Ser Gly Glu Gly Ala
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 Ala Ala Leu Ser Ser Ala Asn Ile Ala Glu Phe Asp Glu Tyr Trp Gln
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 His Pro Glu Glu Val Thr Asn His Phe Asn Lys Ala Val His Ser Ser
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 Gln Cys Leu Ala Thr Asn Pro Ile Asp Arg Cys Trp Arg Cys Lys Lys
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 Asn Trp Ser Ala Asn Arg Lys Asp Leu Val Lys Cys Val Lys Gly Phe
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PF59082SeqList_PF59082.txt

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Trp	Gly	Val	Ile	Gln	Asp	Arg	Pro	Leu	Trp	Ile	Ile	Phe	Gly	Lys	Ser	
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Asp	Ile	Lys	Pro	Gly	Glu	Gly	Gly	Leu	Ile	Arg	Asp	Ser	Glu	Lys	His	
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Val	His	Val	Val	Asn	Asp	Tyr	Thr	His	Trp	Ile	Met	Tyr	Ala	Val		
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Ala	Pro	His	Ile	Glu	Ala	Ala	Lys	Glu	Val	Thr	Lys	Arg	Asp	Tyr	Ala	
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gag	cca	gca	gag	tgg	agc	aaa	tgg	act	tgg	aag	tcc	cag	ggt	gac	ttg	1152
Glu	Pro	Ala	Glu	Trp	Ser	Lys	Trp	Thr	Trp	Lys	Ser	Gln	Gly	Asp	Leu	
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Phe	Val	Ser	Gly	Ala	Phe	Phe	Val	Glu	Ser	Gly	Gly	Pro	Phe	Glu	Asn	
385				390					395					400		
aag	tac	tct	aag	aag	gac	tta	atc	aaa	gcc	aag	ccg	gga	aca	ttc	gtg	1248
Lys	Tyr	Ser	Lys	Lys	Asp	Leu	Ile	Lys	Ala	Lys	Pro	Gly	Thr	Phe	Val	
				405				410						415		
cag	agg	ctc	aca	cgc	ttc	tcg	ggc	gcc	ctc	aac	tgc	aag	gaa	aat	atg	1296
Gln	Arg	Leu	Thr	Arg	Phe	Ser	Gly	Ala	Leu	Asn	Cys	Lys	Glu	Asn	Met	
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<211> 434

<212> PRT

<213> Lilium longiflorum

<400> 902

PF59082SeqList_PF59082.txt

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20 25 30
Lys Lys Ser Lys Val Ala Gln Ala Lys Lys Ala Tyr Thr Pro
35 40 45
His Pro Glu Glu Val Thr Asn His Phe Asn Lys Ala Val His Ser Ser
50 55 60
Phe Glu Gly Asn Ser Thr Arg Arg Asn Leu Arg Thr Asn Lys Leu Gly
65 70 75 80
Gln Cys Leu Ala Thr Asn Pro Ile Asp Arg Cys Trp Arg Cys Lys Lys
85 90 95
Asn Trp Ser Ala Asn Arg Lys Asp Leu Val Lys Cys Val Lys Gly Phe
100 105 110
Gly Arg Lys Thr Thr Gly Gly Ala Gly Glu Ile Tyr Val Val Thr
115 120 125
Asp Pro Ser Asp Asp Ser Leu Thr Asp Pro Lys Phe Gly Thr Leu Arg
130 135 140
Trp Gly Val Ile Gln Asp Arg Pro Leu Trp Ile Ile Phe Gly Lys Ser
145 150 155 160
Met Val Ile Arg Leu Lys Gln Glu Leu Ile Ile Asn Asn Asp Lys Thr
165 170 175
Ile Asp Gly Arg Gly Ala Asn Val Gln Ile Ala Gly Gly Ala Gln Leu
180 185 190
Thr Val Gln Phe Val His Asn Val Ile Ile His Gly Ile His Ile His
195 200 205
Asp Ile Lys Pro Gly Glu Gly Gly Leu Ile Arg Asp Ser Glu Lys His
210 215 220
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225 230 235 240
Ser Ser Asn Ile Trp Ile Asp His Val Ser Leu Ala Arg Cys Ser Asp
245 250 255
Gly Leu Ile Asp Val Ile Leu Gly Ser Thr Ala Ile Thr Ile Ser Asn
260 265 270
Cys His Leu Thr Glu His Asp Asp Val Met Leu Leu Gly Ala Ser Asp
275 280 285
Thr Tyr Thr Gln Asp Glu Ile Met Gln Val Thr Val Ala Phe Asn His
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Phe Gly Arg Gly Leu Val Gln Arg Met Pro Arg Cys Arg Tyr Gly Phe
305 310 315 320
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325 330 335
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340 345 350
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355 360 365
Glu Pro Ala Glu Trp Ser Lys Trp Thr Trp Lys Ser Gln Gly Asp Leu
370 375 380
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385 390 395 400
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glu cys

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seite 1135

PF59082SeqList_PF59082.txt

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gac Asp	tcc Ser	tcc Ser	ttg Leu	240
gcc Ala	ggc Gly	gcc Ala	ggc Gly	288
cac His	gcg Ala	tcc Ser	atc Ile	336
tcg Ser	tgc Cys	ggg Gly	aca Thr	384
gac Asp	tgg Trp	cac His	aac Asn	432
gtg Val	ggc Gly	aag Lys	ccg Pro	480
gac Asp	ccg Pro	agc Ser	gac Asp	528
cac His	gcc Ala	gtc Val	atc Ile	576
atg Met	gtg Val	atc Ile	agc Ser	624
atc Ile	gac Asp	gga Gly	cgc Arg	672
acc Thr	atc Ile	cag Gln	tac Tyr	720
gac Asp	tgc Cys	agg Arg	ccc Pro	768
tac Tyr	ggc Gly	tgg Trp	cgc Arg	816
tcc Ser	agc Ser	cac His	gtc Val	864
ggc Gly	ctc Leu	atc Ile	gac Asp	912
aac Asn	tac Tyr	ttc Phe	acc Thr	960
tcc Ser	tat Tyr	gtg Val	aag Lys	1008
ttc Phe	ggc Gly	gaa Glu	ggc Gly	1056
ttc Phe	cac His	gtt Val	gtg Val	1104
ggg Gly	ggc Gly	agc Ser	gag Glu	1152

PF59082SeqList_PF59082.txt

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Ala Gln Thr Val Trp Lys Ser Trp Asn Trp Arg Ser Glu Gly Asp Leu		
405	ctg ctg aac ggc gcc tac ttc acc ccg tcc ggc gcg ggc gcc tcg gcc	1296
Leu Leu Asn Gly Ala Tyr Phe Thr Pro Ser Gly Ala Gly Ala Ser Ala		
420	agc tac tcg cgc gcg tcc agc ctc ggc aag tcg tcg tcc atg gtc	1344
Ser Tyr Ser Arg Ala Ser Ser Leu Gly Ala Lys Ser Ser Ser Met Val		
435	ggc acc atc acc tcg gac gcc ggc gca ctg tcg tgc cgc aag ggc gcg	1392
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Ala Cys		
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35	Gln Arg Ser Thr Ser Val Val Ala Gly Gly Ala Arg Arg Trp Leu Arg
50	Asp Ser Ser Leu Pro Ala Thr Thr Arg Gly Arg Ala Asp Gly Asp
65	Ala Gly Ala Gly Ala Val Glu Asp Pro Glu Ala Val Ala Asn Asp Val
85	His Ala Ser Ile Asn Asn Ile Thr Ala Arg Arg Asn Leu Gly Tyr Leu
100	Ser Cys Gly Thr Gly Asn Pro Ile Asp Asp Cys Trp Arg Cys Asp Ser
115	Asp Trp His Asn Asn Arg Lys Arg Leu Ala Asp Cys Gly Thr Ala Gly
130	Val Gly Lys Pro Glu Trp Leu Ser Asp Gly Lys Val Tyr Val Val Thr
145	Asp Pro Ser Asp Asp Asp Pro Val Asn Pro Arg Glu Gly Thr Leu Arg
165	His Ala Val Ile Gln Glu Glu Pro Leu Trp Ile Ile Phe Lys Arg Asp
180	Met Val Ile Thr Leu Arg Glu Glu Leu Ile Met Asn Ser Phe Lys Thr
195	Ile Asp Gly Arg Gly Ala Asn Val His Ile Ala Asn Gly Ala Cys Ile
210	Thr Ile Gln Tyr Ile Thr Asn Val Ile Ile His Gly Leu His Ile His
225	Asp Cys Arg Pro Thr Gly Asn Ala Met Val Arg Ser Ser Pro Ser His
245	Tyr Gly Trp Arg Thr Met Ala Asp Gly Asp Gly Val Ser Ile Phe Gly
260	Ser Ser His Val Trp Val Asp His Cys Ser Leu Ser Asn Cys Ala Asp
275	Gly Leu Ile Asp Ala Ile Met Gly Ser Thr Ala Ile Thr Leu Ser Asn
290	Asn Tyr Phe Thr His His Asn Glu Val Met Leu Gly His Ser Asp
305	Ser Tyr Val Lys Asp Lys Ala Met Gln Val Thr Ile Ala Phe Asn His
325	Phe Gly Glu Gly Leu Ile Gln Arg Met Pro Arg Cys Arg His Gly Tyr

PF59082SeqList_PF59082.txt

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 Phe His Val Val Asn Asn Asp Tyr Thr His Trp Glu Met Tyr Ala Ile
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 Gly Gly Ser Ala Glu Pro Thr Ile Asn Ser Gln Gly Asn Arg Tyr Leu
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 385
 Ala Gln Thr Val Trp Lys Ser Trp Asn Trp Arg Ser Glu Gly Asp Leu
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 Leu Leu Asn Gly Ala Tyr Phe Thr Pro Ser Gly Ala Gly Ala Ser Ala
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 Ala Cys
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 ttg cct cat gga aca gca atg ctc aac ctc act ctc cca gga caa cac 96
 Leu Pro His Gly Thr Ala Met Leu Asn Leu Thr Leu Pro Gly Gln His 20
 20
 cca gac cct gaa gcc gtt gct cga gaa gtt cat agg aaa gtg aat gct 144
 Pro Asp Pro Glu Ala Val Ala Arg Glu Val His Arg Lys Val Asn Ala 35
 35
 tca atg gca aga agg gaa atg ctg gga gtg tca gag aaa gag gtg gca 192
 Ser Met Ala Arg Arg Glu Met Leu Gly Val Ser Glu Lys Glu Val Ala 50
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 Ser Cys Leu Thr Gly Asn Pro Ile Asp Asp Cys Trp Lys Cys Asp Pro 65
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 gat tgg gcc aac aac agg cag agg cta gca gat tgt gca ata ggg ttc 288
 Asp Trp Ala Asn Asn Arg Gln Arg Leu Ala Asp Cys Ala Ile Gly Phe 80
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 ggg cag aac gca aag gga gga aaa ggt ggc caa ttt tac ata gtc act 336
 Gly Gln Asn Ala Lys Gly Gly Lys Gly Gly Gln Phe Tyr Ile Val Thr 100
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 Asp Ser Ser Asp Glu Asp Pro Val Asn Pro Lys Pro Gly Thr Leu Arg 115
 115
 tat gca gtg ata cag aac gag cca ctg tgg ata gtg ttc ccc agt aac 432
 Tyr Ala Val Ile Gln Asn Glu Pro Leu Trp Ile Val Phe Pro Ser Asn 130
 130
 atg atg att aag ctg tct caa gaa ctc att ttt aat agc tac aag acc 480
 Met Met Ile Lys Leu Ser Gln Glu Leu Ile Phe Asn Ser Tyr Lys Thr 145
 145
 att gat ggg cgt gga gct gac gtg cac att gtg ggt gga ggc tgc att 528
 Ile Asp Gly Arg Gly Ala Asp Val His Ile Val Gly Gly Gly Cys Ile 165
 165
 act ctt cag tat att agc aat gtc att att cac aac att cac atc cac 576
 Thr Leu Gln Tyr Ile Ser Asn Val Ile Ile His Asn Ile His Ile His 180
 180
 cat tgc cat ccc tct ggc aac gct aac gtg cgg tcg agc ccg gaa cat 624
 His Cys His Pro Ser Gly Asn Ala Asn Val Arg Ser Ser Pro Glu His 195
 195
 tat ggg tac cgc acg gag tcg gac ggc gac ggg atc tcc atc ttc ggc 672
 Tyr Gly Tyr Arg Thr Glu Ser Asp Gly Asp Gly Ile Ser Ile Phe Gly 200
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PF59082SeqList_PF59082.txt

210	tcg cgt gac att tgg atc	215	gac cac tgc acc ctc tcc cgg tgc aag gac	720
Ser Arg Asp Ile Trp	230	Asp His Cys Thr Leu Ser Arg Cys Lys Asp		
225	ggc ctg atc gat gca gtg atg ggt tcc agc gct atc acg atc tcc aac	235	gag ggt tcc agc gct atc acg atc tcc aac	768
Gly Leu Ile Asp Ala	245	Val Met Gly Ser Ser Ala Ile Thr Ile Ser Asn		
250	aac cac ttc tcc cac cac aat gac gtg atg ctc ctg tgc cac agc gac	255	Asn His Phe Ser His His Asn Asp Val Met Leu Leu Cys His Ser Asp	816
Asn His Phe Ser His His Asn Asp Val Met Leu Leu Cys His Ser Asp	260			
270	cac tac ctc cca gac tcc agc atg cag gtg acc att ggc ttc aac cac	275	His Tyr Leu Pro Asp Ser Ser Met Gln Val Thr Ile Gly Phe Asn His	864
His Tyr Leu Pro Asp Ser Ser Met Gln Val Thr Ile Gly Phe Asn His	280			
285	ttt cgg gag ggc ctc gtc cag cgc atg ccg cgt tgc cga cga ggt tac	290	Phe Arg Glu Gly Leu Val Gln Arg Met Pro Arg Cys Arg Arg Gly Tyr	912
Phe Arg Glu Gly Leu Val Gln Arg Met Pro Arg Cys Arg Arg Gly Tyr	295			
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Ile His Val Glu Asn Asn Asp Phe Thr Arg Trp Glu Met Tyr Ala Ile	310			
315	ggc ggc agt gcg gga ccc acc att aac agc cag gga aac cgc tac acc	320	Gly Gly Ser Ala Gly Pro Thr Ile Asn Ser Gln Gly Asn Arg Tyr Thr	1008
Gly Gly Ser Ala Gly Pro Thr Ile Asn Ser Gln Gly Asn Arg Tyr Thr	325			
330	gcg ccg gag gat ccg tac gcg aag cag gtt acg aag agg ctg gat gcc	335	Ala Pro Glu Asp Pro Tyr Ala Lys Gln Val Thr Lys Arg Leu Asp Ala	1056
Ala Pro Glu Asp Pro Tyr Ala Lys Gln Val Thr Lys Arg Leu Asp Ala	340			
345	gaa aaa ggg gag tgg agc ggg tgg aat tgg cgg tcc gaa ggg gat gtt	350	Glu Lys Gly Glu Trp Ser Gly Trp Asn Trp Arg Ser Glu Gly Asp Val	1104
Glu Lys Gly Glu Trp Ser Gly Trp Asn Trp Arg Ser Glu Gly Asp Val	355			
360	ttg ttg aat ggc gcg ttc ttc gtt gct tgc gga gca gtt gct gaa cct	365	Leu Leu Asn Gly Ala Phe Phe Val Ala Ser Gly Ala Val Ala Glu Pro	1152
Leu Leu Asn Gly Ala Phe Phe Val Ala Ser Gly Ala Val Ala Glu Pro	370			
375	aac tat cag aac gcc tac agc acc caa cct aag aac gtg gat cgc att	380	Asn Tyr Gln Asn Ala Tyr Ser Thr Gln Pro Lys Asn Val Asp Arg Ile	1200
Asn Tyr Gln Asn Ala Tyr Ser Thr Gln Pro Lys Asn Val Asp Arg Ile	385			
390	tcg ctt ctc act atg tcc gcc ggt gtt ctc ggc gtt gct agg gac aat	395	Ser Leu Leu Thr Met Ser Ala Gly Val Leu Gly Val Ala Arg Asp Asn	1248
Ser Leu Leu Thr Met Ser Ala Gly Val Leu Gly Val Ala Arg Asp Asn	400			
405	aat ctg gga atg tgg atc aga gga ccc aac gat ggc act gta tat ttt	410	Asn Leu Gly Met Trp Ile Arg Gly Pro Asn Asp Gly Thr Val Tyr Phe	1296
Asn Leu Gly Met Trp Ile Arg Gly Pro Asn Asp Gly Thr Val Tyr Phe	415			
420	tca gat tct ggc cca gaa tac aca gac gaa atg tcc cgg agt aca atg	425	Ser Asp Ser Gly Pro Glu Tyr Thr Asp Glu Met Ser Arg Ser Thr Met	1344
Ser Asp Ser Gly Pro Glu Tyr Thr Asp Glu Met Ser Arg Ser Thr Met	430			
435	ccg ttg cta cct tca cgt att ttg att ctt gta tct gca ctc tta tgc	440	Pro Leu Leu Pro Ser Arg Ile Leu Ile Leu Val Ser Ala Leu Leu Cys	1392
Pro Leu Leu Pro Ser Arg Ile Leu Ile Leu Val Ser Ala Leu Leu Cys	445			
450	ttc tta ggt cat aca aca acc tta aca aca cta ccc aat tag	455	Phe Leu Gly His Thr Thr Thr Leu Thr Thr Leu Pro Asn	1434
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<211> 477

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Pro Asp Pro Glu Ala Val Ala Arg Glu Val His Arg Lys Val Asn Ala	40	45	50	55
Ser Met Ala Arg Arg Glu Met Leu Gly Val Ser Glu Lys Glu Val Ala	60	65	70	75
Ser Cys Leu Thr Gly Asn Pro Ile Asp Asp Cys Trp Lys Cys Asp Pro	80	85	90	95
Asp Trp Ala Asn Asn Arg Gln Arg Leu Ala Asp Cys Ala Ile Gly Phe	100	105	110	115
Gly Gln Asn Ala Lys Gly Gly Lys Gly Gln Phe Tyr Ile Val Thr	120	125	130	135

PF59082SeqList_PF59082.txt

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	130					135					140				
Met	Met	Ile	Lys	Leu	Ser	Gln	Glu	Leu	Ile	Phe	Asn	Ser	Tyr	Lys	Thr
145					150					155					160
Ile	Asp	Gly	Arg	Gly	Ala	Asp	Val	His	Ile	Val	Gly	Gly	Gly	Cys	Ile
				165					170					175	
Thr	Leu	Gln	Tyr	Ile	Ser	Asn	Val	Ile	Ile	His	Asn	Ile	His	Ile	His
			180					185					190		
His	Cys	His	Pro	Ser	Gly	Asn	Ala	Asn	Val	Arg	Ser	Ser	Pro	Glu	His
		195					200					205			
Tyr	Gly	Tyr	Arg	Thr	Glu	Ser	Asp	Gly	Asp	Gly	Ile	Ser	Ile	Phe	Gly
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225					230					235					240
Gly	Leu	Ile	Asp	Ala	Val	Met	Gly	Ser	Ser	Ala	Ile	Thr	Ile	Ser	Asn
				245					250					255	
Asn	His	Phe	Ser	His	His	Asn	Asp	Val	Met	Leu	Leu	Cys	His	Ser	Asp
			260					265					270		
His	Tyr	Leu	Pro	Asp	Ser	Ser	Met	Gln	Val	Thr	Ile	Gly	Phe	Asn	His
		275					280					285			
Phe	Arg	Glu	Gly	Leu	Val	Gln	Arg	Met	Pro	Arg	Cys	Arg	Arg	Gly	Tyr
	290					295					300				
Ile	His	Val	Glu	Asn	Asn	Asp	Phe	Thr	Arg	Trp	Glu	Met	Tyr	Ala	Ile
305					310					315					320
Gly	Gly	Ser	Ala	Gly	Pro	Thr	Ile	Asn	Ser	Gln	Gly	Asn	Arg	Tyr	Thr
				325					330					335	
Ala	Pro	Glu	Asp	Pro	Tyr	Ala	Lys	Gln	Val	Thr	Lys	Arg	Leu	Asp	Ala
			340					345					350		
Glu	Lys	Gly	Glu	Trp	Ser	Gly	Trp	Asn	Trp	Arg	Ser	Glu	Gly	Asp	Val
		355					360					365			
Leu	Leu	Asn	Gly	Ala	Phe	Phe	Val	Ala	Ser	Gly	Ala	Val	Ala	Glu	Pro
	370					375					380				
Asn	Tyr	Gln	Asn	Ala	Tyr	Ser	Thr	Gln	Pro	Lys	Asn	Val	Asp	Arg	Ile
385					390					395					400
Ser	Leu	Leu	Thr	Met	Ser	Ala	Gly	Val	Leu	Gly	Val	Ala	Arg	Asp	Asn
				405					410				415		
Asn	Leu	Gly	Met	Trp	Ile	Arg	Gly	Pro	Asn	Asp	Gly	Thr	Val	Tyr	Phe
			420					425					430		
Ser	Asp	Ser	Gly	Pro	Glu	Tyr	Thr	Asp	Glu	Met	Ser	Arg	Ser	Thr	Met
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<223> Xaa in position 127 to 128 is any amino acid

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<223> Xaa in position 143 to 144 is any amino acid

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<223> Xaa in position 156 is any amino acid

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<220>
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 <223> Xaa in position 209 is any amino acid

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<223> Xaa in position 257 to 258 is any amino acid

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<223> Xaa in position 281 is any amino acid

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<223> Xaa in position 356 to 357 is any amino acid

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<223> Xaa in position 360 to 364 is any amino acid

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<223> Xaa in position 365 to 367 is any or no amino acid

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<223> Xaa in position 369 is any amino acid

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<223> Xaa in position 374 to 381 is any amino acid

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<223> Xaa in position 383 to 385 is any amino acid

<220>
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<223> Xaa in position 387 to 389 is any amino acid

<220>
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<223> Xaa in position 391 is any amino acid

<220>
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<222> (393)..(393)
<223> Xaa in position 393 is any amino acid

<220>
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<223> Xaa in position 395 is any amino acid

<220>
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<222> (396)..(440)
<223> Xaa in position 396 to 440 is any or no amino acid

<220>
<221> Variant
<222> (442)..(443)
<223> Xaa in position 442 to 443 is any amino acid

<400> 915
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Xaa Arg Xaa Xaa Arg Xaa Leu Xaa Xaa Xaa Ser Xaa Xaa Xaa Xaa Xaa
      20      25      30
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Thr Gly Asn Pro Ile Asp
      35      40      45
Asp Cys Trp Arg Cys Xaa Asp Xaa Xaa Trp Xaa Xaa Xaa Arg Xaa Xaa
      50      55      60
Leu Ala Asp Cys Xaa Xaa Ile Gly Phe Gly Xaa Xaa Ala Xaa Gly Gly
65      70      75      80
Xaa Xaa Gly Xaa Xaa Tyr Val Val Thr Asp Xaa Xaa Asp Xaa Asp Xaa
      85      90      95
Val Asn Pro Xaa Pro Gly Thr Leu Arg Xaa Ala Val Ile Gln Xaa Xaa
      100      105      110
Pro Leu Trp Ile Xaa Phe Xaa Xaa Asp Met Xaa Ile Xaa Leu Xaa Xaa
      115      120      125
Glu Leu Xaa Xaa Asn Ser Xaa Lys Thr Ile Asp Gly Arg Gly Xaa Xaa
      130      135      140
Val His Ile Xaa Xaa Gly Xaa Cys Ile Thr Xaa Gln Xaa Xaa Xaa
145      150      155      160
Asn Xaa Ile Ile His Gly Xaa His Ile His Asp Cys Xaa Xaa Xaa Gly
      165      170      175
Asn Xaa Xaa Val Arg Xaa Ser Pro Xaa His Xaa Gly Xaa Arg Thr Xaa
      180      185      190
Xaa Asp Gly Asp Xaa Xaa Ser Ile Phe Gly Xaa Xaa Xaa Xaa Xaa Trp
      195

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<223> Xaa in position 28 is any or no amino acid
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 <223> Xaa in position 33 is Phe or Tyr
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 <223> Xaa in position 35 is any amino acid
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 <222> (37)..(37)
 <223> Xaa in position 37 is any amino acid
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 <222> (39)..(39)
 <223> Xaa in position 39 is Phe or Tyr
 <220>
 <221> Variant
 <222> (45)..(45)
 <223> Xaa in position 45 is Ala or Gly
 <220>
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 <222> (46)..(46)
 <223> Xaa in position 46 is Ala, Asp, Glu, Gly, Asn or Ser
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 <221> Variant
 <222> (50)..(50)
 <223> Xaa in position 50 is any amino acid
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 <221> Variant
 <222> (51)..(51)
 <223> Xaa in position 51 is Cys or Ser
 <220>
 <221> Variant
 <222> (56)..(56)
 <223> Xaa in position 56 is Phe or Tyr
 <220>
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 <222> (57)..(57)
 <223> Xaa in position 57 is any amino acid
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 1 5 10 15
 Arg Met Pro Arg Cys Arg Xaa Gly Tyr Xaa His Xaa Val Asn Asn Asp
 20 25 30
 Xaa Thr Xaa Trp Xaa Met Xaa Ala Ile Gly Gly Ser Xaa Xaa Pro Thr
 35 40 45
 Ile Xaa Xaa Gln Gly Asn Arg Xaa Xaa Ala Pro
 50 55
 <210> 917
 <211> 59
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 <213> Artificial sequence
 <220>

<223> protein pattern

<220>

<221> Variant

<222> (3)..(3)

<223> Xaa in position 3 is Glu, Asn, Ser or Thr

<220>

<221> Variant

<222> (5)..(6)

<223> Xaa in position 5 to 6 is any amino acid

<220>

<221> Variant

<222> (7)..(7)

<223> Xaa in position 7 is Asp or Asn

<220>

<221> Variant

<222> (8)..(8)

<223> Xaa in position 8 is any amino acid

<220>

<221> Variant

<222> (9)..(9)

<223> Xaa in position 9 is Asp, Asn or Ser

<220>

<221> Variant

<222> (10)..(10)

<223> Xaa in position 10 is Ala, Leu, Pro or Val

<220>

<221> Variant

<222> (11)..(11)

<223> Xaa in position 11 is Ser, Thr or Val

<220>

<221> Variant

<222> (12)..(12)

<223> Xaa in position 12 is Asp, Asn or Ser

<220>

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<222> (14)..(15)

<223> Xaa in position 14 to 15 is any amino acid

<220>

<221> Variant

<222> (20)..(20)

<223> Xaa in position 20 is His, Trp or Tyr

<220>

<221> Variant

<222> (21)..(21)

<223> Xaa in position 21 is Ala or Gly

<220>

<221> Variant

<222> (22)..(22)

<223> Xaa in position 22 is Ala or Val

<220>

<221> Variant

<222> (23)..(23)

<223> Xaa in position 23 is any amino acid

<220>

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<222> (25)..(26)
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<223> Xaa in position 31 is any amino acid

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<223> Xaa in position 33 to 34 is any amino acid

<220>
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<223> Xaa in position 35 is Asp, Asn or Ser

<220>
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<222> (36)..(36)
<223> Xaa in position 36 is Ile or Met

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<223> Xaa in position 37 is any amino acid

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<222> (39)..(39)
<223> Xaa in position 39 is any amino acid

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<223> Xaa in position 41 to 42 is any amino acid

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<223> Xaa in position 45 to 46 is Ile, Leu, Met or Val

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<223> Xaa in position 47 is Asn or Thr

<220>
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<223> Xaa in position 48 is Asp, Asn or Ser

<220>
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<223> Xaa in position 49 is any amino acid

<220>
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<223> Xaa in position 52 is Ile or Leu

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<223> Xaa in position 54 is Ala or Gly

<220>

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 <223> Xaa in position 57 is Ala, Ser or Val

 <220>
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 <223> Xaa in position 58 is Ala, Asn or Ser

 <400> 917
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 Thr Leu Arg Xaa Xaa Xaa Xaa Gln Xaa Xaa Pro Leu Trp Ile Xaa Phe
 20 25 30
 Xaa Xaa Xaa Xaa Xaa Ile Xaa Leu Xaa Xaa Glu Leu Xaa Xaa Xaa Xaa
 35 40 45
 Xaa Lys Thr Xaa Asp Xaa Arg Gly Xaa Xaa Val
 50 55

 <210> 918
 <211> 41
 <212> PRT
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 <220>
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 <223> Xaa in position 2 is Ile or Val

 <220>
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 <222> (5)..(5)
 <223> Xaa in position 5 is Cys or Asn

 <220>
 <221> Variant
 <222> (6)..(6)
 <223> Xaa in position 6 is Ser or Thr

 <220>
 <221> Variant
 <222> (7)..(7)
 <223> Xaa in position 7 is Phe, Leu or Met

 <220>
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 <222> (8)..(9)
 <223> Xaa in position 8 to 9 is any amino acid

 <220>
 <221> Variant
 <222> (11)..(11)
 <223> Xaa in position 11 is any amino acid

 <220>
 <221> Variant
 <222> (15)..(15)
 <223> Xaa in position 15 is Ile or Val

 <220>
 <221> Variant
 <222> (17)..(17)
 <223> Xaa in position 17 is Ala, Pro or Val

 <220>

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<221> Variant
<222> (18)..(18)
<223> Xaa in position 18 is Ile or Val

<220>
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<222> (19)..(19)
<223> Xaa in position 19 is any amino acid

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<222> (20)..(20)
<223> Xaa in position 20 is Ala, Gly or Ser

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<222> (26)..(26)
<223> Xaa in position 26 is Ile, Leu or Val

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<223> Xaa in position 30 is Phe, His or Tyr

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<222> (31)..(31)
<223> Xaa in position 31 is Phe, Leu or Met

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<223> Xaa in position 36 is Glu or Lys

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<223> Xaa in position 37 is Ala or Val

<220>
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<223> Xaa in position 38 is Ile or Met

<220>
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<222> (40)..(40)
<223> Xaa in position 40 is Leu or Met

<400> 918
Trp Xaa Asp His Xaa Xaa Xaa Xaa Xaa Cys Xaa Asp Gly Leu Xaa Asp
1      5      10      15
Xaa Xaa Xaa Xaa Ser Thr Ala Ile Thr Xaa Ser Asn Asn Xaa Xaa Xaa
20      25      30
His His Xaa Xaa Xaa Xaa Leu Xaa Gly
35      40

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<210> 919

<211> 14
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 <220>
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 <222> (14)..(14)
 <223> Xaa in position 14 is Ala, Asp, Glu, Ser or Thr

 <400> 919
 Cys Xaa Xaa Gly Asn Pro Ile Asp Asp Cys Trp Arg Cys Xaa
 1 5 10

<210> 920
 <211> 25
 <212> PRT
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 <220>
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 <223> Xaa in position 3 is Lys or Arg

 <220>
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 <223> Xaa in position 4 is any amino acid

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 <222> (5)..(5)
 <223> Xaa in position 5 is Asp or Ser

 <220>
 <221> Variant
 <222> (6)..(8)
 <223> Xaa in position 6 to 8 is any amino acid

 <220>
 <221> Variant
 <222> (9)..(9)
 <223> Xaa in position 9 is Ala, Pro or Val

 <220>
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 <222> (10)..(10)
 <223> Xaa in position 10 is Lys or Arg

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<220>
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<223> Xaa in position 11 is Ala, Pro or Ser

<220>
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<222> (12)..(12)
<223> Xaa in position 12 is Ala, Gly or Ser

<220>
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<223> Xaa in position 13 is Ala, Ser or Thr

<220>
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<222> (14)..(14)
<223> Xaa in position 14 is any amino acid

<220>
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<222> (16)..(16)
<223> Xaa in position 16 is Ala, Asp, Gly, Gln or Ser

<220>
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<222> (17)..(17)
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<222> (18)..(18)
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<220>
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<222> (20)..(21)
<223> Xaa in position 20 to 21 is any amino acid

<220>
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<222> (22)..(23)
<223> Xaa in position 22 to 23 is any or no amino acid

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<222> (25)..(25)
<223> Xaa in position 25 is Gly or Leu

<400> 920
Tyr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Xaa
1      5      10      15
Xaa Xaa Thr Xaa Xaa Xaa Ala Xaa
      20      25

<210> 921
<211> 21
<212> PRT
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<220>
<223> protein pattern

<220>
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<222> (2)..(2)

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<223> Xaa in position 2 is any amino acid

<220>

<221> Variant

<222> (3)..(3)

<223> Xaa in position 3 is His, Lys or Arg

<220>

<221> Variant

<222> (6)..(6)

<223> Xaa in position 6 is Asp or Asn

<220>

<221> Variant

<222> (8)..(8)

<223> Xaa in position 8 is Ala, Gly or Ser

<220>

<221> Variant

<222> (13)..(14)

<223> Xaa in position 13 to 14 is any amino acid

<220>

<221> Variant

<222> (15)..(15)

<223> Xaa in position 15 is Ala or Thr

<220>

<221> Variant

<222> (16)..(16)

<223> Xaa in position 16 is any amino acid

<220>

<221> Variant

<222> (19)..(19)

<223> Xaa in position 19 is Lys or Arg

<220>

<221> Variant

<222> (20)..(20)

<223> Xaa in position 20 is any amino acid

<400> 921

Arg Xaa Xaa Leu Ala Xaa Cys Xaa Ile Gly Phe Gly Xaa Xaa Xaa Xaa
 1 5 10 15
 Gly Gly Xaa Xaa Gly
 20

<210> 922

<211> 13

<212> PRT

<213> Artificial sequence

<220>

<223> protein pattern

<220>

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<222> (4)..(4)

<223> Xaa in position 4 is Ala or Gly

<220>

<221> Variant

<222> (5)..(5)

<223> Xaa in position 5 is Ile or Val

<220>

<221> Variant

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<222> (9)..(9)

<223> Xaa in position 9 is Ala, Glu, Gly or Asn

<220>

<221> Variant

<222> (10)..(10)

<223> Xaa in position 10 is Ala, Gly or Ser

<220>

<221> Variant

<222> (11)..(12)

<223> Xaa in position 11 to 12 is any amino acid

<220>

<221> Variant

<222> (13)..(13)

<223> Xaa in position 13 is Ile, Pro or Val

<400> 922

Asp Gly Asp Xaa Xaa Ser Ile Phe Xaa Xaa Xaa Xaa Xaa
1 5 10

<210> 923

<211> 1530

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1530)

<400> 923

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1 5 10 15	
aag agt gat ttg ggg att tct tcg ttt cct aaa tct tct cag att tcg	96
Lys Ser Asp Leu Gly Ile Ser Ser Phe Pro Lys Ser Ser Gln Ile Ser	
20 25 30	
att cat cga tgt cag aag aaa tcg atc tca cgg aag att gtt tcc gtt	144
Ile His Arg Cys Gln Lys Lys Ser Ile Ser Arg Lys Ile Val Ser Val	
35 40 45	
atg gct cct caa aag gat cgg tct cct gga act aca gga tcg gtg aaa	192
Met Ala Pro Gln Lys Asp Arg Ser Pro Gly Thr Thr Gly Ser Val Lys	
50 55 60	
act ggg atg aca atg acg gat aag att cta gct aga gct tcg gag aag	240
Thr Gly Met Thr Met Thr Glu Lys Ile Leu Ala Arg Ala Ser Glu Lys	
65 70 75 80	
tca tta gtg gtt cct ggt gat aac att tgg gtt aat gtt gat gtt ctt	288
Ser Leu Val Val Pro Gly Asp Asn Ile Trp Val Asn Val Asp Val Leu	
85 90 95	
atg act cat gat gtt tgt ggt cct ggt gct ttt ggt atc ttc aag aga	336
Met Thr His Asp Val Cys Gly Pro Gly Ala Phe Gly Ile Phe Lys Arg	
100 105 110	
gag ttt ggt gaa aaa gcc aag gtt tgg gat ccg gag aag att gtt gtg	384
Glu Phe Gly Glu Lys Ala Lys Val Trp Asp Pro Glu Lys Ile Val Val	
115 120 125	
att ccg gat cat tat att ttc act gct gat aag cgt gca aac cgg aat	432
Ile Pro Asp His Tyr Ile Phe Thr Ala Asp Lys Arg Ala Asn Arg Asn	
130 135 140	
gtt gac atc atg agg gag cat tgc agg gaa cag aat att aag tat ttc	480
Val Asp Ile Met Arg Glu His Cys Arg Glu Gln Asn Ile Lys Tyr Phe	
145 150 155 160	
tat gat atc act gac ctt gga aat ttt aag gct aat cct gac tac aaa	528
Tyr Asp Ile Thr Asp Leu Gly Asn Phe Lys Ala Asn Pro Asp Tyr Lys	
165 170 175	
ggg gtt tgc cat gtt gca ctt gca caa gaa ggt cat tgc agg cca gga	576
Gly Val Cys His Val Ala Leu Ala Gln Glu Gly His Cys Arg Pro Gly	
180 185 190	
gag gtt ttg tta gga aca gac tca cac act tgt act gct gga gca ttt	624

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ggc	act	gga	aaa	atc	ctc	ctt	aag	ggt	cca	cca	acg	atg	agg	ttt	atc	720
Gly	Thr	Gly	Lys	Ile	Leu	Leu	Lys	Val	Pro	Pro	Thr	Met	Arg	Phe	Ile	
225					230					235					240	
ttg	gat	ggt	gag	atg	cct	agt	tat	ttg	caa	gca	aag	gat	ctg	att	tta	768
Leu	Asp	Gly	Glu	Met	Pro	Ser	Tyr	Leu	Gln	Ala	Lys	Asp	Leu	Ile	Leu	
				245					250					255		
caa	att	att	ggt	gaa	ata	tct	ggt	gct	ggt	gca	act	tac	aag	acg	atg	816
Gln	Ile	Ile	Gly	Glu	Ile	Ser	Val	Ala	Gly	Ala	Thr	Tyr	Lys	Thr	Met	
			260				265						270			
gag	ttc	agt	ggt	aca	act	atc	gaa	agt	ctg	agt	atg	gaa	gaa	aga	atg	864
Glu	Phe	Ser	Gly	Thr	Thr	Ile	Glu	Ser	Leu	Ser	Met	Glu	Glu	Arg	Met	
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aca	ttg	tgc	aac	atg	gtt	gtg	gaa	gct	ggg	gga	aag	aat	ggt	gtc	atc	912
Thr	Leu	Cys	Asn	Met	Val	Val	Glu	Ala	Gly	Gly	Lys	Asn	Gly	Val	Ile	
290					295					300						
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Pro	Pro	Asp	Ala	Thr	Thr	Leu	Asn	Tyr	Val	Glu	Asn	Arg	Thr	Ser	Val	
305					310					315					320	
cca	ttt	gag	cca	gta	tat	agt	gat	gga	aat	gca	agc	ttt	gtc	gca	gat	1008
Pro	Phe	Glu	Pro	Val	Tyr	Ser	Asp	Gly	Asn	Ala	Ser	Phe	Val	Ala	Asp	
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tat	aga	ttt	gac	gtg	tca	aag	ctg	gag	cct	gtg	gtg	gct	aag	cct	cat	1056
Tyr	Arg	Phe	Asp	Val	Ser	Lys	Leu	Glu	Pro	Val	Val	Ala	Lys	Pro	His	
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Ser	Pro	Asp	Asn	Arg	Ala	Leu	Ala	Arg	Glu	Cys	Lys	Asp	Val	Lys	Ile	
			355				360					365				
gac	aga	gta	tac	atc	ggt	tct	tgt	act	ggt	ggg	aag	aca	gag	gat	ttt	1152
Asp	Arg	Val	Tyr	Ile	Gly	Ser	Cys	Thr	Gly	Gly	Lys	Thr	Glu	Asp	Phe	
			370			375				380						
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Met	Ala	Ala	Ala	Lys	Leu	Phe	His	Ala	Ala	Gly	Arg	Lys	Val	Lys	Val	
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cca	act	ttc	ctt	gtc	ccg	gct	act	cag	aag	gtg	tgg	atg	gat	gtg	tat	1248
Pro	Thr	Phe	Leu	Val	Pro	Ala	Thr	Gln	Lys	Val	Trp	Met	Asp	Val	Tyr	
				405					410					415		
gct	ctc	ccg	gta	cct	gga	gca	ggt	gga	aag	aca	tgt	gcg	cag	atc	ttt	1296
Ala	Leu	Pro	Val	Pro	Gly	Ala	Gly	Gly	Lys	Thr	Cys	Ala	Gln	Ile	Phe	
			420				425						430			
gaa	gaa	gct	ggc	tgt	gac	aca	cca	gcc	agc	cct	agc	tgt	ggg	gct	tgc	1344
Glu	Glu	Ala	Gly	Cys	Asp	Thr	Pro	Ala	Ser	Pro	Ser	Cys	Gly	Ala	Cys	
			435				440					445				
ctt	ggt	ggc	cca	gca	gac	acc	tac	gct	cgc	ttg	aat	gaa	cct	caa	gtg	1392
Leu	Gly	Gly	Pro	Ala	Asp	Thr	Tyr	Ala	Arg	Leu	Asn	Glu	Pro	Gln	Val	
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tgt	gtc	tca	acg	aca	aac	agg	aac	ttc	ccc	ggt	cgg	atg	gga	cac	aaa	1440
Cys	Val	Ser	Thr	Thr	Asn	Arg	Asn	Phe	Pro	Gly	Arg	Met	Gly	His	Lys	
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Glu	Gly	Gln	Ile	Tyr	Leu	Ala	Ser	Pro	Tyr	Thr	Ala	Ala	Ala	Ser	Ala	
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tta	acc	ggc	cgt	gtc	gct	gac	cca	agg	gag	ttc	ttg	cag	tag			1530
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<211> 509

<212> PRT

<213> Arabidopsis thaliana

<400> 924

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 Lys Ser Asp Leu Gly Ile Ser Ser Phe Pro Lys Ser Ser Gln Ile Ser
 Seite 1159

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Thr	Gly	Met	Thr	Met	Thr	Glu	Lys	Ile	Leu	Ala	Arg	Ala	Ser	Glu	Lys
Ser	Leu	Val	Val	Pro	Gly	Asp	Asn	Ile	Trp	Val	Asn	Val	Asp	Val	Leu
Met	Thr	His	Asp	Val	Cys	Gly	Pro	Gly	Ala	Phe	Gly	Ile	Phe	Lys	Arg
Glu	Phe	Gly	Glu	Lys	Ala	Lys	Val	Trp	Asp	Pro	Glu	Lys	Ile	Val	Val
Ile	Pro	Asp	His	Tyr	Ile	Phe	Thr	Ala	Asp	Lys	Arg	Ala	Asn	Arg	Asn
Val	Asp	Ile	Met	Arg	Glu	His	Cys	Arg	Glu	Gln	Asn	Ile	Lys	Tyr	Phe
Tyr	Asp	Ile	Thr	Asp	Leu	Gly	Asn	Phe	Lys	Ala	Asn	Pro	Asp	Tyr	Lys
Gly	Val	Cys	His	Val	Ala	Leu	Ala	Gln	Glu	Gly	His	Cys	Arg	Pro	Gly
Glu	Val	Leu	Leu	Gly	Thr	Asp	Ser	His	Thr	Cys	Thr	Ala	Gly	Ala	Phe
Gly	Gln	Phe	Ala	Thr	Gly	Ile	Gly	Asn	Thr	Asp	Ala	Gly	Phe	Val	Leu
Gly	Thr	Gly	Lys	Ile	Leu	Leu	Lys	Val	Pro	Pro	Thr	Met	Arg	Phe	Ile
Leu	Asp	Gly	Glu	Met	Pro	Ser	Tyr	Leu	Gln	Ala	Lys	Asp	Leu	Ile	Leu
Gln	Ile	Ile	Gly	Glu	Ile	Ser	Val	Ala	Gly	Ala	Thr	Tyr	Lys	Thr	Met
Glu	Phe	Ser	Gly	Thr	Thr	Ile	Glu	Ser	Leu	Ser	Met	Glu	Glu	Arg	Met
Thr	Leu	Cys	Asn	Met	Val	Val	Glu	Ala	Gly	Gly	Lys	Asn	Gly	Val	Ile
Pro	Pro	Asp	Ala	Thr	Thr	Leu	Asn	Tyr	Val	Glu	Asn	Arg	Thr	Ser	Val
Pro	Phe	Glu	Pro	Val	Tyr	Ser	Asp	Gly	Asn	Ala	Ser	Phe	Val	Ala	Asp
Tyr	Arg	Phe	Asp	Val	Ser	Lys	Leu	Glu	Pro	Val	Val	Ala	Lys	Pro	His
Ser	Pro	Asp	Asn	Arg	Ala	Leu	Ala	Arg	Glu	Cys	Lys	Asp	Val	Lys	Ile
Asp	Arg	Val	Tyr	Ile	Gly	Ser	Cys	Thr	Gly	Gly	Lys	Thr	Glu	Asp	Phe
Met	Ala	Ala	Ala	Lys	Leu	Phe	His	Ala	Ala	Gly	Arg	Lys	Val	Lys	Val
Pro	Thr	Phe	Leu	Val	Pro	Ala	Thr	Gln	Lys	Val	Trp	Met	Asp	Val	Tyr
Ala	Leu	Pro	Val	Pro	Gly	Ala	Gly	Gly	Lys	Thr	Cys	Ala	Gln	Ile	Phe
Glu	Glu	Ala	Gly	Cys	Asp	Thr	Pro	Ala	Ser	Pro	Ser	Cys	Gly	Ala	Cys
Leu	Gly	Gly	Pro	Ala	Asp	Thr	Tyr	Ala	Arg	Leu	Asn	Glu	Pro	Gln	Val
Cys	Val	Ser	Thr	Thr	Asn	Arg	Asn	Phe	Pro	Gly	Arg	Met	Gly	His	Lys
Glu	Gly	Gln	Ile	Tyr	Leu	Ala	Ser	Pro	Tyr	Thr	Ala	Ala	Ala	Ser	Ala
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<222> (1)..(1515)

<400> 925

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Gln Lys Asp Leu Gly Phe Pro Lys Pro Ser Gln Ile Ser Val His Arg	
20 25 30 35 40 45	
tgt cag aag aga gcg att tct cgg aag atc gtc tcc gtc atg gcg ccg	144
Cys Gln Lys Arg Ala Ile Ser Arg Lys Ile Val Ser Val Met Ala Pro	
50 55 60	
cag cga tca tcc agc gcc act gga tcg gtg aaa act ggg atg acg atg	192
Gln Arg Ser Ser Ser Ala Thr Gly Ser Val Lys Thr Gly Met Thr Met	
65 70 75	
acg gag aag att ctt gcc aag gca gca gag aaa tca gtt gtt cct	240
Thr Glu Lys Ile Leu Ala Lys Ala Ala Glu Lys Ser Gln Val Val Pro	
80 85 90 95	
ggg gat aac atc tgg gtt aac gtt gac gtt ctc atg act cat gat gtc	288
Gly Asp Asn Ile Trp Val Asn Val Asp Val Leu Met Thr His Asp Val	
100 105 110	
tgt ggc cct ggt gct ttt ggt atc ttc aag aga gag ttc ggt gaa aaa	336
Cys Gly Pro Gly Ala Phe Gly Ile Phe Lys Arg Glu Phe Gly Glu Lys	
115 120 125	
gct aag gtt tgg gac ccg gag aag att gtt gtt att cca gac cat tac	384
Ala Lys Val Trp Asp Pro Glu Lys Ile Val Val Ile Pro Asp His Tyr	
130 135 140	
atc ttc act act gat aag cgt gcc aac cgc aat gtc gac att atg agg	432
Ile Phe Thr Thr Asp Lys Arg Ala Asn Arg Asn Val Asp Ile Met Arg	
145 150 155	
gaa cat tgc agg gaa cag aac atc aag tat ttc gat atc acc gac	480
Glu His Cys Arg Glu Gln Asn Ile Lys Tyr Phe Tyr Asp Ile Thr Asp	
160 165 170 175	
ctt gga gat ttt cgg gct aat cct gac tac aaa ggt gtt tgc cat gtg	528
Leu Gly Asp Phe Arg Ala Asn Pro Asp Tyr Lys Gly Val Cys His Val	
180 185 190	
gcg ctt gca caa gaa ggt cat tgc agg cca gga gag gtt ttg tta gga	576
Ala Leu Ala Gln Glu Gly His Cys Arg Pro Gly Glu Val Leu Leu Gly	
195 200 205	
aca gac tcg cac aca tgt act gct gga gcg ttt ggt cag ttt gct aca	624
Thr Asp Ser His Thr Cys Thr Ala Gly Ala Phe Gly Gln Phe Ala Thr	
210 215 220	
ggg att gga aac acc gat gca gga ttt gtg tta ggc act gga aaa atc	672
Gly Ile Gly Asn Thr Asp Ala Gly Phe Val Leu Gly Thr Gly Lys Ile	
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ctc ctt aag gtt cca cca aca atg agg ttt atc ttg gat ggt gaa atg	720
Leu Leu Lys Val Pro Pro Thr Met Arg Phe Ile Leu Asp Gly Glu Met	
240 245 250 255	
ccc agt tat ctg caa gca aag gat ctg att cta caa atc att gga gaa	768
Pro Ser Tyr Leu Gln Ala Lys Asp Leu Ile Leu Gln Ile Ile Gly Glu	
260 265 270	
ata tct gtt gct ggt gca act tac aag acg atg gag ttc agt gga aca	816
Ile Ser Val Ala Gly Ala Thr Tyr Lys Thr Met Glu Phe Ser Gly Thr	
275 280 285	
act att gaa agt cta act atg gaa gaa aga atg aca ttg tgc aac atg	864
Thr Ile Glu Ser Leu Thr Met Glu Glu Arg Met Thr Leu Cys Asn Met	
290 295 300	
gtt gtg gaa gct ggg gga aag aat ggt gtc atc cct cct gat gcg acg	912
Val Val Glu Ala Gly Gly Lys Asn Gly Val Ile Pro Pro Asp Ala Thr	
305 310 315	
aca ttt aat tac gtt gag aac agg aca tct gta ccc ttt gag ccc gta	960
Thr Phe Asn Tyr Val Glu Asn Arg Thr Ser Val Pro Phe Glu Pro Val	
320 325 330 335	
tat agt gat gga aat gca agc ttt att gca gat tat cga ttt gac gtg	1008
Tyr Ser Asp Gly Asn Ala Ser Phe Ile Ala Asp Tyr Arg Phe Asp Val	
340 345 350	
tca aag ctg gag cct gtg gtg gct aag cct cat tct cct gac aac agg	1056
Ser Lys Leu Glu Pro Val Val Ala Lys Pro His Ser Pro Asp Asn Arg	

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Ala Leu Ala Arg Glu Cys Lys	Asp Val Lys Ile Asp Arg Val Tyr Ile	
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ggg tct tgt act ggt ggg aag act gag gat ttt atg gct gca gct aaa	1152	
Gly Ser Cys Thr Gly Gly Lys Thr Glu Asp Phe Met Ala Ala Ala Lys		
	370 375 380	
ctt ttc cat gca gca gga aag caa gtc aaa gtc cca act ttc ctt gtc	1200	
Leu Phe His Ala Ala Gly Lys Gln Val Lys Val Pro Thr Phe Leu Val		
	385 390 395 400	
ccc gct act cag aag gtg tgg atg gat gtg tat gcc ctc cct gtg cct	1248	
Pro Ala Thr Gln Lys Val Trp Met Asp Val Tyr Ala Leu Pro Val Pro		
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gga gca ggt gga aag acg tgt gcg cag ata ttc aaa gaa gct ggc tgc	1296	
Gly Ala Gly Gly Lys Thr Cys Ala Gln Ile Phe Lys Glu Ala Gly Cys		
	420 425 430	
gac aca cca acc agt cct agt tgt ggt gcc tgc ctt ggt ggc cca gct	1344	
Asp Thr Pro Thr Ser Pro Ser Cys Gly Ala Cys Leu Gly Gly Pro Ala		
	435 440 445	
gac acc tat gct cgc ttg aat gaa cct caa gtg tgt gtc tcg aca acg	1392	
Asp Thr Tyr Ala Arg Leu Asn Glu Pro Gln Val Cys Val Ser Thr Thr		
	450 455 460	
aac aga aac ttt cct ggt cgg atg gga cac aaa gaa ggg cag att tac	1440	
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ttg gct tct cct tac acc gct gca gcc tcg ctg acc ggc cat gtc	1488	
Leu Ala Ser Pro Tyr Thr Ala Ala Ala Ser Ala Leu Thr Gly His Val		
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 <213> Brassica napus

<400> 926

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Cys Gln Lys Arg Ala Ile Ser Arg Lys Ile Val Ser Val Met Ala Pro	
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Gln Arg Ser Ser Ser Ala Thr Gly Ser Val Lys Thr Gly Met Thr Met	
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Thr Glu Lys Ile Leu Ala Lys Ala Ala Glu Lys Ser Gln Val Val Pro	
	65 70 75 80
Gly Asp Asn Ile Trp Val Asn Val Asp Val Leu Met Thr His Asp Val	
	85 90 95
Cys Gly Pro Gly Ala Phe Gly Ile Phe Lys Arg Glu Phe Gly Glu Lys	
	100 105 110
Ala Lys Val Trp Asp Pro Glu Lys Ile Val Val Ile Pro Asp His Tyr	
	115 120 125
Ile Phe Thr Thr Asp Lys Arg Ala Asn Arg Asn Val Asp Ile Met Arg	
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Glu His Cys Arg Glu Gln Asn Ile Lys Tyr Phe Tyr Asp Ile Thr Asp	
	145 150 155 160
Leu Gly Asp Phe Arg Ala Asn Pro Asp Tyr Lys Gly Val Cys His Val	
	165 170 175
Ala Leu Ala Gln Glu Gly His Cys Arg Pro Gly Glu Val Leu Leu Gly	
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Thr Asp Ser His Thr Cys Thr Ala Gly Ala Phe Gly Gln Phe Ala Thr	
	195 200 205
Gly Ile Gly Asn Thr Asp Ala Gly Phe Val Leu Gly Thr Gly Lys Ile	
	210 215 220
Leu Leu Lys Val Pro Pro Thr Met Arg Phe Ile Leu Asp Gly Glu Met	
	225 230 235 240
Pro Ser Tyr Leu Gln Ala Lys Asp Leu Ile Leu Gln Ile Ile Gly Glu	
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PF59082SeqList_PF59082.txt

Ile Ser Val Ala Gly Ala Thr Tyr Lys Thr Met Glu Phe Ser Gly Thr
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 Thr Ile Glu Ser Leu Thr Met Glu Glu Arg Met Thr Leu Cys Asn Met
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 290 295 300
 Thr Phe Asn Tyr Val Glu Asn Arg Thr Ser Val Pro Phe Glu Pro Val
 305 310 315 320
 Tyr Ser Asp Gly Asn Ala Ser Phe Ile Ala Asp Tyr Arg Phe Asp Val
 325 330 335
 Ser Lys Leu Glu Pro Val Val Ala Lys Pro His Ser Pro Asp Asn Arg
 340 345 350
 Ala Leu Ala Arg Glu Cys Lys Asp Val Lys Ile Asp Arg Val Tyr Ile
 355 360 365
 Gly Ser Cys Thr Gly Gly Lys Thr Glu Asp Phe Met Ala Ala Lys
 370 375 380
 Leu Phe His Ala Ala Gly Lys Gln Val Lys Val Pro Thr Phe Leu Val
 385 390 395 400
 Pro Ala Thr Gln Lys Val Trp Met Asp Val Tyr Ala Leu Pro Val Pro
 405 410 415
 Gly Ala Gly Gly Lys Thr Cys Ala Gln Ile Phe Lys Glu Ala Gly Cys
 420 425 430
 Asp Thr Pro Thr Ser Pro Ser Cys Gly Ala Cys Leu Gly Gly Pro Ala
 435 440 445
 Asp Thr Tyr Ala Arg Leu Asn Glu Pro Gln Val Cys Val Ser Thr Thr
 450 455 460
 Asn Arg Asn Phe Pro Gly Arg Met Gly His Lys Glu Gly Gln Ile Tyr
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gccgccacgc c atg gcc tcc tcc atc tcc gcc gcc gcc aag gcc tcc acg 230
 Met Ala Ser Ser Ile Ser Ala Ala Ala Lys Ala Ser Thr
 1 5 10

gcc ttc gcc cac aag aag gag ctc gcc gcg ccg gcg ccc gcg cag cac 278
 Ala Phe Ala His Lys Lys Glu Leu Ala Ala Pro Ala Pro Ala Gln His
 15 20 25

cgc gcg ggc tcg agc cgc cgg acc aag cca tgc cgc gtg cgc gcc gtc 326
 Arg Ala Gly Ser Ser Arg Arg Thr Lys Pro Cys Arg Val Arg Ala Val
 30 35 40 45

gcc tcg cct gcg cgc gct ccc cgc gcc ccg tcg tcc acc ggc tcg gtg 374
 Ala Ser Pro Ala Arg Ala Pro Arg Ala Pro Ser Ser Thr Gly Ser Val
 50 55 60

aag agc gcg atg acg atg acg gag aag atc ctg gcg cgg gcg tcg gag 422
 Lys Ser Ala Met Thr Met Thr Glu Lys Ile Leu Ala Arg Ala Ser Glu
 65 70 75

cgc gcg gcg ctg gag ccc ggg gag aac gtg tgg gtg gac gtc gac gtg 470
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PF59082SeqList_PF59082.txt

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Lys	Glu	Phe	Gly	Glu	Asp	Ala	Lys	Val	Trp	Asp	Arg	Glu	Lys	Val	Val		
110					115					120					125		
atc	atc	ccg	gac	cac	tac	atc	ttc	acc	acc	gac	gag	cgt	gcc	aac	cgc		614
Ile	Ile	Pro	Asp	His	Tyr	Ile	Phe	Thr	Thr	Asp	Glu	Arg	Ala	Asn	Arg		
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Asn	Val	Asp	Ile	Leu	Arg	Asp	Phe	Cys	Leu	Glu	Gln	Asn	Ile	Lys	Tyr		
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Phe	Tyr	Asp	Ile	Lys	Asp	Leu	Ser	Asn	Phe	Lys	Ala	Asn	Pro	Asp	Tyr		
		160						165					170				
aaa	ggg	gtc	tgc	cac	gtt	gca	ctt	gct	cag	gaa	ggc	cac	tgc	cga	cca		758
Lys	Gly	Val	Cys	His	Val	Ala	Leu	Ala	Gln	Glu	Gly	His	Cys	Arg	Pro		
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Gly	Glu	Val	Leu	Leu	Gly	Thr	Asp	Ser	His	Thr	Cys	Asn	Ala	Gly	Ala		
190					195					200					205		
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Phe	Gly	Gln	Phe	Ala	Thr	Gly	Ile	Gly	Asn	Thr	Asp	Ala	Gly	Phe	Val		
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Leu	Gly	Thr	Gly	Lys	Ala	Leu	Leu	Lys	Val	Pro	Pro	Thr	Ile	Arg	Phe		
			225					230					235				
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Leu	Gln	Ile	Ile	Gly	Glu	Ile	Ser	Val	Ser	Gly	Ala	Thr	Tyr	Lys	Ser		
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Val	Pro	Ala	Asp	Glu	Thr	Thr	Phe	Lys	Tyr	Leu	Glu	Gly	Lys	Thr	Ser		
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Val	Asp	Tyr	Glu	Pro	Val	Tyr	Ser	Asp	Ala	Gln	Ala	Arg	Phe	Phe	Ser		
		320					325					330					
gac	tac	cgt	ttt	gat	gta	tca	aaa	ctg	gag	cca	gta	gtt	gcc	aag	cca		1238
Asp	Tyr	Arg	Phe	Asp	Val	Ser	Lys	Leu	Glu	Pro	Val	Val	Ala	Lys	Pro		
		335				340				345							
cat	tcg	cct	gac	aac	cgt	cta	gca	aga	gaa	gaa	aaa	gat	gtc	aag			1286
His	Ser	Pro	Asp	Asn	Arg	Ala	Leu	Ala	Arg	Glu	Cys	Lys	Asp	Val	Lys		
350				355					360					365			
gtt	gac	cga	gtc	tat	att	ggg	tct	tgc	act	ggg	ggg	aag	act	gag	gac		1334
Val	Asp	Arg	Val	Tyr	Ile	Gly	Ser	Cys	Thr	Gly	Gly	Lys	Thr	Glu	Asp		
			370					375						380			
ttc	ctt	gct	gct	gca	aag	gtg	ttc	tta	gcc	tcg	gga	aag	aag	gtt	aaa		1382
Phe	Leu	Ala	Ala	Ala	Lys	Val	Phe	Leu	Ala	Ser	Gly	Lys	Lys	Val	Lys		
			385					390					395				
gtt	ccc	aca	ttt	ctt	gtc	cct	gcc	aca	caa	aag	gtg	tgg	atg	gac	gta		1430
Val	Pro	Thr	Phe	Leu	Val	Pro	Ala	Thr	Gln	Lys	Val	Trp	Met	Asp	Val		
		400				405						410					
tat	agc	ctc	cct	gta	cca	gga	tct	ggg	ggc	aaa	act	tgc	tcc	cag	ata		1478
Tyr	Ser	Leu	Pro	Val	Pro	Gly	Ser	Gly	Gly	Lys	Thr	Cys	Ser	Gln	Ile		
		415				420				425							
ttt	gag	gag	gct	ggg	tgt	gat	aca	cca	gca	agt	cct	agc	tgt	ggg	gct		1526
Phe	Glu	Glu	Ala	Gly	Cys	Asp	Thr	Pro	Ala	Ser	Pro	Ser	Cys	Gly	Ala		
430				435				440						445			
tgt	ttg	ggg	ggg	cct	cgt	gat	aca	tat	gca	cgg	atg	aat	gaa	cct	atg		1574
Cys	Leu	Gly	Gly	Pro	Arg	Asp	Thr	Tyr	Ala	Arg	Met	Asn	Glu	Pro	Met		

PF59082SeqList_PF59082.txt

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Val Cys Val Ser Thr Thr Asn Arg Asn Phe Pro Gly Arg Met Gly His
          465          470          475
aag gaa ggg cag atc tac ctg gcg tct ccc tac act gca gct gcc tca      1670
Lys Glu Gly Gln Ile Tyr Leu Ala Ser Pro Tyr Thr Ala Ala Ala Ser
          480          485          490
gcc ctg acg ggg tat gtt acg gac ccc agg gac ttc ctc atg taattttgaa      1722
Ala Leu Thr Gly Tyr Val Thr Asp Pro Arg Asp Phe Leu Met
          495          500          505
acaacagagt tcatgatgta acagattgcc tgtagcctct gtttttcgtg ttgaacctta      1782

gttttaggcgt gtctttcgtt gaggaataag ctgcatgtcg ggaggttggc atgtatggtt      1842

ttgcattatt acagtgtact accaattaag aacatacttg agtgttacaa gggaaataca      1902

ttcttctgag tattgatggc agttcctaga ctcaaaactt cttgctataa ggcctgttga      1962

gtgatct      1969

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 <212> PRT
 <213> sorghum bicolor

<400> 928

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Ser Ser Arg Arg Thr Lys Pro Cys Arg Val Arg Ala Val Ala Ser Pro
35      40      45
Ala Arg Ala Pro Arg Ala Pro Ser Ser Thr Gly Ser Val Lys Ser Ala
50      55      60
Met Thr Met Thr Glu Lys Ile Leu Ala Arg Ala Ser Glu Arg Ala Ala
65      70      75      80
Leu Glu Pro Gly Glu Asn Val Trp Val Asp Val Asp Val Leu Met Thr
85      90      95
His Asp Val Cys Gly Pro Gly Thr Ile Gly Ile Phe Lys Lys Glu Phe
100     105     110
Gly Glu Asp Ala Lys Val Trp Asp Arg Glu Lys Val Val Ile Ile Pro
115     120     125
Asp His Tyr Ile Phe Thr Thr Asp Glu Arg Ala Asn Arg Asn Val Asp
130     135     140
Ile Leu Arg Asp Phe Cys Leu Glu Gln Asn Ile Lys Tyr Phe Tyr Asp
145     150     155     160
Ile Lys Asp Leu Ser Asn Phe Lys Ala Asn Pro Asp Tyr Lys Gly Val
165     170     175
Cys His Val Ala Leu Ala Gln Glu Gly His Cys Arg Pro Gly Glu Val
180     185     190
Leu Leu Gly Thr Asp Ser His Thr Cys Asn Ala Gly Ala Phe Gly Gln
195     200     205
Phe Ala Thr Gly Ile Gly Asn Thr Asp Ala Gly Phe Val Leu Gly Thr
210     215     220
Gly Lys Ala Leu Leu Lys Val Pro Pro Thr Ile Arg Phe Val Leu Asp
225     230     235     240
Gly Glu Met Pro Tyr Leu Leu Ala Lys Asp Leu Ile Leu Gln Ile
245     250     255
Ile Gly Glu Ile Ser Val Ser Gly Ala Thr Tyr Lys Ser Met Glu Phe
260     265     270
Val Gly Ser Thr Val Glu Ser Leu Thr Met Glu Glu Arg Met Thr Leu
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Cys Asn Met Val Ile Glu Ala Gly Gly Lys Asn Gly Val Val Pro Ala

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PF59082SeqList_PF59082.txt

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Phe Asp Val Ser 325 Lys Leu Glu Pro Val 330 Ala Lys Pro His Ser Pro
Asp Asn Arg Ala Leu Ala Arg Glu Cys Lys Asp Val Lys Val Asp Arg
355 360 365
Val Tyr Ile Gly Ser Cys Thr Gly Gly Lys Thr Glu Asp Phe Leu Ala
370 375 380
Ala Ala Lys Val Phe Leu Ala Ser Gly Lys Lys Val Lys Val Pro Thr
385 390 395
Phe Leu Val Pro Ala Thr Gln Lys Val Trp Met Asp Val Tyr Ser Leu
405 410 415
Pro Val Pro Gly Ser Gly Gly Lys Thr Cys Ser Gln Ile Phe Glu Gly
420 425 430
Ala Gly Cys Asp Thr Pro Ala Ser Pro Ser Cys Gly Ala Cys Leu Gly
435 440 445
Gly Pro Arg Asp Thr Tyr Ala Arg Met Asn Glu Pro Met Val Cys Val
450 455 460
Ser Thr Thr Asn Arg Asn Phe Pro Gly Arg Met Gly His Lys Glu Gly
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Gln Ile Tyr Leu Ala Ser Pro Tyr Thr Ala Ala Ala Ser Ala Leu Thr
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Gly Tyr Val Thr Asp Pro Arg Asp Phe Leu Met
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 <222> (36)..(1544)

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                               1          5
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Ser Pro Ser Phe Thr Ser Phe Pro Arg Ile Lys Lys Asp Val Ser Leu
10 15 20
tct gct ttc act tct cag cga tgc ttc aaa gcg ctt cca agg aga ata      149
Ser Ala Phe Thr Ser Gln Arg Cys Phe Lys Ala Leu Pro Arg Arg Ile
25 30 35
atc cgt tgt gct gtg gcg gcg cct cag cgc caa cct tcc acc act gga      197
Ile Arg Cys Ala Val Ala Ala Pro Gln Arg Gln Pro Ser Thr Thr Gly
40 45 50
tca gtg agg act gca atg acc atg act gag aag ata ctg gcc aga gct      245
Ser Val Arg Thr Ala Met Thr Met Thr Glu Lys Ile Leu Ala Arg Ala
55 60 65 70
tct gag aag gta cag ctg acc cct ggc gat aat gtt tgg gtc aat gtt      293
Ser Glu Lys Val Gln Leu Thr Pro Gly Asp Asn Val Trp Val Asn Val
75 80 85
gat att ttg atg aca cat gat gtg tgt ggc cct ggt tct att ggg att      341
Asp Ile Leu Met Thr His Asp Val Cys Gly Pro Gly Ser Ile Gly Ile
90 95 100
ttc aag agg gag ttt ggt gac gat gcc aag gtt tgg gac cgt gaa aag      389
Phe Lys Arg Glu Phe Gly Asp Asp Ala Lys Val Trp Asp Arg Glu Lys
105 110 115
ctt gta ata ata ccc gac cat tat ata ttc aca agt gat gaa cgt gcc      437
Leu Val Ile Ile Pro Asp His Tyr Ile Phe Thr Ser Asp Glu Arg Ala
120 125 130
aat cgc aat gta gac ata tta aga gat ttc tgc cat gag cag aat atc      485
Asn Arg Asn Val Asp Ile Leu Arg Asp Phe Cys His Glu Gln Asn Ile
135 140 145 150
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Asp	Tyr	Lys	Gly	Val	Cys	His	Val	Ala	Leu	Ala	Gln	Glu	Gly	His	Cys	
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agg	cct	gga	gag	ggt	ctc	tta	ggt	act	gat	tct	cac	act	tgt	act	gct	629
Arg	Pro	Gly	Glu	Val	Leu	Leu	Gly	Thr	Asp	Ser	His	Thr	Cys	Thr	Ala	
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Gly	Ala	Phe	Gly	Gln	Phe	Ala	Thr	Gly	Ile	Gly	Asn	Thr	Asp	Ala	Gly	
	200					205					210					
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Phe	Val	Leu	Gly	Thr	Gly	Lys	Leu	Leu	Leu	Lys	Val	Pro	Pro	Thr	Leu	
215					220					225					230	
aga	ttt	gta	atg	gat	gga	gaa	atg	cct	gat	tat	ttg	ctt	tct	aag	gat	773
Arg	Phe	Val	Met	Asp	Gly	Glu	Met	Pro	Asp	Tyr	Leu	Leu	Ser	Lys	Asp	
				235					240					245		
ttg	att	ctg	caa	att	att	ggt	gaa	ata	act	gtg	gct	ggt	gca	aca	tat	821
Leu	Ile	Leu	Gln	Ile	Ile	Gly	Glu	Ile	Thr	Val	Ala	Gly	Ala	Thr	Tyr	
			250					255					260			
aaa	tcg	atg	gag	ttt	gtc	ggt	aca	act	ggt	gaa	agt	tta	act	atg	gaa	869
Lys	Ser	Met	Glu	Phe	Val	Gly	Thr	Thr	Val	Glu	Ser	Leu	Thr	Met	Glu	
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gaa	cgg	atg	aca	ttg	tgc	aac	atg	ggt	ggt	gaa	gct	ggt	gga	aag	aat	917
Glu	Arg	Met	Thr	Leu	Cys	Asn	Met	Val	Val	Glu	Gly	Gly	Gly	Lys	Asn	
	280					285					290					
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Gly	Val	Val	Pro	Ala	Asp	Ser	Thr	Thr	Phe	Lys	Tyr	Leu	Glu	Gly	Lys	
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Thr	Ser	Leu	Pro	Tyr	Glu	Pro	Val	Tyr	Ser	Asp	Asp	Gln	Ala	Arg	Phe	
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ctt	gct	gag	tat	aga	ttt	gat	gtc	tca	aaa	ttg	gag	cca	gtg	gtg	gcc	1061
Leu	Ala	Glu	Tyr	Arg	Phe	Asp	Val	Ser	Lys	Leu	Glu	Pro	Val	Val	Ala	
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aag	cct	cat	tct	cca	gat	aat	cgt	gct	ttg	gca	agg	gag	tgc	aag	gat	1109
Lys	Pro	His	Ser	Pro	Asp	Asn	Arg	Ala	Leu	Ala	Arg	Glu	Cys	Lys	Asp	
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Val	Lys	Ile	Asp	Arg	Val	Tyr	Ile	Gly	Ser	Cys	Thr	Gly	Gly	Lys	Thr	
	360					365					370					
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Glu	Asp	Phe	Met	Ala	Ala	Ala	Lys	Val	Phe	Leu	Ala	Ser	Gly	Lys	Gln	
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gtc	aaa	ggt	cct	aca	ttt	ctt	gtg	cct	gca	aca	caa	aag	ggt	tgg	atg	1253
Val	Lys	Val	Pro	Thr	Phe	Leu	Val	Pro	Ala	Thr	Gln	Lys	Val	Trp	Met	
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gac	tta	tac	tcc	ctt	cca	gtc	cct	gga	tct	ggt	ggt	aag	acg	tgc	tcc	1301
Asp	Leu	Tyr	Ser	Leu	Pro	Val	Pro	Gly	Ser	Gly	Gly	Lys	Thr	Cys	Ser	
			410					415					420			
cag	ata	ttt	gaa	gaa	gct	ggg	tgt	gac	aca	cca	gct	agt	cct	agt	tgc	1349
Gln	Ile	Phe	Glu	Glu	Ala	Gly	Cys	Asp	Thr	Pro	Ala	Ser	Pro	Ser	Cys	
		425					430					435				
ggt	gct	tgt	ttg	ggt	ggc	ccg	aaa	gat	act	tac	gca	cgc	atg	aat	gaa	1397
Gly	Ala	Cys	Leu	Gly	Gly	Pro	Lys	Asp	Thr	Tyr	Ala	Arg	Met	Asn	Glu	
	440					445					450					
cct	aag	ggt	tgt	ggt	tca	act	acg	aac	agg	aac	ttc	ccg	ggc	cga	atg	1445
Pro	Lys	Val	Cys	Val	Ser	Thr	Thr	Asn	Arg	Asn	Phe	Pro	Gly	Arg	Met	
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gga	cac	aag	gaa	ggt	caa	atc	tat	ttg	gct	tcc	cca	tat	aca	gct	gct	1493
Gly	His	Lys	Glu	Gly	Gln	Ile	Tyr	Leu	Ala	Ser	Pro	Tyr	Thr	Ala	Ala	
				475					480					485		
gca	tct	gca	ttg	acc	ggt	tat	ggt	act	gat	cct	aaa	gag	ttc	ttg	cag	1541
Ala	Ser	Ala	Leu	Thr	Gly	Tyr	Val	Thr	Asp	Pro	Lys	Glu	Phe	Leu	Gln	
			490					495						500		
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tctagccata agttaaaact gatagctatt taagccgacc aatcttttgg tattttttgt 1661
 Seite 1167

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 35 40 45
 Gln Pro Ser Thr Thr Gly Ser Val Arg Thr Ala Met Thr Met Thr Glu
 50 55 60
 Lys Ile Leu Ala Arg Ala Ser Glu Lys Val Gln Leu Thr Pro Gly Asp
 65 70 75 80
 Asn Val Trp Val Asn Val Asp Ile Leu Met Thr His Asp Val Cys Gly
 85 90 95
 Pro Gly Ser Ile Gly Ile Phe Lys Arg Glu Phe Gly Asp Asp Ala Lys
 100 105 110
 Val Trp Asp Arg Glu Lys Leu Val Ile Ile Pro Asp His Tyr Ile Phe
 115 120 125
 Thr Ser Asp Glu Arg Ala Asn Arg Asn Val Asp Ile Leu Arg Asp Phe
 130 135 140
 Cys His Glu Gln Asn Ile Lys Tyr Phe Tyr Asp Ile Lys Asp Leu Ser
 145 150 155 160
 Asn Phe Lys Val Asn Pro Asp Tyr Lys Gly Val Cys His Val Ala Leu
 165 170 175
 Ala Gln Glu Gly His Cys Arg Pro Gly Glu Val Leu Leu Gly Thr Asp
 180 185 190
 Ser His Thr Cys Thr Ala Gly Ala Phe Gly Gln Phe Ala Thr Gly Ile
 195 200 205
 Gly Asn Thr Asp Ala Gly Phe Val Leu Gly Thr Gly Lys Leu Leu Leu
 210 215 220
 Lys Val Pro Pro Thr Leu Arg Phe Val Met Asp Gly Glu Met Pro Asp
 225 230 235 240
 Tyr Leu Leu Ser Lys Asp Leu Ile Leu Gln Ile Ile Gly Glu Ile Thr
 245 250 255
 Val Ala Gly Ala Thr Tyr Lys Ser Met Glu Phe Val Gly Thr Thr Val
 260 265 270
 Glu Ser Leu Thr Met Glu Glu Arg Met Thr Leu Cys Asn Met Val Val
 275 280 285
 Glu Ala Gly Gly Lys Asn Gly Val Val Pro Ala Asp Ser Thr Thr Phe
 290 295 300
 Lys Tyr Leu Glu Gly Lys Thr Ser Leu Pro Tyr Glu Pro Val Tyr Ser
 305 310 315 320
 Asp Asp Gln Ala Arg Phe Leu Ala Glu Tyr Arg Phe Asp Val Ser Lys
 325 330 335
 Leu Glu Pro Val Val Ala Lys Pro His Ser Pro Asp Asn Arg Ala Leu
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 Ala Arg Glu Cys Lys Asp Val Lys Ile Asp Arg Val Tyr Ile Gly Ser
 355 360 365
 Cys Thr Gly Gly Lys Thr Glu Asp Phe Met Ala Ala Lys Val Phe
 370 375 380

PF59082SeqList_PF59082.txt

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 420 425 430
 Pro Ala Ser Pro Ser Cys Gly Ala Cys Leu Gly Gly Pro Lys Asp Thr
 435 440 445
 Tyr Ala Arg Met Asn Glu Pro Lys Val Cys Val Ser Thr Thr Asn Arg
 450 455 460
 Asn Phe Pro Gly Arg Met Gly His Lys Glu Gly Gln Ile Tyr Leu Ala
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 Pro Lys Glu Phe Leu Gln
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 gggaaggcct cagcgtgctc gctcacctcc tctgtcgctt gacctacccc cctccgcccc 240

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 Arg Arg Thr Lys Pro Cys Arg Val Arg Ala Val Ala Ser Pro Ala Arg
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 Thr Pro Arg Ala Pro Ser Ser Thr Gly Ser Val Lys Thr Ala Met Thr
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 Pro Gly Glu Asn Val Trp Val Asp Ile Asp Val Leu Met Thr His Asp
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 Asp Ala Lys Val Trp Asp Arg Glu Lys Val Val Ile Ile Pro Asp His
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 130 135 140

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Asp	Leu	Ser	Asp	Phe	Arg	Ala	Asn	Pro	Asp	Tyr	Lys	Gly	Val	Cys	His	
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Ile	Ala	Leu	Ala	Gln	Glu	Gly	His	Cys	Arg	Pro	Gly	Glu	Val	Leu	Leu	
			180					185					190			
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Gly	Thr	Asp	Ser	His	Thr	Cys	Asn	Ala	Gly	Ala	Phe	Gly	Gln	Phe	Ala	
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Thr	Gly	Ile	Gly	Asn	Thr	Asp	Ala	Gly	Phe	Val	Met	Gly	Thr	Gly	Lys	
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Ala	Leu	Leu	Lys	Val	Pro	Pro	Thr	Ile	Arg	Phe	Val	Leu	Asp	Gly	Glu	
225					230					235					240	
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Met	Pro	Pro	Tyr	Leu	Ala	Lys	Asp	Leu	Ile	Leu	Gln	Ile	Ile	Ile	Gly	
				245				250						255		
gag	att	tca	gta	tct	ggt	gca	acc	tac	aaa	tcg	atg	gag	ttt	ggt	gga	1113
Glu	Ile	Ser	Val	Ser	Gly	Ala	Thr	Tyr	Lys	Ser	Met	Glu	Phe	Val	Gly	
			260					265					270			
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Ser	Thr	Val	Glu	Ser	Leu	Thr	Met	Glu	Glu	Arg	Met	Thr	Leu	Cys	Asn	
		275					280					285				
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Met	Val	Val	Glu	Ala	Gly	Gly	Lys	Asn	Gly	Val	Val	Pro	Ala	Asp	Glu	
	290				295					300						
act	aca	ttt	aaa	tac	ctt	gag	ggt	agg	aca	tca	gtt	gat	tat	caa	cct	1257
Thr	Thr	Phe	Lys	Tyr	Leu	Glu	Gly	Arg	Thr	Ser	Val	Asp	Tyr	Gln	Pro	
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Val	Ser	Lys	Leu	Glu	Pro	Val	Val	Ala	Lys	Pro	His	Ser	Pro	Asp	Asn	
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Arg	Ala	Leu	Ala	Arg	Glu	Cys	Lys	Asp	Val	Lys	Ile	Asp	Arg	Val	Tyr	
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Ile	Gly	Ser	Cys	Thr	Gly	Gly	Lys	Thr	Glu	Asp	Phe	Leu	Ala	Ala	Ala	
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Lys	Val	Phe	Leu	Ala	Ser	Gly	Lys	Lys	Val	Lys	Val	Pro	Thr	Phe	Leu	
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Pro	Gly	Ser	Gly	Gly	Lys	Thr	Cys	Ala	Gln	Ile	Phe	Glu	Glu	Ala	Gly	
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Cys	Asp	Thr	Pro	Ala	Ser	Pro	Asn	Cys	Gly	Ala	Cys	Leu	Gly	Gly	Pro	
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Arg	Asp	Thr	Tyr	Ala	Arg	Met	Asn	Glu	Pro	Thr	Val	Cys	Val	Ser	Thr	
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Thr	Asn	Arg	Asn	Phe	Pro	Gly	Arg	Met	Gly	His	Lys	Glu	Gly	Gln	Ile	
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Tyr	Leu	Ala	Ser	Pro	Tyr	Thr	Ala	Ala	Ala	Ser	Ala	Leu	Thr	Gly	Tyr	
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Val	Thr	Asp	Pro	Arg	Asp	Phe	Leu	Met								
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PF59082SeqList_PF59082.txt

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 Met Thr Glu Lys Ile Leu Ala Arg Ala Ser Glu Arg Ala Ala Leu Glu
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 Val Cys Gly Pro Gly Thr Ile Gly Ile Phe Lys Lys Glu Phe Gly Glu
 100 105 110
 Asp Ala Lys Val Trp Asp Arg Glu Lys Val Val Ile Ile Pro Asp His
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 Tyr Ile Phe Thr Ser Asp Glu Arg Ala Asn Arg Asn Val Asp Ile Leu
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 Arg Asp Phe Cys Leu Glu Gln Asn Ile Lys Tyr Phe Tyr Asp Ile Lys
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 Asp Leu Ser Asp Phe Arg Ala Asn Pro Asp Tyr Lys Gly Val Cys His
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 Ile Ala Leu Ala Gln Glu Gly His Cys Arg Pro Gly Glu Val Leu Leu
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 Gly Thr Asp Ser His Thr Cys Asn Ala Gly Ala Phe Gly Gln Phe Ala
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 Thr Gly Ile Gly Asn Thr Asp Ala Gly Phe Val Met Gly Thr Gly Lys
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 Ala Leu Leu Lys Val Pro Thr Ile Arg Phe Val Leu Asp Gly Glu
 225 230 235 240
 Met Pro Pro Tyr Leu Leu Ala Lys Asp Leu Ile Leu Gln Ile Ile Gly
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 Glu Ile Ser Val Ser Gly Ala Thr Tyr Lys Ser Met Glu Phe Val Gly
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PF59082SeqList_PF59082.txt

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 Thr Asn Arg Asn Phe Pro Gly Arg Met Gly His Lys Glu Gly Gln Ile
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 Thr Arg Arg Thr Lys Pro Cys Ser Val Arg Ala Val Ala Ser Pro Ala
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cgc gcc ctg tgc tcc acc ggc tgc gtg aag agc gcg atg acg atg acg 310
 Arg Ala Leu Ser Ser Thr Gly Ser Val Lys Ser Ala Met Thr Met Thr
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 Glu Lys Ile Leu Ala Arg Ala Ser Glu Arg Ala Ala Leu Glu Pro Gly
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 Glu Asn Val Trp Val Asp Val Asp Val Leu Met Thr His Asp Val Cys
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 115 120 125

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PF59082SeqList_PF59082.txt

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	Asp	Ser	His	Thr	Cys	Asn	Ala	Gly	Ala	Phe	Gly	Gln	Phe	Ala	Thr	Gly	
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	Ile	Gly	Asn	Thr	Asp	Ala	Gly	Phe	Val	Leu	Gly	Thr	Gly	Lys	Ala	Leu	
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	Leu	Lys	Val	Pro	Pro	Thr	Ile	Arg	Phe	Ile	Leu	Asp	Gly	Glu	Met	Pro	
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	Pro	Tyr	Leu	Leu	Ala	Lys	Asp	Leu	Ile	Leu	Gln	Ile	Ile	Gly	Glu	Ile	
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	Ser	Asp	Ala	Gln	Ala	Arg	Phe	Phe	Ser	Asp	Tyr	Arg	Phe	Asp	Val	Ser	
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	Phe	Leu	Ala	Ser	Gly	Lys	Lys	Val	Lys	Val	Pro	Thr	Phe	Leu	Val	Pro	
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	Ala	Thr	Gln	Lys	Val	Trp	Leu	Asp	Ile	Tyr	Ser	Leu	Pro	Val	Pro	Gly	
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	Arg	Asn	Phe	Pro	Gly	Arg	Met	Gly	His	Lys	Glu	Gly	Gln	Ile	Tyr	Leu	
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PF59082SeqList_PF59082.txt

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Gly Glu Asn Val Trp Val Asp Val Asp Val Leu Met Thr His Asp Val
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PF59082SeqList_PF59082.txt

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 Asn Arg Asn Phe Pro Gly Arg Met Gly His Lys Glu Gly Gln Ile Tyr
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PF59082SeqList_PF59082.txt

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Phe	Lys	Tyr	Leu	Glu	Gly	Arg	Thr	Val	Val	Asp	Tyr	Gln	Pro	Val	Tyr	
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agt	gat	gct	gag	gcc	aga	ttt	ttt	agt	gac	tac	cgg	ttt	gat	gta	tcg	1124
Ser	Asp	Ala	Glu	Ala	Arg	Phe	Phe	Ser	Asp	Tyr	Arg	Phe	Asp	Val	Ser	
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Lys	Leu	Glu	Pro	Val	Val	Ala	Lys	Pro	His	Ser	Pro	Asp	Asn	Arg	Ala	
						345					350					
cta	gca	aga	gaa	tgc	aaa	gat	gtc	aag	atc	gac	cga	gtc	tat	att	ggc	1220
Leu	Ala	Arg	Glu	Cys	Lys	Asp	Val	Lys	Ile	Asp	Arg	Val	Tyr	Ile	Gly	
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Ser	Cys	Thr	Gly	Gly	Lys	Thr	Glu	Asp	Phe	Leu	Ala	Ala	Ala	Lys	Val	
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Phe	Leu	Ala	Ser	Gly	Lys	Lys	Val	Lys	Val	Pro	Thr	Phe	Leu	Val	Pro	
				390				395					400			
gcc	aca	caa	aag	gtg	tgg	atg	gac	gta	tat	agc	ctt	cct	gta	cca	gga	1364
Ala	Thr	Gln	Lys	Val	Trp	Met	Asp	Val	Tyr	Ser	Leu	Pro	Val	Pro	Gly	
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tct	ggc	ggc	aaa	act	tgc	gcc	cag	ata	ttc	gag	gag	gct	ggc	tgt	gat	1412
Ser	Gly	Gly	Lys	Thr	Cys	Ala	Gln	Ile	Phe	Glu	Glu	Ala	Gly	Cys	Asp	
						425					430					
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Thr	Pro	Ala	Ser	Pro	Asn	Cys	Gly	Ala	Cys	Leu	Gly	Gly	Pro	Arg	Asp	
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acg	tat	gca	cgg	atg	aat	gaa	cct	acg	gtc	tgc	gtg	tcc	acc	acg	aac	1508
Thr	Tyr	Ala	Arg	Met	Asn	Glu	Pro	Thr	Val	Cys	Val	Ser	Thr	Thr	Asn	
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agg	aac	ttc	ccg	ggc	agg	atg	ggg	cac	aag	gaa	ggg	cag	atc	tac	ctg	1556
Arg	Asn	Phe	Pro	Gly	Arg	Met	Gly	His	Lys	Glu	Gly	Gln	Ile	Tyr	Leu	
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Ala	Ser	Pro	Tyr	Thr	Ala	Ala	Ala	Ser	Ala	Leu	Thr	Gly	Tyr	Val	Thr	
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gac	ccc	agg	gac	ttc	ctc	atg	tgaaacgatc	ttgaaacagc	cacagagtgc							1655
Asp	Pro	Arg	Asp	Phe	Leu	Met										
				500		505										
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aactcccatg	tcgggaggct	gccattgcc	tttatgtttt	ttgcgttata	tttattacag											1775
tgactgccga	taacgtagtt	gagcggtaca	agggaaatac	attcattctt	cccagtatcg											1835

PF59082SeqList_PF59082.txt

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 cttgttttgc 1965

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 <212> PRT
 <213> Zea mays subsp. mays

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 35 40 45
 Thr Pro Arg Ala Pro Ser Ser Thr Gly Ser Val Lys Thr Ala Met Thr
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 Met Thr Glu Lys Ile Leu Ala Arg Ala Ser Glu Arg Ala Ala Leu Glu
 65 70 75 80
 Pro Gly Glu Asn Val Trp Val Asp Ile Asp Val Leu Met Thr His Asp
 85 90 95
 Val Cys Gly Pro Gly Thr Ile Gly Ile Phe Lys Lys Glu Phe Gly Glu
 100 105 110
 Asp Ala Lys Val Trp Asp Arg Glu Lys Val Val Ile Ile Pro Asp His
 115 120 125
 Tyr Ile Phe Thr Ser Asp Glu Arg Ala Asn Arg Asn Val Asp Ile Leu
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 Arg Asp Phe Cys Leu Glu Gln Asn Ile Lys Tyr Phe Tyr Asp Ile Lys
 145 150 155 160
 Asp Leu Ser Asp Phe Arg Ala Asn Pro Asp Tyr Lys Gly Val Cys His
 165 170 175
 Ile Ala Leu Ala Gln Glu Gly His Cys Arg Pro Gly Glu Val Leu Leu
 180 185 190
 Gly Thr Asp Ser His Thr Cys Asn Ala Gly Ala Phe Gly Gln Phe Ala
 195 200 205
 Thr Gly Ile Gly Asn Thr Asp Ala Gly Phe Val Met Gly Thr Gly Lys
 210 215 220
 Ala Leu Leu Lys Val Pro Pro Thr Ile Arg Phe Val Leu Asp Gly Glu
 225 230 235 240
 Met Pro Pro Tyr Leu Ala Lys Asp Leu Ile Leu Gln Ile Ile Gly
 245 250 255
 Glu Ile Ser Val Ser Gly Ala Thr Tyr Lys Ser Met Glu Phe Val Gly
 260 265 270
 Ser Thr Val Glu Ser Leu Thr Met Glu Glu Arg Met Thr Leu Cys Asn
 275 280 285
 Met Val Val Glu Ala Gly Gly Lys Asn Gly Val Val Pro Ala Asp Glu
 290 295 300
 Thr Thr Phe Lys Tyr Leu Glu Gly Arg Thr Ser Val Asp Tyr Gln Pro
 305 310 315 320
 Val Tyr Ser Asp Ala Glu Ala Arg Phe Phe Ser Asp Tyr Arg Phe Asp
 325 330 335
 Val Ser Lys Leu Glu Pro Val Val Ala Lys Pro His Ser Pro Asp Asn
 340 345 350
 Arg Ala Leu Ala Arg Glu Cys Lys Asp Val Lys Ile Asp Arg Val Tyr
 355 360 365
 Ile Gly Ser Cys Thr Gly Gly Lys Thr Glu Asp Phe Leu Ala Ala Ala
 370 375 380
 Lys Val Phe Leu Ala Ser Gly Lys Lys Val Lys Val Pro Thr Phe Leu
 385 390 395 400
 Val Pro Ala Thr Gln Lys Val Trp Met Asp Val Tyr Ser Leu Pro Val

PF59082SeqList_PF59082.txt

405 410 415
 Pro Gly Ser Gly Gly Lys Thr Cys Ala Gln Ile Phe Glu Glu Ala Gly
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 Arg Asp Thr Tyr Ala Arg Met Asn Glu Pro Thr Val Cys Val Ser Thr
 450 455 460
 Thr Asn Arg Asn Phe Pro Gly Arg Met Gly His Lys Glu Gly Gln Ile
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 Val Thr Asp Pro Arg Asp Phe Leu Met
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<211> 1965

<212> DNA

<213> Zea mays subsp. mays

<220>

<221> CDS

<222> (297)..(1628)

<400> 937

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 ccatctccgc cgccgctaag gcctccgcgg cctttgccca aaagaaggag ctggccgcgc 180

 cggcgccgca ccgcgcgggc tcgagccgtc ggaccaagcc gtgccgcgtg cgcgccgtcg 240

 cgtcgccgc gcgcaccccc cgcgccccgt cgtccaccgg ctcggtgaag accgcg atg 299
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 acg atg acg gag aag atc ctg gcg agg gcg tcg gag cgc gcg gcg ctg 347
 Thr Met Thr Glu Lys Ile Leu Ala Arg Ala Ser Glu Arg Ala Ala Leu
 5 10 15
 gag ccc ggg gag aac gtg tgg gtg gac atc gac gtg ctc atg acg cac 395
 Glu Pro Gly Glu Asn Val Trp Val Asp Ile Asp Val Leu Met Thr His
 20 25 30
 gac gtc tgc ggg ccc ggc acc atc ggc atc ttc aag aag gag ttc ggg 443
 Asp Val Cys Gly Pro Gly Thr Ile Gly Ile Phe Lys Lys Glu Phe Gly
 35 40 45
 gag gat gcc aag gtc tgg gac cgc gag aag gtc gtc atc atc ccc gac 491
 Glu Asp Ala Lys Val Trp Asp Arg Glu Lys Val Ile Ile Pro Asp
 50 55 60 65
 cac tac atc ttc acc agc gac gag cgc gcc aac cgc aac gtc gat atc 539
 His Tyr Ile Phe Thr Ser Asp Glu Arg Ala Asn Arg Asn Val Asp Ile
 70 75 80
 ctc agg gac ttc tgt ctg gag cag aac atc aag tac ttc tat gat atc 587
 Leu Arg Asp Phe Cys Leu Glu Gln Asn Ile Lys Tyr Phe Tyr Asp Ile
 85 90 95
 aag gac ctc agc gat ttc agg gct aat cca gac tac aag ggt gtc tgc 635
 Lys Asp Leu Ser Asp Phe Arg Ala Asn Pro Asp Tyr Lys Gly Val Cys
 100 105 110
 cac att gca ctt gct cag gaa ggc cac tgc cga cca ggc gag gtt ctc 683
 His Ile Ala Leu Ala Gln Glu Gly His Cys Arg Pro Gly Glu Val Leu
 115 120 125
 ctg ggt act gat tct cat acg tgc aat gct gga gcc ttt ggt caa ttt 731
 Leu Gly Thr Asp Ser His Thr Cys Asn Ala Gly Ala Phe Gly Gln Phe
 130 135 140 145
 gca acc gga att gga aac act gat gca ggt ttt gtg atg ggc act gga 779
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PF59082SeqList_PF59082.txt

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gaa atg ccg cct tat tta ctt gcg aag gat ctg att ttg caa att att	875
Glu Met Pro Pro Tyr Leu Leu Ala Lys Asp Leu Ile Leu Gln Ile Ile	
	180
	185
	190
ggt gag att tca gta tct ggt gca acc tac aaa tcg atg gag ttt gtt	923
Gly Glu Ile Ser Val Ser Gly Ala Thr Tyr Lys Ser Met Glu Phe Val	
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Gly Ser Thr Val Glu Ser Leu Thr Met Glu Glu Arg Met Thr Leu Cys	
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Asn Met Val Val Glu Ala Gly Gly Lys Asn Gly Val Val Pro Ala Asp	
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	240
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Glu Thr Thr Phe Lys Tyr Leu Glu Gly Arg Thr Ser Val Asp Tyr Gln	
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cct gtc tac agt gat gct gag gcc aga ttt ttt agt gac tac cgg ttt	1115
Pro Val Tyr Ser Asp Ala Glu Ala Arg Phe Phe Ser Asp Tyr Arg Phe	
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gat gta tcg aaa ctg gag cca gta gtt gcc aag cca cat tcg cct gac	1163
Asp Val Ser Lys Leu Glu Pro Val Val Ala Lys Pro His Ser Pro Asp	
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aac cgt gcc cta gca aga gaa tgc aaa gat gtc aag atc gac cga gtc	1211
Asn Arg Ala Leu Ala Arg Glu Cys Lys Asp Val Lys Ile Asp Arg Val	
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Tyr Ile Gly Ser Cys Thr Gly Gly Lys Thr Glu Asp Phe Leu Ala Ala	
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	320
gca aag gtg ttc tta gcc tcg gga aag aag gtt aaa gtt ccc aca ttc	1307
Ala Lys Val Phe Leu Ala Ser Gly Lys Lys Val Lys Val Pro Thr Phe	
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	335
ctt gtc cct gcc aca caa aag gtg tgg atg gac gta tat agc ctt cct	1355
Leu Val Pro Ala Thr Gln Lys Val Trp Met Asp Val Tyr Ser Leu Pro	
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gta cca gga tct ggc ggc aaa act tgc gcc cag ata ttc gag gag gct	1403
Val Pro Gly Ser Gly Gly Lys Thr Cys Ala Gln Ile Phe Glu Glu Ala	
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	360
	365
ggt tgt gat aca cca gca agt cct aat tgc ggc gct tgt ctg ggt ggc	1451
Gly Cys Asp Thr Pro Ala Ser Pro Asn Cys Gly Ala Cys Leu Gly Gly	
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	375
	380
	385
cct cgc gat acg tat gca cgg atg aat gaa cct acg gtc tgc gtg tcc	1499
Pro Arg Asp Thr Tyr Ala Arg Met Asn Glu Pro Thr Val Cys Val Ser	
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	400
acc acg aac agg aac ttc ccg ggc agg atg ggg cac aag gaa ggg cag	1547
Thr Thr Asn Arg Asn Phe Pro Gly Arg Met Gly His Lys Glu Gly Gln	
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	410
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atc tac ctg gcg tcc ccc tac acc gct gca gcc tcg gcc ctg acg ggg	1595
Ile Tyr Leu Ala Ser Pro Tyr Thr Ala Ala Ala Ser Ala Leu Thr Gly	
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	425
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tac gtc acg gac ccc agg gac ttc ctc atg tgaaacgatc ttgaaacagc	1645
Tyr Val Thr Asp Pro Arg Asp Phe Leu Met	
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tttattacag tgactgccga taacgtagtt gagcggttaca agggaaatac attcattctt	1825
cccagtatcg atggcagtca ctagactccg ttcttacaaa aaaaaaggca tgtcgagaga	1885
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1965

<210> 938

<211> 443

<212> PRT

<213> Zea mays subsp. mays

<400> 938

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His Asp Val Cys Gly Pro Gly Thr Ile Gly Ile Phe Lys Lys Glu Phe
      35      40      45
Gly Glu Asp Ala Lys Val Trp Asp Arg Glu Lys Val Val Ile Ile Pro
      50      55      60
Asp His Tyr Ile Phe Thr Ser Asp Glu Arg Ala Asn Arg Asn Val Asp
65      70      75      80
Ile Leu Arg Asp Phe Cys Leu Glu Gln Asn Ile Lys Tyr Phe Tyr Asp
      85      90      95
Ile Lys Asp Leu Ser Asp Phe Arg Ala Asn Pro Asp Tyr Lys Gly Val
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Cys His Ile Ala Leu Ala Gln Glu Gly His Cys Arg Pro Gly Glu Val
      115      120      125
Leu Leu Gly Thr Asp Ser His Thr Cys Asn Ala Gly Ala Phe Gly Gln
      130      135      140
Phe Ala Thr Gly Ile Gly Asn Thr Asp Ala Gly Phe Val Met Gly Thr
145      150      155      160
Gly Lys Ala Leu Leu Lys Val Pro Pro Thr Ile Arg Phe Val Leu Asp
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Gly Glu Met Pro Pro Tyr Leu Leu Ala Lys Asp Leu Ile Leu Gln Ile
      180      185      190
Ile Gly Glu Ile Ser Val Ser Gly Ala Thr Tyr Lys Ser Met Glu Phe
      195      200      205
Val Gly Ser Thr Val Glu Ser Leu Thr Met Glu Glu Arg Met Thr Leu
      210      215      220
Cys Asn Met Val Val Glu Ala Gly Gly Lys Asn Gly Val Val Pro Ala
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Asp Glu Thr Thr Phe Lys Tyr Leu Glu Gly Arg Thr Ser Val Asp Tyr
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Gln Pro Val Tyr Ser Asp Ala Glu Ala Arg Phe Phe Ser Asp Tyr Arg
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Phe Asp Val Ser Lys Leu Glu Pro Val Val Ala Lys Pro His Ser Pro
      275      280      285
Asp Asn Arg Ala Leu Ala Arg Glu Cys Lys Asp Val Lys Ile Asp Arg
      290      295      300
Val Tyr Ile Gly Ser Cys Thr Gly Gly Lys Thr Glu Asp Phe Leu Ala
305      310      315      320
Ala Ala Lys Val Phe Leu Ala Ser Gly Lys Lys Val Lys Val Pro Thr
      325      330      335
Phe Leu Val Pro Ala Thr Gln Lys Val Trp Met Asp Val Tyr Ser Leu
      340      345      350
Pro Val Pro Gly Ser Gly Gly Lys Thr Cys Ala Gln Ile Phe Glu Glu
      355      360      365
Ala Gly Cys Asp Thr Pro Ala Ser Pro Asn Cys Gly Ala Cys Leu Gly
      370      375      380
Gly Pro Arg Asp Thr Tyr Ala Arg Met Asn Glu Pro Thr Val Cys Val
385      390      395      400
Ser Thr Thr Asn Arg Asn Phe Pro Gly Arg Met Gly His Lys Glu Gly
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<210> 939

<211> 1965

PF59082SeqList_PF59082.txt

<212> DNA

<213> Zea mays subsp. mays

<220>

<221> CDS

<222> (303)..(1628)

<400> 939

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cgtcgcccgc gcgcaccccc cgcgccccgt cgtccaccgg ctcggtgaag accgcgatga      300

cg atg acg gag aag atc ctg gcg agg gcg tcg gag cgc gcg gcg ctg      347
Met Thr Glu Lys Ile Leu Ala Arg Ala Ser Glu Arg Ala Ala Leu
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Glu Pro Gly Glu Asn Val Trp Val Asp Ile Asp Val Leu Met Thr His
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Asp Val Cys Gly Pro Gly Thr Ile Gly Ile Phe Lys Lys Glu Phe Gly
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Glu Asp Ala Lys Val Trp Asp Arg Glu Lys Val Val Ile Ile Pro Asp
50      55      60
cac tac atc ttc acc agc gac gag cgc gcc aac cgc aac gtc gat atc      539
His Tyr Ile Phe Thr Ser Asp Glu Arg Ala Asn Arg Asn Val Asp Ile
65      70      75
ctc agg gac ttc tgt ctg gag cag aac atc aag tac ttc tat gat atc      587
Leu Arg Asp Phe Cys Leu Glu Gln Asn Ile Lys Tyr Phe Tyr Asp Ile
80      85      90      95
aag gac ctc agc gat ttc agg gct aat cca gac tac aag ggt gtc tgc      635
Lys Asp Leu Ser Asp Phe Arg Ala Asn Pro Asp Tyr Lys Gly Val Cys
100      105      110
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His Ile Ala Leu Ala Gln Glu Gly His Cys Arg Pro Gly Glu Val Leu
115      120      125
ctg ggt act gat tct cat acg tgc aat gct gga gcc ttt ggt caa ttt      731
Leu Gly Thr Asp Ser His Thr Cys Asn Ala Gly Ala Phe Gly Gln Phe
130      135      140
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Ala Thr Gly Ile Gly Asn Thr Asp Ala Gly Phe Val Met Gly Thr Gly
145      150      155
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Lys Ala Leu Leu Lys Val Pro Pro Thr Ile Arg Phe Val Leu Asp Gly
160      165      170      175
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Glu Met Pro Pro Tyr Leu Leu Ala Lys Asp Leu Ile Leu Gln Ile Ile
180      185      190
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Gly Glu Ile Ser Val Ser Gly Ala Thr Tyr Lys Ser Met Glu Phe Val
195      200      205
gga tca act gta gaa agt cta acc atg gaa gaa cgt atg aca cta tgc      971
Gly Ser Thr Val Glu Ser Leu Thr Met Glu Glu Arg Met Thr Leu Cys
210      215      220
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Asn Met Val Val Glu Ala Gly Gly Lys Asn Gly Val Val Pro Ala Asp
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PF59082SeqList_PF59082.txt

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Asp	Val	Ser	Lys	Leu	Glu	Pro	Val	Val	Ala	Lys	Pro	His	Ser	Pro	Asp	
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Asn	Arg	Ala	Leu	Ala	Arg	Glu	Cys	Lys	Asp	Val	Lys	Ile	Asp	Arg	Val	
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Tyr	Ile	Gly	Ser	Cys	Thr	Gly	Gly	Lys	Thr	Glu	Asp	Phe	Leu	Ala	Ala	
	305				310					315						
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Ala	Lys	Val	Phe	Leu	Ala	Ser	Gly	Lys	Lys	Val	Lys	Val	Pro	Thr	Phe	
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Val	Pro	Gly	Ser	Gly	Gly	Lys	Thr	Cys	Ala	Gln	Ile	Phe	Glu	Glu	Ala	
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Pro	Arg	Asp	Thr	Tyr	Ala	Arg	Met	Asn	Glu	Pro	Thr	Val	Cys	Val	Ser	
	385				390					395						
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Thr	Thr	Asn	Arg	Asn	Phe	Pro	Gly	Arg	Met	Gly	His	Lys	Glu	Gly	Gln	
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Ile	Tyr	Leu	Ala	Ser	Pro	Tyr	Thr	Ala	Ala	Ala	Ser	Ala	Leu	Thr	Gly	
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tac	gtc	acg	gac	ccc	agg	gac	ttc	ctc	atg	tgaacg	atc	ttgaaacagc				1645
Tyr	Val	Thr	Asp	Pro	Arg	Asp	Phe	Leu	Met							
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 Val Cys Gly Pro Gly Thr Ile Gly Ile Phe Lys Lys Glu Phe Gly Glu
 35 40 45

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Asp Ala Lys Val Trp Asp Arg Glu Lys Val Val Ile Ile Pro Asp His
50 55 60
Tyr Ile Phe Thr Ser Asp Glu Arg Ala Asn Arg Asn Val Asp Ile Leu
65 70 75 80
Arg Asp Phe Cys Leu Glu Gln Asn Ile Lys Tyr Phe Tyr Asp Ile Lys
85 90 95
Asp Leu Ser Asp Phe Arg Ala Asn Pro Asp Tyr Lys Gly Val Cys His
100 105 110
Ile Ala Leu Ala Gln Glu Gly His Cys Arg Pro Gly Glu Val Leu Leu
115 120 125
Gly Thr Asp Ser His Thr Cys Asn Ala Gly Ala Phe Gly Gln Phe Ala
130 135 140
Thr Gly Ile Gly Asn Thr Asp Ala Gly Phe Val Met Gly Thr Gly Lys
145 150 155 160
Ala Leu Leu Lys Val Pro Pro Thr Ile Arg Phe Val Leu Asp Gly Glu
165 170 175
Met Pro Pro Tyr Leu Leu Ala Lys Asp Leu Ile Leu Gln Ile Ile Gly
180 185 190
Glu Ile Ser Val Ser Gly Ala Thr Tyr Lys Ser Met Glu Phe Val Gly
195 200 205
Ser Thr Val Glu Ser Leu Thr Met Glu Glu Arg Met Thr Leu Cys Asn
210 215 220
Met Val Val Glu Ala Gly Gly Lys Asn Gly Val Val Pro Ala Asp Glu
225 230 235 240
Thr Thr Phe Lys Tyr Leu Glu Gly Arg Thr Ser Val Asp Tyr Gln Pro
245 250 255
Val Tyr Ser Asp Ala Glu Ala Arg Phe Phe Ser Asp Tyr Arg Phe Asp
260 265 270
Val Ser Lys Leu Glu Pro Val Val Ala Lys Pro His Ser Pro Asp Asn
275 280 285
Arg Ala Leu Ala Arg Glu Cys Lys Asp Val Lys Ile Asp Arg Val Tyr
290 295 300
Ile Gly Ser Cys Thr Gly Gly Lys Thr Glu Asp Phe Leu Ala Ala Ala
305 310 315 320
Lys Val Phe Leu Ala Ser Gly Lys Lys Val Lys Val Pro Thr Phe Leu
325 330 335
Val Pro Ala Thr Gln Lys Val Trp Met Asp Val Tyr Ser Leu Pro Val
340 345 350
Pro Gly Ser Gly Gly Lys Thr Cys Ala Gln Ile Phe Glu Glu Ala Gly
355 360 365
Cys Asp Thr Pro Ala Ser Pro Asn Cys Gly Ala Cys Leu Gly Gly Pro
370 375 380
Arg Asp Thr Tyr Ala Arg Met Asn Glu Pro Thr Val Cys Val Ser Thr
385 390 395 400
Thr Asn Arg Asn Phe Pro Gly Arg Met Gly His Lys Glu Gly Gln Ile
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Val Thr Asp Pro Arg Asp Phe Leu Met
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Met Ala Ser Ser Leu Leu Ser Pro Ser Phe Thr Ser
1 5 10
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Phe Leu Arg Thr Lys Asp Leu Ser Leu Ser Ala Phe Thr Ser Gln Arg

110

158

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	30					35					40						
cct	cag	cg	caa	cct	tcc	acc	act	gga	tca	gtg	agg	act	gca	atg	acc		254
Pro	Gln	Arg	Gln	Pro	Ser	Thr	Thr	Gly	Ser	Val	Arg	Thr	Ala	Met	Thr		
	45				50					55					60		
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Met	Thr	Glu	Lys	Ile	Leu	Ala	Arg	Ala	Ser	Glu	Lys	Ala	Gln	Leu	Thr		
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Pro	Gly	Asp	Asn	Val	Trp	Val	Asn	Val	Asp	Ile	Leu	Met	Thr	His	Asp		
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gtg	tgt	ggc	cct	ggt	tct	att	ggg	att	ttc	aag	agg	gag	ttt	ggc	gag		398
Val	Cys	Gly	Pro	Gly	Ser	Ile	Gly	Ile	Phe	Lys	Arg	Glu	Phe	Gly	Glu		
		95					100					105					
gat	gcc	aag	gtt	tgg	gac	cgt	gaa	aag	ctt	gta	ata	ata	cct	gac	cac		446
Asp	Ala	Lys	Val	Trp	Asp	Arg	Glu	Lys	Leu	Val	Ile	Ile	Pro	Asp	His		
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tat	att	ttc	aca	agt	gat	gaa	cgt	gcc	aat	cg	aat	gta	gac	ata	tta		494
Tyr	Ile	Phe	Thr	Ser	Asp	Glu	Arg	Ala	Asn	Arg	Asn	Val	Asp	Ile	Leu		
	125				130					135					140		
aga	gat	ttc	tgc	cat	gag	cag	aat	atc	aag	tac	ttt	tat	gat	att	aag		542
Arg	Asp	Phe	Cys	His	Glu	Gln	Asn	Ile	Lys	Tyr	Phe	Tyr	Asp	Ile	Lys		
			145						150					155			
gat	ctt	agt	aat	ttt	aag	gta	aat	cca	gac	tat	aag	ggt	gtt	tgc	cat		590
Asp	Leu	Ser	Asn	Phe	Lys	Val	Asn	Pro	Asp	Tyr	Lys	Gly	Val	Cys	His		
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Val	Ala	Leu	Ala	Gln	Glu	Gly	His	Cys	Arg	Pro	Gly	Glu	Val	Leu	Leu		
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ggt	act	gat	tct	cac	act	tgt	act	gct	gga	gca	ttt	ggt	caa	ttt	gct		686
Gly	Thr	Asp	Ser	His	Thr	Cys	Thr	Ala	Gly	Ala	Phe	Gly	Gln	Phe	Ala		
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Thr	Gly	Ile	Gly	Asn	Thr	Asp	Ala	Gly	Phe	Val	Leu	Gly	Thr	Gly	Lys		
	205				210					215					220		
ctt	ctg	ctc	aag	gtg	ccc	cca	act	ttg	aga	ttt	gta	atg	gat	gga	gaa		782
Leu	Leu	Leu	Lys	Val	Pro	Pro	Thr	Leu	Arg	Phe	Val	Met	Asp	Gly	Glu		
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Met	Pro	Asp	Tyr	Leu	Leu	Ser	Lys	Asp	Leu	Ile	Leu	Gln	Ile	Ile	Gly		
		240						245				250					
gaa	ata	act	gtg	gct	ggg	gca	aca	tat	aaa	tcg	atg	gag	ttt	gtt	ggt		878
Glu	Ile	Thr	Val	Ala	Gly	Ala	Thr	Tyr	Lys	Ser	Met	Glu	Phe	Val	Gly		
		255				260						265					
aca	acc	gtt	gaa	agt	tta	act	atg	gaa	gaa	cg	atg	aca	ttg	tgc	aac		926
Thr	Thr	Val	Glu	Ser	Leu	Thr	Met	Glu	Glu	Arg	Met	Thr	Leu	Cys	Asn		
	270					275					280						
atg	gtt	gtt	gaa	gct	ggt	gga	aag	aat	ggt	gtt	cct	gct	gac	agc			974
Met	Val	Val	Glu	Ala	Gly	Gly	Lys	Asn	Gly	Val	Val	Pro	Ala	Asp	Ser		
	285				290					295				300			
act	aca	ttt	aaa	tat	ctt	gag	ggc	aag	aca	tct	ctg	cca	tat	gaa	cct		1022
Thr	Thr	Phe	Lys	Tyr	Leu	Glu	Gly	Lys	Thr	Ser	Leu	Pro	Tyr	Glu	Pro		
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Val	Tyr	Ser	Asp	Asp	Gln	Ala	Arg	Phe	Leu	Ala	Glu	Tyr	Arg	Phe	Asp		
		320						325				330					
gtc	tca	aaa	ttg	gag	cca	gtg	gtg	gcc	aag	cct	cat	tct	ccg	gat	aat		1118
Val	Ser	Lys	Leu	Glu	Pro	Val	Val	Ala	Lys	Pro	His	Ser	Pro	Asp	Asn		
		335				340						345					
cgt	gct	ttg	gca	aga	gag	tgc	aag	gat	gtg	aaa	att	gac	aga	gta	tac		1166
Arg	Ala	Leu	Ala	Arg	Glu	Cys	Lys	Asp	Val	Lys	Ile	Asp	Arg	Val	Tyr		
	350					355					360						
ata	gga	tct	tgt	aca	ggt	ggc	aaa	aca	gag	gat	ttc	atg	gct	gca	gca		1214
Ile	Gly	Ser	Cys	Thr	Gly	Gly	Lys	Thr	Glu	Asp	Phe	Met	Ala	Ala	Ala		
	365				370				375					380			
aaa	gtt	ttt	ctg	gca	tca	ggt	aaa	cag	gtc	aaa	gtt	cct	aca	ttt	ctt		1262
Lys	Val	Phe	Leu	Ala	Ser	Gly	Lys	Gln	Val	Lys	Val	Pro	Thr	Phe	Leu		

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Pro	Gly	Ser	Gly	Gly	Lys	Thr	Cys	Ser	Gln	Ile	Phe	Glu	Glu	Val	Gly	
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Cys	Asp	Thr	Pro	Ala	Ser	Pro	Ser	Cys	Gly	Ala	Cys	Leu	Gly	Gly	Pro	
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aaa	gat	act	tac	gca	cgc	atg	aat	gaa	cct	aag	gtt	tgt	gtt	tca	act	1454
Lys	Asp	Thr	Tyr	Ala	Arg	Met	Asn	Glu	Pro	Lys	Val	Cys	Val	Ser	Thr	
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Thr	Asn	Arg	Asn	Phe	Pro	Gly	Arg	Met	Gly	His	Lys	Glu	Gly	Gln	Ile	
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Tyr	Leu	Ala	Ser	Pro	Tyr	Thr	Ala	Ala	Ala	Ser	Ala	Leu	Thr	Gly	Tyr	
			480				485						490			
gtt	act	gat	cct	aga	gag	ttc	ttg	tagtagaatg	ttgttacaat	catctcattg						1604
Val	Thr	Asp	Pro	Arg	Glu	Phe	Leu									
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<400> 942

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			20					25					30			
Val	Pro	Arg	Lys	Ile	Ile	Arg	Cys	Ala	Ile	Ala	Ala	Pro	Gln	Arg	Gln	
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Pro	Ser	Thr	Thr	Gly	Ser	Val	Arg	Thr	Ala	Met	Thr	Met	Thr	Glu	Lys	
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Ile	Leu	Ala	Arg	Ala	Ser	Glu	Lys	Ala	Gln	Leu	Thr	Pro	Gly	Asp	Asn	
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Val	Trp	Val	Asn	Val	Asp	Ile	Leu	Met	Thr	His	Asp	Val	Cys	Gly	Pro	
			85						90					95		
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		100						105					110			
Trp	Asp	Arg	Glu	Lys	Leu	Val	Ile	Ile	Pro	Asp	His	Tyr	Ile	Phe	Thr	
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Ser	Asp	Glu	Arg	Ala	Asn	Arg	Asn	Val	Asp	Ile	Leu	Arg	Asp	Phe	Cys	
	130				135						140					
His	Glu	Gln	Asn	Ile	Lys	Tyr	Phe	Tyr	Asp	Ile	Lys	Asp	Leu	Ser	Asn	
145					150				155						160	
Phe	Lys	Val	Asn	Pro	Asp	Tyr	Lys	Gly	Val	Cys	His	Val	Ala	Leu	Ala	
			165					170						175		
Gln	Glu	Gly	His	Cys	Arg	Pro	Gly	Glu	Val	Leu	Leu	Gly	Thr	Asp	Ser	
		180						185					190			
His	Thr	Cys	Thr	Ala	Gly	Ala	Phe	Gly	Gln	Phe	Ala	Thr	Gly	Ile	Gly	
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Asn	Thr	Asp	Ala	Gly	Phe	Val	Leu	Gly	Thr	Gly	Lys	Leu	Leu	Leu	Lys	
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Val	Pro	Pro	Thr	Leu	Arg	Phe	Val	Met	Asp	Gly	Glu	Met	Pro	Asp	Tyr	
	225				230				235						240	
Leu	Leu	Ser	Lys	Asp	Leu	Ile	Leu	Gln	Ile	Ile	Gly	Glu	Ile	Thr	Val	
			245					250						255		
Ala	Gly	Ala	Thr	Tyr	Lys	Ser	Met	Glu	Phe	Val	Gly	Thr	Thr	Val	Glu	
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PF59082SeqList_PF59082.txt

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 Ala Gly Gly Lys Asn Gly Val Val Pro Ala Asp Ser Thr Thr Phe Lys
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 305 310 315 320
 Asp Gln Ala Arg Phe Leu Ala Glu Tyr Arg Phe Asp Val Ser Lys Leu
 325 330 335
 Glu Pro Val Val Ala Lys Pro His Ser Pro Asp Asn Arg Ala Leu Ala
 340 345 350
 Arg Glu Cys Lys Asp Val Lys Ile Asp Arg Val Tyr Ile Gly Ser Cys
 355 360 365
 Thr Gly Gly Lys Thr Glu Asp Phe Met Ala Ala Ala Lys Val Phe Leu
 370 375 380
 Ala Ser Gly Lys Gln Val Lys Val Pro Thr Phe Leu Val Pro Ala Thr
 385 390 395 400
 Gln Lys Val Trp Met Asp Leu Tyr Ser Leu Pro Val Pro Gly Ser Gly
 405 410 415
 Gly Lys Thr Cys Ser Gln Ile Phe Glu Glu Val Gly Cys Asp Thr Pro
 420 425 430
 Ala Ser Pro Ser Cys Gly Ala Cys Leu Gly Gly Pro Lys Asp Thr Tyr
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 Ala Arg Met Asn Glu Pro Lys Val Cys Val Ser Thr Thr Asn Arg Asn
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<222> (249)..(1577)

<400> 943

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ccaaggatct ctctctctct gctttcactt ctcagcgatg cttcaaagcg gtgccaagga 180

aaataatccg ttgtgctatt gcggcgccctc agcgccaacc ttccaccact ggatcagtga 240

ggactgca atg acc atg act gag aag ata ttg gcc aga gct tct gag aag 290
 Met Thr Met Thr Glu Lys Ile Leu Ala Arg Ala Ser Glu Lys
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gca cag ctg acc cct ggg gat aat gtt tgg gtc aat gtt gat att ttg 338
 Ala Gln Leu Thr Pro Gly Asp Asn Val Trp Val Asn Val Asp Ile Leu
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atg aca cat gat gtg tgt ggc cct ggt tct att ggg att ttc aag agg 386
 Met Thr His Asp Val Cys Gly Pro Gly Ser Ile Gly Ile Phe Lys Arg
 35 40 45

gag ttt ggc gag gat gcc aag gtt tgg gac cgt gaa aag ctt gta ata 434
 Glu Phe Gly Glu Asp Ala Lys Val Trp Asp Arg Glu Lys Leu Val Ile
 50 55 60

ata cct gac cac tat att ttc aca agt gat gaa cgt gcc aat cgc aat 482
 Ile Pro Asp His Tyr Ile Phe Thr Ser Asp Glu Arg Ala Asn Arg Asn
 65 70 75

gta gac ata tta aga gat ttc tgc cat gag cag aat atc aag tac ttt 530

PF59082SeqList_PF59082.txt

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Tyr	Asp	Ile	Lys	Asp	Leu	Ser	Asn	Phe	Lys	Val	Asn	Pro	Asp	Tyr	Lys	
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Gly	Val	Cys	His	Val	Ala	Leu	Ala	Gln	Glu	Gly	His	Cys	Arg	Pro	Gly	
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gag	gtt	ctc	tta	ggt	act	gat	tct	cac	act	tgt	act	gct	gga	gca	ttt	674
Glu	Val	Leu	Leu	Gly	Thr	Asp	Ser	His	Thr	Cys	Thr	Ala	Gly	Ala	Phe	
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ggt	caa	ttt	gct	aca	ggg	att	ggt	aat	act	gat	gcc	ggc	ttt	gtg	ctg	722
Gly	Gln	Phe	Ala	Thr	Gly	Ile	Gly	Asn	Thr	Asp	Ala	Gly	Phe	Val	Leu	
	145				150						155					
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Gly	Thr	Gly	Lys	Leu	Leu	Leu	Lys	Val	Pro	Pro	Thr	Leu	Arg	Phe	Val	
	160				165						170					
atg	gat	gga	gaa	atg	ccc	gat	tat	ttg	ctt	tct	aag	gat	ttg	att	ctg	818
Met	Asp	Gly	Glu	Met	Pro	Asp	Tyr	Leu	Leu	Ser	Lys	Asp	Leu	Ile	Leu	
175					180					185					190	
caa	att	att	ggt	gaa	ata	act	gtg	gct	ggg	gca	aca	tat	aaa	tcg	atg	866
Gln	Ile	Ile	Gly	Glu	Ile	Thr	Val	Ala	Gly	Ala	Thr	Tyr	Lys	Ser	Met	
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gag	ttt	gtt	ggt	aca	acc	gtt	gaa	agt	tta	act	atg	gaa	gaa	cgg	atg	914
Glu	Phe	Val	Gly	Thr	Thr	Val	Glu	Ser	Leu	Thr	Met	Glu	Glu	Arg	Met	
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Thr	Leu	Cys	Asn	Met	Val	Val	Glu	Ala	Gly	Gly	Lys	Asn	Gly	Val	Val	
		225					230					235				
cct	gct	gac	agc	act	aca	ttt	aaa	tat	ctt	gag	ggc	aag	aca	tct	ctg	1010
Pro	Ala	Asp	Ser	Thr	Thr	Phe	Lys	Tyr	Leu	Glu	Gly	Lys	Thr	Ser	Leu	
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cca	tat	gaa	cct	gtt	tat	agt	gac	gat	caa	gca	aga	ttt	ctc	gca	gag	1058
Pro	Tyr	Glu	Pro	Val	Tyr	Ser	Asp	Asp	Gln	Ala	Arg	Phe	Leu	Ala	Glu	
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tat	aga	ttt	gat	gtc	tca	aaa	ttg	gag	cca	gtg	gtg	gcc	aag	cct	cat	1106
Tyr	Arg	Phe	Asp	Val	Ser	Lys	Leu	Glu	Pro	Val	Val	Ala	Lys	Pro	His	
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tct	ccg	gat	aat	cgt	gct	ttg	gca	aga	gag	tgc	aag	gat	gtg	aaa	att	1154
Ser	Pro	Asp	Asn	Arg	Ala	Leu	Ala	Arg	Glu	Cys	Lys	Asp	Val	Lys	Ile	
				290				295					300			
gac	aga	gta	tac	ata	gga	tct	tgt	aca	ggt	ggc	aaa	aca	gag	gat	ttc	1202
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Met	Ala	Ala	Ala	Lys	Val	Phe	Leu	Ala	Ser	Gly	Lys	Gln	Val	Lys	Val	
	320					325					330					
cct	aca	ttt	ctt	gtg	cct	gca	aca	caa	aag	gtt	tgg	atg	gac	ttg	tac	1298
Pro	Thr	Phe	Leu	Val	Pro	Ala	Thr	Gln	Lys	Val	Trp	Met	Asp	Leu	Tyr	
335					340					345					350	
tcc	ctc	cct	gtc	cct	gga	tct	ggt	ggt	aag	aca	tgc	tca	cag	ata	ttt	1346
Ser	Leu	Pro	Val	Pro	Gly	Ser	Gly	Gly	Lys	Thr	Cys	Ser	Gln	Ile	Phe	
				355				360						365		
gaa	gaa	gtt	ggg	tgt	gac	aca	cca	gct	agt	cct	agt	tgt	ggt	gct	tgt	1394
Glu	Glu	Val	Gly	Cys	Asp	Thr	Pro	Ala	Ser	Pro	Ser	Cys	Gly	Ala	Cys	
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Leu	Gly	Gly	Pro	Lys	Asp	Thr	Tyr	Ala	Arg	Met	Asn	Glu	Pro	Lys	Val	
		385					390					395				
tgt	gtt	tca	act	acg	aac	agg	aac	ttc	ccg	ggc	cga	atg	gga	cac	aag	1490
Cys	Val	Ser	Thr	Thr	Asn	Arg	Asn	Phe	Pro	Gly	Arg	Met	Gly	His	Lys	
	400				405						410					
gaa	ggt	caa	atc	tat	ttg	gct	tcc	cct	tat	aca	gct	gct	gca	tct	gca	1538
Glu	Gly	Gln	Ile	Tyr	Leu	Ala	Ser	Pro	Tyr	Ala	Ala	Ala	Ala	Ser	Ala	
415					420					425					430	
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Leu	Thr	Gly	Tyr	Val	Thr	Asp	Pro	Arg	Glu	Phe	Leu					
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1683

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 35 40 45
 Gly Glu Asp Ala Lys Val Trp Asp Arg Glu Lys Leu Val Ile Ile Pro
 50 55 60
 Asp His Tyr Ile Phe Thr Ser Asp Glu Arg Ala Asn Arg Asn Val Asp
 65 70 75 80
 Ile Leu Arg Asp Phe Cys His Glu Gln Asn Ile Lys Tyr Phe Tyr Asp
 85 90 95
 Ile Lys Asp Leu Ser Asn Phe Lys Val Asn Pro Asp Tyr Lys Gly Val
 100 105 110
 Cys His Val Ala Leu Ala Gln Glu Gly His Cys Arg Pro Gly Glu Val
 115 120 125
 Leu Leu Gly Thr Asp Ser His Thr Cys Thr Ala Gly Ala Phe Gly Gln
 130 135 140
 Phe Ala Thr Gly Ile Gly Asn Thr Asp Ala Gly Phe Val Leu Gly Thr
 145 150 155 160
 Gly Lys Leu Leu Lys Val Pro Pro Thr Leu Arg Phe Val Met Asp
 165 170 175
 Gly Glu Met Pro Asp Tyr Leu Leu Ser Lys Asp Leu Ile Leu Gln Ile
 180 185 190
 Ile Gly Glu Ile Thr Val Ala Gly Ala Thr Tyr Lys Ser Met Glu Phe
 195 200 205
 Val Gly Thr Thr Val Glu Ser Leu Thr Met Glu Glu Arg Met Thr Leu
 210 215 220
 Cys Asn Met Val Val Glu Ala Gly Gly Lys Asn Gly Val Val Pro Ala
 225 230 235 240
 Asp Ser Thr Thr Phe Lys Tyr Leu Glu Gly Lys Thr Ser Leu Pro Tyr
 245 250 255
 Glu Pro Val Tyr Ser Asp Asp Gln Ala Arg Phe Leu Ala Glu Tyr Arg
 260 265 270
 Phe Asp Val Ser Lys Leu Glu Pro Val Val Ala Lys Pro His Ser Pro
 275 280 285
 Asp Asn Arg Ala Leu Ala Arg Glu Cys Lys Asp Val Lys Ile Asp Arg
 290 295 300
 Val Tyr Ile Gly Ser Cys Thr Gly Gly Lys Thr Glu Asp Phe Met Ala
 305 310 315 320
 Ala Ala Lys Val Phe Leu Ala Ser Gly Lys Gln Val Lys Val Pro Thr
 325 330 335
 Phe Leu Val Pro Ala Thr Gln Lys Val Trp Met Asp Leu Tyr Ser Leu
 340 345 350
 Pro Val Pro Gly Ser Gly Gly Lys Thr Cys Ser Gln Ile Phe Glu Glu
 355 360 365
 Val Gly Cys Asp Thr Pro Ala Ser Pro Ser Cys Gly Ala Cys Leu Gly
 370 375 380
 Gly Pro Lys Asp Thr Tyr Ala Arg Met Asn Glu Pro Lys Val Cys Val
 385 390 395 400
 Ser Thr Thr Asn Arg Asn Phe Pro Gly Arg Met Gly His Lys Glu Gly
 405 410 415
 Gln Ile Tyr Leu Ala Ser Pro Tyr Thr Ala Ala Ser Ala Leu Thr
 420 425 430
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PF59082SeqList_PF59082.txt

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ccaaggatct ctctctctct gctttcactt ctcagcgatg cttcaaagcg gtgccaagga      180

aaataatccg ttgtgctatt gcggcgccctc agcgccaacc ttccaccact ggatcagtga      240

ggactgcaat gacc atg act gag aag ata ttg gcc aga gct tct gag aag      290
                Met Thr Glu Lys Ile Leu Ala Arg Ala Ser Glu Lys
                1      5      10
gca cag ctg acc cct ggg gat aat gtt tgg gtc aat gtt gat att ttg      338
Ala Gln Leu Thr Pro Gly Asp Asn Val Trp Val Asn Val Asp Ile Leu
                15      20      25
atg aca cat gat gtg tgt ggc cct ggt tct att ggg att ttc aag agg      386
Met Thr His Asp Val Cys Gly Pro Gly Ser Ile Gly Ile Phe Lys Arg
                30      35      40
gag ttt ggc gag gat gcc aag gtt tgg gac cgt gaa aag ctt gta ata      434
Glu Phe Gly Glu Asp Ala Lys Val Trp Asp Arg Glu Lys Leu Val Ile
                45      50      55      60
ata cct gac cac tat att ttc aca agt gat gaa cgt gcc aat cgc aat      482
Ile Pro Asp His Tyr Ile Phe Thr Ser Asp Glu Arg Ala Asn Arg Asn
                65      70      75
gta gac ata tta aga gat ttc tgc cat gag cag aat atc aag tac ttt      530
Val Asp Ile Leu Arg Asp Phe Cys His Glu Gln Asn Ile Lys Tyr Phe
                80      85      90
tat gat att aag gat ctt agt aat ttt aag gta aat cca gac tat aag      578
Tyr Asp Ile Lys Asp Leu Ser Asn Phe Lys Val Asn Pro Asp Tyr Lys
                95      100      105
ggg gtt tgc cat gtt gct ctt gct cag gaa ggt cat tgt agg cca gga      626
Gly Val Cys His Val Ala Leu Ala Gln Glu Gly His Cys Arg Pro Gly
                110      115      120
gag gtt ctc tta ggt act gat tct cac act tgt act gct gga gca ttt      674
Glu Val Leu Leu Gly Thr Asp Ser His Thr Cys Thr Ala Gly Ala Phe
                125      130      135      140
ggg caa ttt gct aca ggg att ggt aat act gat gcc ggc ttt gtg ctg      722
Gly Gln Phe Ala Thr Gly Ile Gly Asn Thr Asp Ala Gly Phe Val Leu
                145      150      155
gga act ggg aaa ctt ctg ctc aag gtg ccc cca act ttg aga ttt gta      770
Gly Thr Gly Lys Leu Leu Leu Lys Val Pro Pro Thr Leu Arg Phe Val
                160      165      170
atg gat gga gaa atg ccc gat tat ttg ctt tct aag gat ttg att ctg      818
Met Asp Gly Glu Met Pro Asp Tyr Leu Leu Ser Lys Asp Leu Ile Leu
                175      180      185
caa att att ggt gaa ata act gtg gct ggg gca aca tat aaa tcg atg      866
Gln Ile Ile Gly Glu Ile Thr Val Ala Gly Ala Thr Tyr Lys Ser Met
                190      195      200
gag ttt gtt ggt aca acc gtt gaa agt tta act atg gaa gaa cgg atg      914
Glu Phe Val Gly Thr Thr Val Glu Ser Leu Thr Met Glu Glu Arg Met
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aca ttg tgc aac atg gtt gtt gaa gct ggt gga aag aat ggt gtt gtt      962
Thr Leu Cys Asn Met Val Val Glu Ala Gly Gly Lys Asn Gly Val Val
                225      230      235
cct gct gac agc act aca ttt aaa tat ctt gag ggc aag aca tct ctg      1010
Pro Ala Asp Ser Thr Thr Phe Lys Tyr Leu Glu Gly Lys Thr Ser Leu

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PF59082SeqList_PF59082.txt

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Pro	Tyr	Glu	Pro	Val	Tyr	Ser	Asp	Asp	Gln	Ala	Arg	Phe	Leu	Ala	Glu		
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tat	aga	ttt	gat	gtc	tca	aaa	ttg	gag	cca	gtg	gtg	gcc	aag	cct	cat		1106
Tyr	Arg	Phe	Asp	Val	Ser	Lys	Leu	Glu	Pro	Val	Val	Ala	Lys	Pro	His		
		270					275					280					
tct	ccg	gat	aat	cgt	gct	ttg	gca	aga	gag	tgc	aag	gat	gtg	aaa	att		1154
Ser	Pro	Asp	Asn	Arg	Ala	Leu	Ala	Arg	Glu	Cys	Lys	Asp	Val	Lys	Ile		
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gac	aga	gta	tac	ata	gga	tct	tgt	aca	ggt	ggc	aaa	aca	gag	gat	ttc		1202
Asp	Arg	Val	Tyr	Ile	Gly	Ser	Cys	Thr	Gly	Gly	Lys	Thr	Glu	Asp	Phe		
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Met	Ala	Ala	Ala	Lys	Val	Phe	Leu	Ala	Ser	Gly	Lys	Gln	Val	Lys	Val		
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cct	aca	ttt	ctt	gtg	cct	gca	aca	caa	aag	gtt	tgg	atg	gac	ttg	tac		1298
Pro	Thr	Phe	Leu	Val	Pro	Ala	Thr	Gln	Lys	Val	Trp	Met	Asp	Leu	Tyr		
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tcc	ctc	cct	gtc	cct	gga	tct	ggt	ggt	aag	aca	tgc	tca	cag	ata	ttt		1346
Ser	Leu	Pro	Val	Pro	Gly	Ser	Gly	Gly	Lys	Thr	Cys	Ser	Gln	Ile	Phe		
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Glu	Glu	Val	Gly	Cys	Asp	Thr	Pro	Ala	Ser	Pro	Ser	Cys	Gly	Ala	Cys		
365					370					375					380		
ttg	ggt	ggc	cca	aaa	gat	act	tac	gca	cgc	atg	aat	gaa	cct	aag	gtt		1442
Leu	Gly	Gly	Pro	Lys	Asp	Thr	Tyr	Ala	Arg	Met	Asn	Glu	Pro	Lys	Val		
				385					390						395		
tgt	gtt	tca	act	acg	aac	agg	aac	ttc	ccg	ggc	cga	atg	gga	cac	aag		1490
Cys	Val	Ser	Thr	Thr	Asn	Arg	Asn	Phe	Pro	Gly	Arg	Met	Gly	His	Lys		
				400				405						410			
gaa	ggt	caa	atc	tat	ttg	gct	tcc	cct	tat	aca	gct	gct	gca	tct	gca		1538
Glu	Gly	Gln	Ile	Tyr	Leu	Ala	Ser	Pro	Tyr	Thr	Ala	Ala	Ala	Ser	Ala		
		415				420					425						
ttg	acc	ggt	tat	gtt	act	gat	cct	aga	gag	ttc	ttg	tagtagaatg					1584
Leu	Thr	Gly	Tyr	Val	Thr	Asp	Pro	Arg	Glu	Phe	Leu						
		430				435					440						
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 35 40 45
 Asp Ala Lys Val Trp Asp Arg Glu Lys Leu Val Ile Ile Pro Asp His
 50 55 60
 Tyr Ile Phe Thr Ser Asp Glu Arg Ala Asn Arg Asn Val Asp Ile Leu
 65 70 75 80
 Arg Asp Phe Cys His Glu Gln Asn Ile Lys Tyr Phe Tyr Asp Ile Lys
 85 90 95
 Asp Leu Ser Asn Phe Lys Val Asn Pro Asp Tyr Lys Gly Val Cys His
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 Val Ala Leu Ala Gln Glu Gly His Cys Arg Pro Gly Glu Val Leu Leu
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 Gly Thr Asp Ser His Thr Cys Thr Ala Gly Ala Phe Gly Gln Phe Ala
 130 135 140
 Thr Gly Ile Gly Asn Thr Asp Ala Gly Phe Val Leu Gly Thr Gly Lys

PF59082SeqList_PF59082.txt

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 Glu Ile Thr Val Ala Gly Ala Thr Tyr Lys Ser Met Glu Phe Val Gly
 195 200 205
 Thr Thr Val Glu Ser Leu Thr Met Glu Glu Arg Met Thr Leu Cys Asn
 210 215 220
 Met Val Val Glu Ala Gly Lys Asn Gly Val Val Pro Ala Asp Ser
 225 230 235 240
 Thr Thr Phe Lys Tyr Leu Glu Gly Lys Thr Ser Leu Pro Tyr Glu Pro
 245 250 255
 Val Tyr Ser Asp Asp Gln Ala Arg Phe Leu Ala Glu Tyr Arg Phe Asp
 260 265 270
 Val Ser Lys Leu Glu Pro Val Val Ala Lys Pro His Ser Pro Asp Asn
 275 280 285
 Arg Ala Leu Ala Arg Glu Cys Lys Asp Val Lys Ile Asp Arg Val Tyr
 290 295 300
 Ile Gly Ser Cys Thr Gly Gly Lys Thr Glu Asp Phe Met Ala Ala Ala
 305 310 315 320
 Lys Val Phe Leu Ala Ser Gly Lys Gln Val Lys Val Pro Thr Phe Leu
 325 330 335
 Val Pro Ala Thr Gln Lys Val Trp Met Asp Leu Tyr Ser Leu Pro Val
 340 345 350
 Pro Gly Ser Gly Gly Lys Thr Cys Ser Gln Ile Phe Glu Glu Val Gly
 355 360 365
 Cys Asp Thr Pro Ala Ser Pro Ser Cys Gly Ala Cys Leu Gly Gly Pro
 370 375 380
 Lys Asp Thr Tyr Ala Arg Met Asn Glu Pro Lys Val Cys Val Ser Thr
 385 390 395 400
 Thr Asn Arg Asn Phe Pro Gly Arg Met Gly His Lys Glu Gly Gln Ile
 405 410 415
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 His Lys Val Gln Lys Glu Leu Ala Ala Pro Ala Gln Arg Arg Ala Gly 20 25 30
 ttg acc cgc cgg acc aag ccg tgc agc gtg cgc gcc gtc gct tcg ccc 144
 Leu Thr Arg Arg Thr Lys Pro Cys Ser Val Arg Ala Val Ala Ser Pro 35 40 45
 gcg cgc gcc ctg tcg tcc acc ggc tcg gtg aag agc gcg atg acg atg 192
 Ala Arg Ala Leu Ser Ser Thr Gly Ser Val Lys Ser Ala Met Thr Met 50 55 60
 acg gag aag ata ctg gcg cgg gcg tcg gag cgc gcg gcg ctg gag ccc 240
 Thr Glu Lys Ile Leu Ala Arg Ala Ser Glu Arg Ala Ala Leu Glu Pro 65 70 75 80
 ggg gag aac gtg tgg gtc gac gtc gac gtg ctc atg acg cac gac gtc 288
 Gly Glu Asn Val Trp 85 Val Asp Val Asp Val 90 Leu Met Thr His Asp Val 95
 tgc ggg ccc ggc gcc ttc gac atc ttc aag aag gag ttc ggg gag gac 336
 Cys Gly Pro Gly Ala Phe Asp Ile Phe Lys Lys Glu Phe Gly Glu Asp 100 105 110

PF59082SeqList_PF59082.txt

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atc Ile	ttc Phe 130	acc Thr	agc Ser	gac Asp	ggc Gly	cgt Arg 135	gcc Ala	aaa Lys	cgc Arg	aac Asn	gtc Val 140	gac Asp	atc Ile	ctc Leu	agg Arg	432
gac Asp 145	ttc Phe	tgt Cys	gcg Ala	gag Glu	cag Gln 150	aac Asn	atc Ile	aag Lys	tac Tyr	ttc Phe 155	tat Tyr	gac Asp	atc Ile	aag Lys	gac Asp 160	480
ctc Leu	agc Ser	gat Asp	ttc Phe	agg Arg 165	gct Ala	aat Asn	ccg Pro	gac Asp	tac Tyr 170	aaa Lys	ggc Gly	gtc Val	tgc Cys	cac His 175	atc Ile	528
gca Ala	ctt Leu	gct Ala	cag Gln 180	gaa Glu	ggc Gly	cac His	tgc Cys	cga Arg 185	cca Pro	ggc Gly	gag Glu	ggt Val	ctc Leu 190	ttg Leu	ggc Gly	576
act Thr	gat Asp	tct Ser 195	cat His	aca Thr	tgc Cys	aat Asn 200	gct Ala 205	gga Gly	gct Ala	ttt Phe	ggt Gly 205	cag Gln	ttt Phe	gca Ala	act Thr	624
gga Gly 210	atc Ile	gga Gly	aac Asn	act Thr	gat Asp	gca Ala 215	ggt Gly	ttt Phe	gtg Val	ttg Leu	ggc Gly 220	act Thr	gga Gly	aag Lys	gct Ala	672
ctt Leu 225	ctc Leu	cag Gln	gtg Val	cca Pro	cct Pro 230	act Thr	atc Ile	agg Arg	ttt Phe	ata Ile 235	tta Leu	gat Asp	gga Gly	gag Glu	atg Met 240	720
ccg Pro	cct Pro	tat Tyr	tta Leu	ctt Leu 245	gcg Ala	aag Lys	gat Asp	ctg Leu	att Ile 250	ttg Leu	caa Gln	att Ile	att Ile	gga Gly 255	gag Glu	768
att Ile	tca Ser	gta Val	tct Ser 260	ggt Gly	gcg Ala	acc Thr	tac Tyr 265	aaa Lys	tca Ser	atg Met	gag Glu	ttt Phe	ggt Val 270	gga Gly	tca Ser	816
act Thr	gta Val 275	gaa Glu	agt Ser	cta Leu	acc Thr	atg Met 280	gaa Glu 285	gag Glu	cgt Arg	atg Met	aca Thr 285	cta Leu	tgc Cys	aac Asn	atg Met	864
gtt Val	att Ile 290	gaa Glu	gct Ala	ggt Gly	gga Gly	aag Lys 295	aac Asn	ggt Gly	gtt Val	gtg Val	cct Pro 300	gct Ala	gat Asp	gaa Glu	act Thr	912
aca Thr 305	ttt Phe	aaa Lys	tac Tyr	ctt Leu	gag Glu 310	ggt Gly	aag Lys	aca Thr	tca Ser	gtc Val 315	gat Asp	tat Tyr	gaa Glu	cct Pro	gtc Val 320	960
tac Tyr	agt Ser	gat Asp	gct Ala	caa Gln 325	gcc Ala	aga Arg	ttt Phe	ttt Phe	agc Ser 330	tac Asp	cgg Tyr	ttt Arg	gat Phe 335	gat Asp 335	gta Val	1008
tca Ser	aaa Lys	ctg Leu	gag Glu 340	cca Pro	gta Val	gtt Val	gcc Ala 345	aag Lys	cca Pro	cat His	tcg Ser	cct Pro	gac Asp 350	aac Asn	cgt Arg	1056
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gtg Val 385	ttc Phe	tta Leu	gcc Ala	tcg Ser	gga Gly 390	aag Lys	aag Lys	gtt Val	aaa Lys	gtt Val 395	ccc Pro	aca Thr	ttt Phe	ctt Leu	gtc Val 400	1200
cct Pro	gcc Ala	aca Thr	caa Gln 405	aag Lys	gtg Val	tgg Trp	ttg Leu	gac Asp	ata Ile 410	tat Tyr	agc Ser	ctc Leu	cct Pro	gta Val 415	cca Pro	1248
gga Gly	tct Ser	ggt Gly 420	ggc Lys	aaa Thr	act Cys	tgc Cys	tcc Ser	cag Gln 425	ata Ile	ttt Phe	gag Glu	gag Glu	gct Ala 430	ggt Gly	tgt Cys	1296
gac Asp	aca Thr 435	cca Pro	gca Ala	agt Ser	cct Pro	aat Asn	tgt Cys 440	ggt Gly	gct Ala	tgt Cys	ttg Leu	ggt Gly 445	ggc Gly	cct Pro	cgt Arg	1344
gat Asp	aca Thr 450	tat Tyr	gca Ala	cgg Arg	atg Met	aat Asn 455	gaa Glu	cct Pro	act Thr	gtc Val	tgc Cys 460	gtg Val	tcc Ser	acc Thr	acg Thr	1392
aac Asn 465	agg Arg	aac Asn	ttt Phe	ccg Pro	ggc Gly 470	agg Arg	atg Met	ggc Gly	cac His	aag Lys 475	gaa Glu	ggg Gly	caa Gln	atc Ile	tac Tyr 480	1440

PF59082SeqList_PF59082.txt

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35 40 45
Ala Arg Ala Leu Ser Ser Thr Gly Ser Val Lys Ser Ala Met Thr Met
50 55 60
Thr Glu Lys Ile Leu Ala Arg Ala Ser Glu Arg Ala Ala Leu Glu Pro
65 70 75 80
Gly Glu Asn Val Trp Val Asp Val Asp Val Leu Met Thr His Asp Val
85 90 95
Cys Gly Pro Gly Ala Phe Asp Ile Phe Lys Lys Glu Phe Gly Glu Asp
100 105 110
Ala Arg Val Trp Asp Arg Glu Lys Leu Val Val Ile Pro Asp His Tyr
115 120 125
Ile Phe Thr Ser Asp Gly Arg Ala Lys Arg Asn Val Asp Ile Leu Arg
130 135 140
Asp Phe Cys Ala Glu Gln Asn Ile Lys Tyr Phe Tyr Asp Ile Lys Asp
145 150 155 160
Leu Ser Asp Phe Arg Ala Asn Pro Asp Tyr Lys Gly Val Cys His Ile
165 170 175
Ala Leu Ala Gln Glu Gly His Cys Arg Pro Gly Glu Val Leu Leu Gly
180 185 190
Thr Asp Ser His Thr Cys Asn Ala Gly Ala Phe Gly Gln Phe Ala Thr
195 200 205
Gly Ile Gly Asn Thr Asp Ala Gly Phe Val Leu Gly Thr Gly Lys Ala
210 215 220
Leu Leu Gln Val Pro Pro Thr Ile Arg Phe Ile Leu Asp Gly Glu Met
225 230 235 240
Pro Pro Tyr Leu Leu Ala Lys Asp Leu Ile Leu Gln Ile Ile Gly Glu
245 250 255
Ile Ser Val Ser Gly Ala Thr Tyr Lys Ser Met Glu Phe Val Gly Ser
260 265 270
Thr Val Glu Ser Leu Thr Met Glu Glu Arg Met Thr Leu Cys Asn Met
275 280 285
Val Ile Glu Ala Gly Gly Lys Asn Gly Val Val Pro Ala Asp Glu Thr
290 295 300
Thr Phe Lys Tyr Leu Glu Gly Lys Thr Ser Val Asp Tyr Glu Pro Val
305 310 315 320
Tyr Ser Asp Ala Gln Ala Arg Phe Phe Ser Asp Tyr Arg Phe Asp Val
325 330 335
Ser Lys Leu Glu Pro Val Val Ala Lys Pro His Ser Pro Asp Asn Arg
340 345 350
Ala Pro Ala Arg Glu Cys Lys Asp Val Lys Ile Asp Arg Val Tyr Ile
355 360 365
Gly Ser Cys Thr Gly Gly Lys Thr Glu Asp Phe Leu Ala Ala Lys
370 375 380
Val Phe Leu Ala Ser Gly Lys Lys Val Lys Val Pro Thr Phe Leu Val
385 390 395 400
Pro Ala Thr Gln Lys Val Trp Leu Asp Ile Tyr Ser Leu Pro Val Pro
405 410 415
Gly Ser Gly Gly Lys Thr Cys Ser Gln Ile Phe Glu Glu Ala Gly Cys
420 425 430
Asp Thr Pro Ala Ser Pro Asn Cys Gly Ala Cys Leu Gly Gly Pro Arg
435 440 445

PF59082SeqList_PF59082.txt

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 Asn Arg Asn Phe Pro Gly Arg Met Gly His Lys Glu Gly Gln Ile Tyr
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 485 490 495
 Thr Asp Pro Arg Asp Phe Leu Met
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 <222> (1673)..(1673)
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 cgttcgcgca caaggtccag aaggagctgg ccgcgccggc gcagcgccgc gcgggcttga 180

 cccgccggac caagccgtgc agcgtgcgcg ccgtcgcttc gcccgcgcg cccctgtcgt 240

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 Met Thr Met Thr Glu Lys Ile Leu Ala Arg
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 gcg tcg gag cgc gcg gcg ctg gag ccc ggg gag aac gtg tgg gtc gac 341
 Ala Ser Glu Arg Ala Ala Leu Glu Pro Gly Glu Asn Val Trp Val Asp
 15 20 25
 gtc gac gtg ctc atg acg cac gac gtc tgc ggg ccc ggc gcc ttc gac 389
 Val Asp Val Leu Met Thr His Asp Val Cys Gly Pro Gly Ala Phe Asp
 30 35 40
 atc ttc aag aag gag ttc ggg gag gac gcc agg gtc tgg gac cgc gag 437
 Ile Phe Lys Lys Glu Phe Gly Glu Asp Ala Arg Val Trp Asp Arg Glu
 45 50 55
 aag ctc gtc gtc atc ccg gac cac tac atc ttc acc agc gac ggc cgt 485
 Lys Leu Val Val Ile Pro Asp His Tyr Ile Phe Thr Ser Asp Gly Arg
 60 65 70
 gcc aaa cgc aac gtc gac atc ctc agg gac ttc tgt gcg gag cag aac 533
 Ala Lys Arg Asn Val Asp Ile Leu Arg Asp Phe Cys Ala Glu Gln Asn
 75 80 85 90
 atc aag tac ttc tat gac atc aag gac ctc agc gat ttc agg gct aat 581
 Ile Lys Tyr Phe Tyr Asp Ile Lys Asp Leu Ser Asp Phe Arg Ala Asn
 95 100 105
 ccg gac tac aaa ggc gtc tgc cac atc gca ctt gct cag gaa gcc cac 629
 Pro Asp Tyr Lys Gly Val Cys His Ile Ala Leu Ala Gln Glu Ala His
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 Cys Arg Pro Gly Glu Val Leu Leu Gly Thr Asp Ser His Thr Cys Asn
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 Ala Gly Ala Phe Gly Gln Phe Ala Thr Gly Ile Gly Asn Thr Asp Ala
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 Gly Phe Val Leu Gly Thr Gly Lys Ala Leu Leu Lys Val Pro Pro Thr
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Lys	Thr	Ser	Val	Asp	Tyr	Glu	Pro	Val	Tyr	Ser	Asp	Ala	Gln	Ala	Arg	
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Ser	Gln	Ile	Phe	Glu	Glu	Ala	Gly	Cys	Asp	Thr	Pro	Ala	Ser	Pro	Asn	
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Cys	Gly	Ala	Cys	Leu	Gly	Gly	Pro	Arg	Asp	Thr	Tyr	Ala	Arg	Met	Asn	
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Ala	Ala	Ser	Ala	Leu	Thr	Gly	Tyr	Val	Thr	Asp	Pro	Lys	Asp	Phe	Leu	
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PF59082SeqList_PF59082.txt

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 85 90 95
 Ile Lys Asp Leu Ser Asp Phe Arg Ala Asn Pro Asp Tyr Lys Gly Val
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 Cys His Ile Ala Leu Ala Gln Glu Ala His Cys Arg Pro Gly Glu Val
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 Leu Leu Gly Thr Asp Ser His Thr Cys Asn Ala Gly Ala Phe Gly Gln
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 Phe Ala Thr Gly Ile Gly Asn Thr Asp Ala Gly Phe Val Leu Gly Thr
 145 150 155 160
 Gly Lys Ala Leu Leu Lys Val Pro Pro Thr Ile Arg Phe Ile Leu Asp
 165 170 175
 Gly Glu Met Pro Pro Tyr Leu Leu Ala Lys Asp Leu Ile Leu Gln Ile
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 Ile Gly Glu Ile Ser Val Ser Gly Ala Thr Tyr Lys Ser Met Glu Phe
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 245 250 255
 Glu Pro Val Tyr Ser Asp Ala Gln Ala Arg Phe Phe Ser Asp Tyr Arg
 260 265 270
 Phe Asp Val Ser Lys Leu Glu Pro Val Val Ala Lys Pro His Ser Pro
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 Ser Thr Thr Asn Arg Asn Phe Pro Gly Arg Met Gly His Lys Glu Gly
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Ala	Gln	Arg	Arg	Ala	Gly	Leu	Thr	Arg	Arg	Thr	Lys	Pro	Cys	Ser	Val	
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Lys	Ser	Ala	Met	Thr	Met	Thr	Glu	Lys	Ile	Leu	Ala	Arg	Ala	Ser	Glu	
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Arg	Ala	Ala	Leu	Glu	Pro	Gly	Glu	Asn	Val	Trp	Val	Asp	Val	Asp	Val	
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Leu	Met	Thr	His	Asp	Val	Cys	Gly	Pro	Gly	Ala	Phe	Asp	Ile	Phe	Lys	
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Lys	Glu	Phe	Gly	Glu	Asp	Ala	Arg	Val	Trp	Asp	Arg	Glu	Lys	Leu	Val	
				110					115					120		
gtc	atc	ccg	gac	cac	tac	atc	ttc	acc	agc	gac	gac	cgc	gcc	aac	cgc	497
Val	Ile	Pro	Asp	His	Tyr	Ile	Phe	Thr	Ser	Asp	Asp	Arg	Ala	Asn	Arg	
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aac	gtc	gac	atc	ctc	agg	gac	ttc	tgt	gcg	gag	cag	aac	atc	aag	tac	545
Asn	Val	Asp	Ile	Leu	Arg	Asp	Phe	Cys	Ala	Glu	Gln	Asn	Ile	Lys	Tyr	
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Phe	Tyr	Asp	Ile	Lys	Asp	Leu	Ser	Asp	Phe	Arg	Ala	Asn	Pro	Asp	Tyr	
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Phe	Gly	Gln	Phe	Ala	Thr	Gly	Ile	Gly	Asn	Thr	Asp	Ala	Gly	Phe	Val	
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Ile	Leu	Asp	Gly	Glu	Met	Pro	Pro	Tyr	Leu	Leu	Ala	Lys	Asp	Leu	Ile	
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Leu	Gln	Ile	Ile	Gly	Glu	Ile	Ser	Val	Ser	Gly	Ala	Thr	Tyr	Lys	Ser	
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Val	Asp	Tyr	Glu	Pro	Val	Tyr	Ser	Asp	Ala	Gln	Ala	Arg	Phe	Phe	Ser	
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Asp	Tyr	Arg	Phe	Asp	Val	Ser	Lys	Leu	Glu	Pro	Val	Val	Ala	Lys	Pro	
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His	Ser	Pro	Asp	Asn	Arg	Ala	Pro	Ala	Arg	Glu	Cys	Lys	Asp	Val	Lys	
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Ile	Asp	Arg	Val	Tyr	Ile	Gly	Ser	Cys	Thr	Gly	Gly	Lys	Thr	Glu	Asp	
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PF59082SeqList_PF59082.txt

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Ile Ser Val Ser Gly Ala Thr Tyr Lys Ser Met Glu Phe Val Gly Ser
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355          360          365          370
Ala Pro Ala Arg Glu Cys Lys Asp Val Lys Ile Asp Arg Val Tyr Ile
375          380          385          390
Gly Ser Cys Thr Gly Gly Lys Thr Glu Asp Phe Leu Ala Ala Lys
395          400          405          410
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455          460          465          470
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475          480          485          490
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ccg atg acc gtt tcg gag aag atc ttt tcg aaa gcc tcc gga act ccc      144
Pro Met Thr Val Ser Glu Lys Ile Phe Ser Lys Ala Ser Gly Thr Pro
35          40          45          50
gtg aaa gcc ggg gat ttc gta ctg gca aat ata gac ctg gca atg acc      192
Val Lys Ala Gly Asp Phe Val Leu Ala Asn Ile Asp Leu Ala Met Thr
55          60          65          70
cac gac atc aca ggt ccg ctg gca gtc cag ggc ttc tac gaa atc atg      240
His Asp Ile Thr Gly Pro Leu Ala Val Gln Gly Phe Tyr Glu Ile Met
75          80          85          90
aga gat gaa gaa gac aag aaa gta tgg gac ccg agc aaa att gta att      288
Arg Asp Glu Glu Asp Lys Lys Val Trp Asp Pro Ser Lys Ile Val Ile
95          100          105          110
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His	Ile	Met	Leu	Arg	Lys	Phe	Ala	Lys	Glu	Gln	Gly	Ile	Leu	Asn	Tyr		
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Asp	Val	Tyr	Glu	Gly	Val	Cys	His	Gln	Val	Leu	Pro	Glu	Lys	Gly	His		
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Val	Lys	Pro	Gly	Asp	Leu	Ile	Val	Gly	Ser	Asp	Ser	His	Thr	Cys	Ala		
145					150					155					160		
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Tyr	Gly	Ser	Leu	Gly	Ala	Phe	Ser	Thr	Gly	Ile	Gly	Ser	Thr	Asp	Met		
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Ala	Ala	Val	Phe	Ala	Thr	Gly	Lys	Leu	Trp	Phe	Arg	Val	Pro	Glu	Thr		
			180					185					190				
ttc	cgc	ttt	gaa	gtg	gaa	gga	aaa	cta	cca	gag	cgc	gtt	tat	tcc	aaa		624
Phe	Arg	Phe	Glu	Val	Glu	Gly	Lys	Leu	Pro	Glu	Arg	Val	Tyr	Ser	Lys		
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Asp	Leu	Ile	Leu	His	Leu	Ile	Gly	Asp	Val	Gly	Val	Glu	Gly	Val	Arg		
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Pro	Glu	Arg	Met	Thr	Met	Ser	Asn	Met	Ala	Ile	Glu	Met	Gly	Gly	Lys		
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			260				265						270				
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Ala	Lys	Tyr	Leu	Asp	Ile	Arg	Tyr	Tyr	Asp	Val	Ser	Asp	Leu	Glu	Pro		
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Gln	Val	Ala	Cys	Pro	His	Asn	Val	Asp	Asn	Val	Lys	Pro	Val	Ser	Glu		
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gtt	gaa	ggc	aca	aaa	ctc	gac	cag	atc	ttt	atg	gga	tcc	tgc	aca	aac		1008
Val	Glu	Gly	Thr	Lys	Leu	Asp	Gln	Ile	Phe	Met	Gly	Ser	Cys	Thr	Asn		
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Gly	Arg	Phe	Glu	Asp	Ile	Lys	Ile	Met	Ala	Asp	Ile	Met	Gly	Asp	Glu		
			340				345					350					
cct	gtt	gcg	aaa	aat	ttg	cg	ctc	ctt	gtt	gtt	ccc	gct	tca	aaa	act		1104
Pro	Val	Ala	Lys	Asn	Leu	Arg	Leu	Leu	Val	Val	Pro	Ala	Ser	Lys	Thr		
		355				360					365						
gaa	tat	atg	aag	ctg	tta	aaa	gcc	gga	tat	att	gaa	aaa	ctc	gtg	aac		1152
Glu	Tyr	Met	Lys	Leu	Leu	Lys	Ala	Gly	Tyr	Ile	Glu	Lys	Leu	Val	Asn		
	370				375					380							
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Ser	Phe	Gly	Leu	Leu	Gly	Pro	Gly	Glu	Val	Gly	Leu	Ala	Thr	Ser	Asn		
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cgc	aat	ttc	aag	ggc	aga	gaa	gga	agt	gca	gag	tct	ttt	gtt	tac	ctt		1296
Arg	Asn	Phe	Lys	Gly	Arg	Glu	Gly	Ser	Ala	Glu	Ser	Phe	Val	Tyr	Leu		
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Ser	Ser	Pro	Ala	Thr	Ala	Gly	Ala	Ser	Ala	Leu	Thr	Gly	Glu	Ile	Thr		
		435				440					445						
gat	ccc	agg	aag	gtt	taa												1362
Asp	Pro	Arg	Lys	Val													
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PF59082SeqList_PF59082.txt

<211> 453

<212> PRT

<213> Methanosarcina mazei Go1

<400> 954

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      35      40      45
Val Lys Ala Gly Asp Phe Val Leu Ala Asn Ile Asp Leu Ala Met Thr
      50      55      60
His Asp Ile Thr Gly Pro Leu Ala Val Gln Gly Phe Tyr Glu Ile Met
65      70      75      80
Arg Asp Glu Glu Asp Lys Lys Val Trp Asp Pro Ser Lys Ile Val Ile
      85      90      95
Ile Phe Asp His Gln Val Pro Ala Asp Ser Ile Asn Ala Ala Gln Asn
      100      105      110
His Ile Met Leu Arg Lys Phe Ala Lys Glu Gln Gly Ile Leu Asn Tyr
      115      120      125
Asp Val Tyr Glu Gly Val Cys His Gln Val Leu Pro Glu Lys Gly His
      130      135      140
Val Lys Pro Gly Asp Leu Ile Val Gly Ser Asp Ser His Thr Cys Ala
145      150      155      160
Tyr Gly Ser Leu Gly Ala Phe Ser Thr Gly Ile Gly Ser Thr Asp Met
      165      170      175
Ala Ala Val Phe Ala Thr Gly Lys Leu Trp Phe Arg Val Pro Glu Thr
      180      185      190
Phe Arg Phe Glu Val Glu Gly Lys Leu Pro Glu Arg Val Tyr Ser Lys
      195      200      205
Asp Leu Ile Leu His Leu Ile Gly Asp Val Gly Val Glu Gly Val Arg
      210      215      220
Tyr Met Ala Ala Glu Tyr Ala Gly Ser Thr Ile Arg Ser Leu Ser Ile
225      230      235      240
Pro Glu Arg Met Thr Met Ser Asn Met Ala Ile Glu Met Gly Gly Lys
      245      250      255
Ala Gly Ile Ile Glu Ala Asp Glu Val Thr Glu Ala Tyr Leu Lys Glu
      260      265      270
Arg Ile Pro Gly Phe Lys Leu Asp Pro Tyr Trp Lys Ser Asp Glu Gly
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Ala Lys Tyr Leu Asp Ile Arg Tyr Tyr Asp Val Ser Asp Leu Glu Pro
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Gln Val Ala Cys Pro His Asn Val Asp Asn Val Lys Pro Val Ser Glu
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      325      330      335
Gly Arg Phe Glu Asp Ile Lys Ile Met Ala Asp Ile Met Gly Asp Glu
      340      345      350
Pro Val Ala Lys Asn Leu Arg Leu Leu Val Val Pro Ala Ser Lys Thr
      355      360      365
Glu Tyr Met Lys Leu Leu Lys Ala Gly Tyr Ile Glu Lys Leu Val Asn
      370      375      380
Ala Gly Ala Ile Val Glu Ala Pro Cys Cys Gly Pro Cys Met Gly Gly
385      390      395      400
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      405      410      415
Arg Asn Phe Lys Gly Arg Glu Gly Ser Ala Glu Ser Phe Val Tyr Leu
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<211> 1296

<212> DNA

<213> Chlorobium tepidum TLS

PF59082SeqList_PF59082.txt

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<223> transl_table=11

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Lys Phe Val Asp Pro Gly Gln Ser Val Trp Leu Asn Val Asp Val Leu	
20 25 30	
ttg acg cac gac gtc tgc ggc ccg ccg acc ttc gat atc ttc aag cag	144
Leu Thr His Asp Val Cys Gly Pro Pro Thr Phe Asp Ile Phe Lys Gln	
35 40 45	
gag ttc ggc ccg aac gcc aag gtg tgg gat ccg tcg aaa gtg gtg gtg	192
Glu Phe Gly Pro Asn Ala Lys Val Trp Asp Pro Ser Lys Val Val Val	
50 55 60	
ctt ccc gac cac tac atc ttc acg gcc aac gag cac gcg cac cgc aat	240
Leu Pro Asp His Tyr Ile Phe Thr Ala Asn Glu His Ala His Arg Asn	
65 70 75 80	
atc gac ctc ttg cgc cag ttc gcc gcc gag cag ggc ttg ccg aac tac	288
Ile Asp Leu Leu Arg Gln Phe Ala Ala Glu Gln Gly Leu Pro Asn Tyr	
85 90 95	
tat gat gta ggc acc gac cgc tac cgc ggc gtc tgc cac gtc gcg ctg	336
Tyr Asp Val Gly Thr Asp Arg Tyr Arg Gly Val Cys His Val Ala Leu	
100 105 110	
gcc gaa gag ggc ttt aac ctc ccc ggc acc gtg ctg ttc ggc acc gac	384
Ala Glu Glu Gly Phe Asn Leu Pro Gly Thr Val Leu Phe Gly Thr Asp	
115 120 125	
tcg cac acc tgc acc tcg ggc gca ttc ggc atg ttc ggc tcc ggc atc	432
Ser His Thr Cys Thr Ser Gly Ala Phe Gly Met Phe Gly Ser Gly Ile	
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ggc aac acc gac gca gcc ttc atc ctc ggc acc ggc aag ctc tgg gag	480
Gly Asn Thr Asp Ala Ala Phe Ile Leu Gly Thr Lys Lys Leu Trp Glu	
145 150 155 160	
aag gtg cct gat tcg atg aag ttc acc ttt gaa ggc cag atg ccc gag	528
Lys Val Pro Asp Ser Met Lys Phe Thr Phe Glu Gly Gln Met Pro Glu	
165 170 175	
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Tyr Leu Thr Ala Lys Asp Leu Ile Leu Gln Ile Leu Gly Asp Ile Thr	
180 185 190	
acc gac ggc gcg acc tac cgc gcc atg gag ttc gat ggc gaa gcg gtc	624
Thr Asp Gly Ala Thr Tyr Arg Ala Met Glu Phe Asp Gly Glu Ala Val	
195 200 205	
tat tcg ctg ccg atc gac gag cgc atg acg ctc tgc aac atg gcc atc	672
Tyr Ser Leu Pro Ile Asp Glu Arg Met Thr Leu Cys Asn Met Ala Ile	
210 215 220	
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Glu Ala Gly Gly Met Asn Gly Ile Ile Ala Asp Ala Val Thr Glu	
225 230 235 240	
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245 250 255	
gat ccc gac gcg cag tac cac agc atg tac cgc tac aac gtc gaa aag	816
Asp Pro Asp Ala Gln Tyr His Ser Met Tyr Arg Tyr Asn Val Glu Lys	
260 265 270	
atg gag ccg atc gtc gcc aag ccg cac agc ccg gac aac cgc gcc acc	864
Met Glu Pro Ile Val Ala Lys Pro His Ser Pro Asp Asn Arg Ala Thr	
275 280 285	
gtg cac agc gtg gcc gga acg ccg atc acc aaa tcg tac atc ggc tcc	912
Val His Ser Val Ala Gly Thr Pro Ile Thr Lys Ser Tyr Ile Gly Ser	
290 295 300	
tgt acc ggc ggc aag ctg acc gac ttc aag ctc gca gcg aag att ctc	960
Cys Thr Gly Gly Lys Leu Thr Asp Phe Lys Leu Ala Ala Lys Ile Leu	
305 310 315 320	
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Lys Gly Lys Lys Val Ala Val Thr Thr Asn Ile Val Pro Ala Thr Val	
325 330 335	

PF59082SeqList_PF59082.txt

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cgc	cat	att	ttc	gag	gaa	gct	ggc	tgc	aac	atc	gcc	ctg	cca	tcg	tgc	1104
Arg	His	Ile	Phe	Glu	Glu	Ala	Gly	Cys	Asn	Ile	Ala	Leu	Pro	Ser	Cys	
		355					360					365				
gcg	gcg	tgt	ctc	ggc	ggc	cct	tcg	gac	acg	gtc	ggg	cgc	tcg	gtg	gac	1152
Ala	Ala	Cys	Leu	Gly	Gly	Pro	Ser	Asp	Thr	Val	Gly	Arg	Ser	Val	Asp	
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aac	gac	gtc	gtc	gtt	tcg	acc	acc	aac	cgc	aac	ttc	cct	ggc	cgc	atg	1200
Asn	Asp	Val	Val	Val	Ser	Thr	Thr	Asn	Arg	Asn	Phe	Pro	Gly	Arg	Met	
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ggc	agc	aag	ttc	gcg	agc	gtc	tat	ctg	gcc	tcg	ccg	ctg	act	gcg	gca	1248
Gly	Ser	Lys	Phe	Ala	Ser	Val	Tyr	Leu	Ala	Ser	Pro	Leu	Thr	Ala	Ala	
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gcc	tct	gcc	ata	acg	ggc	aaa	ctc	acc	gat	ccg	aga	gat	ttc	ctc		1293
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		20					25					30				
Leu	Thr	His	Asp	Val	Cys	Gly	Pro	Pro	Thr	Phe	Asp	Ile	Phe	Lys	Gln	
	35					40					45					
Glu	Phe	Gly	Pro	Asn	Ala	Lys	Val	Trp	Asp	Pro	Ser	Lys	Val	Val	Val	
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Leu	Pro	Asp	His	Tyr	Ile	Phe	Thr	Ala	Asn	Glu	His	Ala	His	Arg	Asn	
65					70				75					80		
Ile	Asp	Leu	Leu	Arg	Gln	Phe	Ala	Ala	Glu	Gln	Gly	Leu	Pro	Asn	Tyr	
		85					90					95				
Tyr	Asp	Val	Gly	Thr	Asp	Arg	Tyr	Arg	Gly	Val	Cys	His	Val	Ala	Leu	
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Ala	Glu	Glu	Gly	Phe	Asn	Leu	Pro	Gly	Thr	Val	Leu	Phe	Gly	Thr	Asp	
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Ser	His	Thr	Cys	Thr	Ser	Gly	Ala	Phe	Gly	Met	Phe	Gly	Ser	Gly	Ile	
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Tyr	Leu	Thr	Ala	Lys	Asp	Leu	Ile	Leu	Gln	Ile	Leu	Gly	Asp	Ile	Thr	
		180				185						190				
Thr	Asp	Gly	Ala	Thr	Tyr	Arg	Ala	Met	Glu	Phe	Asp	Gly	Glu	Ala	Val	
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Tyr	Ser	Leu	Pro	Ile	Asp	Glu	Arg	Met	Thr	Leu	Cys	Asn	Met	Ala	Ile	
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225				230					235					240		
Ala	Phe	Val	Lys	Ala	Arg	Thr	Ser	Lys	Pro	Tyr	Glu	Ile	Phe	Thr	Ser	
		245							250				255			
Asp	Pro	Asp	Ala	Gln	Tyr	His	Ser	Met	Tyr	Arg	Tyr	Asn	Val	Glu	Lys	
		260					265					270				
Met	Glu	Pro	Ile	Val	Ala	Lys	Pro	His	Ser	Pro	Asp	Asn	Arg	Ala	Thr	
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Val	His	Ser	Val	Ala	Gly	Thr	Pro	Ile	Thr	Lys	Ser	Tyr	Ile	Gly	Ser	
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Cys	Thr	Gly	Gly	Lys	Leu	Thr	Asp	Phe	Lys	Leu	Ala	Ala	Lys	Ile	Leu	
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Lys	Gly	Lys	Lys	Val	Ala	Val	Thr	Thr	Asn	Ile	Val	Pro	Ala	Thr	Val	

PF59082SeqList_PF59082.txt

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          355          360          365
Ala Ala Cys Leu Gly Gly Pro Ser Asp Thr Val Gly Arg Ser Val Asp
          370          375          380
Asn Asp Val Val Val Ser Thr Thr Asn Arg Asn Phe Pro Gly Arg Met
385          390          395          400
Gly Ser Lys Phe Ala Ser Val Tyr Leu Ala Ser Pro Leu Thr Ala Ala
          405          410          415
Ala Ser Ala Ile Thr Gly Lys Leu Thr Asp Pro Arg Asp Phe Leu
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<211> 1275

<212> DNA

<213> Methanococcus maripaludis s2

<220>

<221> CDS

<222> (1)..(1275)

<223> transl_table=11

<400> 957

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tca gag gtt tca cct gga gac atc gtt atg gct aaa gta gaa acc gcg      96
Ser Glu Val Ser Pro Gly Asp Ile Val Met Ala Lys Val Glu Thr Ala
          20          25          30
atg gtc cac gat att aca ggc ccg ctt tca gta aat aca tta aaa aaa      144
Met Val His Asp Ile Thr Gly Pro Leu Ser Val Asn Thr Leu Lys Lys
          35          40          45
gaa ggt att tca aaa gtt tgg gac aat gaa aag att gtg att cca ttc      192
Glu Gly Ile Ser Lys Val Trp Asp Asn Glu Lys Ile Val Ile Pro Phe
          50          55          60
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Asp His Gln Ile Pro Ala Asp Ser Ile Asn Ala Ala Glu Asn His Ile
          65          70          75
tta atg aga aac ttt gta aaa gaa caa aat atc aaa cac ttc tat gac      288
Leu Met Arg Asn Phe Val Lys Glu Gln Asn Ile Lys His Phe Tyr Asp
          80          85          90
att aga gaa gga gtt tgc cat cag gta tta cct gaa aaa ggt cac ata      336
Ile Arg Glu Gly Val Cys His Gln Val Leu Pro Glu Lys Gly His Ile
          100          105          110
gtt cca gga act gtt gta gtt ggt gca gac agc cac acc tgt aca tac      384
Val Pro Gly Thr Val Val Val Gly Ala Asp Ser His Thr Cys Thr Tyr
          115          120          125
ggt gca ttt ggt gca ttt gca aca gga att gga agt acc gac atg gct      432
Gly Ala Phe Gly Ala Phe Ala Thr Gly Ile Gly Ser Thr Asp Met Ala
          130          135          140
gct gca ttt gca act ggt gaa tta tgg ttt aaa gtt cct gaa aca ctt      480
Ala Ala Phe Ala Thr Gly Glu Leu Trp Phe Lys Val Pro Glu Thr Leu
          145          150          155
tac ttc aat ata act ggt gag tta aaa cca gaa gta atg tct aaa gat      528
Tyr Phe Asn Ile Thr Gly Glu Leu Lys Pro Glu Val Met Ser Lys Asp
          160          165          170
gta atc ttg agc att atc gga atg gtt gga gct gac ggt gca aca tac      576
Val Ile Leu Ser Ile Ile Gly Met Val Gly Ala Asp Gly Ala Thr Tyr
          175          180          185
aaa gct gca cag ttt gcc gga aac aca gta gat aac atg act att gca      624
Lys Ala Ala Gln Phe Ala Gly Asn Thr Val Asp Asn Met Thr Ile Ala
          190          195          200
tca aga atg aca atg tca aac atg gct atc gaa atg ggt gga aaa gca      672
Ser Arg Met Thr Met Ser Asn Met Ala Ile Glu Met Gly Gly Lys Ala
          205          210          215
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Gly Leu Ile Ala Pro Asp Asp Lys Thr Ile Asn Tyr Val Lys Asn Ala

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PF59082SeqList_PF59082.txt

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Lys Asn Ala Glu Phe Glu Glu Lys Phe Glu Ile Asp Val Ser Asn Leu					
gaa cct gtt atg gca tgc ccg cac aac gtg gac aat gta aaa gct gtt	260	265	270	864	
Glu Pro Val Met Ala Cys Pro His Asn Val Asp Asn Val Lys Ala Val					
aga gaa gtt gca gga acc cca att gat cag gta ttc att ggt tca tgt	275	280	285	912	
Arg Glu Val Ala Gly Thr Pro Ile Asp Gln Val Phe Ile Gly Ser Cys					
act aac gga aga ctt gaa gat ttg aga gct gct tta aac gtt att gaa	290	295	300	960	
Thr Asn Gly Arg Leu Glu Asp Leu Arg Ala Leu Asn Val Ile Glu					
aaa cac ggc gga att tca aaa gat atc aga gtt gtt gta acc cct gca	305	310	315	1008	
Lys His Gly Gly Ile Ser Lys Asp Ile Arg Val Val Val Thr Pro Ala					
tca aga agc atc atg ctt gaa gct att gat gaa gga tta att aaa aaa	325	330	335	1056	
Ser Arg Ser Ile Met Leu Glu Ala Ile Asp Glu Gly Leu Ile Lys Lys					
ttc tac cag tac ggc tgt gtt gta aca aat cca tca tgt tct gca tgt	340	345	350	1104	
Phe Tyr Gln Tyr Gly Cys Val Val Thr Asn Pro Ser Cys Ser Ala Cys					
atg ggt gca tta tac ggt ctt tta ggt cct gga gaa gtt gga att gca	355	360	365	1152	
Met Gly Ala Leu Tyr Gly Leu Leu Gly Pro Gly Glu Val Gly Ile Ala					
act tca aac aga aac ttc aga gga aga gaa ggt tct tta gaa tca gac	370	375	380	1200	
Thr Ser Asn Arg Asn Phe Arg Gly Arg Glu Gly Ser Leu Glu Ser Asp					
gtg tac ctt gca tcg cca att act gct gca gca tgt gct gtt aaa gga	385	390	395	1248	
Val Tyr Leu Ala Ser Pro Ile Thr Ala Ala Ala Cys Ala Val Lys Gly					
gaa att gtt gac cca aga gat ctc taa	405	410	415	1275	
Glu Ile Val Asp Pro Arg Asp Leu	420				

<210> 958

<211> 424

<212> PRT

<213> Methanococcus maripaludis S2

<400> 958

Met Ala Met Thr Leu Ala Glu Lys Ile Leu Ala Lys Ala Ser Gly Asn	1	5	10	15
Ser Glu Val Ser Pro Gly Asp Ile Val Met Ala Lys Val Glu Thr Ala	20	25	30	
Met Val His Asp Ile Thr Gly Pro Leu Ser Val Asn Thr Leu Lys Lys	35	40	45	
Glu Gly Ile Ser Lys Val Trp Asp Asn Glu Lys Ile Val Ile Pro Phe	50	55	60	
Asp His Gln Ile Pro Ala Asp Ser Ile Asn Ala Ala Glu Asn His Ile	65	70	75	80
Leu Met Arg Asn Phe Val Lys Glu Gln Asn Ile Lys His Phe Tyr Asp	85	90	95	
Ile Arg Glu Gly Val Cys His Gln Val Leu Pro Glu Lys Gly His Ile	100	105	110	
Val Pro Gly Thr Val Val Val Gly Ala Asp Ser His Thr Cys Thr Tyr	115	120	125	
Gly Ala Phe Gly Ala Phe Ala Thr Gly Ile Gly Ser Thr Asp Met Ala	130	135	140	
Ala Ala Phe Ala Thr Gly Glu Leu Trp Phe Lys Val Pro Glu Thr Leu	145	150	155	160
Tyr Phe Asn Ile Thr Gly Glu Leu Lys Pro Glu Val Met Ser Lys Asp	165	170	175	
Val Ile Leu Ser Ile Ile Gly Met Val Gly Ala Asp Gly Ala Thr Tyr	180	185	190	
Lys Ala Ala Gln Phe Ala Gly Asn Thr Val Asp Asn Met Thr Ile Ala				

PF59082SeqList_PF59082.txt

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195
Ser Arg Met Thr Met Ser Asn Met Ala Ile Glu Met Gly Gly Lys Ala
210 215 220
Gly Leu Ile Ala Pro Asp Asp Lys Thr Ile Asn Tyr Val Lys Asn Ala
225 230 235
Met Glu Ala Asn Asn Thr Ala Lys Pro Phe Glu Leu Val Leu Gly Asp
245 250 255
Lys Asn Ala Glu Phe Glu Glu Lys Phe Glu Ile Asp Val Ser Asn Leu
260 265 270
Glu Pro Val Met Ala Cys Pro His Asn Val Asp Asn Val Lys Ala Val
275 280 285
Arg Glu Val Ala Gly Thr Pro Ile Asp Gln Val Phe Ile Gly Ser Cys
290 295 300
Thr Asn Gly Arg Leu Glu Asp Leu Arg Ala Ala Leu Asn Val Ile Glu
305 310 315
Lys His Gly Gly Ile Ser Lys Asp Ile Arg Val Val Val Thr Pro Ala
325 330 335
Ser Arg Ser Ile Met Leu Glu Ala Ile Asp Glu Gly Leu Ile Lys Lys
340 345 350
Phe Tyr Gln Tyr Gly Cys Val Val Thr Asn Pro Ser Cys Ser Ala Cys
355 360 365
Met Gly Ala Leu Tyr Gly Leu Leu Gly Pro Gly Glu Val Gly Ile Ala
370 375 380
Thr Ser Asn Arg Asn Phe Arg Gly Arg Glu Gly Ser Leu Glu Ser Asp
385 390 395
Val Tyr Leu Ala Ser Pro Ile Thr Ala Ala Cys Ala Val Lys Gly
405 410 415
Glu Ile Val Asp Pro Arg Asp Leu
420

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<210> 959

<211> 1545

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<221> CDS

<222> (1)..(1545)

<400> 959

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1      5      10      15
ttc gcc cac aag aac gag ctc gcc gcc gcc gct gct ccg tcc cag      96
Phe Ala His Lys Asn Glu Leu Ala Ala Val Ala Pro Ser Gln
20      25      30
cag cag ctg cag cgg agg gtg agt ggg agg agg gcg cgt tcc ggg agg      144
Gln Gln Leu Gln Arg Arg Val Ser Gly Arg Arg Ala Arg Ser Gly Arg
35      40      45
gtc cgc gcc gtc gcc acg ccc gcc cgc gcc ccc cgc gcc ccg tcc tcc      192
Val Arg Ala Val Ala Thr Pro Ala Arg Ala Pro Arg Ala Pro Ser Ser
50      55      60
act ggc tcg gtg aag agc gcc atg acg atg aca gag aag atc ctg gcg      240
Thr Gly Ser Val Lys Ser Ala Met Thr Met Thr Glu Lys Ile Leu Ala
65      70      75      80
agg gcg tcg gag cgc gcc agc ttg gag ccc ggg gag aac gtg tgg gtg      288
Arg Ala Ser Glu Arg Ala Ser Leu Glu Pro Gly Glu Asn Val Trp Val
85      90      95
gac gtc gac gtg ctg atg acg cac gac gtc tgc ggc cct ggc acc atc      336
Asp Val Asp Val Leu Met Thr His Asp Val Cys Gly Pro Gly Thr Ile
100      105      110
ggg atc ttc aag cgg gag ttc ggg gag gac gcc aag gtt tgg gac cga      384
Gly Ile Phe Lys Arg Glu Phe Gly Glu Asp Ala Lys Val Trp Asp Arg
115      120      125
gag aag gtg gtc atc atc ccg gac cac tac atc ttc acc agc gat gag      432
Glu Lys Val Val Ile Ile Pro Asp His Tyr Ile Phe Thr Ser Asp Glu
130      135      140
cga gca aac cga aat gtt gat atc ctc agg gat ttc tgt atg gag cag      480
Arg Ala Asn Arg Asn Val Asp Ile Leu Arg Asp Phe Cys Met Glu Gln

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PF59082SeqList_PF59082.txt

145	aac atc aag tac ttc tat gac atc aag gac ctg agc aat ttc aaa gca	150	155	160	528
Asn Ile Lys Tyr Phe Tyr Asp Ile Lys Asp Leu Ser Asn Phe Lys Ala					
aat cca gac tac aag ggt gtt tgc cac gtt gct ctt gct caa gag ggt	165	170			576
Asn Pro Asp Tyr Lys Gly Val Cys His Val Ala Leu Ala Gln Glu Gly	180	185			
cat tgc aga cca ggc gag gtt ctc ctt ggt act gat tct cat aca tgc	190	200			624
His Cys Arg Pro Gly Glu Val Leu Leu Gly Thr Asp Ser His Thr Cys	195	205			
aat gct gga gcc ttt ggc caa gca act gga att gga aac act gat	210	215	220		672
Asn Ala Gly Ala Phe Gly Gln Phe Ala Thr Gly Ile Gly Asn Thr Asp					
gct ggt ttt gtg atg ggc act ggg aag gct ctt ctt aag gtg cct cca	225	230	235		720
Ala Gly Phe Val Met Gly Thr Gly Lys Ala Leu Leu Lys Val Pro Pro					
act atc agg ttt gta tta gat gga gaa atg cca cct tat tta ctt gca	245	250			768
Thr Ile Arg Phe Val Leu Asp Gly Glu Met Pro Pro Tyr Leu Leu Ala					
aag gat ctg att tta caa att att ggt gag att tct gta tct ggc gca	260	265	270		816
Lys Asp Leu Ile Leu Gln Ile Ile Gly Glu Ile Ser Val Ser Gly Ala					
aca tac aaa tcc atg gag ttt gtt gga tca act gtg gaa agt cta aat	275	280	285		864
Thr Tyr Lys Ser Met Glu Phe Val Gly Ser Thr Val Glu Ser Leu Asn					
atg gaa gag cga atg aca ctg tgc aac atg gtt att gaa gct ggt ggc	290	295	300		912
Met Glu Glu Arg Met Thr Leu Cys Asn Met Val Ile Glu Ala Gly Gly					
aag aat ggt gtt gtg cct gcc gat caa act aca ttt aac tat ctt gag	305	310	315		960
Lys Asn Gly Val Val Pro Ala Asp Gln Thr Thr Phe Asn Tyr Leu Glu					
ggc aag aca tca gtt gaa tac gag cct gtc tat agt gat gct cag gcc	325	330			1008
Gly Lys Thr Ser Val Glu Tyr Glu Pro Val Tyr Ser Asp Ala Gln Ala					
aga ttt gtt agt tat tac cgg ttt gat gta tcc aaa ttg gag cca gtt	340	345	350		1056
Arg Phe Val Ser Asp Tyr Arg Phe Asp Val Ser Lys Leu Glu Pro Val					
att gcc aag cca cat tca cct gac aac cgt gct cta gca aga gag tgc	355	360	365		1104
Ile Ala Lys Pro His Ser Pro Asp Asn Arg Ala Leu Ala Arg Glu Cys					
aaa gat gtc aag att gac cgg gtc tat atc ggt tct tgt act gga ggt	370	375	380		1152
Lys Asp Val Lys Ile Asp Arg Val Tyr Ile Gly Ser Cys Thr Gly Gly					
aaa act gag gac ttc ttt gct gct gcg aag gtg ttc tta gct tcg ggg	385	390	395		1200
Lys Thr Glu Asp Phe Phe Ala Ala Lys Val Phe Leu Ala Ser Gly					
aag aag gtt aaa gtt ccc act ttt ctc gtt ccg gcg aca caa aag gtg	405	410			1248
Lys Lys Val Lys Val Pro Thr Phe Leu Val Pro Ala Thr Gln Lys Val					
tgg atg gac att tat agc atc cct gta cca gga gcc ggt ggc aaa act	420	425	430		1296
Trp Met Asp Ile Tyr Ser Ile Pro Val Pro Gly Ala Gly Lys Thr					
tgc tca cag ata ttt gag gag gct ggt tgt gat aca cca gct agc cct	435	440	445		1344
Cys Ser Gln Ile Phe Glu Glu Ala Gly Cys Asp Thr Pro Ala Ser Pro					
agt tgt ggt gct tgt ttg ggt ggt cct cgt gat aca tat gct cgc atg	450	455	460		1392
Ser Cys Gly Ala Cys Leu Gly Gly Pro Arg Asp Thr Tyr Ala Arg Met					
aat gaa cct atg gtg tgt gtg tcg acg acg aac agg aat ttc ccc ggc	465	470	475		1440
Asn Glu Pro Met Val Cys Val Ser Thr Thr Asn Arg Asn Phe Pro Gly					
agg atg ggg cac aag gaa ggg cag atc tac ctg gct tcg ccg ttc acc	485	490	495		1488
Arg Met Gly His Lys Glu Gly Gln Ile Tyr Leu Ala Ser Pro Phe Thr					
gcg gcg gct tca gcc ctc acc gga tac gtc act gac ccc agg gac ttc	500	505	510		1536
Ala Ala Ala Ser Ala Leu Thr Gly Tyr Val Thr Asp Pro Arg Asp Phe					
ctg atg taa					1545
Leu Met					

PF59082SeqList_PF59082.txt

<210> 960

<211> 514

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<400> 960

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Met Ala Ser Ile Ser Ala Ala Ser Pro Val Ala Gly Lys Ala Ala Ala
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Phe Ala His Lys Asn Glu Leu Ala Ala Val Ala Pro Ser Gln
      20      25      30
Gln Gln Leu Gln Arg Arg Val Ser Gly Arg Arg Ala Arg Ser Gly Arg
      35      40      45
Val Arg Ala Val Ala Thr Pro Ala Arg Ala Pro Arg Ala Pro Ser Ser
      50      55      60
Thr Gly Ser Val Lys Ser Ala Met Thr Met Thr Glu Lys Ile Leu Ala
65      70      75      80
Arg Ala Ser Glu Arg Ala Ser Leu Glu Pro Gly Glu Asn Val Trp Val
      85      90      95
Asp Val Asp Val Leu Met Thr His Asp Val Cys Gly Pro Gly Thr Ile
      100      105      110
Gly Ile Phe Lys Arg Glu Phe Gly Glu Asp Ala Lys Val Trp Asp Arg
      115      120      125
Glu Lys Val Val Ile Ile Pro Asp His Tyr Ile Phe Thr Ser Asp Glu
130      135      140
Arg Ala Asn Arg Asn Val Asp Ile Leu Arg Asp Phe Cys Met Glu Gln
145      150      155      160
Asn Ile Lys Tyr Phe Tyr Asp Ile Lys Asp Leu Ser Asn Phe Lys Ala
      165      170      175
Asn Pro Asp Tyr Lys Gly Val Cys His Val Ala Leu Ala Gln Glu Gly
      180      185      190
His Cys Arg Pro Gly Glu Val Leu Leu Gly Thr Asp Ser His Thr Cys
195      200      205
Asn Ala Gly Ala Phe Gly Gln Phe Ala Thr Gly Ile Gly Asn Thr Asp
210      215      220
Ala Gly Phe Val Met Gly Thr Gly Lys Ala Leu Leu Lys Val Pro Pro
225      230      235      240
Thr Ile Arg Phe Val Leu Asp Gly Glu Met Pro Pro Tyr Leu Leu Ala
      245      250      255
Lys Asp Leu Ile Leu Gln Ile Ile Gly Glu Ile Ser Val Ser Gly Ala
260      265      270
Thr Tyr Lys Ser Met Glu Phe Val Gly Ser Thr Val Glu Ser Leu Asn
275      280      285
Met Glu Gly Arg Met Thr Leu Cys Asn Met Val Ile Glu Ala Gly Gly
290      295      300
Lys Asn Gly Val Val Pro Ala Asp Gln Thr Thr Phe Asn Tyr Leu Glu
305      310      315      320
Gly Lys Thr Ser Val Glu Tyr Glu Pro Val Tyr Ser Asp Ala Gln Ala
      325      330      335
Arg Phe Val Ser Asp Tyr Arg Phe Asp Val Ser Lys Leu Glu Pro Val
340      345      350
Ile Ala Lys Pro His Ser Pro Asp Asn Arg Ala Leu Ala Arg Glu Cys
355      360      365
Lys Asp Val Lys Ile Asp Arg Val Tyr Ile Gly Ser Cys Thr Gly Gly
370      375      380
Lys Thr Glu Asp Phe Phe Ala Ala Ala Lys Val Phe Leu Ala Ser Gly
385      390      395      400
Lys Lys Val Lys Val Pro Thr Phe Leu Val Pro Ala Thr Gln Lys Val
405      410      415
Trp Met Asp Ile Tyr Ser Ile Pro Val Pro Gly Ala Gly Gly Lys Thr
420      425      430
Cys Ser Gln Ile Phe Glu Glu Ala Gly Cys Asp Thr Pro Ala Ser Pro
435      440      445
Ser Cys Gly Ala Cys Leu Gly Pro Arg Asp Thr Tyr Ala Arg Met
450      455      460
Asn Glu Pro Met Val Cys Val Ser Thr Thr Asn Arg Asn Phe Pro Gly
465      470      475      480
Arg Met Gly His Lys Glu Gly Gln Ile Tyr Leu Ala Ser Pro Phe Thr

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PF59082SeqList_PF59082.txt

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<210> 961
 <211> 1251
 <212> DNA
 <213> Dehalococcoides ethenogenes 195

<220>
 <221> CDS
 <222> (1)..(1251)
 <223> transl_table=11

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 gtc agc ccg ggt gat ttt ata aac gcc aag gta gac ctg gtg ctg gct 96
 Val Ser Pro Gly Asp Phe Ile Asn Ala Lys Val Asp Leu Val Leu Ala
 20 25 30
 aat gac att acc gca cct ata gcc gta aaa gag ttt aag aag att ggg 144
 Asn Asp Ile Thr Ala Pro Ile Ala Val Lys Glu Phe Lys Lys Ile Gly
 35 40 45
 gtc agc aaa gta ttt gac ccc aaa aag ata gtt ttt gtg cct gac cat 192
 Val Ser Lys Val Phe Asp Pro Lys Lys Ile Val Phe Val Pro Asp His
 50 55 60
 ttt gta ccc aac aag gac att gca tct gcc gaa cag gta aaa atg gtg 240
 Phe Val Pro Asn Lys Asp Ile Ala Ser Ala Glu Gln Val Lys Met Val
 65 70 75 80
 cgt gag ttt gcc cgt gag cag ggt ata ctc ttt ttt gaa tgc ggt aaa 288
 Arg Glu Phe Ala Arg Glu Gln Gly Ile Leu Phe Phe Glu Cys Gly Lys
 85 90 95
 atg ggt gtt gag cat gta atc ctg cac gag cag ggt ctg gta ctg ccg 336
 Met Gly Val Glu His Val Ile Leu His Glu Gln Gly Leu Val Leu Pro
 100 105 110
 ggg gat att gtg gta ggc gct gac tcc cat acc tgc act tac ggg gca 384
 Gly Asp Ile Val Val Gly Ala Asp Ser His Thr Cys Thr Tyr Gly Ala
 115 120 125
 ctg ggc gct ttt act acc ggc atg ggc tca acc gat ata gcc gcc gcc 432
 Leu Gly Ala Phe Thr Thr Gly Met Gly Ser Thr Asp Ile Ala Ala Ala
 130 135 140
 atg gcc acc ggt gag gtt tgg atg aaa gtc ccc acc atc aaa ttt 480
 Met Ala Thr Gly Glu Val Trp Met Lys Val Pro Pro Thr Ile Lys Phe
 145 150 155 160
 aac tat tcg ggt aag ctg ccc aaa tgg att ggc ggt aaa gac ctt att 528
 Asn Tyr Ser Gly Lys Leu Pro Lys Trp Ile Gly Gly Lys Asp Leu Ile
 165 170 175
 ttg ttt acc ata ggt cag ata ggg gta gac ggg gct ttg tac tct gcc 576
 Leu Phe Thr Ile Gly Gln Ile Gly Val Asp Gly Ala Leu Tyr Ser Ala
 180 185 190
 atg tat ttc tgc gga gag gct att gat gcc ctt tcc atg gaa aac cgc 624
 Met Tyr Phe Cys Gly Glu Ala Ile Asp Ala Leu Ser Met Glu Asn Arg
 195 200 205
 ttt acc atg tcc aat atg gcc ata gag gcc ggc ggc aag gca ggt ctt 672
 Phe Thr Met Ser Asn Met Ala Ile Glu Ala Gly Gly Lys Ala Gly Leu
 210 215 220
 ttc agg gtt gac gaa aag act ctg gaa tat gtg acc ccc aga gcc aaa 720
 Phe Arg Val Asp Glu Lys Thr Leu Glu Tyr Val Thr Pro Arg Ala Lys
 225 230 235 240
 cgc cag tat acg gtt tat gat aat gat gct gat gcg tct tat gcc aaa 768
 Arg Gln Tyr Thr Val Tyr Asp Asn Asp Ala Asp Ala Ser Tyr Ala Lys
 245 250 255
 aca tat aac ttt gat att tcc aag ctt gag ccg cag gta tca ctg ccg 816
 Thr Tyr Asn Phe Asp Ile Ser Lys Leu Glu Pro Gln Val Ser Leu Pro
 260 265 270
 cat tca ccg gca aat gcc cgc ccc atc agc cag att ggt aaa ata aag 864

PF59082SeqList_PF59082.txt

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Val	Asp	Gln	Val	Ile	Ile	Gly	Ser	Cys	Thr	Asn	Gly	Arg	Leu	Glu	Asp	
290						295					300					
ctg	gcc	ata	tct	gcc	aaa	ctg	ctt	gaa	ggg	aat	aaa	gtc	agc	cct	gat	960
Leu	Ala	Ile	Ser	Ala	Lys	Leu	Leu	Glu	Gly	Asn	Lys	Val	Ser	Pro	Asp	
305					310					315					320	
ttg	agg	act	att	gtt	ata	ccc	ggg	tcg	cag	cag	gtc	tat	ctg	gat	gcc	1008
Leu	Arg	Thr	Ile	Val	Ile	Pro	Gly	Ser	Gln	Gln	Val	Tyr	Leu	Asp	Ala	
					325				330					335		
ctg	aaa	gcc	ggc	tat	att	gaa	acc	ttt	atc	aat	gcc	ggg	gtt	gcg	gtt	1056
Leu	Lys	Ala	Gly	Tyr	Ile	Glu	Thr	Phe	Ile	Asn	Ala	Gly	Val	Ala	Val	
					340			345					350			
tcc	act	ccc	acc	tgc	ggg	cct	tgc	ctc	ggc	ggg	cat	atg	ggg	att	ttg	1104
Ser	Thr	Pro	Thr	Cys	Gly	Pro	Cys	Leu	Gly	Gly	His	Met	Gly	Ile	Leu	
						360						365				
gcc	gcc	ggg	gaa	cgc	tgt	ctg	gca	act	acc	aac	cgc	aat	ttc	gta	ggg	1152
Ala	Ala	Gly	Glu	Arg	Cys	Leu	Ala	Thr	Thr	Asn	Arg	Asn	Phe	Val	Gly	
370						375					380					
cgt	atg	ggc	agc	ccc	aag	gac	gaa	gta	tac	ctg	ggc	ggg	ccg	gcc	gtt	1200
Arg	Met	Gly	Ser	Pro	Lys	Ser	Glu	Val	Tyr	Leu	Ala	Gly	Pro	Ala	Val	
385					390					395					400	
gcc	gcc	gct	acc	gcc	atc	aag	gga	tat	att	gcc	cat	ccc	gat	gaa	att	1248
Ala	Ala	Ala	Thr	Ala	Ile	Lys	Gly	Tyr	Ile	Ala	His	Pro	Asp	Glu	Ile	
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taa																1251

<210> 962

<211> 416

<212> PRT

<213> Dehalococcoides ethenogenes 195

<400> 962

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			20					25				30				
Asn	Asp	Ile	Thr	Ala	Pro	Ile	Ala	Val	Lys	Glu	Phe	Lys	Lys	Ile	Gly	
		35					40					45				
Val	Ser	Lys	Val	Phe	Asp	Pro	Lys	Lys	Ile	Val	Phe	Val	Pro	Asp	His	
	50					55				60						
Phe	Val	Pro	Asn	Lys	Asp	Ile	Ala	Ser	Ala	Glu	Gln	Val	Lys	Met	Val	
65					70					75					80	
Arg	Glu	Phe	Ala	Arg	Glu	Gln	Gly	Ile	Leu	Phe	Phe	Glu	Cys	Gly	Lys	
				85					90					95		
Met	Gly	Val	Glu	His	Val	Ile	Leu	His	Glu	Gln	Gly	Leu	Val	Leu	Pro	
		100					105					110				
Gly	Asp	Ile	Val	Val	Gly	Ala	Asp	Ser	His	Thr	Cys	Thr	Tyr	Gly	Ala	
		115				120						125				
Leu	Gly	Ala	Phe	Thr	Thr	Gly	Met	Gly	Ser	Thr	Asp	Ile	Ala	Ala	Ala	
	130					135					140					
Met	Ala	Thr	Gly	Glu	Val	Trp	Met	Lys	Val	Pro	Pro	Thr	Ile	Lys	Phe	
145					150					155					160	
Asn	Tyr	Ser	Gly	Lys	Leu	Pro	Lys	Trp	Ile	Gly	Gly	Lys	Asp	Leu	Ile	
				165					170					175		
Leu	Phe	Thr	Ile	Gly	Gln	Ile	Gly	Val	Asp	Gly	Ala	Leu	Tyr	Ser	Ala	
			180					185					190			
Met	Tyr	Phe	Cys	Gly	Glu	Ala	Ile	Asp	Ala	Leu	Ser	Met	Glu	Asn	Arg	
		195				200						205				
Phe	Thr	Met	Ser	Asn	Met	Ala	Ile	Glu	Ala	Gly	Gly	Lys	Ala	Gly	Leu	
	210					215					220					
Phe	Arg	Val	Asp	Glu	Lys	Thr	Leu	Glu	Tyr	Val	Thr	Pro	Arg	Ala	Lys	
225					230					235					240	
Arg	Gln	Tyr	Thr	Val	Tyr	Asp	Asn	Asp	Ala	Asp	Ala	Ser	Tyr	Ala	Lys	
				245					250					255		
Thr	Tyr	Asn	Phe	Asp	Ile	Ser	Lys	Leu	Glu	Pro	Gln	Val	Ser	Leu	Pro	

PF59082SeqList_PF59082.txt

195	200	205	
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gtg cca ccg gac gaa aaa acc ttt gcc ttc ctg aaa aat cgg gcg gct	Val Pro Pro Asp Glu Lys Thr Phe Ala Phe Leu Lys Asn Arg Ala Ala	720	
gct cct tat gat ccg gtt tat gcc gat cag gat gca gtc tat gta aaa	Ala Pro Tyr Asp Pro Val Tyr Ala Asp Gln Asp Ala Val Tyr Val Lys	768	
gaa ccc gtt tac tct gct gaa gat atc gag cct cag gta gcc tgt ccg	Glu Pro Val Tyr Ser Ala Glu Asp Ile Glu Pro Gln Val Ala Cys Pro	816	
cat cag gtt gac aac gta aaa cct gtg gga gaa gtt gaa ggt acc cac	His Gln Val Asp Asn Val Lys Pro Val Gly Glu Val Glu Gly Thr His	864	
ata gac cag gtt ttc ata ggg acg tgc aca aat ggc aga ctt gaa gac	Ile Asp Gln Val Phe Ile Gly Thr Cys Thr Asn Gly Arg Leu Glu Asp	912	
ctc gag gtc gca gca gca atc ctt aaa gga aaa aag gtt gca gtc agg	Leu Glu Val Ala Ala Ala Ile Leu Lys Gly Lys Val Ala Val Arg	960	
act att gta att cct gca tct cgc acg act ctc ctt gca gca att gaa	Thr Ile Val Ile Pro Ala Ser Arg Thr Thr Leu Leu Ala Ala Ile Glu	1008	
aac gga acg atg gaa att ctg ctc aaa gca ggc att acg ctt gca acc	Asn Gly Thr Met Glu Ile Leu Leu Lys Ala Gly Ile Thr Leu Ala Thr	1056	
cct ggc tgc ggg ccc tgt ctt ggc gct cac cag gga gtg ctc ggt gaa	Pro Gly Cys Gly Pro Cys Leu Gly Ala His Gln Gly Val Leu Gly Glu	1104	
gga gaa gtt tgc ctt tca acc gca aac cga aac ttc aag ggc agg atg	Gly Glu Val Cys Leu Ser Thr Ala Asn Arg Asn Phe Lys Gly Arg Met	1152	
gga aaa agt ggt ttt atc ctg gca tcc cct gca acc gca gca gcc	Gly Lys Ser Gly Phe Ile Tyr Leu Ala Ser Pro Ala Thr Ala Ala Ala	1200	
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<210> 964

<211> 413

<212> PRT

<213> Methanosarcina barkeri str. fusaro

<400> 964

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Met Lys Lys Val Trp Asp Pro Ser Arg Ile Val Ile Pro Phe Asp His	60	65	70	75
Ile Ala Pro Ala Asn Asn Glu Ile Ser Ala Thr Leu Gln Lys Glu Ile	80	85	90	95
Arg Glu Trp Val Lys Glu Gln Gly Ile Pro Asn Phe Tyr Glu Leu Gly	100	105	110	115
Glu Gly Ile Cys His Gln Val Leu Pro Glu Asn Gly Phe Ala Leu Pro	120	125	130	135
Gly Lys Leu Val Val Gly Ala Asp Ser His Ser Cys Thr Tyr Gly Ala	140	145	150	155
Phe Gly Ala Phe Ala Thr Gly Val Gly Ala Thr Asp Met Ala Glu Ile	160	165	170	175
Phe Ala Thr Gly Lys Leu Trp Phe Lys Val Pro Glu Ser Phe Arg Phe	180	185	190	195
Thr Val Glu Gly Arg Leu Gly Lys Gly Val Tyr Ala Lys Asp Leu Thr	200	205	210	215

PF59082SeqList_PF59082.txt

Leu Tyr Leu Ile Gly Lys Thr Gly Ile Asp Gly Ala Thr Tyr Lys Ala
 180 185 190
 Val Glu Phe Tyr Gly Gln Ala Ile Ser Glu Leu Ser Val Ser Gly Arg
 195 200 205
 Met Thr Leu Cys Asn Met Ala Ile Glu Met Gly Ala Lys Thr Gly Ile
 210 215 220
 Val Pro Pro Asp Glu Lys Thr Phe Ala Phe Leu Lys Asn Arg Ala Ala
 225 230 235 240
 Ala Pro Tyr Asp Pro Val Tyr Ala Asp Gln Asp Ala Val Tyr Val Lys
 245 250 255
 Glu Pro Val Tyr Ser Ala Glu Asp Ile Glu Pro Gln Val Ala Cys Pro
 260 265 270
 His Gln Val Asp Asn Val Lys Pro Val Gly Glu Val Glu Gly Thr His
 275 280 285
 Ile Asp Gln Val Phe Ile Gly Thr Cys Thr Asn Gly Arg Leu Glu Asp
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 Leu Glu Val Ala Ala Ala Ile Leu Lys Gly Lys Lys Val Ala Val Arg
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 325 330 335
 Asn Gly Thr Met Glu Ile Leu Leu Lys Ala Gly Ile Thr Leu Ala Thr
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 Pro Gly Cys Gly Pro Cys Leu Gly Ala His Gln Gly Val Leu Gly Glu
 355 360 365
 Gly Glu Val Cys Leu Ser Thr Ala Asn Arg Asn Phe Lys Gly Arg Met
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<211> 1296

<212> DNA

<213> Methanosarcina barkeri str. fusaro

<220>

<221> CDS

<222> (1)..(1296)

<223> transl_table=11

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gta ctg gca aat ata gac cta gca atg act cac gac att aca ggt ccg	144
Val Leu Ala Asn Ile Asp Leu Ala Met Thr His Asp Ile Thr Gly Pro	
35 40 45	
cta gca gtc aaa ggc ttc tat gag att atg aag gac aaa gaa gag aag	192
Leu Ala Val Lys Gly Phe Tyr Glu Ile Met Lys Asp Lys Glu Glu Lys	
50 55 60	
aaa gta tgg gat cca acg aaa ata gtg atc gta ttt gat cat cag gtt	240
Lys Val Trp Asp Pro Thr Lys Ile Val Ile Val Phe Asp His Gln Val	
65 70 75 80	
cct gcg gac tcc att aac gcc acc gca aat cat att atg ctc cga aaa	288
Pro Ala Asp Ser Ile Asn Ala Thr Ala Asn His Ile Met Leu Arg Lys	
85 90 95	
ttt gct gaa gaa cag ggc att tta aat tat gat gta tac gaa gga gtt	336
Phe Ala Glu Glu Gln Gly Ile Leu Asn Tyr Asp Val Tyr Glu Gly Val	
100 105 110	
tgc cat cag gtt ctt ccc gag aaa gga cat gtc ctg cca gga gac ctt	384
Cys His Gln Val Leu Pro Glu Lys Gly His Val Leu Pro Gly Asp Leu	
115 120 125	
att gtt ggc tcg gat tcg cat aca tgt gcg tat ggt gca ctt ggt gcg	432
Ile Val Gly Ser Asp Ser His Thr Cys Ala Tyr Gly Ala Leu Gly Ala	
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Gly	Lys	Leu	Trp	Phe	Lys	Val	Pro	Glu	Thr	Phe	Arg	Phe	Glu	Val	Glu	
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Gly	Asn	Leu	Pro	Glu	Arg	Val	Tyr	Ser	Lys	Asp	Leu	Ile	Leu	His	Leu	
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Ser	Asn	Met	Ala	Ile	Glu	Met	Gly	Gly	Lys	Ala	Gly	Ile	Ile	Glu	Ala	
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gat	gaa	gtg	act	gca	aac	tac	ctc	aaa	gag	cgg	att	atg	tat	tac	gaa	768
Asp	Glu	Val	Thr	Ala	Asn	Tyr	Leu	Lys	Glu	Arg	Ile	Met	Tyr	Tyr	Glu	
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Phe	Asp	Pro	Tyr	Trp	Lys	Ser	Asp	Glu	Asp	Ala	Lys	Tyr	Val	Gly	Ile	
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Arg	His	Tyr	Asp	Val	Ser	Asp	Leu	Glu	Pro	Gln	Val	Ala	Cys	Pro	His	
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His	Val	Asp	Asn	Val	Lys	Pro	Val	Thr	Glu	Val	Glu	Gly	Thr	Lys	Leu	
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Arg	Leu	Leu	Val	Val	Pro	Ala	Ser	Arg	Thr	Glu	Tyr	Leu	Lys	Leu	Leu	
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aaa	gcc	ggg	tat	ata	gaa	aag	ctc	atg	aat	gca	ggc	gca	atc	gta	gaa	1104
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Ser	Pro	Cys	Cys	Gly	Pro	Cys	Met	Gly	Gly	Ser	Phe	Gly	Leu	Leu	Gly	
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Glu	Gly	Ser	Pro	Glu	Ser	Phe	Val	Tyr	Leu	Ser	Ser	Pro	Ala	Thr	Ala	
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gga	gca	tca	gcc	ctt	aca	gga	gaa	atc	act	gat	cca	agg	aaa	gtt		1293
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<212> PRT

<213> Methanosarcina barkeri str. fusaro

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Pro Ala Asp Ser Ile Asn Ala Thr Ala Asn His Ile Met Leu Arg Lys
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Phe Ala Glu Glu Gln Gly Ile Leu Asn Tyr Asp Val Tyr Glu Gly Val
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Cys His Gln Val Leu Pro Glu Lys Gly His Val Leu Pro Gly Asp Leu
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    130      135
Phe Ser Thr Gly Ile Gly Ser Thr Asp Met Ala Ala Val Phe Ala Thr
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    180      185
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Gly Gly Ser Thr Ile His Ser Leu Ser Ile Pro Glu Arg Met Thr Met
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Ser Asn Met Ala Ile Glu Met Gly Gly Lys Ala Gly Ile Ile Glu Ala
225      230      235
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    20      25      30
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Leu Ala Asn Asp Ile Thr Gly Pro Val Ala Ile Ser Glu Phe Lys Lys

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PF59082SeqList_PF59082.txt

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1266

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 35 40 45
 Ile Gly Val Asp Ser Val Phe Asp Arg Asp Arg Val Tyr Leu Val Pro
 50 55 60
 Asp His Phe Thr Pro Asn Lys Asp Ile Lys Ser Ala Glu Gln Ala Lys
 65 70 75 80
 Ile Leu Arg Asp Phe Ala Lys Glu Gln Asn Leu Thr Tyr Tyr Phe Glu
 85 90 95
 Val Gly Lys Met Gly Ile Glu His Val Leu Leu Pro Glu Gly Leu
 100 105 110
 Val Leu Pro Gly Glu Val Ile Ile Gly Ala Asp Ser His Thr Cys Thr
 115 120 125
 Tyr Gly Gly Leu Gly Ala Phe Ala Thr Gly Val Gly Ser Thr Asp Leu
 130 135 140
 Ala Ala Ala Met Ala Leu Gly Glu Thr Trp Phe Lys Val Pro Glu Ser
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 Ile Lys Phe Tyr Leu Tyr Gly Glu Lys Leu Leu Pro Tyr Val Ser Ala
 165 170 175
 Lys Asp Ile Ile Leu Phe Ile Ile Gly Gln Ile Gly Val Asp Gly Ala
 180 185 190
 Leu Tyr Lys Ala Met Glu Phe Ala Gly Ser Ala Leu Lys Leu Ile Ser
 195 200 205
 Val Glu Gly Arg Leu Thr Met Ala Asn Met Ala Ile Glu Ala Gly Ala
 210 215 220
 Lys Asn Gly Ile Phe Pro Val Asp Glu Leu Thr Leu Glu Tyr Val Lys
 225 230 235 240
 Gly Arg Ala Lys Arg Glu Phe Lys Val Phe Ala Ser Asp Pro Asp Ala
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 Arg Tyr Glu Ala Val Tyr Glu Ile Asn Val Glu Glu Ile Glu Pro Gln
 260 265 270
 Val Ala Leu Pro His Leu Pro Glu Asn Ala Val Pro Val Lys Glu Val
 275 280 285
 Ser Gly Lys Asp Ile Asp Gln Val Val Ile Gly Ser Cys Thr Asn Gly
 290 295 300
 Arg Ile Glu Asp Leu Arg Val Ala Ala Ala Ile Leu Lys Gly Lys Lys
 305 310 315 320
 Val Lys Asp Tyr Val Arg Cys Ile Ile Ile Pro Gly Ser Gln Ser Val
 325 330 335
 Tyr Arg Gln Ala Leu Lys Glu Gly Leu Ile Asp Ile Phe Leu Glu Ala
 340 345 350
 Gly Ala Ala Val Ser Thr Pro Thr Cys Gly Pro Cys Leu Gly Gly His
 355 360 365
 Met Gly Ile Leu Ala Lys Gly Glu Arg Ala Val Ala Thr Thr Asn Arg
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Leu Gly Asn Asp Ile Thr Thr Pro Val Ala Val Lys Glu Phe Arg Lys	
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att ggc gtg aac aag gtg ttc gat gta aat aaa ata gca att gtt cct	192
Ile Gly Val Asn Lys Val Phe Asp Val Asn Lys Ile Ala Ile Val Pro	
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gac cat ttt aca ccc aac aaa gac atc aag tcc gcg gag cag gtc aag	240
Asp His Phe Thr Pro Asn Lys Asp Ile Lys Ser Ala Glu Gln Val Lys	
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Phe Ile Arg Glu Phe Ala Arg Glu Met Gly Ile Val Asn Phe Phe Glu	
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Ala Ala Gly Met Ala Thr Gly Glu Ala Trp Phe Lys Val Pro Glu Ala	
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Tyr Arg Ser Met Glu Phe Thr Gly Asp Gly Val Ala His Leu Ser Met	
195 200 205	
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Asp Asp Arg Phe Ala Met Ala Asn Met Ala Ile Glu Ala Gly Ala Lys	
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Ala Phe Pro His Leu Pro Ser Asn Thr Arg Thr Ile Asp Asn Val Gly	
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Asn Ile Lys Ile Asp Gln Val Val Ile Gly Ser Cys Thr Asn Gly Arg	
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Ile Glu Asp Leu Arg Val Ala Ala Glu Val Leu Lys Gly Arg Lys Val	
305 310 315 320	
cac aag gac gta aga tgt ata atc atc cct gca act cag aag ata tgg	1008

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gct	gcg	gta	agt	act	ccc	acc	tgc	gga	ccg	tgt	ctt	gga	ggt	cat	atg	1104
Ala	Ala	Val	Ser	Thr	Pro	Thr	Cys	Gly	Pro	Cys	Leu	Gly	Gly	His	Met	
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Phe	Val	Gly	Arg	Met	Gly	His	Pro	Glu	Ser	Glu	Ile	Tyr	Leu	Ala	Ser	
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ccg	gct	gta	gct	gcg	gca	tcg	gct	gtt	ttg	gga	aga	ata	ggt	tca	ccg	1248
Pro	Ala	Val	Ala	Ala	Ala	Ser	Ala	Val	Leu	Gly	Arg	Ile	Gly	Ser	Pro	
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gat	gaa	ctt	taa													1260
Asp	Glu	Leu														

<210> 970

<211> 419

<212> PRT

<213> Clostridium thermocellum ATCC 27405

<400> 970

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			20					25					30			
Leu	Gly	Asn	Asp	Ile	Thr	Thr	Pro	Val	Ala	Val	Lys	Glu	Phe	Arg	Lys	
		35				40						45				
Ile	Gly	Val	Asn	Lys	Val	Phe	Asp	Val	Asn	Lys	Ile	Ala	Ile	Val	Pro	
	50					55					60					
Asp	His	Phe	Thr	Pro	Asn	Lys	Asp	Ile	Lys	Ser	Ala	Glu	Gln	Val	Lys	
65					70				75						80	
Phe	Ile	Arg	Glu	Phe	Ala	Arg	Glu	Met	Gly	Ile	Val	Asn	Phe	Phe	Glu	
				85				90						95		
Val	Gly	Gln	Met	Gly	Val	Glu	His	Ala	Leu	Leu	Pro	Glu	Lys	Gly	Leu	
			100					105					110			
Val	Val	Pro	Gly	Asp	Val	Val	Ile	Gly	Ala	Asp	Ser	His	Thr	Cys	Thr	
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Tyr	Gly	Ala	Leu	Gly	Ala	Phe	Ser	Thr	Gly	Ile	Gly	Ser	Thr	Asp	Met	
	130					135					140					
Ala	Ala	Gly	Met	Ala	Thr	Gly	Glu	Ala	Trp	Phe	Lys	Val	Pro	Glu	Ala	
145					150					155					160	
Met	Lys	Phe	Val	Leu	Lys	Gly	Lys	Pro	Gly	Lys	Trp	Val	Ser	Gly	Lys	
				165				170						175		
Asp	Ile	Ile	Leu	His	Ile	Ile	Gly	Met	Ile	Gly	Val	Asp	Gly	Ala	Leu	
			180					185					190			
Tyr	Arg	Ser	Met	Glu	Phe	Thr	Gly	Asp	Gly	Val	Ala	His	Leu	Ser	Met	
		195					200					205				
Asp	Asp	Arg	Phe	Ala	Met	Ala	Asn	Met	Ala	Ile	Glu	Ala	Gly	Ala	Lys	
	210					215					220					
Asn	Gly	Ile	Phe	Glu	Val	Asp	Glu	Lys	Thr	Ile	Glu	Tyr	Val	Lys	Glu	
225					230					235					240	
His	Ser	Thr	Arg	Gln	Tyr	Lys	Val	Tyr	Lys	Ala	Asp	Glu	Asp	Ala	Glu	
				245					250					255		
Tyr	Val	Ala	Thr	Tyr	Glu	Ile	Asp	Leu	Ser	Gln	Val	Lys	Pro	Thr	Val	
			260					265					270			
Ala	Phe	Pro	His	Leu	Pro	Ser	Asn	Thr	Arg	Thr	Ile	Asp	Asn	Val	Gly	
		275					280					285				
Asn	Ile	Lys	Ile	Asp	Gln	Val	Val	Ile	Gly	Ser	Cys	Thr	Asn	Gly	Arg	
	290					295					300					
Ile	Glu	Asp	Leu	Arg	Val	Ala	Ala	Glu	Val	Leu	Lys	Gly	Arg	Lys	Val	
305					310					315					320	
His	Lys	Asp	Val	Arg	Cys	Ile	Ile	Ile	Pro	Ala	Thr	Gln	Lys	Ile	Trp	
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PF59082SeqList_PF59082.txt

Lys Gln Ala Met Asn Glu Gly Leu Phe Asp Ile Phe Ile Asp Ala Gly
 340 345 350
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 355 360 365
 Gly Ile Leu Ala Lys Gly Glu Arg Ala Val Ala Thr Thr Asn Arg Asn
 370 375 380
 Phe Val Gly Arg Met Gly His Pro Glu Ser Glu Ile Tyr Leu Ala Ser
 385 390 395 400
 Pro Ala Val Ala Ala Ser Ala Val Leu Gly Arg Ile Gly Ser Pro
 405 410 415
 Asp Glu Leu

<210> 971
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 <212> DNA
 <213> Prosthecochloris aestuarii DSM 271

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 aaa ttt gtt aac gca ggt gaa aat gtc tgg ctc aac gtc gat att ctc 96
 Lys Phe Val Asn Ala Gly Glu Asn Val Trp Leu Asn Val Asp Ile Leu
 20 25 30
 ctt acg cat gac gta tgc gga cct ccg acc ttc gat att ttc aag gaa 144
 Leu Thr His Asp Val Cys Gly Pro Pro Thr Phe Asp Ile Phe Lys Glu
 35 40 45
 aaa ttc ggc ccg gac gcc aaa gta tgg gat cct gaa aaa gtc gtt gta 192
 Lys Phe Gly Pro Asp Ala Lys Val Trp Asp Pro Glu Lys Val Val Val
 50 55 60
 cta ccc gac cac tac att ttc aca gaa aac gaa cac gca cac cgt aat 240
 Leu Pro Asp His Tyr Ile Phe Thr Glu Asn Glu His Ala His Arg Asn
 65 70 75 80
 atc gat ctt ctg cgc act ttc gct gca gaa aac ctc ccc aac tat 288
 Ile Asp Leu Leu Arg Thr Phe Ala Ala Glu Gln Asn Leu Pro Asn Tyr
 85 90 95
 tac gat gtc ggt acc gat cgt tac aaa gga gtc tgc cat gtt gcg ctt 336
 Tyr Asp Val Gly Thr Asp Arg Tyr Lys Gly Val Cys His Val Ala Leu
 100 105 110
 gca cag gaa ggc ttc aac ctt ccc ggc acc gtc ctc ttc ggg acc gat 384
 Ala Gln Glu Gly Phe Asn Leu Pro Gly Thr Val Leu Phe Gly Thr Asp
 115 120 125
 tcc cat acc tgt aca tcg ggt gcg ttc ggc atg ttc ggg acc ggt atc 432
 Ser His Thr Cys Thr Ser Gly Ala Phe Gly Met Phe Gly Thr Gly Ile
 130 135 140
 ggc aac acc gat gcc gcc ttc atc ctg gga aca gga aaa ctc tgg gaa 480
 Gly Asn Thr Asp Ala Ala Phe Ile Leu Gly Thr Gly Lys Leu Trp Glu
 145 150 155 160
 aaa gtc cct gaa tca atg aaa ttc gtt ttt gac ggt gcc atg ccg gac 528
 Lys Val Pro Glu Ser Met Lys Phe Val Phe Asp Gly Ala Met Pro Asp
 165 170 175
 tat ctc acc gcc aaa gac ctt atc ctt cag atc ctc ggc gat atc ggt 576
 Tyr Leu Thr Ala Lys Asp Leu Ile Leu Gln Ile Leu Gly Asp Ile Gly
 180 185 190
 acc gat ggg gcg acc tac cgg gcc atg gaa ttt gac ggt tcg gca gtc 624
 Thr Asp Gly Ala Thr Tyr Arg Ala Met Glu Phe Asp Gly Ser Ala Val
 195 200 205
 tat cag ctt cct gtc gaa gag cgt atg acc ctt acc aat atg gca atc 672
 Tyr Gln Leu Pro Val Glu Glu Arg Met Thr Leu Thr Asn Met Ala Ile
 210 215 220
 gaa gcc ggc ggc atg aac ggc atc att gct gct gat gag gtc aca gaa 720
 Glu Ala Gly Gly Met Asn Gly Ile Ile Ala Ala Asp Glu Val Thr Glu
 225 230 235 240

PF59082SeqList_PF59082.txt

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gac	ccg	gat	gcc	atc	tat	cac	agc	atc	tac	cac	tat	aat	gtt	gaa	gaa	816
Asp	Pro	Asp	Ala	Ile	Tyr	His	Ser	Ile	Tyr	His	Tyr	Asn	Val	Glu	Glu	
			260					265					270			
ctc	gag	cct	gtc	gta	gcc	cag	ccg	cac	agc	ccg	gac	aac	cgc	gca	act	864
Leu	Glu	Pro	Val	Val	Ala	Gln	Pro	His	Ser	Pro	Asp	Asn	Arg	Ala	Thr	
		275					280					285				
gta	cga	agc	gtt	cag	ggc	acg	aga	atc	acc	aaa	tcc	tac	atc	ggc	tca	912
Val	Arg	Ser	Val	Gln	Gly	Thr	Arg	Ile	Thr	Lys	Ser	Tyr	Ile	Gly	Ser	
	290					295					300					
tgc	acc	gga	ggc	aag	ctt	tcc	gat	ttc	aaa	atg	gct	gca	aaa	att	ctc	960
Cys	Thr	Gly	Gly	Lys	Leu	Ser	Asp	Phe	Lys	Met	Ala	Ala	Lys	Ile	Leu	
305					310					315					320	
aac	ggc	cag	cag	gtg	tcg	ata	caa	aca	aat	att	gtt	cct	gca	acc	gtt	1008
Asn	Gly	Gln	Gln	Val	Ser	Ile	Gln	Thr	Asn	Ile	Val	Pro	Ala	Thr	Val	
			325						330				335			
gaa	gtt	gcc	aaa	agt	ctg	gaa	aca	gaa	cag	tat	gaa	ggc	aag	tca	atc	1056
Glu	Val	Ala	Lys	Ser	Leu	Glu	Thr	Glu	Gln	Tyr	Glu	Gly	Lys	Ser	Ile	
			340					345					350			
cgc	aaa	gtc	ctg	gaa	gat	gcg	ggc	tgc	act	atc	gca	cag	cca	tcc	tgt	1104
Arg	Lys	Val	Leu	Glu	Asp	Ala	Gly	Cys	Thr	Ile	Ala	Gln	Pro	Ser	Cys	
		355				360					365					
gca	gca	tgc	ctt	ggc	ggc	ccg	gcc	gat	acc	ttt	ggg	cgt	tcg	gaa	gac	1152
Ala	Ala	Cys	Leu	Gly	Gly	Pro	Ala	Asp	Thr	Phe	Gly	Arg	Ser	Glu	Asp	
	370					375					380					
aac	gac	ctg	gtc	gta	tca	acg	aca	aac	aga	aac	ttc	ccc	ggc	cgt	atg	1200
Asn	Asp	Leu	Val	Val	Ser	Thr	Thr	Asn	Arg	Asn	Phe	Pro	Gly	Arg	Met	
385					390					395					400	
ggc	agc	aaa	aaa	gca	ggg	gtc	tat	ctt	gct	tcg	ccc	ctg	acg	gcc	gct	1248
Gly	Ser	Lys	Lys	Ala	Gly	Val	Tyr	Leu	Ala	Ser	Pro	Leu	Thr	Ala	Ala	
			405					410						415		
gca	tcc	gcc	att	acc	gga	agg	ctt	acc	gac	ccg	aga	gag	ttt	ctc	tct	1296
Ala	Ser	Ala	Ile	Thr	Gly	Arg	Leu	Thr	Asp	Pro	Arg	Glu	Phe	Leu	Ser	
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taa																1299

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<211> 432

<212> PRT

<213> Prosthecochloris aestuarii DSM 271

<400> 972

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Lys	Phe	Val	Asn	Ala	Gly	Glu	Asn	Val	Trp	Leu	Asn	Val	Asp	Ile	Leu	
			20					25					30			
Leu	Thr	His	Asp	Val	Cys	Gly	Pro	Pro	Thr	Phe	Asp	Ile	Phe	Lys	Glu	
		35					40				45					
Lys	Phe	Gly	Pro	Asp	Ala	Lys	Val	Trp	Asp	Pro	Glu	Lys	Val	Val	Val	
	50					55				60						
Leu	Pro	Asp	His	Tyr	Ile	Phe	Thr	Glu	Asn	Glu	His	Ala	His	Arg	Asn	
65					70				75						80	
Ile	Asp	Leu	Leu	Arg	Thr	Phe	Ala	Ala	Glu	Gln	Asn	Leu	Pro	Asn	Tyr	
			85					90						95		
Tyr	Asp	Val	Gly	Thr	Asp	Arg	Tyr	Lys	Gly	Val	Cys	His	Val	Ala	Leu	
		100					105						110			
Ala	Gln	Glu	Gly	Phe	Asn	Leu	Pro	Gly	Thr	Val	Leu	Phe	Gly	Thr	Asp	
		115				120						125				
Ser	His	Thr	Cys	Thr	Ser	Gly	Ala	Phe	Gly	Met	Phe	Gly	Thr	Gly	Ile	
	130					135				140						
Gly	Asn	Thr	Asp	Ala	Ala	Phe	Ile	Leu	Gly	Thr	Gly	Lys	Leu	Trp	Glu	
145					150				155						160	
Lys	Val	Pro	Glu	Ser	Met	Lys	Phe	Val	Phe	Asp	Gly	Ala	Met	Pro	Asp	
			165					170						175		
Tyr	Leu	Thr	Ala	Lys	Asp	Leu	Ile	Leu	Gln	Ile	Leu	Gly	Asp	Ile	Gly	

PF59082SeqList_PF59082.txt

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Gly Glu Phe Ala Thr Gly Ile Gly Asn Thr Asp Ala Ala Phe Ile Ala				
145	150	155	160	
ggt aca ggc aaa cta ttg gtc aaa gtg cca gca act atg cgc ttt atc				528
Gly Thr Gly Lys Leu Val Lys Val Pro Ala Thr Met Arg Phe Ile				
165	170	175		
ttg aat ggg gaa atg ccc aat tat tta tta gca aaa gat ttg ata ctt				576
Leu Asn Gly Glu Met Pro Asn Tyr Leu Leu Ala Lys Asp Leu Ile Leu				
180	185	190		
caa att att gga gat att tct gta tca ggt gct act tat aga aca atg				624
Gln Ile Ile Gly Asp Ile Ser Val Ser Gly Ala Thr Tyr Arg Thr Met				
195	200	205		
gaa ttt gct ggg gaa act gtt gga caa atg acc atg gaa gaa cgg atg				672
Glu Phe Ala Gly Glu Thr Val Gly Gln Met Thr Met Glu Glu Arg Met				
210	215	220		
acc cta tgc aat atg gtt att gaa gcg ggg ggt aaa aat gga gtt att				720
Thr Leu Cys Asn Met Val Ile Glu Ala Gly Gly Lys Asn Gly Val Ile				
225	230	235	240	
gct ccc gat gag atg acc ttt gaa tat ttg cgg ggt aga acc gat aaa				768
Ala Pro Asp Glu Met Thr Phe Glu Tyr Leu Arg Gly Arg Thr Asp Lys				
245	250	255		
cca ttt gag tca ttt tat tct gat aaa aat gcc gaa ttt tat agc gat				816
Pro Phe Glu Ser Phe Tyr Ser Asp Lys Asn Ala Glu Phe Tyr Ser Asp				
260	265	270		
cgc tcc tat gat gtc aca aaa tta gaa cct gta gta gct aaa ccc cat				864
Arg Ser Tyr Asp Val Thr Lys Leu Glu Pro Val Val Ala Lys Pro His				
275	280	285		
tct cca gat aat aag gaa ctt gcc cgt aac tgt cag gat gtt aaa att				912
Ser Pro Asp Asn Lys Glu Leu Ala Arg Asn Cys Gln Asp Val Lys Ile				
290	295	300		
gac cga gtt tat att ggt tcc tgt act gga gga aaa act tct gac ttt				960
Asp Arg Val Tyr Ile Gly Ser Cys Thr Gly Gly Lys Thr Ser Asp Phe				
305	310	315	320	
ctt cat gca gcg aaa ctt att aaa gat cat caa gtg aaa gtt ccg act				1008
Leu His Ala Ala Lys Leu Ile Lys Asp His Gln Val Lys Val Pro Thr				
325	330	335		
tat tta gta cca gca act cag aaa gtt tat gag gat tta ttt att att				1056
Tyr Leu Val Pro Ala Thr Gln Lys Val Tyr Glu Asp Leu Phe Ile Ile				
340	345	350		
aaa cat gat gga aaa act ctc tca gaa ata ttt tta gat gct ggt tgt				1104
Lys His Asp Gly Lys Thr Leu Ser Glu Ile Phe Leu Asp Ala Gly Cys				
355	360	365		
att gaa cct gca gct cca tct tgt gcc gct tgt tta gga gga cca aaa				1152
Ile Glu Pro Ala Ala Pro Ser Cys Ala Ala Cys Leu Gly Gly Pro Lys				
370	375	380		
gat aca ttt ggg cga tta aat gaa ccg gaa att tgt gtg tct aca act				1200
Asp Thr Phe Gly Arg Leu Asn Glu Pro Glu Ile Cys Val Ser Thr Thr				
385	390	395	400	
aat cgt aat ttt cct ggt cga atg gga aat aaa cag gca caa gtc tat				1248
Asn Arg Asn Phe Pro Gly Arg Met Gly Asn Lys Gln Ala Gln Val Tyr				
405	410	415		
tta gct tct ccc tat aca gca gca gct tca gct tta act gga tat gtt				1296
Leu Ala Ser Pro Tyr Thr Ala Ala Ala Ser Ala Leu Thr Gly Tyr Val				
420	425	430		
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Thr Asp Pro Arg Glu Phe Met				
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<211> 439

<212> PRT

<213> Trichodesmium erythraeum IMS101

<400> 974

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Ser Thr Val Asn Pro Gly Glu Asn Ile Trp Val Asn Val Asp Val Leu

20

25

30

PF59082SeqList_PF59082.txt

Met Thr His Asp Val Cys Gly Pro Gly Thr Ile Gly Ile Phe Lys Arg
 35 40 45
 Glu Phe Gly Glu Asn Ala Lys Val Trp Asp Lys Glu Lys Ile Val Leu
 50 55 60
 Ile Pro Asp His Tyr Ile Phe Thr Ala Asp Glu Arg Ala Asn Arg Asn
 65 70 75 80
 Val Asp Ile Leu Arg Asp Phe Ala Gln Glu Gln Asn Ile Lys Tyr Phe
 85 90 95
 Tyr Asp Ile Ile Glu Arg Ser Asn Phe Lys Ala Asn Pro Asp Tyr Lys
 100 105 110
 Gly Val Cys His Val Ala Leu Ala Gln Glu Gly His Thr Arg Pro Gly
 115 120 125
 Glu Val Leu Phe Gly Thr Asp Ser His Thr Cys Asn Ala Gly Ala Phe
 130 135 140
 Gly Glu Phe Ala Thr Gly Ile Gly Asn Thr Asp Ala Ala Phe Ile Ala
 145 150 155 160
 Gly Thr Gly Lys Leu Leu Val Lys Val Pro Ala Thr Met Arg Phe Ile
 165 170 175
 Leu Asn Gly Glu Met Pro Asn Tyr Leu Leu Ala Lys Asp Leu Ile Leu
 180 185 190
 Gln Ile Ile Gly Asp Ile Ser Val Ser Gly Ala Thr Tyr Arg Thr Met
 195 200 205
 Glu Phe Ala Gly Glu Thr Val Gly Gln Met Thr Met Glu Glu Arg Met
 210 215 220
 Thr Leu Cys Asn Met Val Ile Glu Ala Gly Gly Lys Asn Gly Val Ile
 225 230 235 240
 Ala Pro Asp Glu Met Thr Phe Glu Tyr Leu Arg Gly Arg Thr Asp Lys
 245 250 255
 Pro Phe Glu Ser Phe Tyr Ser Asp Lys Asn Ala Glu Phe Tyr Ser Asp
 260 265 270
 Arg Ser Tyr Asp Val Thr Lys Leu Glu Pro Val Val Ala Lys Pro His
 275 280 285
 Ser Pro Asp Asn Lys Glu Leu Ala Arg Asn Cys Gln Asp Val Lys Ile
 290 295 300
 Asp Arg Val Tyr Ile Gly Ser Cys Thr Gly Gly Lys Thr Ser Asp Phe
 305 310 315 320
 Leu His Ala Ala Lys Leu Ile Lys Asp His Gln Val Lys Val Pro Thr
 325 330 335
 Tyr Leu Val Pro Ala Thr Gln Lys Val Tyr Glu Asp Leu Phe Ile Ile
 340 345 350
 Lys His Asp Gly Lys Thr Leu Ser Glu Ile Phe Leu Asp Ala Gly Cys
 355 360 365
 Ile Glu Pro Ala Ala Pro Ser Cys Ala Ala Cys Leu Gly Gly Pro Lys
 370 375 380
 Asp Thr Phe Gly Arg Leu Asn Glu Pro Glu Ile Cys Val Ser Thr Thr
 385 390 395 400
 Asn Arg Asn Phe Pro Gly Arg Met Gly Asn Lys Gln Ala Gln Val Tyr
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 Thr Asp Pro Arg Glu Phe Met
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<220>

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 gag aaa atc ttt tcc cgg gca gcg gga aca gag gca aaa gct aac gat
 Glu Lys Ile Phe Ser Arg Ala Ala Gly Thr Glu Ala Lys Ala Asn Asp
 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95

48

96

PF59082SeqList_PF59082.txt

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192	gta ctt gcc gtg aat gct ttt aag gaa atg gag atg gaa aag gtc tgg Val Leu Ala Val Asn Ala Phe Lys Glu Met Glu Met Glu Lys Val Trp			
240	gac cct tca agg atc gta gtc ccc ttt gac cac atc gcg cct gcg aat Asp Pro Ser Arg Ile Val Val Pro Phe Asp His Ile Ala Pro Ala Asn			
288	aat gag acc tca gcc acc ctg cag aga gag atc agg gaa tgg gta aag Asn Glu Thr Ser Ala Thr Leu Gln Arg Glu Ile Arg Glu Trp Val Lys			
336	gag cag ggg atc cct aac ttc tat gag gtc ggg gaa ggg atc tgt cac Glu Gln Gly Ile Pro Asn Phe Tyr Glu Val Gly Glu Gly Ile Cys His			
384	cag gtc ctt ccg gaa aac ggt ttt gca ttg ccc gga aag ctg gtt gtt Gln Val Leu Pro Glu Asn Gly Phe Ala Leu Pro Gly Lys Leu Val Val			
432	ggg gct gat tcg cat tcc tgc acg tac ggg gct ttt gga gct ttt gca Gly Ala Asp Ser His Ser Cys Thr Tyr Gly Ala Phe Gly Ala Phe Ala			
480	aca ggg gta ggg gct acc gat atg gct gaa atc ttt gct acg gga aaa Thr Gly Val Gly Ala Thr Asp Met Ala Glu Ile Phe Ala Thr Gly Lys			
528	ctc tgg ttt aag gtt ccg gaa agc ttc agg atg acg gtt gaa ggg agc Leu Trp Phe Lys Val Pro Glu Ser Phe Arg Met Thr Val Glu Gly Ser			
576	ctt cgg aaa ggg gtc tat gca aag gat ctg act ctt tac ctg atc gga Leu Arg Lys Gly Val Tyr Ala Lys Asp Leu Thr Leu Tyr Ile Gly			
624	aag acc gga att gcc ggg gcg acc tat aaa gca gtt gag ttt tac ggg Lys Thr Gly Ile Ala Gly Ala Thr Tyr Lys Ala Val Glu Phe Tyr Gly			
672	cag gca atc cgc gaa ctt acg gtt gct ggc agg atg acg ctc tgc aat Gln Ala Ile Arg Glu Leu Thr Val Ala Gly Arg Met Thr Leu Cys Asn			
720	atg gca att gag atg ggc gca aag acc ggg atc gtc cct ccg gac gaa Met Ala Ile Glu Met Gly Ala Lys Thr Gly Ile Val Pro Pro Asp Glu			
768	aag acc ttc gag ttc ctg aaa aac agg gca gca gct act tat gaa cct Lys Thr Phe Glu Phe Leu Lys Asn Arg Ala Ala Ala Thr Tyr Glu Pro			
816	gtc tat gcc gac ccg gat gct gtt tat ctg gaa gag ttc act tat gat Val Tyr Ala Asp Pro Asp Ala Val Tyr Leu Glu Glu Phe Thr Tyr Asp			
864	gcc gac gat atc gaa ccc cag gtt gcc tgc ccg cat cag gtg gat aat Ala Asp Asp Ile Glu Pro Gln Val Ala Cys Pro His Gln Val Asp Asn			
912	gta aag ccc gta gga gag gtt gaa ggc act cat gta gac cag gtc ttt Val Lys Pro Val Gly Glu Val Glu Gly Thr His Val Asp Gln Val Phe			
960	atc ggg acg tgc acg aac ggc agg ctt gaa gac ctc gag gtc gca gca Ile Gly Thr Cys Thr Asn Gly Arg Leu Glu Asp Leu Glu Val Ala Ala			
1008	gca gtc ctg aaa gga aaa cag gtt gca gtc agg aca att gtg atc cct Ala Val Leu Lys Gly Lys Gln Val Ala Val Arg Thr Ile Val Ile Pro			
1056	gcc tct cgc acc acc ctc ctt gca gca atc gaa aac ggg aca atg gaa Ala Ser Arg Thr Thr Leu Leu Ala Ala Ile Glu Asn Gly Thr Met Glu			
1104	act ctg ctg aaa gcc ggg gta acc ctt gca acc ccg ggc tgc gga ccc Thr Leu Leu Lys Ala Gly Val Thr Leu Ala Thr Pro Gly Cys Gly Pro			
1152	tgc ctc ggt gcc cat cag ggg gtg ctc gga gaa ggc gag gtc tgc gtt Cys Leu Gly Ala His Gln Gly Val Leu Gly Glu Gly Glu Val Cys Val			
1200	tca acc gca aac agg aac ttc aaa ggc agg atg gga aaa ggc ggt ttt Ser Thr Ala Asn Arg Asn Phe Lys Gly Arg Met Glu Lys Gly Gly Phe			

PF59082SeqList_PF59082.txt

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	405		410	415	
gaa atc acc gat ccg agg aca gtt tga					1275
Glu Ile Thr Asp Pro Arg Thr Val					
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 <213> Methanosarcina acetivorans

<400> 976

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Glu	Lys	Ile	Phe	Ser	Arg	Ala	Ala	Gly	Thr	Glu	Ala	Lys	Ala	Asn	Asp
			20					25					30		
Phe	Val	Leu	Ala	Asp	Val	Asp	Tyr	Ala	Met	Ala	His	Asp	Gly	Thr	Ser
		35				40						45			
Val	Leu	Ala	Val	Asn	Ala	Phe	Lys	Glu	Met	Glu	Met	Glu	Lys	Val	Trp
	50					55				60					
Asp	Pro	Ser	Arg	Ile	Val	Val	Pro	Phe	Asp	His	Ile	Ala	Pro	Ala	Asn
65				70				75						80	
Asn	Glu	Thr	Ser	Ala	Thr	Leu	Gln	Arg	Glu	Ile	Arg	Glu	Trp	Val	Lys
			85					90					95		
Glu	Gln	Gly	Ile	Pro	Asn	Phe	Tyr	Glu	Val	Gly	Glu	Gly	Ile	Cys	His
			100					105					110		
Gln	Val	Leu	Pro	Glu	Asn	Gly	Phe	Ala	Leu	Pro	Gly	Lys	Leu	Val	Val
		115				120						125			
Gly	Ala	Asp	Ser	His	Ser	Cys	Thr	Tyr	Gly	Ala	Phe	Gly	Ala	Phe	Ala
	130					135					140				
Thr	Gly	Val	Gly	Ala	Thr	Asp	Met	Ala	Glu	Ile	Phe	Ala	Thr	Gly	Lys
145					150					155				160	
Leu	Trp	Phe	Lys	Val	Pro	Glu	Ser	Phe	Arg	Met	Thr	Val	Glu	Gly	Ser
			165					170					175		
Leu	Arg	Lys	Gly	Val	Tyr	Ala	Lys	Asp	Leu	Thr	Leu	Tyr	Leu	Ile	Gly
			180					185					190		
Lys	Thr	Gly	Ile	Ala	Gly	Ala	Thr	Tyr	Lys	Ala	Val	Glu	Phe	Tyr	Gly
		195				200						205			
Gln	Ala	Ile	Arg	Glu	Leu	Thr	Val	Ala	Gly	Arg	Met	Thr	Leu	Cys	Asn
	210				215					220					
Met	Ala	Ile	Glu	Met	Gly	Ala	Lys	Thr	Gly	Ile	Val	Pro	Pro	Asp	Glu
225				230						235				240	
Lys	Thr	Phe	Glu	Phe	Leu	Lys	Asn	Arg	Ala	Ala	Ala	Thr	Tyr	Glu	Pro
			245					250						255	
Val	Tyr	Ala	Asp	Pro	Asp	Ala	Val	Tyr	Leu	Glu	Glu	Phe	Thr	Tyr	Asp
			260					265					270		
Ala	Asp	Asp	Ile	Glu	Pro	Gln	Val	Ala	Cys	Pro	His	Gln	Val	Asp	Asn
		275				280						285			
Val	Lys	Pro	Val	Gly	Glu	Val	Glu	Gly	Thr	His	Val	Asp	Gln	Val	Phe
	290					295					300				
Ile	Gly	Thr	Cys	Thr	Asn	Gly	Arg	Leu	Glu	Asp	Leu	Glu	Val	Ala	Ala
305				310						315				320	
Ala	Val	Leu	Lys	Gly	Lys	Gln	Val	Ala	Val	Arg	Thr	Ile	Val	Ile	Pro
			325					330					335		
Ala	Ser	Arg	Thr	Thr	Leu	Leu	Ala	Ala	Ile	Glu	Asn	Gly	Thr	Met	Glu
			340					345					350		
Thr	Leu	Leu	Lys	Ala	Gly	Val	Thr	Leu	Ala	Thr	Pro	Gly	Cys	Gly	Pro
		355				360						365			
Cys	Leu	Gly	Ala	His	Gln	Gly	Val	Leu	Gly	Glu	Gly	Glu	Val	Cys	Val
	370				375					380					
Ser	Thr	Ala	Asn	Arg	Asn	Phe	Lys	Gly	Arg	Met	Gly	Lys	Gly	Gly	Phe
385				390						395				400	
Ile	Tyr	Leu	Ala	Ser	Pro	Ala	Thr	Ala	Ala	Ser	Ala	Leu	Thr	Gly	
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Glu	Ile	Thr	Asp	Pro	Arg	Thr	Val								
			420												

PF59082SeqList_PF59082.txt

<210> 977
 <211> 1257
 <212> DNA
 <213> Methanopyrus kandleri

<220>
 <221> CDS
 <222> (1)..(1257)
 <223> transl_table=11

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gac gct gag gcg ggg gat atc gtc gtc gcc aac atc gac gtg gcg atg      96
Asp Ala Glu Ala Gly Asp Ile Val Val Ala Asn Ile Asp Val Ala Met
          20          25          30
gtc cac gat atc acg ggc ccg atc acg gtt cag cgg ctc gag gag atg      144
Val His Asp Ile Thr Gly Pro Ile Thr Val Gln Arg Leu Glu Glu Met
          35          40          45
gga gtc gag cgc gtg tgg gac ccg tcc aag atc gtc gtg ctg ttc gac      192
Gly Val Glu Arg Val Trp Asp Pro Ser Lys Ile Val Val Leu Phe Asp
          50          55          60
cat cag gtg ccc gcg gac tcc gtg gaa gcc gcg gag aac cac aaa ata      240
His Gln Val Pro Ala Asp Ser Val Glu Ala Ala Glu Asn His Lys Ile
          65          70          75          80
atg cgg gag ttc gtc gaa gaa cag ggt atc gag cac ttc tac gac gtt      288
Met Arg Glu Phe Val Glu Glu Gln Gly Ile Glu His Phe Tyr Asp Val
          85          90          95
cgg gag ggt gtc tgt cac cag gtc ctc ccg gag aag ggt cac gtg cgt      336
Arg Glu Gly Val Cys His Gln Val Leu Pro Glu Lys Gly His Val Arg
          100          105          110
ccc ggg gac gtg atc gtg ggg gcc gac tct cac acc tgc acc cac gga      384
Pro Gly Asp Val Ile Val Gly Ala Asp Ser His Thr Cys Thr His Gly
          115          120          125
gcg ctc gga gcc ttc gcc acc ggg atc ggt tcc acc gac atg gcg gcg      432
Ala Leu Gly Ala Phe Ala Thr Gly Ile Gly Ser Thr Asp Met Ala Ala
          130          135          140
gtc ttt gcg acc ggt aag ctg tgg ttc cgc gtc ccg gaa act tac cgc      480
Val Phe Ala Thr Gly Lys Leu Trp Phe Arg Val Pro Glu Thr Tyr Arg
          145          150          155          160
gta gag atc acg gga gag ctt ccg gaa ggt gtg tac gcg aag gat gtc      528
Val Glu Ile Thr Gly Glu Leu Pro Glu Gly Val Tyr Ala Lys Asp Val
          165          170          175
gtg ctc aag gtg acg gga gaa atc ggt gcc gac ggt gcg acg tac atg      576
Val Leu Lys Val Thr Gly Glu Ile Gly Ala Asp Gly Ala Thr Tyr Met
          180          185          190
gcg atc gag tac cac ggc gag gtc gtc cga gag atg tcc gta tcg gac      624
Ala Ile Glu Tyr His Gly Glu Val Val Arg Glu Met Ser Val Ser Asp
          195          200          205
cgt atg tgc ctg tgc aac atg gcg atc gag atg gga gcg aag acg gga      672
Arg Met Cys Leu Cys Asn Met Ala Ile Glu Met Gly Ala Lys Thr Gly
          210          215          220
atg gtt cca ccc gac gag aag acg ctc gag tac gtc aag aag cgt gcg      720
Met Val Pro Pro Asp Glu Lys Thr Leu Glu Tyr Val Lys Lys Arg Ala
          225          230          235          240
ggt acg gaa ggg cgc ccg gtt gag ccg gac ccg gac gcc cgg tac gag      768
Gly Thr Glu Gly Arg Pro Val Glu Pro Asp Pro Asp Ala Arg Tyr Glu
          245          250          255
gcc gag ctg acc ttg gac gtg agc gac ctc gag ccg cag gtc gcg aag      816
Ala Glu Leu Thr Leu Asp Val Ser Asp Leu Glu Pro Gln Val Ala Lys
          260          265          270
ccg ttc tct ccg gac aac gtg gtg ccc gtg ggg gag gtc gaa ggt atc      864
Pro Phe Ser Pro Asp Asn Val Val Pro Val Gly Glu Val Glu Gly Ile
          275          280          285
gcg atc gac caa gtc ttc atc ggt tcc tgt acc aac ggt cgg tac gag      912
Ala Ile Asp Gln Val Phe Ile Gly Ser Cys Thr Asn Gly Arg Tyr Glu
          290          295          300
gac ctg aag gtt gcg gcg gag gta ctt gaa ggc gag gtc cac gac      960
    
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PF59082SeqList_PF59082.txt

Asp 305	Leu	Lys	Val	Ala	Ala 310	Glu	Val	Leu	Glu	Gly 315	Glu	Glu	Val	His	Asp 320	
gac	gtc	cgg	ctg	atc	gtc	atc	ccg	gcg	tcg	agg	gaa	gtt	tac	cac	cgg	1008
Asp	Val	Arg	Leu	Ile 325	Val	Ile	Pro	Ala	Ser 330	Arg	Glu	Val	Tyr	His 335	Arg	
acg	ctc	aag	gac	ggc	gtg	ctc	gaa	gta	ctc	cac	gag	gcg	ggg	gca	ctg	1056
Thr	Leu	Lys	Asp	Gly 340	Val	Leu	Glu	Val	Leu	His	Glu	Ala	Gly 350	Ala	Leu	
atc	tgc	ccg	ccg	aac	tgc	ggc	ccg	tgc	ctg	ggc	cat	atg	gga	gtg		1104
Ile	Cys	Pro 355	Pro	Asn	Cys	Gly 360	Pro	Cys	Leu	Gly	Gly	His 365	Met	Gly	Val	
cta	gcg	gaa	ggc	gag	cga	tgc	gta	gcg	acg	tcc	aac	agg	aac	ttt	ccg	1152
Leu	Ala	Glu	Gly	Glu	Arg	Cys 375	Val	Ala	Thr	Ser	Asn	Arg	Asn	Phe	Pro	
ggc	agg	atg	gga	cac	cg	gag	tcg	gaa	gtg	tat	cta	gcc	agt	ccg	gcg	1200
Gly 385	Arg	Met	Gly	His	Arg 390	Glu	Ser	Glu	Val	Tyr 395	Leu	Ala	Ser	Pro	Ala 400	
acg	gcc	gcc	gcc	agc	gct	atc	gag	ggc	gag	atc	acc	gac	cct	cgt	ccc	1248
Thr	Ala	Ala	Ala	Ser 405	Ala	Ile	Glu	Gly	Glu 410	Ile	Thr	Asp	Pro	Arg 415	Pro	
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Tyr	Leu															

<210> 978

<211> 418

<212> PRT

<213> Methanopyrus kandleri

<400> 978

Met 1	Gly	Lys	Thr	Met 5	Ala	Glu	Lys	Ile	Leu 10	Ser	Arg	Ala	Ser	Gly 15	Glu	
Asp	Ala	Glu	Ala	Gly 20	Asp	Ile	Val	Val 25	Ala	Asn	Ile	Asp	Val 30	Ala	Met	
Val	His	Asp 35	Ile	Thr	Gly	Pro	Ile 40	Thr	Val	Gln	Arg	Leu 45	Glu	Glu	Met	
Gly	Val	Glu	Arg	Val	Trp	Asp 55	Pro	Ser	Lys	Ile	Val 60	Val	Leu	Phe	Asp	
His 65	Gln	Val	Pro	Ala	Asp 70	Ser	Val	Glu	Ala	Ala 75	Glu	Asn	His	Lys	Ile 80	
Met	Arg	Glu	Phe	Val 85	Glu	Glu	Gln	Gly	Ile 90	Glu	His	Phe	Tyr	Asp 95	Val	
Arg	Glu	Gly	Val 100	Cys	His	Gln	Val	Leu 105	Pro	Glu	Lys	Gly	His 110	Val	Arg	
Pro	Gly	Asp 115	Val	Ile	Val	Gly	Ala 120	Asp	Ser	His	Thr	Cys 125	Thr	His	Gly	
Ala	Leu	Gly	Ala	Phe	Ala	Thr 135	Gly	Ile	Gly	Ser	Thr	Asp	Met	Ala	Ala	
Val 145	Phe	Ala	Thr	Gly	Lys 150	Leu	Trp	Phe	Arg	Val 155	Pro	Glu	Thr	Tyr	Arg 160	
Val	Glu	Ile	Thr	Gly 165	Glu	Leu	Pro	Glu	Gly 170	Val	Tyr	Ala	Lys	Asp 175	Val	
Val	Leu	Lys	Val 180	Thr	Gly	Glu	Ile	Gly 185	Ala	Asp	Gly	Ala	Thr 190	Tyr	Met	
Ala	Ile	Glu 195	Tyr	His	Gly	Glu	Val 200	Val	Arg	Glu	Met	Ser 205	Val	Ser	Asp	
Arg	Met 210	Cys	Leu	Cys	Asn	Met 215	Ala	Ile	Glu	Met	Gly 220	Ala	Lys	Thr	Gly	
Met	Val	Pro	Pro	Asp	Glu 230	Lys	Thr	Leu	Glu	Tyr 235	Val	Lys	Lys	Arg	Ala 240	
Gly	Thr	Glu	Gly	Arg 245	Pro	Val	Glu	Pro	Asp 250	Pro	Asp	Ala	Arg	Tyr 255	Glu	
Ala	Glu	Leu	Thr 260	Leu	Asp	Val	Ser	Asp 265	Leu	Glu	Pro	Gln	Val 270	Ala	Lys	
Pro	Phe	Ser 275	Pro	Asp	Asn	Val 280	Val	Pro	Val	Gly	Glu	Val 285	Glu	Gly	Ile	
Ala	Ile	Asp 290	Gln	Val	Phe	Ile 295	Gly	Ser	Cys	Thr	Asn 300	Gly	Arg	Tyr	Glu	
Asp	Leu	Lys	Val	Ala	Ala	Glu	Val	Leu	Glu	Gly	Glu	Val	His	Asp		

PF59082SeqList_PF59082.txt

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305          310          315          320
Asp Val Arg Leu Ile Val Ile Pro Ala Ser Arg Glu Val Tyr His Arg
          325          330          335
Thr Leu Lys Asp Gly Val Leu Glu Val Leu His Glu Ala Gly Ala Leu
          340          345          350
Ile Cys Pro Asn Cys Gly Pro Cys Leu Gly Gly His Met Gly Val
          355          360          365
Leu Ala Glu Gly Glu Arg Cys Val Ala Thr Ser Asn Arg Asn Phe Pro
          370          375          380
Gly Arg Met Gly His Arg Glu Ser Glu Val Tyr Leu Ala Ser Pro Ala
385          390          395          400
Thr Ala Ala Ala Ser Ala Ile Glu Gly Glu Ile Thr Asp Pro Arg Pro
          405          410          415
Tyr Leu

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<210> 979
 <211> 1260
 <212> DNA
 <213> Methanobacterium thermoautotrophicum

<220>
 <221> CDS
 <222> (1)..(1260)
 <223> transl_table=11

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1          5          10          15
gat agg gtg gaa gcc ggt gaa ata gtt atg gcg gat ata gat gtt gcg      96
Asp Arg Val Glu Ala Gly Glu Ile Val Met Ala Asp Ile Asp Val Ala
          20          25          30
atg acc cat gac ctc aca ggt ccc ctg tcg gtt gag tcc ttc agg gcc      144
Met Thr His Asp Leu Thr Gly Pro Leu Ser Val Glu Ser Phe Arg Ala
          35          40          45
ata ggt gag gat agg gtc tgg gac cct gaa aaa atc gtt gtg ata ttc      192
Ile Gly Glu Asp Arg Val Trp Asp Pro Glu Lys Ile Val Val Ile Phe
50          55          60
gat cac cag gtc cct gca gac tcc att gaa gcc gcc cag aac cac atg      240
Asp His Gln Val Pro Ala Asp Ser Ile Glu Ala Ala Gln Asn His Met
65          70          75          80
ata atg agg gac ttc gta gag gag cag gga ata cgg aac ttc tat gac      288
Ile Met Arg Asp Phe Val Glu Glu Gln Gly Ile Arg Asn Phe Tyr Asp
85          90          95
gtt cgt gaa ggc gtc tgt cac cag gtg ctc cct gag aag ggc cat gtt      336
Val Arg Glu Gly Val Cys His Gln Val Leu Pro Glu Lys Gly His Val
100          105          110
gtg ccc ggt gag gtc gtg gtg ggt aca gac tcc cac acc tgc acc cac      384
Val Pro Gly Glu Val Val Val Thr Asp Ser His Thr Cys Thr His
115          120          125
ggg gcc ctc gga gcc ttc gca acg ggt ata ggt tca aca gat atg gcc      432
Gly Ala Leu Gly Ala Phe Ala Thr Gly Ile Gly Ser Thr Asp Met Ala
130          135          140
atg gta ttt gca act ggg aaa ctt tgg ttc agg gtc cct gaa acc ctg      480
Met Val Phe Ala Thr Gly Lys Leu Trp Phe Arg Val Pro Glu Thr Leu
145          150          155          160
aga ttt gat gtg agg gga aaa ctc agg gag cac gtc tat gca aag gac      528
Arg Phe Asp Val Arg Gly Lys Leu Arg Glu His Val Tyr Ala Lys Asp
165          170          175
gtc ata ctg aac ata ata ggg agg gtt ggt gcc gat ggc gca acc tac      576
Val Ile Leu Asn Ile Ile Gly Arg Val Gly Ala Asp Gly Ala Thr Tyr
180          185          190
atg gcc tgt gaa ttt gca ggt gaa acc gtt gca gaa atg agt gta tcc      624
Met Ala Cys Glu Phe Ala Gly Thr Val Ala Glu Met Ser Val Ser
195          200          205          210
gac cgt atg gtc ctc tca aat atg gca ata gag atg ggt ggt aag aca      672
Asp Arg Met Val Leu Ser Asn Met Ala Ile Glu Met Gly Gly Lys Thr
210          215          220

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PF59082SeqList_PF59082.txt

gga atc gtg gaa cct gac gaa aaa acc ctg aac tat gtc agg agg agg	720
Gly Ile Val Glu Pro Asp Glu Lys Thr Leu Asn Tyr Val Arg Arg Arg	
225 230 235 240	
tca ggt aaa ccc tgg agg gtc ttc aaa aca gac cct gac gct cca tcc	768
Ser Gly Lys Pro Trp Arg Val Phe Lys Thr Asp Pro Asp Ala Pro Ser	
245 250 255	
ctc agt gtc atg gag gtc gac gtg agt gac ctt gaa ccc cag gtc gcc	816
Leu Ser Val Met Glu Val Asp Val Ser Asp Leu Glu Pro Gln Val Ala	
260 265 270	
tgt cca cac aat gtg gac aat gtg aaa ccc gtc acc gag gtg gag ggg	864
Cys Pro His Asn Val Asp Asn Val Lys Pro Val Thr Glu Val Glu Gly	
275 280 285	
aca gag ata gac cag gtc ttc ctt ggt tca tgc aca aat gga agg ctc	912
Thr Glu Ile Asp Gln Val Phe Leu Gly Ser Cys Thr Asn Gly Arg Leu	
290 295 300	
agt gac ctc agg gac gct gcc ata ctg aag aac agg aag gtc tca	960
Ser Asp Leu Arg Asp Ala Ala Ile Leu Lys Asn Arg Lys Val Ser	
305 310 315 320	
gac agt gtc agg atg ctc gtc ata cct gcc tcc agg gag gtc tac cgc	1008
Asp Ser Val Arg Met Leu Val Ile Pro Ala Ser Arg Glu Val Tyr Arg	
325 330 335	
agg gcc ctt gac gag gga ctg att gag ata ttc gtg gat gca gga gcc	1056
Arg Ala Leu Asp Glu Gly Leu Ile Glu Ile Phe Val Asp Ala Gly Ala	
340 345 350	
ctg gta tgc aac ccc tgc tgc ggc ccc tgc ctc gga gga cac gtt gga	1104
Leu Val Cys Asn Pro Cys Cys Gly Pro Cys Leu Gly Gly His Val Gly	
355 360 365	
ctg gtc gga cca ggg gag gtg agc ctc tca acc tca aac agg aac ttc	1152
Leu Val Gly Pro Gly Glu Val Ser Leu Ser Thr Ser Asn Arg Asn Phe	
370 375 380	
agg ggg agg cag gga agc ccc gaa gca gag gtc ctc tcc tca gca	1200
Arg Gly Arg Gln Gly Ser Pro Glu Ala Glu Val Tyr Leu Ser Ser Ala	
385 390 395 400	
gcc gtg gca gcc gca tct gca gtg aag ggc agc ata acc cac cct ggg	1248
Ala Val Ala Ala Ser Ala Val Lys Gly Ser Ile Thr His Pro Gly	
405 410 415	
agt ctg aag tag	1260
Ser Leu Lys	

<210> 980

<211> 419

<212> PRT

<213> Methanobacterium thermoautotrophicum

<400> 980

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20 25 30	
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35 40 45	
Ile Gly Glu Asp Arg Val Trp Asp Pro Glu Lys Ile Val Val Ile Phe	
50 55 60	
Asp His Gln Val Pro Ala Asp Ser Ile Glu Ala Ala Gln Asn His Met	
65 70 75 80	
Ile Met Arg Asp Phe Val Glu Glu Gln Gly Ile Arg Asn Phe Tyr Asp	
85 90 95	
Val Arg Glu Gly Val Cys His Gln Val Leu Pro Glu Lys Gly His Val	
100 105 110	
Val Pro Gly Glu Val Val Val Gly Thr Asp Ser His Thr Cys Thr His	
115 120 125	
Gly Ala Leu Gly Ala Phe Ala Thr Gly Ile Gly Ser Thr Asp Met Ala	
130 135 140	
Met Val Phe Ala Thr Gly Lys Leu Trp Phe Arg Val Pro Glu Thr Leu	
145 150 155 160	
Arg Phe Asp Val Arg Gly Lys Leu Arg Glu His Val Tyr Ala Lys Asp	
165 170 175	
Val Ile Leu Asn Ile Ile Gly Arg Val Gly Ala Asp Gly Ala Thr Tyr	

PF59082SeqList_PF59082.txt

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Met Ala Cys Glu Phe Ala Gly Glu Thr Val Ala Glu Met Ser Val Ser
      195      200      205
Asp Arg Met Val Leu Ser Asn Met Ala Ile Glu Met Gly Gly Lys Thr
      210      215      220
Gly Ile Val Glu Pro Asp Glu Lys Thr Leu Asn Tyr Val Arg Arg Arg
      225      230      235
Ser Gly Lys Pro Trp Arg Val Phe Lys Thr Asp Pro Asp Ala Pro Ser
      240      245      250
Leu Ser Val Met Glu Val Asp Val Ser Asp Leu Glu Pro Gln Val Ala
      255      260      265
Cys Pro His Asn Val Asp Asn Val Lys Pro Val Thr Glu Val Glu Gly
      270      275      280
Thr Glu Ile Asp Gln Val Phe Leu Gly Ser Cys Thr Asn Gly Arg Leu
      285      290      295
Ser Asp Leu Arg Asp Ala Ala Ile Leu Lys Asn Arg Lys Val Ser
      300      305      310
Asp Ser Val Arg Met Leu Val Ile Pro Ala Ser Arg Glu Val Tyr Arg
      315      320      325
Arg Ala Leu Asp Glu Gly Leu Ile Glu Ile Phe Val Asp Ala Gly Ala
      330      335      340
Leu Val Cys Asn Pro Cys Cys Gly Pro Cys Leu Gly Gly His Val Gly
      345      350      355
Leu Val Gly Pro Gly Glu Val Ser Leu Ser Thr Ser Asn Arg Asn Phe
      360      365      370
Arg Gly Arg Gln Gly Ser Pro Glu Ala Glu Val Tyr Leu Ser Ser Ala
      375      380      385
Ala Val Ala Ala Ala Ser Ala Val Lys Gly Ser Ile Thr His Pro Gly
      390      395      400
Ser Leu Lys
      405      410      415

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<210> 981
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 <213> Pyrococcus abyssi

<220>
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 <223> transl_table=11

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      1      5      10      15
gag gag gtt aaa cct gga gaa ata gtc atg gcc aag ttg gat ttc gtg      96
Glu Glu Val Lys Pro Gly Glu Ile Val Met Ala Lys Leu Asp Phe Val
      20      25      30
ttt gga aac gat gta acg atg cct cta gct ata aag aag ttt agg gaa      144
Phe Gly Asn Asp Val Thr Met Pro Leu Ala Ile Lys Lys Phe Arg Glu
      35      40      45
ctt gga gtt aag agg gtt ttc gat agg gaa agg ata gcg ata gtt cta      192
Leu Gly Val Lys Arg Val Phe Asp Arg Glu Arg Ile Ala Ile Val Leu
      50      55      60
gat cac ttc acg cca aac aag gat ata aag agc gcc gag cag tgc aaa      240
Asp His Phe Thr Pro Asn Lys Asp Ile Lys Ser Ala Glu Gln Cys Lys
      65      70      75      80
tct tca agg gag ttc gcc aaa gag atg gga ata aaa tgg ttt ttc gaa      288
Ser Ser Arg Glu Phe Ala Lys Glu Met Gly Ile Lys Trp Phe Phe Glu
      85      90      95
gga gga agt gtc gga gtt gaa cac tgc tta ctt cca gag cta ggt ctt      336
Gly Gly Ser Val Gly Val Glu His Cys Leu Leu Pro Glu Leu Gly Leu
      100      105      110
gtt ctt cct gga gac tta att atc ggt gca gat tcg cac aca tgc acg      384
Val Leu Pro Gly Asp Leu Ile Ile Gly Ala Asp Ser His Thr Cys Thr
      115      120      125
tat ggt gct ctc ggt gcc ttc gca aca gga gtt ggg agt act gat tta      432
Tyr Gly Ala Leu Gly Ala Phe Ala Thr Gly Val Gly Ser Thr Asp Leu

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PF59082SeqList_PF59082.txt

130	gcc gtc gcg atg gct act	135	ggg gaa gcc tgg ttc agg gtt ccc gaa acc	480
Ala Val Ala Met Ala Thr	140	Gly Glu Ala Trp Phe Arg Val Pro Glu Thr		
145	atg aaa ttc atc tac	150	gag gga gag ctc caa cct tat gta act ggt aag	528
Met Lys Phe Ile Tyr	155	Glu Gly Glu Leu Gln Pro Tyr Val Thr Gly Lys		
165	gat ttg atc ctt cac aca atc gga gat ata gga gta aat gga gcc cta	170	Asp Leu Ile Gly Val Asn Gly Ala Leu	576
Asp Leu Ile Leu His Thr Ile Gly Asp Ile Gly Val Asn Gly Ala Leu	185			
180	tac aag gtc atg gaa ttc agt gga agc gta ata gag gag ctc tcg gtg	190	Tyr Lys Val Met Glu Phe Ser Gly Ser Val Ile Glu Glu Leu Ser Val	624
Tyr Lys Val Met Glu Phe Ser Gly Ser Val Ile Glu Glu Leu Ser Val	200			
195	gaa cag agg atg acc atg agt aat atg gct ata gaa gct gga gca aag	205	Glu Gln Arg Met Thr Met Ser Asn Met Ala Ile Glu Ala Gly Ala Lys	672
Glu Gln Arg Met Thr Met Ser Asn Met Ala Ile Glu Ala Gly Ala Lys	210			
215	act ggg ata ata gaa ccg gat aag aaa acc cta gat tac gtt aag gag	220	Thr Gly Ile Ile Glu Pro Asp Lys Lys Thr Leu Asp Tyr Val Lys Glu	720
Thr Gly Ile Ile Glu Pro Asp Lys Lys Thr Leu Asp Tyr Val Lys Glu	230			
235	aga gca aaa agg aag ttt aag gtt tac aaa agc gag gat gct aag	240	Arg Ala Lys Arg Lys Phe Lys Val Tyr Lys Ser Asp Glu Asp Ala Lys	768
Arg Ala Lys Arg Lys Phe Lys Val Tyr Lys Ser Asp Glu Asp Ala Lys	245			
250	tac tac aaa gtt atc gag tac gac gtt acc aac tgg gaa cct gta gtt	255	Tyr Tyr Lys Val Ile Glu Tyr Asp Val Thr Asn Trp Glu Pro Val Val	816
Tyr Tyr Lys Val Ile Glu Tyr Asp Val Thr Asn Trp Glu Pro Val Val	260			
265	gcc ttt ccc cat tta ccg gag aac acg gtt cca ata agt aag gct gca	270	Ala Phe Pro His Leu Pro Glu Asn Thr Val Pro Ile Ser Lys Ala Ala	864
Ala Phe Pro His Leu Pro Glu Asn Thr Val Pro Ile Ser Lys Ala Ala	275			
280	aag atg aac ata aag ata gat cag gtc ttc ata ggt tct tgc aca aat	285	Lys Met Asn Ile Lys Ile Asp Gln Val Phe Ile Gly Ser Cys Thr Asn	912
Lys Met Asn Ile Lys Ile Asp Gln Val Phe Ile Gly Ser Cys Thr Asn	290			
295	ggg aga ata gaa gat cta aga atg gcg gct gaa att tta gaa ggg caa	300	Gly Arg Ile Glu Asp Leu Arg Met Ala Ala Glu Ile Leu Glu Gly Gln	960
Gly Arg Ile Glu Asp Leu Arg Met Ala Ala Glu Ile Leu Glu Gly Gln	305			
310	aaa gtc gcc aag tgg gtt agg tta atc gtc att ccg tgc tct cca acg	315	Lys Val Ala Lys Trp Val Arg Leu Ile Val Ile Pro Cys Ser Pro Thr	1008
Lys Val Ala Lys Trp Val Arg Leu Ile Val Ile Pro Cys Ser Pro Thr	320			
325	gtt tac tgg aaa gcc ttg aag gaa ggt ttg ata gag ata ttc ttg gag	330	Val Tyr Trp Lys Ala Leu Lys Glu Gly Leu Ile Glu Ile Phe Leu Glu	1056
Val Tyr Trp Lys Ala Leu Lys Glu Gly Leu Ile Glu Ile Phe Leu Glu	335			
340	gcc gga gct gta ata gga cct ccc acg tgt gga ccc tgt ctc gga ggt	345	Ala Gly Ala Val Ile Gly Pro Pro Thr Cys Gly Pro Cys Leu Gly Gly	1104
Ala Gly Ala Val Ile Gly Pro Pro Thr Cys Gly Pro Cys Leu Gly Gly	350			
355	cac atg gga gtg ctt gca agt ggt gaa agg gct gtc tct aca act aac	360	His Met Gly Val Leu Ala Ser Gly Glu Arg Ala Val Ser Thr Thr Asn	1152
His Met Gly Val Leu Ala Ser Gly Glu Arg Ala Val Ser Thr Thr Asn	365			
370	agg aac ttc gtt ggg aga atg ggg cat cca aag agc gag gtt tac tta	375	Arg Asn Phe Val Gly Arg Met Gly His Pro Lys Ser Glu Val Tyr Leu	1200
Arg Asn Phe Val Gly Arg Met Gly His Pro Lys Ser Glu Val Tyr Leu	380			
385	gct aac cca tac gtc gct gct tca gct gtt ttg ggt agg ata gca	390	Ala Asn Pro Tyr Val Ala Ala Ala Ser Ala Val Leu Gly Arg Ile Ala	1248
Ala Asn Pro Tyr Val Ala Ala Ala Ser Ala Val Leu Gly Arg Ile Ala	395			
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Ser Pro Glu Glu Val Val Lys	410			
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<210> 982

<211> 423

<212> PRT

<213> Pyrococcus abyssi

<400> 982

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Phe Gly Asn Asp Val Thr Met Pro Leu Ala Ile Lys Lys Phe Arg Glu	40	45	50	55
Leu Gly Val Lys Arg Val Phe Asp Arg Glu Arg Ile Ala Ile Val Leu	60	65	70	75

PF59082SeqList_PF59082.txt

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Ser Ser Arg Glu Phe Ala Lys Glu Met Gly Ile Lys Trp Phe Phe Glu
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Val Leu Pro Gly Asp Leu Ile Ile Gly Ala Asp Ser His Thr Cys Thr
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Tyr Gly Ala Leu Gly Ala Phe Ala Thr Gly Val Gly Ser Thr Asp Leu
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Ala Val Ala Met Ala Thr Gly Glu Ala Trp Phe Arg Val Pro Glu Thr
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Met Lys Phe Ile Tyr Glu Gly Glu Leu Gln Pro Tyr Val Thr Gly Lys
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Asp Leu Ile Leu His Thr Ile Gly Asp Ile Gly Val Asn Gly Ala Leu
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Tyr Lys Val Met Glu Phe Ser Gly Ser Val Ile Glu Glu Leu Ser Val
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Glu Gln Arg Met Thr Met Ser Asn Met Ala Ile Glu Ala Gly Ala Lys
170
Thr Gly Ile Ile Glu Pro Asp Lys Lys Thr Leu Asp Tyr Val Lys Glu
185
Arg Ala Lys Arg Lys Phe Lys Val Tyr Lys Ser Asp Glu Asp Ala Lys
190
Tyr Tyr Lys Val Ile Glu Tyr Asp Val Thr Asn Trp Glu Pro Val Val
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Ala Phe Pro His Leu Pro Glu Asn Thr Val Pro Ile Ser Lys Ala Ala
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Lys Met Asn Ile Lys Ile Asp Gln Val Phe Ile Gly Ser Cys Thr Asn
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Gly Arg Ile Glu Asp Leu Arg Met Ala Ala Glu Ile Leu Glu Gly Gln
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Lys Val Ala Lys Trp Val Arg Leu Ile Val Ile Pro Cys Ser Pro Thr
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Val Tyr Trp Lys Ala Leu Lys Glu Gly Leu Ile Glu Ile Phe Leu Glu
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His Met Gly Val Leu Ala Ser Gly Glu Arg Ala Val Ser Thr Thr Asn
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Ser Pro Glu Glu Val Val Lys
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<220>

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<222> (1)..(1275)

<223> transl_table=11

<400> 983

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aag gaa gag gta aaa cct gga gag ata gtt ttg gca aaa gtg gac ttc      96
Lys Glu Glu Val Lys Pro Gly Glu Ile Val Leu Ala Lys Val Asp Phe
20          25          30
atg ttt ggg aat gat gta aca acc ccc tta gcc ata aaa acg ttt aga     144
Met Phe Gly Asn Asp Val Thr Thr Pro Leu Ala Ile Lys Thr Phe Arg
35          40          45
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PF59082SeqList_PF59082.txt

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Leu	Asp	His	Phe	Thr	Pro	Asn	Lys	Asp	Ile	Lys	Ala	Ala	Glu	Gln	Cys		
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aaa	ttc	tca	cga	gaa	ttt	gcc	aga	gaa	cag	gga	atc	aag	tgg	ttc	ttt	288	
Lys	Phe	Ser	Arg	Glu	Phe	Ala	Arg	Glu	Gln	Gly	Ile	Lys	Trp	Phe	Phe		
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gag	gga	gga	aac	ggt	ggt	gtc	gag	cat	tgt	tta	ctc	cct	gag	tta	gga	336	
Glu	Gly	Gly	Asn	Val	Gly	Val	Glu	His	Cys	Leu	Leu	Pro	Glu	Leu	Gly		
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Leu	Val	Leu	Pro	Gly	Glu	Leu	Ile	Ile	Gly	Ala	Asp	Ser	His	Thr	Cys		
		115					120					125					
act	tat	gga	gcc	ctg	ggt	gcc	ttt	gca	act	gga	ggt	ggt	agt	act	gac	432	
Thr	Tyr	Gly	Ala	Leu	Gly	Ala	Phe	Ala	Thr	Gly	Val	Gly	Ser	Thr	Asp		
	130					135					140						
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Leu	Ala	Val	Ala	Met	Ala	Thr	Gly	Glu	Ala	Trp	Phe	Arg	Val	Pro	Glu		
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Thr	Ile	Lys	Phe	Val	Tyr	Glu	Gly	Asp	Leu	Gln	Pro	Trp	Val	Thr	Ser		
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Lys	Asp	Leu	Ile	Leu	Tyr	Thr	Ile	Gly	Asp	Ile	Gly	Val	Asn	Gly	Ala		
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ctc	tac	aaa	gtc	atg	gaa	ttt	tcg	gga	gaa	ggt	ata	gag	aag	ctt	tcc	624	
Leu	Tyr	Lys	Val	Met	Glu	Phe	Ser	Gly	Glu	Val	Ile	Glu	Lys	Leu	Ser		
		195					200					205					
gtg	gaa	cag	agg	atg	acg	atg	act	aat	atg	gcc	ata	gag	gcc	gga	gca	672	
Val	Glu	Gln	Arg	Met	Thr	Met	Thr	Asn	Met	Ala	Ile	Glu	Ala	Gly	Ala		
	210					215					220						
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Gly	Arg	Ala	Lys	Arg	Glu	Tyr	Lys	Ile	Tyr	Lys	Ser	Asp	Glu	Asp	Ala		
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Lys	Tyr	Tyr	Lys	Val	Ile	Glu	Tyr	Asp	Val	Ser	Lys	Ile	Glu	Pro	Gln		
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Val	Ala	Phe	Pro	His	Leu	Pro	Glu	Asn	Thr	Val	Pro	Ile	Ser	Lys	Ala		
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Asn	Gly	Arg	Leu	Glu	Asp	Leu	Arg	Met	Ala	Ala	Glu	Val	Leu	Glu	Gly		
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cag	aaa	gtg	gcc	ccc	tgg	gta	agg	ctt	atc	att	ctt	cca	tgt	tca	ccg	1008	
Gln	Lys	Val	Ala	Pro	Trp	Val	Arg	Leu	Ile	Ile	Leu	Pro	Cys	Ser	Pro		
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Thr	Val	Tyr	Phe	Lys	Ala	Met	Lys	Glu	Gly	Leu	Leu	Glu	Ile	Phe	Leu		
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Glu	Ala	Gly	Ala	Val	Ile	Gly	Pro	Pro	Thr	Cys	Gly	Pro	Cys	Leu	Gly		
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Gly	His	Met	Gly	Ile	Leu	Ala	Ser	Gly	Glu	Arg	Ala	Val	Ser	Thr	Thr		
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Asn	Arg	Asn	Phe	Val	Gly	Arg	Met	Gly	His	Pro	Lys	Ser	Glu	Val	Tyr		
				390						395					400		
ttg	gca	agt	ccc	tat	gta	gct	gca	gct	tcg	gct	att	ctt	ggt	aga	att	1248	
Leu	Ala	Ser	Pro	Tyr	Val	Ala	Ala	Ala	Ser	Ala	Ile	Leu	Gly	Arg	Ile		
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<212> PRT

<213> Pyrococcus furiosus

<400> 984

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35 40 45
Lys Ile Gly Val Glu Lys Val Phe Asp Pro Glu Arg Ile Ala Ile Val
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Leu Asp His Phe Thr Pro Asn Lys Asp Ile Lys Ala Ala Glu Gln Cys
65 70 75 80
Lys Phe Ser Arg Glu Phe Ala Arg Glu Gln Gly Ile Lys Trp Phe Phe
85 90 95
Glu Gly Gly Asn Val Gly Val Glu His Cys Leu Leu Pro Glu Leu Gly
100 105 110
Leu Val Leu Pro Gly Glu Leu Ile Ile Gly Ala Asp Ser His Thr Cys
115 120 125
Thr Tyr Gly Ala Leu Gly Ala Phe Ala Thr Gly Val Gly Ser Thr Asp
130 135 140
Leu Ala Val Ala Met Ala Thr Gly Glu Ala Trp Phe Arg Val Pro Glu
145 150 155 160
Thr Ile Lys Phe Val Tyr Glu Gly Asp Leu Gln Pro Trp Val Thr Ser
165 170 175
Lys Asp Leu Ile Leu Tyr Thr Ile Gly Asp Ile Gly Val Asn Gly Ala
180 185 190
Leu Tyr Lys Val Met Glu Phe Ser Gly Glu Val Ile Glu Lys Leu Ser
195 200 205
Val Glu Gln Arg Met Thr Met Thr Asn Met Ala Ile Glu Ala Gly Ala
210 215 220
Lys Thr Gly Ile Ile Glu Pro Asp Lys Lys Thr Ile Glu Tyr Val Lys
225 230 235 240
Gly Arg Ala Lys Arg Glu Tyr Lys Ile Tyr Lys Ser Asp Glu Asp Ala
245 250 255
Lys Tyr Tyr Lys Val Ile Glu Tyr Asp Val Ser Lys Ile Glu Pro Gln
260 265 270
Val Ala Phe Pro His Leu Pro Glu Asn Thr Val Pro Ile Ser Lys Ala
275 280 285
Ala Lys Met Asn Ile Lys Ile Asp Gln Val Val Ile Gly Ser Cys Thr
290 295 300
Asn Gly Arg Leu Glu Asp Leu Arg Met Ala Ala Glu Val Leu Glu Gly
305 310 315 320
Gln Lys Val Ala Pro Trp Val Arg Leu Ile Ile Leu Pro Cys Ser Pro
325 330 335
Thr Val Tyr Phe Lys Ala Met Lys Glu Gly Leu Leu Glu Ile Phe Leu
340 345 350
Glu Ala Gly Ala Val Ile Gly Pro Pro Thr Cys Gly Pro Cys Leu Gly
355 360 365
Gly His Met Gly Ile Leu Ala Ser Gly Glu Arg Ala Val Ser Thr Thr
370 375 380
Asn Arg Asn Phe Val Gly Arg Met Gly His Pro Lys Ser Glu Val Tyr
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Ala Ser Pro Glu Glu Val Val Lys
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<211> 1263

<212> DNA

<213> Methanosarcina acetivorans

PF59082SeqList_PF59082.txt

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 <223> transl_table=11

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Lys Ala Gly Asp Phe Val Leu Ala Asn Ile Asp Leu Ala Met Thr His	
20 25 30	
gac atc aca ggt ccg ctg gca gtc cag ggc ttt tac gaa atc atg aga	144
Asp Ile Thr Gly Pro Leu Ala Val Gln Gly Phe Tyr Glu Ile Met Arg	
35 40 45	
gat gaa gaa gaa aaa gtc tgg gac ccc agc aaa atc gta atc att	192
Asp Glu Glu Glu Lys Lys Val Trp Asp Pro Ser Lys Ile Val Ile Ile	
50 55 60	
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Phe Asp His Gln Val Pro Ala Asp Ser Ile Asn Ala Ala Glu Asn His	
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Ile Met Leu Arg Lys Phe Ala Lys Glu Gln Gly Ile Leu Asn Tyr Asp	
85 90 95	
gtg tac gag gga gtc tgc cat cag gtt ctg ccc gaa aaa ggg cat gta	336
Val Tyr Glu Gly Val Cys His Gln Val Leu Pro Glu Lys Gly His Val	
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ctg ccc gga gac ctt att gtg ggc tct gac tct cat acc tgc gca tac	384
Leu Pro Gly Asp Leu Ile Val Gly Ser Asp Ser His Thr Cys Ala Tyr	
115 120 125	
ggg tct tta ggg gca ttt tct acc ggt ata gga tct act gac atg gca	432
Gly Ser Leu Gly Ala Phe Ser Thr Gly Ile Gly Ser Thr Asp Met Ala	
130 135 140	
gct gtt ttt gct aca ggc aaa ctc tgg ttc agg gtt ccc gag acc ttc	480
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145 150 155 160	
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Arg Phe Glu Val Glu Gly Lys Leu Pro Glu Arg Val Tyr Ser Lys Asp	
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ctt atc ctg cac ctc atc ggg gat gta gga gtg gaa ggt gcc aga tat	576
Leu Ile Leu His Leu Ile Gly Asp Val Gly Val Glu Gly Ala Arg Tyr	
180 185 190	
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Met Ala Ala Glu Tyr Ala Gly Ser Thr Ile Arg Ser Leu Ser Ile Pro	
195 200 205	
gag cgc atg acc atc tcc aac atg gca ata gag atg gga gga aag gca	672
Glu Arg Met Thr Ile Ser Asn Met Ala Ile Glu Met Gly Gly Lys Ala	
210 215 220	
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Gly Ile Ile Glu Ala Asp Glu Val Thr Glu Ala Tyr Leu Gln Glu Arg	
225 230 235 240	
att ccg ggc tac aaa ctt gac cca tac tgg aag tcc gat gaa gag gct	768
Ile Pro Gly Tyr Lys Leu Asp Pro Tyr Trp Lys Ser Asp Glu Glu Ala	
245 250 255	
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Lys Tyr Leu Asp Ile Arg His Tyr Asp Val Ser Asp Leu Glu Pro Gln	
260 265 270	
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Val Ala Cys Pro His Asn Val Asp Asn Val Lys Ser Val Ser Glu Val	
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Glu Gly Thr Lys Leu Asp Gln Val Phe Met Gly Ser Cys Thr Asn Gly	
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Arg Phe Glu Asp Ile Lys Ile Met Ala Asp Ile Met Gly Asp Glu Pro	
305 310 315 320	
gta gca aaa ggt gtg cgt ctc ctt gtt gtg cct gct tcg aaa acc gaa	1008
Val Ala Lys Gly Val Arg Leu Leu Val Val Pro Ala Ser Lys Thr Glu	
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PF59082SeqList_PF59082.txt

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Gly	Ala	Ile	Val	Glu	Ala	Pro	Cys	Cys	Gly	Pro	Cys	Met	Gly	Gly	Ser	
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Phe	Gly	Leu	Leu	Gly	Pro	Gly	Glu	Val	Gly	Leu	Ala	Thr	Ser	Asn	Arg	
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Asn	Phe	Lys	Gly	Arg	Glu	Gly	Ser	Ala	Glu	Ser	Phe	Val	Tyr	Leu	Ser	
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Ser	Pro	Ala	Thr	Ala	Gly	Ala	Ser	Ala	Leu	Thr	Gly	Glu	Ile	Thr	Asp	
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<213> Methanosarcina acetivorans

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			35					40					45			
Asp	Glu	Glu	Glu	Lys	Lys	Val	Trp	Asp	Pro	Ser	Lys	Ile	Val	Ile	Ile	
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Phe	Asp	His	Gln	Val	Pro	Ala	Asp	Ser	Ile	Asn	Ala	Ala	Glu	Asn	His	
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Ile	Met	Leu	Arg	Lys	Phe	Ala	Lys	Glu	Gln	Gly	Ile	Leu	Asn	Tyr	Asp	
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Val	Tyr	Glu	Gly	Val	Cys	His	Gln	Val	Leu	Pro	Glu	Lys	Gly	His	Val	
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Leu	Pro	Gly	Asp	Leu	Ile	Val	Gly	Ser	Asp	Ser	His	Thr	Cys	Ala	Tyr	
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Gly	Ser	Leu	Gly	Ala	Phe	Ser	Thr	Gly	Ile	Gly	Ser	Thr	Asp	Met	Ala	
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Ala	Val	Phe	Ala	Thr	Gly	Lys	Leu	Trp	Phe	Arg	Val	Pro	Glu	Thr	Phe	
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Arg	Phe	Glu	Val	Glu	Gly	Lys	Leu	Pro	Glu	Arg	Val	Tyr	Ser	Lys	Asp	
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Leu	Ile	Leu	His	Leu	Ile	Gly	Asp	Val	Gly	Val	Glu	Gly	Ala	Arg	Tyr	
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Glu	Arg	Met	Thr	Ile	Ser	Asn	Met	Ala	Ile	Glu	Met	Gly	Gly	Lys	Ala	
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225									235						240	
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Lys	Tyr	Leu	Asp	Ile	Arg	His	Tyr	Asp	Val	Ser	Asp	Leu	Glu	Pro	Gln	
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Val	Ala	Cys	Pro	His	Asn	Val	Asp	Asn	Val	Lys	Ser	Val	Ser	Glu	Val	
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Glu	Gly	Thr	Lys	Leu	Asp	Gln	Val	Phe	Met	Gly	Ser	Cys	Thr	Asn	Gly	
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Arg	Phe	Glu	Asp	Ile	Lys	Ile	Met	Ala	Asp	Ile	Met	Gly	Asp	Glu	Pro	
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Val	Ala	Lys	Gly	Val	Arg	Leu	Leu	Val	Val	Pro	Ala	Ser	Lys	Thr	Glu	
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Tyr	Met	Lys	Leu	Leu	Lys	Ala	Gly	Tyr	Val	Glu	Lys	Leu	Met	Asn	Ala	
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PF59082SeqList_PF59082.txt

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 Asn Phe Lys Gly Arg Glu Gly Ser Ala Glu Ser Phe Val Tyr Leu Ser
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 Ser Pro Ala Thr Ala Gly Ala Ser Ala Leu Thr Gly Glu Ile Thr Asp
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 Pro Arg Lys Val
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 <212> DNA
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 Lys Glu Val Ser Pro Gly Asp Ile Val Met Ala Asn Ile Asp Val Ala
 20 25 30
 atg gtt cat gat att aca ggg cct tta aca gtc aat aca tta aag gag 144
 Met Val His Asp Ile Thr Gly Pro Leu Thr Val Asn Thr Leu Lys Glu
 35 40 45
 tat gga att gaa aaa gtt tgg aat cca gaa aag ata gtt att tta ttt 192
 Tyr Gly Ile Glu Lys Val Trp Asn Pro Glu Lys Ile Val Ile Leu Phe
 50 55 60
 gac cac caa gtt cct gct gat agt ata aaa gcg gct gaa aac cat ata 240
 Asp His Gln Val Pro Ala Asp Ser Ile Lys Ala Ala Glu Asn His Ile
 65 70 75 80
 tta atg aga aag ttc gta aaa gaa cag ggt att aaa tac ttc tac gat 288
 Leu Met Arg Lys Phe Val Lys Glu Gln Gly Ile Lys Tyr Phe Tyr Asp
 85 90 95
 att aga gag gga gtt tgt cac caa gtt tta cca gag aaa gga cat gta 336
 Ile Arg Glu Gly Val Cys His Gln Val Leu Pro Glu Lys Gly His Val
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 gct cca gga gag gta gtt gtt gga gct gat tca cac aca tgc aca cat 384
 Ala Pro Gly Glu Val Val Val Gly Ala Asp Ser His Thr Cys Thr His
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 Gly Ala Phe Gly Ala Phe Ala Thr Gly Ile Gly Ser Thr Asp Met Ala
 130 135 140
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 His Val Phe Ala Thr Gly Lys Leu Trp Phe Lys Val Pro Glu Thr Ile
 145 150 155 160
 tac ttc aac att act gga gat tta caa cct tac gtt act tca aag gat 528
 Tyr Phe Asn Ile Thr Gly Asp Leu Gln Pro Tyr Val Thr Ser Lys Asp
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 Val Ile Leu Ser Ile Ile Gly Glu Val Gly Val Asp Gly Ala Thr Tyr
 180 185 190
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 Lys Ala Cys Gln Phe Gly Gly Thr Val Lys Lys Met Ser Ile Ala
 195 200 205
 tca aga atg aca atg aca aac atg gct att gag atg ggg gga aaa aca 672
 Ser Arg Met Thr Met Thr Asn Met Ala Ile Glu Met Gly Gly Lys Thr
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 Gly Ile Ile Glu Pro Asp Glu Lys Thr Ile Gln Tyr Val Lys Glu Ala
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Glu	Pro	Val	Phe	Ala	Cys	Pro	His	Asn	Val	Asp	Asn	Val	Lys	Gln	Ala		
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Arg	Glu	Val	Ala	Gly	Lys	Pro	Ile	Asp	Gln	Val	Phe	Ile	Gly	Ser	Cys		
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acg	aac	gga	aga	ttg	gaa	gat	tta	aga	atg	gct	att	aag	att	att	gag		960
Thr	Asn	Gly	Arg	Leu	Glu	Asp	Leu	Arg	Met	Ala	Ile	Lys	Ile	Ile	Glu		
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aag	cat	ggg	gga	att	gct	gat	gat	gtt	agg	gtt	gtt	gta	act	cca	gct		1008
Lys	His	Gly	Gly	Ile	Ala	Asp	Asp	Val	Arg	Val	Val	Val	Thr	Pro	Ala		
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tca	agg	gaa	gag	tat	cta	aaa	gca	tta	aaa	gag	gga	ata	att	gag	aaa		1056
Ser	Arg	Glu	Glu	Tyr	Leu	Lys	Ala	Leu	Lys	Glu	Gly	Ile	Ile	Glu	Lys		
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Phe	Leu	Lys	Tyr	Gly	Cys	Val	Val	Thr	Asn	Pro	Ser	Cys	Ser	Ala	Cys		
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Met	Gly	Ser	Leu	Tyr	Gly	Val	Leu	Gly	Pro	Gly	Glu	Val	Cys	Val	Ser		
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Thr	Ser	Asn	Arg	Asn	Phe	Arg	Gly	Arg	Gln	Gly	Ser	Leu	Glu	Ala	Glu		
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Ile	Tyr	Leu	Ala	Ser	Pro	Ile	Thr	Ala	Ala	Ala	Cys	Ala	Val	Lys	Gly		
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<212> PRT

<213> Methanococcus jannaschii

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Tyr	Gly	Ile	Glu	Lys	Val	Trp	Asn	Pro	Glu	Lys	Ile	Val	Ile	Leu	Phe	
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Asp	His	Gln	Val	Pro	Ala	Asp	Ser	Ile	Lys	Ala	Ala	Glu	Asn	His	Ile	
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Gly	Ala	Phe	Gly	Ala	Phe	Ala	Thr	Gly	Ile	Gly	Ser	Thr	Asp	Met	Ala	
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His	Val	Phe	Ala	Thr	Gly	Lys	Leu	Trp	Phe	Lys	Val	Pro	Glu	Thr	Ile	
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Tyr	Phe	Asn	Ile	Thr	Gly	Asp	Leu	Gln	Pro	Tyr	Val	Thr	Ser	Lys	Asp	
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Val	Ile	Leu	Ser	Ile	Ile	Gly	Glu	Val	Gly	Val	Asp	Gly	Ala	Thr	Tyr	
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Lys	Ala	Cys	Gln	Phe	Gly	Gly	Glu	Thr	Val	Lys	Lys	Met	Ser	Ile	Ala	
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 260 265 270
 Glu Pro Val Phe Ala Cys Pro His Asn Val Asp Asn Val Lys Gln Ala
 275 280 285
 Arg Glu Val Ala Gly Lys Pro Ile Asp Gln Val Phe Ile Gly Ser Cys
 290 295 300
 Thr Asn Gly Arg Leu Glu Asp Leu Arg Met Ala Ile Lys Ile Ile Glu
 305 310 315 320
 Lys His Gly Gly Ile Ala Asp Asp Val Arg Val Val Val Thr Pro Ala
 325 330 335
 Ser Arg Glu Glu Tyr Leu Lys Ala Leu Lys Glu Gly Ile Ile Glu Lys
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 Phe Leu Lys Tyr Gly Cys Val Val Thr Asn Pro Ser Cys Ser Ala Cys
 355 360 365
 Met Gly Ser Leu Tyr Gly Val Leu Gly Pro Gly Glu Val Cys Val Ser
 370 375 380
 Thr Ser Asn Arg Asn Phe Arg Gly Arg Gln Gly Ser Leu Glu Ala Glu
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 405 410 415
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<212> DNA

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Met Ala Asn Asp Val Thr Ala Pro Leu Ala Ile Lys Ile Leu Glu Lys	
35 40 45	
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Tyr Gly Ile Asp Lys Val Phe Asp Pro Glu Arg Ile Ala Leu Val Leu	
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tca cac ttc gtt ccc gca aag gac ata aag tcc gct gag cag gca aag	240
Ser His Phe Val Pro Ala Lys Asp Ile Lys Ser Ala Glu Gln Ala Lys	
65 70 75 80	
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Ile Val Arg Glu Phe Val Lys Lys His Gly Ile Lys Trp Phe Phe Glu	
85 90 95	
gag gga gaa ggt ata gaa cac gcc ata ctc ccc gag caa gga ctc gtc	336
Glu Gly Glu Gly Ile Glu His Ala Ile Leu Pro Glu Gln Gly Leu Val	
100 105 110	
gtt ccc ggg gac ctc gtt gta ggt gcg gac tcc cac acc tgc act tac	384
Val Pro Gly Asp Leu Val Val Gly Ala Asp Ser His Thr Cys Thr Tyr	
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Gly Ala Leu Gly Ala Phe Ala Thr Gly Val Gly Ser Thr Asp Ile Ala	
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tac gct atg gct acc gga gaa gtt tgg ctc aga gtt ccc gaa agt atg	480
Tyr Ala Met Ala Thr Gly Glu Val Trp Leu Arg Val Pro Glu Ser Met	
145 150 155 160	
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PF59082SeqList_PF59082.txt

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Leu	Ile	Leu	Tyr	Thr	Ile	Gly	Gln	Ile	Gly	Val	Asp	Gly	Ala	Leu	Tyr	
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Arg	Ala	Met	Glu	Phe	Asp	Gly	Glu	Thr	Ile	Arg	Asn	Leu	Ser	Met	Glu	
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Gln	Arg	Phe	Thr	Ile	Ala	Asn	Met	Ala	Ile	Glu	Ala	Gly	Gly	Lys	Ser	
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Gly	Ile	Ile	Ser	Pro	Asp	Glu	Lys	Thr	Ile	Glu	Tyr	Val	Lys	Gln	Arg	
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gca	aag	aga	cca	tgg	aaa	gtt	tac	cag	agc	gac	cct	gac	gct	gag	tac	768
Ala	Lys	Arg	Pro	Trp	Lys	Val	Tyr	Gln	Ser	Asp	Pro	Asp	Ala	Glu	Tyr	
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cac	tcc	gtt	tac	gag	tgg	gac	gct	tct	cag	ata	gaa	ccc	tta	gta	gcg	816
His	Ser	Val	Tyr	Glu	Trp	Asp	Ala	Ser	Gln	Ile	Glu	Pro	Leu	Val	Ala	
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Trp	Pro	Tyr	Leu	Pro	Ser	Asn	Val	His	Pro	Val	Ser	Glu	Ser	Thr	His	
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Gly	Lys	Lys	Val	His	Pro	Tyr	Val	Arg	Cys	Ile	Val	Ile	Pro	Ala	Ser	
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Lys	Ala	Ile	Tyr	Lys	Gln	Ala	Leu	Lys	Glu	Gly	Leu	Ile	Asp	Ile	Phe	
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ggg	gga	cac	atg	gga	gtg	ctt	gcg	gaa	ggg	gaa	agg	tgt	ata	tcc	aca	1152
Gly	Gly	His	Met	Gly	Val	Leu	Ala	Glu	Gly	Glu	Arg	Cys	Ile	Ser	Thr	
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Ser	Asn	Arg	Asn	Phe	Pro	Gly	Arg	Met	Gly	His	Pro	Lys	Ser	Glu	Ser	
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Tyr	Leu	Ala	Asn	Pro	Ala	Val	Val	Ala	Ala	Ser	Ala	Ile	Met	Gly	Arg	
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Met	Ala	Asn	Asp	Val	Thr	Ala	Pro	Leu	Ala	Ile	Lys	Ile	Leu	Glu	Lys
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Tyr	Gly	Ile	Asp	Lys	Val	Phe	Asp	Pro	Glu	Arg	Ile	Ala	Leu	Val	Leu
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Tyr Ala Met Ala Thr Gly Glu Val Trp Leu Arg Val Pro Glu Ser Met
145      150      155
Lys Phe Ile Phe Tyr Gly Lys Leu Lys Pro Trp Val Met Gly Lys Asp
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Leu Ile Leu Tyr Thr Ile Gly Gln Ile Gly Val Asp Gly Ala Leu Tyr
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Arg Ala Met Glu Phe Asp Gly Glu Thr Ile Arg Asn Leu Ser Met Glu
      195      200      205
Gln Arg Phe Thr Ile Ala Asn Met Ala Ile Glu Ala Gly Gly Lys Ser
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Ala Lys Arg Pro Trp Lys Val Tyr Gln Ser Asp Pro Asp Ala Glu Tyr
      245      250      255
His Ser Val Tyr Glu Trp Asp Ala Ser Gln Ile Glu Pro Leu Val Ala
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Lys Ala Ile Tyr Lys Gln Ala Leu Lys Glu Gly Leu Ile Asp Ile Phe
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      370      375      380
Ser Asn Arg Asn Phe Pro Gly Arg Met Gly His Pro Lys Ser Glu Ser
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cat gaa gtg acc tct ccg cag gcg ttc gac ggc ctg cgt gcg atg ggc      144
His Glu Val Thr Ser Pro Gln Ala Phe Asp Gly Leu Arg Ala Met Gly
      35      40      45
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PF59082SeqList_PF59082.txt

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Leu	Tyr	Asp	Leu	Asn	His	Pro	Tyr	Gln 105	Gly	Ile	Val	His	Val	Ile	Gly	
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Pro	Glu	Gln 115	Gly	Met	Thr	Leu	Pro	Gly	Met	Thr	Ile	Val	Cys	Gly	Asp	
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Ser	His 130	Thr	Ala	Thr	His	Gly 135	Ala	Phe	Gly	Ser	Leu	Ala	Phe	Gly	Ile	
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Gly 145	Thr	Ser	Glu	Val	Glu 150	His	Val	Leu	Ala	Thr 155	Gln	Thr	Leu	Lys	Gln 160	
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Gly	Arg	Ala	Lys	Thr 165	Met	Lys	Ile	Glu	Val 170	Thr	Gly	Asp	Ala	Ala 175	His	
ggc	atc	acc	gcg	aaa	gac	atc	gtg	ctg	gcg	atc	atc	ggt	aaa	acc	ggt	576
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Glu 225	Met	Gly	Ala	Lys	Ala 230	Gly	Leu	Val	Ala	Pro 235	Asp	Glu	Thr	Thr	Phe 240	
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Ala	Ala	Val 260	Ala	Tyr	Trp	Ser	Thr	Leu 265	Lys	Ser	Asp	Asp	Asp	Ala	Gln	
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Phe	Asp 275	Thr	Ile	Val	Thr	Leu	Asp 280	Ala	Ala	Gln	Ile	Ala 285	Pro	Gln	Val	
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Thr	Trp 290	Gly	Thr	Asn	Pro	Gly 295	Gln	Val	Ile	Ala	Val 300	Asn	Gln	Glu	Ile	
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Pro	Asn	Pro	Asp	Ser	Phe 310	Ser	Asp	Pro	Val	Glu 315	Arg	Ala	Ser	Ala 320	Ala	
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Glu	Asp	Leu 355	Arg	Ala	Ala	Ala	Glu 360	Ile	Ala	Lys	Gly	Arg 365	Lys	Val	Ala	
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Glu	Trp	Arg	Leu	Pro 405	Gly	Cys	Ser	Met	Cys 410	Leu	Ala	Met	Asn	Asn 415	Asp	
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Arg	Leu	Asn	Pro 420	Gly	Glu	Arg	Cys	Ala 425	Ser	Thr	Ser	Asn	Arg 430	Asn	Phe	
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PF59082SeqList_PF59082.txt

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1392

1401

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 Arg Lys Val Arg Gln Pro Gly Lys Thr Phe Ala Thr Met Asp His Asn
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 Val Ser Thr Gln Thr Lys Asp Ile Asn Ala Ser Gly Glu Met Ala Arg
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 Leu Tyr Asp Leu Asn His Pro Tyr Gln Gly Ile Val His Val Ile Gly
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 Pro Glu Gln Gly Met Thr Leu Pro Gly Met Thr Ile Val Cys Gly Asp
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 Ser His Thr Ala Thr His Gly Ala Phe Gly Ser Leu Ala Phe Gly Ile
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 Gly Arg Ala Lys Thr Met Lys Ile Glu Val Thr Gly Asp Ala Ala His
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 Gly Ile Thr Ala Lys Asp Ile Val Leu Ala Ile Ile Gly Lys Thr Gly
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 Arg Ala Leu Ser Met Glu Gly Arg Met Thr Leu Cys Asn Met Ala Ile
 210 215 220
 Glu Met Gly Ala Lys Ala Gly Leu Val Ala Pro Asp Glu Thr Thr Phe
 225 230 235 240
 Asn Tyr Leu Lys Gly Arg Gln Phe Ala Pro Lys Asp Ala Asn Trp Asp
 245 250 255
 Ala Ala Val Ala Tyr Trp Ser Thr Leu Lys Ser Asp Asp Ala Gln
 260 265 270
 Phe Asp Thr Ile Val Thr Leu Asp Ala Ala Gln Ile Ala Pro Gln Val
 275 280 285
 Thr Trp Gly Thr Asn Pro Gly Gln Val Ile Ala Val Asn Gln Glu Ile
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 Pro Asn Pro Asp Ser Phe Ser Asp Pro Val Glu Arg Ala Ser Ala Ala
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PF59082SeqList_PF59082.txt

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 Leu Asn
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 Met Ala Ser Ser Val Ile

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 Phe Pro Lys Ser Ser Gln Ile Ser Val His Arg Cys Gln Lys Arg Ala
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 Ile Ser Arg Lys Ile Val Ser Val Met Ala Pro Gln Arg Ser Ser Ser
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 Ala Thr Gly Ser Val Lys Thr Gly Met Thr Met Thr Glu Lys Ile Leu
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 Ala Lys Ala Ala Glu Lys Ser Gln Val Val Pro Gly Asp Asn Ile Trp
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 135 140 145 150

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 Gly His Cys Arg Pro Gly Glu Val Leu Leu Gly Thr Asp Ser His Thr
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 Asp Ala Gly Phe Val Leu Gly Thr Gly Lys Ile Leu Leu Lys Val Pro
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PF59082SeqList_PF59082.txt

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Pro	Ser	Cys	Gly	Ala	Cys	Leu	Gly	Gly	Pro	Ala	Asp	Thr	Tyr	Ala	Arg		
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Thr	Ala	Ala	Ala	Ser	Ala	Leu	Thr	Gly	His	Val	Thr	Asp	Pro	Arg	Glu		
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Phe	Leu	Gln															
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<213> Brassica napus

<400> 994

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Pro Gln Arg Ser Ser Ser Ala Thr Gly Ser Val Lys Thr Gly Met Thr
50      55      60
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65      70      75      80
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Val Cys Gly Pro Gly Ala Phe Gly Ile Phe Lys Arg Glu Phe Gly Glu
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115     120     125
Tyr Ile Phe Thr Thr Asp Lys Arg Ala Asn Arg Asn Val Asp Ile Met
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Arg Glu His Cys Arg Glu Gln Asn Ile Lys Tyr Phe Tyr Asp Ile Thr
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Asp Leu Gly Asp Phe Arg Ala Asn Pro Asp Tyr Lys Gly Val Cys His
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Val Ala Leu Ala Gln Glu Gly His Cys Arg Pro Gly Glu Val Leu Leu
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Met Pro Ser Tyr Leu Gln Ala Lys Asp Leu Ile Leu Gln Ile Ile Gly
245     250     255
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Val Tyr Ser Asp Gly Asn Ala Ser Phe Ile Ala Asp Tyr Arg Phe Asp
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405     410     415
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Val Trp Val Asn Val 85 Asp Ile Leu Met Thr 90 His Asp Val Cys Gly 95 Pro	
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Gly Ser Ile Gly 100 Ile Phe Lys Arg Glu Phe Gly Glu Asp Ala Lys Val	
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Ser Leu Thr Met Glu Glu Arg Met Thr Leu Cys Asn Met Val Val Glu	
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Ala Gly 290 Gly Lys Asn Gly Val 295 Val Pro Ala Asp Ser 300 Thr Thr Phe Lys	
tat ctt gag ggc aag aca tct ctg cca tat gaa cct gtt tat agt gac	960
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PF59082SeqList_PF59082.txt

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Pro	Ser	Thr	Thr	Gly	Ser	Val	Arg	Thr	Ala	Met	Thr	Met	Thr	Glu	Lys	
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Ile	Leu	Ala	Arg	Ala	Ser	Glu	Lys	Ala	Gln	Leu	Thr	Pro	Gly	Asp	Asn	
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Val	Trp	Val	Asn	Val	Asp	Ile	Leu	Met	Thr	His	Asp	Val	Cys	Gly	Pro	
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Gly	Ser	Ile	Gly	Ile	Phe	Lys	Arg	Glu	Phe	Gly	Glu	Asp	Ala	Lys	Val	
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Trp	Asp	Arg	Glu	Lys	Leu	Val	Ile	Ile	Pro	Asp	His	Tyr	Ile	Phe	Thr	
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Ser	Asp	Glu	Arg	Ala	Asn	Arg	Asn	Val	Asp	Ile	Leu	Arg	Asp	Phe	Cys	
	130					135					140					
His	Glu	Gln	Asn	Ile	Lys	Tyr	Phe	Tyr	Asp	Ile	Lys	Asp	Leu	Ser	Asn	
	145				150					155					160	
Phe	Lys	Val	Asn	Pro	Asp	Tyr	Lys	Gly	Val	Cys	His	Val	Ala	Leu	Ala	
			165					170						175		
Gln	Glu	Gly	His	Cys	Arg	Pro	Gly	Glu	Val	Leu	Leu	Gly	Thr	Asp	Ser	
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His	Thr	Cys	Thr	Ala	Gly	Ala	Phe	Gly	Gln	Phe	Ala	Thr	Gly	Ile	Gly	
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PF59082SeqList_PF59082.txt

Asn Thr Asp Ala Gly Phe Val Leu Gly Thr Gly Lys Leu Leu Leu Lys
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 Leu Leu Ser Lys Asp Leu Ile Leu Gln Ile Gly Glu Ile Thr Val
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 Ala Gly Ala Thr Tyr Lys Ser Met Glu Phe Val Gly Thr Thr Val Glu
 260 265 270
 Ser Leu Thr Met Glu Glu Arg Met Thr Leu Cys Asn Met Val Val Glu
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 Ala Gly Gly Lys Asn Gly Val Val Pro Ala Asp Ser Thr Thr Phe Lys
 290 295 300
 Tyr Leu Glu Gly Lys Thr Ser Leu Pro Tyr Glu Pro Val Tyr Ser Asp
 305 310 315 320
 Asp Gln Ala Arg Phe Leu Ala Glu Tyr Arg Phe Asp Val Ser Lys Leu
 325 330 335
 Glu Pro Val Val Ala Lys Pro His Ser Pro Asp Asn Arg Ala Leu Ala
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 Arg Glu Cys Lys Asp Val Lys Ile Asp Arg Val Tyr Ile Gly Ser Cys
 355 360 365
 Thr Gly Gly Lys Thr Glu Asp Phe Met Ala Ala Ala Lys Val Phe Leu
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 Ala Ser Gly Lys Gln Val Lys Val Pro Thr Phe Leu Val Pro Ala Thr
 385 390 395 400
 Gln Lys Val Trp Met Asp Leu Tyr Ser Leu Pro Val Pro Gly Ser Gly
 405 410 415
 Gly Lys Thr Cys Ser Gln Ile Phe Glu Glu Val Gly Cys Asp Thr Pro
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 Lys Lys Asp Val Ser Leu Ser Ala Phe Thr Ser Gln Arg Cys Phe Lys
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 Ala Leu Pro Arg Arg Ile Ile Arg Cys Ala Val Ala Ala Pro Gln Arg
 35 40 45
 caa cct tcc acc act gga tca gtg agg act gca atg acc atg act gac 192
 Gln Pro Ser Thr Thr Gly Ser Val Arg Thr Ala Met Thr Met Thr Asp
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 aag ata ctg gcc aga gct tct gag aag gta cag ctg acc cct ggc gat 240
 Lys Ile Leu Ala Arg Ala Ser Glu Lys Val Gln Leu Thr Pro Gly Asp
 65 70 75 80
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 Asn Val Trp Val Asn Val Asp Ile Leu Met Thr His Asp Val Cys Gly
 85 90 95
 cct ggt tct att ggg att ttc aag agg gag tgt ggt gac gat gcc aag 336
 Pro Gly Ser Ile Gly Ile Phe Lys Arg Glu Cys Gly Asp Asp Ala Lys

PF59082SeqList_PF59082.txt

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aca agt gat gaa cgt gcc aat cgc aat gta gac ata tta aga gat ttc	432			
Thr Ser 115 Asp Glu Arg Ala Asn 120 Arg Asn Val Asp 125 Ile Leu Arg Asp Phe				
tgc cat gag cag aat atc aag tac ttt tat gat att aag gat ctc agt	480			
Cys His 130 Glu Gln Asn Ile 135 Lys Tyr Phe Tyr Asp 140 Ile Lys Asp Leu Ser				
aat ttt aag gta aat cca gac tat aag ggt gtt tgc cat gtt gcc ctt	528			
Asn Phe 145 Lys Val Asn Pro Asp Tyr Lys Gly Val Cys His Val Ala Leu				
gct cag gaa ggt cat tgt agg cct gga gag gtt ctc tta ggt act gat	576			
Ala Gln 150 Glu His Cys Arg Pro Gly Glu Val Leu Leu Gly Thr Asp				
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Ser His 165 Thr Cys Thr Ala Gly Ala Phe Gly Gln Phe Ala Thr Gly Ile				
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Gly Asn 180 Thr Asp Ala Gly Phe Val Leu Gly Thr Gly Lys Leu Leu				
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Lys Val 195 Pro Pro Thr Leu Arg Phe Val Met Asp Gly Glu Met Pro Asp				
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Tyr Leu 200 Leu Ser Lys Asp Leu Ile Leu Gln Ile Ile Gly Glu Ile Thr				
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Val Ala 210 Gly Ala Thr Tyr Lys Ser Met Glu Phe Val Gly Thr Val				
gaa agt tta act atg gaa gaa cgg atg aca ttg tgc aac atg gtt gtt	864			
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Glu Ala 230 Gly Gly Lys Asn Gly Val Val Pro Ala Asp Ser Thr Thr Phe				
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Lys Tyr 240 Leu Glu Gly Lys Thr Ser Leu Pro Tyr Glu Pro Val Tyr Ser				
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Leu Glu 260 Pro Val Ala Lys Pro His Ser Pro Asp Asn Arg Ala Leu				
gca agg gag tgc aag gat gta aaa att gac aga gta tac ata gga tct	1104			
Ala Arg 270 Glu Cys Lys Asp Val Lys Ile Asp Arg Val Tyr Ile Gly Ser				
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Cys Thr 280 Gly Gly Lys Thr Glu Asp Phe Met Ala Ala Ala Lys Val Phe				
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Thr Gln 300 Lys Val Trp Met Asp Leu Tyr Ser Leu Pro Val Pro Gly Ser				
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Gly Gly 310 Lys Thr Cys Ser Gln Ile Phe Glu Glu Ala Gly Cys Asp Thr				
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Pro Ala 320 Ser Pro Ser Cys Gly Ala Cys Leu Gly Gly Pro Lys Asp Thr				
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Tyr Ala 330 Arg Met Asn Glu Pro Lys Val Cys Val Ser Thr Thr Asn Arg				
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PF59082SeqList_PF59082.txt

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			20					25					30		
Ala	Leu	Pro	Arg	Arg	Ile	Ile	Arg	Cys	Ala	Val	Ala	Ala	Pro	Gln	Arg
			35				40					45			
Gln	Pro	Ser	Thr	Thr	Gly	Ser	Val	Arg	Thr	Ala	Met	Thr	Met	Thr	Asp
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Lys	Ile	Leu	Ala	Arg	Ala	Ser	Glu	Lys	Val	Gln	Leu	Thr	Pro	Gly	Asp
65					70					75					80
Asn	Val	Trp	Val	Asn	Val	Asp	Ile	Leu	Met	Thr	His	Asp	Val	Cys	Gly
				85					90					95	
Pro	Gly	Ser	Ile	Gly	Ile	Phe	Lys	Arg	Glu	Cys	Gly	Asp	Asp	Ala	Lys
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Val	Trp	Asp	Arg	Glu	Lys	Leu	Val	Ile	Ile	Pro	Asp	His	Tyr	Ile	Phe
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Thr	Ser	Asp	Glu	Arg	Ala	Asn	Arg	Asn	Val	Asp	Ile	Leu	Arg	Asp	Phe
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Cys	His	Glu	Gln	Asn	Ile	Lys	Tyr	Phe	Tyr	Asp	Ile	Lys	Asp	Leu	Ser
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Asn	Phe	Lys	Val	Asn	Pro	Asp	Tyr	Lys	Gly	Val	Cys	His	Val	Ala	Leu
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Ala	Arg	Glu	Cys	Lys	Asp	Val	Lys	Ile	Asp	Arg	Val	Tyr	Ile	Gly	Ser
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Cys	Thr	Gly	Gly	Lys	Thr	Glu	Asp	Phe	Met	Ala	Ala	Ala	Lys	Val	Phe
	370					375					380				
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Thr	Gln	Lys	Val	Trp	Met	Asp	Leu	Tyr	Ser	Leu	Pro	Val	Pro	Gly	Ser
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PF59082SeqList_PF59082.txt

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 Ala Leu Pro Arg Arg Ile Ile Arg Cys Ala Val Ala Ala Pro Gln Arg
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 Val Trp Asp Arg Glu Lys Leu Val Ile Ile Pro Asp His Tyr Ile Phe
 115 120 125
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 Thr Ser Asp Glu Arg Ala Asn Arg Asn Val Asp Ile Leu Arg Asp Phe
 130 135 140
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 Cys His Glu Gln Asn Ile Lys Tyr Phe Tyr Asp Ile Lys Asp Leu Ser
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 Ala Gln Glu Gly His Cys Arg Pro Gly Glu Val Leu Leu Gly Thr Asp
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 Ser His Thr Cys Thr Ala Gly Ala Phe Gly Gln Phe Ala Thr Gly Ile
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Leu	Glu	Pro	Val	Val	Ala	Lys	Pro	His	Ser	Pro	Asp	Asn	Arg	Ala	Leu	
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gca	agg	gag	tgc	aag	gat	gta	aaa	att	gac	aga	gta	tac	ata	gga	tct	1104
Ala	Arg	Glu	Cys	Lys	Asp	Val	Lys	Ile	Asp	Arg	Val	Tyr	Ile	Gly	Ser	
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Gly	Gly	Lys	Thr	Cys	Ser	Gln	Ile	Phe	Glu	Glu	Ala	Gly	Cys	Asp	Thr	
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Pro	Ala	Ser	Pro	Ser	Cys	Gly	Ala	Cys	Leu	Gly	Gly	Pro	Lys	Asp	Thr	
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Tyr	Ala	Arg	Met	Asn	Glu	Pro	Lys	Val	Cys	Val	Ser	Thr	Thr	Asn	Arg	
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Asn	Phe	Pro	Gly	Arg	Met	Gly	His	Lys	Glu	Gly	Gln	Ile	Tyr	Leu	Ala	
	465				470				475						480	
tcc	cca	tat	aca	gct	gct	gca	tct	gca	ttg	acc	ggt	tat	gtt	act	gat	1488
Ser	Pro	Tyr	Thr	Ala	Ala	Ala	Ser	Ala	Leu	Thr	Gly	Tyr	Val	Thr	Asp	
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Lys	Ile	Leu	Ala	Arg	Ala	Ser	Glu	Lys	Val	Gln	Leu	Thr	Pro	Gly	Asp	
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Asn	Val	Trp	Val	Asn	Val	Asp	Ile	Leu	Met	Thr	His	Asp	Val	Cys	Gly	
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Pro	Gly	Ser	Ile	Gly	Ile	Phe	Lys	Arg	Glu	Phe	Gly	Asp	Asp	Ala	Lys	
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PF59082SeqList_PF59082.txt

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 Ala Gln Glu Gly His Cys Arg Pro Gly Glu Val Leu Leu Gly Thr Asp
 180 185 190
 Ser His Thr Cys Thr Ala Gly Ala Phe Gly Gln Phe Ala Thr Gly Ile
 195 200 205
 Gly Asn Thr Asp Ala Gly Phe Val Leu Gly Thr Gly Lys Leu Leu Leu
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 Lys Val Pro Pro Thr Leu Arg Phe Val Met Asp Gly Glu Met Pro Asp
 225 230 235
 Tyr Leu Leu Ser Lys Asp Leu Ile Leu Gln Ile Ile Gly Glu Ile Thr
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 Val Ala Gly Ala Thr Tyr Lys Ser Met Glu Phe Val Gly Thr Thr Val
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 Glu Ser Leu Thr Met Glu Glu Arg Met Thr Leu Cys Asn Met Val Val
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 Glu Ala Gly Gly Lys Asn Gly Val Val Pro Ala Asp Ser Thr Thr Phe
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 Lys Tyr Leu Glu Gly Lys Thr Ser Leu Pro Tyr Glu Pro Val Tyr Ser
 305 310 315
 Asp Asp Gln Ala Arg Phe Leu Ala Glu Tyr Arg Phe Asp Val Ser Lys
 325 330 335
 Leu Glu Pro Val Val Ala Lys Pro His Ser Pro Asp Asn Arg Ala Leu
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 Ala Arg Glu Cys Lys Asp Val Lys Ile Asp Arg Val Tyr Ile Gly Ser
 355 360 365
 Cys Thr Gly Gly Lys Thr Glu Asp Phe Met Ala Ala Ala Lys Val Phe
 370 375 380
 Leu Ala Ser Gly Lys Gln Val Lys Val Pro Thr Phe Leu Val Pro Ala
 385 390 395
 Thr Gln Lys Val Trp Met Asp Leu Tyr Ser Leu Pro Val Pro Gly Ser
 405 410 415
 Gly Gly Lys Thr Cys Ser Gln Ile Phe Glu Glu Ala Gly Cys Asp Thr
 420 425 430
 Pro Ala Ser Pro Ser Cys Gly Ala Cys Leu Gly Gly Pro Lys Asp Thr
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 450 455 460
 Asn Phe Pro Gly Arg Met Gly His Lys Glu Gly Gln Ile Tyr Leu Ala
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Lys Lys Asp Val Ser Leu Ser Ala Phe Thr Ser Gln Arg Cys Phe Lys	
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gcg ctt cca agg aga ata atc cgt tgt gct gtg gcg gcg cct cag cgc	144
Ala Leu Pro Arg Arg Ile Ile Arg Cys Ala Val Ala Ala Pro Gln Arg	
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PF59082SeqList_PF59082.txt

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Asn	Val	Trp	Val	Asn	Val	Asp	Ile	Leu	Met	Thr	His	Asp	Val	Cys	Gly	
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Pro	Gly	Ser	Ile	Gly	Ile	Phe	Lys	Arg	Glu	Phe	Gly	Asp	Asp	Ala	Lys	
			100				105						110			
gtt	tgg	gac	cgt	gaa	aag	ctt	gta	ata	ata	ccc	gac	cat	tat	ata	ttc	384
Val	Trp	Asp	Arg	Glu	Lys	Leu	Val	Ile	Ile	Pro	Asp	His	Tyr	Ile	Phe	
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Thr	Ser	Asp	Glu	Arg	Ala	Asn	Arg	Asn	Val	Asp	Ile	Leu	Arg	Asp	Phe	
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Cys	His	Glu	Gln	Asn	Ile	Lys	Tyr	Phe	Tyr	Asp	Ile	Lys	Asp	Leu	Ser	
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Asn	Phe	Lys	Val	Asn	Pro	Asp	Tyr	Lys	Gly	Val	Cys	His	Val	Ala	Leu	
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Ser	His	Thr	Cys	Thr	Ala	Gly	Ala	Phe	Gly	Gln	Phe	Ala	Thr	Gly	Ile	
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Gly	Asn	Thr	Asp	Ala	Gly	Phe	Val	Leu	Gly	Thr	Gly	Lys	Leu	Leu	Leu	
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Tyr	Leu	Leu	Ser	Lys	Asp	Leu	Ile	Leu	Gln	Ile	Ile	Gly	Glu	Ile	Thr	
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Val	Ala	Gly	Ala	Thr	Tyr	Lys	Ser	Met	Glu	Phe	Val	Gly	Thr	Thr	Val	
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gaa	agt	tta	act	atg	gaa	gaa	cgg	atg	aca	ttg	tgc	aac	atg	gtt	gtt	864
Glu	Ser	Leu	Thr	Met	Glu	Glu	Arg	Met	Thr	Leu	Cys	Asn	Met	Val	Val	
		275					280					285				
gaa	gct	ggg	gga	aag	aat	ggg	gtt	gtt	cct	gct	gac	agc	act	aca	ttt	912
Glu	Ala	Gly	Gly	Lys	Asn	Gly	Val	Val	Pro	Ala	Asp	Ser	Thr	Thr	Phe	
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aaa	tat	ctt	gag	ggc	aag	aca	tct	ctg	cca	tat	gaa	cct	gtt	tat	agt	960
Lys	Tyr	Leu	Glu	Gly	Lys	Thr	Ser	Leu	Pro	Tyr	Glu	Pro	Val	Tyr	Ser	
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gac	gat	caa	gca	aga	ttt	ctt	gct	gag	tat	aga	ttt	gat	gtc	tca	aaa	1008
Asp	Asp	Gln	Ala	Arg	Phe	Leu	Ala	Glu	Tyr	Arg	Phe	Asp	Val	Ser	Lys	
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Leu	Glu	Pro	Val	Val	Ala	Lys	Pro	His	Ser	Pro	Asp	Asn	Arg	Ala	Leu	
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Ala	Arg	Glu	Cys	Lys	Asp	Val	Lys	Ile	Asp	Arg	Val	Tyr	Ile	Gly	Ser	
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Cys	Thr	Gly	Gly	Lys	Thr	Glu	Asp	Phe	Met	Ala	Ala	Ala	Lys	Val	Phe	
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Leu	Ala	Ser	Gly	Lys	Gln	Val	Lys	Val	Pro	Thr	Phe	Leu	Val	Pro	Ala	
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Pro	Ala	Ser	Pro	Ser	Cys	Gly	Ala	Cys	Leu	Gly	Gly	Pro	Lys	Asp	Thr	
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Tyr	Ala	Arg	Met	Asn	Glu	Pro	Lys	Val	Cys	Val	Ser	Thr	Thr	Asn	Arg	
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225				230						235						
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Val	Ala	Gly	Ala	Thr	Tyr	Lys	Ser	Met	Glu	Phe	Val	Gly	Thr	Thr	Val	
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Glu	Ser	Leu	Thr	Met	Glu	Glu	Arg	Met	Thr	Leu	Cys	Asn	Met	Val	Val	
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Glu	Ala	Gly	Gly	Lys	Asn	Gly	Val	Val	Pro	Ala	Asp	Ser	Thr	Thr	Phe	
	290				295					300						
Lys	Tyr	Leu	Glu	Gly	Lys	Thr	Ser	Leu	Pro	Tyr	Glu	Pro	Val	Tyr	Ser	320
305					310					315						
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Leu	Glu	Pro	Val	Val	Ala	Lys	Pro	His	Ser	Pro	Asp	Asn	Arg	Ala	Leu	
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PF59082SeqList_PF59082.txt

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 Tyr Ala Arg Met Asn Glu Pro Lys Val Cys Val Ser Thr Thr Asn Arg
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 Asn Phe Pro Gly Arg Met Gly His Lys Glu Gly Gln Ile Tyr Leu Ala
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 Arg Arg Thr Lys Pro Cys Arg Val Arg Ala Val Ala Ser Pro Ala Arg
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 Thr Pro Arg Ala Pro Ser Ser Thr Gly Ser Val Lys Thr Ala Met Thr
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 Met Thr Glu Lys Ile Leu Ala Arg Ala Ser Glu Arg Ala Ala Leu Glu
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 Pro Gly Glu Asn Val Trp Val Asp Ile Asp Val Leu Met Thr His Asp
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 Val Cys Gly Pro Gly Thr Ile Gly Ile Phe Lys Lys Glu Phe Gly Glu
 100 105 110
 gat gcc aag gtc tgg gac cgc gag aag gtc gtc atc atc ccc gac cac 384
 Asp Ala Lys Val Trp Asp Arg Glu Lys Val Val Ile Ile Pro Asp His
 115 120 125
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 Tyr Ile Phe Thr Ser Asp Glu Arg Ala Asn Arg Asn Val Asp Ile Leu
 130 135 140
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 Arg Asp Phe Cys Leu Gln Asn Ile Lys Tyr Phe Tyr Asp Ile Lys
 145 150 155 160
 gac ctc agc gat ttc agg gct aat cca gac tac aag ggt gtc tgc cac 528
 Asp Leu Ser Asp Phe Arg Ala Asn Pro Asp Tyr Lys Gly Val Cys His
 165 170 175
 att gca ctt gct cag gaa ggc cac tgc cga cca ggc gag gtt ctc ctg 576
 Ile Ala Leu Ala Gln Glu Gly His Cys Arg Pro Gly Glu Val Leu Leu
 180 185 190
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 Gly Thr Asp Ser His Thr Cys Asn Ala Gly Ala Phe Gly Gln Phe Ala

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PF59082SeqList_PF59082.txt

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    65      70      75      80
Pro Gly Glu Asn Val Trp Val Asp Ile Asp Val Leu Met Thr His Asp
    85      90      95
Val Cys Gly Pro Gly Thr Ile Gly Ile Phe Lys Lys Glu Phe Gly Glu
    100      105      110
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Tyr Ile Phe Thr Ser Asp Glu Arg Ala Asn Arg Asn Val Asp Ile Leu
    130      135      140
Arg Asp Phe Cys Leu Glu Gln Asn Ile Lys Tyr Phe Tyr Asp Ile Lys
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Asp Leu Ser Asp Phe Arg Ala Asn Pro Asp Tyr Lys Gly Val Cys His
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Ile Ala Leu Ala Gln Glu Gly His Cys Arg Pro Gly Glu Val Leu Leu
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Gly Thr Asp Ser His Thr Cys Asn Ala Gly Ala Phe Gly Gln Phe Ala
    195      200      205
Thr Gly Ile Gly Asn Thr Asp Ala Gly Phe Val Met Gly Thr Gly Lys
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Ala Leu Leu Lys Val Pro Pro Thr Ile Arg Phe Val Leu Asp Gly Glu
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Met Pro Pro Tyr Leu Leu Ala Lys Asp Leu Ile Leu Gln Ile Ile Gly
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Glu Ile Ser Val Ser Gly Ala Thr Tyr Lys Ser Met Glu Phe Val Gly
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Ser Thr Val Glu Ser Leu Thr Met Glu Glu Arg Met Thr Leu Cys Asn
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Met Val Val Glu Ala Gly Gly Lys Asn Gly Val Val Pro Ala Asp Glu
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Thr Thr Phe Lys Tyr Leu Glu Gly Arg Thr Ser Val Asp Tyr Gln Pro
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Val Tyr Ser Asp Ala Glu Ala Arg Phe Phe Ser Asp Tyr Arg Phe Asp
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Thr Asn Arg Asn Phe Pro Gly Arg Met Gly His Lys Glu Gly Gln Ile
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Leu Thr Arg 35 Arg Thr Lys Pro Cys Ser Val Arg Ala Val Ala Ser Pro
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Ala Arg Ala Leu Ser Ser Thr Gly Ser Val Lys Ser Ala Met Thr Met
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Thr Glu Lys Ile Leu Arg Ala Ser Glu Arg Ala Ala Leu Glu Pro
65
ggg gag aac gtg tgg gtc gac gtc gac gtg ctc atg acg cac gac gtc 288
Gly Glu Asn Val Trp 85 Val Asp Val Asp Val Leu Met Thr His Asp Val
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Cys Gly Pro Gly Ala Phe Asp Ile Phe Lys Lys Glu Phe Gly Glu Asp
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Ala Arg Val Trp Asp Arg Glu Lys 120 Leu Val Val Ile Pro Asp His Tyr
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Ile Phe Thr Ser Asp Gly Arg Ala Lys Arg Asn Val Asp Ile Leu Arg
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Leu Ser Asp Phe Arg 165 Ala Asn Pro Asp Tyr Lys Gly Val Cys His Ile
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Ala Leu Ala Gln Glu Ala His Cys Arg Pro Gly Glu Val Leu Leu Gly
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Thr Asp Ser His Thr Cys Asn Ala Gly Ala Phe Gly Gln Phe Ala Thr
195
gga atc gga aac act gat gca ggt ttt gtg ttg ggc act gga aag gct 672
Gly Ile Gly Asn Thr Asp Ala Gly Phe Val Leu Gly Thr Gly Lys Ala
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Leu Leu Lys Val Pro Pro Thr Ile Arg Phe Ile Leu Asp Gly Glu Met
225
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Pro Pro Tyr Leu 245 Ala Lys Asp Leu Ile Leu Gln Ile Ile Gly Glu
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Ile Ser Val Ser Gly Ala Thr Tyr Lys Ser Met Glu Phe Val Gly Ser
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Val Ile Glu Ala Gly Gly Lys Asn Gly Val Val Pro 300 Ala Asp Glu Thr
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PF59082SeqList_PF59082.txt

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 <223> Xaa in position 11 is any or no amino acid

<220>
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 <223> Xaa in position 13 to 15 is any amino acid

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<223> Xaa in position 19 to 20 is Ile, Leu or Val

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<223> Xaa in position 21 is Phe, Ile, Leu or Val

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<223> Xaa in position 23 is Ala, Ser or Thr

<220>

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<222> (29)..(29)

<223> Xaa in position 29 is Ala, Asn or Thr

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<223> Xaa in position 30 is any amino acid

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<223> Xaa in position 33 is Phe or Leu

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<223> Xaa in position 35 is any amino acid

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<221> Variant

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<223> Xaa in position 38 is Ser or Thr

<220>

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<223> Xaa in position 40 is Ile, Met or Val

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<223> Xaa in position 42 is Asn or Ser

<220>

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<223> Xaa in position 46 is Ala or Gly

<220>

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 <223> Xaa in position 48 is Ala, Gly, Ile or Val

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 <223> Xaa in position 49 is any amino acid

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 <223> Xaa in position 50 is Ala or Gly

 <220>
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 <223> Xaa in position 53 is Glu or Lys

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 <223> Xaa in position 60 is any amino acid

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 <223> Xaa in position 61 is Ala, Ser or Thr

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 Gly Xaa Xaa Xaa Xaa Gly Xaa Asp Ser His Thr Cys Xaa Xaa Gly Xaa
 20 25 30
 Xaa Gly Xaa Phe Xaa Xaa Gly Xaa Gly Xaa Thr Asp Xaa Xaa Xaa Xaa
 35 40 45
 Xaa Xaa Thr Gly Xaa Xaa Xaa Xaa Xaa Val Pro Xaa Xaa
 50 55 60

 <210> 1017
 <211> 59
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<223> Xaa in position 12 is Gly, Ser or Thr

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<222> (21)..(22)
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<223> Xaa in position 27 is Ala, Thr or Val

<220>

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<223> Xaa in position 28 is Ile or Val

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<223> Xaa in position 29 to 30 is any amino acid

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<223> Xaa in position 31 is Leu or Met

<220>
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<223> Xaa in position 32 is Asn, Pro, Ser or Thr

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Xaa Tyr Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20          25          30
Xaa Xaa Xaa Arg Xaa Thr Xaa Xaa Asn Met Xaa Xaa Glu Xaa Gly Xaa
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50          55

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<220>
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<220>
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<400> 1018
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1          5          10          15
Xaa Xaa Xaa Pro Xaa
                20

<210> 1019
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<220>
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 1 5 10 15
 Arg Met Gly

<210> 1020
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<223> Xaa in position 21 is Ala or Ile

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Xaa	Xaa	Xaa	Ala	Xaa										
			20											

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 <400> 1021
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 1 5 10 15
 Asn

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 1 5 10 15
 Xaa Xaa Xaa

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Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25

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1 5

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Cys Gly Val Glu Thr Asp Phe Ser Asn Asp Val Thr His Leu Leu Asn
20 25 30
ttc aac att tcc acc ggc ggt ttt gac tat gtt ctc gct cct ctg gtg 144
Phe Asn Ile Ser Thr Gly Gly Phe Asp Tyr Val Leu Ala Pro Leu Val
35 40 45
gat cct tcg tat agg ccg agc ttg gtg gaa gga aat ggt gta gat act 192
Asp Pro Ser Tyr Arg Pro Ser Leu Val Glu Gly Asn Gly Val Asp Thr
50 55 60
cag gtt ctt cca gtc tgt ggc tct gac tta gtc ttg tca cct tct caa 240
Gln Val Leu Pro Val Cys Gly Ser Asp Leu Val Leu Ser Pro Ser Gln
65 70 75 80
tgg agc agt cat gtt gtt gga aaa att agt tcg tgg att gac ttg gat 288
Trp Ser Ser His Val Val Gly Lys Ile Ser Ser Trp Ile Asp Leu Asp
85 90 95
tct gaa gat gag gtc tta cgg atg gat tca gaa acc aca ttg aag caa 336
Seite 1284

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Glu	Ile	Ala	Trp	Ala	Thr	His	Leu	Ser	Leu	Gln	Ala	Cys	Leu	Leu	Pro	
act	cct	aaa	ggg	aaa	tcg	tgc	gcc	aat	tat	gcc	aga	tgt	gtg	aac	cag	432
Thr	Pro	Lys	Gly	Lys	Ser	Cys	Ala	Asn	Tyr	Ala	Arg	Cys	Val	Asn	Gln	
atc	tta	caa	ggc	ctc	act	acc	ttg	cag	tta	tgg	cta	agg	gtt	cca	ctg	480
Ile	Leu	Gln	Gly	Leu	Thr	Thr	Leu	Gln	Leu	Trp	Leu	Arg	Val	Pro	Leu	
gtg	aag	tct	gaa	ggg	gat	tca	atg	gat	gat	acc	tca	gag	gga	ctg	aat	528
Val	Lys	Ser	Glu	Gly	Asp	Ser	Met	Asp	Asp	Thr	Ser	Glu	Gly	Leu	Asn	
gat	tcc	tgg	gag	ctg	tgg	aat	tcg	ttt	cgt	ctt	ctt	tgt	gag	cat	gac	576
Asp	Ser	Trp	Glu	Leu	Trp	Asn	Ser	Phe	Arg	Leu	Leu	Cys	Glu	His	Asp	
agt	aag	ctg	tct	ggt	gct	ctt	gat	ggt	ctg	agt	aca	cta	ccc	tct	gaa	624
Ser	Lys	Leu	Ser	Val	Ala	Leu	Asp	Val	Leu	Ser	Thr	Leu	Pro	Ser	Glu	
act	tca	cta	ggg	cgc	tgg	atg	gga	gag	tct	gtg	aga	gca	gcc	ata	tta	672
Thr	Ser	Leu	Gly	Arg	Trp	Met	Gly	Glu	Ser	Val	Arg	Ala	Ala	Ile	Leu	
agc	act	gat	gct	ttc	tta	aca	aat	gct	cgg	ggt	tat	cct	tgc	ttg	tcc	720
Ser	Thr	Asp	Ala	Phe	Leu	Thr	Asn	Ala	Arg	Gly	Tyr	Pro	Cys	Leu	Ser	
aaa	cgc	cac	caa	aag	tta	ata	gca	gga	ttt	ttt	gat	cat	gct	gcc	cag	768
Lys	Arg	His	Gln	Lys	Leu	Ile	Ala	Gly	Phe	Phe	Asp	His	Ala	Ala	Gln	
gtt	gta	att	tgt	gga	aag	cct	gtt	cat	aat	ctt	caa	aag	cct	ctt	gat	816
Val	Val	Ile	Cys	Gly	Lys	Pro	Val	His	Asn	Leu	Gln	Lys	Pro	Leu	Asp	
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Ser	Ser	Ser	Glu	Gly	Thr	Glu	Lys	Asn	Pro	Leu	Arg	Ile	Tyr	Leu	Asp	
tat	gtt	gct	tat	ctg	ttc	caa	aag	atg	gaa	tca	ctt	tct	gaa	cag	gaa	912
Tyr	Val	Ala	Tyr	Leu	Phe	Gln	Lys	Met	Glu	Ser	Leu	Ser	Glu	Gln	Glu	
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Arg	Ile	Glu	Leu	Gly	Tyr	Arg	Asp	Phe	Leu	Gln	Ala	Pro	Leu	Gln	Pro	
ctt	atg	gac	aac	ctc	gaa	gcc	caa	acc	tat	gag	acg	ttt	gag	aga	gac	1008
Leu	Met	Asp	Asn	Leu	Glu	Ala	Gln	Thr	Tyr	Glu	Thr	Phe	Glu	Arg	Asp	
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Ser	Val	Lys	Tyr	Ile	Gln	Tyr	Gln	Arg	Ala	Val	Glu	Lys	Ala	Leu	Val	
gac	agg	gta	cct	gat	gaa	aaa	gca	tcc	gag	ttg	act	act	gtc	ctg	atg	1104
Asp	Arg	Val	Pro	Asp	Glu	Lys	Ala	Ser	Glu	Leu	Thr	Thr	Val	Leu	Met	
gtt	gtg	ggg	gca	gga	agg	gga	ccc	ctt	gtg	agg	gca	tcg	tta	cag	gca	1152
Val	Val	Gly	Ala	Gly	Arg	Gly	Pro	Leu	Val	Arg	Ala	Ser	Leu	Gln	Ala	
gct	gaa	gaa	act	gat	cgg	aag	ttg	aaa	gtt	tat	gcc	gtg	gaa	aag	aat	1200
Ala	Glu	Glu	Thr	Asp	Arg	Lys	Leu	Lys	Val	Tyr	Ala	Val	Glu	Lys	Asn	
cct	aat	gcc	gtt	gta	aca	ctc	cat	aat	ttg	gtt	aag	atg	gaa	gga	tg	1248
Pro	Asn	Ala	Val	Val	Thr	Leu	His	Asn	Leu	Val	Lys	Met	Glu	Gly	Trp	
gaa	gac	gtt	gtt	acg	ata	ata	tcc	tgt	gac	atg	cgt	ttt	tgg	aat	gct	1296
Glu	Asp	Val	Val	Thr	Ile	Ile	Ser	Cys	Asp	Met	Arg	Phe	Trp	Asn	Ala	
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Pro	Glu	Gln	Ala	Asp	Ile	Leu	Val	Ser	Glu	Leu	Leu	Gly	Ser	Phe	Gly	
gac	aat	gaa	ctt	tct	cct	gag	tgt	ctt	gat	gga	gcc	caa	agg	ttt	ctg	1392
Asp	Asn	Glu	Leu	Ser	Pro	Glu	Cys	Leu	Asp	Gly	Ala	Gln	Arg	Phe	Leu	
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PF59082SeqList_PF59082.txt

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Pro	Ile	Thr	Ala	Ser 485	Lys	Leu	Tyr	Asn	Asp 490	Val	Lys	Ala	His	Lys 495	Asp	
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Leu	Ala	His	Phe	Glu	Thr	Ala	Tyr	Val	Val	Lys	Leu	His	Ser	Val	Ala	
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Ser	Thr	Lys	Val	Asn	Asn	Gln	Arg	Tyr	Lys	Lys	Leu	Gln	Phe	Ser	Leu	
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cca	agc	gat	gct	ggc	tca	gct	ttg	gtg	cat	gga	ttc	gct	ggc	tat	ttt	1680
Pro	Ser	Asp	Ala	Gly	Ser	Ala	Leu	Val	His	Gly	Phe	Ala	Gly	Tyr	Phe	
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gat	tcc	gtc	ctt	tat	aaa	gat	gtt	cat	ctt	ggg	atc	gag	cct	aca	aca	1728
Asp	Ser	Val	Leu	Tyr	Lys	Asp	Val	His	Leu	Gly	Ile	Glu	Pro	Thr	Thr	
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gca	aca	cca	aac	atg	ttc	agc	tgg	ttc	cca	atc	ttt	ttc	cca	ttg	agg	1776
Ala	Thr	Pro	Asn	Met	Phe	Ser	Trp	Phe	Pro	Ile	Phe	Phe	Pro	Leu	Arg	
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aag	cct	gtg	gag	ggt	cac	cct	gat	act	cca	tta	gaa	gta	cac	ttt	tgg	1824
Lys	Pro	Val	Glu	Val	His	Pro	Asp	Thr	Pro	Leu	Glu	Val	His	Phe	Trp	
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agg	tgt	tgt	ggt	tcc	tca	aag	gtt	tgg	tat	gaa	tgg	tcg	gtg	tct	tca	1872
Arg	Cys	Cys	Gly	Ser	Ser	Lys	Val	Trp	Tyr	Glu	Trp	Ser	Val	Ser	Ser	
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Pro	Thr	Pro	Ser	Pro	Met	His	Asn	Thr	Asn	Gly	Arg	Ser	Tyr	Trp	Val	
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Gln	Val	Leu	Pro	Val 70	Cys	Gly	Ser	Asp	Leu 75	Val	Leu	Ser	Pro	Ser 80	Gln
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Ser	Glu	Asp	Glu	Val 100	Leu	Arg	Met	Asp	Ser 105	Glu	Thr	Thr	Leu	Lys 110	Gln
Glu	Ile	Ala	Trp	Ala 115	Thr	His	Leu	Ser	Leu 120	Gln	Ala	Cys	Leu	Leu 125	Pro
Thr	Pro	Lys	Gly	Lys 130	Ser	Cys	Ala	Asn	Tyr 135	Ala	Arg	Cys	Val	Asn 140	Gln
Ile	Leu	Gln	Gly	Leu 150	Thr	Thr	Leu	Gln	Leu 155	Trp	Leu	Arg	Val	Pro 160	Leu
Val	Lys	Ser	Glu	Gly 165	Asp	Ser	Met	Asp	Asp 170	Thr	Ser	Glu	Gly	Leu 175	Asn
Asp	Ser	Trp	Glu	Leu 180	Trp	Asn	Ser	Phe	Arg 185	Leu	Leu	Cys	Glu	His 190	Asp
Ser	Lys	Leu	Ser	Val 195	Ala	Leu	Asp	Val	Leu 200	Ser	Thr	Leu	Pro	Ser 205	Glu
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PF59082SeqList_PF59082.txt

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Val Val Ile Cys 245 Lys Pro Val His 250 Leu Gln Lys Pro Leu Asp
Ser Ser Ser Glu Gly Thr Glu Lys Asn Pro Leu Arg Ile Tyr Leu Asp
Tyr Val Ala Tyr Leu Phe Gln Lys Met Glu Ser Leu Ser Glu Gln Glu
Arg Ile Glu Leu Gly Tyr Arg Asp Phe Leu Gln Ala Pro Leu Gln Pro
305 Leu Met Asp Asn Leu 310 Ala Gln Thr Tyr Glu Thr Phe Glu Arg Asp
Ser Val Lys Tyr 325 Gln Tyr Gln Arg Ala Val Glu Lys Ala Leu Val
Asp Arg Val Pro Asp Glu Lys Ala Ser Glu Leu Thr Thr Val Leu Met
Val Val Gly Ala Gly Arg Gly Pro Leu Val Arg Ala Ser Leu Gln Ala
370 Ala Glu Glu Thr Asp Arg Lys Leu Lys Val Tyr Ala Val Glu Lys Asn
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Glu Asp Val Val Thr Ile Ile Ser Cys Asp Met Arg Phe Trp Asn Ala
Pro Glu Gln Ala Asp Ile Leu Val Ser Glu Leu Leu Gly Ser Phe Gly
Asp Asn Glu Leu Ser Pro Glu Cys Leu Asp Gly Ala Gln Arg Phe Leu
Lys Pro Asp Gly Ile Ser Ile Pro Ser Ser Tyr Thr Ser Phe Ile Gln
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Leu Ala His Phe Glu Thr Ala Tyr Val Val Lys Leu His Ser Val Ala
Lys Leu Ala Pro Ser Gln Ser Val Phe Thr Phe Thr His Pro Asn Phe
Ser Thr Lys Val Asn Asn Gln Arg Tyr Lys Lys Leu Gln Phe Ser Leu
Pro Ser Asp Ala Gly Ser Ala Leu Val His Gly Phe Ala Gly Tyr Phe
545 Asp Ser Val Leu Tyr Lys Asp Val His Leu Gly Ile Glu Pro Thr Thr
Ala Thr Pro Asn Met Phe Ser Trp Phe Pro Ile Phe Phe Pro Leu Arg
Lys Pro Val Glu Val His Pro Asp Thr Pro Leu Glu Val His Phe Trp
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Ser Asp Ser Arg Tyr 15 Cys Gly Val Glu Val 20 Leu Asp Phe Pro Ala 25 Gly		
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Asp Gly Leu Pro Ala Val Leu Thr His Ser Leu Ser Ser Ala Phe Asp		
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Phe Leu 45 Ala Pro Leu Val 50 Asp Pro Asp Tyr Arg 55 Thr Pro Gly		
gcc gtc ctg ccg gtg gcg gcc tcg gac ctc gtc ctc agc ccg tcc cag		305
Ala Val 60 Leu Pro Val Ala 65 Ser Asp Leu Val 70 Leu Ser Pro Ser Gln		
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Trp Ser Ser His Ile Val 80 Gly Lys Ile Ser Glu Trp Ile Asp Leu Asp		
	75 85 90	
tcc gag gac gag cag ctc cgg ctc gac tcg gag ctc acg ctt aag cag		401
Ser Glu Asp Glu Gln 95 Arg Leu Asp Ser Glu Leu Thr Leu Lys 105 Gln		
gag atc gcc tgg gcg act cat ctc tcc ttg cag gcg tgc gtt att cct		449
Glu Ile Ala Trp Ala Thr His Leu Ser Leu Gln Ala Cys Val Ile Pro		
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cct ccc aag aga tca acc tgt gcc aat tat gct aga gtt gta aat aat		497
Pro Pro Lys Arg Ser Thr Cys Ala Asn Tyr Ala Arg Val Val Asn Asn		
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att ttg caa ggc ctg acc aat atg cag ttg tgg ctt agg ata cct ctg		545
Ile Leu Gln Gly Leu Thr 145 Asn Met Gln Leu Trp Leu Arg Ile Pro Leu		
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Glu Lys Ser Glu Ser Met Glu Glu Asp Arg Asp Lys Ser Glu Thr Val		
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Asp Ser Trp Glu Trp 175 Asn Ser Phe Arg 180 Leu Leu Cys Glu His 185 Ser		
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Ser Gln Leu Tyr Val Ala Leu Asp Ile Leu Ser Ser Leu Pro Ser Met		
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caa aca gat gct ttt cta aca aat gca aga ggt tat cct tgc ttg tcc		785
Gln Thr 220 Asp Ala Phe Leu Thr 225 Asn Ala Arg Gly Tyr 230 Pro Cys Leu Ser		
aaa cgc cac cag act ctg ctt act ggt ttt ttt aac cat tca gtt cag		833
Lys Arg His Gln Thr 240 Leu Leu Thr Gly Phe Phe 245 Asn His Ser Val Gln		
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Val Ile Ile Ser Gly 255 Arg Ser Asn His 260 Val Ser Gln Val 265 Ser Glu		
gga gtg ctc tca cgt gat gaa aac cac acc gaa gat acc ccc act cag		929
Gly Val Leu Ser Arg Asp Glu Asn His Thr Glu Asp Thr Pro Thr Gln		
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cat gca ttg agc ccg tac ctt gac tac atg gcc tac ctc tat cag agg		977
His Ala Leu Ser Pro Tyr Leu Asp Tyr Met Ala Tyr Leu Tyr Gln Arg		
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Phe Leu Gln Ser Pro Leu 320 Gln Pro Leu Met Asp Asn Leu Glu Ala Gln		
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Thr Tyr Glu Thr 335 Glu Lys Asp Thr Val 340 Lys Tyr Thr Gln Tyr Gln		
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Arg Ala Ile Ala Lys Ala Leu Val 355 Asp Lys Val Ser Asp Asp Glu Val		
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PF59082SeqList_PF59082.txt

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Leu	Val	Arg	Ala	Ser	Leu	Gln	Ala	Ala	Glu	Glu	Thr	Gly	Arg	Thr	Leu	
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Lys	Val	Tyr	Ala	Val	Glu	Lys	Asn	Pro	Asn	Ala	Val	Ile	Thr	Leu	His	
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Ser	Asp	Met	Arg	Cys	Trp	Asp	Ala	Pro	Glu	Lys	Ala	Asp	Ile	Leu	Val	
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Leu	Asp	Gly	Ala	Gln	Arg	Phe	Leu	Lys	Pro	Asp	Gly	Ile	Ser	Ile	Pro	
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Phe	Ser	Phe	Ala	His	Pro	Asn	Phe	Ser	Pro	Lys	Ala	Thr	Asn	Gln	Arg	
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Tyr	Thr	Lys	Leu	Gln	Phe	Glu	Leu	Pro	Gln	Asp	Thr	Gly	Ser	Cys	Leu	
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65      70      75      80
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165     170     175
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180     185     190
Leu Asp Ile Leu Ser Ser Leu Pro Ser Met Asn Ser Leu Gly Arg Trp
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290     295     300
Gln Glu Arg Phe Glu Ile Asn Tyr Arg Asp Phe Leu Gln Ser Pro Leu
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Lys Asp Thr Val Lys Tyr Thr Gln Tyr Gln Arg Ala Ile Ala Lys Ala
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 Leu Asn His Ser Leu Ala Ser Ala Phe Asp Phe Ile Leu Val Pro Leu
 35 40 45
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 Val Asp Pro Asn Tyr Arg Pro Ala Pro Gly Ser Val Leu Pro Val Ser
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 Ala Ser Asp Leu Ile Leu Gly Pro Ala Gln Trp Ser Asn His Val Val
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 ggg aag atc agc gag tgg att gat ttg gac tct gag gac gag cgg ctc 288
 Gly Lys Ile Ser Glu Trp Ile Asp Leu Asp Ser Glu Asp Glu Arg Leu
 85 90 95
 cgc ttt gac tcc gag ctc acg ctg aag cag gag att gcg tgg gcg tct 336
 Arg Phe Asp Ser Glu Leu Thr Leu Lys Gln Glu Ile Ala Trp Ala Ser
 100 105 110
 cac gtc tcg ctg cag gca tgt gtt ctt cct gcc ccc agg aga tct ttt 384
 His Val Ser Leu Gln Ala Cys Val Leu Pro Ala Pro Arg Arg Ser Phe
 115 120 125
 tgt ggc aat tat gcc aga gtc gtg aat caa att ttg caa ggc ctg acc 432
 Cys Gly Asn Tyr Ala Arg Val Val Asn Gln Ile Leu Gln Gly Leu Thr
 130 135 140
 aat atg cat ttg tgg ctc agg ttg cct ctg gag aag tcc gag cct atg 480
 Asn Met His Leu Trp Leu Arg Leu Pro Leu Glu Lys Ser Glu Pro Met
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 gat gat gat ctt gat aaa ata aag aat aac agc cac acg agt gaa att 528
 Asp Asp Asp Leu Asp Lys Ile Lys Asn Asn Ser His Thr Ser Glu Ile
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 Val Asp Ser Trp Glu Leu Trp Asn Ser Phe Arg Leu Leu Cys Asp His
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 Ser Ser Gln Leu Cys Val Ala Leu Asp Ile Leu Ser Thr Leu Pro Ser
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 Ile Asn Ser Leu Ala Arg Trp Phe Gly Glu Pro Val Arg Ala Ala Ile
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	Glu	Gly	Val	Leu	Ser	Gly	Asp	Glu	Ser	Tyr	Thr	Glu	Asp	Ser	His	Val	
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	Arg	His	Ala	Leu	Thr	Pro	Tyr	Leu	Glu	Tyr	Ile	Ala	Tyr	Leu	Tyr	Arg	
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	Gln	Thr	Tyr	Glu	Thr	Phe	Glu	Lys	Asp	Val	Val	Lys	Tyr	Thr	Gln	Tyr	
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	Arg	Arg	Ala	Val	Ala	Lys	Ala	Leu	Val	Asp	Arg	Val	Ala	Asp	Asp	Ala	
	gtc	tct	aca	act	agg	acg	gtg	ctg	atg	gtt	gtg	gga	gca	gga	cgg	gga	1152
	Val	Ser	Thr	Thr	Arg	Thr	Val	Leu	Met	Val	Val	Gly	Ala	Gly	Arg	Gly	
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	Pro	Leu	Val	Arg	Ala	Ser	Leu	Gln	Ala	Ala	Glu	Glu	Thr	Gly	Arg	Lys	
	tta	aaa	gta	tat	gct	gtt	gaa	aaa	aat	cct	aac	gct	gtt	att	act	ctt	1248
	Leu	Lys	Val	Tyr	Ala	Val	Glu	Lys	Asn	Pro	Asn	Ala	Val	Ile	Thr	Leu	
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	Ser	Ser	Asp	Met	Arg	Cys	Trp	Asp	Ala	Pro	Glu	Lys	Ala	Asp	Val	Leu	
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	Val	Ser	Glu	Leu	Leu	Gly	Ser	Phe	Gly	Asp	Asn	Glu	Leu	Ser	Pro	Glu	
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	Cys	Leu	Asp	Gly	Ala	Gln	Arg	Phe	Leu	Lys	Pro	Asp	Gly	Ile	Ser	Ile	
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	Pro	Ser	Ser	Tyr	Thr	Ser	Phe	Ile	Gln	Pro	Ile	Ile	Ala	Ser	Lys	Leu	
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	Val	Phe	Thr	Phe	Thr	His	Pro	Asn	Phe	Ser	Pro	Asn	Ala	Ser	Asn	Gln	
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Val Trp Tyr Glu Trp Ala Val Thr Thr Pro Thr Pro Ser Pro Ile His				
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aac agc aat ggc cgg tcc tat tgg gtt ggt cta tag				1956
Asn Ser Asn Gly Arg Ser Tyr Trp Val Gly Leu				
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Val Asp Pro Asn Tyr Arg Pro Ala Pro Gly Ser Val Leu Pro Val Ser	
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Ala Ser Asp Leu Ile Leu Gly Pro Ala Gln Trp Ser Asn His Val Val	
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Gly Lys Ile Ser Glu Trp Ile Asp Leu Asp Ser Glu Asp Glu Arg Leu	
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Arg Phe Asp Ser Glu Leu Thr Leu Lys Gln Glu Ile Ala Trp Ala Ser	
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His Val Ser Leu Gln Ala Cys Val Leu Pro Ala Pro Arg Arg Ser Phe	
115 120 125	
Cys Gly Asn Tyr Ala Arg Val Val Asn Gln Ile Leu Gln Gly Leu Thr	
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Ser Lys Arg His Gln Ser Leu Leu Thr Gly Phe Phe Lys His Ser Val	
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Gln Val Ile Ile Ser Gly Arg Ser Asn His Asn Val Phe Pro Val Ser	
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Glu Gly Val Leu Ser Gly Asp Glu Ser Tyr Thr Glu Asp Ser His Val	
275 280 285	
Arg His Ala Leu Thr Pro Tyr Leu Glu Tyr Ile Ala Tyr Leu Tyr Arg	
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Lys Met Asp Pro Leu Pro Glu Gln Glu Arg Ile Glu Ile Asn Tyr Arg	
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Arg Arg Ala Val Ala Lys Ala Leu Val Asp Arg Val Ala Asp Asp Ala	
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370 375 380	
Pro Leu Val Arg Ala Ser Leu Gln Ala Ala Glu Glu Thr Gly Arg Lys	
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Leu Lys Val Tyr Ala Val Glu Lys Asn Pro Asn Ala Val Ile Thr Leu	
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 450 455 460
 Cys Leu Asp Gly Ala Gln Arg Phe Leu Lys Pro Asp Gly Ile Ser Ile
 465 470 475 480
 Pro Ser Ser Tyr Thr Ser Phe Ile Gln Pro Ile Ile Ala Ser Lys Leu
 485 490 495
 His Asn Asp Ile Lys Ala His Lys Asp Ile Ala His Phe Glu Thr Ala
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 Tyr Val Val Lys Leu His Arg Ile Ala Thr Leu Ala Pro Pro Gln Gln
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 Val Phe Thr Phe Thr His Pro Asn Phe Ser Pro Asn Ala Ser Asn Gln
 530 535 540
 Arg Tyr Thr Lys Leu Gln Phe Glu Met Leu Pro Asp Met Gly Ser Cys
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 565 570 575
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 580 585 590
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 Gly Ser Pro Ile Glu Val His Phe Trp Arg Cys Cys Ala Pro Thr Lys
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gactagtacc agcgaggagg aggagaagaa ggcaaccgga g atg ccg ctg ggg caa 176
 Met Pro Leu Gly Gln
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 Arg Ala Gly Asp Lys Ser Glu Ser Arg Tyr Cys Gly Val Glu Val Leu
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 Asp Phe Pro Ala Gly Glu Glu Leu Pro Ala Val Leu Ser His Ser Leu
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 Ser Ser Ser Phe Asp Phe Leu Leu Ala Pro Leu Val Asp Pro Asp Tyr
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 Arg Pro Thr Pro Gly Ser Val Leu Pro Val Ala Ala Ser Asp Leu Val
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 Leu Gly Pro Ala Gln Trp Ser Ser His Ile Val Gly Lys Ile Ser Glu
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 Trp Ile Asp Leu Asp Ala Glu Asp Glu Gln Leu Arg Leu Asp Ser Glu
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Arg	Val	Val	Asn	His	Ile	Leu	Gln	Gly	Leu	Thr	Asn	Leu	Gln	Leu	Trp	
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Leu	Arg	Ile	Pro	Leu	Glu	Lys	Ser	Glu	Pro	Met	Asp	Glu	Asp	His	Asp	
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Phe	Leu	Thr	Asn	Ala	Arg	Gly	Tyr	Pro	Cys	Leu	Ser	Lys	Arg	His	Gln	
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Lys	Leu	Leu	Thr	Gly	Phe	Phe	Asn	His	Ser	Val	Gln	Val	Ile	Ile	Ser	
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Gly	Arg	Ser	Asn	His	Asn	Val	Ser	Gln	Gly	Gly	Val	Leu	Ser	Gly	Asp	
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Pro	Glu	Lys	Ala	Asp	Ile	Leu	Val	Ser	Glu	Leu	Leu	Gly	Ser	Phe	Gly	
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Pro	Ile	Thr	Ala	Ser	Lys	Leu	His	Asn	Asp	Ile	Lys	Ala	His	Lys	Asp	
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Ile	Ala	His	Phe	Glu	Thr	Ala	Tyr	Val	Val	Lys	Leu	His	Arg	Ile	Ala	
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Ser	Pro	Asn	Ala	Ser	Asn	Gln	Arg	Tyr	Thr	Lys	Leu	Lys	Phe	Glu	Ile		
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Ala	Thr	Pro	Asn	Met	Phe	Ser	Trp	Phe	Pro	Ile	Phe	Phe	Pro	Leu	Arg		
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Glu																	
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 <213> Oryza sativa

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 Val Asp Pro Asp Tyr Arg Pro Thr Pro Gly Ser Val Leu Pro Val Ala
 50 55 60
 Ala Ser Asp Leu Val Leu Gly Pro Ala Gln Trp Ser Ser His Ile Val
 65 70 75 80
 Gly Lys Ile Ser Glu Trp Ile Asp Leu Asp Ala Glu Asp Glu Gln Leu
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 Arg Leu Asp Ser Glu Ile Thr Leu Lys Gln Glu Ile Ala Trp Ala Ser
 100 105 110
 His Leu Ser Leu Gln Ala Cys Val Leu Pro Pro Pro Lys Arg Ser Ser
 115 120 125
 Cys Ala Asn Tyr Ala Arg Val Val Asn His Ile Leu Gln Gly Leu Thr
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 Asn Leu Gln Leu Trp Leu Arg Ile Pro Leu Glu Lys Ser Glu Pro Met
 145 150 155 160
 Asp Glu Asp His Asp Gly Ala Lys Asp Asn Ser Asp Met Val Gly Tyr
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 Ser Leu Ile Arg Ser Thr Leu Pro Ser Met Asn Ser Leu Gly Arg Trp
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 Phe Gly Glu Pro Ala Phe Leu Thr Asn Ala Arg Gly Tyr Pro Cys Leu
 195 200 205
 Ser Lys Arg His Gln Lys Leu Leu Thr Gly Phe Phe Asn His Ser Val
 210 215 220
 Gln Val Ile Ile Ser Gly Arg Ser Asn His Asn Val Ser Gln Gly Gly
 225 230 235 240
 Val Leu Ser Gly Asp Glu Asn His Thr Glu Asp Thr Ala Val Arg His
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 Ala Leu Ser Pro Tyr Leu Asp Tyr Ile Ala Tyr Ile Tyr Gln Arg Met
 260 265 270
 Asp Pro Leu Pro Glu Gln Glu Arg Phe Glu Ile Asn Tyr Arg Asp Phe
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 Tyr Glu Thr Phe Glu Lys Asp Thr Val Lys Tyr Thr Gln Tyr Gln Arg
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 325 330 335
 Thr Thr Lys Thr Ala Ala Glu Glu Thr Gly Arg Lys Leu Lys Val Tyr
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 Ala Gln Arg Phe Leu Lys Pro Asp Gly Ile Ser Ile Pro Ser Ser Tyr
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 Thr Ser Phe Ile Glu Pro Ile Thr Ala Ser Lys Leu His Asn Asp Ile
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PF59082SeqList_PF59082.txt

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 515 520 525
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 Gly Ser Asp Leu Val Leu Ser Pro Ser Gln Trp Ser Ser His Val Val
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 Gly Lys Ile Ser Ser Trp Ile Asp Leu Asp Ser Glu Asp Glu Val Leu
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 Arg Met Asp Ser Glu Thr Thr Leu Lys Gln Glu Ile Ala Trp Ala Thr
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 His Leu Ser Leu Gln Ala Cys Leu Leu Pro Thr Pro Lys Gly Lys Ser
 75 80 85

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 Cys Ala Asn Tyr Ala Arg Cys Val Asn Gln Ile Leu Gln Gly Leu Thr
 90 95 100

acc ttg cag tta tgg cta agg gtt cca ctg atg aag tct gaa ggt gat 568
 Thr Leu Gln Leu Trp Leu Arg Val Pro Leu Met Lys Ser Glu Gly Asp
 105 110 115 120

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 Ser Met Asp Asp Thr Ser Glu Gly Leu Val Arg His Asn Asp Ser Trp
 125 130 135

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PF59082SeqList_PF59082.txt

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Gln Lys Leu Ile Ala	Gly Phe Phe Asp His Ala Ala Gln Val Val Ile	195		
205	tct gga aag cct gtt cat	210	aat ctt caa aag cct ctt gat tct agc acg	904
Ser Gly Lys Pro Val His	Asn Leu Gln Lys Pro Leu Asp Ser Ser Thr	215		
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Glu Gly Thr Glu Lys Asn	Pro Leu Arg Ile Tyr Leu Asp Tyr Val Ala	230		
235	tat ctg ttc caa aag atg	240	gaa tca ctt cct gaa cag gaa cgc atc gag	1000
Tyr Leu Phe Gln Lys Met	Glu Ser Leu Pro Glu Gln Glu Arg Ile Glu	245		
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Tyr Ile Gln Tyr Gln Arg	Ala Val Glu Lys Ala Leu Val Asp Arg Val	295		
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Pro Asp Glu Lys Ala Ser	Glu Leu Thr Thr Val Leu Met Val Val Gly	310		
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425	gct tcg aag ctt tac aat	435	gac gtt aag gct cat aaa gat ctt gcg cac	1576
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475	gtc aac aac caa cgc tat	480	aag aag ctt cag ttc aat cta cca agc gat	1720
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Leu Tyr Lys Asp Val His	Leu Gly Ile Glu Pro Thr Thr Ala Thr Pro	515		
525	aac atg ttc agc tgg ttc	530	cca atc ttt ttc cca ttg agg aag cct gtg	1864
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Gly Ser Ser Lys Val Trp Tyr Glu Trp Ser Val Ser Ser Pro Thr Pro
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Ser Pro Met His Asn Thr Asn Gly Arg Ser Tyr Trp Val Gly Leu
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ttgtcttaag aaagactaaa gtttacgagt gaattaaatc tcttttgacc ttatttatgt 2125

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Lys Gln Glu Ile Ala Trp Ala Thr His Leu Ser Leu Gln Ala Cys Leu
65          70          75          80
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85          90          95
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130          135          140
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260          265          270
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290          295          300
Glu Lys Ala Leu Val Asp Arg Val Pro Asp Glu Lys Ala Ser Glu Leu
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PF59082SeqList_PF59082.txt

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Phe Asn Ile Ser Thr Gly Gly Phe Asp Tyr Val Leu Ala Pro Leu Val	
35 40 45	
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Trp Ser Ser His Val Val Gly Lys Ile Ser Ser Trp Ile Asp Leu Asp	
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Ser Glu Asp Glu Val Leu Arg Met Asp Ser Glu Thr Thr Leu Lys Gln	
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PF59082SeqList_PF59082.txt

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Lys	Arg	His	Gln	Lys	Leu	Ile	Ala	Gly	Phe	Phe	Asp	His	Ala	Ala	Gln	
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Tyr	Val	Ala	Tyr	Leu	Phe	Gln	Lys	Met	Glu	Ser	Leu	Ser	Glu	Gln	Glu	
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Pro	Asn	Ala	Val	Val	Thr	Leu	His	Asn	Leu	Val	Lys	Met	Glu	Gly	Trp	
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Pro	Glu	Gln	Ala	Asp	Ile	Leu	Val	Ser	Glu	Leu	Leu	Gly	Ser	Phe	Gly	
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Lys	Pro	Asp	Gly	Ile	Ser	Ile	Pro	Ser	Ser	Thr	Thr	Ser	Phe	Ile	Gln	
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cct	ata	aca	gct	tcg	aag	ctt	tac	aat	gac	gtt	aag	gct	cat	aaa	gat	1488
Pro	Ile	Thr	Ala	Ser	Lys	Leu	Tyr	Asn	Asp	Val	Lys	Ala	His	Lys	Asp	
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PF59082SeqList_PF59082.txt

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Lys	Leu	Ala	Pro	Ser	Gln	Ser	Val	Phe	Thr	Phe	Thr	His	Pro	Asn	Phe		
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Ser	Thr	Lys	Val	Asn	Asn	Gln	Arg	Tyr	Lys	Lys	Leu	Gln	Phe	Ser	Leu		
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cca	agc	gat	gct	ggc	tca	gct	ttg	gtg	cat	gga	ttc	gct	ggc	tat	ttt		1680
Pro	Ser	Asp	Ala	Gly	Ser	Ala	Leu	Val	His	Gly	Phe	Ala	Gly	Tyr	Phe		
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<211> 584

<212> PRT

<213> Arabidopsis thaliana

<400> 1036

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Phe	Asn	Ile	Ser	Thr	Gly	Gly	Phe	Asp	Tyr	Val	Leu	Ala	Pro	Leu	Val		
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Gln	Val	Leu	Pro	Val	Cys	Gly	Ser	Asp	Leu	Val	Leu	Ser	Pro	Ser	Gln		
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Trp	Ser	Ser	His	Val	Gly	Lys	Ile	Ser	Trp	Ile	Asp	Leu	Asp				
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Ser	Glu	Asp	Glu	Val	Leu	Arg	Met	Asp	Ser	Glu	Thr	Thr	Leu	Lys	Gln		
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Thr	Pro	Lys	Gly	Lys	Ser	Cys	Ala	Asn	Tyr	Ala	Arg	Cys	Val	Asn	Gln		
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Ile	Leu	Gln	Gly	Leu	Thr	Thr	Leu	Gln	Leu	Trp	Leu	Arg	Val	Pro	Leu		
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Val	Lys	Ser	Glu	Gly	Asp	Ser	Met	Asp	Asp	Thr	Ser	Glu	Gly	Leu	Asn		
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Thr	Ser	Leu	Gly	Arg	Trp	Met	Gly	Glu	Ser	Val	Arg	Ala	Ala	Ile	Leu		
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PF59082SeqList_PF59082.txt

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 385 390 395 400
 Pro Asn Ala Val Val Thr Leu His Asn Leu Val Lys Met Glu Gly Trp
 405 410 415
 Glu Asp Val Val Thr Ile Ile Ser Cys Asp Met Arg Phe Trp Asn Ala
 420 425 430
 Pro Glu Gln Ala Asp Ile Leu Val Ser Glu Leu Leu Gly Ser Phe Gly
 435 440 445
 Asp Asn Glu Leu Ser Pro Glu Cys Leu Asp Gly Ala Gln Arg Phe Leu
 450 455 460
 Lys Pro Asp Gly Ile Ser Ile Pro Ser Ser Tyr Thr Ser Phe Ile Gln
 465 470 475 480
 Pro Ile Thr Ala Ser Lys Leu Tyr Asn Asp Val Lys Ala His Lys Asp
 485 490 495
 Leu Ala His Phe Glu Thr Ala Tyr Val Val Lys Leu His Ser Val Ala
 500 505 510
 Lys Leu Ala Pro Ser Gln Ser Val Phe Thr Phe Thr His Pro Asn Phe
 515 520 525
 Ser Thr Lys Val Asn Asn Gln Arg Tyr Lys Lys Leu Gln Phe Ser Leu
 530 535 540
 Pro Ser Asp Ala Gly Ser Ala Leu Val His Gly Phe Ala Gly Tyr Phe
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 Ala Thr Pro Asn Met Phe Ser Trp
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<211> 1950

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<221> CDS

<222> (1)..(1950)

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Gly Val Glu Val Leu Asp Phe Pro Ala Gly Glu Glu Leu Pro Ala Val	
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ctc tcc cac tcc ctc tcc tcc tcc ttc gac ttc ctc ctc gcc ccc ctc	144
Leu Ser His Ser Leu Ser Ser Ser Phe Asp Phe Leu Leu Ala Pro Leu	
35 40 45	
gtt gat ccc gac tac cgg ccg acg ccc ggg tcc gtc ctc ccc gtg gcg	192
Val Asp Pro Asp Tyr Arg Pro Thr Pro Gly Ser Val Leu Pro Val Ala	
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Ala Ser Asp Leu Val Leu Gly Pro Ala Gln Trp Ser Ser His Ile Val	
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Gly Lys Ile Ser Glu Trp Ile Asp Leu Asp Ala Glu Asp Glu Gln Leu	
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cgg ttg gac tcc gag atc act ctg aag cag gag att gcg tgg gcg tct	336
Arg Leu Asp Ser Glu Ile Thr Leu Lys Gln Glu Ile Ala Trp Ala Ser	
100 105 110	
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His Leu Ser Leu Gln Ala Cys Val Leu Pro Pro Pro Lys Arg Ser Ser	
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Cys Ala Asn Tyr Ala Arg Val Val Asn His Ile Leu Gln Gly Leu Thr	
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aat ttg cag ttg tgg ctt agg ata cct ctg gag aag tct gaa cct atg	480
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PF59082SeqList_PF59082.txt

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	Val	Asp	Ser	Trp	Glu	Trp	Trp	Asn	Ser	Phe	Arg	Leu	Leu	Cys	Glu	His	
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	Leu	Gln	Thr	Asn	Ala	Phe	Leu	Thr	Asn	Ala	Arg	Gly	Tyr	Pro	Cys	Leu	
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	Ser	Lys	Arg	His	Gln	Lys	Leu	Leu	Thr	Gly	Phe	Phe	Asn	His	Ser	Val	
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	Gln	Val	Ile	Ile	Ser	Gly	Arg	Ser	Asn	His	Asn	Val	Ser	Gln	Gly	Gly	
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	Val	Leu	Ser	Gly	Asp	Glu	Asn	His	Thr	Glu	Asp	Thr	Ala	Val	Arg	His	
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	Ala	Leu	Ser	Pro	Tyr	Leu	Asp	Tyr	Ile	Ala	Tyr	Ile	Tyr	Gln	Arg	Met	
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	Asp	Pro	Leu	Pro	Glu	Gln	Glu	Arg	Phe	Glu	Ile	Asn	Tyr	Arg	Asp	Phe	
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	Leu	Gln	Ser	Pro	Leu	Gln	Pro	Leu	Met	Asp	Asn	Leu	Glu	Ala	Gln	Thr	
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	Tyr	Glu	Thr	Phe	Glu	Lys	Asp	Thr	Val	Lys	Tyr	Thr	Gln	Tyr	Gln	Arg	
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	gca	att	gct	aag	gca	ttg	gtt	gat	aga	gtt	tcc	gat	gat	gat	gtc	tca	1104
	Ala	Ile	Ala	Lys	Ala	Leu	Val	Asp	Arg	Val	Ser	Asp	Asp	Asp	Val	Ser	
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	Val	Tyr	Ala	Val	Glu	Lys	Asn	Pro	Asn	Ala	Val	Ile	Thr	Leu	His	Ser	
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	Leu	Ile	Lys	Leu	Glu	Gly	Trp	Glu	Ser	Leu	Val	Thr	Ile	Ile	Ser	Ser	
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	Asp	Gly	Ala	Gln	Arg	Phe	Leu	Lys	Pro	Asp	Gly	Ile	Ser	Ile	Pro	Ser	
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PF59082SeqList_PF59082.txt

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535	Thr Lys Leu Lys Phe Glu Ile Pro Gln Glu Thr Gly Ser Cys Leu Val	
540	545 cac gga ttt gct gga tat ttt gat gcc gta ttg tat aaa gat gtt cat	1728
550	His Gly Phe Ala Gly Tyr Phe Asp Ala Val Leu Tyr Lys Asp Val His	
555	560 ctt gga att gaa cca aac acg gct aca cca aac atg ttt agc tgg ttc	1776
565	Leu Gly Ile Glu Pro Asn Thr Ala Thr Pro Asn Met Phe Ser Trp Phe	
570	575 ccg atc ttc ttc cca ttg aga aag ccc atc tac gta ccg tcg aag acg	1824
580	Pro Ile Phe Phe Pro Leu Arg Lys Pro Ile Tyr Val Pro Ser Lys Thr	
585	590 cct ata gaa gtg cac ttt tgg cga tgc tgc ggt gca aca aag gtg tgg	1872
595	Pro Ile Glu Val His Phe Trp Arg Cys Cys Gly Ala Thr Lys Val Trp	
600	605 tac gag tgg gct gtg acg gca cct tct cca tca cca atc cat aac agc	1920
610	Tyr Glu Trp Ala Val Thr Ala Pro Ser Pro Ser Pro Ile His Asn Ser	
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625	Asn Gly Arg Ser Tyr Trp Val Gly Leu	
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<211> 649

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<400> 1038

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Arg Leu Asp Ser Glu Ile Thr Leu Lys Gln Glu Ile Ala Trp Ala Ser	
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Gln Val Ile Ile Ser Gly Arg Ser Asn His Asn Val Ser Gln Gly Gly	
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PF59082SeqList_PF59082.txt

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 Thr Thr Lys Thr Val Leu Met Val Val Gly Ala Gly Arg Gly Pro Leu
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 Asp Met Arg Cys Trp Glu Ala Pro Glu Lys Ala Asp Ile Leu Val Ser
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 580 585 590
 Pro Ile Phe Phe Pro Leu Arg Lys Pro Ile Tyr Val Pro Ser Lys Thr
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 ttc aac att tcc acc ggc ggt ttt gac tat gtt ctc gct cct ctg gtg 144
 Phe Asn Ile Ser Thr Gly Gly Phe Asp Tyr Val Leu Ala Pro Leu Val
 35 40 45
 gat cct tcg tat agg ccg agc ttg gtg gaa gga aat ggt gta gat act 192
 Asp Pro Ser Tyr Arg Pro Ser Leu Val Glu Gly Asn Gly Val Asp Thr
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 Seite 1307

PF59082SeqList_PF59082.txt

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Trp	Ser	Ser	His	Val 85	Val	Gly	Lys	Ile	Ser 90	Ser	Trp	Ile	Asp	Leu 95	Asp	
tct	gaa	gat	gag	gtc	tta	cgg	atg	gat	tca	gaa	acc	aca	ttg	aag	caa	336
Ser	Glu	Asp	Glu	Val	Leu	Arg	Met	Asp	Ser	Glu	Thr	Thr	Leu	Lys	Gln	
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Glu	Ile	Ala	Trp	Ala	Thr	His	Leu	Ser	Leu	Gln	Ala	Cys	Leu	Leu	Pro	
act	cct	aaa	ggg	aaa	tcg	tgc	gcc	aat	tat	gcc	aga	tgt	gtg	aac	cag	432
Thr	Pro	Lys	Gly	Lys	Ser	Cys	Ala	Asn	Tyr	Ala	Arg	Cys	Val	Asn	Gln	
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Lys	Arg	His	Gln	Lys 245	Leu	Ile	Ala	Gly	Phe	Phe	Asp	His	Ala	Ala	Gln	
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Ser	Ser	Ser	Glu	Gly	Thr	Glu	Lys	Asn	Pro	Leu	Arg	Ile	Tyr	Leu	Asp	
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Tyr	Val 290	Ala	Tyr	Leu	Phe	Gln 295	Lys	Met	Glu	Ser	Leu 300	Ser	Glu	Gln	Glu	
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<212> PRT

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 420 425 430
 Pro Glu Gln Ala Asp Ile Leu Val Ser Glu Leu Leu Gly Ser Phe Gly
 435 440 445
 Asp Asn Glu Leu Ser Pro Glu Cys Leu Asp Gly Ala Gln Arg Phe Leu
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 Lys Pro Asp Gly Ile Ser Ile Pro Ser Ser Tyr Thr Ser Phe Ile Gln
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 Gly Val Glu Val Leu Asp Phe Pro Ala Gly Glu Gly Leu Pro Ala Val
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 Leu Asn His Ser Leu Ala Ser Ala Phe Asp Phe Ile Leu Ala Pro Leu
 35 40 45
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 Val Asp Pro Asn Tyr Arg Pro Ala Pro Gly Ala Val Leu Pro Val Ser
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 Ala Ser Asp Leu Val Leu Gly Pro Ser Gln Trp Ser Asn His Val Val
 65 70 75 80
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 Gly Lys Ile Ser Glu Trp Ile Asp Leu Asp Ala Glu Asp Glu Arg Leu
 85 90 95
 ctg ctg gac tcc gag ctc acg ctg aag cag gag atc gct tgg gca tct 336
 Leu Leu Asp Ser Glu Leu Thr Leu Lys Gln Glu Ile Ala Trp Ala Ser
 100 105 110
 cac gtt tcg ctg cag gca tgt gtt att cct gcc ccc agg aga tct ttt 384
 His Val Ser Leu Gln Ala Cys Val Ile Pro Ala Pro Arg Arg Ser Phe
 115 120 125
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 Cys Gly Asn Tyr Ala Arg Val Val Asn Gln Ile Leu Gln Gly Leu Thr
 130 135 140
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 Asn Met Asn Leu Trp Leu Arg Leu Pro Leu Glu Lys Ser Glu Pro Met
 145 150 155 160
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 195 200 205
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Cys	Leu	Ser	Lys	Arg	His	Gln	Arg	Leu	Leu	Thr	Gly	Leu	Phe	Asn	His	
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PF59082SeqList_PF59082.txt

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 Pro Glu Cys Leu Asp Gly Ala Gln Arg Phe Leu Lys Pro Asp Gly Ile
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 Lys Leu His Asp Asp Ile Lys Ala His Lys Asp Ile Ala His Phe Glu
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 Ser Cys Leu Val His Gly Phe Ala Gly Tyr Phe Asp Ser Val Leu Tyr
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 Lys Asp Val His Leu Gly Ile Glu Pro Asn Thr Ala Thr Pro Asn Met
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 Pro Glu Gly Ser Pro Ile Glu Val His Phe Trp Arg Cys Cys Ala Pro
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Gly Ala Glu Val Leu Asp Phe Pro Ala Gly Glu Asp Leu Pro Ala Val	
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Leu Asn His Ser Leu Ala Ser Ala Phe Asp Phe Ile Leu Val Pro Leu	
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Val Asp Pro Asn Tyr Arg Pro Ala Pro Gly Ser Val Leu Pro Val Ser	
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Gly Lys Ile Ser Glu Trp Ile Asp Leu Asp Ser Glu Asp Glu Arg Leu	
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Arg Phe Asp Ser Glu Leu Thr Leu Lys Gln Glu Ile Ala Trp Ala Ser	
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His Val Ser Leu Gln Ala Cys Val Leu Pro Ala Pro Arg Arg Ser Phe	
115 120 125	
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Leu Gln Thr Glu Ala Phe Leu Thr Asn Ala Lys Gly Tyr Pro Cys Leu				
225	tca aag cgc cat cag agt ctg cta act gga ttt ttt aaa cat tct gtt	230	tca aag cgc cat cag agt ctg cta act gga ttt ttt aaa cat tct gtt	768
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Gln Val Ile Ile Ser Gly Arg Ser Asn His Asn Val Phe Pro Val Ser				
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Lys Met Asp Pro Leu Pro Glu Gln Glu Arg Ile Glu Ile Asn Tyr Arg				
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Asp Phe Leu Gln Ser Pro Leu Gln Pro Leu Met Asp Asn Leu Glu Ala				
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Gln Thr Tyr Glu Thr Phe Glu Lys Asp Val Val Lys Tyr Thr Gln Tyr				
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Arg Arg Ala Val Ala Lys Ala Leu Val Asp Arg Val Ala Asp Asp Ala				
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Val Ser Thr Thr Arg Thr Val Leu Met Val Val Gly Ala Gly Arg Gly				
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Pro Leu Val Arg Ala Ser Leu Gln Ala Ala Glu Glu Thr Gly Arg Lys				
385	tta aaa gta tat gct gtt gaa aaa aat cct aac gct gtt att act ctt	390	tta aaa gta tat gct gtt gaa aaa aat cct aac gct gtt att act ctt	1248
Leu Lys Val Tyr Ala Val Glu Lys Asn Pro Asn Ala Val Ile Thr Leu				
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His Ser Leu Ile Lys Leu Glu Gly Trp Glu Ser Leu Val Thr Val Ile				
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Cys Leu Asp Gly Ala Gln Arg Phe Leu Lys Pro Asp Gly Ile Ser Ile				
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Pro Ser Ser Tyr Thr Ser Phe Ile Gln Pro Ile Thr Ala Ser Lys Leu				
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Leu 35	Asn 35	His 35	Ser 35	Leu 40	Ala 40	Ser 40	Ala 40	Phe 40	Asp 40	Phe 40	Ile 40	Leu 45	Val 45	Pro 45	Leu 45
Val 50	Asp 50	Pro 50	Asn 50	Tyr 50	Arg 50	Pro 55	Ala 55	Pro 55	Gly 55	Ser 55	Val 60	Leu 60	Pro 60	Val 60	Ser 60
Ala 65	Ser 65	Asp 65	Leu 65	Ile 65	Leu 70	Gly 70	Pro 70	Ala 70	Gln 70	Trp 75	Ser 75	Asn 75	His 75	Val 80	Val 80
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His 115	Val 115	Ser 115	Leu 115	Gln 115	Ala 115	Cys 115	Val 120	Leu 120	Pro 120	Ala 120	Pro 120	Arg 125	Arg 125	Ser 125	Phe 125
Cys 130	Gly 130	Asn 130	Tyr 130	Ala 130	Arg 130	Val 135	Val 135	Asn 135	Gln 135	Ile 135	Leu 140	Gln 140	Gly 140	Leu 140	Thr 140
Asn 145	Met 145	His 145	Leu 145	Trp 145	Leu 150	Arg 150	Leu 150	Pro 150	Leu 150	Glu 155	Lys 155	Ser 155	Glu 155	Pro 160	Met 160
Asp 165	Asp 165	Asp 165	Leu 165	Asp 165	Lys 165	Ile 165	Lys 165	Asn 170	Asn 170	Ser 170	His 170	Thr 170	Ser 175	Glu 175	Ile 175
Val 180	Asp 180	Ser 180	Trp 180	Glu 180	Leu 180	Trp 180	Asn 185	Ser 185	Phe 185	Arg 185	Leu 185	Leu 190	Cys 190	Asp 190	His 190
Ser 195	Ser 195	Gln 195	Leu 195	Cys 195	Val 195	Ala 195	Leu 200	Asp 200	Ile 200	Leu 200	Ser 200	Thr 205	Leu 205	Pro 205	Ser 205
Ile 210	Asn 210	Ser 210	Leu 210	Ala 210	Arg 210	Trp 215	Phe 215	Gly 215	Glu 215	Pro 215	Val 220	Arg 220	Ala 220	Ala 220	Ile 220
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 Met

117

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165

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213

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Ser	Tyr	Arg	Pro	Ser	Leu	Val	Gln	Lys	Asp	Ala	Leu	Gly	Ser	Gly	Val	
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ttg	atg	gat	aat	tta	gag	gct	cag	act	tac	gag	act	ttt	gag	aga	gat	1125
Leu	Met	Asp	Asn	Leu	Glu	Ala	Gln	Thr	Tyr	Glu	Thr	Phe	Glu	Arg	Asp	
		325						330					335			
gca	gtg	aaa	tac	att	cag	tac	caa	cga	gca	gtc	agt	aaa	gca	ttg	ctg	1173
Ala	Val	Lys	Tyr	Ile	Gln	Tyr	Gln	Arg	Ala	Val	Ser	Lys	Ala	Leu	Leu	
		340					345					350				
gac	agg	gtt	cct	gat	gaa	gag	gca	tct	gtt	aaa	acc	att	gta	ttg	atg	1221
Asp	Arg	Val	Pro	Asp	Glu	Glu	Ala	Ser	Val	Lys	Thr	Ile	Val	Leu	Met	
	355					360					365					
gtt	gtg	gggt	gca	gga	cgt	gggt	cct	ctt	gtg	cgg	gca	tca	tta	cag	gct	1269
Val	Val	Gly	Ala	Gly	Arg	Gly	Pro	Leu	Val	Arg	Ala	Ser	Leu	Gln	Ala	
				375				380							385	
gct	gaa	gaa	act	gggt	cgg	aag	ctc	aaa	gtt	tat	gct	gtt	gaa	aag	aat	1317

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cca	aat	gct	ggt	ggt	acc	cta	cat	gca	tta	gtc	aag	tta	gaa	gga	tgg	1365
Pro	Asn	Ala	Val	Val	Thr	Leu	His	Ala	Leu	Val	Lys	Leu	Glu	Gly	Trp	
				405				410					415			
gag	gat	act	gtg	acc	ata	gtc	tca	agt	gac	atg	cgt	cat	tgg	agt	gcc	1413
Glu	Asp	Thr	Val	Thr	Ile	Val	Ser	Ser	Asp	Met	Arg	His	Trp	Ser	Ala	
				420				425					430			
cct	gaa	aaa	gct	gac	ata	ttg	ggt	agt	gaa	ttg	cta	ggg	tct	ttt	ggc	1461
Pro	Glu	Lys	Ala	Asp	Ile	Leu	Val	Ser	Glu	Leu	Leu	Gly	Ser	Phe	Gly	
				435				440					445			
gac	aat	gag	ctg	tct	cct	gag	tgc	ctt	gat	gga	gcc	cag	aga	ttt	cta	1509
Asp	Asn	Glu	Leu	Ser	Pro	Glu	Cys	Leu	Asp	Gly	Ala	Gln	Arg	Phe	Leu	
					455					460					465	
aag	caa	gat	gga	att	tca	ata	cca	tct	tcg	tac	aca	agt	ttc	ctc	caa	1557
Lys	Gln	Asp	Gly	Ile	Ser	Ile	Pro	Ser	Ser	Tyr	Thr	Ser	Phe	Leu	Gln	
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cca	gtg	aca	gct	tca	aag	tta	tat	aat	gat	ggt	aag	gca	cat	aaa	gat	1605
Pro	Val	Thr	Ala	Ser	Lys	Leu	Tyr	Asn	Asp	Val	Lys	Ala	His	Lys	Asp	
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ctt	gta	cac	ttt	gaa	act	gct	tat	ggt	gtc	aaa	atg	cac	aat	gta	gcc	1653
Leu	Val	His	Phe	Glu	Thr	Ala	Tyr	Val	Val	Lys	Met	His	Asn	Val	Ala	
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Lys	Leu	Ala	Pro	Thr	Gln	Pro	Val	Phe	Thr	Phe	Thr	His	Pro	Lys	His	
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Ser	Asp	Lys	Glu	Ile	Asn	Gln	Arg	Tyr	Lys	Lys	Leu	Asn	Phe	Ile	Ile	
				530						540				545		
cct	aat	gac	act	ggg	tca	gca	atg	gta	cac	gga	ttt	gct	ggg	tat	ttt	1797
Pro	Asn	Asp	Thr	Gly	Ser	Ala	Met	Val	His	Gly	Phe	Ala	Gly	Tyr	Phe	
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gat	gca	act	ctt	tac	aag	gat	gtg	cat	ctt	gga	att	gaa	cct	tca	act	1845
Asp	Ala	Thr	Leu	Tyr	Lys	Asp	Val	His	Leu	Gly	Ile	Glu	Pro	Ser	Thr	
				565				570					575			
gca	aca	cca	aac	atg	ttc	agt	tgg	ttt	gca	ata	ttt	ttc	cca	tta	agg	1893
Ala	Thr	Pro	Asn	Met	Phe	Ser	Trp	Phe	Ala	Ile	Phe	Phe	Pro	Leu	Arg	
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aca	ccc	att	tgt	gtg	gat	ccc	ggg	tct	aca	ctt	gaa	gta	cat	ttt	tgg	1941
Thr	Pro	Ile	Cys	Val	Asp	Pro	Gly	Ser	Thr	Leu	Glu	Val	His	Phe	Trp	
				595		600					605					
cgt	tgt	tgt	ggg	tct	acg	aag	gtt	tgg	tat	gag	tgg	tgt	ggt	gct	tct	1989
Arg	Cys	Cys	Gly	Ser	Thr	Lys	Val	Trp	Tyr	Glu	Trp	Cys	Val	Ala	Ser	
				610						620				625		
ccc	gcg	tcg	tcc	cca	atg	cac	aac	agt	aat	gga	cgt	tca	tac	tgg	gtt	2037
Pro	Ala	Ser	Ser	Pro	Met	His	Asn	Ser	Asn	Gly	Arg	Ser	Tyr	Trp	Val	
				630					635					640		
ggg	ctt	tag	tgcc	ttgtat	tttttagaat	gtttatcagt	cttgagtagt	caagtttata								2096
Gly	Leu															
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aattcaattc	atgttgaggaa	atgttggtgt	acaataagat	atgttggttg	ctataggtgt											2216
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Ser	Ser	His	Val	Val	Gly	Lys	Ile	Ser	Ser	Trp	Ile	Asp	Leu	Asp	Ser
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Glu	Asp	Glu	Thr	Leu	Arg	Ile	Asp	Ser	Glu	Thr	Thr	Leu	Lys	Gln	Glu
			100					105					110		
Ile	Ala	Trp	Ala	Ser	His	Leu	Ser	Leu	Gln	Ala	Cys	Leu	Leu	Pro	Ala
		115					120					125			
Pro	Lys	Gly	Thr	Ser	Cys	Ala	Asn	Tyr	Ala	Arg	Cys	Val	Asn	Gln	Ile
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Leu	Gln	Gly	Ser	Asn	Asn	Met	Gln	Leu	Trp	Leu	Arg	Val	Pro	Leu	Val
145				150						155					160
Lys	Pro	Asp	Asp	Asp	Ser	Met	Asp	Ala	Lys	Ser	Val	Ala	Leu	Val	Asp
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Ser	Trp	Glu	Thr	Trp	Asn	Ser	Phe	Arg	Leu	Leu	Cys	Glu	His	His	Ser
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Gln	Leu	Ser	Val	Ala	Leu	Asp	Ile	Leu	Ser	Thr	Leu	Pro	Ser	Pro	Asn
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Thr	Asp	Cys	Phe	Leu	Thr	Asn	Ser	His	Gly	Cys	Pro	Cys	Leu	Ser	Lys
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Arg	His	Gln	Ser	Leu	Ile	Thr	Gly	Phe	Phe	Asn	His	Ser	Ile	Gln	Ile
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Ile	Val	Ser	Gly	Asn	Ser	Val	His	Pro	Lys	Ala	Ser	Val	Asp	Ala	Asn
			260					265					270		
Asp	Asn	Ser	Gly	Thr	Asn	Ser	Gln	Arg	His	Pro	Leu	Arg	Pro	Tyr	Leu
		275					280					285			
Asp	Tyr	Ile	Gly	Tyr	Leu	Tyr	Gln	Arg	Met	Asp	Pro	Leu	Pro	Glu	Gln
		290				295					300				
Glu	Arg	Phe	Glu	Leu	Gly	Tyr	Arg	Asp	Phe	Leu	Gln	Ser	Pro	Leu	Gln
305					310					315					320
Pro	Leu	Met	Asp	Asn	Leu	Glu	Ala	Gln	Thr	Tyr	Glu	Thr	Phe	Glu	Arg
				325					330					335	
Asp	Ala	Val	Lys	Tyr	Ile	Gln	Tyr	Gln	Arg	Ala	Val	Ser	Lys	Ala	Leu
			340					345					350		
Leu	Asp	Arg	Val	Pro	Asp	Glu	Glu	Ala	Ser	Val	Lys	Thr	Ile	Val	Leu
		355					360					365			
Met	Val	Val	Gly	Ala	Gly	Arg	Gly	Pro	Leu	Val	Arg	Ala	Ser	Leu	Gln
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 595 600 605
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 610 615 620
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 Val Gly Leu

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catcgtacgg ggaagaagcg ccgtttacac ccatctggcg gag atg ccg ctg ggg 175
 Met Pro Leu Gly

cag cgt ccg ggg gac aag agt gac gcc cgc tac tgc ggg gcg gag gtg 223
 Gln Arg Pro Gly Asp Lys Ser Asp Ala Arg Tyr Cys Gly Ala Glu Val
 5 10 15 20

ctc gac ttc cct gcc ggc gag gac ctc ccc gcc gtc ctc aac cac tcc 271
 Leu Asp Phe Pro Ala Gly Glu Asp Leu Pro Ala Val Leu Asn His Ser
 25 30 35

ctc gcc tcc gcc ttc gac ttc atc ctc gtc cct ctg gtt gat ccc aac 319
 Leu Ala Ser Ala Phe Asp Phe Ile Leu Val Pro Leu Val Asp Pro Asn
 40 45 50

tac cgg ccg gcc ccc ggc tcc gtt ctg ctc gtc ggc tgc gac ctc 367
 Tyr Arg Pro Ala Pro Gly Ser Val Leu Pro Val Ser Ala Ser Asp Leu
 55 60 65

atc ctt ggc ccg gcc cag tgg agc aac cac gtc gtc ggg aag atc agc 415
 Ile Leu Gly Pro Ala Gln Trp Ser Asn His Val Val Gly Lys Ile Ser
 70 75 80

gag tgg att gat ttg gac tct gag gac gag cgg ctc cgc ttt gac tcc 463
 Glu Trp Ile Asp Leu Asp Ser Glu Asp Glu Arg Leu Arg Phe Asp Ser
 85 90 95 100

gag ctc acg ctg aag gag att gcg tgg gcg tct cac gtc tcg ctg 511
 Glu Leu Thr Leu Lys Gln Glu Ile Ala Trp Ala Ser His Val Ser Leu
 105 110 115

cag gca tgt gtt ctt cct gcc ccc agg aga tct ttt tgt ggc aat tat 559
 Gln Ala Cys Val Leu Pro Ala Pro Arg Arg Ser Phe Cys Gly Asn Tyr
 120 125 130

gcc aga gtc gtg aat caa att ttg caa ggc ctg acc aat atg cat ttg 607
 Ala Arg Val Val Asn Gln Ile Leu Gln Gly Leu Thr Asn Met His Leu
 135 140 145

tgg ctc agg ttg cct ctg gag aag tcc gag cct atg gat gat gat ctt 655
 Trp Leu Arg Leu Pro Leu Glu Lys Ser Glu Pro Met Asp Asp Asp Leu
 150 155 160

gat aaa ata aag aat aac agc cac acg agt gaa att gta gac tca tgg 703
 Asp Lys Ile Lys Asn Asn Ser His Thr Ser Glu Ile Val Asp Ser Trp
 165 170 175 180

gaa tta tgg aat tca ttg aga ttg cta tgt gac cat agt agc caa cta 751
 Glu Leu Trp Asn Ser Phe Arg Leu Leu Cys Asp His Ser Ser Gln Leu
 185 190 195

tgt gtg gca ctc gat att ttg agc act ctg cca tca ata aac tca tta 799
 Cys Val Ala Leu Asp Ile Leu Ser Thr Leu Pro Ser Ile Asn Ser Leu
 200 205 210

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Ala	Phe	Leu	Thr	Asn	Ala	Lys	Gly	Tyr	Pro	Cys	Leu	Ser	Lys	Arg	His	
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cag	agt	ctg	cta	act	gga	ttt	ttt	aaa	cat	tct	gtt	cag	gtg	ata	ata	943
Gln	Ser	Leu	Leu	Thr	Gly	Phe	Phe	Lys	His	Ser	Val	Gln	Val	Ile	Ile	
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Ser	Gly	Arg	Ser	Asn	His	Asn	Val	Phe	Pro	Val	Ser	Glu	Gly	Val	Leu	
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Ser	Gly	Asp	Glu	Ser	Tyr	Thr	Glu	Asp	Ser	His	Val	Arg	His	Ala	Leu	
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Thr	Pro	Tyr	Leu	Glu	Tyr	Ile	Ala	Tyr	Leu	Tyr	Arg	Lys	Met	Asp	Pro	
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Leu	Pro	Glu	Gln	Glu	Arg	Ile	Glu	Ile	Asn	Tyr	Arg	Asp	Phe	Leu	Gln	
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Thr	Phe	Glu	Lys	Asp	Val	Val	Lys	Tyr	Thr	Gln	Tyr	Arg	Arg	Ala	Val	
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Ala	Lys	Ala	Leu	Val	Asp	Arg	Val	Ala	Asp	Asp	Ala	Val	Ser	Thr	Thr	
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Arg	Thr	Val	Leu	Met	Val	Val	Gly	Ala	Gly	Arg	Gly	Pro	Leu	Val	Arg	
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Ala	Ser	Leu	Gln	Ala	Ala	Glu	Glu	Thr	Gly	Arg	Lys	Leu	Lys	Val	Tyr	
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Leu	His	Arg	Ile	Ala	Thr	Leu	Ala	Pro	Pro	Gln	Gln	Val	Phe	Thr	Phe	
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Phe Phe Pro Leu Arg Lys Pro Ile Tyr Val Pro Glu Gly Ser Pro Ile	
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gaa gtg cac ttc tgg cgg tgc tgt gcc ccc aca aag gtg tgg tac gag	2047
Glu Val His Phe Trp Arg Cys Cys Ala Pro Thr Lys Val Trp Tyr Glu	
615 620 625	
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Trp Ala Val Thr Thr Pro Thr Pro Ser Pro Ile His Asn Ser Asn Gly	
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Arg Ser Tyr Trp Val Gly Leu	
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Val Asp Pro Asn Tyr Arg Pro Ala Pro Gly Ser Val Leu Pro Val Ser	50 55 60
Ala Ser Asp Leu Ile Leu Gly Pro Ala Gln Trp Ser Asn His Val Val	65 70 75 80
Gly Lys Ile Ser Glu Trp Ile Asp Leu Asp Ser Glu Asp Glu Arg Leu	85 90 95
Arg Phe Asp Ser Glu Leu Thr Leu Lys Gln Glu Ile Ala Trp Ala Ser	100 105 110
His Val Ser Leu Gln Ala Cys Val Leu Pro Ala Pro Arg Arg Ser Phe	115 120 125
Cys Gly Asn Tyr Ala Arg Val Val Asn Gln Ile Leu Gln Gly Leu Thr	130 135 140
Asn Met His Leu Trp Leu Arg Leu Pro Leu Glu Lys Ser Glu Pro Met	145 150 155 160
Asp Asp Asp Leu Asp Lys Ile Lys Asn Asn Ser His Thr Ser Glu Ile	165 170 175
Val Asp Ser Trp Glu Leu Trp Asn Ser Phe Arg Leu Leu Cys Asp His	180 185 190
Ser Ser Gln Leu Cys Val Ala Leu Asp Ile Leu Ser Thr Leu Pro Ser	195 200 205
Ile Asn Ser Leu Ala Arg Trp Phe Gly Glu Pro Val Arg Ala Ala Ile	210 215 220
Leu Gln Thr Glu Ala Phe Leu Thr Asn Ala Lys Gly Tyr Pro Cys Leu	225 230 235 240
Ser Lys Arg His Gln Ser Leu Leu Thr Gly Phe Phe Lys His Ser Val	245 250 255
Gln Val Ile Ile Ser Gly Arg Ser Asn His Asn Val Phe Pro Val Ser	260 265 270
Glu Gly Val Leu Ser Gly Asp Glu Ser Tyr Thr Glu Asp Ser His Val	275 280 285
Arg His Ala Leu Thr Pro Tyr Leu Glu Tyr Ile Ala Tyr Leu Tyr Arg	290 295 300

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 Val Ser Thr Thr Arg Thr Val Leu Met Val Val Gly Ala Gly Arg Gly
 370 375 380
 Pro Leu Val Arg Ala Ser Glu Gln Ala Ala Glu Thr Gly Arg Lys
 385 390 395 400
 Leu Lys Val Tyr Ala Val Glu Lys Asn Pro Asn Ala Val Ile Thr Leu
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 Ser Ser Asp Met Arg Cys Trp Asp Ala Pro Glu Lys Ala Asp Val Leu
 435 440 445
 Val Ser Glu Leu Leu Gly Ser Phe Gly Asp Asn Glu Leu Ser Pro Glu
 450 455 460
 Cys Leu Asp Gly Ala Gln Arg Phe Leu Lys Pro Asp Gly Ile Ser Ile
 465 470 475 480
 Pro Ser Ser Tyr Thr Ser Phe Ile Gln Pro Ile Ile Ala Ser Lys Leu
 485 490 495
 His Asn Asp Ile Lys Ala His Lys Asp Ile Ala His Phe Glu Thr Ala
 500 505 510
 Tyr Val Val Lys Leu His Arg Ile Ala Thr Leu Ala Pro Pro Gln Gln
 515 520 525
 Val Phe Thr Phe Thr His Pro Asn Phe Ser Pro Asn Ala Ser Asn Gln
 530 535 540
 Arg Tyr Thr Lys Leu Gln Phe Glu Met Leu Pro Asp Met Gly Ser Cys
 545 550 555 560
 Leu Val His Gly Phe Ala Gly Tyr Phe Asp Ser Val Leu Tyr Lys Asp
 565 570 575
 Val His Leu Gly Ile Glu Pro Asn Thr Ala Thr Pro Asn Met Phe Ser
 580 585 590
 Trp Phe Pro Ile Phe Phe Pro Leu Arg Lys Pro Ile Tyr Val Pro Glu
 595 600 605
 Gly Ser Pro Ile Glu Val His Phe Trp Arg Cys Cys Ala Pro Thr Lys
 610 615 620
 Val Trp Tyr Glu Trp Ala Val Thr Thr Pro Thr Pro Ser Pro Ile His
 625 630 635 640
 Asn Ser Asn Gly Arg Ser Tyr Trp Val Gly Leu
 645 650

<210> 1049
 <211> 1932
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (1)..(1932)

<400> 1049
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 Met Pro Leu Gly Glu Arg Ala Gly Asp Lys Ser Glu Ser Arg Tyr Cys
 1 5 10 15
 ggt gta gag acc gac ttc aac gat gac atg cca cac gtc ctc cat ttc 96
 Gly Val Glu Thr Asp Phe Asn Asp Asp Met Pro His Val Leu His Phe
 20 25 30
 aac ctt tat tct gga agc ttc gat ttc gtt gtt gct cct ctg atg gat 144
 Asn Leu Tyr Ser Gly Ser Phe Asp Phe Val Val Ala Pro Leu Met Asp
 35 40 45
 cat tct tat cgg cca agt tta gtg caa aag gat gct ttg ggg tct ggt 192
 His Ser Tyr Arg Pro Ser Leu Val Gln Lys Asp Ala Leu Gly Ser Gly
 50 55 60
 gtt ctg cca ttt gct ggg tca gac ttg gtc ttg agt cca tcc cag tgg 240
 Val Leu Pro Phe Ala Gly Ser Asp Leu Val Leu Ser Pro Ser Gln Trp
 65 70 75 80 85 90 95
 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650
 1049 1932
 DNA
 Glycine max
 CDS
 (1)..(1932)

PF59082SeqList_PF59082.txt

65	70	75	80	
agt agt cat gta gtg gga aaa att agc tca tgg ata gat ttg gat tca				288
Ser Ser His Val Val Gly Lys Ile Ser Ser Trp Ile Asp Leu Asp Ser				
	85	90	95	
gag gat gaa acc ctc agg ata gat tct gaa acc act ctt aaa caa gaa				336
Glu Asp Glu Thr Leu Arg Ile Asp Ser Glu Thr Thr Leu Lys Gln Glu				
	100	105	110	
att gct tgg gct tct cat ctc tct tta cag gcc tgc ctg ctt cct gcc				384
Ile Ala Trp Ala Ser His Leu Ser Leu Gln Ala Cys Leu Leu Pro Ala				
	115	120	125	
ccg aag gga act tct tgt gct aat tat gct aga tgt gtg aat cag atc				432
Pro Lys Gly Thr Ser Cys Ala Asn Tyr Ala Arg Cys Val Asn Gln Ile				
	130	135	140	
tta cag ggt tca aat aat atg cag ttg tgg ctt agg gtt cca ttg gtg				480
Leu Gln Gly Ser Asn Asn Met Gln Leu Trp Leu Arg Val Pro Leu Val				
	145	150	155	
aag cct gat gat gac tct atg gat gca aag tct gtt gct ttg gtt gac				528
Lys Pro Asp Asp Asp Ser Met Asp Ala Lys Ser Val Ala Leu Val Asp				
	165	170	175	
tct tgg gaa act tgg aat tca ttt cgt ctg ctg tgt gag cat cat agt				576
Ser Trp Glu Thr Trp Asn Ser Phe Arg Leu Leu Cys Glu His His Ser				
	180	185	190	
caa ctg tca gtt gca ctt gat att ctg agt act ctt cct tcc cca aat				624
Gln Leu Ser Val Ala Leu Asp Ile Leu Ser Thr Leu Pro Ser Pro Asn				
	195	200	205	
tca cta gga cgc tgg ttt ggg gag cct gtt aga gca gct ata tta cat				672
Ser Leu Gly Arg Trp Phe Gly Glu Pro Val Arg Ala Ala Ile Leu His				
	210	215	220	
act gat tgc ttt cta act aat tct cat ggc tgt cca tgc ctc tcc aag				720
Thr Asp Cys Phe Leu Thr Asn Ser His Gly Cys Pro Cys Leu Ser Lys				
	225	230	235	
cgc cac cag agt tta att act ggt ttt ttt aac cat tct att cag atc				768
Arg His Gln Ser Leu Ile Thr Gly Phe Phe Asn His Ser Ile Gln Ile				
	245	250	255	
att gta tct gca aat tca gtt cat cca aaa gca agt gta gat gca aat				816
Ile Val Ser Ala Asn Ser Val His Pro Lys Ala Ser Val Asp Ala Asn				
	260	265	270	
gat aat tct gat aca aat tca caa aag cat ccc ttg cgg cca tat ctg				864
Asp Asn Ser Asp Thr Asn Ser Gln Lys His Pro Leu Arg Pro Tyr Leu				
	275	280	285	
gac tac att gga tat ctt tac caa aga atg gat cct ctt cct gag caa				912
Asp Tyr Ile Gly Tyr Leu Tyr Gln Arg Met Asp Pro Leu Pro Glu Gln				
	290	295	300	
gaa cgt ttt gag ctt ggt tac agg gat ttt tta cag tca ccc ttg caa				960
Glu Arg Phe Glu Leu Gly Tyr Arg Asp Phe Leu Gln Ser Pro Leu Gln				
	305	310	315	
cct ttg atg gat aat tta gag gct cag act tac gag act ttt gag aga				1008
Pro Leu Met Asp Asn Leu Glu Ala Gln Thr Tyr Glu Thr Phe Glu Arg				
	325	330	335	
gat gca gtg aaa tac att cag tac caa cga gca gtc agt aaa gca ttg				1056
Asp Ala Val Lys Tyr Ile Gln Tyr Gln Arg Ala Val Ser Lys Ala Leu				
	340	345	350	
ctg gac agg gtt cct gat gaa gag gca tct gtt aaa acc att gta ttg				1104
Leu Asp Arg Val Pro Asp Glu Glu Ala Ser Val Lys Thr Ile Val Leu				
	355	360	365	
atg gtt gtg ggg gca gga cgt ggg cct ctt gtg cgg gca tca tta cag				1152
Met Val Val Gly Ala Gly Arg Gly Pro Leu Val Arg Ala Ser Leu Gln				
	370	375	380	
gct gct gaa gaa act ggg cgg aag ctc aaa gtt tat gct gtt gaa aag				1200
Ala Ala Glu Glu Thr Gly Arg Lys Leu Lys Val Tyr Ala Val Glu Lys				
	385	390	395	
aat cca aat gct gtt gtt acc cta cat gca tta gtc aag tta gaa gga				1248
Asn Pro Asn Ala Val Val Thr Leu His Ala Leu Val Lys Leu Glu Gly				
	405	410	415	
tgg gag gat act gtg acc ata gtc tca agt gac atg cgt cat tgg agt				1296
Trp Glu Asp Thr Val Thr Ile Val Ser Ser Asp Met Arg His Trp Ser				
	420	425	430	
gcc cct gaa aaa gct gac ata ttg gtt agt gaa ttg cta ggt tct ttt				1344
Ala Pro Glu Lys Ala Asp Ile Leu Val Ser Glu Leu Gly Ser Phe				

PF59082SeqList_PF59082.txt

435	440	445		
ggc gac aat gag ctg tct cct gag tgc ctt gat gga gcc cag aga ttt	450	455	460	1392
Gly Asp Asn Glu Leu Ser Pro Glu Cys Leu Asp Gly Ala Gln Arg Phe				
cta aag caa gat gga att tca ata cca tct tcg tac aca agt ttc ctc	465	470	475	1440
Leu Lys Gln Asp Gly Ile Ser Ile Pro Ser Ser Tyr Thr Ser Phe Leu				
caa cca gtg aca gct tca aag tta tat aat gat gtt aag gca cat aaa	485	490	495	1488
Gln Pro Val Thr Ala Ser Lys Leu Tyr Asn Asp Val Lys Ala His Lys				
gat ctt gta cac ttt gaa act gct tat gtt gtc aaa atg cac aat gta	500	505	510	1536
Asp Leu Val His Phe Glu Thr Ala Tyr Val Val Lys Met His Asn Val				
gcc aaa ctt gca cca acc caa cct gtt ttt aca ttt act cat cca aag	515	520	525	1584
Ala Lys Leu Ala Pro Thr Gln Pro Val Phe Thr Phe Thr His Pro Lys				
cac tct gat aaa gaa atc aat cag cgc tat aaa aag ttg aat ttt ata	530	535	540	1632
His Ser Asp Lys Glu Ile Asn Gln Arg Tyr Lys Lys Leu Asn Phe Ile				
ata cct aat gac act ggg tca gca atg gta cac gga ttt gct ggt tat	545	550	555	1680
Ile Pro Asn Asp Thr Gly Ser Ala Met Val His Gly Phe Ala Gly Tyr				
ttt gat gca act ctt tac aag gat gtg cat ctt gga att gaa cct tca	565	570	575	1728
Phe Asp Ala Thr Leu Tyr Lys Asp Val His Leu Gly Ile Glu Pro Ser				
act gca aca cca aac atg ttc agt tgg ttt gca ata ttt ttc cca tta	580	585	590	1776
Thr Ala Thr Pro Asn Met Phe Ser Trp Phe Ala Ile Phe Phe Pro Leu				
agg aca ccc att tgt gtg gat ccc ggt tct aca ctt gaa gta cat ttt	595	600	605	1824
Arg Thr Pro Ile Cys Val Asp Gly Ser Thr Leu Glu Val His Phe				
tgg cgt tgt tgt ggt tct acg aag gtt tgg tat gag tgg tgt gtt gct	610	615	620	1872
Trp Arg Cys Cys Gly Ser Thr Lys Val Trp Tyr Glu Trp Cys Val Ala				
tct ccc gcg tcg tcc cca atg cac aac agt aat gga cgt tca tac tgg	625	630	635	1920
Ser Pro Ala Ser Ser Pro Met His Asn Ser Asn Gly Arg Ser Tyr Trp				
gtt ggg ctt tag				1932
Val Gly Leu				

<210> 1050
 <211> 643
 <212> PRT
 <213> Glycine max

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 Met Pro Leu Gly Glu Arg Ala Gly Asp Lys Ser Glu Ser Arg Tyr Cys
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 Gly Val Glu Thr Asp Phe Asn Asp Asp Met Pro His Val Leu His Phe
 20 25 30
 Asn Leu Tyr Ser Gly Ser Phe Asp Phe Val Val Ala Pro Leu Met Asp
 35 40 45
 His Ser Tyr Arg Pro Ser Leu Val Gln Lys Asp Ala Leu Gly Ser Gly
 50 55 60
 Val Leu Pro Phe Ala Gly Ser Asp Leu Val Leu Ser Pro Ser Gln Trp
 65 70 75 80
 Ser Ser His Val Val Gly Lys Ile Ser Ser Trp Ile Asp Leu Asp Ser
 85 90 95
 Glu Asp Glu Thr Leu Arg Ile Asp Ser Glu Thr Thr Leu Lys Gln Glu
 100 105 110
 Ile Ala Trp Ala Ser His Leu Ser Leu Gln Ala Cys Leu Leu Pro Ala
 115 120 125
 Pro Lys Gly Thr Ser Cys Ala Asn Tyr Ala Arg Cys Val Asn Gln Ile
 130 135 140
 Leu Gln Gly Ser Asn Asn Met Gln Leu Trp Leu Arg Val Pro Leu Val
 145 150 155 160
 Lys Pro Asp Asp Asp Ser Met Asp Ala Lys Ser Val Ala Leu Val Asp
 165 170 175

PF59082SeqList_PF59082.txt

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Ser Trp Glu Thr Trp Asn Ser Phe Arg Leu Leu Cys Glu His His Ser
180 185 190
Gln Leu Ser Val Ala Leu Asp Ile Leu Ser Thr Leu Pro Ser Pro Asn
195 200 205
Ser Leu Gly Arg Trp Phe Gly Glu Pro Val Arg Ala Ile Leu His
210 215 220
Thr Asp Cys Phe Leu Thr Asn Ser His Gly Cys Pro Cys Leu Ser Lys
225 230 235 240
Arg His Gln Ser Leu Ile Thr Gly Phe Phe Asn His Ser Ile Gln Ile
245 250 255
Ile Val Ser Ala Asn Ser Val His Pro Lys Ala Ser Val Asp Ala Asn
260 265 270
Asp Asn Ser Asp Thr Asn Ser Gln Lys His Pro Leu Arg Pro Tyr Leu
275 280 285
Asp Tyr Ile Gly Tyr Leu Tyr Gln Arg Met Asp Pro Leu Pro Glu Gln
290 295 300
Glu Arg Phe Glu Leu Gly Tyr Arg Asp Phe Leu Gln Ser Pro Leu Gln
305 310 315 320
Pro Leu Met Asp Asn Leu Glu Ala Gln Thr Tyr Glu Thr Phe Glu Arg
325 330 335
Asp Ala Val Lys Tyr Ile Gln Tyr Gln Arg Ala Val Ser Lys Ala Leu
340 345 350
Leu Asp Arg Val Pro Asp Glu Glu Ala Ser Val Lys Thr Ile Val Leu
355 360 365
Met Val Val Gly Ala Gly Arg Gly Pro Leu Val Arg Ala Ser Leu Gln
370 375 380
Ala Ala Glu Glu Thr Gly Arg Lys Leu Lys Val Tyr Ala Val Glu Lys
385 390 395 400
Asn Pro Asn Ala Val Thr Leu His Ala Leu Val Lys Leu Glu Gly
405 410 415
Trp Glu Asp Thr Val Thr Ile Val Ser Ser Asp Met Arg His Trp Ser
420 425 430
Ala Pro Glu Lys Ala Asp Ile Leu Val Ser Glu Leu Leu Gly Ser Phe
435 440 445
Gly Asp Asn Glu Leu Ser Pro Glu Cys Leu Asp Gly Ala Gln Arg Phe
450 455 460
Leu Lys Gln Asp Gly Ile Ser Ile Pro Ser Ser Tyr Thr Ser Phe Leu
465 470 475 480
Gln Pro Val Thr Ala Ser Lys Leu Tyr Asn Asp Val Lys Ala His Lys
485 490 495
Asp Leu Val His Phe Glu Thr Ala Tyr Val Val Lys Met His Asn Val
500 505 510
Ala Lys Leu Ala Pro Thr Gln Pro Val Phe Thr Phe Thr His Pro Lys
515 520 525
His Ser Asp Lys Glu Ile Asn Gln Arg Tyr Lys Lys Leu Asn Phe Ile
530 535 540
Ile Pro Asn Asp Thr Gly Ser Ala Met Val His Gly Phe Ala Gly Tyr
545 550 555 560
Phe Asp Ala Thr Leu Tyr Lys Asp Val His Leu Gly Ile Glu Pro Ser
565 570 575
Thr Ala Thr Pro Asn Met Phe Ser Trp Phe Ala Ile Phe Phe Pro Leu
580 585 590
Arg Thr Pro Ile Cys Val Asp Pro Gly Ser Thr Leu Glu Val His Phe
595 600 605
Trp Arg Cys Cys Gly Ser Thr Lys Val Trp Tyr Glu Trp Cys Val Ala
610 615 620
Ser Pro Ala Ser Ser Pro Met His Asn Ser Asn Gly Arg Ser Tyr Trp
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Val Gly Leu

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<210> 1051
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 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (1)..(1932)

PF59082SeqList_PF59082.txt

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ggc gta gag acc gac ttc aac gat gac atg gcg cac gtc ctc cat ttc      96
Gly Val Glu Thr Asp Phe Asn Asp Asp Met Ala His Val Leu His Phe
20      25      30
aac ctt tat tct gga agc ttc gat ttc gtt gtt gct cct ctg atg gat      144
Asn Leu Tyr Ser Gly Ser Phe Asp Phe Val Val Ala Pro Leu Met Asp
35      40      45
cct tct tat agg cca agt tta gtt caa aat gat gct ttg ggg tct ggt      192
Pro Ser Tyr Arg Pro Ser Leu Val Gln Asn Asp Ala Leu Gly Ser Gly
50      55      60
ctt ctg cca ttt gct ggg tca gac ttg gtc ttg agt cca tcc caa tgg      240
Leu Leu Pro Phe Ala Gly Ser Asp Leu Val Leu Ser Pro Ser Gln Trp
65      70      75      80
agc agt cat gta gtg gga aaa att agc tca tgg ata gat ttg gat tca      288
Ser Ser His Val Val Gly Lys Ile Ser Ser Trp Ile Asp Leu Asp Ser
85      90      95
gag gat gaa acc ctc agg gta gat tct gaa acc act ctt aga caa gaa      336
Glu Asp Glu Thr Leu Arg Val Asp Ser Glu Thr Thr Leu Arg Gln Glu
100      105      110
att gct tgg gct tct cat ctc tct tta cag gcc tgc ctt ctt cct gcc      384
Ile Ala Trp Ala Ser His Leu Ser Leu Gln Ala Cys Leu Leu Pro Ala
115      120      125
ccc aag gga act tct tgt gct aat tat gct aga tgt gtg aat cag att      432
Pro Lys Gly Thr Ser Cys Ala Asn Tyr Ala Arg Cys Val Asn Gln Ile
130      135      140
tta cag ggt tca aat aat atg cag ttg tgg ctt agg ctt cca ttg gtg      480
Leu Gln Gly Ser Asn Asn Met Gln Leu Trp Leu Arg Leu Pro Leu Val
145      150      155      160
aag cct gat gat gac tct atg gat gca aag tct gtt gct ttg gtt gac      528
Lys Pro Asp Asp Asp Ser Met Asp Ala Lys Ser Val Ala Leu Val Asp
165      170      175
tac tgg gaa act tgg aat tca ttt cgt ctg ctg tgt gag cat cat agt      576
Tyr Trp Glu Thr Trp Asn Ser Phe Arg Leu Leu Cys Glu His His Ser
180      185      190
caa ctg tca gtt gca ctt gat att ctg agt act ctc cct tcc cca aat      624
Gln Leu Ser Val Ala Leu Asp Ile Leu Ser Thr Leu Pro Ser Pro Asn
195      200      205
tca cta gga cgt tgg ttt ggg gag cct ctt aga gca gct ata tta cat      672
Ser Leu Gly Arg Trp Phe Gly Glu Pro Leu Arg Ala Ala Ile Leu His
210      215      220
act gat tgc ttt cta act aat tct cat ggc tct cca tgc ctc tcc aag      720
Thr Asp Cys Phe Leu Thr Asn Ser His Gly Ser Pro Cys Leu Ser Lys
225      230      235      240
cgt cac cag agt tta att act ggt gtt ttt aat cat tct att cag atc      768
Arg His Gln Ser Leu Ile Thr Gly Val Phe Asn His Ser Ile Gln Ile
245      250      255
att ata tct gga aat tca gtt cat aca aaa gca agt atg gat gca aat      816
Ile Ile Ser Gly Asn Ser Val His Thr Lys Ala Ser Met Asp Ala Asn
260      265      270
gat aat tct ggt aca gat tca caa aga cat ccc ttg cgg cca tat ctg      864
Asp Asn Ser Gly Thr Asp Ser Gln Arg His Pro Leu Arg Pro Tyr Leu
275      280      285
gac tac gtt gga tat ctt tac caa aga atg gat cct ctt cct gag caa      912
Asp Tyr Val Gly Tyr Leu Tyr Gln Arg Met Asp Pro Leu Pro Glu Gln
290      295      300
gaa cgt ttt gag ctt ggt tac agg gat ttt tta cag tca ccc ttg caa      960
Glu Arg Phe Glu Leu Gly Tyr Arg Asp Phe Leu Gln Ser Pro Leu Gln
305      310      315      320
cct ttg atg gat aat tta gag gct cag act tac gag act ttt gag aga      1008
Pro Leu Met Asp Asn Leu Glu Ala Gln Thr Tyr Glu Thr Phe Glu Arg
325      330      335
gat gca atg aaa tac att cag tac caa aga gca gtt agt aaa gca ttg      1056
Asp Ala Met Lys Tyr Ile Gln Tyr Gln Arg Ala Val Ser Lys Ala Leu
340      345      350
ctg gac agg gtt cct gat gaa gag gca tct gtt aaa acc att gta ttg      1104

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PF59082SeqList_PF59082.txt

Leu	Asp	Arg	Val	Pro	Asp	Glu	Glu	Ala	Ser	Val	Lys	Thr	Ile	Val	Leu	
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Met	Val	Val	Gly	Ala	Gly	Arg	Gly	Pro	Leu	Val	Arg	Ala	Ser	Leu	Gln	
	370					375					380					
gct	gct	gaa	gaa	act	ggg	cgg	aag	ctc	aaa	gtt	tat	gct	gtt	gaa	aag	1200
Ala	Ala	Glu	Glu	Thr	Gly	Arg	Lys	Leu	Lys	Val	Tyr	Ala	Val	Glu	Lys	
	385				390					395					400	
aat	ccg	aat	gct	gtt	gtt	acc	cta	cat	gca	tta	gtc	aag	tta	gaa	gga	1248
Asn	Pro	Asn	Ala	Val	Val	Thr	Leu	His	Ala	Leu	Val	Lys	Leu	Glu	Gly	
				405					410					415		
tgg	gag	tat	act	gtg	acc	ata	gtc	tca	agt	gac	atg	cgt	cat	tgg	aat	1296
Trp	Glu	Tyr	Thr	Val	Thr	Ile	Val	Ser	Ser	Asp	Met	Arg	His	Trp	Asn	
			420					425					430			
gcc	cct	gaa	aaa	gct	gac	ata	ttg	gtt	agt	gaa	ttg	cta	ggt	tct	ttt	1344
Ala	Pro	Glu	Lys	Ala	Asp	Ile	Leu	Val	Ser	Glu	Leu	Leu	Gly	Ser	Phe	
		435					440					445				
ggt	gac	aac	gaa	ctg	tct	cct	gag	tgc	ctt	gat	gga	gcc	cag	aga	ttt	1392
Gly	Asp	Asn	Glu	Leu	Ser	Pro	Glu	Cys	Leu	Asp	Gly	Ala	Gln	Arg	Phe	
	450					455					460					
cta	aag	caa	gat	gga	att	tca	ata	cca	tct	tcg	tac	aca	agt	ttc	ctc	1440
Leu	Lys	Gln	Asp	Gly	Ile	Ser	Ile	Pro	Ser	Ser	Tyr	Thr	Ser	Phe	Leu	
	465			470					475						480	
caa	cca	gtg	aca	gct	tca	aag	tta	tat	aat	gat	gtt	aag	gct	cat	aaa	1488
Gln	Pro	Val	Thr	Ala	Ser	Lys	Leu	Tyr	Asn	Asp	Val	Lys	Ala	His	Lys	
				485					490					495		
gac	ctt	gta	cac	ttt	gaa	act	gct	tat	gtt	gtg	aaa	atg	cac	aat	gta	1536
Asp	Leu	Val	His	Phe	Glu	Thr	Ala	Tyr	Val	Val	Lys	Met	His	Asn	Val	
			500					505					510			
gcc	aga	ctt	gca	cca	acc	caa	cct	gtt	ttt	aca	ttt	act	cat	cca	aag	1584
Ala	Arg	Leu	Ala	Pro	Thr	Gln	Pro	Val	Phe	Thr	Phe	Thr	His	Pro	Lys	
		515					520					525				
cac	tct	gat	aca	gaa	agc	aat	cag	cgc	cat	aaa	aag	ttg	aat	ttt	gtg	1632
His	Ser	Asp	Thr	Glu	Ser	Asn	Gln	Arg	His	Lys	Lys	Leu	Asn	Phe	Val	
	530					535					540					
ata	cct	aat	gac	act	ggg	tca	gca	atg	gta	cac	gga	ttt	gct	ggt	tat	1680
Ile	Pro	Asn	Asp	Thr	Gly	Ser	Ala	Met	Val	His	Gly	Phe	Ala	Gly	Tyr	
	545				550				555						560	
ttt	gat	gca	act	ctt	tac	aag	gat	gtg	cat	ctt	gga	att	gaa	cct	tca	1728
Phe	Asp	Ala	Thr	Leu	Tyr	Lys	Asp	Val	His	Leu	Gly	Ile	Glu	Pro	Ser	
				565					570					575		
acg	gca	aca	cca	aac	atg	ttc	agt	tgg	ttt	gca	ata	ttt	ttc	cca	tta	1776
Thr	Ala	Thr	Pro	Asn	Met	Phe	Ser	Trp	Phe	Ala	Ile	Phe	Phe	Pro	Leu	
			580					585					590			
agg	aca	ccc	att	tgt	gtg	gat	ccc	ggt	tct	aca	ctt	gaa	gta	cat	ttt	1824
Arg	Thr	Pro	Ile	Cys	Val	Asp	Pro	Gly	Ser	Thr	Leu	Glu	Val	His	Phe	
		595					600					605				
tgg	cgt	tgt	tgt	ggt	tct	aca	aag	gtt	tgg	tat	gag	tgg	tgt	gtt	gcc	1872
Trp	Arg	Cys	Cys	Gly	Ser	Thr	Lys	Val	Trp	Tyr	Glu	Trp	Cys	Val	Ala	
	610					615					620					
tct	ccc	tcg	tcg	tcc	cca	att	cac	aac	agt	aat	gga	cgt	tca	tac	tgg	1920
Ser	Pro	Ser	Ser	Ser	Pro	Ile	His	Asn	Ser	Asn	Gly	Arg	Ser	Tyr	Trp	
	625				630					635					640	
gtt	ggg	ctt	tag													1932
Val	Gly	Leu														

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 <212> PRT
 <213> Glycine max

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 Asn Leu Tyr Ser Gly Ser Phe Asp Phe Val Val Ala Pro Leu Met Asp
 35 40 45

PF59082SeqList_PF59082.txt

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Leu	Leu	Pro	Phe	Ala	Gly	Ser	Asp	Leu	Val	Leu	Ser	Pro	Ser	Gln	Trp
65					70					75					80
Ser	Ser	His	Val	Val	Gly	Lys	Ile	Ser	Ser	Trp	Ile	Asp	Leu	Asp	Ser
				85					90					95	
Glu	Asp	Glu	Thr	Leu	Arg	Val	Asp	Ser	Glu	Thr	Thr	Leu	Arg	Gln	Glu
			100					105					110		
Ile	Ala	Trp	Ala	Ser	His	Leu	Ser	Leu	Gln	Ala	Cys	Leu	Leu	Pro	Ala
		115					120					125			
Pro	Lys	Gly	Thr	Ser	Cys	Ala	Asn	Tyr	Ala	Arg	Cys	Val	Asn	Gln	Ile
	130					135					140				
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Lys	Pro	Asp	Asp	Asp	Ser	Met	Asp	Ala	Lys	Ser	Val	Ala	Leu	Val	Asp
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Tyr	Trp	Glu	Thr	Trp	Asn	Ser	Phe	Arg	Leu	Leu	Cys	Glu	His	His	Ser
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Gln	Leu	Ser	Val	Ala	Leu	Asp	Ile	Leu	Ser	Thr	Leu	Pro	Ser	Pro	Asn
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Ser	Leu	Gly	Arg	Trp	Phe	Gly	Glu	Pro	Leu	Arg	Ala	Ala	Ile	Leu	His
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Thr	Asp	Cys	Phe	Leu	Thr	Asn	Ser	His	Gly	Ser	Pro	Cys	Leu	Ser	Lys
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Arg	His	Gln	Ser	Leu	Ile	Thr	Gly	Val	Phe	Asn	His	Ser	Ile	Gln	Ile
				245				250						255	
Ile	Ile	Ser	Gly	Asn	Ser	Val	His	Thr	Lys	Ala	Ser	Met	Asp	Ala	Asn
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Asp	Asn	Ser	Gly	Thr	Asp	Ser	Gln	Arg	His	Pro	Leu	Arg	Pro	Tyr	Leu
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Asp	Tyr	Val	Gly	Tyr	Leu	Tyr	Gln	Arg	Met	Asp	Pro	Leu	Pro	Glu	Gln
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Glu	Arg	Phe	Glu	Leu	Gly	Tyr	Arg	Asp	Phe	Leu	Gln	Ser	Pro	Leu	Gln
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Pro	Leu	Met	Asp	Asn	Leu	Glu	Ala	Gln	Thr	Tyr	Glu	Thr	Phe	Glu	Arg
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Asp	Ala	Met	Lys	Tyr	Ile	Gln	Tyr	Gln	Arg	Ala	Val	Ser	Lys	Ala	Leu
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Asn	Pro	Asn	Ala	Val	Thr	Leu	His	Ala	Leu	Val	Lys	Leu	Glu	Gly	
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Trp	Glu	Tyr	Thr	Val	Thr	Ile	Val	Ser	Ser	Asp	Met	Arg	His	Trp	Asn
			420					425					430		
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Gly	Asp	Asn	Glu	Leu	Ser	Pro	Glu	Cys	Leu	Asp	Gly	Ala	Gln	Arg	Phe
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Gln	Pro	Val	Thr	Ala	Ser	Lys	Leu	Tyr	Asn	Asp	Val	Lys	Ala	His	Lys
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His	Ser	Asp	Thr	Glu	Ser	Asn	Gln	Arg	His	Lys	Lys	Leu	Asn	Phe	Val
	530					535					540				
Ile	Pro	Asn	Asp	Thr	Gly	Ser	Ala	Met	Val	His	Gly	Phe	Ala	Gly	Tyr
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Phe	Asp	Ala	Thr	Leu	Tyr	Lys	Asp	Val	His	Leu	Gly	Ile	Glu	Pro	Ser
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Thr	Ala	Thr	Pro	Asn	Met	Phe	Ser	Trp	Phe	Ala	Ile	Phe	Phe	Pro	Leu
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Arg	Thr	Pro	Ile	Cys	Val	Asp	Pro	Gly	Ser	Thr	Leu	Glu	Val	His	Phe

PF59082SeqList_PF59082.txt

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Gly Val Glu Thr Asp Phe Asn Asp Asp Met Pro His Val Leu His Phe
20 25 30
aac ctt tat tct gga agc ttc gat ttc gtt gtt gct cct ctg atg gat 144
Asn Leu Tyr Ser Gly Ser Phe Asp Phe Val Val Ala Pro Leu Met Asp
35 40 45
cat tct tat cgg cca agt tta gtg caa aag gat gct ttg ggg tct ggt 192
His Ser Tyr Arg Pro Ser Leu Val Gln Lys Asp Ala Leu Gly Ser Gly
50 55 60
gtt ctg cca ttt gct ggg tca gac ttg gtc ttg agt cca tcc cag tgg 240
Val Leu Pro Phe Ala Gly Ser Asp Leu Val Leu Ser Pro Ser Gln Trp
65 70 75 80
agt agt cat gta gtg gga aaa att agc tca tgg ata gat ttg gat tca 288
Ser Ser His Val Val Gly Lys Ile Ser Ser Trp Ile Asp Leu Asp Ser
85 90 95
gag gat gaa acc ctc agg ata gat tct gaa acc act ctt aaa caa gaa 336
Glu Asp Glu Thr Leu Arg Ile Asp Ser Glu Thr Thr Leu Lys Gln Glu
100 105 110
att gct tgg gct tct cat ctc tct tta cag gcc tgc ctg ctt cct gcc 384
Ile Ala Trp Ala Ser His Leu Ser Leu Gln Ala Cys Leu Leu Pro Ala
115 120 125
ccg aag gga act tct tgt gct aat tat gct aga tgt gtg aat cag atc 432
Pro Lys Gly Thr Ser Cys Ala Asn Tyr Ala Arg Cys Val Asn Gln Ile
130 135 140
tta cag ggt tca aat aat atg cag ttg tgg ctt agg gtt cca ttg gtg 480
Leu Gln Gly Ser Asn Asn Met Gln Leu Trp Leu Arg Val Pro Leu Val
145 150 155 160
aag cct gat gat gac tct atg gat gca aag tct gtt gct ttg gtt gac 528
Lys Pro Asp Asp Asp Ser Met Asp Ala Lys Ser Val Ala Leu Val Asp
165 170 175
tct tgg gaa act tgg aat tca ttt cgt ctg ctg tgt gag cat cat agt 576
Ser Trp Glu Thr Trp Asn Ser Phe Arg Leu Leu Cys Glu His His Ser
180 185 190
caa ctg tca gtt gca ctt gat att ctg agt act ctt cct tcc cca aat 624
Gln Leu Ser Val Ala Leu Asp Ile Leu Ser Thr Leu Pro Ser Pro Asn
195 200 205
tca cta gga cgc tgg ttt ggg gag cct gtt aga gca gct ata tta cat 672
Ser Leu Gly Arg Trp Phe Gly Glu Pro Val Arg Ala Ala Ile Leu His
210 215 220
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Thr Asp Cys Phe Leu Thr Asn Ser His Gly Cys Pro Cys Leu Ser Lys
225 230 235 240
cgc cac cag agt tta att act ggt ttt ttt aac cat tct att cag atc 768
Arg His Gln Ser Leu Ile Thr Gly Phe Phe Asn His Ser Ile Gln Ile
245 250 255
att gta tct gga aat tca gtt cat cca aaa gca agt gtg gat gca aat 816
Ile Val Ser Gly Asn Ser Val His Pro Lys Ala Ser Val Asp Ala Asn
260 265 270

PF59082SeqList_PF59082.txt

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Glu	Arg	Phe	Glu	Leu	Gly	Tyr	Arg	Asp	Phe	Leu	Gln	Ser	Pro	Leu	Gln	
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cct	ttg	atg	gat	aat	tta	gag	gct	cag	act	tac	gag	act	ttt	gag	aga	1008
Pro	Leu	Met	Asp	Asn	Leu	Glu	Ala	Gln	Thr	Tyr	Glu	Thr	Phe	Glu	Arg	
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Asp	Ala	Val	Lys	Tyr	Ile	Gln	Tyr	Gln	Arg	Ala	Val	Ser	Lys	Ala	Leu	
			340					345					350			
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Leu	Asp	Arg	Val	Pro	Asp	Glu	Glu	Ala	Ser	Val	Lys	Thr	Ile	Val	Leu	
		355				360						365				
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Met	Val	Val	Gly	Ala	Gly	Arg	Gly	Pro	Leu	Val	Arg	Ala	Ser	Leu	Gln	
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385					390					395				400		
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Asn	Pro	Asn	Ala	Val	Val	Thr	Leu	His	Ala	Leu	Val	Lys	Leu	Glu	Gly	
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tgg	gag	gat	act	gtg	acc	ata	gtc	tca	agt	gac	atg	cgt	cat	tgg	agt	1296
Trp	Glu	Asp	Thr	Val	Thr	Ile	Val	Ser	Ser	Asp	Met	Arg	His	Trp	Ser	
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gcc	cct	gaa	aaa	gct	gac	ata	ttg	gtt	agt	gaa	ttg	cta	ggt	tct	ttt	1344
Ala	Pro	Glu	Lys	Ala	Asp	Ile	Leu	Val	Ser	Glu	Leu	Leu	Gly	Ser	Phe	
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ggc	gac	aat	gag	ctg	tct	cct	gag	tgc	ctt	gat	gga	gcc	cag	aga	ttt	1392
Gly	Asp	Asn	Glu	Leu	Ser	Pro	Glu	Cys	Leu	Asp	Gly	Ala	Gln	Arg	Phe	
	450					455					460					
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Leu	Lys	Gln	Asp	Gly	Ile	Ser	Ile	Pro	Ser	Ser	Tyr	Thr	Ser	Phe	Leu	
465					470					475					480	
caa	cca	gtg	aca	gct	tca	aag	tta	tat	aat	gat	gtt	aag	gca	cat	aaa	1488
Gln	Pro	Val	Thr	Ala	Ser	Lys	Leu	Tyr	Asn	Asp	Val	Lys	Ala	His	Lys	
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Asp	Leu	Val	His	Phe	Glu	Thr	Ala	Tyr	Val	Val	Lys	Met	His	Asn	Val	
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gcc	aaa	ctt	gca	cca	acc	caa	cct	gtt	ttt	aca	ttt	act	cat	cca	aag	1584
Ala	Lys	Leu	Ala	Pro	Thr	Gln	Pro	Val	Phe	Thr	Phe	Thr	His	Pro	Lys	
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His	Ser	Asp	Lys	Glu	Ile	Asn	Gln	Arg	Tyr	Lys	Lys	Leu	Asn	Phe	Ile	
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ata	cct	aat	gac	act	ggg	tca	gca	atg	gta	cac	gga	ttt	gct	ggt	tat	1680
Ile	Pro	Asn	Asp	Thr	Gly	Ser	Ala	Met	Val	His	Gly	Phe	Ala	Gly	Tyr	
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ttt	gat	gca	act	ctt	tac	aag	gat	gtg	cat	ctt	gga	att	gaa	cct	tca	1728
Phe	Asp	Ala	Thr	Leu	Tyr	Lys	Asp	Val	His	Leu	Gly	Ile	Glu	Pro	Ser	
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Thr	Ala	Thr	Pro	Asn	Met	Phe	Ser	Trp	Phe	Ala	Ile	Phe	Phe	Pro	Leu	
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agg	aca	ccc	att	tgt	gtg	gat	ccc	ggt	tct	aca	ctt	gaa	gta	cat	ttt	1824
Arg	Thr	Pro	Ile	Cys	Val	Asp	Pro	Gly	Ser	Thr	Leu	Glu	Val	His	Phe	
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tgg	cgt	tgt	tgt	ggt	tct	acg	aag	gtt	tgg	tat	gag	tgg	tgt	gtt	gct	1872
Trp	Arg	Cys	Cys	Gly	Ser	Thr	Lys	Val	Trp	Tyr	Glu	Trp	Cys	Val	Ala	
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tct	ccc	gcg	tcg	tcc	cca	atg	cac	aac	agt	aat	gga	cgt	tca	tac	tgg	1920
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35 40 45
His Ser Tyr Arg Pro Ser Leu Val Gln Lys Asp Ala Leu Gly Ser Gly
50 55 60
Val Leu Pro Phe Ala Gly Ser Asp Leu Val Leu Ser Pro Ser Gln Trp
65 70 75 80
Ser Ser His Val Val Gly Lys Ile Ser Ser Trp Ile Asp Leu Asp Ser
85 90 95
Glu Asp Glu Thr Leu Arg Ile Asp Ser Glu Thr Thr Leu Lys Gln Glu
100 105 110
Ile Ala Trp Ala Ser His Leu Ser Leu Gln Ala Cys Leu Leu Pro Ala
115 120 125
Pro Lys Gly Thr Ser Cys Ala Asn Tyr Ala Arg Cys Val Asn Gln Ile
130 135 140
Leu Gln Gly Ser Asn Asn Met Gln Leu Trp Leu Arg Val Pro Leu Val
145 150 155 160
Lys Pro Asp Asp Asp Ser Met Asp Ala Lys Ser Val Ala Leu Val Asp
165 170 175
Ser Trp Glu Thr Trp Asn Ser Phe Arg Leu Leu Cys Glu His His Ser
180 185 190
Gln Leu Ser Val Ala Leu Asp Ile Leu Ser Thr Leu Pro Ser Pro Asn
195 200 205
Ser Leu Gly Arg Trp Phe Gly Glu Pro Val Arg Ala Ala Ile Leu His
210 215 220
Thr Asp Cys Phe Leu Thr Asn Ser His Gly Cys Pro Cys Leu Ser Lys
225 230 235 240
Arg His Gln Ser Leu Ile Thr Gly Phe Phe Asn His Ser Ile Gln Ile
245 250 255
Ile Val Ser Gly Asn Ser Val His Pro Lys Ala Ser Val Asp Ala Asn
260 265 270
Asp Asn Ser Gly Thr Asn Ser Gln Arg His Pro Leu Arg Pro Tyr Leu
275 280 285
Asp Tyr Ile Gly Tyr Leu Tyr Gln Arg Met Asp Pro Leu Pro Glu Gln
290 295 300
Glu Arg Phe Glu Leu Gly Tyr Arg Asp Phe Leu Gln Ser Pro Leu Gln
305 310 315 320
Pro Leu Met Asp Asn Leu Glu Ala Gln Thr Tyr Glu Thr Phe Glu Arg
325 330 335
Asp Ala Val Lys Tyr Ile Gln Tyr Gln Arg Ala Val Ser Lys Ala Leu
340 345 350
Leu Asp Arg Val Pro Asp Glu Glu Ala Ser Val Lys Thr Ile Val Leu
355 360 365
Met Val Val Gly Ala Gly Arg Gly Pro Leu Val Arg Ala Ser Leu Gln
370 375 380
Ala Ala Glu Glu Thr Gly Arg Lys Leu Lys Val Tyr Ala Val Glu Lys
385 390 395 400
Asn Pro Asn Ala Val Val Thr Leu His Ala Leu Val Lys Leu Glu Gly
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420 425 430
Ala Pro Glu Lys Ala Asp Ile Leu Val Ser Glu Leu Leu Gly Ser Phe
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Gly Asp Asn Glu Leu Ser Pro Glu Cys Leu Asp Gly Ala Gln Arg Phe
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PF59082SeqList_PF59082.txt

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Ala Lys Leu Ala Pro Thr Gln Pro Val Phe Thr Phe Thr His Pro Lys
          515          520          525
His Ser Asp Lys Glu Ile Asn Gln Arg Tyr Lys Lys Leu Asn Phe Ile
          530          535          540
Ile Pro Asn Asp Thr Gly Ser Ala Met Val His Gly Phe Ala Gly Tyr
          545          550          555
Phe Asp Ala Thr Leu Tyr Lys Asp Val His Leu Gly Ile Glu Pro Ser
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Thr Ala Thr Pro Asn Met Phe Ser Trp Phe Ala Ile Phe Phe Pro Leu
          580          585          590          595
Arg Thr Pro Ile Cys Val Asp Pro Gly Ser Thr Leu Glu Val His Phe
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Trp Arg Cys Cys Gly Ser Thr Lys Val Trp Tyr Glu Trp Cys Val Ala
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20          25          30
ctc aat cac tcc ctc gcc tcc gcc ttc gac ttc atc ctc gcc cct ctg      144
Leu Asn His Ser Leu Ala Ser Ala Phe Asp Phe Ile Leu Ala Pro Leu
35          40          45
gtt gat ccc aac tac cgg ccg gcg ccc ggc gcc gtt ctg cca gtg tca      192
Val Asp Pro Asn Tyr Arg Pro Ala Pro Gly Ala Val Leu Pro Val Ser
50          55          60
gcg tca gac ctc gtc ctc ggc ccg tcc cag tgg agc aac cac gtc gtc      240
Ala Ser Asp Leu Val Leu Gly Pro Ser Gln Trp Ser Asn His Val Val
65          70          75          80
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Gly Lys Ile Ser Glu Trp Ile Asp Leu Asp Ala Glu Asp Glu Arg Leu
85          90          95
cgc ctg cac tcc aag ctc acg ctg aag cag gag atc gct tgg gca tct      336
Arg Leu His Ser Lys Leu Thr Leu Lys Gln Glu Ile Ala Trp Ala Ser
100          105          110          115
cac gtc tcg ctg cag gca tgt gtt att cct gcc ccc agg aga tct ttt      384
His Val Ser Leu Gln Ala Cys Val Ile Pro Ala Pro Arg Arg Ser Phe
120          125          130          135
tgc ggc aat tat gcc aga gtc gtg aat caa att ttg caa ggc ctg acc      432
Cys Gly Asn Tyr Ala Arg Val Val Asn Gln Ile Leu Gln Gly Leu Thr
140          145          150          155
aat atg aat ttg tgg ctc agg ttg cct ctg gag aag tcc gag cct atg      480
Asn Met Asn Leu Trp Leu Arg Leu Pro Leu Glu Lys Ser Glu Pro Met
160          165          170          175
gat gat gat ctt gat aaa ata aag aac aac cac acg cta cag agt      528
Asp Asp Asp Leu Asp Lys Ile Lys Asn Asn Asn His Thr Leu Gln Ser
180          185          190          195
gaa att gta gac tca tgg gaa tta tgg aat tca ttc aga ttg cta tgt      576
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PF59082SeqList_PF59082.txt

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cca	tca	ata	aac	tca	tta	gca	agg	tg	ttt	gga	gag	cct	gta	agg	gct		672
Pro	Ser	Ile	Asn	Ser	Leu	Ala	Arg	Trp	Phe	Gly	Glu	Pro	Val	Arg	Ala		
	210					215					220						
gct	att	ctg	caa	acc	gag	gct	ttt	ctt	aca	aat	gca	aaa	gga	tat	cct		720
Ala	Ile	Leu	Gln	Thr	Glu	Ala	Phe	Leu	Thr	Asn	Ala	Lys	Gly	Tyr	Pro		
225					230					235					240		
tgt	tta	tca	aag	cgc	cat	cag	agt	ctg	cta	act	gga	ttt	ttt	aaa	cat		768
Cys	Leu	Ser	Lys	Arg	His	Gln	Ser	Leu	Leu	Thr	Gly	Phe	Phe	Lys	His		
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Ser	Val	Gln	Val	Ile	Ile	Ser	Gly	Arg	Ser	Asn	His	Asn	Val	Phe	Pro		
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gta	tct	gaa	gga	gtg	ctc	tca	ggt	gat	gag	agc	tac	aca	gaa	gat	tcc		864
Val	Ser	Glu	Gly	Val	Leu	Ser	Gly	Asp	Glu	Ser	Tyr	Thr	Glu	Asp	Ser		
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Tyr	Arg	Lys	Met	Asp	Pro	Leu	Pro	Glu	Gln	Glu	Arg	Ile	Glu	Ile	Asn		
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Tyr	Arg	Asp	Phe	Leu	Gln	Ser	Pro	Leu	Gln	Pro	Leu	Met	Asp	Asn	Leu		
			325					330						335			
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Glu	Ala	Gln	Thr	Tyr	Glu	Thr	Phe	Glu	Lys	Asp	Val	Val	Lys	Tyr	Thr		
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cag	tat	cga	aga	gca	gtt	gct	aag	gcc	ttg	gtt	gat	agg	gtt	gca	gat		1104
Gln	Tyr	Arg	Arg	Ala	Val	Ala	Lys	Ala	Leu	Val	Asp	Arg	Val	Ala	Asp		
		355				360						365					
gat	gca	gtc	tcc	aca	act	agg	acg	gtt	ctg	atg	gtt	gtg	gga	gca	ggc		1152
Asp	Ala	Val	Ser	Thr	Thr	Arg	Thr	Val	Leu	Met	Val	Val	Gly	Ala	Gly		
	370				375			380									
cga	ggg	cct	cta	gta	cga	gca	tca	ttg	cag	gct	gct	gaa	gaa	act	ggt		1200
Arg	Gly	Pro	Leu	Val	Arg	Ala	Ser	Leu	Gln	Ala	Ala	Glu	Glu	Thr	Gly		
385					390					395					400		
cgc	aag	tta	aaa	gta	tat	gct	gtt	gaa	aaa	aat	cct	aac	gct	gtt	att		1248
Arg	Lys	Leu	Lys	Val	Tyr	Ala	Val	Glu	Lys	Asn	Pro	Asn	Ala	Val	Ile		
			405					410						415			
act	ctt	cat	agt	ttg	atc	aaa	ttg	gag	ggt	tg	gaa	agc	ctg	gtt	act		1296
Thr	Leu	His	Ser	Leu	Ile	Lys	Leu	Glu	Gly	Trp	Glu	Ser	Leu	Val	Thr		
			420				425						430				
gta	att	tct	agt	gac	atg	cgg	tgt	tg	gat	gcc	cct	gaa	aag	aca	gag		1344
Val	Ile	Ser	Ser	Asp	Met	Arg	Cys	Trp	Asp	Ala	Pro	Glu	Lys	Thr	Glu		
		435				440					445						
att	ttg	gta	agt	gaa	ttg	ctt	ggg	tcc	ttt	ggg	gac	aaa	gaa	cta	tct		1392
Ile	Leu	Val	Ser	Glu	Leu	Leu	Gly	Ser	Phe	Gly	Asp	Lys	Glu	Leu	Ser		
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ccg	gag	tgt	ctg	gat	ggt	gca	caa	aga	tac	ctg	aag	cct	gat	gcg	att		1440
Pro	Glu	Cys	Leu	Asp	Gly	Ala	Gln	Arg	Tyr	Leu	Lys	Pro	Asp	Ala	Ile		
465					470					475					480		
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Ser	Thr	Pro	Ser	Ser	Tyr	Thr	Ser	Phe	Thr	Gln	Pro	Ile	Thr	Glu	Ser		
			485					490						495			
aaa	ttg	cac	gac	gac	atc	aaa	gca	cac	aaa	gat	att	gca	cat	ttt	gaa		1536
Lys	Leu	His	Asp	Asp	Ile	Lys	Ala	His	Lys	Asp	Ile	Ala	His	Phe	Glu		
			500					505					510				
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Thr	Ala	Tyr	Val	Val	Lys	Leu	His	Arg	Ile	Ala	Thr	Leu	Ala	Pro	Pro		
		515				520					525						
caa	cag	gtt	ttt	act	ttc	acc	cat	cca	aat	ttc	tca	cca	aat	gcc	agc		1632
Gln	Gln	Val	Phe	Thr	Phe	Thr	His	Pro	Asn	Phe	Ser	Pro	Asn	Ala	Ser		
	530				535						540						
aac	caa	agg	tac	acc	aag	ttg	caa	ttt	gaa	atg	ctg	cca	gac	atg	ggt		1680
Asn	Gln	Arg	Tyr	Thr	Lys	Leu	Gln	Phe	Glu	Met	Leu	Pro	Asp	Met	Gly		

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	Ser	Cys	Leu	Val	His	Gly	Phe	Ala	Gly	Tyr	Phe	Asp	Ser	Val	Leu	Tyr	
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aag	gat	gtt	cat	ctt	gga	atc	gag	cca	aac	acc	gct	aca	cca	aac	atg		1776
Lys	Asp	Val	His	Leu	Gly	Ile	Glu	Pro	Asn	Thr	Ala	Thr	Pro	Asn	Met		
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ttc	agc	tgg	ttc	ccg	atc	ttc	ttc	cca	ttg	aga	aag	ccc	atc	tac	gtg		1824
Phe	Ser	Trp	Phe	Pro	Ile	Phe	Phe	Pro	Leu	Arg	Lys	Pro	Ile	Tyr	Val		
		595					600					605					
ccc	gaa	ggg	tct	cct	ata	gaa	gtg	cac	ttc	tgg	cgg	tgc	tgt	gcc	ccc		1872
Pro	Glu	Gly	Ser	Pro	Ile	Glu	Val	His	Phe	Trp	Arg	Cys	Cys	Ala	Pro		
	610					615					620						
acg	aag	gtg	tgg	tac	gag	tgg	gct	gtg	act	acg	ccg	acc	ccg	tcg	ccg		1920
Thr	Lys	Val	Trp	Tyr	Glu	Trp	Ala	Val	Thr	Thr	Pro	Thr	Pro	Ser	Pro		
625					630				635						640		
atc	cac	aac	agc	aat	ggc	cgg	tcc	tat	tgg	gtt	ggg	cta	taa				1962
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 35 40 45
 Val Asp Pro Asn Tyr Arg Pro Ala Pro Gly Ala Val Leu Pro Val Ser
 50 55 60
 Ala Ser Asp Leu Val Leu Gly Pro Ser Gln Trp Ser Asn His Val Val
 65 70 75 80
 Gly Lys Ile Ser Glu Trp Ile Asp Leu Asp Ala Glu Asp Glu Arg Leu
 85 90 95
 Arg Leu His Ser Lys Leu Thr Leu Lys Gln Glu Ile Ala Trp Ala Ser
 100 105 110
 His Val Ser Leu Gln Ala Cys Val Ile Pro Ala Pro Arg Arg Ser Phe
 115 120 125
 Cys Gly Asn Tyr Ala Arg Val Val Asn Gln Ile Leu Gln Gly Leu Thr
 130 135 140
 Asn Met Asn Leu Trp Leu Arg Leu Pro Leu Glu Lys Ser Glu Pro Met
 145 150 155 160
 Asp Asp Asp Leu Asp Lys Ile Lys Asn Asn Asn His Thr Leu Gln Ser
 165 170 175
 Glu Ile Val Asp Ser Trp Glu Leu Trp Asn Ser Phe Arg Leu Leu Cys
 180 185 190
 Asp His Ser Ser Gln Leu Cys Val Ala Leu Asp Ile Leu Ser Thr Leu
 195 200 205
 Pro Ser Ile Asn Ser Leu Ala Arg Trp Phe Gly Glu Pro Val Arg Ala
 210 215 220
 Ala Ile Leu Gln Thr Glu Ala Phe Leu Thr Asn Ala Lys Gly Tyr Pro
 225 230 235 240
 Cys Leu Ser Lys Arg His Gln Ser Leu Leu Thr Gly Phe Phe Lys His
 245 250 255
 Ser Val Gln Val Ile Ile Ser Gly Arg Ser Asn His Asn Val Phe Pro
 260 265 270
 Val Ser Glu Gly Val Leu Ser Gly Asp Glu Ser Tyr Thr Glu Asp Ser
 275 280 285
 His Val Arg His Ala Leu Thr Pro Tyr Leu Glu Tyr Ile Ala Tyr Leu
 290 295 300
 Tyr Arg Lys Met Asp Pro Leu Pro Glu Gln Glu Arg Ile Glu Ile Asn
 305 310 315 320
 Tyr Arg Asp Phe Leu Gln Ser Pro Leu Gln Pro Leu Met Asp Asn Leu
 325 330 335
 Glu Ala Gln Thr Tyr Glu Thr Phe Glu Lys Asp Val Val Lys Tyr Thr
 340 345 350
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 Arg Gly Pro Leu Val Arg Ala Ser Leu Gln Ala Glu Glu Thr Gly
 385 390 395
 Arg Lys Leu Lys Val Tyr Ala Val Glu Lys Asn Pro Asn Ala Val Ile
 400 405 410 415
 Thr Leu His Ser Leu Ile Lys Leu Glu Gly Trp Glu Ser Leu Val Thr
 420 425 430
 Val Ile Ser Ser Asp Met Arg Cys Trp Asp Ala Pro Glu Lys Thr Glu
 435 440 445
 Ile Leu Val Ser Glu Leu Leu Gly Ser Phe Gly Asp Lys Glu Leu Ser
 450 455 460
 Pro Glu Cys Leu Asp Gly Ala Gln Arg Tyr Leu Lys Pro Asp Ala Ile
 465 470 475 480
 Ser Thr Pro Ser Ser Tyr Thr Ser Phe Thr Gln Pro Ile Thr Glu Ser
 485 490 495
 Lys Leu His Asp Asp Ile Lys Ala His Lys Asp Ile Ala His Phe Glu
 500 505 510
 Thr Ala Tyr Val Val Lys Leu His Arg Ile Ala Thr Leu Ala Pro Pro
 515 520 525
 Gln Gln Val Phe Thr Phe Thr His Pro Asn Phe Ser Pro Asn Ala Ser
 530 535 540
 Asn Gln Arg Tyr Thr Lys Leu Gln Phe Glu Met Leu Pro Asp Met Gly
 545 550 555 560
 Ser Cys Leu Val His Gly Phe Ala Gly Tyr Phe Asp Ser Val Leu Tyr
 565 570 575
 Lys Asp Val His Leu Gly Ile Glu Pro Asn Thr Ala Thr Pro Asn Met
 580 585 590
 Phe Ser Trp Phe Pro Ile Phe Phe Pro Leu Arg Lys Pro Ile Tyr Val
 595 600 605
 Pro Glu Gly Ser Pro Ile Glu Val His Phe Trp Arg Cys Cys Ala Pro
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 645 650

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 Gly Ala Glu Val Leu Asp Phe Pro Ala Gly Glu Asp Leu Pro Ala Val
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 ctc aac cac tcc ctc gcc tcc gcc ttc gac ttc atc ctc gtc cct ctg 144
 Leu Asn His Ser Leu Ala Ser Ala Phe Asp Phe Ile Leu Val Pro Leu
 35 40 45
 gtt gat ccc aac tac cgg ccg gcc ggc tcc gtt ctg ccc gtg tcg 192
 Val Asp Pro Asn Tyr Arg Pro Ala Pro Gly Ser Val Leu Pro Val Ser
 50 55 60
 gcg tcg gac ctc atc ctt ggc ccg gcc cag tgg agc aac cac gtc gtc 240
 Ala Ser Asp Leu Ile Leu Gly Pro Ala Gln Trp Ser Asn His Val Val
 65 70 75 80
 ggg aag atc agc gag tgg att gat ttg gac tct gag gac gag cgg ctc 288
 Gly Lys Ile Ser Glu Trp Ile Asp Leu Asp Ser Glu Asp Glu Arg Leu
 85 90 95
 cgc ttt gac tcc gag ctc acg ctg aag cag gag att gcg tgg gcg tct 336
 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200

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His	Val	Ser	Leu	Gln	Ala	Cys	Gly	Leu	Pro	Ala	Pro	Lys	Arg	Ser	Phe	
tgg	ggc	aat	tat	gcc	aga	gtc	gtg	aat	caa	att	ttg	caa	ggc	ctg	acc	432
Trp	Gly	Asn	Tyr	Ala	Arg	Val	Val	Asn	Gln	Ile	Leu	Gln	Gly	Leu	Thr	
aat	atg	cat	ttg	ttg	ctc	agg	ttg	cct	ctg	gag	aag	tcc	gag	cct	atg	480
Asn	Met	His	Leu	Trp	Leu	Arg	Leu	Pro	Leu	Glu	Lys	Ser	Glu	Pro	Met	
gat	gat	gat	ctt	gat	aaa	ata	aag	aat	aac	agc	cac	acg	agt	gaa	att	528
Asp	Asp	Asp	Leu	Asp	Lys	Ile	Lys	Asn	Asn	Ser	His	Thr	Ser	Glu	Ile	
gta	gac	tca	ttg	gaa	tta	ttg	aat	tca	ttc	aga	ttg	cta	tgt	gac	cat	576
Val	Asp	Ser	Trp	Glu	Leu	Trp	Asn	Ser	Phe	Arg	Leu	Leu	Cys	Asp	His	
agt	agc	caa	cta	tgt	gtg	gca	ctc	gat	att	ttg	agc	act	ctg	cca	tca	624
Ser	Ser	Gln	Leu	Cys	Val	Ala	Leu	Asp	Ile	Leu	Ser	Thr	Leu	Pro	Ser	
ata	aac	tca	tta	gca	agg	ttg	ttt	gga	gag	cct	gta	agg	gct	gct	att	672
Ile	Asn	Ser	Leu	Ala	Arg	Trp	Phe	Gly	Glu	Pro	Val	Arg	Ala	Ala	Ile	
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Leu	Gln	Thr	Glu	Ala	Phe	Leu	Thr	Asn	Ala	Lys	Gly	Tyr	Pro	Cys	Leu	
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Ser	Lys	Arg	His	Gln	Ser	Leu	Leu	Thr	Gly	Phe	Phe	Lys	His	Ser	Val	
cag	gtg	ata	ata	tct	gga	aga	tca	aat	cac	aat	gtt	ttc	cca	gta	tct	816
Gln	Val	Ile	Ile	Ser	Gly	Arg	Ser	Asn	His	Asn	Val	Phe	Pro	Val	Ser	
gaa	gga	gtg	ctc	tca	ggt	gat	gag	agc	tac	aca	gaa	gat	tcc	cat	gtt	864
Glu	Gly	Val	Leu	Ser	Gly	Asp	Glu	Ser	Tyr	Thr	Glu	Asp	Ser	His	Val	
cga	cat	gca	tta	act	cct	tac	ctt	gaa	tac	att	gcg	tac	cta	tat	cgg	912
Arg	His	Ala	Leu	Thr	Pro	Tyr	Leu	Glu	Tyr	Ile	Ala	Tyr	Leu	Tyr	Arg	
aag	atg	gat	ccg	ctt	cct	gag	cag	gaa	cgc	att	gag	att	aat	tac	agg	960
Lys	Met	Asp	Pro	Leu	Pro	Glu	Gln	Glu	Arg	Ile	Glu	Ile	Asn	Tyr	Arg	
gac	ttt	ttg	cag	tct	cct	ctg	cag	cct	cta	atg	gac	aat	ttg	gaa	gct	1008
Asp	Phe	Leu	Gln	Ser	Pro	Leu	Gln	Pro	Leu	Met	Asp	Asn	Leu	Glu	Ala	
caa	act	tat	gag	aca	ttt	gag	aag	gat	gtt	gtg	aag	tac	act	cag	tat	1056
Gln	Thr	Tyr	Glu	Thr	Phe	Glu	Lys	Asp	Val	Val	Lys	Tyr	Thr	Gln	Tyr	
cga	aga	gca	gtt	gct	aag	gcc	ttg	gtt	gat	agg	gtt	gct	gat	gat	gca	1104
Arg	Arg	Ala	Val	Ala	Lys	Ala	Leu	Val	Asp	Arg	Val	Ala	Asp	Asp	Ala	
gtc	tct	aca	act	agg	acg	gtg	ctg	atg	gtt	gtg	gga	gca	gga	cgg	gga	1152
Val	Ser	Thr	Thr	Arg	Thr	Val	Leu	Met	Val	Val	Gly	Ala	Gly	Arg	Gly	
cct	cta	gta	cga	gca	tca	ttg	cag	gcc	gct	gaa	gaa	act	ggt	cgc	aaa	1200
Pro	Leu	Val	Arg	Ala	Ser	Leu	Gln	Ala	Ala	Glu	Glu	Thr	Gly	Arg	Lys	
tta	aaa	gta	tat	gct	gtt	gaa	aaa	aat	cct	aac	gct	gtt	att	act	ctt	1248
Leu	Lys	Val	Tyr	Ala	Val	Glu	Lys	Asn	Pro	Asn	Ala	Val	Ile	Thr	Leu	
cat	agt	ttg	atc	aaa	ttg	gag	ggt	ttg	gaa	agc	ctg	gtt	act	gta	att	1296
His	Ser	Leu	Ile	Lys	Leu	Glu	Gly	Trp	Glu	Ser	Leu	Val	Thr	Val	Ile	
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Ser	Ser	Asp	Met	Arg	Cys	Trp	Asp	Ala	Pro	Glu	Lys	Ala	Asp	Val	Leu	
gtc	agt	gaa	ttg	ctt	ggg	tcc	ttt	ggt	gac	aat	gaa	cta	tct	cct	gag	1392
Val	Ser	Glu	Leu	Leu	Gly	Ser	Phe	Gly	Asp	Asn	Glu	Leu	Ser	Pro	Glu	
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PF59082SeqList_PF59082.txt

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Pro	Ser	Ser	Tyr	Thr 485	Ser	Phe	Ile	Gln	Pro 490	Ile	Ile	Ala	Ser	Lys 495	Leu	
cac	aac	gat	atc	aaa	gca	cac	aaa	gac	att	gca	cat	ttt	gaa	acc	gca	1536
His	Asn	Asp	Ile	Lys	Ala	His	Lys	Asp	Ile	Ala	His	Phe	Glu	Thr	Ala	
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tat	gtt	gtc	aaa	cta	cac	cgc	ata	gcg	aca	ctt	gca	cct	cca	caa	cag	1584
Tyr	Val	Val	Lys	Leu	His	Arg	Ile	Ala	Thr	Leu	Ala	Pro	Pro	Gln	Gln	
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Val	Phe	Thr	Phe	Thr	His	Pro	Asn	Phe	Ser	Pro	Asn	Ala	Ser	Asn	Gln	
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Arg	Tyr	Thr	Lys	Leu	Gln	Phe	Glu	Met	Leu	Pro	Asp	Met	Gly	Ser	Cys	
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Leu	Val	His	Gly	Phe	Ala	Gly	Tyr	Phe	Asp	Ser	Val	Leu	Tyr	Lys	Asp	
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Val	His	Leu	Gly	Ile	Glu	Pro	Asn	Thr	Ala	Thr	Pro	Asn	Met	Phe	Ser	
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tgg	ttc	ccc	atc	ttc	ttc	cca	ttg	aga	aaa	ccc	atc	tac	gtg	ccg	gaa	1824
Trp	Phe	Pro	Ile	Phe	Phe	Pro	Leu	Arg	Lys	Pro	Ile	Tyr	Val	Pro	Glu	
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Val	Trp	Tyr	Glu	Trp	Ala	Val	Thr	Thr	Pro	Thr	Pro	Ser	Pro	Ile	His	
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		35					40					45			
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Ala	Ser	Asp	Leu	Ile	Leu	Gly	Pro	Ala	Gln	Trp	Ser	Asn	His	Val	Val
65					70				75						80
Gly	Lys	Ile	Ser	Glu	Trp	Ile	Asp	Leu	Asp	Ser	Glu	Asp	Glu	Arg	Leu
			85						90					95	
Arg	Phe	Asp	Ser	Glu	Leu	Thr	Leu	Lys	Gln	Glu	Ile	Ala	Trp	Ala	Ser
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His	Val	Ser	Leu	Gln	Ala	Cys	Gly	Leu	Pro	Ala	Pro	Lys	Arg	Ser	Phe
		115					120					125			
Trp	Gly	Asn	Tyr	Ala	Arg	Val	Val	Asn	Gln	Ile	Leu	Gln	Gly	Leu	Thr
	130					135						140			
Asn	Met	His	Leu	Trp	Leu	Arg	Leu	Pro	Leu	Glu	Lys	Ser	Glu	Pro	Met
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Val	Asp	Ser	Trp	Glu	Leu	Trp	Asn	Ser	Phe	Arg	Leu	Leu	Cys	Asp	His
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Ser	Ser	Gln	Leu	Cys	Val	Ala	Leu	Asp	Ile	Leu	Ser	Thr	Leu	Pro	Ser
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Glu Gly Val Leu Ser Gly Asp Glu Ser Tyr Thr Glu Asp Ser His Val
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Arg His Ala Leu Thr Pro Tyr Leu Glu Tyr Ile Ala Tyr Leu Tyr Arg
          290          295          300
Lys Met Asp Pro Leu Pro Glu Gln Glu Arg Ile Glu Ile Asn Tyr Arg
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          310          315          320
Gln Thr Tyr Glu Thr Phe Glu Lys Asp Val Val Lys Tyr Thr Gln Tyr
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Arg Arg Ala Val Ala Lys Ala Leu Val Asp Arg Val Ala Asp Asp Ala
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Val Ser Thr Thr Arg Thr Val Leu Met Val Val Gly Ala Gly Arg Gly
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Pro Leu Val Arg Ala Ser Leu Gln Ala Ala Glu Glu Thr Gly Arg Lys
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Val Ser Glu Leu Leu Gly Ser Phe Gly Asp Asn Glu Leu Ser Pro Glu
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Cys Leu Asp Gly Ala Gln Arg Phe Leu Lys Pro Asp Gly Ile Ser Ile
465 Pro Ser Ser Tyr Thr Ser Phe Ile Gln Pro Ile Ile Ala Ser Lys Leu
          435          440          445
His Asn Asp Ile Lys Ala His Lys Asp Ile Ala His Phe Glu Thr Ala
          450          455          460
Tyr Val Val Lys Leu His Arg Ile Ala Thr Leu Ala Pro Pro Gln Gln
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 20 25 30
 Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Asp Xaa Xaa Xaa Xaa
 35 40 45
 Pro Leu Xaa Asp Pro Xaa Tyr Arg Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 50 55 60
 Xaa Xaa Xaa Xaa Val Leu Pro Xaa Xaa Xaa Ser Asp Leu Xaa Leu Xaa
 65 70 75 80
 Pro Xaa Gln Trp Ser Xaa His Val Val Gly Lys Ile Ser Xaa Trp Ile
 85 90 95
 Asp Leu Asp Xaa Glu Asp Glu Xaa Leu Arg Xaa Asp Ser Glu Xaa Thr
 100 105 110
 Leu Lys Gln Glu Ile Ala Trp Ala Xaa His Xaa Ser Leu Gln Ala Cys
 115 120 125
 Xaa Xaa Pro Xaa Pro Xaa Xaa Xaa Xaa Cys Xaa Asn Tyr Ala Arg Xaa
 130 135 140
 Val Asn Gln Ile Leu Gln Gly Xaa Xaa Xaa Xaa Xaa Leu Trp Leu Arg
 145 150 155 160
 Xaa Pro Leu Xaa Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Xaa Xaa
 165 170 175
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp Glu
 180 185 190
 Xaa Trp Asn Ser Phe Arg Leu Leu Cys Xaa His Xaa Ser Xaa Leu Xaa
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 Val Ala Leu Asp Xaa Leu Ser Thr Leu Pro Ser Xaa Xaa Ser Leu Xaa
 210 215 220
 Arg Trp Xaa Gly Glu Xaa Val Arg Ala Ala Ile Leu Xaa Thr Xaa Xaa
 225 230 235 240
 Phe Leu Thr Asn Xaa Xaa Gly Xaa Pro Cys Leu Ser Lys Arg His Gln
 245 250 255
 Xaa Leu Xaa Xaa Gly Phe Phe Xaa His Xaa Xaa Gln Xaa Xaa Ile Ser
 260 265 270
 Gly Xaa Xaa Xaa His Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser
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PF59082SeqList_PF59082.txt

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				325					330					335	
Pro	Leu	Gln	Pro	Leu	Met	Asp	Asn	Leu	Glu	Ala	Gln	Thr	Tyr	Glu	Thr
			340					345					350		
Phe	Glu	Xaa	Asp	Xaa	Val	Lys	Tyr	Xaa	Gln	Tyr	Xaa	Arg	Ala	Val	Xaa
		355				360						365			
Lys	Ala	Leu	Xaa	Asp	Arg	Val	Xaa	Asp	Xaa	Xaa	Xaa	Ser	Xaa	Xaa	Xaa
	370				375						380				
Xaa	Val	Leu	Met	Val	Val	Gly	Ala	Gly	Arg	Gly	Pro	Leu	Val	Arg	Ala
385				390						395					400
Ser	Leu	Gln	Ala	Ala	Glu	Glu	Thr	Xaa	Arg	Lys	Leu	Lys	Val	Tyr	Ala
			405						410					415	
Val	Glu	Lys	Asn	Pro	Asn	Ala	Val	Xaa	Thr	Leu	His	Xaa	Leu	Xaa	Lys
			420					425					430		
Xaa	Glu	Gly	Trp	Glu	Xaa	Xaa	Val	Thr	Xaa	Xaa	Ser	Xaa	Asp	Met	Arg
		435					440					445			
Xaa	Trp	Xaa	Ala	Pro	Glu	Xaa	Ala	Asp	Xaa	Leu	Val	Ser	Glu	Leu	Leu
	450				455						460				
Gly	Ser	Phe	Gly	Asp	Asn	Glu	Leu	Ser	Pro	Glu	Cys	Leu	Asp	Gly	Ala
465				470						475					480
Gln	Arg	Phe	Leu	Lys	Xaa	Asp	Gly	Ile	Ser	Ile	Pro	Ser	Ser	Tyr	Thr
			485						490					495	
Ser	Phe	Xaa	Gln	Pro	Xaa	Thr	Ala	Ser	Lys	Leu	Xaa	Asn	Asp	Xaa	Lys
			500					505					510		
Ala	His	Lys	Asp	Xaa	Xaa	His	Phe	Glu	Thr	Ala	Tyr	Val	Val	Lys	Xaa
		515					520					525			
His	Xaa	Xaa	Ala	Xaa	Leu	Ala	Pro	Xaa	Gln	Xaa	Val	Phe	Thr	Phe	Xaa
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His	Pro	Xaa	Xaa	Ser	Xaa	Xaa	Xaa	Asn	Gln	Arg	Tyr	Xaa	Lys	Leu	
545				550					555					560	
Xaa	Phe	Xaa	Xaa	Xaa	Xaa	Asp	Xaa	Gly	Ser	Xaa	Xaa	Val	His	Gly	Phe
			565						570					575	
Ala	Gly	Tyr	Phe	Asp	Xaa	Xaa	Leu	Tyr	Lys	Asp	Val	His	Leu	Gly	Ile
			580					585					590		
Glu	Pro	Xaa	Thr	Ala	Thr	Pro	Asn	Met	Phe	Ser	Trp	Phe	Xaa	Ile	Phe
		595					600					605			
Phe	Pro	Leu	Arg	Xaa	Pro	Xaa	Xaa	Val	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Glu
	610					615					620				
Val	His	Phe	Trp	Arg	Cys	Cys	Xaa	Xaa	Xaa	Lys	Val	Trp	Tyr	Glu	Trp
625				630						635					640
Xaa	Xaa	Xaa	Xaa	Pro	Xaa	Xaa	Ser	Pro	Xaa	His	Asn	Xaa	Asn	Gly	Arg
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Gly	Asp	Asn	Glu	Leu	Ser	Pro	Glu	Cys	Leu	Asp	Gly	Ala	Gln	Arg	Phe
		20						25					30		
Leu	Lys	Xaa	Asp	Gly	Ile	Ser	Ile	Pro	Ser	Ser	Tyr	Thr	Ser	Phe	Xaa
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Xaa	Pro	Xaa	Xaa	Ala	Ser	Lys									
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Leu	Arg	Xaa	Asp	Ser	Glu	Xaa	Thr	Leu	Lys	Gln	Glu	Ile	Ala	Trp	Ala
			20				25					30			
Xaa	His	Xaa	Ser	Leu	Gln	Ala	Cys	Xaa	Xaa	Pro	Xaa	Pro	Xaa	Xaa	Xaa
		35				40					45				
Xaa	Xaa	Xaa	Asn	Tyr	Ala	Arg	Xaa	Val	Asn	Xaa	Ile				
	50				55						60				

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Thr Asn Xaa Xaa Gly Xaa Pro Cys Leu Ser Lys Arg His Gln Xaa Leu
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Xaa Xaa His Xaa
          35

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<210> 1074

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Leu Gly Ile Glu Pro Xaa Thr Ala Thr Pro Asn Met Phe
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<223> Xaa in position 41 to 42 is any amino acid

<220>
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<222> (44)..(44)
<223> Xaa in position 44 is Asp, Pro or Thr

<220>
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<222> (45)..(47)
<223> Xaa in position 45 to 47 is any amino acid

<220>
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<222> (52)..(52)
<223> Xaa in position 52 is any amino acid

<220>
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<223> Xaa in position 55 is any amino acid

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Leu Xaa Xaa Asp Xaa Lys Ala His Lys Asp Xaa Xaa His Phe Glu Thr
1      5      10      15
Ala Tyr Val Val Lys Xaa His Xaa Xaa Ala Xaa Leu Ala Pro Xaa Gln
20      25      30
Xaa Val Phe Thr Phe Xaa His Pro Xaa Xaa Ser Xaa Xaa Xaa Xaa Asn
35      40      45
Gln Arg Tyr Xaa Lys Leu Xaa Phe

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<210> 1076
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<212> PRT
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<220>
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<222> (7)..(7)
<223> Xaa in position 7 is Ala or Gly

<220>
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<222> (8)..(8)
<223> Xaa in position 8 is Ala, Pro or Ser

<220>
<221> Variant
<222> (9)..(9)
<223> Xaa in position 9 is Ser or Thr

<400> 1076
His Phe Trp Arg Cys Cys Xaa Xaa Xaa Lys Val Trp Tyr Glu Trp
1 5 10 15

<210> 1077
<211> 20
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<220>
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<222> (4)..(4)
<223> Xaa in position 4 is any amino acid

<220>
<221> Variant
<222> (5)..(6)
<223> Xaa in position 5 to 6 is Asn or Thr

<220>
<221> Variant
<222> (7)..(7)
<223> Xaa in position 7 is Leu or Met

<220>
<221> Variant
<222> (8)..(8)
<223> Xaa in position 8 is any amino acid

<220>
<221> Variant
<222> (13)..(13)
<223> Xaa in position 13 is Leu or Val

<220>
<221> Variant
<222> (16)..(16)
<223> Xaa in position 16 is any amino acid

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<220>
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<222> (18)..(18)
<223> Xaa in position 18 is Pro or Ser

<220>
<221> Variant
<222> (19)..(19)
<223> Xaa in position 19 is Asp or Glu

<220>
<221> Variant
<222> (20)..(20)
<223> Xaa in position 20 is Asp, Gly or Pro

<400> 1077
Leu Gln Gly Xaa Xaa Xaa Xaa Xaa Leu Trp Leu Arg Xaa Pro Leu Xaa
1          5          10          15
Lys Xaa Xaa Xaa
          20

<210> 1078
<211> 19
<212> PRT
<213> Artificial sequence

<220>
<223> protein pattern

<220>
<221> Variant
<222> (3)..(3)
<223> Xaa in position 3 is Phe or Val

<220>
<221> Variant
<222> (4)..(4)
<223> Xaa in position 4 is Ala, Cys or Ser

<220>
<221> Variant
<222> (5)..(5)
<223> Xaa in position 5 is Ala or Gly

<220>
<221> Variant
<222> (9)..(9)
<223> Xaa in position 9 is Ile or Val

<220>
<221> Variant
<222> (11)..(11)
<223> Xaa in position 11 is Gly or Ser

<220>
<221> Variant
<222> (13)..(13)
<223> Xaa in position 13 is Ala or Ser

<220>
<221> Variant
<222> (17)..(17)
<223> Xaa in position 17 is Asn or Ser

<400> 1078
Leu Pro Xaa Xaa Xaa Ser Asp Leu Xaa Leu Xaa Pro Xaa Gln Trp Ser
1          5          10          15
Xaa His Val

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PF59082SeqList_PF59082.txt

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<210> 1079
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<212> PRT
<213> Artificial sequence

<220>
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<220>
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<222> (13)..(13)
<223> Xaa in position 13 is Asp or Glu

<220>
<221> Variant
<222> (15)..(15)
<223> Xaa in position 15 is any or no amino acid

<220>
<221> Variant
<222> (17)..(17)
<223> Xaa in position 17 is any amino acid

<220>
<221> Variant
<222> (18)..(18)
<223> Xaa in position 18 is any or no amino acid

<220>
<221> Variant
<222> (20)..(20)
<223> Xaa in position 20 is any amino acid

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Ser Trp Glu Xaa Trp Asn Ser Phe Arg Leu Leu Cys Xaa His Xaa Ser
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Xaa Xaa Leu Xaa Val Ala
          20

<210> 1080
<211> 22
<212> PRT
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<220>
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<222> (3)..(3)
<223> Xaa in position 3 is Ala or Pro

<220>
<221> Variant
<222> (10)..(10)
<223> Xaa in position 10 is any amino acid

<220>
<221> Variant
<222> (12)..(12)

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<223> Xaa in position 12 is Ile or Val

<220>

<221> Variant

<222> (13)..(13)

<223> Xaa in position 13 is any amino acid

<220>

<221> Variant

<222> (15)..(15)

<223> Xaa in position 15 is any or no amino acid

<220>

<221> Variant

<222> (17)..(20)

<223> Xaa in position 17 to 20 is any amino acid

<220>

<221> Variant

<222> (21)..(21)

<223> Xaa in position 21 is any or no amino acid

<400> 1080

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Xaa	Xaa	Xaa	Xaa	Xaa	Glu										
				20											

<210> 1081

<211> 21

<212> PRT

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<220>

<223> protein pattern

<220>

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<222> (3)..(3)

<223> Xaa in position 3 is any amino acid

<220>

<221> Variant

<222> (4)..(4)

<223> Xaa in position 4 is Asn or Thr

<220>

<221> Variant

<222> (7)..(7)

<223> Xaa in position 7 is Ala or Gly

<220>

<221> Variant

<222> (10)..(10)

<223> Xaa in position 10 is Phe or Met

<220>

<221> Variant

<222> (13)..(13)

<223> Xaa in position 13 is Pro or Ser

<220>

<221> Variant

<222> (20)..(20)

<223> Xaa in position 20 is any amino acid

<400> 1081

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1 5 10 15
Ala Ile Leu Xaa Thr
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<210> 1082
<211> 15
<212> PRT
<213> Artificial sequence

<220>
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<220>
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<223> Xaa in position 3 is Ile or Met

<220>
<221> Variant
<222> (6)..(6)
<223> Xaa in position 6 is Ser or Thr

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1 5 10 15

<210> 1083
<211> 1971
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<213> Arabidopsis thaliana

<220>
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1 5 10 15
aaa cca ttc cac aca tac act tta tca tct caa aca gac acc aca acc 96
Lys Pro Phe His Thr Tyr Thr Leu Ser Ser Gln Thr Asp Thr Thr Thr 20 25 30
cct tct tct tcc ggt gaa aca gcc att gat ggc gac gac cat ctc tct 144
Pro Ser Ser Ser Gly Glu Thr Ala Ile Asp Gly Asp Asp His Leu Ser 35 40 45
ctt caa caa cct ctt ttc ctc tgt cct tct tta cgt ctt aaa gct gac 192
Leu Gln Gln Pro Leu Phe Leu Cys Pro Ser Leu Arg Leu Lys Ala Asp 50 55 60
gag ata aac tat tct tat agt gaa att cta ccg ttc aat att tcc ccg 240
Glu Ile Asn Tyr Ser Tyr Ser Glu Ile Leu Pro Phe Asn Ile Ser Pro 65 70 75 80
tac ttc ccc agc ata aga ggc gct gat caa caa gtc cag cat ttg ctt 288
Tyr Phe Pro Ser Ile Arg Gly Ala Asp Gln Gln Val Gln His Leu Leu 85 90 95
gat tcc gac agc caa caa gtc cat gat ttg ctt cat tcc gac aac agc 336
Asp Ser Asp Ser Gln Gln Val His Asp Leu Leu His Ser Asp Asn Ser 100 105 110
cat gat gat gat ggt gat gaa atc tgt aag ctc cca gtt gtc cct atc 384
His Asp Asp Asp Gly Asp Glu Ile Cys Lys Leu Pro Val Val Pro Ile 115 120 125
tat tgg tgt aac agt aaa gaa att gag ttc gat caa ttc aat tgc ggt 432
Tyr Trp Cys Asn Ser Lys Glu Ile Glu Phe Asp Gln Phe Asn Cys Gly 130 135 140
gca tgt gaa cga tca aag att ggc aca gac tat tat atc tgt ctc acg 480
Ala Cys Glu Arg Ser Lys Ile Gly Thr Asp Tyr Tyr Ile Cys Leu Thr 145 150 155 160
tgt gat cta atg ttc cac aaa gaa tgc gtg gag tct ccc ctt gag atc 528
Cys Asp Leu Met Phe His Lys Glu Cys Val Glu Ser Pro Leu Glu Ile

PF59082SeqList_PF59082.txt

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			180					185					190			
gag	cag	ctc	atg	agt	tgc	atg	tgc	tgt	aaa	cac	cct	tcc	aat	ctt	att	624
Glu	Gln	Leu	Met	Ser	Cys	Met	Cys	Cys	Lys	His	Pro	Ser	Asn	Leu	Ile	
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ttt	tat	tat	tgt	ccc	acc	tac	aaa	ttg	agt	ttg	cat	ccc	gat	tgt	gcg	672
Phe	Tyr	Tyr	Cys	Pro	Thr	Tyr	Lys	Leu	Ser	Leu	His	Pro	Asp	Cys	Ala	
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Met	Lys	Pro	Ile	Ser	Ile	Phe	Ile	Asp	His	Pro	Lys	Arg	His	Pro	His	
225					230					235					240	
ctt	ctc	acc	ttt	ttt	ccc	aaa	caa	gct	tcc	tta	ctt	tgc	gat	gtt	tgt	768
Leu	Leu	Thr	Phe	Phe	Pro	Lys	Gln	Ala	Ser	Leu	Leu	Cys	Asp	Val	Cys	
				245					250					255		
agc	ctc	att	aaa	gaa	gct	ttc	ccc	acc	tat	gtg	tgt	ctt	cga	tgt	atc	816
Ser	Leu	Ile	Lys	Glu	Ala	Phe	Pro	Thr	Tyr	Val	Cys	Leu	Arg	Cys	Ile	
			260					265					270			
ttt	gta	gcc	cat	cga	gat	tgt	atc	tat	ttc	ccg	tat	gtc	att	aaa	ata	864
Phe	Val	Ala	His	Arg	Asp	Cys	Ile	Tyr	Phe	Pro	Tyr	Val	Ile	Lys	Ile	
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Cys	Arg	His	Gln	His	Arg	Ile	Ser	Phe	Thr	Ser	Ser	Leu	Pro	Ser	Gly	
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Lys	Trp	Ser	Cys	Gly	Val	Cys	Arg	Lys	Lys	Val	Asp	Asn	Asn	Cys	Gly	
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gca	tac	act	tgc	aac	aag	tgt	agc	cac	tat	ttt	gtt	cat	aca	aga	tgt	1008
Ala	Tyr	Thr	Cys	Asn	Lys	Cys	Ser	His	Tyr	Phe	Val	His	Thr	Arg	Cys	
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gcg	tta	cgg	gaa	gac	ttg	tgg	gat	gga	aag	gat	ctc	gag	gga	gta	cct	1056
Ala	Leu	Arg	Glu	Asp	Leu	Trp	Asp	Gly	Lys	Asp	Leu	Glu	Gly	Val	Pro	
			340				345					350				
gaa	gaa	cct	gaa	ata	att	ctc	gag	cca	ttt	gag	acg	ata	gct	gat	gga	1104
Glu	Glu	Pro	Glu	Ile	Ile	Leu	Glu	Pro	Phe	Glu	Thr	Ile	Ala	Asp	Gly	
		355					360					365				
ata	ata	ctc	cat	ttt	tct	cat	ggc	cat	cat	ctg	aaa	ctc	aag	acc	agt	1152
Ile	Ile	Leu	His	Phe	Ser	His	Gly	His	His	Leu	Lys	Leu	Lys	Thr	Ser	
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gga	gtt	tac	aac	gaa	aac	att	att	tgt	caa	gcg	tgc	atc	ctt	cca	atc	1200
Gly	Val	Tyr	Asn	Glu	Asn	Ile	Ile	Cys	Gln	Ala	Cys	Ile	Leu	Pro	Ile	
385				390				395							400	
tat	gag	ggt	aat	tat	tac	tcg	tgt	atg	gat	caa	tgc	aac	ttc	atc	ctc	1248
Tyr	Glu	Gly	Asn	Tyr	Tyr	Ser	Cys	Met	Asp	Gln	Cys	Asn	Phe	Ile	Leu	
				405				410						415		
cac	gaa	gca	tgt	gca	aat	gct	tct	cgc	aag	aaa	gat	cat	gcc	tta	cac	1296
His	Glu	Ala	Cys	Ala	Asn	Ala	Ser	Arg	Lys	Lys	Asp	His	Ala	Leu	His	
			420				425						430			
agt	cac	cca	ctt	acg	cta	aaa	gtt	gtc	tct	gat	ata	cag	aat	gaa	tac	1344
Ser	His	Pro	Leu	Thr	Leu	Lys	Val	Val	Ser	Asp	Ile	Gln	Asn	Glu	Tyr	
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Phe	Lys	Gly	Tyr	Phe	Arg	Cys	Ser	Ala	Cys	Asp	Arg	Glu	Ser	Cys	Gly	
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Phe	Ile	Tyr	Glu	Glu	Asp	Gln	Tyr	Ser	Ile	Asp	Ile	Arg	Cys	Ala	Ser	
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gtt	tct	gaa	cca	ttt	gat	tat	caa	ggc	cat	gag	cat	ccc	tta	ttc	caa	1488
Val	Ser	Glu	Pro	Phe	Asp	Tyr	Gln	Gly	His	Glu	His	Pro	Leu	Phe	Gln	
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gct	tta	gac	cga	aaa	gaa	gaa	agg	gag	gca	att	tgt	caa	att	tgc	cga	1536
Ala	Leu	Asp	Arg	Lys	Glu	Glu	Arg	Glu	Ala	Ile	Cys	Gln	Ile	Cys	Arg	
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Lys	Lys	Tyr	Gly	Arg	Lys	Leu	Asn	Cys	Ile	Glu	Cys	Asn	Tyr	Ile	Ile	
		515					520					525				
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Lys His Phe Leu Thr	Phe Arg Glu Gly Glu Glu Gly Ser Asp Gln Leu	540		
545	gac tgg tgt gag gta tgc	550	gaa aag aaa tta gaa tac tca aga gaa ggt	1728
Asp Trp Cys Glu Val Cys	Glu Lys Lys Leu Glu Tyr Ser Arg Glu Gly	555		
565	ggg ttc tat gcg tgt gat gac tgc tgc acc act ctc cat gtt gat tgt	570		1776
Gly Phe Tyr Ala Cys Asp	Asp Cys Cys Thr Thr Leu His Val Asp Cys	575		
580	ttg ctt gga aaa gag atg tat atg ttg aat cct ggt cat act gta atg	585		1824
Leu Leu Gly Lys Glu Met Tyr Met Leu Asn Pro Gly His Thr Val Met		590		
595	gct tat agg tca aac att tat att ctt ccc aac aat acc atg act cga	600		1872
Ala Tyr Arg Ser Asn Ile Tyr Ile Leu Pro Asn Asn Thr Met Thr Arg		605		
610	cca ttc tgc caa ctt cat aaa gaa gat cgt tgt cca cac aaa gta att	620		1920
Pro Phe Cys Gln Leu His Lys Glu Asp Arg Cys Pro His Lys Val Ile		625		
625	ttc aat tgg cat gac atg aca ttt tgc tct tac agt tgt tcg atg gat	635		1968
Phe Asn Trp His Asp Met Thr Phe Cys Ser Tyr Ser Cys Ser Met Asp		640		
645	tag	650		1971

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<400> 1084

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Leu Gln Gln Pro Leu Phe Leu Cys Pro Ser Leu Arg Leu Lys Ala Asp	50	55	60	
Glu Ile Asn Tyr Ser Tyr Ser Glu Ile Leu Pro Phe Asn Ile Ser Pro	65	70	75	80
Tyr Phe Pro Ser Ile Arg Gly Ala Asp Gln Gln Val Gln His Leu Leu	85	90	95	
Asp Ser Asp Ser Gln Gln Val His Asp Leu Leu His Ser Asp Asn Ser	100	105	110	
His Asp Asp Asp Gly Asp Glu Ile Cys Lys Leu Pro Val Val Pro Ile	115	120	125	
Tyr Trp Cys Asn Ser Lys Glu Ile Glu Phe Asp Gln Phe Asn Cys Gly	130	135	140	
Ala Cys Glu Arg Ser Lys Ile Gly Thr Asp Tyr Tyr Ile Cys Leu Thr	145	150	155	160
Cys Asp Leu Met Phe His Lys Glu Cys Val Glu Ser Pro Leu Glu Ile	165	170	175	
Lys His Pro Ser Tyr Pro Phe Leu Ser Leu Lys Leu Tyr Thr Arg His	180	185	190	
Glu Gln Leu Met Ser Cys Met Cys Cys Lys His Pro Ser Asn Leu Ile	195	200	205	
Phe Tyr Tyr Cys Pro Thr Tyr Lys Leu Ser Leu His Pro Asp Cys Ala	210	215	220	
Met Lys Pro Ile Ser Ile Phe Ile Asp His Pro Lys Arg His Pro His	225	230	235	240
Leu Leu Thr Phe Phe Pro Lys Gln Ala Ser Leu Leu Cys Asp Val Cys	245	250	255	
Ser Leu Ile Lys Glu Ala Phe Pro Thr Tyr Val Cys Leu Arg Cys Ile	260	265	270	
Phe Val Ala His Arg Asp Cys Ile Tyr Phe Pro Tyr Val Ile Lys Ile	275	280	285	
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PF59082SeqList_PF59082.txt

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290          295          300
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305 Ala Tyr Thr Cys Asn 310 Lys Cys Ser His Tyr Phe Val His Thr Arg Cys
Ala Leu Arg Glu 325 Leu Trp Asp Gly 330 Lys Asp Leu Glu Gly Val Pro
Glu Glu Pro Glu Ile Ile Leu Glu 345 Pro Phe Glu Thr Ile Ala Asp Gly
Ile Ile 355 Leu His Phe Ser His 360 Gly His His Leu Lys 365 Leu Lys Thr Ser
Gly Val Tyr Asn Glu Asn 375 Ile Ile Cys Gln Ala Cys Ile Leu Pro Ile
385 Tyr Glu Gly Asn Tyr 390 Ser Cys Met Asp Gln Cys Asn Phe Ile Leu
His Glu Ala Cys 405 Asn Ala Ser Arg 410 Lys Lys Asp His Ala Leu His
Ser His Pro Leu Thr Leu Lys Val 425 Val Ser Asp Ile Gln Asn Glu Tyr
Phe Lys 435 Gly Tyr Phe Arg Cys 440 Ser Ala Cys Asp Arg Glu Ser Cys Gly
Phe Ile Tyr Glu Glu Asp Gln Tyr Ser Ile Asp 450 Ile Arg Cys Ala Ser
465 Val Ser Glu Pro Phe 470 Asp Tyr Gln Gly His 475 Glu His Pro Leu Phe Gln
Ala Leu Asp Arg 485 Lys Glu Glu Arg Glu 490 Ala Ile Cys Gln Ile Cys Arg
Lys Lys Tyr Gly Arg Lys Leu Asn Cys Ile Glu Cys Asn Tyr Ile Ile
Cys Phe 500 Ser Cys Ala Thr Leu 510 Pro Tyr Lys Ala Lys Tyr Lys Leu Asp
Lys His Phe Leu Thr Phe Arg Glu Gly Glu Glu 520 Glu Gly Ser Asp Gln Leu
545 Asp Trp Cys Glu Val 535 Cys Glu Lys Lys Leu Glu Tyr Ser Arg Glu Gly
Gly Phe Tyr Ala Cys Asp Asp Cys Cys Thr Thr Leu His Val Asp Cys
Leu Leu Gly Lys Glu Met Tyr Met Leu Asn Pro Gly His Thr Val Met
Ala Tyr Arg Ser Asn Ile Tyr 600 Ile Leu Pro Asn Asn Thr Met Thr Arg
610 Pro Phe Cys Gln Leu His Lys Glu Asp Arg Cys Pro His Lys Val Ile
625 Phe Asn Trp His Asp 630 Met Thr Phe Cys Ser Tyr Ser Cys Ser Met Asp
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ccg aat tgg cat cag cat aca ctt gct ctc ttt cct aga caa gct ttc      96
Pro Asn Trp His Gln His Thr Leu Ala Leu Phe Pro Arg Gln Ala Phe
20
tta act tgc aat gtg tgc gcc ttg gcc gat gca agc tct cct atc tat      144
Leu Thr Cys Asn Val Cys Ala Leu Ala Asp Ala Ser Ser 45 Pro Ile Tyr
35
atg tgt ccc cct tgt gat ttt gtg gtc cat cta aga tgt atc aac tta      192
Met Cys Pro Pro Cys Asp Phe Val Val His Leu Arg Cys Ile Asn Leu
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cca cgt gtc ata agg ata tct cgc cac ccc cat cgc atc tct ttt acc      240
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Pro	Leu	Phe	Asp	Gln 85	Arg	Asp	Arg	Ser	Cys 90	Gly	Val	Cys	Arg	Glu 95	Thr	
atc	gac	aac	gat	ttt	ggg	ggg	tat	tct	tgc	atc	aag	gat	gat	tgt	tcg	336
Ile	Asp	Asn	Asp	Phe	Gly	Gly	Tyr	Ser	Cys	Ile	Lys	Asp	Asp	Cys	Ser	
tac	gga	gca	cat	tca	aga	tgt	gcc	aca	caa	aga	aat	gtg	tgg	gat	ggc	384
Tyr	Gly	Ala	His	Ser	Arg	Cys	Ala	Thr	Gln	Arg	Asn	Val	Trp	Asp	Gly	
ata	gag	ctt	gaa	ggg	gtg	tta	gaa	gag	att	gaa	gaa	gaa	ggt	gag	ccg	432
Ile	Glu	Leu	Glu	Gly	Val	Leu	Glu	Glu	Ile	Glu	Glu	Glu	Val	Glu	Pro	
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Phe 145	Val	Thr	Ile	Ser	Asp 150	Gly	Ile	Ile	Gln	His 155	Phe	Ser	His	Gln	Gln 160	
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His	His	Leu	Arg	Leu 165	Asp	Glu	Asn	Lys	Asp 170	Arg	Asp	Tyr	Asp	Asp 175	Ser	
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Ser	Cys	Ile	Gln	Cys	Ser	Phe	Ile	Leu	His	Glu	Glu	Cys	Ala	Asn	Leu	
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Ser	Arg	Lys	Ile	His	His	Pro	Ile	His	Pro	Pro	Met	Leu	Ser	Leu	Val	
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Pro	Trp	Ser	Cys	Ile 245	Ala	Gly	Phe	Phe	Tyr	Val	Cys	Asp	Lys	Glu	Gly 255	
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Glu	Gln	Arg	Gly	Cys	Ser	Val	Cys	Lys	Asp	Ser	Arg	Leu	Glu	Cys	Thr	
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Asp	Glu	Tyr	Cys	Cys	Val	Thr	Leu	His	Ile	Arg	Cys	Leu	Ile	Gly	Lys	
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Lys	Leu	Phe	Val	Leu	Pro	Asn	Asn	His	Met	Ser	Arg	Pro	Ser	Cys	Thr	
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Gly	Cys	Arg	Lys	Arg	Cys	Pro	Tyr	Lys	Thr	Val	Leu	Val	Leu	Ile	Arg	
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Phe Val Thr Ile Ser Asp Gly Ile Ile Gln His Phe Ser His Gln Gln
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Pro Trp Ser Cys Ile Ala Gly Phe Phe Tyr Val Cys Asp Lys Glu Gly
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Lys Asp Ser Pro Val Leu Val Leu Tyr Pro Leu Asp Glu Arg Lys Val	
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Leu Arg Ser Thr His Thr Ser Ser Ser His Pro Leu Val Trp Cys Asn	
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Asn Gly Glu Asn Lys Asp Lys Tyr Cys Lys Arg Glu Ser Arg Cys Arg	
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Tyr Tyr Tyr Cys Thr Thr Cys Glu Val Thr Phe His Asn Gly Cys His	
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Tyr Glu Phe Val Asp Ile Val Pro Tyr Lys Ser Asp Ile Ile Phe Asn	
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Lys Cys Thr Trp Cys Ala Lys Asp Phe Lys Gly Asp Trp Phe Tyr Arg	
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Cys Leu Ile Cys Ser Phe Cys Leu Asp Leu Ser Cys Ala Ala Thr Leu	
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Pro Leu Leu Thr Ile Thr Asn Pro Lys Ser His His His Ser Leu Val	
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Phe Leu Pro Arg Pro Leu Leu Val Pro Cys Asp Ala Cys Gly Leu Val	
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Asp Gly Leu Glu Pro Ser Tyr Ala Cys Phe Gln Cys Asn Tyr Met Val	
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His Gln Asn Cys Ile Asp Leu Pro Arg Val Ile Lys Ile Thr Arg His	
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Pro His Arg Leu Ser His Thr Pro Tyr Cys Ser Ser Leu Thr Ser Ser	
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Cys Gln Ile Cys Tyr Lys Glu Val Asp Ile Lys Tyr Gly Gln Tyr Ser	
245 250 255	
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Cys His Leu Gln Asp Cys Phe Tyr Val Val His Ser Lys Cys Ala Thr	
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His Glu Asn Val Trp Asp Gly Lys Glu Leu Glu Trp Glu Ile Glu Ser	
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Asp Glu Thr Glu Asp Ile Ser Pro Phe Arg Asn Leu Gly Asp Gly Phe	
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Ile Lys His Phe Cys His Lys His Arg Leu Lys Leu Lys Asn His Asp	
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Val	Ser	His	Gln	Phe	Tyr	His	Cys	Lys	Lys	Cys	Asn	Tyr	Ser	Leu	His		
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Glu	Val	Cys	Ala	Gly	Leu	Ser	Arg	Lys	Leu	Asp	His	Ala	Leu	His	Asn		
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cac	act	ctt	atc	cta	tct	cca	tct	ccc	gga	aag	ttt	tgt	tgt	tca	gct		1152
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Cys	Ser	Arg	Glu	Ser	Thr	Gly	Phe	Ser	Tyr	Ile	Cys	Ser	Asn	Lys	Gly		
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Cys	Gln	Asp	Phe	Val	Leu	Asp	Val	Arg	Cys	Ile	Ser	Val	Leu	Glu	Tyr		
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Phe	Ile	His	Arg	Ser	His	Glu	His	Pro	Ile	Phe	Ile	Ser	Thr	Ser	Tyr		
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Asn	Ser	Lys	Asp	Glu	Ile	Leu	Cys	Lys	Val	Cys	Lys	Lys	Arg	Cys	Leu		
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Leu	Thr	Leu	Ser	Cys	Gly	Glu	Ser	Ala	Asp	Asn	Thr	Tyr	Trp	Cys	Glu		
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Lys	Cys	Cys	Ile	Thr	Ile	His	Leu	His	Cys	Ile	Phe	Gly	Ser	Ser	Val		
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Thr	Tyr	Tyr	Tyr	Asn	His	Ser	Asn	Arg	Ser	Thr	His	Arg	Met	Ile	Phe		
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Cys	Ser	Leu	Glu	Cys	Glu	Ile	Leu	Gly	Met	Arg	Lys	Arg	Arg	Leu	Ile		
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Tyr	Glu	Phe	Val	Asp	Ile	Val	Pro	Tyr	Lys	Ser	Asp	Ile	Ile	Phe	Asn
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Pro	Leu	Leu	Thr	Ile	Thr	Asn	Pro	Lys	Ser	His	His	His	Ser	Leu	Val
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Phe	Leu	Pro	Arg	Pro	Leu	Leu	Val	Pro	Cys	Asp	Ala	Cys	Gly	Leu	Val
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Cys	Gln	Ile	Cys	Tyr	Lys	Glu	Val	Asp	Ile	Lys	Tyr	Gly	Gln	Tyr	Ser
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Thr Thr Cys Asn Leu Ser Met His Pro Val Cys Ala Met Arg Pro Val
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Pro Leu Val Val Asp His Pro Lys Ser His Pro His Pro Leu Ser Phe
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His Leu Asp Pro Thr Tyr Ile Cys Ile Gln Cys Val Phe Val Ile His
115      120      125
aaa ggt tgt atg ggt ttc cca cat acc ata aga ata tct cgt cac cct      432
Lys Gly Cys Met Gly Phe Pro His Thr Ile Arg Ile Ser Arg His Pro
130      135      140
cac cgt atc tct ttt acc tct tcc ctt cca tct aga acg ctg tct tgt      480
His Arg Ile Ser Phe Thr Ser Ser Leu Pro Ser Arg Thr Leu Ser Cys
145      150      155      160
gga gtc tgt cat caa caa gtt gac aac aat tat ggt gca tac tct tgc      528
Gly Val Cys His Gln Gln Val Asp Asn Asn Tyr Gly Ala Tyr Ser Cys
165      170      175
aat aat tgt gac ggt tat ttt gtt cat tca aaa tgt gca ata cat cca      576
Asn Asn Cys Asp Gly Tyr Phe Val His Ser Lys Cys Ala Ile His Pro
180      185      190
aaa gtg tgg gat gga aaa gaa ctc gaa gga gta cca gaa gaa gat gat      624
Lys Val Trp Asp Gly Lys Glu Leu Glu Gly Val Pro Glu Glu Asp Asp
195      200      205
ttg ata gac gat ggt gag ccg ttc gag agg ata tct gat gga att ata      672
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His His Pro Phe His Ser His His Leu Arg His Glu Met Ser Ile Thr
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Tyr Asp Glu Ser Lys Tyr Cys Gln Gly Cys Ala Leu Pro Ile Tyr Glu
245      250      255
ggt cag ttt tat tca tgc atg gaa tgt gac ttc atc ctc cat gac agt      816
Gly Gln Phe Tyr Ser Cys Met Glu Cys Asp Phe Ile Leu His Asp Ser
260      265      270
tgt gca aat gct cca cgg atg aaa cgg tat cct tta tat cca cat cca      864
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 Asn Asn Cys Asp Gly Tyr Phe Val His Ser Lys Cys Ala Ile His Pro
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 His Arg Gly Cys His Ile Phe Leu Pro Glu Ile Arg His Pro Phe His
 65 70 75 80
 Pro Ser His Pro Leu Thr Phe Ile Ser Leu Leu Leu Pro Lys Phe Asp
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 Val Thr Lys Ile Pro Lys Asn Trp Met Asp Ser Ser Ser Ser Ser Asp
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 Glu Ser Glu Asp Asp Asp Asp Glu Lys Ser Ile Lys Glu Glu Cys
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 Glu Asp Asp Gly Asp Asp Asp Asp Gly Asp Ser Ser Asp Ser Asp Asp
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 Asp Asp Asn Asn Phe Asp Ala Asn Asn Asp Gly Ala Ser Leu Ser Asp
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 Gly Asn His Leu Lys Cys Lys Cys Cys Gln Val Pro Leu Glu Lys Ile
 165 170 175
 Tyr Tyr His Cys Ser Ile Cys Lys Phe Asn Leu Asn Val Glu Cys Ser
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 Ile Leu Thr Leu Phe Pro Ile Arg Leu Pro Leu Pro Cys Gly Ala Cys
 210 215 220
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 225 230 235 240
 Cys Asn Leu Leu Val His Arg Ser Cys Ile Tyr Leu Pro Arg Val Ile
 245 250 255
 Lys Ile Thr Arg His Pro His Arg Leu Ser Leu Thr Pro Ser Leu Gln
 260 265 270
 Pro Gly Asp Phe Ser Cys Gly Val Cys Arg Gln Thr Val Asp Val Asn
 275 280 285
 Tyr Gly Gln Tyr Ser Cys Asp Lys Glu Cys His Tyr Ala Val His Ser
 290 295 300
 Lys Cys Ala Thr Arg Asn Asp Val Trp Asp Gly Lys Asp Leu Asp Gly
 305 310 315 320
 Val Pro Glu Glu Pro Asp Glu Phe Ile Glu Pro Pro Phe Leu Lys Ile
 325 330 335
 Asp Glu Glu Thr Ile Gln His Phe Ser His His His His Leu Lys Leu
 340 345 350
 His Glu Lys Lys Thr Ile Gly Gly Lys Asp Lys Phe Cys Glu Ala Cys
 355 360 365
 Thr Leu Pro Val Met Ile Ser Gln Arg Tyr Tyr Gly Cys Met Gln Cys
 370 375 380
 Asp Phe Val Leu Asp Glu Thr Cys Ala Ser Leu Pro Arg Lys Lys Asn
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 His Pro Leu His Lys His Pro Leu Asn Leu His Ile Leu Pro Leu Gly
 405 410 415
 Glu Ser Ala Met Ile Asn Lys Gly Ala Thr Ser Lys Asp Ile Phe Gln
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 Cys Ile Gly Cys Gly Arg Ile Gly Cys Gly Phe Phe Tyr Lys Cys Asp
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 Glu Lys Asp Cys Asp Glu Phe Leu Leu Asp Val Arg Cys Ala Ser Leu
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Pro Asp Pro Phe Val His Asp Cys His Pro His Asp His Pro Leu Phe
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 Phe Asn Leu Thr Lys Gly Asn Cys Met Gly Cys Gly Ser Asp Asn Cys
 Ser Ser Tyr Phe Leu Glu Cys Ile Lys Cys Lys Ser Phe Leu Gly Ile
 Lys Cys Ala Thr Leu Pro Cys Glu Ala His Tyr Ile His Asp Arg His
 Pro Ile Thr Leu Cys Tyr Gly Glu Glu Asp Thr Thr Ser Gly Gln Tyr
 Trp Cys Glu Ile Cys Glu Leu Lys Leu Asp Pro Lys Thr Trp Phe Tyr
 Ser Cys Asp Phe Cys Lys Ile Thr Leu His Val Asn Cys Leu Leu Gly
 Glu Asp Ile Tyr Leu Lys Pro Cys His Ile Phe Lys Val Gly Leu Tyr
 Tyr Lys Glu Val Glu Ile Ala Arg Asn Asp Gly Asn Ser Arg Leu Phe
 Cys Tyr Thr Cys Glu Leu Arg Cys Gly Gln Thr Leu Val Phe Lys Tyr
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 Ser Asp Pro Ala Gln Pro His Lys Leu Cys Arg Arg Arg Arg Arg Ser
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 cac ggt cca ctt tct atc tgc ttt tcg tgc aaa ggc aag cat tta gag 144
 His Gly Pro Leu Ser Ile Cys Phe Ser Cys Lys Gly Lys His Leu Glu
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 Gly Arg Lys Tyr Tyr Tyr Tyr Cys Ala Thr Cys Lys Leu Glu Phe His
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 aga ggc tgt cac ctc ctt ccg gtg ata aga cac cct ttt cac ccc 240
 Arg Gly Cys His Leu Leu Pro Pro Val Ile Arg His Pro Phe His Pro
 65 70 75 80
 tct cac ctt ctc acc ctc atc tcc tta cca cct ggt ttt gat att tct 288
 Ser His Leu Leu Thr Leu Ile Ser Leu Pro Pro Gly Phe Asp Ile Ser
 85 90 95
 aag ata ccc cgc aat acc gac gac ggc tcc gcg gct tca gaa aga tcg 336
 Lys Ile Pro Arg Asn Thr Asp Asp Gly Ser Ala Ala Ser Glu Arg Ser
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 Ile Asn Glu Thr Asp Asp Asp Asp Ser Glu Asp Gly Gly His Asp
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 gat gaa gat aac aat ttt gtt gac gat gat gtt att gtt aat gat ggt 432
 Asp Glu Asp Asn Asn Phe Val Asp Asp Asp Val Ile Val Asn Asp Gly
 130 135 140
 gat ggt gtt ggt gaa gat cgt gat ggt gac agt gat ggg gat ggt gat 480
 Asp Gly Val Gly Glu Asp Arg Asp Gly Asp Ser Asp Gly Asp Gly Asp
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ata Ile	cga Arg	ctc Leu	cct Pro	tca Ser	cca Pro	tgt Cys	gat Asp	gct Ala	tgt Cys	ggg Gly	ttg Leu	tct Ser	cta Leu	agc Ser	gac Asp																																	
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acc Thr	ata Ile	gac Asp	ctc Leu	atc Ile	tac Tyr	gct Ala	tgt Cys	ctc Leu	cct Pro	tgc Cys	agc Ser	cac His	atg Met	atc Ile	cat His																																	
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gca Ala	tgt Cys	gct Ala	tct Ser	ctt Leu	cct Pro	cgg Arg	aaa Lys	ata Ile	tac Tyr	aac Asn	cca Pro	cta Leu	cat His	aaa Lys	cac His																																	
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cct Pro	ctt Leu	acc Thr	ctc Leu	cag Gln	ccc Pro	ttc Phe	cct Pro	att Ile	gat Asp	gag Glu	aca Thr	tcc Ser	aat Asn	atc Ile	gca Ala																																	
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His Tyr Lys His Asp Arg His Pro Leu Ile Leu Cys Arg Asp Glu Asp			
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Thr Ser Ser Gly Leu Tyr Trp Cys Glu Ile Cys Glu Ser Glu Leu Asp			
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Pro Lys Thr Trp Phe Tyr Thr Cys Asp Phe Cys Thr Ile Thr Leu His			
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Gly Asn Ser Arg Leu Phe Cys Thr Arg Cys Lys Arg His Cys Met Gln			
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Asn Leu Ile Tyr Lys Arg Ile Gly Arg Asp Gln Ser Tyr Cys Thr Leu			
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Lys Ile Pro Arg Asn Thr Asp Asp Gly Ser Ala Ala Ser Glu Arg Ser	
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Ile Asn Glu Thr Asp Asp Asp Asp Ser Glu Asp Gly Gly His Asp	
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Asp Gly Val Gly Glu Asp Arg Asp Gly Asp Ser Asp Gly Asp Gly Asp	
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Gly Gly Asp Asp Asp Asp Asp Asp Phe Gln Gln Asp Ile Tyr Tyr	
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Arg Val Asn Gly Tyr Asp Tyr Tyr Tyr Asn Asn Tyr Asp Asp Gly Asp	
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Asn Ala Ala Tyr Ala Ser Ile Ser Asp Gly Asn Asp His Arg Lys Cys	
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Lys Cys Cys Gln Asp Pro Leu Lys Lys Val His Tyr His Cys Ser Ile	
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Cys Lys Phe Asn Leu Asn Leu Ser Cys Ser Met Arg Pro Pro Pro Pro	
225 230 235 240	
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PF59082SeqList_PF59082.txt

Thr Ile Asp Leu Ile Tyr Ala Cys Leu Pro Cys Ser His Met Ile His
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 305 310 315 320
 Gly Val Cys Arg Gln Thr Val Asp Ile Asn Tyr Gly His Tyr Ser Cys
 325 330 335
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 Glu Asp Ile Glu Pro Phe Val Arg Ile Asp Glu Glu Thr Ile Gln His
 370 375 380
 Phe Ser His His Glu His Tyr Met Lys Leu His Glu Lys Glu Thr Ile
 385 390 395 400
 Ser Glu Lys Asp Lys Phe Cys Glu Ala Cys Thr Leu Pro Val Met Ile
 405 410 415
 Ser Gln Arg Tyr Tyr Gly Cys Thr Glu Cys Asp Phe Val Leu Asp Glu
 420 425 430
 Ala Cys Ala Ser Leu Pro Arg Lys Ile Tyr Asn Pro Leu His Lys His
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 Pro Leu Thr Leu Gln Pro Phe Pro Ile Asp Glu Thr Ser Asn Ile Ala
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 Asp Asn Ile Ser Thr Lys Gly Ile Phe Glu Cys Asp Gly Cys His Arg
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 485 490 495
 Arg Leu Asp Val Arg Cys Ala Ser Leu Pro Asp Pro Phe Ile His Asp
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 Cys His Pro His Asp Leu Phe Phe Asn Ser Thr Lys Gly Asn Cys Ile
 515 520 525
 Gly Cys Gly Ser Asp Glu Cys Ser Ser Tyr Phe Leu Glu Cys Ile Lys
 530 535 540
 Cys Asn Ser Phe Leu Gly Ile Arg Cys Ala Ser Leu Pro Phe Glu Ala
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 His Tyr Lys His Asp Arg His Pro Leu Ile Leu Cys Arg Asp Glu Asp
 565 570 575
 Thr Ser Ser Gly Leu Tyr Trp Cys Glu Ile Cys Glu Ser Glu Leu Asp
 580 585 590
 Pro Lys Thr Trp Phe Tyr Thr Cys Asp Phe Cys Thr Ile Thr Leu His
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 Val Asn Cys Leu Leu Gly Lys Asp Met Tyr Met Lys Pro Gln Tyr Ile
 610 615 620
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 Gly Asn Ser Arg Leu Phe Cys Thr Arg Cys Lys Arg His Cys Met Gln
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<212> DNA

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 Thr Lys Pro Pro Cys Arg Leu Ser Asp Pro Ala Gln Pro His Lys Leu
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48

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Cys	Lys	Gly	Lys	His	Leu	Lys	Arg	Ser	Lys	Tyr	Tyr	Tyr	Tyr	Cys	Ala	
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Thr	Cys	Asn	Leu	Glu	Phe	His	Arg	Gly	Cys	His	Val	Phe	Leu	Pro	Glu	
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tcc	gct	tca	gag	gaa	tct	tcc	gaa	gag	ttg	ata	aac	gaa	ggt	gac		384
Ser	Ala	Ser	Glu	Glu	Ser	Ser	Glu	Glu	Leu	Ile	Asn	Glu	Val	Val	Asp	
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Tyr	Asp	His	Glu	Asp	Ala	Gly	Asp	Asp	Ala	Val	Ala	Asn	Glu	Asp	Asp	
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gat	gaa	gat	gct	ggt	cct	aat	gat	gac	gat	aat	ggc	ggt	ggc	ggt	ggc	480
Asp	Glu	Asp	Ala	Val	Pro	Asn	Asp	Asp	Asp	Asn	Gly	Gly	Gly	Gly	Gly	
145					150					155					160	
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Asp	Ile	Tyr	Ala	Val	Ala	Tyr	Asn	Asp	Gly	Ala	Ser	Leu	Ser	Tyr	Gly	
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aat	cac	ctg	aaa	tgc	aaa	tgt	tgt	gct	tct	cct	tta	gaa	aag	cta	tat	576
Asn	His	Leu	Lys	Cys	Lys	Cys	Cys	Ala	Ser	Pro	Leu	Glu	Lys	Leu	Tyr	
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Tyr	His	Cys	Ser	Thr	Cys	Lys	Phe	Asn	Leu	Asn	Leu	Thr	Cys	Ser	Met	
		195					200					205				
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Arg	Pro	Pro	Pro	Thr	Thr	Ile	Ser	His	Leu	Lys	Phe	His	Glu	His	Thr	
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ttt	ctt	cta	aac	aaa	gac	acc	gac	gat	ctc	ggt	tac	gct	tgt	cta	cct	768
Phe	Leu	Leu	Asn	Lys	Asp	Thr	Asp	Asp	Leu	Val	Tyr	Ala	Cys	Leu	Pro	
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tgc	agc	ctt	atg	gtc	cac	aga	tca	tgt	atc	tat	cta	cct	cgt	gtc	att	816
Cys	Ser	Leu	Met	Val	His	Arg	Ser	Cys	Ile	Tyr	Leu	Pro	Arg	Val	Ile	
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Lys	Ile	Thr	Arg	His	Pro	His	Arg	Leu	Ser	Leu	Thr	Ser	Ser	Leu	Gln	
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Cys	Gly	Gln	Tyr	Ser	Cys	Asp	Lys	Gly	Cys	Gln	Tyr	Ala	Ile	His	Ser	
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Lys	Cys	Ala	Thr	Trp	Arg	Asp	Val	Trp	Asp	Gly	Ile	Asp	Leu	Asp	Gly	
				325					330					335		
gtg	cct	gaa	gaa	ccc	gag	gag	tat	atc	gaa	ccg	cca	ttc	ctg	aag	att	1056
Val	Pro	Glu	Glu	Pro	Glu	Glu	Tyr	Ile	Glu	Pro	Pro	Phe	Leu	Lys	Ile	
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gat	gag	gac	aca	att	caa	cat	ttc	agt	cat	cat	gag	cat	tat	atg	aag	1104
Asp	Glu	Asp	Thr	Ile	Gln	His	Phe	Ser	His	His	Glu	His	Tyr	Met	Lys	
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PF59082SeqList_PF59082.txt

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Tyr	Asn	Pro	Leu	His	Lys	His	Pro	Leu	Thr	Leu	His	Val	Val	Pro	Thr	
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att	gac	acc	tac	acg	gac	ccg	aat	atg	cct	att	acc	aaa	gtc	ata	ttc	1344
Ile	Asp	Thr	Tyr	Thr	Asp	Pro	Asn	Met	Pro	Ile	Thr	Lys	Val	Ile	Phe	
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Cys Phe Thr Cys Lys Gly Lys Asn Leu Thr Cys Arg Lys Tyr Tyr Tyr
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 Ala Gln Tyr Trp Cys Asp Ile Cys Glu Ala Lys Leu Asp Ala Glu Glu
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 Trp Phe Tyr Thr Cys Asn Asp Tyr Cys Asn Val Thr Val His Val Ser
 595 600 605
 Cys Leu Leu Gly Asn Pro Ile Phe Leu Lys Pro Thr Ser Phe Tyr Ile
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Thr Lys Ser Pro Thr Ser Ser His Lys Thr Ala Ser His Asp Leu Leu
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Ile His Glu Ile Cys Ala Lys Asp Arg Arg Arg Ile Gln His Ala Leu
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Glu Ser His Ile Pro Leu Asn Cys Ile Lys Cys Asp Phe Val Val Cys
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Asn	Ile	Ala	Cys	Val	Glu	Lys	Leu	Pro	Leu	Leu	Ser	Ile	His	His	Pro	
		275					280					285				
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Lys	Trp	His	Glu	His	Thr	Leu	Ser	Leu	Phe	Pro	Ile	Leu	Ile	Ser	Leu	
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Thr	Cys	Asn	Val	Cys	Ala	Leu	Asp	His	Phe	Asn	Cys	Pro	Phe	Tyr	Ile	
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Cys	Ser	Pro	Cys	Asp	Phe	Val	Val	His	Gln	Ser	Cys	Ile	Thr	Leu	Pro	
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cgt	gtt	ata	agg	ata	tct	cgc	cat	ctc	cac	cgt	att	tcc	ttt	acc	cct	1056
Arg	Val	Ile	Arg	Ile	Ser	Arg	His	Leu	His	Arg	Ile	Ser	Phe	Thr	Pro	
			340				345						350			
tca	ttt	gaa	caa	gga	gat	tgg	tct	tgt	ggg	gta	tgt	cgc	aaa	aaa	atc	1104
Ser	Phe	Glu	Gln	Gly	Asp	Trp	Ser	Cys	Gly	Val	Cys	Arg	Lys	Lys	Ile	
		355				360						365				
gac	aat	gat	tgt	ggg	ggg	tat	tct	tgc	gga	aac	agc	ggg	tgt	acg	tat	1152
Asp	Asn	Asp	Cys	Gly	Gly	Tyr	Ser	Cys	Gly	Asn	Ser	Gly	Cys	Thr	Tyr	
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Val	Ala	His	Ser	Lys	Cys	Ala	Thr	Gln	Ser	Asn	Val	Trp	Asp	Gly	Glu	
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Asp	Leu	Glu	Gly	Lys	Pro	Glu	Ala	Ile	Asp	Glu	Ile	Gly	Val	Asn	Pro	
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Phe	Val	Arg	Ile	Ser	Leu	Gly	Ile	Ile	Gln	His	Phe	Ser	His	Gln	Gln	
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His	Tyr	Leu	Arg	Leu	Asp	Asp	Asn	Thr	Gly	Arg	Asp	Tyr	Asp	Glu	Ser	
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aag	ctg	tgt	caa	gca	tgc	atc	acg	cca	atc	tat	ttt	ggg	aaa	ttc	tac	1392
Lys	Leu	Cys	Gln	Ala	Cys	Ile	Thr	Pro	Ile	Tyr		Gly	Lys	Phe	Tyr	
	450					455					460					
tct	tgt	atg	gaa	tgc	aat	ttc	att	ctc	cac	gaa	gaa	tgt	gca	aat	ttt	1440
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Thr	Ser	Ala	Thr	Asp	Lys	Ala	Asn	Thr	His	Asp	Leu	Cys	Ser	Ala	Cys		
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Pro	Trp	Leu	Phe	Thr	Thr	Gly	Phe	Phe	Tyr	Glu	Cys	His	Arg	Glu	Gly		
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Asp	Trp	Arg	Thr	Cys	Ser	Val	Cys	Lys	Glu	Ser	Ser	Arg	Tyr	Val	Thr		
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His	Glu	Thr	Phe	Asn	Cys	Val	Gln	Cys	Val	Phe	Ala	Leu	Cys	Phe	Lys		
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Leu	Ile	Leu	Ser	Tyr	Gly	Lys	Glu	Ile	Glu	Thr	Ser	Thr	Met	Ala	Tyr		
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Trp	Cys	Glu	Ala	Cys	Glu	Arg	Lys	Ile	Asn	Pro	Lys	Gly	Gln	Phe	Tyr		
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aat	tgt	gat	gag	tat	ggt	tgt	gtc	acc	cta	cac	att	gaa	tgt	ttg	att	1968	
Asn	Cys	Asp	Glu	Tyr	Gly	Cys	Val	Thr	Leu	His	Ile	Glu	Cys	Leu	Ile		
				645					650					655			
ggg	aag	gac	tta	tat	atg	aag	ccc	ggt	tca	tct	tgg	tta	ttc	aaa	ggt	2016	
Gly	Lys	Asp	Leu	Tyr	Met	Lys	Pro	Gly	Ser	Ser	Trp	Leu	Phe	Lys	Gly		
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Arg	Lys	Val	Arg	Val	Leu	Arg	Asn	Asn	His	Arg	Met	Thr	Arg	Pro	Ile		
		675					680					685					
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Cys	Arg	Glu	Cys	Lys	Asp	Arg	Cys	Pro	His	Lys	Ile	Val	Phe	Arg	Arg		
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Lys	Phe	Leu	Leu	Phe	Ile	Thr	Arg	Ile	Ile	Ser	Ile	Val	Ser	Ser	Leu		
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Asn	Leu	Asn	Val	Gln	Pro	Glu	Pro	Gly	Val	Ile	Ser	Leu	Ile	Ser	Gln		
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Met	Ile	Ser	Leu	Ser	Ser	Ser	Ile	Ser	Asp	Ser	Lys	Pro	Glu	Leu	Glu		
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Leu	Ile	Ser	Leu	Val	Asn	His	Met	Ile	Ser	Leu	Val	Asn	Ser	Ile	Asp		
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Ser	Glu	Pro	Glu	Pro	Asp	Pro	Asp	Leu	Met	Ser	Leu	Ile	Thr	Gln	Ile		
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Phe	Lys	Leu	Glu	Leu	Ser	Asn	Gly	Lys	Asn	Leu	Val	Thr	Gly	Phe	Val
				165					170					175	
Lys	Arg	Asp	Gly	Arg	Lys	Tyr	Asp	Pro	Glu	Tyr	Cys	Asn	Pro	Glu	Tyr
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Trp	Arg	Val	Leu	Arg	Leu	Thr	Thr	Gly	Glu	Ile	Ser	His	Phe	Leu	Cys
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Pro	Ser	Cys	Glu	Gly	Asp	Asn	His	Glu	Glu	Tyr	Glu	Lys	Ala	Pro	Leu
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Glu	Asn	Ser	Trp	Gly	Cys	Arg	Lys	Lys	Lys	Cys	Tyr	Cys	Cys	Asp	Glu
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Ile	Leu	Leu	Trp	Ile	Phe	Tyr	Tyr	Cys	Trp	Val	Cys	Asp	Cys	Gly	Met
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Lys	Trp	His	Glu	His	Thr	Leu	Ser	Leu	Phe	Pro	Ile	Leu	Ile	Ser	Leu
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Thr	Cys	Asn	Val	Cys	Ala	Leu	Asp	His	Phe	Asn	Cys	Pro	Phe	Tyr	Ile
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Cys	Ser	Pro	Cys	Asp	Phe	Val	Val	His	Gln	Ser	Cys	Ile	Thr	Leu	Pro
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Arg	Val	Ile	Arg	Ile	Ser	Arg	His	Leu	His	Arg	Ile	Ser	Phe	Thr	Pro
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Val	Ala	His	Ser	Lys	Cys	Ala	Thr	Gln	Ser	Asn	Val	Trp	Asp	Gly	Glu
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Asp	Leu	Glu	Gly	Lys	Pro	Glu	Ala	Ile	Asp	Glu	Ile	Gly	Val	Asn	Pro
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Ser	Arg	Lys	Ile	Gln	His	Pro	Ile	His	Pro	His	Leu	Leu	Thr	Leu	Val
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		500						505					510		
Pro	Trp	Leu	Phe	Thr	Thr	Gly	Phe	Phe	Tyr	Glu	Cys	His	Arg	Glu	Gly
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Asp	Trp	Arg	Thr	Cys	Ser	Val	Cys	Lys	Glu	Ser	Ser	Arg	Tyr	Val	Thr
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Cys	Ala	Ala	Ile	Pro	Gln	Lys	Val	Arg	Tyr	Lys	His	Asp	Asn	His	Val
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Leu	Ile	Leu	Ser	Tyr	Gly	Lys	Glu	Ile	Glu	Thr	Ser	Thr	Met	Ala	Tyr
	610					615					620				
Trp	Cys	Glu	Ala	Cys	Glu	Arg	Lys	Ile	Asn	Pro	Lys	Gly	Gln	Phe	Tyr
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Asn	Cys	Asp	Glu	Tyr	Gly	Cys	Val	Thr	Leu	His	Ile	Glu	Cys	Leu	Ile
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Ile Phe Phe Ile Tyr Gln Leu Ile Ser Phe Gly Arg Ser Leu Ser Gly
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Ser Lys Pro Glu Arg Gln Ile Leu Leu Val Thr Glu Met Ile Ser
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ctc atc agc tct act gat ccg aag cag gaa ccg gaa cct gag gtc atg 240
Leu Ile Ser Ser Thr Asp Pro Lys Gln Glu Pro Glu Pro Glu Val Met
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tca ctg acc agt aaa aca tta tca agt tta tac tca ctg gat cct tat 288
Ser Leu Thr Ser Lys Thr Leu Ser Ser Leu Tyr Ser Leu Asp Pro Tyr
85 90 95
tcg gag ctc caa cta ctc att gct aaa aca ttc tct ttc gtc gaa cta 336
Ser Glu Leu Gln Leu Leu Ile Ala Lys Thr Phe Ser Phe Val Glu Leu
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Met Asp Ser Asp Ser Asp Pro Glu Ala Asp Ala Glu Arg Glu Ser Glu
115 120 125
cgg cta att tcc tta tgc cct cag ttt gaa gta gaa ctt gtg caa gga 432
Arg Leu Ile Ser Leu Cys Pro Gln Phe Glu Val Glu Leu Val Gln Gly
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Lys Cys Asn Pro Gly Asn Arg Lys Val Leu Arg Leu Arg Lys Gly Ala
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Val Cys Asp Lys Ala Pro Leu Glu Val Lys His Pro Leu His Pro Arg
195 200 205
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Ser Ala Cys Asp Cys Gly Met Asn Ile Ala Cys Val Glu Lys Lys Pro
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Leu Leu Ser Ile Asp His Pro Glu Trp His Glu Ile Leu Ser Leu

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275	280	285	
tca agg tct act ttt tat ata tgt tcc ccg tgt caa ttt ata gtt cat	280	285	912
Ser Arg Ser Thr Phe Tyr Ile Cys Ser Pro Cys Gln Phe Ile Val His			
290	295	300	
caa agt tgt atc aac tta cca agc gtc ata agg ata tct cgt cat ctc	295	300	960
Gln Ser Cys Ile Asn Leu Pro Ser Val Ile Arg Ile Ser Arg His Leu			
305	310	315	
cac cgt atc tct ttt atc cgt tct ttc gac caa gga gat tgg tct tgt	310	315	1008
His Arg Ile Ser Phe Ile Arg Ser Phe Asp Gln Gly Asp Trp Ser Cys			
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Gly Val Cys Arg Lys Ile Tyr Asn Asp Tyr Gly Gly Tyr Ser Cys			
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Ser Asn Val Trp Asp Gly Asn Glu Leu Lys Gly Lys Pro Glu Glu Ile			
370	375	380	
gat gga gaa gga gtt gag cca tat gtg agt aaa ggg aat gga att ata	375	380	1200
Asp Gly Glu Gly Val Glu Pro Tyr Val Ser Lys Gly Asn Gly Ile Ile			
385	390	395	
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Gln His Phe Ser His Gln Gln His Tyr Leu Ser Leu Asp Glu Asn Thr			
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Gly Arg Asp Asn Asn Glu Asn Lys Cys Gln Ala Cys Ile Thr Pro			
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Ile Tyr Ser Gly Lys Phe Tyr Ser Cys Met Lys Cys Asn Phe Ile Leu			
435	440	445	
cac gaa gaa tgt gca aat ttt tct cgc aaa ata cat cac ccg ata cat	440	445	1392
His Glu Glu Cys Ala Asn Phe Ser Arg Lys Ile His His Pro Ile His			
450	455	460	
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Pro His Met Leu Thr Leu Met Thr Pro Thr Thr Asp Arg Ile Asn Ile			
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Glu Asn Ser Cys Ser Ala Cys Pro Trp Leu Cys Thr Thr Gly Phe Phe			
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Tyr Glu Cys Asp Arg Glu Gly Cys Phe Ile Leu His Val Gln Cys			
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Ser Lys Ile Ser Glu Pro Leu Val His Glu Ser His Met His Pro Leu			
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Phe Leu Thr Ser Arg Pro Gly Glu Arg Lys His Cys Asp Val Cys Lys			
530	535	540	
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Lys Pro Arg Asp Thr Ser Thr Ser Glu Thr Phe Asn Cys Asn Glu Cys			
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Val Phe Ser Leu Cys Phe Lys Cys Ala Ala Ile Pro Tyr Lys Val Arg			
565	570	575	
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Tyr Lys His Asp Lys His Met Leu Thr Ser Tyr Gly Asn Glu Thr			
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Ser Met Leu Thr His Trp Cys Glu Val Cys Glu Gly Lys Ile Asn Pro			
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Lys Tyr Arg Phe Tyr Arg Cys Asp Glu Tyr Cys Cys Val Thr Leu His			
610	615	620	
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Met Glu Cys Leu Leu Gly Leu Asp Leu Tyr Met Thr Pro Gly Leu Ser			

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Glu Asn Ser Cys Ser Ala Cys Pro Trp Leu Cys Thr Thr Gly Phe Phe
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Ser Lys Tyr Ser Ser Ser Pro Leu Phe Asp Glu Thr Ser Asn Asn His	
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Ala	Glu	Glu	Gly	Asp	Glu	Cys	Tyr	Ser	Cys	Ser	Ile	Gln	Thr	Ile	Gly	
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Thr	Asp	Tyr	Tyr	Phe	Cys	Ala	Thr	Cys	Asp	Lys	Arg	Phe	His	Lys	Glu	
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Cys	Val	Glu	Cys	Pro	Leu	Glu	Ile	Ser	Tyr	Pro	Thr	His	Thr	Lys	His	
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Ser	Leu	Gln	Leu	Phe	Tyr	Ser	Lys	Tyr	Arg	Phe	Asp	His	Cys	Ile	Tyr	
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Cys	Arg	Lys	Arg	Ala	Thr	Tyr	Met	Ile	Tyr	Phe	Cys	Ala	Leu	Cys	Asp	
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Ser	Tyr	Met	His	Val	Leu	Cys	Ala	Gln	Ser	Lys	Ile	Pro	Phe	Phe	Ile	
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Val	Cys	Ala	Ser	Thr	Ala	Glu	Pro	Phe	Asn	Tyr	Gln	Gly	His	Arg	His	
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 cca aaa aga cat gac cat acc ctc acc ctt ttt cct aga caa gct tcc 96
 Pro Lys Arg His Asp His Thr Leu Thr Leu Phe Pro Arg Gln Ala Ser
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 Leu Thr Cys Asn Ile Cys Gly Leu Val Asn Lys Leu His Leu Thr Tyr
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 att tgc cct ata tgc gat ttc gta gcc cat agt gat tgt atc tat atc 192
 Ile Cys Pro Ile Cys Asp Phe Val Ala His Ser Asp Cys Ile Tyr Ile
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 Pro Gln Thr Ile Arg Ile Ser Arg His His His Arg Val Ser Phe Ile
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 Ser Ser Leu Pro Phe Glu Glu Lys Ser Cys Gly Val Cys Arg Gln Met
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 ctt gac agt gat tat ggt gca tat att tgc aaa ggg tgt agt ggc ttt 336
 Leu Asp Ser Asp Tyr Gly Ala Tyr Ile Cys Lys Gly Cys Ser Gly Phe
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 Val Ala His Ile Arg Cys Ala Leu Arg Ser Asp Ile Trp Asp Gly Lys
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 Glu Leu Glu Gly Val Pro Glu Glu Val Glu Glu Asp Asp Val Glu Ser
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 Phe Lys Arg Ile Ala Asp Gly Val Ile Leu His Phe Ser His Arg His
 145 150 155 160
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 His Leu Tyr Phe Glu Ile Ser Gly Val Tyr Asn Gly Asn Lys Phe Cys

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Lys	Val	His	Pro	Leu	His	Pro	His	Pro	Leu	Lys	Leu	Ile	Phe	Tyr	Glu	
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Asp	Asn	Cys	Phe	His	Cys	Lys	Ala	Cys	Trp	Arg	Thr	Ser	Thr	Ala	Phe	
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Gly	Tyr	Arg	Cys	Ile	Asn	His	Asn	Cys	Lys	Tyr	Met	Ile	Asp	Ile	Val	
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Cys	Ala	Ser	Thr	Ala	Glu	Pro	Phe	Asp	Tyr	Gln	Gly	His	Arg	His	Pro	
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Leu	Phe	Leu	Ser	Leu	Asp	Pro	Lys	Glu	Lys	Pro	Met	Cys	His	Ile	Cys	
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Arg	Ser	Thr	Lys	Asp	Lys	Lys	Val	Leu	Asn	Cys	Ile	Glu	Cys	Asp	Phe	
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Glu	Gly	Phe	Tyr	Glu	Cys	Lys	Asp	Cys	Cys	Thr	Thr	Leu	His	Ile	Asn	
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Cys	Leu	Leu	Gly	Pro	Asp	Pro	Tyr	Leu	Met	Val	Gly	Gln	Arg	Leu	Pro	
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Pro	Phe	Cys	Ser	Ile	Cys	Asn	Ile	Arg	Cys	Pro	Tyr	Pro	Thr	Phe	Val	
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Ser	Tyr	Ile	Lys	Asp	Met	Phe	Ile	Ser	Tyr	Ile	Leu	Cys	Ser	Ser	Lys	
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Leu	Thr	Cys	Asn	Ile	Cys	Gly	Leu	Val	Asn	Lys	Leu	His	Leu	Thr	Tyr	
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 Glu Leu Glu Gly Val Pro Glu Glu Val Glu Glu Asp Asp Val Glu Ser
 Phe 130 Lys Arg Ile Ala Asp 135 Gly Val Ile Leu His Phe Ser His Arg His
 145 His Leu Tyr Phe Glu 150 Ile Ser Gly Val Tyr 155 Asn Gly Asn Lys Phe Cys
 Gln Ala Cys Ala Leu Pro Val Asn Glu Gly Asn Leu Tyr Val Cys Val
 Gly Cys Asp Phe Ile Leu His Glu Thr Cys Ala Asp Ala Pro Arg Arg
 Lys Val His Pro Leu His Pro His Pro Leu Lys Leu Ile Phe Tyr Glu
 Asp 210 Asn Cys Phe His Cys 215 Lys Ala Cys Trp Arg Thr Ser Thr Ala Phe
 225 Gly Tyr Arg Cys Ile Asn His Asn Cys Lys Tyr Met Ile Asp Ile Val
 Cys Ala Ser Thr Ala Glu Pro Phe Asp Tyr Gln Gly His Arg His Pro
 Leu Phe Leu Ser Leu Asp Pro Lys Glu Lys Pro Met Cys His Ile Cys
 Arg Ser Thr Lys Asp Lys Lys Val Leu Asn Cys Ile Glu Cys Asp Phe
 Ile Val Cys Phe Glu Cys Ala Thr Leu Pro Tyr Met Ile Arg Tyr Lys
 305 His Asp Glu His Tyr Leu Thr Phe Cys His 315 Gly Asp Glu Ala Ser Asp
 Ser Asp Trp Cys Glu Leu Cys Glu Gly Lys Leu Ala Ile Gly Gly Lys
 Glu Gly Phe Tyr Glu Cys Lys Asp Cys Cys Thr Thr Leu His Ile Asn
 Cys Leu Leu Gly Pro Asp Pro Tyr Leu Met Val Gly Gln Arg Leu Pro
 Val 370 Pro Asn Gly Glu Ile Phe Phe Arg His Asn Asn Tyr Thr Thr Arg
 385 Pro Phe Cys Ser Ile Cys Asn Ile Arg Cys Pro Tyr Pro Thr Phe Val
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Phe Leu Val Tyr Arg Asn Val Ile Lys Pro Leu Pro Gln Thr Gln Thr
 20 25 30

tca aac tcc ttt gat aaa caa tcc att gat tcc gtc tac gat ctc cct 144

Ser Asn Ser Phe Asp Lys Gln Ser Ile Asp Ser Val Tyr Asp Leu Pro
 35 40 45

cct caa cct ctt ttc tta tgc cct aga ctc cga acc cgt ata tta ttg 192

Pro Gln Pro Leu Phe Leu Cys Pro Arg Leu Arg Thr Arg Ile Leu Leu
 50 55 60

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Ser	Lys	Tyr	Ser	Ser	Ser	Pro	Leu	Phe	Asp	Glu	Thr	Ser	Asn	Asn	His	
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Thr	Asp	Tyr	Tyr	Phe	Cys	Ala	Thr	Cys	Asp	Lys	Arg	Phe	His	Lys	Glu	
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Ser	Leu	Gln	Leu	Phe	Tyr	Ser	Lys	Tyr	Arg	Phe	Asp	His	Cys	Ile	Tyr	
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Cys	Arg	Lys	Arg	Ala	Thr	Tyr	Met	Ile	Tyr	Phe	Cys	Ala	Leu	Cys	Asp	
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Ser	Tyr	Met	His	Val	Leu	Cys	Ala	Gln	Ser	Lys	Ile	Pro	Phe	Phe	Ile	
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Asp	Gln	Pro	Lys	Arg	His	Asp	His	Thr	Leu	Thr	Leu	Phe	Pro	Arg	Gln	
	210					215					220					
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Ala	Ser	Leu	Thr	Cys	Asn	Ile	Cys	Gly	Leu	Ile	Asn	Lys	Leu	His	Phe	
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Tyr	Ile	Pro	Gln	Thr	Ile	Arg	Ile	Ser	Arg	His	His	His	Arg	Val	Ser	
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Cys	Lys	Ser	Thr	Lys	Asp	Lys	Lys	Val	Leu	Asn	Cys	Ile	Glu	Cys	Asp	
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Phe	Ile	Ile	Cys	Phe	Glu	Cys	Ala	Thr	Leu	Pro	Tyr	Met	Val	Arg	Tyr	
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Cys	Ala	Gln	Ala	Lys	Ile	Pro	Phe	Leu	Ile	Asp	Gln	Pro	Lys	Lys	His	
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Pro Arg Asp Pro Ala His Glu Val Leu Pro Asn Asn Gly Val Thr Arg					
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Ser Phe Cys Ser Arg 85 Cys Glu Gly Arg Phe 90 Glu Asn Gly Tyr 95 Cys	
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Ser Ile Cys Asp Phe Lys Leu Asp Phe 105 Arg Cys Ala Lys 110 Gly Pro Ala	
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Pro Leu Leu Ile Leu Glu Lys Ser Asn Leu His Glu His Leu Leu Glu	
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Phe Phe Val Gly Trp His 135 Ser Trp Lys Gly His 140 Arg Glu Cys Lys Ala	
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Cys Gly Gly Ala Gly Phe 150 Arg Gly Tyr Arg Trp Tyr Gly Cys Tyr Gln 160	
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Cys Asp Thr Leu Phe 165 His Gly Glu Cys Ala 170 Glu Phe Phe Pro Glu 175 Ala	
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Lys His Thr Ser His Pro Gln His Thr 185 Leu Lys His Ile Thr 190 Ser Glu	

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Phe	Asp	Gln	Gln	His	Pro	Lys	Ile	His	His	Cys	Asp	Val	Cys	Asn	Phe	
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Gln	Cys	Ser	Phe	Ile	Leu	His	Glu	Lys	Cys	Ala	Asn	His	Pro	Arg	Lys	
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 385 390 400
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 Pro Ser Ser Ser Gly Glu Thr Ala Ile Asp Gly Asp Asp His Leu Ser
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 Leu Gln Pro Leu Phe Leu Cys Pro Ser Leu Arg Leu Arg Val His
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Thr	Ile	Thr	Tyr	Ile	Lys	Arg	Glu	Val	His	Ile	Leu	Pro	Asn	Asn	Thr	
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Arg	Ser	Arg	Pro	Phe	Cys	His	His	His	Asp	Glu	Asp	Arg	Cys	Pro	His	
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Lys	Val	Val	Phe	Lys	Trp	Gln	Asp	Gln	Tyr	Thr	Ile	Phe	Cys	Ser	Tyr	
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 Ser Met Leu Tyr His Cys Pro Thr Tyr Lys Leu Ser Met His Pro Val
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 Cys Ala Met Lys Pro Ile Pro Ile Phe Ile Asp His Ser Lys Arg His
 225 230 235 240
 Pro His Leu Leu Thr Phe Phe Pro Lys Gln Ala Ser Leu Leu Cys Asp
 245 250 255
 Val Cys Gly Leu Val Lys Glu Ser Phe Pro Thr Tyr Val Cys Val Arg
 260 265 270
 Cys Ile Phe Val Val His Arg Asp Cys Ile Tyr Phe Pro Phe Val Ile
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 Ser Gly Lys Trp Ser Cys Gly Val Cys Arg Gln Lys Val Asp Asn Asn
 305 310 315 320
 Cys Gly Ala Tyr Thr Cys Asn Lys Cys Asn His Tyr Phe Val His Thr
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 Val Pro Glu Glu Pro Glu Ile Ile Leu Glu Pro Phe Glu Thr Ile Ala
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 Asp Gly Ile Ile Leu His Phe Ser His Gly His His Leu Thr Leu Glu
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 580 585 590
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Pro	Leu	Phe	Trp	Cys	Asn	Asn	Lys	Glu	Pro	Asn	Gly	Ala	Asp	Phe	Cys	
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tgt	agt	gca	tgc	aaa	ctc	aca	aat	ctt	ggc	aca	gcc	tac	tat	ttt	tgt	144
Cys	Ser	Ala	Cys	Lys	Leu	Thr	Asn	Leu	Gly	Thr	Ala	Tyr	Tyr	Phe	Cys	
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gcc	aca	tgt	cgt	aag	aag	ttc	cac	aaa	gaa	tgt	gtg	gag	tct	cca	ctt	192
Ala	Thr	Cys	Arg	Lys	Lys	Phe	His	Lys	Glu	Cys	Val	Glu	Ser	Pro	Leu	
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Glu	Ile	Lys	His	Pro	Ser	Tyr	Pro	Phe	Gln	Ser	Leu	Gln	Leu	Tyr	Ser	
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Ser	Pro	Phe	Ala	Leu	Val	Asn	Cys	Ile	Cys	Cys	Asp	Ile	Ser	Phe	Gln	
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gac	att	att	tat	cat	tct	tct	aat	cac	aaa	ctg	agt	atg	cat	cct	gtt	336
Asp	Ile	Ile	Tyr	His	Ser	Ser	Asn	His	Lys	Leu	Ser	Met	His	Pro	Val	
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Cys	Ala	Met	Lys	Pro	Val	Pro	Ile	Phe	Ile	Asp	His	Thr	Lys	Arg	His	
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Tyr	Gly	Lys	Trp	Ser	Cys	Gly	Val	Cys	Arg	Arg	Glu	Val	Asp	Asn	His	
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Val	Pro	Glu	Glu	Pro	Glu	Ile	Asp	Val	Glu	Pro	Tyr	Glu	Thr	Ile	Ala	
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 Cys Cys Thr Thr Leu His Val Asp Cys Leu Leu Gly Glu Met Ser Leu
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 Leu Leu Ile Ser Ser Lys Val Ser Gly Gln Glu Glu Glu Ile Cys Arg
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 Leu Ser His Pro Ser His Pro His Thr Leu Ser Arg Tyr Gly Glu
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 cac cct ccg tct ggt tgt ttt gca agc tca gac tcc aca ttc ata agg 192
 His Pro Pro Ser Gly Cys Phe Ala Ser Ser Asp Ser Thr Phe Ile Arg
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 His Ser Leu Tyr Phe Tyr Phe Phe Cys Thr Thr Cys Asp Leu Glu Phe
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 85 90 95

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Glu	Asp	Ser	Ser	Ile	Leu	Gly	Asn	Cys	Asn	Trp	Cys	Gly	Asn	Asp	Leu	
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gat	tct	agt	tgt	tcc	caa	agc	ttt	cca	ctt	cct	acc	atc	tca	aat	cca	528
Asp	Ser	Ser	Cys	Ser	Gln	Ser	Phe	Pro	Leu	Pro	Thr	Ile	Ser	Asn	Pro	
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Lys	Ser	His	His	His	Ser	Leu	Ile	Phe	Leu	Pro	Arg	Pro	Leu	Leu	Phe	
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Pro	Cys	Asp	Ala	Cys	Gly	Leu	Val	Glu	Gln	Trp	Arg	Pro	Ser	Tyr	Ala	
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Cys	Phe	Gln	Cys	Asn	Tyr	Val	Val	His	Lys	Asp	Cys	Ile	Asp	Leu	Pro	
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Arg	Val	Ile	Lys	Ile	Thr	Arg	His	Pro	His	Arg	Leu	Phe	Tyr	Thr	Pro	
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Phe	Leu	Ser	Pro	Ser	Thr	Ser	Ser	Leu	Cys	Arg	Leu	Cys	Tyr	Glu	Thr	
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Val	Asp	Ile	Asn	Tyr	Gly	Gln	Tyr	Thr	Cys	Asn	His	Asp	Asp	Cys	Ser	
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Arg	Glu	Leu	Glu	Trp	Glu	Pro	Glu	Glu	Phe	Asp	Glu	Thr	Glu	Asp	Val	
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Lys	Gln	Cys	Gln	Ala	Cys	Val	Leu	His	Val	Asp	Ser	Arg	His	Phe	Tyr	
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Asn	Cys	Phe	Gln	Cys	Asp	Tyr	Val	Leu	His	Glu	Val	Cys	Ala	Asn	Leu	
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Pro	Arg	Lys	Leu	Asp	His	Gly	Leu	His	Asn	His	Pro	Leu	Phe	Leu	Asp	
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Pro	Val	Pro	Leu	Asn	Ala	Trp	Asp	Ser	Ser	Asn	Cys	Ser	Val	Cys	Glu	
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Arg	Val	Thr	Val	Gly	Phe	Val	Tyr	Lys	Cys	Ser	Lys	Lys	Arg	Cys	Thr	
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cgt	att	tac	cag	caa	aaa	agg	ttc	cag	gta	gat	gtt	aga	tgc	atc	tta	1296
Arg	Ile	Tyr	Gln	Gln	Lys	Arg	Phe	Gln	Val	Asp	Val	Arg	Cys	Ile	Leu	
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gtt	cct	gat	tgt	ttc	acc	cac	aaa	agt	cat	gaa	cat	ccc	tta	ttc	ctc	1344
Val	Pro	Asp	Cys	Phe	Thr	His	Lys	Ser	His	Glu	His	Pro	Leu	Phe	Leu	
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Gly	Trp	Ser	Ala	Tyr	Met	Met	Pro	Gly	Tyr	Thr	Leu	Leu	Phe	Gly	Asn	
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His	Asn	Cys	Asp	Asn	Arg	Cys	Ser	Ser	Thr	Val	Tyr	Leu	Lys	Leu	Ser	
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tgg	tac	tta	gct	gca	tta	gca	gat	tga								1899
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<212> PRT

<213> Arabidopsis thaliana

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Ile	His	Asp	Ser	Asp	Ile	His	Ser	Tyr	Asp	Val	Ser	Ser	Ile	Ile	Pro	
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Arg Glu Leu Glu Trp Glu Pro Glu Glu Phe Asp Glu Thr Glu Asp Val
Ala Pro Phe Lys Lys Val Gly Asp Asp Leu Ile Lys Tyr Phe Cys His
Asp His His Leu Lys Leu Glu Lys Tyr Asp Arg Val Arg Asp Met Asp
Lys Gln Cys Gln Ala Cys Val Leu His Val Asp Ser Arg His Phe Tyr
Asn Cys Phe Gln Cys Asp Tyr Val Leu His Glu Val Cys Ala Asn Leu
Pro Arg Lys Leu Asp His Gly Leu His Asn His Pro Leu Phe Leu Asp
Pro Val Pro Leu Asn Ala Trp Asp Ser Ser Asn Cys Ser Val Cys Glu
Arg Val Thr Val Gly Phe Val Tyr Lys Cys Ser Lys Lys Arg Cys Thr
Arg Ile Tyr Gln Gln Lys Arg Phe Gln Val Asp Val Arg Cys Ile Leu
Val Pro Asp Cys Phe Thr His Lys Ser His Glu His Pro Leu Phe Leu
Pro Ile His Asn Tyr Asp Thr Arg Leu Cys Asn Gly Cys Asn His Thr
Gly Ser Thr Ser Ser Tyr Tyr Leu Gln Cys Thr Leu Cys Lys Val Phe
Leu Cys Tyr Glu Cys Ala Thr Ile Pro Asp Lys Leu His Asn Lys Tyr
Asp Ala Val Pro Phe Ser Leu Cys Tyr Gly Glu Val Ser Asp Gln Thr
Tyr Trp Cys Glu Val Cys Glu Gly Ile Leu Asp Pro Arg Glu Trp Phe
Tyr Thr Cys Ser Lys Pro Tyr Ile Thr Ile His Arg Ser Cys Val Phe
Gly Trp Ser Ala Tyr Met Met Pro Gly Tyr Thr Leu Leu Phe Gly Asn
Leu Ser Ile Lys Val Ile Cys Asn Ser Ser Asn Thr Arg Leu Met Cys
His Asn Cys Asp Asn Arg Cys Ser Ser Thr Val Tyr Leu Lys Leu Ser
Asn Gly Ile Ala Ile Cys Ser Tyr Gln Cys Leu Arg Asp Phe Asn Ser
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His Ser His Thr Leu Ser Arg Arg Ala Gly Arg Ile Pro Pro Ser Gly
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48

96

144

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Tyr	Pro	Arg	Lys	Leu	Thr	His	Pro	Tyr	His	Leu	Gln	His	Pro	Leu	Thr	
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Leu	Thr	Thr	Gln	Asn	Thr	Glu	Ile	Glu	Ile	Ile	Ser	Lys	Asn	Pro	Glu	
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Tyr	Gly	Tyr	Ile	Phe	Lys	Asn	Cys	Asn	Trp	Cys	Gly	Asp	Asp	Leu	Arg	
		100					105					110				
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Asp	Gly	Ser	Gln	Phe	Tyr	His	Cys	Ser	Ile	Cys	Asn	Phe	Cys	Leu	Asp	
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Leu	Ser	Cys	Ser	Gln	Asn	Phe	Pro	Thr	Leu	Thr	Ile	Thr	Asn	Pro	Lys	
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Ser	His	His	His	Ser	Leu	Phe	Leu	Phe	Pro	Trp	Pro	Leu	Leu	Ile	Pro	
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Cys	Glu	Ala	Cys	Glu	Leu	Val	Ser	Leu	Glu	Glu	Pro	Ser	Tyr	Thr	Cys	
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Phe	Gln	Cys	Asn	Tyr	Leu	Val	His	Glu	Ser	Cys	Ile	Asn	Leu	Pro	Arg	
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Leu	Pro	Pro	Thr	Thr	Pro	Ser	Cys	Arg	Val	Cys	Tyr	Lys	Thr	Val	Asp	
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Cys	Gln	Ala	Cys	Ile	Leu	Arg	Ile	Asp	Ser	Tyr	Asp	Phe	Tyr	Asn	Cys	
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Pro	Ile	Leu	Asp	Tyr	Ser	Ser	Thr	Ser	Cys	Ser	Thr	Cys	Ala	Arg	Glu	
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Ile	Thr	Ile	Gln	Ile	Asp	Phe	Arg	Cys	Ile	Leu	Val	Pro	Asp	Cys	Phe	
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Cys	Ala	Thr	Ile	Pro	Tyr	Glu	Leu	Tyr	Tyr	Lys	Tyr	Asp	Ala	His	Leu		
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Tyr	Gly	Tyr	Ile	Phe	Lys	Asn	Cys	Asn	Trp	Cys	Gly	Asp	Asp	Leu	Arg		
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Phe	Gln	Cys	Asn	Tyr	Leu	Val	His	Glu	Ser	Cys	Ile	Asn	Leu	Pro	Arg		
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PF59082SeqList_PF59082.txt

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 Leu Glu Trp Glu Pro Glu Glu Leu Asp Glu Thr Glu Asp Ile Val Pro
 260 265 270
 Phe Lys Lys Val Gly Asp Asn Met Ile Lys Tyr Phe Cys His Glu His
 275 280 285
 His Leu Lys Leu Glu Lys Tyr Asp Ser Val Arg Asp Ala Lys Lys Gln
 290 295 300
 Cys Gln Ala Cys Ile Leu Arg Ile Asp Ser Tyr Asp Phe Tyr Asn Cys
 305 310 315 320
 Val Gln Cys Asp Phe Phe Leu His Glu Val Cys Ala Gly Leu Pro Arg
 325 330 335
 Lys Leu Ala His Ala Leu His Lys His Pro Leu Val Leu Asp Pro Ser
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 Pro Ile Leu Asp Tyr Ser Ser Thr Ser Cys Ser Thr Cys Ala Arg Glu
 355 360 365
 Ser Thr Gly Phe Arg Tyr Lys Cys Ser Lys Thr Asp Cys Asp Asp Glu
 370 375 380
 Ile Thr Ile Gln Ile Asp Phe Arg Cys Ile Leu Val Pro Asp Cys Phe
 385 390 395 400
 Thr His Lys Ser His Glu His Pro Leu Phe Ile Ser Thr Ser Tyr Ser
 405 410 415
 Arg Lys Gly Asn Ile Ser Cys Asp Gly Cys Lys Asp Ser Val Arg Asp
 420 425 430
 Glu Tyr Tyr Leu Gln Cys Thr Ile Cys Ser Phe Ala Met Cys Tyr Arg
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 Cys Ala Thr Ile Pro Tyr Glu Leu Tyr Tyr Lys Tyr Asp Ala His Leu
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 Leu Ser Leu Cys Tyr Gly Glu Asp Ala Glu Lys Ala Tyr Trp Cys Glu
 465 470 475 480
 Val Cys Glu Lys Glu Leu Asn Pro Arg Glu Trp Phe Tyr Ser Cys Asn
 485 490 495
 Lys Cys Cys Ile Thr Ile His Leu Glu Cys Ile Phe Gly Ser Ser Val
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 Tyr Ile Lys Ser Gly Tyr Thr Phe Tyr Phe Gly Ser Ala Ser Met Lys
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Phe Thr Arg Phe Ser Tyr Lys Ala Cys Lys Gly Cys Gly Tyr Val Gly	
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Tyr Ile Tyr Gly Gly Tyr His Cys Asn Glu Leu Gly Cys Glu Ser Val	
35 40 45	
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Phe His Lys Glu Cys Ala Asp Pro Leu Pro Glu Ile Asn His Tyr Ser	

PF59082SeqList_PF59082.txt

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Ser	Cys	Ser	Gln	Cys	Pro	Ser	Ser	Phe	Glu	Asn	Gly	Tyr	Leu	Cys	Ser	
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att	tgt	gac	ttc	aag	ttg	gat	ttt	cgt	tgc	gcg	acg	agg	ttg	cct	ttg	336
Ile	Cys	Asp	Phe	Lys	Leu	Asp	Phe	Arg	Cys	Ala	Thr	Arg	Leu	Pro	Leu	
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Ser	Asp	Gly	Thr	Arg	Asp	Gly	Phe	Val	Gln	Leu	Cys	Lys	Thr	Cys	Lys	
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Trp	Gly	Val	Phe	Asp	Ala	Val	His	Tyr	Lys	Cys	Asn	Lys	Cys	Asp	Leu	
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Leu	His	Pro	Gln	His	Pro	Leu	Lys	Leu	Leu	Arg	Cys	Glu	Glu	Ala	Pro	
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Asp	Tyr	Ala	Asp	Asn	Lys	Cys	Leu	Leu	Cys	Gly	Asn	Lys	Phe	Asp	Gly	
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Cys	Gly	Thr	Gln	Ala	Asp	Gln	Ser	Pro	Tyr	Phe	Cys	Leu	Gln	Cys	Asn	
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Phe	Met	Ile	His	Trp	Glu	Cys	Ile	Asp	Leu	Pro	Arg	Val	Ile	Asn	Ile	
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Asn	Arg	His	Asp	His	Arg	Ile	Ser	Tyr	Thr	Arg	Arg	Leu	Gly	His	Gly	
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Gly	Tyr	Ser	Cys	Ser	Lys	Cys	Ser	Asn	Tyr	Val	Val	His	Ser	Arg	Cys	
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Glu	Glu	Pro	Glu	Glu	Asp	Ala	Pro	Phe	Glu	Val	Ile	Asp	Asp	Asn	Thr	
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Cys	Ser	Asp	Ala	Phe	Tyr	Ser	Cys	Glu	Asn	Cys	Asp	Phe	Ile	Leu	His	
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<212> PRT

<213> Arabidopsis thaliana

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Ser	Cys	Ser	Gln	Cys	Pro	Ser	Ser	Phe	Glu	Asn	Gly	Tyr	Leu	Cys	Ser
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PF59082SeqList_PF59082.txt

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 Arg Ile His His Cys Asp Val Cys Asn Phe Thr Ile Cys Gly Gly Cys
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 Ile Lys His Phe Ser His Asp His Asn Leu Val Ile Asn Lys Asp Gly
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 Arg Ile Leu His Glu Ser Thr Leu Cys Lys Ala Cys Val Phe Gln Ile
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 Leu Pro Phe Thr Leu Val Thr Asn Asp Thr Ser Asp Glu Thr Ser Cys
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 Asp Leu Cys Trp Gln Ser Phe Thr Gly Phe Arg Tyr Glu Cys Leu Thr
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 Arg Met Val Thr Leu Asp Val Arg Cys Gly Ser Ile Arg Glu Pro Leu
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 Tyr Met Pro Gly Ser Lys Ile Gly Trp Glu Glu Asp Leu Val Val Ser
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 Asn Thr Ser Met Cys Arg Pro Phe Cys Tyr Val Cys Asn Ser Gln Cys
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His Met Ala Ser Leu Arg Lys Lys Leu Pro Leu Asn Arg Phe Arg Arg
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cgc ttg gac aag ctg cga tct aga cat aac att cga tct gta agg caa      144
Arg Leu Asp Lys Leu Arg Ser Arg His Asn Ile Arg Ser Val Arg Gln
          35          40          45
agg ttt ggc aat ggc ggc aac acg cag cag caa cgg cca act aaa      192
Arg Phe Gly Asn Gly Gly Asn Thr Gln Gln Gln Arg Pro Pro Thr Lys
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cac ctt tgc cct ttc tcc gat cca gtt gaa ccg cac aag ctc caa cgc      240
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cgc cgt tta cta agt cag tct caa ctc tct gaa tgc ttc gga tgc aaa      288
Arg Arg Leu Leu Ser Gln Ser Gln Leu Ser Glu Cys Phe Gly Cys Lys
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Gly Lys His Leu Glu Gly Lys Arg Tyr Tyr Phe Cys Pro Leu Cys
          100          105          110
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Asn Leu Glu Phe His Arg Gly Cys His Val Leu Pro Gln Gln Met Lys
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Arg Arg Leu Leu Arg Arg Arg Ala Arg Phe Phe Ser Pro Phe Asp
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gtt gaa gat gat gat gat gat gat gtt gat ctt gat gat gat gac gat      624
Val Glu Asp Asp Asp Asp Asp Asp Val Asp Leu Asp Asp Asp Asp
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gtt tgc aac ttc agc ctc aat ttc act tgt acg ata aag cca cca cct      768
Val Cys Asn Phe Ser Leu Asn Phe Thr Cys Thr Ile Lys Pro Pro Pro
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ctc act atc act cac cta aaa agc cac agc cac att ctc act ctt ttt      816
Leu Thr Ile Thr His Leu Lys Ser His Ser His Ile Leu Thr Leu Phe
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Pro Arg Arg Ile Pro Leu Pro Cys Asp Val Cys Gly Leu Ser Leu Asn
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gac gct cat gat cca gtt tac gct tgt ctt cct tgt aac tac atg gtt      912
Asp Ala His Asp Pro Val Tyr Ala Cys Leu Pro Cys Asn Tyr Met Val
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	Ser	Thr	Gly	Phe	Val	Tyr	Ser	Cys	Asn	Val	Glu	Phe	Cys	Asp	Phe	Gln	
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Gly Lys His Leu Glu Gly Lys Arg Tyr Tyr Tyr Phe Cys Pro Leu Cys
100 105 110
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His Pro Leu His Leu Ser His Pro Leu Thr Leu Ile Ser Leu Asp Pro
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Ser Asp Ser Glu Gly Ser Phe Asp Ser Asp Glu Phe Gly Gly Arg
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325 330 335
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Cys Ile Lys Gly Cys Cys Tyr Gly Ala His Ser Lys Cys Ala Thr Asn
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His Phe Thr His Ser Cys His Leu Lys Leu Gln Gly Lys Gly Ser Ile
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PF59082SeqList_PF59082.txt

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 act act caa ata ttc tct cta ctc cac tct atg gat tcg gat tcc atg 192
 Thr Thr Gln Ile Phe Ser Leu Leu His Ser Met Asp Ser Asp Ser Met
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 Asp His Asn Thr Asp Phe Arg Leu Phe Phe Arg Gln Thr Met Ala Leu
 85 90 95
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 Glu Pro Glu Pro Ile Phe Met Ser Leu Ile Tyr Gln Ile Phe Ser Leu
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Arg Ser Arg Arg Arg Lys Ile Lys Ser Tyr Ser Asp Thr Tyr Pro Leu
50      55      60
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Ser Pro Leu Ile Ile Lys His Pro Tyr His Pro Glu His Tyr Leu Gln
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Gly Arg Lys Ala His Trp Leu Ile Tyr His Cys Thr Thr Cys Gln Ala
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Gly	Pro	Phe	Glu	Val	Ile	Ser	Glu	Gly	Val	Ile	Leu	Tyr	Phe	His	His	
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 Asp Ile Asn Thr Cys Ala Gly Cys Asp Glu Asp Tyr Gly Phe Cys Tyr
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 Arg Val Ile Asn Ile 165 Asn Arg His Asp His Arg Ile Ser Arg Thr Tyr
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	Leu	Arg	Asn	Ser	Asn	Ser	Thr	Arg	Pro	Gln	Cys	Thr	Arg	Cys	Gly	Asp	
	545					550				555						560	
	cgt	tgt	cca	ggt	tac	atc	tac	ttc	aaa	cgc	aaa	cgc	gat	aaa	cac	cct	1728
	Arg	Cys	Pro	Gly	Tyr	Ile	Tyr	Phe	Lys	Arg	Lys	Arg	Asp	Lys	His	Pro	
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	gta	acg	ttt	tcc	tgt	tct	gtg	caa	tgt	tta	gag	gga	gga	tga			1770
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<212> PRT

<213> Arabidopsis thaliana

<400> 1152

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Cys	Gly	Lys	Lys	Ala	Pro	Leu	Ser	Lys	Arg	Asp	Arg	Arg	Phe	Ser	Tyr
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Thr	Phe	Pro	Asp	Tyr	Glu	Ser	Gly	Ile	Thr	Ser	Asp	Ser	Phe	Asp	Tyr
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Glu	Thr	Tyr	Arg	Thr	Ala	Val	Lys	Cys	His	Ser	Gln	Phe	Ile	Ile	Thr
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Tyr	Ser	Leu	Lys	Lys	Pro	Gly	Ser	Ile	Glu	Cys	Ser	Trp	Cys	Gly	Lys
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Asn	Ile	Glu	Asp	Asp	Cys	Phe	Tyr	Arg	Cys	Ser	Ile	Cys	Asn	Phe	Tyr
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Leu	Asp	Leu	Ser	Cys	Ser	Gln	Ser	Ile	Pro	Leu	Leu	Leu	Val	Ala	Asn
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 Pro Arg Val Ile Lys Ile Thr Arg His Arg His Arg Leu Ser His Ile
 210 215 220
 Pro Cys Val Gln Ser Pro Val Ser Pro Cys Gly Val Cys Tyr Gln Lys
 225 230 235 240
 Val Glu Asn Lys Tyr Gly Leu Tyr Ser Cys Asn Arg Tyr Glu Asp His
 245 250 255
 Ser Tyr Val Val His Ser Lys Cys Ala Thr His Glu Asn Ile Trp Asp
 260 265 270
 Gly Lys Glu Leu Glu Trp Glu Pro Glu Glu Pro Glu Asn Ile Glu Asp
 275 280 285
 Ile Leu Pro Phe Lys Lys Val Gly Thr Asp Met Ile Lys Tyr Phe Ser
 290 295 300
 His Glu His Asn Leu Lys Leu Glu Lys Tyr Asp Ala Val Arg Asp Ala
 305 310 315 320
 Glu Lys Leu Cys Gln Ala Cys Val Cys Pro Ile Asn Ser Arg Asp Phe
 325 330 335
 Tyr Asn Cys Ile His Cys Asp Phe Phe Leu His Glu Val Cys Ala Gly
 340 345 350
 Leu Leu Arg Lys Leu Asp His Ala Leu His Lys His Thr Leu Ile Leu
 355 360 365
 Asp Pro Tyr Pro Arg Asp Ser Tyr Tyr Leu Leu Asp Cys Pro Ile Cys
 370 375 380
 Ser Arg Gly Ser Thr Gly Phe Arg Tyr Ile Cys Ser Ile Ser Asn Cys
 385 390 395 400
 Asn Ser His Arg Ile Gly Ile Asp Ile Arg Cys Ile Leu Val Pro Asp
 405 410 415
 His Phe Thr His Glu Ser His Glu His Pro Leu Phe Ile Ser Thr Ser
 420 425 430
 Phe Lys Ala Glu Ile Arg Cys Gln Gly Cys Gln Lys Glu Cys Met Gln
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 Ser Tyr Leu Gln Cys Thr Ile Cys Ile Phe Ile Met Cys Tyr Lys Cys
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 Ala Thr Ile Pro Thr Glu Val Ser Tyr Lys His Asp Lys His Pro Leu
 465 470 475 480
 Ser Leu Cys Tyr Gly Glu Lys Ala Asp Asp Thr Tyr Trp Cys Glu Leu
 485 490 495
 Cys Glu Lys Glu Val Asn Pro Arg Asn Trp Phe Tyr Thr Cys Asn Ile
 500 505 510
 Cys Cys Ile Thr Ile His Leu His Cys Ile Phe Gly Ser Ser Ser Tyr
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 agc aga aag atg gac aaa gaa gaa gta tct cca ctt cct ccg cct ctt
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48

96

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gac Asp	aaa Lys 50	gaa Glu	gaa Glu	gta Val	tct Ser	cca Pro 55	cct Pro	cct Pro	ccg Pro	cct Pro	ctt Leu 60	ccg Pro	ctt Leu	ttt Phe	gga Gly	192
tat Tyr 65	gga Gly	cga Arg	tat Tyr	caa Gln	acc Thr 70	aga Arg	aac Asn	cac His	aaa Lys	aag Lys 75	atg Met	gac Asp	aaa Lys	gaa Glu	aaa Lys 80	240
gtt Val	cct Pro	cca Pro	cct Pro	cct Pro 85	tca Ser	cct Pro	cat His	cca Pro	cct Pro 90	ctt Leu	cac His	tcc Ser	ctt Leu	cca Pro 95	tca Ser	288
agc Ser	aaa Lys	cct Pro	gaa Glu 100	gta Val	aaa Lys	cct Pro	cac His	cct Pro 105	cgt Arg	cct Pro	aca Thr	gga Gly 110	aac Asn	cca Pro	ata Ile	336
tgt Cys	cct Pro	gtg Val 115	tct Ser	cat His	cca Pro	agt Ser	caa Gln 120	cct Pro	cac His	acc Thr	ctc Leu 125	tct Ser	ctt Leu	aga Arg	tct Ser	384
ggc Gly	aga Arg 130	aac Asn	acc Thr	aag Lys	ttt Phe	gat Asp 135	tgt Cys	ttt Phe	tca Ser	tgc Cys	cgt Arg 140	aaa Lys	cat His	atg Met	tct Ser	432
ccc Pro 145	ttg Leu	act Thr	tac Tyr	cat His	aat Asn 150	tac Tyr	cat His	tac Tyr	tac Tyr	tgc Cys 155	aag Lys	acg Thr	tgc Cys	gat Asp 160	atg Met 160	480
gag Glu	ttt Phe	cac His	cat His	ggt Gly 165	tgt Cys	cac His	acg Thr	ttt Phe	cca Pro 170	agg Arg	aag Lys	tta Leu	aca Thr	cat His 175	cct Pro	528
tat Tyr	cac His	ctc Leu	caa Gln 180	cac His	cct Pro	ctt Leu	act Thr	ttc Phe 185	acc Thr	ttc Phe	agg Arg	aac Asn 190	aat Asn	gaa Glu	acc Thr	576
gga Gly	ttc Phe	cta Leu 195	tct Ser	gat Asp	ggc Gly	aat Asn 200	ata Ile	gat Asp	gta Val	tcc Ser	ttt Phe 205	tcc Ser	act Thr	aca Thr	ctt Leu	624
tcg Ser	tcc Ser 210	tac Tyr	tcc Ser	aac Asn	ctg Leu	cct Pro 215	gga Gly	tcc Ser	aac Asn	aaa Lys	tct Ser 220	gat Asp	cat His	aac Asn	aag Lys	672
ttt Phe 225	gaa Glu	tct Ser	acg Thr	gaa Glu	tct Ser 230	gat Asp	caa Gln	tgc Cys	aca Thr	tgg Trp 235	tgt Cys	gga Gly	aaa Lys	tat Tyr	atc Ile 240	720
caa Gln	ggc Gly	aat Asn	tgg Trp	ttt Phe 245	tat Tyr	cat His	tgt Cys	cct Pro 250	ata Ile	tgc Cys	aac Asn	ttt Phe	tgt Cys	ttg Leu 255	gat Asp	768
ctc Leu	tct Ser	tgc Cys	tcc Ser 260	caa Gln	caa Gln	agt Ser	gtt Val 265	cca Pro	ctt Leu	ctc Leu	ctc Leu	gtc Val 270	gcg Ala	aaa Lys	cca Pro	816
aag Lys	agt Ser	cat His	cac His	cat His	cca Pro	ctc Leu	gtc Val 280	ttc Phe	tac Tyr	acg Thr	cga Arg	cca Pro 285	ctc Leu	ttg Leu	act Thr	864
cca Pro	tgt Cys 290	gat Asp	gcg Ala	tgt Cys	ggg Gly	ttg Leu 295	gtc Val	aat Asn	gtg Val	ttg Leu	gag Glu 300	cca Pro	agc Ser	tat Tyr	gct Ala	912
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cga Arg	gtc Val	ata Ile	aag Lys	atc Ile	acg Thr	cgt Arg	cac His	gag Glu	cat His	cgt Arg	ctt Leu	cat His	cat His	act Thr 335	cct Pro	1008
tac Tyr	ctc Leu	cgt Arg	tcc Ser 340	aca Thr	att Ile	tca Ser	cca Pro	tgc Cys 345	cgg Arg	atc Ile	tgc Cys	tac Tyr	caa Gln 350	cca Pro	gtt Val	1056
gac Asp	atc Ile	aag Lys 355	tac Tyr	ggc Gly	caa Gln	tat Tyr	tat Tyr 360	tgc Cys	aac Asn	cgc Arg	gag Glu	aat Asn 365	tgc Cys	tct Ser	tat Tyr	1104
gta Val	gtt Val 370	cat His	tca Ser	aaa Lys	tgt Cys	gca Ala 375	aca Thr	cat His	gag Glu	aac Asn	ata Ile 380	tgg Trp	gac Asp	agg Arg	aaa Lys	1152
gaa Glu 385	ctc Leu	gaa Glu	tgg Trp	gaa Glu	ccc Pro 390	gaa Glu	gaa Glu	tct Ser	gac Asp	gaa Glu 395	att Ile	gaa Glu	gat Asp	atc Ile	atg Met 400	1200

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cat	ctt	cta	aag	ctc	gag	aca	tat	gat	ggt	gct	cga	gat	gca	gag	aag	1296
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Gln	Cys	Gln	Ala	Cys	Ile	Leu	Pro	Ile	Asn	Ser	His	Asp	Phe	Tyr	Asn	
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Cys	Met	Glu	Cys	Asp	Phe	Phe	Leu	His	Glu	Val	Cys	Ala	Cys	Leu	Leu	
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Arg	Lys	Leu	Asn	His	Ala	Leu	His	Lys	His	Thr	Leu	Ile	Leu	Asp	Thr	
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Ser	Pro	Gln	Asn	His	Tyr	Asp	Leu	Ile	Asn	Cys	Ser	Val	Cys	Ser	Arg	
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Lys	Ser	Thr		Phe	Met	Tyr	Arg	Cys	Ser	Glu	Thr	Asp	Cys	Arg	Leu	
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tta	aaa	gat	caa	ggt	ctt	cag	ata	gat	ggt	cga	tgt	att	tta	ggt	ctt	1584
Leu	Lys	Asp	Gln	Val	Leu	Gln	Ile	Asp	Val	Arg	Cys	Ile	Leu	Val	Leu	
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Asp	Tyr	Phe	Thr	His	Glu	Ser	His	Glu	His	Pro	Leu	Phe	Ile	Cys	Thr	
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Ser	Ser	Lys	Gly	Glu	Asn	Lys	Ile	Cys	Cys	Glu	Gly	Cys	Lys	Glu	Ile	
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Cys	Gln	Gln	Pro	Tyr	Leu	Gln	Cys	Thr	Arg	Cys	Lys	Phe	Ala	Met	Cys	
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Tyr	Gln	Cys	Thr	Thr	Val	Pro	Thr	Glu	Val	Cys	Tyr	Lys	Tyr	Asp	Lys	
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Cys	Asn	Ile	Cys	Cys	Ile	Thr	Ile	His	Leu	His	Cys	Ile	Phe	Gly	Asn	
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Ser	Val	Tyr	Met	Lys	Pro	Gly	Leu	Thr	Phe	Glu	Tyr	Gly	Phe	Thr	Ser	
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Ser	Tyr	Gly	Gln	Trp	Thr	Leu	Lys	Ser	Val	Thr	Cys	Ser	Leu	Lys	Cys	
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Tyr Gly Arg Tyr Gln Thr Arg Asn His Lys Lys Met Asp Lys Glu Lys
65 70 75 80
Val Pro Pro Pro Pro Ser Pro His Pro Pro Leu His Ser Leu Pro Ser
85 90 95
Ser Lys Pro Glu Val Lys Pro His Pro Arg Pro Thr Gly Asn Pro Ile
100 105 110
Cys Pro Val Ser His Pro Ser Gln Pro His Thr Leu Ser Leu Arg Ser
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Gly Arg Asn Thr Lys Phe Asp Cys Phe Ser Cys Arg Lys His Met Ser
130 135 140
Pro Leu Thr Tyr His Asn Tyr His Tyr Tyr Cys Lys Thr Cys Asp Met
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Glu Phe His His Gly Cys His Thr Phe Pro Arg Lys Leu Thr His Pro
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Tyr His Leu Gln His Pro Leu Thr Phe Thr Phe Arg Asn Asn Glu Thr
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Gly Phe Leu Ser Asp Gly Asn Ile Asp Val Ser Phe Ser Thr Thr Leu
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225 230 235 240
Gln Gly Asn Trp Phe Tyr His Cys Pro Ile Cys Asn Phe Cys Leu Asp
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275 280 285
Pro Cys Asp Ala Cys Gly Leu Val Asn Val Leu Glu Pro Ser Tyr Ala
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Arg Val Ile Lys Ile Thr Arg His Glu His Arg Leu His His Thr Pro
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Asp Ile Lys Tyr Gly Gln Tyr Tyr Cys Asn Arg Glu Asn Cys Ser Tyr
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Gln Cys Gln Ala Cys Ile Leu Pro Ile Asn Ser His Asp Phe Tyr Asn
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Cys Met Glu Cys Asp Phe Phe Leu His Glu Val Cys Ala Cys Leu Leu
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PF59082SeqList_PF59082.txt

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 610 615 620 625
 Ser Val Tyr Met Lys Pro Gly Leu Thr Phe Glu Tyr Gly Phe Thr Ser
 630 635 640
 Lys Val Glu Val Leu Arg Asn Ser Asn Ser Thr Arg Pro Leu Cys Val
 645 650 655 660
 Arg Cys Gly Asn His Cys Pro Gly Tyr Ser Tyr Tyr Cys His Ile Gly
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Ser Lys Thr Lys Thr Gly Ser Val Trp Phe Ser Tyr Leu Glu Glu His	
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cta gta aat gta cac ata ttt gaa gaa tct cca cgc gat tct aga gat	144
Leu Val Asn Val His Ile Phe Glu Glu Ser Pro Arg Asp Ser Arg Asp	
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gca att tgc aaa ttg tgt aaa agt acg gtt tct ttt gaa tct ttc gca	192
Ala Ile Cys Lys Leu Cys Lys Ser Thr Val Ser Phe Glu Ser Phe Ala	
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Tyr Tyr Cys Arg Glu Cys Arg Ser His Phe His Lys Asp Cys Leu Thr	
65 70 75 80	
ata atc aat gca aag att cat gag cat aca cta act ttc att cgt aga	288
Ile Ile Asn Ala Lys Ile His Glu His Thr Leu Thr Phe Ile Arg Arg	
85 90 95	
gag aat ccg ttc cct tgt gat gtt tgt ggg agg gat gat aaa ggt atg	336
Glu Asn Pro Phe Pro Cys Asp Val Cys Gly Arg Asp Asp Lys Gly Met	
100 105 110	
gat atg tac gga tgt tta caa tgc gat ttc ttt gta cat aga cag tgt	384
Asp Met Tyr Gly Cys Leu Gln Cys Asp Phe Phe Val His Arg Gln Cys	
115 120 125	
ata ttc cta cca aag gtt ata aag ctc aca cgt cac tca cag cgt ctc	432
Ile Phe Leu Pro Lys Val Ile Lys Leu Thr Arg His Ser Gln Arg Leu	
130 135 140	
tct cac gtt ttt cgt atc tct gat ggt gat aac att tgt gga gtt tgc	480
Ser His Val Phe Arg Ile Ser Asp Gly Asp Asn Ile Cys Gly Val Cys	
145 150 155 160	
cgg agc caa gtt gat gtt aga tat gga gga tat tct tgt att gag aag	528
Arg Ser Gln Val Asp Val Arg Tyr Gly Gly Tyr Ser Cys Ile Glu Lys	
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Trp Asp Gly Lys Asp Leu Glu Glu Glu Pro Glu Pro Glu Glu Ile Asp	
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Arg	His	Phe	Ser	His	Glu	His	Asp	Leu	Leu	Arg	Leu	Asp	Met	Gly	Glu	
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aaa	gaa	gaa	agt	gga	caa	gta	tgt	caa	gcc	tgt	gtc	ctt	cca	att	gaa	768
Lys	Glu	Glu	Ser	Gly	Gln	Val	Cys	Gln	Ala	Cys	Val	Leu	Pro	Ile	Glu	
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ttt	ggg	agt	ttc	ttg	ggg	tgc	aag	caa	tgc	gac	ttt	gct	ctt	cac	gac	816
Phe	Gly	Ser	Phe	Leu	Gly	Cys	Lys	Gln	Cys	Asp	Phe	Ala	Leu	His	Asp	
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Val	Cys	Ala	Ser	Leu	Pro	Arg	Lys	Met	Glu	His	Gly	Ile	His	Ile	His	
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Ala	Glu	Pro	Phe	Asp	His	Ser	Met	His	Lys	His	Pro	Leu	Tyr	Leu	Ala	
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Ile	Tyr	Phe	Asp	Glu	Phe	Ile	Tyr	Arg	Cys	Glu	Gly	Cys	Thr	Gln	Ser	
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His	Ser	Leu	Thr	Leu	Tyr	Ser	Asp	Lys	Tyr	Tyr	Ser	Lys	Ser	Phe	Gln	
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Leu	Glu	Trp	Trp	Cys	Glu	Ile	Cys	Glu	Asn	Ile	Asn	Lys	Lys	Lys	Lys	
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Leu	Phe	Tyr	Thr	Cys	His	Glu	Cys	Cys	Thr	Thr	Leu	His	Val	Glu	Cys	
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Ile	Leu	Gly	Lys	Tyr	Pro	Tyr	Leu	Lys	Ser	Gly	His	Arg	Ile	Lys	Val	
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Ser	Gly	Leu	Glu	Val	Glu	Ile	Ala	Ser	Asn	Asn	Gly	Val	Ser	Arg	Pro	
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Gly	Lys	Asp	Asp	Val	Tyr	Phe	Cys	Ser	Ile	Lys	Cys	Ile	His	Ser	Thr	
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Lys																

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 Tyr Tyr Cys Arg Glu Cys₇₀ Arg Ser His Phe His₇₅ Lys Asp Cys Leu Thr
 65 Ile Ile Asn Ala Lys₈₅ Ile His Glu His Thr₉₀ Leu Thr Phe Ile Arg Arg
 Glu Asn Pro Phe₁₀₀ Pro Cys Asp Val Cys₁₀₅ Gly Arg Asp Asp Lys₁₁₀ Gly Met
 Asp Met Tyr₁₁₅ Gly Cys Leu Gln Cys₁₂₀ Asp Phe Phe Val His₁₂₅ Arg Gln Cys
 Ile Phe₁₃₀ Leu Pro Lys Val Ile₁₃₅ Lys Leu Thr Arg His₁₄₀ Ser Gln Arg Leu
 Ser His Val Phe Arg Ile Ser Asp Gly Asp Asn₁₅₅ Ile Cys Gly Val Cys
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 Thr Cys Asn Tyr₁₈₀ Val Val His Ser Ser₁₈₅ Cys Ile Ile Arg Phe₁₉₀ Asp Val
 Trp Asp Gly₁₉₅ Lys Asp Leu Glu Glu₂₀₀ Glu Pro Glu Pro Glu₂₀₅ Glu Ile Asp
 Ser Gln Val Asp Leu Ala Ala₂₁₅ Leu Val Glu Ile Asp₂₂₀ Gly Lys Ser Val
 Arg His Phe Ser His Glu His Asp Leu Leu Arg Leu Asp Met Gly Glu
 225 Lys Glu Glu Ser Gly₂₄₅ Gln Val Cys Gln Ala₂₅₀ Cys Val Leu Pro Ile Glu
 Phe Gly Ser Phe₂₆₀ Leu Gly Cys Lys Gln Cys Asp Phe Ala Leu His Asp
 Val Cys Ala₂₇₅ Ser Leu Pro Arg Lys₂₈₀ Met Glu His Gly Ile His Ile His
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 Ile Tyr Phe Asp Glu Phe Ile Tyr Arg Cys Glu Gly Cys₃₆₅ Thr Gln Ser
 Ser Arg Phe Ala Ala Lys Cys Tyr Lys Gly Cys Trp Phe Pro Leu Glu
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 385 His Ser Leu Thr Leu Tyr Ser Asp Lys Tyr Tyr Ser Lys Ser Phe Gln
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gaa atg tat gat gca gaa aaa cca aga tgc ctt ctg tct cat cca gct	144
Glu Met Tyr Asp Ala Glu Lys Pro Arg Cys Leu Leu Ser His Pro Ala	
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Asp Ser Pro His Asn Leu Ser Val Gly Cys Asp Pro Lys Leu Pro Leu	
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Gly Cys Phe Thr Cys Gly Gly Lys Thr Thr Val Arg Arg Gln Asp Tyr	
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Leu His Phe His Cys Thr Thr Cys Asp Val Lys Phe His Glu Gly Cys	
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caa acg cgt ccg aga agg ata aca cat cct tat cac ctc caa cac cct	336
Gln Thr Arg Pro Arg Arg Ile Thr His Pro Tyr His Leu Gln His Pro	
100 105 110	
ctc act ctc ttc tat cga aac cct gaa acc gga att ata tcc aac atc	384
Leu Thr Leu Phe Tyr Arg Asn Pro Glu Thr Gly Ile Ile Ser Asn Ile	
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Ile Pro Tyr Ser Ser Pro Tyr Glu Ser Asp Thr Ser Asp Pro Glu Ser	
130 135 140	
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Asn Ser Ser Gly Glu Gly Lys Ser Glu Leu Val Asp Ile Ile Pro Ser	
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Lys Ser Asp Ile Ile Phe Asp Lys Cys Thr Trp Cys Gly Lys Asp Phe	
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Lys Gly Asp Val Trp Phe Tyr Arg Cys Leu Ile Cys Gly Phe Cys Leu	
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Asp Leu Ser Cys Ala Leu Thr Leu Pro Pro Leu Thr Ile Ala Asn Pro	
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Lys Ser His His His Ser Leu Leu Phe Leu Pro Arg Pro Leu Leu Val	
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Cys Phe Gln Cys Asn Tyr Met Ile His Gln Asn Cys Ile Asp Leu Pro	
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Arg Val Ile Lys Ile Thr Arg His His His Arg Leu Ser Phe Thr Pro	
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Phe Gly Pro Pro Leu Ile Ser Leu Cys Arg Val Cys Tyr Lys Glu Val	
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Val Ala His Ser Lys Cys Ala Thr His Lys Asn Val Trp Asp Gly Thr	
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Arg	Lys	Leu	Asp	His	Ala	Leu	His	Lys	His	Arg	Leu	Val	Leu	Asp	Pro	
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Ser	Pro	Leu	His	Asp	Tyr	Arg	Asn	Met	His	Cys	Ser	Thr	Cys	Ser	Arg	
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Gln	Pro	His	Ile	Lys	Cys	Thr	Lys	Cys	Asp	Phe	Ala	Met	Cys	Tyr	Thr	
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Cys	Ala	Thr	Ile	Pro	Asn	Glu	Val	His	Tyr	Lys	Phe	Asp	Glu	His	Pro	
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Lys	Cys	Cys	Thr	Thr	Val	His	Arg	Glu	Cys	Leu	Phe	Gly	Ser	Thr	Val	
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Glu Leu Glu Trp Glu Thr Glu Glu Ser Asp Glu Asn Glu Asp Ile Ala
325 330 335
Pro Phe Lys Val Val Gly Glu Asp Leu Ile Lys His Phe Cys His Lys
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His His Leu Arg Leu Lys Lys His Asp Gly Phe Arg Glu Ala Glu Lys
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      115      120      125
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      130      135      140
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Val Arg Tyr Pro Asp Gly Pro Gly Ser Val Glu Gly Thr Arg Ala Ala
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cct att gta act ttc aaa tca cgt acg gat gat gac gaa gag ata gat     528
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Lys Ala Lys Thr Ala Leu Thr Ala Ser Val His His Gln His Ile Lys
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gcc atg gat tcg gtg tca aag cag cct ctt ctc ttt tgc cct cgt gca     624
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Pro Pro Asn Leu Ser Ser Pro Ser Phe His Leu Thr Ser Leu Val Leu
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Gly Asn Asp Phe Asn Ile Thr Arg Lys Tyr Tyr Tyr Asp Arg His Gly

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Cys	Glu	Val	Cys	Glu	Lys	Gln	Ala	Asn	Pro	Lys	Asn	Gly	Val	Tyr	Met
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Phe 145	Leu 145	Ser 145	Leu 145	Ser 145	Arg 145	Tyr 145	Ile 145	Ile 145	Ser 145	Leu 145	Ala 145	Thr 145	Ser 145	Val 145	Asp 145
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 Val Glu Ser Ser Gly Asp Asp Leu Pro Leu Gln Pro Leu Phe Ser Cys
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 Pro Tyr Ala Arg Ile Arg Ser His Lys Phe Lys Val Glu Lys Asn Tyr
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 Asp Gly Val Asn Phe Phe Asn Phe His Pro Phe Asn Ser Tyr Pro His
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 Cys Asn Asn Lys Thr Pro Asp Ser Asn Glu Phe Glu Cys Gly Gly Cys
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 Glu Glu Ser Lys Thr Ser Arg Ser Tyr Tyr Ala Cys Leu Glu Cys Gly
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Tyr Asp Cys Lys Val Asn Leu Asp Ile Asp Cys Met Ile Asp Gly Ile	
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Cys Thr Leu Ala Arg Leu Ser Lys Pro Trp His Pro His Leu Leu Leu	
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	Arg	Asp	Lys	Phe	Asp	Leu		Leu	Cys	Ser	Ser	Ile	Thr	Val	Pro	Phe	Ile	
	465					470						475					480	
	cat	gga	agt	cat	gat	cat	485	cat	tta	ctc	tac	aaa	cta	cga	tat	ggt	Gly	1488
	His	Gly	Ser	His	Asp	His		His	Leu	Leu	Tyr	Tyr	Lys	Leu	Arg	Tyr		
					485						490					495		
	caa	gtg	aag	act	tgt	cag	1536	aac	tgc	ggt	att	gat	gaa	aca	gaa	gta	ctt	
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PF59082SeqList_PF59082.txt

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Gly Cys Ser Lys Cys Asn Tyr Tyr Leu Asp Phe Cys Cys Ala Thr Leu					
cca aaa acg gta atg ctt ccc aga tac gat gat cat cca ctc act ctt					1632
Pro Lys Thr Val Met Leu Pro Arg Tyr Asp Asp His Pro Leu Thr Leu					
tgt tat ggt gat gaa aac gca agc ggc aaa tat tgg tgt gat att tgt					1680
Cys Tyr Gly Asp Glu Asn Ala Ser Gly Lys Tyr Trp Cys Asp Ile Cys					
gaa agg gaa aca aat cca aaa act tgg ttc tat act tgt aaa gat tgc					1728
Glu Arg Glu Thr Asn Pro Lys Thr Trp Phe Tyr Thr Cys Lys Asp Cys					
gga gtc acg ttt cat ata ttg tgt gta gtt gga gat atc agg tat gcc					1776
Gly Val Thr Phe His Ile Leu Cys Val Gly Asp Ile Arg Tyr Ala					
aaa cca gga gga aag att aac ggc gat tat gaa ttg ctg gct aac aat					1824
Lys Pro Gly Gly Lys Ile Asn Gly Asp Tyr Glu Leu Leu Ala Asn Asn					
agc tct tca cgg ccg ctt tgc agc acg tgt cat tgt cgt tgc cca ggt					1872
Ser Ser Ser Arg Pro Leu Cys Ser Thr Cys His Cys Arg Cys Pro Gly					
ccc ttc att ctt aat aag gaa aga aac aac ata ttc ttt tgt tct tat					1920
Pro Phe Ile Leu Asn Lys Glu Arg Asn Asn Ile Phe Phe Cys Ser Tyr					
tat tgt ctc ggg ctc agc cgg gag cat gcg tac tca tca gtg gac gtg					1968
Tyr Cys Leu Gly Leu Ser Arg Glu His Ala Tyr Ser Ser Val Asp Val					
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Cys Pro Pro Trp Ala Ile					

<210> 1168

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<213> Arabidopsis thaliana

<400> 1168

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Phe Val Phe Met Thr Glu Asp Ile Phe His His Pro Ser His Asp Gly	50	55	60	
His Cys Leu Lys Leu Thr Thr Gly Ala Pro Val His Thr Asp Ser	65	70	75	80
Lys Cys His Leu Cys Gly Lys Asn Thr Lys His Leu Leu Tyr His Cys	85	90	95	
Tyr Asp Cys Lys Val Asn Leu Asp Ile Asp Cys Met Ile Asp Gly Ile	100	105	110	
Cys Thr Leu Ala Arg Leu Ser Lys Pro Trp His Pro His Leu Leu Leu	115	120	125	
Met Val Asp Phe Ser Ser Asp Met Trp Cys Asp Phe Cys Tyr Glu Gly	130	135	140	
Gly Lys His Gly Tyr Phe Cys Pro Arg Cys Arg Leu Val Ile His Glu	145	150	155	160
Ser Cys Val Ser Val Phe Asp Ser Pro Glu Ile Asn His Pro Ser His	165	170	175	
Leu Ser His Pro Leu Lys Leu Ile Thr Asn Gly Ala Pro Asp Tyr Thr	180	185	190	
Glu Asp Arg Ser Cys His Ile Cys Gly Lys Glu Thr Gly Asn Leu Leu	195	200	205	
Tyr His Cys Asp Ile Cys Lys Phe Asn Leu Asp Met Glu Cys Ala Val	210	215	220	
Glu Asn Pro Ile Pro Val Ala Leu Ser Asp Leu Lys Val His Glu His	225	230	235	240
Thr Leu Thr Leu Met Pro Arg Leu Ile Ser Phe Ile Cys Asp Ala Cys				

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Asp	Phe	Ser	Ile	His	His	Ile	Cys	Ala	Phe	Leu	Phe	Asn	Ile	Pro	Glu	
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Thr	Gly	Ala	Pro	His	His	Thr	Asp	Pro	Asn	Cys	His	Leu	Cys	Gly	Lys	
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Tyr	Thr	Lys	Ser	Ile	Leu	Tyr	His	Cys	Ser	Asp	Cys	Lys	Leu	Asn	Leu	
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Asp	Ile	Asp	Cys	Ile	Ser	His	His	Ile	Phe	Ala	Ala	Ser	Lys	Asp	His	
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Leu	Leu	Val	Ser	Trp	His	His	His	Pro	Ile	Gln	Ile	Cys	Tyr	Thr	Asp	
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145					150					155					160	
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Gln	Cys	Gly	Phe	Arg	Ile	His	Leu	Thr	Cys	Val	Pro	Val	Phe	Asp	Ser	
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Pro	Glu	Ile	Thr	His	Pro	Ser	His	Val	Arg	Leu	Pro	Leu	Lys	Leu	Leu	
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acc	gat	gga	gct	cca	aat	tac	aca	gac	cca	aga	tgt	cat	ata	tgt	gga	624
Thr	Asp	Gly	Ala	Pro	Asn	Tyr	Thr	Asp	Pro	Arg	Cys	His	Ile	Cys	Gly	
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Glu	Asp	Thr	Gln	His	Leu	Leu	Tyr	His	Cys	Asp	Ile	Cys	Lys	Phe	Asn	
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Leu	Asp	Leu	Arg	Cys	Ala	Ala	Lys	Ser	Pro	Pro	Pro	Ile	Ala	Leu	Ser	
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aat	cta	aag	gtc	cat	gag	cat	aca	ctc	aca	ctc	atg	cca	aga	ttg	atc	768
Asn	Leu	Lys	Val	His	Glu	His	Thr	Leu	Thr	Leu	Met	Pro	Arg	Leu	Ile	
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Ser	Phe	Val	Cys	Asp	Ala	Cys	Gly	Thr	Glu	Gly	Asp	Arg	Ser	Pro	Tyr	
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atc	tgt	gtt	caa	tgt	gat	ttc	atg	att	ttc	cat	caa	aag	tgt	gct	caa	864
Ile	Cys	Val	Gln	Cys	Asp	Phe	Met	Ile	Phe	His	Gln	Lys	Cys	Ala	Gln	
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Leu	Pro	Arg	Val	Ile	His	Val	Asn	His	His	Asp	His	Arg	Ile	Ser	Tyr	
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Glu	Ile	Asp	Trp	Ser	Tyr	Gly	Ala	Tyr	Pro	Cys	Ser	Leu	Cys	Pro	Asn	
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Tyr	Ala	Ile	His	Ser	Leu	Cys	Ala	Thr	Arg	Lys	Asp	Val	Trp	Asp	Gly	
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Lys	Glu	Leu	Asp	Glu	Val	Pro	Glu	Glu	Val	Glu	Asp	Ile	Glu	Pro	Phe	
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Lys	Arg	Asn	Asp	Asp	Asn	Thr	Ile	Thr	His	Phe	Ala	His	Glu	His	Asn	
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ctc	atg	agc	ctc	gga	aaa	gac	ggt	gaa	gaa	ggc	agt	tat	tgt	gga	gca	1200
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gat	tgc	agt	ttc	att	ctc	cat	gaa	acg	tgt	gct	aat	tta	cgc	aag	aag	1296
Asp	Cys	Ser	Phe	Ile	Leu	His	Glu	Thr	Cys	Ala	Asn	Leu	Arg	Lys	Lys	
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Lys	Arg	His	Phe	Leu	Ser	Pro	Glu	Gln	Leu	Val	Ile	Ser	Gln	Trp	Lys	
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Asn	Tyr	Gly	Asn	Phe	Pro	Lys	Trp	Cys	Asp	Ala	Cys	Leu	Leu	Val	Cys	
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Ile	Asp	Val	Pro	Phe	Ile	His	Glu	Ser	His	Pro	His	His	Leu	Leu	Tyr	
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ctt	aaa	cta	caa	gac	ggc	cac	ttt	aag	act	tgc	cag	agc	tgt	ggc	atc	1536
Leu	Lys	Leu	Gln	Asp	Gly	His	Phe	Lys	Thr	Cys	Gln	Ser	Cys	Gly	Ile	
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Asp	His	Thr	Lys	Val	Val	Ile	Gly	Cys	Leu	Lys	Cys	Asn	Tyr	Phe	Leu	
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gat	ttt	cat	tgt	gcc	aca	cta	ccg	tta	aca	gtc	agt	ctt	ccc	aga	tac	1632
Asp	Phe	His	Cys	Ala	Thr	Leu	Pro	Leu	Thr	Val	Ser	Leu	Pro	Arg	Tyr	
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Tyr	Thr	Gly	Leu	Glu	Ser	Gly	Val	Thr	Leu	His	Ile	Leu	Cys	Val	Leu	
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Gly	Asp	Ile	Arg	Tyr	Ala	Lys	Pro	Gly	Gly	Asn	Ile	Cys	Glu	Gly	Phe	
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Glu	Leu	Gln	Leu	Asn	Ser	Ser	Ser	Thr	Arg	Pro	Ile	Cys	Leu	Asn	Cys	
	610				615						620					
aaa	tgt	cgt	tgc	cca	ggt	acc	ttt	ttt	att	aat	ttt	ggt	ggc	tac	ggc	1920
Lys	Cys	Arg	Cys	Pro	Gly	Thr	Phe	Phe	Ile	Asn	Phe	Val	Gly	Tyr	Gly	
625					630					635					640	
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Glu	Asp	His	Asp	Gly	Tyr	Asn	Val	Phe	Phe	Cys	Ser	Phe	Tyr	Cys	Leu	
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PF59082SeqList_PF59082.txt

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Tyr	Thr	Lys	Ser	Ile	Leu	Tyr	His	Cys	Ser	Asp	Cys	Lys	Leu	Asn	Leu
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Thr	Asp	Gly	Ala	Pro	Asn	Tyr	Thr	Asp	Pro	Arg	Cys	His	Ile	Cys	Gly
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Asn	Leu	Lys	Val	His	Glu	His	Thr	Leu	Thr	Leu	Met	Pro	Arg	Leu	Ile
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Lys	Glu	Leu	Asp	Glu	Val	Pro	Glu	Glu	Val	Glu	Asp	Ile	Glu	Pro	Phe
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Tyr	Thr	Gly	Leu	Glu	Ser	Gly	Val	Thr	Leu	His	Ile	Leu	Cys	Val	Leu
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PF59082SeqList_PF59082.txt

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 Asn Val Asp Gly Tyr Ser Cys Ser Glu Cys Lys Phe Asn Ile His Val
 35 40 45
 gca tgt aca ttt gtg ttc gat aaa caa gag ata gtc gac cac cct tct 192
 Ala Cys Thr Phe Val Phe Asp Lys Gln Glu Ile Val Asp His Pro Ser
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 Phe His Cys Ser Val Cys Gln Leu Asn Leu Asp Ile Phe Cys Ile Ala
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Pro Gln Pro Leu Thr Leu Ser Tyr His Arg Leu Gln Arg Arg Trp Gly
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Tyr Ser Ser Tyr Leu Glu Glu Asn Phe Asp Leu Pro Cys Ser Ser Ile
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Glu Lys Arg Val Ala Ile Gly Cys Thr Lys Cys Asn Tyr Phe Leu Asp
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Tyr Cys Arg Cys Pro Gly Pro Phe Ile Leu Arg Ile Arg Lys Gln His
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Gly Phe Tyr Cys Ser Glu Cys Lys Phe Thr Val His Arg Lys Cys Ala
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Val Val Phe Leu Leu Lys Asp Ile Phe Asp His Pro Ser His Val Gly
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465	470	475	480	
aaa cat cga agc cat gat cat cat tta ctc tac ctc aaa cta gag gtt	1488			
Lys His Arg Ser His Asp His His Leu Leu Tyr Leu Lys Leu Glu Val				
	485	490	495	
gat cac acg aag act tgc caa aac tgc ggc att gac gaa aaa gaa gtc	1536			
Asp His Thr Lys Thr Cys Gln Asn Cys Gly Ile Asp Glu Lys Glu Val				
	500	505	510	
gtc cta ggt tgt tta aaa tgc aac tac ttt ttg gat ttt cgt tgt gcc	1584			
Val Leu Gly Cys Leu Lys Cys Asn Tyr Phe Leu Asp Phe Arg Cys Ala				
	515	520	525	
act cta cca tat aca gta agg ctt ccc agg tac gat gat cat cca ctc	1632			
Thr Leu Pro Tyr Thr Val Arg Leu Pro Arg Tyr Asp Asp His Pro Leu				
	530	535	540	
act ctt tgt tat ggt gaa aag gca agc gga aaa tat tgg tgt gat att	1680			
Thr Leu Cys Tyr Gly Glu Lys Ala Ser Gly Lys Tyr Trp Cys Asp Ile				
	545	550	555	560
tgc gaa aga gaa aca aat tca aag act tgg ttc tac act tgt aaa ggt	1728			
Cys Glu Arg Glu Thr Asn Ser Lys Thr Trp Phe Tyr Thr Cys Lys Gly				
	565	570	575	
tgc ggg gtc act ttg cat gtc ttt tgt gta ctt ggg gat att cga tat	1776			
Cys Gly Val Thr Leu His Val Phe Cys Val Leu Gly Asp Ile Arg Tyr				
	580	585	590	
gct aaa cca gga gga agc atc aac aac aat gtt gaa ttg gtg cct aac	1824			
Ala Lys Pro Gly Gly Ser Ile Asn Asn Asn Val Glu Leu Val Pro Asn				
	595	600	605	
aat aga tct tca aga cca ctt tgc cac aat tgt cat tgt cat tgc cca	1872			
Asn Arg Ser Ser Arg Pro Leu Cys His Asn Cys His Cys Cys Pro				
	610	615	620	
ggt ccc ttc att ctt aag gat ttt gtc gaa gaa tgt ttt tgt tct tac	1920			
Gly Pro Phe Ile Leu Lys Asp Phe Val Glu Glu Cys Phe Cys Ser Tyr				
	625	630	635	640
tat tgt ttc agc cgt tgc aaa tcc tgg atg tcc atc gtg aag aag gaa	1968			
Tyr Cys Phe Ser Arg Cys Lys Ser Trp Met Ser Ile Val Lys Lys Glu				
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<211> 665

<212> PRT

<213> Arabidopsis thaliana

<400> 1174

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35 40 45	
Val Val Phe Leu Leu Lys Asp Ile Phe Asp His Pro Ser His Val Gly	
50 55 60	
His Tyr Leu Lys Leu Leu Thr Thr Gly Ala Pro Asp His Thr Asp Pro	
65 70 75 80	
Lys Cys His Leu Cys Gly Lys Asn Thr Lys Arg Ile Leu Tyr His Cys	
85 90 95	
Ser Ile Cys Lys Leu Asn Leu Asp Ile Asp Cys Ile Phe Asp Tyr Phe	
100 105 110	
Ser Asp Gln Gln Ala His Leu Asn Phe Ser Trp His His His Pro Leu	
115 120 125	
His Phe Ile Ser Phe Arg Leu His Leu Gln Cys Asp Val Cys Tyr Met	
130 135 140	
Phe Arg Arg Lys Gly Tyr Phe Cys Phe Gln Cys Lys Leu Val Val His	
145 150 155 160	
Lys Glu Cys Val Ser Lys Ile Glu Ser Ala Val Ile Thr His Pro Phe	
165 170 175	

PF59082SeqList_PF59082.txt

His Ala Arg His Pro Leu Lys Leu Leu Thr Asp Gly Ala Pro Asp Tyr
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 Thr Asp Pro Lys Cys His Ile Cys Gly Val Glu Thr Ala Asn Leu Leu
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 Tyr His Cys Asp Met Cys Met Phe Asn Leu Asp Ile Gly Cys Ala Ile
 210 215 220
 Arg Asn Pro Glu Arg Val Ser Leu Ser Lys Leu Lys Val His Glu His
 225 230 235 240
 Thr Leu Thr Leu Met Pro Lys Leu Met Phe Phe Val Cys Asp Ala Cys
 245 250 255
 Gly Met Lys Gly Asp His Ala Pro Tyr Val Cys Val Gln Cys Asp Phe
 260 265 270
 Met Phe Phe His Gln Lys Cys Ala Tyr Leu Pro Arg Val Ile Asn Val
 275 280 285
 Asn His His Glu His Arg Val Ser Tyr Lys Tyr Pro Leu Gly Pro Gly
 290 295 300
 Asp Trp Ile Cys Gly Val Cys Trp Glu Glu Ile Asn Trp Ser Tyr Gly
 305 310 315 320
 Ala Tyr Ser Cys Ser Cys Pro Asn Tyr Ala Ile His Ser Arg Cys
 325 330 335
 Ala Thr Arg Lys Asp Val Trp Asp Gly Lys Glu Leu Asp Gly Val Pro
 340 345 350
 Glu Leu Ile Glu Asp Ile Lys Pro Phe Lys Met Asn Asp Asp Asn Thr
 355 360 365
 Ile Thr His Phe Ala His Gly His Asn Leu Ser Leu Asn Lys Asp Thr
 370 375 380
 Glu Glu Gly Ser Phe Cys Glu Ala Cys Val Leu Pro Ile Asp Ser Tyr
 385 390 395 400
 Thr Ser Tyr Lys Cys Ser Lys Ser Asp Cys Cys Phe Ile Leu His Glu
 405 410 415
 Thr Cys Ala Asn Phe Pro Lys Lys Lys Arg His Phe Leu Ser Pro Glu
 420 425 430
 Pro Leu Thr Leu Arg Pro Gln Asn Gln Arg Lys Lys Glu Ser Ile Cys
 435 440 445
 Arg Ala Cys Asp Gln Val Phe Cys Gln Gly Phe Val Tyr Ser Thr Tyr
 450 455 460
 Arg Lys Arg Asn Phe Asp Leu Leu Cys Ser Ser Ile Thr Met Pro Phe
 465 470 475 480
 Lys His Arg Ser His Asp His His Leu Leu Tyr Leu Lys Leu Glu Val
 485 490 495
 Asp His Thr Lys Thr Cys Gln Asn Cys Gly Ile Asp Glu Lys Glu Val
 500 505 510
 Val Leu Gly Cys Leu Lys Cys Asn Tyr Phe Leu Asp Phe Arg Cys Ala
 515 520 525
 Thr Leu Pro Tyr Thr Val Arg Leu Pro Arg Tyr Asp Asp His Pro Leu
 530 535 540
 Thr Leu Cys Tyr Gly Glu Lys Ala Ser Gly Lys Tyr Trp Cys Asp Ile
 545 550 555 560
 Cys Glu Arg Glu Thr Asn Ser Lys Thr Trp Phe Tyr Thr Cys Lys Gly
 565 570 575
 Cys Gly Val Thr Leu His Val Phe Cys Val Leu Gly Asp Ile Arg Tyr
 580 585 590
 Ala Lys Pro Gly Gly Ser Ile Asn Asn Asn Val Glu Leu Val Pro Asn
 595 600 605
 Asn Arg Ser Ser Arg Pro Leu Cys His Asn Cys His Cys His Cys Pro
 610 615 620
 Gly Pro Phe Ile Leu Lys Asp Phe Val Glu Glu Cys Phe Cys Ser Tyr
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 Lys Gly Ile Cys Pro Pro Trp Ala Leu
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<211> 1986

<212> DNA

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PF59082SeqList_PF59082.txt

<221> CDS

<222> (1)..(1986)

<400> 1175

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cct gtg aaa atg gag tcg aag tgt gat tgg tgt gga atc aaa ttc ata	96
Pro Val Lys Met Glu Ser Lys Cys Asp Trp Cys Gly Ile Lys Phe Ile	
20 25 30	
cac ata tct gat ggc tac caa tgt gat tcc tgt ttc act cct tta ttc	144
His Ile Ser Asp Gly Tyr Gln Cys Asp Ser Cys Phe Thr Pro Leu Phe	
35 40 45	
cac aag aca tgc gcc aac gat aag aat atc gcc cac cct tct caa gcg	192
His Lys Thr Cys Ala Asn Asp Lys Asn Ile Ala His Pro Ser Gln Ala	
50 55 60	
tgt ggc atc att ctt tat cat aca gtg aat ttt gat agc ggc aag tgg	240
Cys Gly Ile Ile Leu Tyr His Thr Val Asn Phe Asp Ser Gly Lys Trp	
65 70 75 80	
aga tgt gca aaa tgt gga gaa aag atc tac gat tcc tta ttt ttt gta	288
Arg Cys Ala Lys Cys Gly Glu Lys Ile Tyr Asp Ser Leu Phe Phe Val	
85 90 95	
tgt aac gac tgt gtt tta aaa cct aga aga aaa gga agc aga ttt ggt	336
Cys Asn Asp Cys Val Leu Lys Pro Arg Arg Lys Gly Ser Arg Phe Gly	
100 105 110	
ggt tct tca tat ttc cat ttc aac tgt gct aaa tac cca cct tcg gag	384
Gly Ser Ser Tyr Phe His Phe Asn Cys Ala Lys Tyr Pro Pro Ser Glu	
115 120 125	
gtt att gat gtt cct cag cac cat gac cat aaa ctc aag cta gag atg	432
Val Ile Asp Val Pro Gln His Asp His Lys Leu Lys Leu Glu Met	
130 135 140	
gtg ata agc agc ttc act tgt gct gct tgt gga aaa gat ggt gac gga	480
Val Ile Ser Ser Phe Thr Cys Ala Ala Cys Gly Lys Asp Gly Asp Gly	
145 150 155 160	
tat tcg tac aaa tgt cag gaa tgt aat ttg acg ttt cat gtg aat tgc	528
Tyr Ser Tyr Lys Cys Gln Glu Cys Asn Leu Thr Phe His Val Asn Cys	
165 170 175	
gaa aag tat ccg gca gag gta acc cat ttt tcc cac ttc tta cac cct	576
Glu Lys Tyr Pro Ala Glu Val Thr His Phe Ser His Phe Leu His Pro	
180 185 190	
cta aaa ctc ttc aag ggg gaa cca cct gct tac act gat gga aaa tgt	624
Leu Lys Leu Phe Lys Gly Glu Pro Pro Ala Tyr Thr Asp Gly Lys Cys	
195 200 205	
cgt ttg tgt gga gaa aaa ctt gct aat ttt gaa gtc ttt tat cat tgc	672
Arg Leu Cys Gly Glu Lys Cys Ala Asn Phe Glu Val Phe Tyr His Cys	
210 215 220	
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Ser Ala Cys Asn Phe Ser Leu Asp Leu Gln Cys Val Phe His Pro Pro	
225 230 235 240	
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Lys Gln Asn Pro His Asp Leu Asn Ile His Asp His Pro Leu Thr Leu	
245 250 255	
atg cca aaa tcc atc tct ttt acc tgt acc act tgc ggg cta aat gga	816
Met Pro Lys Ser Ile Ser Phe Thr Cys Thr Thr Cys Gly Leu Asn Gly	
260 265 270	
gat cgg agc cca tac gta tgt ctt cct tgc gat ttt aca agc cac aat	864
Asp Arg Ser Pro Tyr Val Cys Leu Pro Cys Asp Phe Thr Ser His Asn	
275 280 285	
gat tgc tct gga tat cca tgg gtc ata aac atc aac cgc cat gat cat	912
Asp Cys Ser Gly Tyr Pro Trp Val Ile Asn Ile Asn Arg His Asp His	
290 295 300 305	
cgt gtt tct cgc act tcc ctt att ggt gtg gtg aat tca gta tgt gga	960
Arg Val Ser Arg Thr Ser Leu Ile Gly Val Val Asn Ser Val Cys Gly	
310 315 320 325	
att tgt cgc aag aaa atg gat tgg agt tgt ggg ggt tat tct tgt cag	1008
Ile Cys Arg Lys Lys Met Asp Trp Ser Cys Gly Gly Tyr Ser Cys Gln	
330 335	
aag tgt tcg agc tat gtg ttt cat acc aaa tgc gct act aga gaa gat	1056
Lys Cys Ser Ser Tyr Val Phe His Thr Lys Cys Ala Thr Arg Glu Asp	

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cat aaa gag cat aac cta aga ctt gac aag tct ggt att ttt att gag	His Lys Glu His Asn Leu Arg Leu Asp Lys Ser Gly Ile Phe Ile Glu	1200		
gag agg att tgt gag gca tgt gtt tat cct att tat cac cac tcc ttc	Glu Arg Ile Cys Glu Ala Cys Val Tyr Pro Ile Tyr His His Ser Phe	1248		
tat agc tgc atg agt tgt agt ttc att ctt cac gag agt tgc gcc tat	Tyr Ser Cys Met Ser Cys Ser Phe Ile Leu His Glu Ser Cys Ala Tyr	1296		
ctg cct cta tgg aaa cga cat gtg gta agc aac gaa cga cat gag tat	Leu Pro Leu Trp Lys Arg His Val Val Ser Asn Glu Arg His Glu Tyr	1344		
aaa tat tgg gac tat ttt att aga tgt tcg gct tgt aga ttg ctt tcc	Lys Tyr Trp Asp Tyr Phe Ile Arg Cys Ser Ala Cys Arg Leu Leu Ser	1392		
aat ggt ttt aga tac gaa aca acg caa act tca ttg gat ttg cga tgt	Asn Gly Phe Arg Tyr Glu Thr Thr Gln Thr Ser Leu Asp Leu Arg Cys	1440		
gct tca act act gag cca ttt ttc cat aaa act cat cct cat ccc tta	Ala Ser Thr Thr Glu Pro Phe Phe His Lys Thr His Pro His Pro Leu	1488		
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ctt cat gtg ctc aga tgc gtt gaa gat ggt tgt gaa tac atc atg gac	Leu His Val Leu Arg Cys Val Glu Asp Gly Cys Glu Tyr Ile Met Asp	1584		
tat aag tgc gct cta tta cca tat gag gta aag cat agt gtc gac caa	Tyr Lys Cys Ala Leu Leu Pro Tyr Glu Val Lys His Ser Val Asp Gln	1632		
cat ttt ctc tct ttg tgc tat ggt gaa gaa aat gca agt ggt aaa cat	His Phe Leu Ser Leu Cys Tyr Gly Glu Glu Asn Ala Ser Gly Lys His	1680		
tgg tgt gat att tgt gag aaa gaa atg gat cca aaa aca tgg ttt tac	Trp Cys Asp Ile Cys Glu Lys Glu Met Asp Pro Lys Thr Trp Phe Tyr	1728		
acc tct aag gat tgt gag ctt act ttg cat aca gac tgt gtg ctc ggc	Thr Ser Lys Asp Cys Glu Leu Thr Leu His Thr Asp Cys Val Leu Gly	1776		
gat ttt cga ggt ctc aag cca gaa agc gaa gaa tcg atg tac atc gac	Asp Phe Arg Gly Leu Lys Pro Glu Ser Glu Glu Ser Met Tyr Ile Asp	1824		
gac ttc gaa atg tat gtt aag gtg gtt cgc aac aac agt atg tct cga	Asp Phe Glu Met Tyr Val Lys Val Val Arg Asn Asn Ser Met Ser Arg	1872		
cca ctt tgc aaa caa tgc aag tct cgt tgc ata ttt cca gtc atc ttg	Pro Leu Cys Lys Gln Cys Lys Ser Arg Cys Ile Phe Pro Val Ile Leu	1920		
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<211> 661

<212> PRT

<213> Arabidopsis thaliana

<400> 1176

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Cys	Gly	Ile	Ile	Leu	Tyr	His	Thr	Val	Asn	Phe	Asp	Ser	Gly	Lys	Trp	
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Arg	Cys	Ala	Lys	Cys	Gly	Glu	Lys	Ile	Tyr	Asp	Ser	Leu	Phe	Phe	Val	
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Val	Ile	Asp	Val	Pro	Gln	His	His	Asp	His	Lys	Leu	Lys	Leu	Glu	Met	
	130					135					140					
Val	Ile	Ser	Ser	Phe	Thr	Cys	Ala	Ala	Cys	Gly	Lys	Asp	Gly	Asp	Gly	
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Tyr	Ser	Tyr	Lys	Cys	Gln	Glu	Cys	Asn	Leu	Thr	Phe	His	Val	Asn	Cys	
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Glu	Lys	Tyr	Pro	Ala	Glu	Val	Thr	His	Phe	Ser	His	Phe	Leu	His	Pro	
			180					185					190			
Leu	Lys	Leu	Phe	Lys	Gly	Glu	Pro	Pro	Ala	Tyr	Thr	Asp	Gly	Lys	Cys	
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Lys	Gln	Asn	Pro	His	Asp	Leu	Asn	Ile	His	Asp	His	Pro	Leu	Thr	Leu	
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Ile	Gln	Pro	Phe	Thr	Ile	Ile	Asp	Glu	Asn	Thr	Ile	Lys	His	Val	Ser	
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Tyr	Ser	Cys	Met	Ser	Cys	Ser	Phe	Ile	Leu	His	Glu	Ser	Cys	Ala	Tyr	
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Lys	Tyr	Trp	Asp	Tyr	Phe	Ile	Arg	Cys	Ser	Ala	Cys	Arg	Leu	Leu	Ser	
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Asn	Gly	Phe	Arg	Tyr	Glu	Thr	Thr	Gln	Thr	Ser	Leu	Asp	Leu	Arg	Cys	
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Phe	Tyr	Thr	Ser	Pro	Gln	Gly	Ile	Cys	Ser	Ile	Cys	Lys	Lys	Asp	His	
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Tyr	Lys	Cys	Ala	Leu	Leu	Pro	Tyr	Glu	Val	Lys	His	Ser	Val	Asp	Gln	
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<210> 1177

<211> 2079

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(2079)

<400> 1177

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Ala Tyr Ser Cys Gly Glu Cys Lys Phe Thr Val His Lys Lys Cys Thr	
35 40 45	
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Phe Leu Phe Glu Val Val Pro Glu Ile Phe Glu His Pro Ser His Val	
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Pro Lys Cys His Leu Cys Gly Lys Asn Thr Lys Arg Leu Leu Tyr His	
85 90 95	
tgc aga gat tgt aaa ctc aat gtg gat atc gat tgc att att gat ccc	336
Cys Arg Asp Cys Lys Leu Asn Val Asp Ile Asp Cys Ile Ile Asp Pro	
100 105 110	
atg tgt gcc caa gcc gat ctg aat atg ccg tgg cac cac cac cct cta	384
Met Cys Ala Gln Ala Asp Leu Asn Met Pro Trp His His His Pro Leu	
115 120 125	
ttc atg ggt aat ttt gcg act aat atg act tgc gat gtt tgt tat gac	432
Phe Met Gly Asn Phe Ala Thr Asn Met Thr Cys Asp Val Cys Tyr Asp	
130 135 140	
aac cac gta gat ggc tat atc tgt ctt tgc tgt cgg ttg ttc gtt ggg	480
Asn His Val Asp Gly Tyr Ile Cys Leu Cys Cys Arg Leu Phe Val Gly	
145 150 155 160	
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Trp Val Cys Ala Ala Leu Val Ile Asp Ser Pro Glu Ile Thr His Pro	
165 170 175	
tgt cac acc aaa cac cct ctc aag ctt ctc acc gaa gga gca ccc act	576
Cys His Thr Lys His Pro Leu Lys Leu Thr Glu Gly Ala Pro Thr	
180 185 190	
tac act gat cca aaa tgt cat cta tgc gga gaa gac act gga aaa ttc	624
Tyr Thr Asp Pro Lys Cys His Leu Cys Gly Glu Asp Thr Gly Lys Phe	
195 200 205	
atc tat cat tgt gat atc tgt aag ttc aat ttg gat ttg gta tgc gca	672
Ile Tyr His Cys Asp Ile Cys Lys Phe Asn Leu Asp Leu Val Cys Ala	
210 215 220	
aaa aca aaa acc cca cca gtt gct ctt tca aat ctc aag gta cat gag	720
Lys Thr Lys Thr Pro Pro Val Ala Leu Ser Asn Leu Lys Val His Glu	

PF59082SeqList_PF59082.txt

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	Cys	Gly	Thr	Lys	Gly	Asp	Arg	Ala	Pro	Tyr	Val	Cys	His	Gln	Cys	Asp	
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	ttc	atg	ggt	cac	aaa	aag	tgt	gct	cat	tta	cca	cgt	ggt	att	aac	gtc	864
	Phe	Met	Val	His	Lys	Lys	Cys	Ala	His	Leu	Pro	Arg	Val	Ile	Asn	Val	
			275										285				
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	Asn	His	His	Asp	His	Arg	Val	Ser	Phe	Lys	Tyr	Pro	Leu	Gly	Leu	Gly	
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Phe Tyr Gly Gly Tyr Val Cys Asn Glu Val Gly Cys Asp Thr Leu Phe	
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His Lys Glu Cys Val Glu Ser Val Pro Glu Ile Lys His Pro Ser His	
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	Asp	Phe	Asn	Val ₁₀₀	His	Leu	Val	Cys	Ala ₁₀₅	Arg	Arg	Pro	Pro	Ser ₁₁₀	Ser	Thr
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PF59082SeqList_PF59082.txt

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Arg	Pro	His	Cys	Ser	Arg	Cys	Ser	Ser	Arg	Cys	Lys	Leu	Pro	Tyr	Ile
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Glu Arg Phe Tyr Phe Gly Arg Cys Ser Gly Cys Ser Arg Glu Gly Tyr
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Phe Tyr Gly Gly Tyr Arg Cys Asn Glu Leu Ala Cys Phe Ala Val Phe
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His Lys Glu Cys Ala Glu Ser Lys Pro Glu Ile Ser His His Ala His
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Gln Leu Ser Ser Ile Glu Asn Tyr Lys Val His Glu His Pro Leu Lys
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Asp Arg Ser Pro Tyr Phe Cys Leu Gln Cys Asn Phe Met Ile His Arg
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Pro	Phe	Val	His	Glu	Arg	His	Pro	His	Pro	Leu	Tyr	Tyr	Lys	Phe	Phe	
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Thr	Phe	Ser	Ala	Val	Ala	Lys	Cys	Asp	Ile	Cys	His	Ile	Thr	Arg	Arg	
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His	Leu	Leu	Cys	Cys	Glu	Glu	Cys	Asp	Phe	Arg	Leu	Asp	Phe	Arg	Cys	
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Ala	Thr	Leu	Pro	Lys	Lys	Val	Met	Lys	Gln	Arg	Tyr	Asp	Asp	His	Pro	
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Asp	Ala	Cys	Gly	Val	Thr	Leu	His	Val	Ser	Cys	Val	Val	Gly	Asp	Phe	
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Ser	Ile	Cys	Arg	Pro	Leu	Cys	Ser	Arg	Cys	His	Thr	Arg	Cys	Lys	Leu	
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cct	tgc	att	ctt	gaa	acc	tcc	gag	gat	ggg	gtt	aat	gtt	tac	ttt	tgt	2016
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PF59082SeqList_PF59082.txt

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Pro Lys His Leu Leu Lys Leu Gly Asn Arg Arg Gln Arg Cys His Leu
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Gly Met His Leu Val Cys Ala Lys Ser Pro Pro Leu Ser Leu Gln Pro
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Asn Tyr Ile Ile Gly Asn Gly Asp Ser Ala Pro Phe Tyr Glu Cys Arg
145 150 155 160
Arg Cys Lys Leu Tyr Ile His Val Thr Cys Leu Glu Leu Phe Phe Thr
165 170 175
Thr Asp Ala Arg His Asn Ser His Leu Lys His Pro Leu Lys Tyr Leu
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Lys Asn Gly Pro Pro Ser Tyr Ala Asp His Lys Cys Leu Cys Gly
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Pro Leu Val Val Val Thr Pro Lys Thr His Glu His Gln Leu His Leu
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Gly Cys Ile Asp Leu Pro Arg Ile Ile Asn Ile Asn Arg His Asp His
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Lys Cys Ser Ser Tyr Val Val His Ser Leu Cys Ala Thr Arg Lys Asp
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Ala Pro Phe Glu Val Val Asp Glu Asn Thr Ile Lys His Met Ser His
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Asp His Asp Leu Ile Phe Asn Asn Asp Gly Ile Asn Leu His Glu Ser
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Lys Leu Cys Glu Ala Cys Val Ser Gln Ile Asn Thr Asp Pro Phe Tyr
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Ser Cys Glu Leu Cys Gly Phe Ile Leu His Gln Thr Cys Ala Asn Met
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Thr Asp Asp Ser Lys Asp Ser Ser Arg Leu Arg Arg Lys Cys Ser Leu
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PF59082SeqList_PF59082.txt

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Ala Thr Leu Pro Lys Lys Val Met Lys Gln Arg Tyr Asp Asp His Pro
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Asp Val Cys Glu Lys Arg Val Asp Ala Lys Thr Trp Phe Tyr Thr Cys
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Asp Ala Cys Gly Val Thr Leu His Val Ser Cys Val Val Gly Asp Phe
                               595                               600                               605
Ser Tyr His Met Pro Gly Pro Leu Ser Thr Val Val Ser Glu Tyr Lys
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Met Val Pro Pro Ala Val Val Ser Leu Tyr Lys Val Val Pro Asn Thr
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Pro Cys Ile Leu Glu Thr Ser Glu Asp Gly Val Asn Val Tyr Phe Cys
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<400> 1185

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Gln Leu Met Phe Val Glu Tyr Phe Asn Leu Tyr Trp Asp Ala Thr Pro
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Leu Leu Thr Glu Leu Ile Leu Leu Val Ser Ser Met Asp Leu Asp Ser
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cag ccg aag ccg gag tca gag ttc atg tca ctc act act caa gca ata      192
Gln Pro Lys Pro Glu Ser Glu Phe Met Ser Leu Thr Thr Gln Ala Ile
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Asp Leu Met Ser Met Val Phe Gln Asn Leu Ser Leu Phe Asn Ser Ala
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ttg gac tcg gaa gcc aca aca ctc ttt ggt aaa ata atc tct ctg gtc      336
Leu Asp Ser Glu Ala Thr Thr Leu Phe Gly Lys Ile Ile Ser Leu Val
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agc tca atg gat ttg act aca gag gag aag cca gag tct gat gag cta      384
Ser Ser Met Asp Leu Thr Thr Glu Glu Lys Pro Glu Ser Asp Glu Leu
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gtg tta ctc atc caa gag ata ctc tct cta gtc aac tct agg gat tca      432
Val Leu Leu Ile Gln Glu Ile Leu Ser Leu Val Asn Ser Arg Asp Ser
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Asp Ser Gln Pro Lys Arg Leu Val Glu Leu Ile Ser Phe Ile Ser Gln
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PF59082SeqList_PF59082.txt

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Leu	Ile	Ser	Leu	Thr	His	Gln	Ile	Leu	Ser	Leu	Val	Val	Ser	Met	Asn		
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195							200					205					
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Leu	Glu	Asn	Gly	Arg	Phe	Arg	Val	Leu	Glu	Asp	Val	Ser	Trp	Arg	Thr		
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Asn	Asn	Lys	Trp	His	Cys	Leu	Ser	Val	Asn	Trp	Arg	Thr	Phe	Lys	Leu		
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Ser	Arg	Glu	Glu	Asp	Thr	Leu	His	Phe	Ile	Cys	Ile	Gly	Cys	Asn	Gly		
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Leu	His	Pro	Asn	His	Ser	Leu	Gln	Leu	Val	Val	Leu	Gln	Glu	Asp	Ser		
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Thr	Arg	Glu	Cys	Tyr	Cys	Cys	Asp	Glu	Ala	Leu	Ser	Arg	Ile	Leu	Tyr		
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Tyr	Cys	Ser	Ala	Cys	Asp	Phe	Ala	Ile	Ser	Ile	Leu	Cys	Ala	Arg	Lys		
305					310					315					320		
cca	cca	gtc	ttt	ttg	ata	aac	cat	cac	cgt	ccg	gag	tgg	cat	ggg	cat		1008
Pro	Pro	Val	Phe	Leu	Ile	Asn	His	His	Arg	Pro	Glu	Trp	His	Gly	His		
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cct	ctt	gct	ctg	ttt	cca	aga	caa	gct	ttc	tta	act	tgc	aac	ctt	tgc		1056
Pro	Leu	Ala	Leu	Phe	Pro	Arg	Gln	Ala	Phe	Leu	Thr	Cys	Asn	Leu	Cys		
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gcc	ttg	gcc	gat	cca	agc	tct	cct	atc	tat	atg	tgt	ccg	cct	tgt	gac		1104
Ala	Leu	Ala	Asp	Pro	Ser	Ser	Pro	Ile	Tyr	Met	Cys	Pro	Pro	Cys	Asp		
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Gly	Leu	Ser	Cys	Gly	Val	Cys	Arg	Arg	Lys	Ile	Asn	Lys	Leu	Tyr	Gly		
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Gly	Tyr	Ser	Cys	Ile	Lys	Asn	Gly	Cys	Trp	Tyr	Ala	Ala	His	Ser	Arg		
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Cys	Ala	Thr	Gln	Lys	Asn	Val	Trp	Asp	Gly	Val	Glu	Leu	Glu	Gly	Val		
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PF59082SeqList_PF59082.txt

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Leu	Tyr	Leu	Thr	Ser	Lys	Pro	Asp	Glu	Glu	Gln	Arg	Lys	Cys	Ser	Val	
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Asn	Asn	His	His	Met	Ser	Arg	Pro	Phe	Cys	Phe	Ile	Cys	Lys	Lys	Arg	
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Cys	Pro	His	Lys	Thr	Phe	Phe	Gln	Cys	Asn	Gly	Phe	Glu	Tyr	Cys	Ser	
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Leu	Asp	Ser	Glu	Ala	Thr	Thr	Leu	Phe	Gly	Lys	Ile	Ile	Ser	Leu	Val	
			100					105					110			
Ser	Ser	Met	Asp	Leu	Thr	Thr	Glu	Glu	Lys	Pro	Glu	Ser	Asp	Glu	Leu	

Val	Leu	Leu	Ile	Gln	Glu	Ile	Leu	Ser	Leu	Val	Asn	Ser	Arg	Asp	Ser
Asp	130	Ser	Gln	Pro	Lys	Arg	135	Leu	Glu	Leu	140	Ser	Phe	Ile	Ser
145	Ile	Ser	Leu	Ile	Asp	Glu	Thr	Leu	Glu	155	Val	Lys	Pro	Glu	Pro
Lys	160			165	Thr	His	Gln	Ile	Leu	Ser	Leu	Val	Val	Ser	Met
Leu	180	Ile	Ser	Leu	Thr	His	Gln	Ile	Leu	Ser	Leu	Val	Val	Ser	Met
Ser	Asn	Ser	195	Gly	Glu	Tyr	Ile	Ser	200	Leu	Cys	Pro	Gln	Ala	205
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Asn	225	Asn	Lys	Trp	His	Cys	230	Leu	Ser	Val	Asn	Trp	Arg	Thr	Phe
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Asp	Asn	His	Lys	Glu	Phe	Asn	Asn	Val	Pro	Val	Glu	Ile	Asn	His	Pro
Leu	His	Pro	275	Asn	His	Ser	Leu	Gln	280	Leu	Val	Val	Leu	Gln	285
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PF59082SeqList_PF59082.txt

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Arg Cys Leu Gln Ile Pro Ser Lys Met Ile His Pro Tyr His Pro Gln
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His Pro Leu Thr Phe Thr Phe Val Ser Tyr Glu Thr Lys Ile Val Val
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Asp Val Asn Tyr Gly Asp Phe Cys Thr Phe Leu Cys Arg Ser Gly Leu
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Cys	Asp	Phe	Asp	Leu	Cys	Leu	Tyr	Cys	Ala	Thr	Leu	Pro	Lys	Lys	Ile	
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Asp	Pro	Ser	Ile	Trp	Phe	Tyr	Thr	Cys	Phe	Asp	Cys	Gly	Val	Thr	Leu	
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 Asp Gly Cys Lys Lys Asn Ile Asp Asp Tyr Met Leu Arg Cys Lys Ala
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 Ser Ile Cys Asp Gly Tyr Tyr Cys Lys Ile Cys Asp Ile Phe Val His
 35 40 45
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 Lys Lys Cys Gly Glu Ser Ser Glu Tyr Ile Glu His Pro Ser His Pro
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 Asn His Thr Leu Gln Leu Leu Ser Thr Arg Gly Asn Ser His Asp Cys
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 Asp Leu Cys Gly Lys Asn Ile Gly Asp Leu Phe Tyr Arg Cys Glu Ile
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 Cys Asp Phe Asp Met Asp Leu Tyr Cys Ala Lys Tyr Pro Pro Pro Glu
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 Val Ile Asn Ile Ser Lys Thr His His His Lys Leu Asn Leu Leu Lys
 115 120 125
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ctt Leu	tgg Trp 210	aat Asn	ttg Leu	aaa Lys	gct Ala	cat His 215	gac Asp	cac His	caa Gln	ctc Leu	acc Thr 220	ctg Leu	ctc Leu	cca Pro	agt Ser	672
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tat Tyr	gtg Val	gta Val	ata Ile 340	gat Asp	gac Asp	aat Asn	aca Thr	ata Ile 345	caa Gln	cat His	ttc Phe	agc Ser 350	cac His	aaa Lys	gag Glu	1056
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His Trp Leu Lys Val Val Arg Ser Cys Asp Leu Cys Gly Lys Asn Ile				
85	90	95		
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Gly Asp Leu Phe Tyr Arg Cys Glu Ile Cys Asp Phe Asp Met Asp Leu				
100	105	110		
cac tgt gcc aag tat cca cca cta gag gtt att gac att ccc gag atg	384			
His Cys Ala Lys Tyr Pro Pro Leu Glu Val Ile Asp Ile Pro Glu Met				
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130	135	140		
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Asp Ala Lys Cys Gly Lys Ile Gly Tyr Gly Phe Pro Tyr Glu Cys His				
145	150	155	160	
gaa tgt gat tca aag ttc cat gtg gat tgc gta agg tac tcc tca tcg	528			
Glu Cys Asp Ser Lys Phe His Val Asp Cys Val Arg Tyr Ser Ser Ser				
165	170	175		
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Glu Glu Val Lys His Pro Leu Glu Val Asn His Ser Tyr His Ser Leu				
180	185	190		
cac cct ctt aag ctc ctc atg ggt caa cca cca gac tac tct gat gga	624			
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Lys Cys Arg Leu Cys Gly Arg Lys Ile Asp Asp Lys Leu Phe Tyr His				
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Cys Ser Ser Cys Asn Phe Thr Leu Asp Met Arg Cys Val Leu Asn Pro				
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Pro Pro Lys Ser Val Leu Asp Leu Lys Thr His Asp His Gln Leu Asn				
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Leu Leu Pro Arg Leu Ile Phe Phe Thr Cys Asn Ala Cys Gly Leu Asn				
260	265	270		
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Gly Asp Arg Ser Pro Tyr Ala Cys Phe Gln Cys Asp Phe Leu Ile His				
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Gly Val Cys Arg Gln Lys Val Asp Trp Thr Cys Gly Gly Tyr Ser Cys				
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Gln Arg Cys Ser Thr Tyr Ile Ala His Ser Lys Cys Ala Thr Arg Glu				
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Asp Val Trp Asn Gly Lys Glu Leu Glu Gly Val Pro Glu Glu Ile Glu				
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Asp Ile Glu Pro Tyr Val Val Ile Asp Asp Asn Thr Ile Gln His Phe				
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Glu Val Asn Lys Arg Cys Asn Ala Cys Asn His Pro Ile Ser Pro Gln				
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gct Ala	tta Leu 450	gtc Val	act Thr	agc Ser	gag Glu	gtt Val 455	aat Asn	att Ile	ttc Phe	ggg Gly 460	tgt Cys	agt Ser	gct Ala	tgt Cys	cac His	1392
aaa Lys 465	att Ile	ttc Phe	aat Asn	ggt Gly 470	ttt Phe	aga Arg	tac Tyr	gag Glu	cat His	gag Glu 475	gat Asp	aca Thr	aaa Lys	tta Leu	gat Asp 480	1440
gtc Val	ctt Leu	tgt Cys	ggt Gly 485	tca Ser	ttt Phe	tct Ser	gag Glu	cca Pro	ttt Phe 490	atc Ile	cat His	cca Pro	agt Ser	cat His 495	cct Pro	1488
cat His	cat His	ccg Pro	tta Leu 500	tat Tyr	tgc Cys	att Ile	tca Ser	cct Pro 505	gag Glu	gat Asp	gat Asp	gaa Glu	gta Val 510	tgc Cys	agt Ser	1536
ggc Gly	tgt Cys	aac Asn 515	gag Glu	agg Arg	agc Ser	tat Tyr	cat His 520	gtg Val	ctt Leu	aga Arg	tgc Cys	att Ile 525	gaa Glu	gac Asp	aat Asn	1584
tgt Cys	ggg Gly 530	ttt Phe	atc Ile	ttg Leu	gat Asp	ttt Phe 535	ggt Gly	tgc Cys	gcc Ala	act Thr	ttt Phe 540	cca Pro	caa Gln	gtg Val	gta Val	1632
aag Lys 545	cat His	aga Arg	att Ile	gaa Glu	gac Asp 550	caa Gln	cct Pro	ctt Leu	tct Ser	cta Leu 555	tgc Cys	tat Tyr	ggt Gly	gaa Glu	aag Lys 560	1680
gca Ala	agt Ser	gga Gly	aaa Lys	tat Tyr 565	tgg Trp	tgt Cys	gac Asp	att Ile	tgt Cys 570	gaa Glu	aag Lys	gaa Glu	acc Thr	aat Asn 575	cca Pro	1728
aac Asn	aca Thr	tgg Trp	ttc Phe 580	tac Tyr	aca Thr	tgt Cys	aaa Lys	gat Asp 585	cat His	cgg Arg	gca Ala	agt Ser	ttg Leu 590	cat His	aca Thr	1776
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gag Glu	cta Leu 610	tgg Trp	aac Asn	ata Ile	tca Ser	tat Tyr 615	gaa Glu	gtg Val	gtg Val	ctc Leu	aat Asn 620	aat Asn	agt Ser	att Ile	tct Ser	1872
cgc Arg 625	cca Pro	att Ile	tgc Cys	agg Arg	cac His 630	tgt Cys	aag Lys	tcg Ser	cat His	tgc Cys 635	att Ile	ccc Pro	cct Pro	att Ile 640	atc Ile 640	1920
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Glu	Cys	Asp	Ser	Lys	Phe	His	Val	Asp	Cys	Val	Arg	Tyr	Ser	Ser	Ser
				165					170					175	
Glu	Glu	Val	Lys	His	Pro	Leu	Glu	Val	Asn	His	Ser	Tyr	His	Ser	Leu
			180					185					190		
His	Pro	Leu	Lys	Leu	Leu	Met	Gly	Gln	Pro	Pro	Asp	Tyr	Ser	Asp	Gly
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	610					615					620				
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 Asp Leu Cys Gly Arg Arg Thr Asn Tyr Leu Ser Tyr Tyr Cys Glu Ile
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 Cys Gly Phe Ile Val Asp Leu His Cys Ala Met Tyr Pro Pro Glu
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 Phe Ile Glu Asn Ser Glu Arg His His His Lys Leu Thr Leu Leu Lys
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 Glu Arg Ile Ala Ala Phe Asp Cys Asp Ala Lys Cys Gly Lys Ile Ser
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 Ile Asn Ile Asn Arg His Asp His Arg Val Ser Arg Thr Ser Val Leu
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His Pro Asn His Thr Leu Glu Leu Cys Ser Asn Leu Arg Phe His Cys
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Phe Ile Glu Asn Ser Glu Arg His His His Lys Leu Thr Leu Lys
115     120     125
Glu Arg Ile Ala Ala Phe Asp Cys Asp Ala Lys Cys Gly Lys Ile Ser
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Gly Asn Glu Phe Ala Tyr Lys Cys Gln Glu Cys Asp Leu Thr Phe His
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Val Asp Cys Val Trp His Pro Ser Glu Val Tyr His Pro Leu Glu Val
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Asn His Ser Tyr His Pro Ser His Pro Leu Lys Leu His Thr Gly Gln
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Asp Asp Arg Tyr Phe Tyr His Cys Ser Ser Cys Asn Phe Thr Leu Asp
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Gln Cys Gly Phe Met Ile His Gln Asp Cys Leu Ser Leu Pro Arg Leu
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Ile Asn Ile Asn Arg His Asp His Arg Val Ser Arg Thr Ser Val Leu
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Val Leu His Asn Glu Arg Leu Thr Leu Val Ser Tyr Glu Tyr Asp Phe
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465     470     475     480
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Asp Glu Glu Thr Lys Ser Ser Cys Asn Gly Cys Asn Lys Ser Ser Tyr
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Ser Trp Leu Met Pro Gly Ser Thr Ile Asp Leu Ser Glu Leu Ser Lys
595 600 605
Val Val Leu Asn Asn Ser Ile Ser Arg Pro Phe Cys Ser Gly Cys Lys
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Arg Phe Glu Ala Ile Ser Asp Gly Tyr Tyr Cys Lys Thr Cys Asp Phe
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ttc gtc cga aaa aat tgt gct gac gag ccc tcc gaa tat atc aag cat      192
Phe Val Arg Lys Asn Cys Ala Asp Glu Pro Ser Glu Tyr Ile Lys His
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cca tct cac ccc aag cac act ctt cag ctg cta aga cct gaa aga cct      240
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Thr Asn Phe Cys Asn Leu Cys Gly Arg Met Cys Pro Ile Phe Tyr Arg
85 90 95
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Cys Asp Leu Cys Asp Phe Asp Met Asp Leu Tyr Cys Ser Lys Tyr Pro
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cca cca gag gtt att gac att tcc aag acg cat cac cac agg ctt acc      384
Pro Pro Glu Val Ile Asp Ile Ser Lys Thr His His His Arg Leu Thr
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130 135 140
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Ile Ile Gly Asn Glu Phe Pro Tyr Asn Cys His Glu Cys Asp Leu Ser
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Glu Val Asn His Ser Tyr His Ser Leu His Pro Leu Lys Leu Tyr Ala
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Lys Gly Gln Leu Pro Asp Tyr Ser Asp Gly Lys Cys Arg Leu Cys Ala
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Ser	Phe	Thr	Cys 260	Asn	Ala	Cys	Gly	Leu	Lys	Gly	Asp	Arg	Ser	Pro	Tyr	
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 465 470 475 480
 Ser Glu Pro His Ile His Pro Ser His Pro Asn His Pro Leu Tyr Tyr
 485 490 495
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 580 585 590
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 595 600 605
 Tyr Glu Val Val Leu Asn Asn Ser Ile Ser Arg Pro Phe Cys Ser Trp
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 Ala Ile Ser Asp Gly Tyr Tyr Cys Lys Thr Cys Asp Phe Phe Val His 35 40 45
 aag agc tgt ggc gat agg tcc tcc gaa tat atc gag cat cca tct cac 192
 Lys Ser Cys Gly Asp Arg Ser Ser Glu Tyr Ile Glu His Pro Ser His 50 55 60
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 Pro Ser His Ala Leu Gln Leu Leu Arg Lys Pro Gly His Thr Arg Asn 65 70 75 80
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 Ile Cys Asn Phe Asn Val His Met Tyr Cys Ala Lys Tyr Pro Pro Pro 100 105 110
 caa gtt att gac att tcc gag acg cat cac cac aag ctc aac ctt tac 384
 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995

PF59082SeqList_PF59082.txt

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Asp	Cys	Ala	Trp	Arg	Pro	Ser	Glu	Ser	Asn	Leu	Pro	Leu	Glu	Val	Asn	
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His	Phe	Tyr	His	Ser	Leu	His	Pro	Leu	Lys	Leu	Val	Arg	Gly	Lys	Leu	
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ccg	gac	tat	tct	gac	aga	aaa	tgt	cgt	ctt	tgc	gga	aga	tat	att	ggg	624
Pro	Asp	Tyr	Ser	Asp	Arg	Lys	Cys	Arg	Leu	Cys	Gly	Arg	Tyr	Ile	Gly	
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 Lys Cys Ala Thr Arg Lys Asp Val Trp Asn Gly Lys Glu Leu Glu Gly
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 Val Pro Glu Glu Thr Glu Asp Ile Gln Pro Tyr Val Val Ile Asp Glu
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 Val Asn Gly Val Leu Cys Asp Asp Asn Lys Trp Cys Ser Ala Cys Thr
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 His Pro Ile Cys Leu Gln Ser Phe Tyr Gly Cys Met Asp Cys Asp Phe
 405 410 415
 Ile Leu His Gln Asn Cys Ala Gly Phe Arg Arg Met Lys Trp His Val
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 Arg Cys Tyr Ala Cys Asp Arg Trp Ser Asn Gly Phe Arg Tyr His Gln
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 Gly Asn Ile Thr Phe Asp Val Arg Cys Gly Ser Ile Ala Glu Pro Phe
 465 470 475 480
 Leu His Pro Ser His Pro Asp His Pro Leu Tyr His Thr Leu Pro Asp
 485 490 495
 Gly Gly Ile Lys Ile Cys Asn Gly Cys Lys Asn Gly Phe Tyr Asp Val
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 Leu Gly Cys Ile Glu Asp Asp Cys Arg Phe Ala Ile Cys Phe Lys Cys
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48

96

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Cys	Asn	Ala	Cys	Gly	Leu	Ser	Gly	Asp	Arg	Ser	Pro	Tyr	Ile	Cys	Ile	
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caa	tgt	gac	ttt	atg	atc	cat	caa	gat	tgt	ctt	gac	ctt	cca	cgc	ctc	1872
Gln	Cys	Asp	Phe	Met	Ile	His	Gln	Asp	Cys	Leu	Asp	Leu	Pro	Arg	Leu	
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Ile	Asn	Val	Asn	Arg	His	Asp	His	Arg	Val	Ser	Arg	Thr	Ser	Val	Leu	
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ggg	gtt	gta	aat	tct	gta	tgt	gga	gtt	tgt	cat	cag	aag	gtg	gat	tgg	1968
Gly	Val	Val	Asn	Ser	Val	Cys	Gly	Val	Cys	His	Gln	Lys	Val	Asp	Trp	
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Gly	Val	Pro	Glu	Glu	Ile	Glu	Asp	Ile	Glu	Pro	Tyr	Val	Val	Ile	Asp	
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Asp	Asn	Thr	Ile	Gln	His	Phe	Ser	His	Lys	Glu	His	Tyr	Leu	Arg	Leu	
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cac	gtt	aat	gat	gtt	cta	tgt	aac	gac	aac	aag	cgg	tgc	aag	gca	tgc	2208
His	Val	Asn	Asp	Val	Leu	Cys	Asn	Asp	Asn	Lys	Arg	Cys	Lys	Ala	Cys	
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acc	cat	ccc	atc	ttt	ctt	caa	tcc	ttc	tac	agt	tgt	atg	gat	tgt	gac	2256
Thr	His	Pro	Ile	Phe	Leu	Gln	Ser	Phe	Tyr	Ser	Cys	Met	Asp	Cys	Asp	
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Phe	Leu	Leu	His	Gln	Asn	Cys	Ala	Gly	Phe	Pro	Arg	Met	Lys	Arg	His	
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cat	gga	tat	aag	tca	ctc	gat	ctt	cag	tgt	ggt	tca	ata	tcc	gag	cca	2448
His	Gly	Tyr	Lys	Ser	Leu	Asp	Leu	Gln	Cys	Gly	Ser	Ile	Ser	Glu	Pro	
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Phe	Val	His	Pro	Ser	His	Pro	Asp	His	Pro	Leu	Tyr	His	Thr	Leu	Leu	
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gat	gga	agg	aat	gag	att	tgt	gat	ggc	tgc	aaa	aag	agt	tgg	tat	tat	2544
Asp	Gly	Arg	Asn	Glu	Ile	Cys	Asp	Gly	Cys	Lys	Lys	Ser	Trp	Tyr	Tyr	
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Cys	Leu	Thr	Leu	Pro	Gln	Val	Val	Lys	His	Arg	Val	Asp	Asp	Asp	Pro	
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Ile	Cys	Glu	Lys	Glu	Thr	Asn	Pro	Glu	Thr	Trp	Phe	Tyr	Thr	Cys	Lys	
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gat	cat	caa	tct	agt	atg	cat	aca	atg	tgt	gtg	ctt	ggt	gac	tct	gta	2784
Asp	His	Gln	Ser	Ser	Met	His	Thr	Met	Cys	Val	Leu	Gly	Asp	Ser	Val	
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Ser	Lys	Ala	Val	Ser	Val	Gly	Tyr	Tyr	Cys	Lys	Ser	Cys	Asp	Phe	Phe	
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Ala	His	Lys	Lys	Cys	Gly	Glu	Ser	Ser	Glu	Phe	Ile	Gln	His	Pro	Ser	
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Cys	Asn	Leu	Cys	Gly	Arg	Thr	Ile	Ser	Asp	Leu	Phe	Tyr	Arg	Cys	Asp	
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 Asn His Ser Tyr His Ser Leu His Pro Leu Lys Leu Leu Ser Gly Gln
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 Leu Pro Asp Asn Cys Asp Gly Lys Cys Arg Leu Cys Ala Arg Lys Ile
 225 230 235 240
 Asp Asp Arg Leu Phe Tyr His Cys Ser Pro Cys Asn Phe Thr Leu Asp
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 Leu Arg Cys Val Leu Asn Pro Pro Gln Gln Ser Leu Leu Asn Leu Lys
 260 265 270
 Ala His Asp His Gln Leu Thr Leu Pro Arg Leu Leu Ser Phe Thr
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 Cys Asn Ala Cys Gly Leu Asn Gly Asp Arg Ser Pro Tyr Thr Cys Val
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 Gln Cys Asp Phe Met Ile His Gln Asp Cys Leu Asp Leu Pro Arg Val
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 Cys Asn Leu Cys Gly Arg Ser Lys Gly Val Asn Val Cys Tyr Arg Cys
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 Asp His Cys Tyr Tyr Gln Leu Asp Leu Tyr Cys Ala Lys Tyr Pro Pro
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 Pro Glu Phe Ile Asp Ile Pro Glu Thr His His His Lys Leu Thr Leu
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 Gly Asp Gly Phe Ala Tyr Lys Cys Pro Glu Cys Asp Leu Phe Phe His
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 Cys Asn Ala Cys Gly Leu Ser Gly Asp Arg Ser Pro Tyr Ile Cys Ile
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 Thr Cys Gly Gly Phe Ser Cys Gln Arg Cys Ser Ser Tyr Val Val His
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 Gly Val Pro Glu Glu Ile Glu Asp Ile Glu Pro Tyr Val Val Ile Asp
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Thr His Pro Ile Phe Leu Gln Ser Phe Tyr Ser Cys Met Asp Cys Asp
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Phe Leu Leu His Gln Asn Cys Ala Gly Phe Pro Arg Met Lys Arg His
755          760          765
Val Leu His Asn Glu Arg Leu Thr Leu Val Thr Asn Glu Thr Lys Leu
770          775          780
Phe Gln Cys Ala Pro Cys Asp Arg Trp Ser Asn Gly Phe Arg Tyr Gln
785          790          795
His Gly Tyr Lys Ser Leu Asp Leu Gln Cys Gly Ser Ile Ser Glu Pro
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Phe Val His Pro Ser His Pro Asp His Pro Leu Tyr His Thr Leu Leu
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835          840          845
Val Leu Ser Cys Ile Glu Asp Asp Cys Arg Phe Val Leu Cys Phe Lys
850          855          860
Cys Leu Thr Leu Pro Gln Val Val Lys His Arg Val Asp Asp Asp Pro
865          870          875
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885          890          895
Ile Cys Glu Lys Glu Thr Asn Pro Glu Thr Trp Phe Tyr Thr Cys Lys
900          905          910
Asp His Gln Ser Ser Met His Thr Met Cys Val Leu Gly Asp Ser Val
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Gly Ile Met Pro Lys Ser Thr Ile Met Gly Trp Tyr Lys Tyr Tyr Glu
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Ile Pro Cys Asn His Leu Arg Lys Gly Asp Cys Cys Gly Arg Phe Glu
20          25          30
gct ata agc gat ggc tac tac tgc aaa aca tgc gat ttt ttc gtc cac      144
Ala Ile Ser Asp Gly Tyr Tyr Cys Lys Thr Cys Asp Phe Phe Val His
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aag aaa tgt gtc gat gag gcc tct gaa tct atc gag cat cca tct cat      192
Lys Lys Cys Val Asp Glu Ala Ser Glu Ser Ile Glu His Pro Ser His
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ccc ggt cac act ctt cag ctt cta agt aaa caa aaa tat cgt tat tgt      240
Pro Gly His Thr Leu Gln Leu Leu Ser Lys Gln Lys Tyr Arg Tyr Cys
65          70          75
aat tta tgt gga agg gac att aag gat cta tgc tat cat ttt ggt aac      288
Asn Leu Cys Gly Arg Asp Ile Lys Asp Leu Cys Tyr His Phe Gly Asn
85          90          95
ttc gac gtg gat cta tat tgt gca aag tac cca cca cca gag gtt att      336
Phe Asp Val Asp Leu Tyr Cys Ala Lys Tyr Pro Pro Pro Glu Val Ile
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Glu Ser Ser Glu Thr Pro Cys His Lys Arg Thr Leu Leu Lys Glu Lys

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Phe	Thr	Leu	Asp	Met	Arg	Cys	Ala	Leu	Asn	Pro	Pro	Ser	Ile	Ser	Phe	
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Glu	Asp	Ser	Lys	Thr	His	Asp	His	Gln	Leu	Thr	Leu	Leu	Pro	Arg	Leu	
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Asp	Tyr	Pro	Leu	Leu	Leu	Cys	Tyr	Gly	Glu	Lys	Ala	Asn	Gly	Ile	Tyr			
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Ser	Tyr	Glu	Val	Val	Leu	Asn	Lys	Asn	Val	Ser	Arg	Pro	Phe	Cys	Arg			
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 Pro Gly His Thr Leu Gln Leu Leu Ser Lys Gln Lys Tyr Arg Tyr Cys
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 Asp Ser Phe Thr Cys Asn Ala Cys Gly Leu Lys Gly Asp Arg Ser Pro
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 Lys Glu Leu Glu Gly Val Ile Glu Glu Thr Glu Asp Ile Glu Pro Tyr
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 Tyr Ile Ser Pro Glu Met Glu Glu Val Cys Asn Gly Cys Asn Met Ser
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gat aca cag atc cca cca atc ttt acg gga aag tct ctc aca tac gat	Asp Thr Gln Ile Pro Pro Ile Phe Thr Gly Lys Ser Leu Thr Tyr Asp	384		
gcg aag ctt ctc ctc tat acg aag acg tta gcg agc cgg gat gca aat	Ala Lys Leu Leu Leu Tyr Thr Lys Thr Leu Ala Ser Arg Asp Ala Asn	432		
gtc gta tca ctc ata gtt gaa att gtc act ctg gtc aac tct acg gat	Val Val Ser Leu Ile Val Glu Ile Val Thr Leu Val Asn Ser Thr Asp	480		
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gaa gat ctc aag aat atc ttt tat tgc tcc gct tgc gag ttt gct	Glu Asp Leu Lys Asn Ile Phe Tyr Tyr Cys Ser Ala Cys Glu Phe Ala	1104		
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gac	tta	tac	atg	aag	cat	ggg	tca	tct	tca	ttt	tat	tta	gag	aaa	acg	1968	
Asp	Leu	Tyr	Met	Lys	His	Gly	Ser	Ser	Ser	Phe	Tyr	Leu	Glu	Lys	Thr		
				645					650					655			
gta	gac	gtt	ctg	tcc	aat	aat	cat	cat	atg	act	cga	cct	att	tgc	tgc	2016	
Val	Asp	Val	Leu	Ser	Asn	Asn	His	His	Met	Thr	Arg	Pro	Ile	Cys	Cys		
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Tyr	Cys	Glu	Lys	Arg	Cys	Pro	Tyr	Lys	Ile	Cys	Leu	Glu	Trp	Ser	Gly		
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Ser	Ile	Tyr	Cys	Ser	Ser	Asp	Cys	Ile	Phe	Thr	Phe	Leu	Ile	Phe			
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Ile	Ile	Ser	Leu	Ile	Ala	Gln	Ile	Ile	Ser	Leu	Val	Ser	Ser	Met	Asp		
		35				40						45					
Leu	His	Ser	Gln	Pro	Lys	Pro	Glu	Ser	Glu	Phe	Met	Ser	Leu	Val	Thr		
	50					55					60						
Gln	Ala	Ile	Ser	Leu	Phe	Asp	Ser	Met	Asp	Leu	Asn	Pro	Glu	Leu	Ser		
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Pro	Leu	Ser	Glu	Leu	Ile	Ser	Leu	Leu	Ser	Gln	Ile	Ile	Ser	Thr	Asp		
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Leu	Cys	Glu	Thr	Leu	Phe	Gly	Gln	Pro	Glu	Pro	Glu	Leu	Val	Ser	Leu		
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Ile	Tyr	Gln	Ile	Phe	Ser	Leu	Val	Ser	Ser	Ile	Asn	Ser	Lys	Ser	Glu		
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			180				185						190				
Tyr	Phe	Gly	Cys	Lys	Gly	Cys	Asn	Gly	Lys	Asn	His	Glu	Glu	Tyr	Glu		
		195					200					205					
Gln	Ala	Pro	Asp	Glu	Ile	Lys	His	His	Leu	His	Arg	Lys	His	Ser	Leu		
	210					215					220						
Gln	Leu	Val	Phe	Phe	Ser	Glu	Gly	Lys	Glu	Arg	Lys	Cys	Tyr	Cys	Cys		
225					230					235					240		
Asp	Asp	Asp	Leu	Glu	Lys	Val	Ile	Tyr	Cys	Cys	Val	Ser	Cys	Asp	Tyr		
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Ala	Met	Asn	Met	Ala	Cys	Ala	Lys	Lys	Pro	Pro	Val	Leu	Ser	Ile	Asp		
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 305 310 315 320
 Leu Pro Arg Val Ile Arg Ile Ser Arg His His Arg Ile Ser Phe
 325 330 335
 Thr Pro Ser Phe Asp Gln Glu Arg Leu Ser Cys Gly Val Cys Gln Lys
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 Asn Ile Asp Asn Asp Tyr Gly Gly Tyr Ser Cys Ile Lys Glu Gly Cys
 355 360 365
 Phe Tyr Ala Ala His Ser Lys Cys Ala Thr Gln Arg Asn Val Trp Asp
 370 375 380
 Gly Lys Glu Leu Glu Gly Glu Gln Glu Glu Glu Ile Lys Glu Val Glu
 385 390 395 400
 Pro Phe Val Lys Ile Ser Asp Gly Ile Ile Gln His Phe Ser His Gln
 405 410 415
 His His His Leu Arg Leu Asp Asp Asn Ile Asn Arg Asp Tyr Asp Glu
 420 425 430
 Asn Lys Glu Cys Gln Ala Cys Ile Arg Pro Ile Tyr Phe Gly Asn Phe
 435 440 445
 Tyr Ser Cys Met Gln Cys Glu Phe Ile Leu His Glu Glu Cys Ala Asn
 450 455 460
 Leu Phe Arg Gln Ile Tyr His Pro Ile His Pro His Met Leu Ser Leu
 465 470 475 480
 Gly Tyr Asp Asn Ile Val Asp His Glu Val Met Cys Ala Ala Tyr Pro
 485 490 495
 Ser Leu Trp Thr Ala Gly Phe Phe Tyr Glu Cys Gly Lys Glu Gly Cys
 500 505 510
 Asp Phe Lys Leu Pro Val Gln Phe Ala Thr Thr Ser Glu Pro Leu Val
 515 520 525
 His Glu Ser His Met His Pro Leu Phe Leu Thr Ser Lys Pro Glu Glu
 530 535 540
 Asp Pro Arg Arg Cys Ser Val Cys Lys Glu Ser Arg Tyr Ala Arg Thr
 545 550 555 560
 Asn Glu Thr Phe Asn Cys Ile Glu Cys Asp Phe Ala Leu Cys Phe Val
 565 570 575
 Cys Ala Thr Leu Pro Gln Lys Val Arg Tyr Lys His Asp Lys His Val
 580 585 590
 Leu Thr Leu Phe Tyr Gly Asn Glu Thr Ser Thr Ile Thr Tyr Trp Cys
 595 600 605
 Glu Ile Cys Glu Gly Thr Ile Asp Pro Thr Lys Arg Phe Tyr Val Cys
 610 615 620
 Asp Glu Tyr Cys Cys Leu Thr Leu His Ile Lys Cys Leu Leu Gly Trp
 625 630 635 640
 Asp Leu Tyr Met Lys His Gly Ser Ser Ser Phe Tyr Leu Glu Lys Thr
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 Val Asp Val Leu Ser Asn Asn His His Met Thr Arg Pro Ile Cys Cys
 660 665 670
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 gct cat gct cac caa ctc atc ttt cgc cca aga ctt gat tct ttt aca
 Ala His Ala His Gln Leu Ile Phe Arg Pro Arg Leu Asp Ser Phe Thr
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48

96

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caa Gln	tgt Cys 50	gat Asp	ttc Phe	atg Met	ata Ile	cat His 55	caa Gln	gag Glu	tgt Cys	ttt Phe	tcc Ser 60	ctt Leu	cca Pro	cgc Arg	ctc Leu	192	
ata Ile 65	aac Asn	atc Ile	aat Asn	cgg Arg	cat His 70	gat Asp	cat His	cgt Arg	gtt Val	gct Ala 75	cgc Arg	aca Thr	tct Ser	gtt Val	ctt Leu 80	240	
ggg Gly	gtt Val	gtg Val	aat Asn	tct Ser 85	gta Val	tgt Cys	gga Gly	gtt Val	tgt Cys 90	cac His	caa Gln	aag Lys	gtg Val	gat Asp 95	tgg Trp	288	
acc Thr	tgg Trp	ggc Gly	ggg Gly 100	tat Tyr	tct Ser	tgc Cys	cag Gln	agg Arg 105	tgt Cys	cct Pro	caa Gln	tat Tyr	gtc Val 110	att Ile	cat His	336	
tcg Ser	aaa Lys	tgt Cys 115	gct Ala	act Thr	aga Arg	aat Asn	gat Asp 120	gtg Val	tgg Trp	aac Asn	ggg Gly 125	aaa Lys	gaa Glu	ctc Leu	gaa Glu	384	
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ggc Gly 145	aac Asn	ata Ile	ata Ile	caa Gln	cat His 150	ttc Phe	agc Ser	cac His	aaa Lys	gag Glu 155	cac His	tac Tyr	ctt Leu	aga Arg	ttc Phe 160	480	
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acc Thr	tac Tyr	ccc Pro	att Ile 180	ggg Gly	ctc Leu	caa Gln	tcc Ser	ttc Phe 185	tat Tyr	gaa Glu	tgt Cys	att Ile	gat Asp 190	tgt Cys	gat Asp	576	
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atg Met	cta Leu 210	cac His	aat Asn	gat Asp	cga Arg	ctt Leu 215	aca Thr	tta Leu	gtt Val	aca Thr	agc Ser 220	gta Val	gcc Ala	gaa Glu	ttc Phe	672	
ttt Phe 225	tgg Trp	tgt Cys	ata Ile	gct Ala	tgt Cys 230	aga Arg	aga Arg	atg Met	tcc Ser	aat Asn 235	ggg Gly	ttc Phe	aag Lys	tac Tyr	cag Gln 240	720	
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ctg Leu	acg Thr 290	tgc Cys	att Ile	gaa Glu	agt Ser	tgt Cys 295	tgt Cys	gga Gly	ttt Phe	gtc Val	tta Leu 300	tgc Cys	ttc Phe	tgt Cys	tgt Cys	912	
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cac His	cga Arg	gct Ala 355	agt Ser	ttg Leu	cat His	aca Thr	aag Lys 360	tgc Cys	gtg Val	tta Leu	gga Gly	gac Asp 365	ttt Phe	gca Ala	ggg Gly	1104	
ctc Leu	atg Met 370	cca Pro	aga Arg	agc Ser	aca Thr	ata Ile 375	aag Lys	tat Tyr	ggc Gly	agc Ser	aga Arg 380	tca Ser	tat Tyr	gag Glu	gtg Val	1152	
gtg Val 385	ctc Leu	aat Asn	aat Asn	agt Ser	gta Val 390	tct Ser	cgt Arg	cca Pro	ttt Phe	tgc Cys 395	agg Arg	gtg Val	tgt Cys	gag Glu	tcg Ser 400	1200	

PF59082SeqList_PF59082.txt

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Tyr	Ile	Cys	Ser	Leu	Asn	Cys	Gln	Lys	Arg	Leu	Asn	Ser	Leu	Asp	Asn	
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Glu	Ser	Asp	Asp	Asp	Asp	Arg	Thr	Gln	Leu	Gln	Ala	Leu	Leu	Leu	Ala	
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Glu	Glu	Thr	Ala	Lys	Lys	Glu	Pro	Asp	Tyr	Ala	Asp	Arg	Met	Gln	Leu	
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gtg	tgt	atg	tac	tgt	aaa	tat	tgc	tgc	tat	gcc	tca	acg	aat	aag	gta	1488
Val	Cys	Met	Tyr	Cys	Lys	Tyr	Cys	Cys	Tyr	Ala	Ser	Thr	Asn	Lys	Val	
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Leu	Thr	Leu	Lys	Arg	His	Ile	Tyr	Gly	Gly	Phe	Glu	Asp	Gln	Arg	Leu	
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Thr	Trp	Gly	Gly	Tyr	Ser	Cys	Gln	Arg	Cys	Pro	Gln	Tyr	Val	Ile	His	
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Thr	Tyr	Pro	Ile	Gly	Leu	Gln	Ser	Phe	Tyr	Glu	Cys	Ile	Asp	Cys	Asp	
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Phe	Met	Leu	His	Gln	Asn	Cys	Ala	Glu	Phe	Pro	Arg	Lys	Lys	Trp	His	
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Met	Leu	His	Asn	Asp	Arg	Leu	Thr	Leu	Val	Thr	Ser	Val	Ala	Glu	Phe	
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Phe	Trp	Cys	Ile	Ala	Cys	Arg	Arg	Met	Ser	Asn	Gly	Phe	Lys	Tyr	Gln	
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Cys	Gly	Tyr	Gly	Val	Leu	Asp	Val	Leu	Cys	Cys	Ser	Val	Ser	Glu	Pro	
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Phe	Val	His	Pro	Ser	His	Pro	Asp	His	Pro	Leu	Tyr	Tyr	Ile	Arg	Gln	
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Val	Lys	Tyr	Arg	Gln	Cys	Tyr	Gly	Cys	Asn	Gly	Arg	Thr	Tyr	Asn	Val	
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Leu	Thr	Cys	Ile	Glu	Ser	Cys	Cys	Gly	Phe	Val	Leu	Cys	Phe	Cys	Cys	
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PF59082SeqList_PF59082.txt

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 370 375 380
 Val Leu Asn Asn Ser Val Ser Arg Pro Phe Cys Arg Val Cys Glu Ser
 385 390 395 400
 His Cys Met Tyr Pro Ile Ser Leu Lys Met Leu Gly Thr Ser Asp Pro
 405 410 415
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 420 425 430
 Leu Thr Lys Lys Leu Glu Ala Leu Tyr Val Leu Lys Thr Thr Lys Lys
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 Glu Ser Asp Asp Asp Asp Arg Thr Gln Leu Gln Ala Leu Leu Leu Ala
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 Glu Glu Thr Ala Lys Lys Glu Pro Asp Tyr Ala Asp Arg Met Gln Leu
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 Val Asp Leu Phe Cys Val Lys Tyr Pro Pro Pro Asp Val Ile Asp Ile
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 Ser Glu Thr His His His Lys Leu Thr His Ile Lys Lys Trp Thr Lys
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 ttc aac tgt att gct aaa tgt ggt aag aag ttt tat ggg ttt cct tac 192
 Phe Asn Cys Ile Ala Lys Cys Gly Lys Lys Phe Tyr Gly Phe Pro Tyr
 50 55 60
 aaa tgt cta gaa tgt cat tta atg ttc gat atg gat tgc gta tgg aac 240
 Lys Cys Leu Glu Cys His Leu Met Phe Asp Met Asp Cys Val Trp Asn
 65 70 75 80
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 Pro Pro Glu Ala Lys Asn Gln Ser Glu Val Asn Ile Ser Ser His Pro
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 Leu His Pro Leu Lys Leu His Thr Ser Gln Pro Pro Asp Tyr Ser Asp
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 Glu Lys Cys Arg Leu Cys Thr Arg Lys Ile Glu Gly Leu Phe Tyr His
 115 120 125
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 Cys Ser Ser Cys Asn Phe Ser Leu Asp Met Arg Cys Val Ile Asn Pro
 130 135 140
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Gln	Asp	Cys	Leu	Ser	Leu	Pro	Arg	Leu	Ile	Asn	Ile	Asn	Arg	His	Ala	
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His	Arg	Val	Ser	Arg	Thr	Ser	Val	Leu	Gly	Val	Val	Asn	Ser	Val	Cys	
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Gly	Val	Cys	His	Gln	Lys	Val	Asp	Trp	Thr	Trp	Gly	Gly	Tyr	Ser	Cys	
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Gln	Arg	Cys	Pro	Gln	Tyr	Val	Val	His	Ser	Lys	Cys	Ala	Thr	Arg	Lys	
			245						250					255		
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Asp	Val	Trp	Asn	Gly	Lys	Glu	Leu	Glu	Gly	Val	Pro	Glu	Glu	Ile	Glu	
			260				265						270			
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Asp	Ile	Glu	Pro	Tyr	Val	Val	Ile	Asp	Asp	Asn	Thr	Ile	Gln	His	Phe	
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Ser	His	Lys	Glu	His	Tyr	Leu	Arg	Phe	His	Val	Asn	Gly	Leu	Leu	Trp	
	290					295					300					
gaa	gaa	aac	aag	cgt	tgc	agt	gct	tgc	acc	cat	ccc	ggt	cgt	ctc	caa	960
Glu	Glu	Asn	Lys	Arg	Cys	Ser	Ala	Cys	Thr	His	Pro	Val	Arg	Leu	Gln	
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Ser	Phe	Tyr	Ala	Cys	Lys	Asp	Cys	Asp	Phe	Ile	Leu	His	Gln	His	Cys	
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gct	gaa	tct	cct	aaa	aaa	gaa	tgg	cac	gtg	cta	cac	aat	gac	cgg	ctt	1056
Ala	Glu	Ser	Pro	Lys	Lys	Glu	Trp	His	Val	Leu	His	Asn	Asp	Arg	Leu	
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Thr	Leu	Val	Thr	Cys	Val	Ala	Asn	Phe	Phe	Ser	Cys	Thr	Ala	Cys	Ser	
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Gly	Cys	Asn	Asn	Arg	Glu	Val	Arg	Val	Leu	Thr	Cys	Ile	Glu	Ser	Gly	
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Cys	Gly	Tyr	Val	Leu	Cys	Phe	Asp	Cys	Ala	Thr	Leu	Pro	Gln	Val	Val	
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Lys	His	Arg	Val	Asp	Gly	His	Pro	Leu	Ser	Leu	Cys	Tyr	Gly	Glu	Glu	
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Lys	Thr	Trp	Phe	Tyr	Thr	Cys	Lys	Asp	His	Arg	Ala	Ser	Leu	His	Thr	
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 Pro Pro Glu Ala Lys Asn Gln Ser Glu Val Asn Ile Ser Ser His Pro
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 Leu His Pro Leu Lys Leu His Thr Ser Gln Pro Pro Asp Tyr Ser Asp
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 Glu Lys Cys Arg Leu Cys Thr Arg Lys Ile Glu Gly Leu Phe Tyr His
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 130 135 140
 Pro Pro Gln Phe Val Met Asp Leu Lys Val His Asp His Glu Leu Thr
 145 150 155 160
 Leu Leu Pro Arg Leu Asp Ser Phe Thr Cys Asn Ala Cys Gly Leu Lys
 165 170 175
 Gly Asp Arg Ser Pro Tyr Ile Cys Val Gln Cys Gly Phe Ile Ile His
 180 185 190
 Gln Asp Cys Leu Ser Leu Pro Arg Leu Ile Asn Ile Asn Arg His Ala
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 His Arg Val Ser Arg Thr Ser Val Leu Gly Val Val Asn Ser Val Cys
 210 215 220
 Gly Val Cys His Gln Lys Val Asp Trp Thr Trp Gly Gly Tyr Ser Cys
 225 230 235 240
 Gln Arg Cys Pro Gln Tyr Val Val His Ser Lys Cys Ala Thr Arg Lys
 245 250 255
 Asp Val Trp Asn Gly Lys Glu Leu Glu Gly Val Pro Glu Glu Ile Glu
 260 265 270
 Asp Ile Glu Pro Tyr Val Val Ile Asp Asp Asn Thr Ile Gln His Phe
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 Ser His Lys Glu His Tyr Leu Arg Phe His Val Asn Gly Leu Leu Trp
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 Glu Glu Asn Lys Arg Cys Ser Ala Cys Thr His Pro Val Arg Leu Gln
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 Ser Phe Tyr Ala Cys Lys Asp Cys Asp Phe Ile Leu His Gln His Cys
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 Thr Leu Val Thr Cys Val Ala Asn Phe Phe Ser Cys Thr Ala Cys Ser
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 Arg Leu Ser Asn Gly Phe Met Tyr Gln Cys Asp Phe Met Lys Leu Asp
 370 375 380
 Val Leu Cys Gly Leu Val Ser Glu Pro Tyr Ile His Pro Gly His Pro
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 Gly Cys Asn Asn Arg Glu Val Arg Val Leu Thr Cys Ile Glu Ser Gly
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 Cys Gly Tyr Val Leu Cys Phe Asp Cys Ala Thr Leu Pro Gln Val Val
 435 440 445
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 Ala Ser Gly Lys Tyr Trp Cys Asp Ile Cys Glu Lys Glu Thr Tyr Pro
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 Lys Thr Trp Phe Tyr Thr Cys Lys Asp His Arg Ala Ser Leu His Thr
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PF59082SeqList_PF59082.txt

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 Arg Phe Gly Phe Thr Ser Gly Gly Tyr Tyr Cys Glu Ser Cys Ser Phe
 35 40 45
 ttg gtt cat agg aaa tgt gtt gaa gat tcc tct gaa tat att gaa cac 192
 Leu Val His Arg Lys Cys Val Glu Asp Ser Ser Glu Tyr Ile Glu His
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 ccg tct cac tct gtt cac cct ctt aag ctt caa agt aaa cca gac cat 240
 Pro Ser His Ser Val His Pro Leu Lys Leu Gln Ser Lys Pro Asp His
 65 70 75 80
 ata tgt gat ata tgt gat aag agg atc gtg gat cta tgc tat cat tgt 288
 Ile Cys Asp Ile Cys Asp Lys Arg Ile Val Asp Leu Cys Tyr His Cys
 85 90 95
 gag atc tgt gac ttc aat gtg gat cta tac tgt gca aag tac cca cca 336
 Glu Ile Cys Asp Phe Asn Val Asp Leu Tyr Cys Ala Lys Tyr Pro Pro
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 Pro Lys Val Ile Asp Ile Ser Glu Thr His His His Lys Leu Thr Leu
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 Leu Lys Lys Gly Ile Lys Phe Asp Cys Gly Ala Ser Lys Cys Gly Glu
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 Val Met Tyr Gly Phe Pro Tyr Lys Cys His Glu Cys Asp Leu Ala Phe
 145 150 155 160
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 165 170 175
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 Val Asn His Ser His His Pro Leu His Pro Leu Lys Leu His Ile Gly
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 Gln Pro Pro Asp Tyr Ser Asp Gly Lys Cys Arg Leu Cys Ala Gln Lys
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 Ile Cys Asp Arg Leu Phe Tyr His Cys Ser Ala Cys Asn Phe Ser Leu
 210 215 220
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 Asp Met Cys Cys Leu Leu Asn Pro Pro Ser Gln Tyr Val Met Asp Leu
 225 230 235 240
 aaa gtt cat gct cac gaa ctc acc ttt cgc cca aga ctt gat tct ttt 768
 Lys Val His Ala His Glu Leu Thr Phe Arg Pro Arg Leu Asp Ser Phe
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 aca tgt aat gct tgc ggg ttg agt gga gac aga aac cct tac ata tgt 816
 Thr Cys Asn Ala Cys Gly Leu Ser Gly Asp Arg Asn Pro Tyr Ile Cys
 260 265 270
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Glu	Gly	Val	Pro	Glu	Glu	Ile	Glu	Asp	Val	Glu	Pro	Tyr	Val	Val	Ile	
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Cys	Thr	Gln	Pro	Ile	Gly	Leu	Gln	Ser	Phe	Tyr	Gly	Cys	Val	Val	Cys	
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Asp	Phe	Ile	Leu	His	Gln	Asn	Cys	Ala	Glu	Ser	Pro	Arg	Lys	Lys	Trp	
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Gln	Cys	Gly	Asp	Met	Lys	Leu	Asp	Val	Leu	Cys	Gly	Ser	Ile	Ser	Glu	
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Pro	Phe	Val	His	Pro	Ser	His	Pro	His	His	Pro	Leu	Tyr	Tyr	Ile	Pro	
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Pro	Glu	Glu	Glu	Lys	Gln	Cys	Asn	Gly	Cys	Asp	Asn	Trp	Ser	Ser	Leu	
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Val	Leu	Thr	Cys	Ile	Glu	Ser	Gly	Cys	Arg	Tyr	Phe	Leu	Cys	Phe	Asp	
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Cys	Ala	Arg	Leu	Pro	Gln	Val	Val	Lys	His	Arg	Val	Asp	Ala	His	Pro	
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Leu	Ser	Leu	Cys	Tyr	Gly	Glu	Lys	Ala	Ser	Gly	Lys	Tyr	Trp	Cys	Asp	
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Ile	Cys	Glu	Lys	Glu	Thr	Asn	Pro	Ser	Thr	Trp	Phe	Tyr	Thr	Cys	Lys	
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Asp	His	Arg	Ala	Ser	Leu	His	Thr	Lys	Cys	Val	Met	Gly	Asp	Phe	Ala	
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Arg	Leu	Met	Pro	Gly	Ser	Thr	Leu	Thr	Tyr	Ser	His	Ile	Ser	Tyr	Glu	
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gtg	gtg	cgc	aat	aat	agt	atg	tct	cgt	cca	ttt	tgc	aga	gcg	tgt	gag	1872
Val	Val	Arg	Asn	Asn	Ser	Met	Ser	Arg	Pro	Phe	Cys	Arg	Ala	Cys	Glu	
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Ser	His	Cys	Met	Tyr	Pro	Ile	Ile	Leu	Lys	Val	Leu	Gly	Ser	Ser	Ala	
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ctt	tac	atc	tgc	tct	tta	aac	tgc	gta	gat	ggg	ttt	tgg	tat	ccg	aag	1968
Leu	Tyr	Ile	Cys	Ser	Leu	Asn	Cys	Val	Asp	Gly	Phe	Trp	Tyr	Pro	Lys	
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 Glu Ile Cys Asp Phe Asn Val Asp Leu Tyr Cys Ala Lys Tyr Pro Pro
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 115 120 125
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 130 135 140
 Val Met Tyr Gly Phe Pro Tyr Lys Cys His Glu Cys Asp Leu Ala Phe
 145 150 155 160
 His Val Asp Cys Val Trp Asn Pro Pro Glu Ala Lys Asn Pro Ser Glu
 165 170 175
 Val Asn His Ser His His Pro Leu His Pro Leu Lys Leu His Ile Gly
 180 185 190
 Gln Pro Pro Asp Tyr Ser Asp Gly Lys Cys Arg Leu Cys Ala Gln Lys
 195 200 205
 Ile Cys Asp Arg Leu Phe Tyr His Cys Ser Ala Cys Asn Phe Ser Leu
 210 215 220
 Asp Met Cys Cys Leu Leu Asn Pro Pro Ser Gln Tyr Val Met Asp Leu
 225 230 235 240
 Lys Val His Ala His Glu Leu Thr Phe Arg Pro Arg Leu Asp Ser Phe
 245 250 255
 Thr Cys Asn Ala Cys Gly Leu Ser Gly Asp Arg Asn Pro Tyr Ile Cys
 260 265 270
 Val Gln Cys Asp Phe Met Ile His Gln Glu Cys Leu Asp Leu Pro Arg
 275 280 285
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 290 295 300
 Leu Gly Val Val Asn Ser Val Cys Gly Val Cys Arg Arg Lys Val Asp
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 Trp Thr Trp Gly Gly Tyr Ser Cys Gln Arg Cys Pro His Tyr Val Val
 325 330 335
 His Ser Lys Cys Ala Thr Arg Glu Asp Val Trp Asn Gly Lys Glu Leu
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 Glu Gly Val Pro Glu Glu Ile Glu Asp Val Glu Pro Tyr Val Val Ile
 355 360 365
 Asp Glu Asn Thr Ile Gln His Phe Ser His Lys Glu His Tyr Leu Arg
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 Phe His Val Ser Ala Leu Trp Glu Glu Asn Lys Arg Cys Asn Ala
 385 390 395 400
 Cys Thr Gln Pro Ile Gly Leu Gln Ser Phe Tyr Gly Cys Val Val Cys
 405 410 415
 Asp Phe Ile Leu His Gln Asn Cys Ala Glu Ser Pro Arg Lys Lys Trp
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 His Phe Leu His Asn Glu Arg Leu Thr Leu Val Thr Ser Lys Asp Asp
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PF59082SeqList_PF59082.txt

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Cys Ala Arg Leu Pro Gln Val Val Lys His Arg Val Asp Ala His Pro
Leu Ser Leu Cys Tyr Gly Glu Lys Ala Ser Gly Lys Tyr Trp Cys Asp
Ile Cys Glu Lys Glu Thr Asn Pro Ser Thr Trp Phe Tyr Thr Cys Lys
Asp His Arg Ala Ser Leu His Thr Lys Cys Val Met Gly Asp Phe Ala
Arg Leu Met Pro Gly Ser Thr Leu Thr Tyr Ser His Ile Ser Tyr Glu
Val Val Arg Asn Asn Ser Met Ser Arg Pro Phe Cys Arg Ala Cys Glu
Ser His Cys Met Tyr Pro Ile Ile Leu Lys Val Leu Gly Ser Ser Ala
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Thr Phe Leu Ile Ser Thr Asn Leu Lys Val Asp Pro Arg Val Ile Ser
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aag tcc ctt tac ccg aag atg gag ttc cat tta ctc ctt cgt caa ata      192
Lys Ser Leu Tyr Pro Lys Met Glu Phe His Leu Leu Leu Arg Gln Ile
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Ser Leu Ile Cys Lys Ile Met Phe Leu Val Ser Ser Met Asp Leu Asp
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tcg gag tca gag ctc aca tct ctc atc aag aaa ata att tct ctc ttc      336
Ser Glu Ser Glu Leu Thr Ser Leu Ile Lys Lys Ile Ile Ser Leu Phe
100                               105                               110
aac tct aaa ccc gat acg ggt tca gag ctc gtt tcc ctc att aca cag      384
Asn Ser Lys Pro Asp Thr Gly Ser Glu Leu Val Ser Leu Ile Thr Gln
115                               120                               125
ttg atg cgt atc gat acc tct gtg gat tcg gat tca gag cca aca caa      432
Leu Met Arg Ile Asp Thr Ser Val Asp Ser Asp Ser Glu Pro Thr Gln
130                               135                               140
gaa tct gag ctt cta tca ctc att agc caa cta gtc tct gcc aag ccg      480
Glu Ser Glu Leu Leu Ser Leu Ile Ser Gln Leu Val Ser Ala Lys Pro
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gag ccg gag ctc aca tca ctc acc agg cgg atc atc tct acc ttc ata      528
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Met	Val	Glu	Leu	Val	His	Gly	Lys	Leu	Thr	Thr	Glu	Val	Val	Arg	Pro	
		195					200					205				
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Arg	Lys	Ala	Lys	Glu	Arg	Glu	Cys	Glu	Leu	Tyr	Ala	Tyr	Glu	Ile	Trp	
	210					215					220					
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Lys	Ser	Thr	Arg	Gln	Ile	His	Phe	His	Cys	Ile	Leu	Cys	Asn	Gly	Glu	
225					230					235					240	
aac	cat	gaa	gag	tat	gac	aag	gtt	cct	ata	gag	gtc	aaa	cac	cct	ctt	768
Asn	His	Glu	Glu	Tyr	Asp	Lys	Val	Pro	Ile	Glu	Val	Lys	His	Pro	Leu	
				245				250						255		
cac	cca	aga	cat	tct	ctt	cag	ctt	gcc	gtt	aga	caa	tgg	tgc	gag	gag	816
His	Pro	Arg	His	Ser	Leu	Gln	Leu	Ala	Val	Arg	Gln	Trp	Ser	Glu	Glu	
		260				265							270			
gaa	acg	atg	att	gaa	tgt	tat	tgt	tgt	gat	gaa	tat	ctc	atg	gat	tat	864
Glu	Thr	Met	Ile	Glu	Cys	Tyr	Cys	Cys	Asp	Glu	Tyr	Leu	Met	Asp	Tyr	
		275				280						285				
tat	tac	tat	tgc	tcc	tct	tgc	gat	ttt	gct	atg	aat	gta	agc	tgt	ttg	912
Tyr	Tyr	Tyr	Cys	Ser	Ser	Cys	Asp	Phe	Ala	Met	Asn	Val	Ser	Cys	Leu	
	290				295						300					
gag	aaa	cca	cca	cca	gtc	tta	tct	ata	gac	cat	ccc	aag	tgg	cat	cag	960
Glu	Lys	Pro	Pro	Pro	Val	Leu	Ser	Ile	Asp	His	Pro	Lys	Trp	His	Gln	
305					310					315					320	
cat	ccc	ctt	att	ttg	ttt	cca	agt	cag	gct	tcc	ttt	cct	tgt	aac	ctt	1008
His	Pro	Leu	Ile	Leu	Phe	Pro	Ser	Gln	Ala	Ser	Phe	Pro	Cys	Asn	Leu	
				325					330					335		
tgt	gcc	ctc	aca	cat	tca	agt	tgt	cct	ttc	tat	att	tgt	ccc	ccc	tgt	1056
Cys	Ala	Leu	Thr	His	Ser	Ser	Cys	Pro	Phe	Tyr	Ile	Cys	Pro	Pro	Cys	
		340						345					350			
gac	ttc	gtg	gtc	cat	caa	aag	tgt	ctc	agc	tta	cca	cat	gtc	ata	agg	1104
Asp	Phe	Val	Val	His	Gln	Lys	Cys	Leu	Ser	Leu	Pro	His	Val	Ile	Arg	
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Ile	Ser	Arg	His	His	His	Arg	Ile	Ser	Phe	Thr	Pro	Ser	Phe	Glu	Lys	
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Gly	Gly	Tyr	Thr	Cys	Leu	Lys	Asp	Gly	Cys	Ser	Tyr	Val	Ala	His	Ser	
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aga	tgt	gca	aca	caa	aag	aat	gtg	tgg	gat	ggt	cta	gac	ctt	gag	gga	1296
Arg	Cys	Ala	Thr	Gln	Lys	Asn	Val	Trp	Asp	Gly	Leu	Asp	Leu	Glu	Gly	
		420						425					430			
gag	cca	gaa	gaa	gtt	gaa	gaa	gaa	gaa	gtt	gag	cca	ttt	gtg	ata	ata	1344
Glu	Pro	Glu	Glu	Val	Glu	Glu	Glu	Glu	Val	Glu	Pro	Phe	Val	Ile	Ile	
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agt	gac	gga	aca	ata	cac	cat	ttt	agt	cat	cca	cat	cat	ttg	aga	atg	1392
Ser	Asp	Gly	Thr	Ile	His	His	Phe	Ser	His	Pro	His	His	Leu	Arg	Met	
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gat	aag	aat	acc	ggc	aga	gac	tac	gac	gag	aat	aag	cag	tgt	caa	gca	1440
Asp	Lys	Asn	Thr	Gly	Arg	Asp	Tyr	Asp	Glu	Asn	Lys	Gln	Cys	Gln	Ala	
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Cys	Ile	Thr	Pro	Ile	Tyr	Phe	Gly	Asn	Ile	Tyr	Ser	Cys	Met	Gln	Cys	
				485				490						495		
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Asn	Phe	Ile	Leu	His	Glu	Glu	Cys	Ala	Asn	Phe	Ser	Arg	Lys	Ile	His	
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aac	ccg	ata	cat	cca	cat	aag	ctc	aat	cta	gtg	gga	gga	tac	gac	ggt	1584
Asn	Pro	Ile	His	Pro	His	Lys	Leu	Asn	Leu	Val	Gly	Gly	Tyr	Asp	Gly	
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gtt	acc	aag	tat	tat	aag	gat	ttc	tgt	tca	gtg	tgt	cct	agg	atg	tgc	1632
Val	Thr	Lys	Tyr	Tyr	Lys	Asp	Phe	Cys	Ser	Val	Cys	Pro	Arg	Met	Cys	
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Lys	Leu	His	Val	Gln	Cys	Ala	Thr	Ile	Ser	Glu	Pro	Leu	Val	His	Glu	
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Ser	His	Val	His	Pro	Leu	Phe	Leu	Thr	Ser	Lys	Pro	Arg	Glu	Arg	Arg	
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Arg	Cys	Gly	Val	Cys	Lys	Lys	Lys	Pro	Leu	Ser	His	Thr	Glu	Thr	Phe	
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Asn	Cys	Ile	Glu	Gly	Glu	Cys	Thr	Phe	Ala	Leu	Cys	Phe	Gly	Cys	Ala	
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Thr	Leu	Pro	His	Glu	Val	Arg	Tyr	Lys	His	Asp	Lys	His	Met	Leu	Thr	
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Leu	Ser	Tyr	Gly	Glu	Thr	Ser	Thr	Met	Met	Tyr	Trp	Cys	Glu	Ala		
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Cys	Glu	Lys	Glu	Ile	Asn	Ser	Glu	Glu	Arg	Phe	Tyr	Lys	Cys	Asp	Glu	
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Tyr	Cys	Cys	Val	Thr	Leu	His	Ile	Gln	Cys	Leu	Ile	Gly	Lys	Glu	Leu	
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Val	Leu	Leu	Lys	Thr	Gln	Val	Met	Ser	Arg	Pro	Ile	Cys	Phe	Gln	Cys	
705					710				715						720	
aag	agt	cgt	tgt	cca	cat	aac	aca	gtt	atc	cag	tgg	tct	gag	tta	gta	2208
Lys	Ser	Arg	Cys	Pro	His	Asn	Thr	Val	Ile	Gln	Trp	Ser	Glu	Leu	Val	
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Tyr	Cys	Thr	Ile	His	Cys	Phe	Leu	Phe	Gly	Arg	Leu	Arg	Trp	Asp	Glu	
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gaa	gaa	aga	aga	aga	aag	caa	gct	gaa	att	gac	aat	aaa	gat	gtt		2301
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Lys	Ser	Leu	Tyr	Pro	Lys	Met	Glu	Phe	His	Leu	Leu	Arg	Gln	Ile		
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Leu	Lys	Phe	Trp	Thr	Ser	Thr	Asp	Met	Gly	Arg	Gln	Trp	Lys	Phe	Val	
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Ser	Leu	Ile	Cys	Lys	Ile	Met	Phe	Leu	Val	Ser	Ser	Met	Asp	Leu	Asp	
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Ser	Glu	Ser	Glu	Leu	Thr	Ser	Leu	Ile	Lys	Lys	Ile	Ile	Ser	Leu	Phe	
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Asn	Ser	Lys	Pro	Asp	Thr	Gly	Ser	Glu	Leu	Val	Ser	Leu	Ile	Thr	Gln	
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Glu Pro Glu Leu Thr Ser	Leu Thr Arg Arg Ile Ile Ser Thr Phe Ile														
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Ser Met Asn Trp Glu Pro	Met Gln Phe Ile Ser Val Cys Pro Gln Val														
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	195	200	205												
Arg Lys Ala Lys Glu Arg	Glu Cys Glu Leu Tyr Ala Tyr Glu Ile Trp														
	210	215	220												
Lys Ser Thr Arg Gln Ile	His Phe His Cys Ile Leu Cys Asn Gly Glu														
225	230	235	240												
Asn His Glu Glu Tyr Asp	Lys Val Pro Ile Glu Val Lys His Pro Leu														
	245	250	255												
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	260	265	270												
Glu Thr Met Ile Glu Cys	Tyr Cys Cys Asp Glu Tyr Leu Met Asp Tyr														
	275	280	285												
Tyr Tyr Tyr Cys Ser Ser	Cys Asp Phe Ala Met Asn Val Ser Cys Leu														
	290	295	300												
Glu Lys Pro Pro Pro Val	Leu Ser Ile Asp His Pro Lys Trp His Gln														
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His Pro Leu Ile Leu Phe	Pro Ser Gln Ala Ser Phe Pro Cys Asn Leu														
	325	330	335												
Cys Ala Leu Thr His Ser	Ser Cys Pro Phe Tyr Ile Cys Pro Pro Cys														
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	370	375	380												
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	405	410	415												
Arg Cys Ala Thr Gln Lys	Asn Val Trp Asp Gly Leu Asp Leu Glu Gly														
	420	425	430												
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	435	440	445												
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	450	455	460												
Asp Lys Asn Thr Gly Arg	Asp Tyr Asp Glu Asn Lys Gln Cys Gln Ala														
465	470	475	480												
Cys Ile Thr Pro Ile Tyr	Phe Gly Asn Ile Tyr Ser Cys Met Gln Cys														
	485	490	495												
Asn Phe Ile Leu His Glu	Glu Cys Ala Asn Phe Ser Arg Lys Ile His														
	500	505	510												
Asn Pro Ile His Pro His	Lys Leu Asn Leu Val Gly Gly Tyr Asp Gly														
	515	520	525												
Val Thr Lys Tyr Tyr Lys	Asp Phe Cys Ser Val Cys Pro Arg Met Cys														
	530	535	540												
Thr Asn Gly Phe Phe Tyr	Glu Cys Gly Lys Glu Glu Cys Asp Arg Phe														
545	550	555	560												
Lys Leu His Val Gln Cys	Ala Thr Ile Ser Glu Pro Leu Val His Glu														
	565	570	575												
Ser His Val His Pro Leu	Phe Leu Thr Ser Lys Pro Arg Glu Arg Arg														
	580	585	590												
Arg Cys Gly Val Cys Lys	Lys Lys Pro Leu Ser His Thr Glu Thr Phe														
	595	600	605												
Asn Cys Ile Glu Gly Glu	Cys Thr Phe Ala Leu Cys Phe Gly Cys Ala														
	610	615	620												
Thr Leu Pro His Glu Val	Arg Tyr Lys His Asp Lys His Met Leu Thr														
625	630	635	640												
Leu Ser Tyr Gly Glu Thr	Ser Thr Met Met Tyr Trp Cys Glu Ala														
	645	650	655												
Cys Glu Lys Glu Ile Asn	Ser Glu Glu Arg Phe Tyr Lys Cys Asp Glu														
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Tyr Cys Cys Val Thr Leu	His Ile Gln Cys Leu Ile Gly Lys Glu Leu														
	675	680	685												

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Val Leu Leu Lys Thr Gln Val Met Ser Arg Pro Ile Cys Phe Gln Cys
705 710 715 720
Lys Ser Arg Cys Pro His Asn Thr Val Ile Gln Trp Ser Glu Leu Val
725 730 735
Tyr Cys Thr Ile His Cys Phe Leu Phe Gly Arg Leu Arg Trp Asp Glu
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Leu	Cys	Lys	Leu	Lys	Thr	Pro	Phe	Ala	Arg	Cys	Thr	Val	Cys	Asn	Ile	
			20					25					30			
aac	att	agt	cca	ctt	tgt	atg	gta	aag	caa	cca	cca	ctc	act	att	tgt	144
Asn	Ile	Ser	Pro	Leu	Cys	Met	Val	Lys	Gln	Pro	Pro	Leu	Thr	Ile	Cys	
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Asn	Pro	Lys	His	His	Lys	His	Ser	Leu	Thr	Leu	Leu	Val	Arg	Leu	Val	
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Ile	Phe	Thr	Cys	Asn	Ala	Cys	Gly	Val	Glu	Gly	Asp	Arg	Asn	Pro	Tyr	
	65				70				75					80		
gta	tgt	ctt	caa	tgc	aat	ctg	atg	gtc	cac	aaa	gac	tgt	att	gag	aat	288
Val	Cys	Leu	Gln	Cys	Asn	Leu	Met	Val	His	Lys	Asp	Cys	Ile	Glu	Asn	
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cta	ccg	cga	gtc	ata	tgc	atc	aat	cgg	cac	gat	cat	cgc	atc	ttt	cat	336
Leu	Pro	Arg	Val	Ile	Cys	Ile	Asn	Arg	His	Asp	His	Arg	Ile	Phe	His	
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Pro	Asn	Tyr	Ala	Val	His	Ser	Arg	Cys	Ala	Thr	Lys	Lys	Glu	Val	Trp	
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Asp	Gly	Ile	Glu	Leu	Glu	Asp	Val	Pro	Glu	Glu	Glu	Glu	Glu	Val	Glu	
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Glu	Pro	Phe	Val	Val	Ile	Asn	Glu	Lys	Glu	Ile	Ile	His	Phe	Ser	His	
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Glu	Glu	His	Val	Leu	Arg	Leu	Asp	Glu	Asn	Tyr	Val	Thr	Asp	Asn	Val	
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Asn	Met	Arg	Cys	Arg	Gly	Cys	Val	Leu	Ala	Ile	Asn	Gly	Asp	Ser	Cys	
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Tyr	Lys	Cys	Val	Glu	Cys	Asp	Tyr	Ile	Leu	His	Lys	Ala	Cys	Ala	Ser	
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Arg	Cys	Gln	Ala	Cys	Gly	Thr	Glu	Thr	Asp	Asp	Asn	Leu	Leu	Asn	Cys	
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Thr	Val	Cys	Asp	Asp	Tyr	Ala	Leu	Cys	Met	Lys	Cys	Ala	Thr	Leu	Pro	
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Arg	Lys	Val	Lys	His	Arg	Cys	Asp	Asp	His	Phe	Leu	Ser	Leu	Cys	Gln	
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Phe	Cys	Gly	Val	Cys	Glu	Val	Arg	Cys	Lys	Phe	Pro	Phe	Ile	Met	Trp	
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Gly	Ala	Val	Gly	Asp	Phe	Thr	Gly	Tyr	Val	Cys	Ser	Ile	Asn	Cys	Val	
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<213> Arabidopsis thaliana

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Asn Met Arg Cys Arg Gly Cys Val Leu Ala Ile Asn Gly Asp Ser Cys
210 215 220
Tyr Lys Cys Val Glu Cys Asp Tyr Ile Leu His Lys Ala Cys Ala Ser
225 230 235 240
Leu Pro Arg Lys Lys Arg His Leu Leu His Asn His Lys Leu Thr
245 250 255
Gln Val Asp Glu Ala Ala Ser Ser Asp Phe Val Cys Thr Ala Cys Arg
260 265 270
Thr Tyr Ser Asn Gly Phe Arg Tyr Lys Cys Phe Glu Gly Cys Glu Asp
275 280 285
Asp Val Val Tyr Asp Val Arg Cys Ser Ser Val Ser Glu Pro Phe Gln
290 295 300
His Asp Leu His Pro His Pro Leu Tyr Trp Thr Leu Glu Ser Ser Lys
305 310 315 320
Arg Cys Gln Ala Cys Gly Thr Glu Thr Asp Asp Asn Leu Leu Asn Cys
325 330 335
Thr Val Cys Asp Asp Tyr Ala Leu Cys Met Lys Cys Ala Thr Leu Pro
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Arg Lys Val Lys His Arg Cys Asp Asp His Phe Leu Ser Leu Cys Gln
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Lys Thr Asp Pro Asn Val Cys Tyr Tyr Thr Cys Glu Glu Cys Gly Leu
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Ser Leu His Leu Asn Cys Val Leu Gly Asp Phe Tyr Tyr Val Lys Val
405 410 415
Ile Pro Asp Gln Pro Lys Val Phe Ala Asn Asn Gly Val Thr Arg Leu
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Phe Cys Gly Val Cys Glu Val Arg Cys Lys Phe Pro Phe Ile Met Trp
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Gln Ile Ser Ser Phe Ser Glu Ser Trp Asn Pro Tyr Leu Gly Phe Asp	
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cca gaa tgg gat tct ata tct aag atg ata tca act att act caa aca	144
Pro Glu Trp Asp Ser Ile Ser Lys Met Ile Ser Thr Ile Thr Gln Thr	
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Ile Ser Leu Val Ser Ser Ile Asp Phe Asp Ser Gln Pro Glu Ser Lys	
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Thr	Asp	Ser	Ala	Pro	Asp	Leu	Glu	Ile	Phe	Met	Leu	Leu	Ile	Gln	Glu	
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Glu	Pro	Glu	Ile	Asp	Leu	Glu	Met	Asn	Leu	Ile	Ser	Leu	Ile	Thr	Gln	
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tgc Cys	att Ile	gag Glu	tgc Cys	gac Asp 805	ttt Phe	gct Ala	ttg Leu	tgt Cys	ttc Phe 810	aag Lys	tgt Cys	gct Ala	act Thr	tta Leu 815	cct Pro	2448
cat His	aag Lys	gtg Val	agg Arg 820	tat Tyr	aag Lys	cat His	gat Asp	aag Lys 825	cat His	atg Met	ctt Leu	act Thr	ctt Leu 830	tct Ser	tat Tyr	2496

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PF59082SeqList_PF59082.txt

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Thr Cys 450 Asn Val Asp Asn 455 His Gly Glu Tyr Glu 460 Lys Ala Pro Val Met
Ile 465 Lys His Ala Leu His 470 Pro Asn His Ser Leu 475 Gln Leu Val Leu Leu
Asn Gly Asp Thr 485 Thr Arg Glu Ser Cys Asp 490 Tyr Ala Met Asn Ile 495 Ala
Cys Val Glu Lys 500 Pro Arg Val Leu Ser 505 Leu Asp Gln Pro Lys Trp His
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Leu Asp Glu Asn 660 Thr Ser Arg Asp Tyr 665 Asn Glu Asn Lys Leu 670 Cys Gln
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Ile Met Asp Ala Thr 725 Lys Ser Cys Ser Val 730 Cys Pro Trp Lys Cys Thr 735
Thr Gly Phe Phe Tyr Glu Cys Arg Glu 745 Arg Glu Cys Arg Phe 750 Lys Val
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Cys 785 Val Cys Lys Glu Leu 790 Gly His Cys Ser Thr 795 Asn Glu Thr Phe Asn 800
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Gln	Pro	Leu	Phe	Leu	Cys	Pro	Leu	Leu	Arg	Val	Lys	Thr	His	Ser	Gln	
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Ile	Tyr	His	Ser	Ser	Thr	Tyr	Lys	Leu	Ser	Met	His	Pro	Val	Cys	Ala	
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Pro	Leu	Thr	Phe	Ser	Pro	Ser	Lys	Ala	Phe	Leu	Pro	Cys	Asn	Val	Cys	
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Ala	Leu	Arg	Lys	Asp	Val	Trp	Asn	Gly	Glu	Asp	Leu	Glu	Gly	Ile	Pro	
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gaa	gag	cct	gag	atg	gat	gtt	gag	cca	tac	gag	acg	ata	acc	gat	gca	1008
Glu	Glu	Pro	Glu	Met	Asp	Val	Glu	Pro	Tyr	Glu	Thr	Ile	Thr	Asp	Ala	
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PF59082SeqList_PF59082.txt

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gcc Ala 450	tcg Ser	ggt Val	ttc Phe	gaa Glu	cca Pro	ttt Phe 455	gaa Glu	tat Tyr	caa Gln	ggc Gly	cac His 460	gag Glu	aat Asn	ccc Pro	tta Leu	1392
ttc Phe 465	cta Leu	gcc Ala	tta Leu	gag Glu	cca Pro	gat Asp 470	gaa Glu	gaa Glu	aaa Lys	gcg Ala 475	gtg Val	ata Ile	tgt Cys	caa Gln	atc Ile 480	1440
tgc Cys	caa Gln	gaa Glu	gat Asp	ggt Gly 485	gat Asp	gga Gly	aat Asn	aac Asn	tat Tyr 490	att Ile	aga Arg	aaa Lys	cta Leu	aat Asn 495	tgc Cys	1488
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ccc Pro	aac Asn	aat Asn 595	acc Thr	atg Met	act Thr	cga Arg	cca Pro 600	ttc Phe	tgc Cys	cat His	ggt Gly 605	cat His	aaa Lys	gaa Glu	gat Asp	1824
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<212> PRT

<213> Arabidopsis thaliana

<400> 1226

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Gln	Pro	Leu 35	Phe	Leu	Cys	Pro	Leu 40	Arg	Val	Lys	Thr 45	His	Ser	Gln	
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Asp	Ser	His	Asn 85	Arg	Gly	Leu	Ile	Cys	Lys 90	Leu	Pro	Val	Leu	Pro 95	Leu
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Pro Ser Ser Tyr Gly Glu Thr Ala Ile Asp Gly Asp Asp His Leu Ser	
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Asp Ser Asp Ser Gln Gln Val His Asp Leu Leu His Ser Asp Asn Ser	
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His Asp Asp Asp Gly Asp Glu Ile Cys Lys Leu Pro Val Val Pro Ile	
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Tyr Trp Cys Asn Ser Lys Lys Asp Glu Tyr Leu Gln Phe Thr Cys Gly	
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Ser Asp Gln Met Phe His Lys Glu Cys Val Glu Ser Pro Leu Glu Ile	
165 170 175	
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Lys His Pro Ser Tyr Pro Phe Leu Ser Leu Lys Leu Tyr His Asn Phe	
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agc gaa aac gtg aat tgc atc tgc tgt gat tta gct ctc ttt agc atg	624
Ser Glu Asn Val Asn Cys Ile Cys Cys Asp Leu Ala Leu Phe Ser Met	
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Leu Tyr His Ser Ser Thr Tyr Lys Leu Ser Met His Pro Val Cys Ala	
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Leu Leu Thr Phe Pro Lys Gln Ala Ser Leu Leu Cys Asp Val Cys	
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Phe Val Ala His Arg Asp Cys Ile Tyr Phe Pro Tyr Val Ile Lys Ile	
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Cys Arg His Gln His Arg Ile Ser Phe Ile Ser Leu Pro Ser Gly	
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Lys Trp Ser Cys Gly Val Cys Arg Gln Lys Val Asn Asn Asn Cys Gly	
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Leu	Leu	Thr	Phe	Phe	Pro	Lys	Gln	Ala	Ser	Leu	Leu	Cys	Asp	Val	Cys
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Thr	Leu	Pro	Tyr	Glu	Ala	Lys	Tyr	Lys	His	Asp	Lys	His	Phe	Leu	Thr
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580 585 590
Val His Ile Leu Pro Asn Asn Thr Arg Ser Arg Pro Phe Cys His His
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Lys Pro Phe Leu Ile Tyr Thr Leu Leu Ser Gln Thr Glu Ser Pro Ser
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Ser Gly Glu Ala Ala Val Asp Ser Asp Gly Gly Asp Gly Arg Leu Ser
35 40 45
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Leu Glu Pro Arg Ile Leu Cys Pro Thr Leu Arg Leu Lys Val Lys Lys
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Val Ser Pro His Phe Pro Thr Ile Gln Ser Gly His Glu Gln Pro Glu
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Tyr Met Leu His Ser Asp Ser Phe His Gln Asp Cys Ile Tyr Phe Pro
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Tyr Val Ile Lys Ile Ser Arg His His His Arg Ile Ser Tyr Thr Ser
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Ser Leu Pro Ser Gly Lys Trp Ser Cys Gly Val Cys Arg Gln Met Val
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His Leu Gln His Pro Leu Phe Leu Thr Tyr Gly Lys His Asp Asn Ile
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145 150 155 160
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Tyr Gly Gln Tyr Ser Cys Lys Asp Glu Asp Cys Ser Tyr Val Leu His
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Gln	Cys	Ser	Thr	Leu	Cys	Glu	Tyr	Ser	Ile	Cys	Tyr	Glu	Cys	Ala	Thr	
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Ile	Pro	Ser	Glu	Leu	His	Tyr	Lys	Tyr	Asp	Lys	His	Pro	Leu	Thr	Leu	
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 Ser Pro Ser His His Lys His Pro Leu Lys Leu His Glu Arg Ile Ile
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 85 90 95
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 Asp Met Phe Tyr Asn Cys Ser Arg Cys Met Phe Glu Val Cys Met Ala
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Pro Glu Ala Leu Ser Lys Val Ile Ser Leu Ile Thr Asp Arg Val Asn
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gat aca gat tcg gat tcc gat atc tat ttg gat tca gat ttt gaa gac      192
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	Pro	Thr	Ile	His	Ile	Glu	Cys	Val	Leu	Gly	Asp	Phe	Arg	Tyr	Val	Lys	
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	Pro	Arg	Leu	His	Phe	Glu	Asn	Lys	Lys	Lys	Lys	Trp	Glu	Val	Ala	Leu	
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	Asn	Gly	Ile	Asn	Arg	Pro	Gly	Cys	Tyr	Lys	Cys	Gly	Phe	Arg	Cys	Lys	
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 Asn Gly Ile Asn Arg Pro Gly Cys Tyr Lys Cys Gly Phe Arg Cys Lys
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 Leu Ser Asp Pro Ala Gln Pro Leu Asn Leu Phe Arg Leu Gly Cys Ser
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 Ser Ser Lys Gly Asn Asp Met Glu Asp Thr Pro Pro Pro Phe Phe Ser
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 Thr Ser Lys Pro Lys Cys Arg Leu Ser Asp Pro Ala Gln Pro His Lys
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 Ser Cys Lys Gly Lys Asp Met Glu Asp Ser Arg Tyr Tyr Tyr Tyr Cys
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 115 120 125
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Pro	Pro	Pro	Pro	Thr	Ile	Ser	His	Ile	Lys	Ser	His	Glu	His	Thr	Leu	
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His	Met	Val	His	Arg	Ser	Cys	Ile	Tyr	Leu	Pro	Arg	Val	Ile	Lys	Ile	
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Glu	Cys	Ile	Lys	Cys	Thr	Ser	Phe	Leu	Gly	Ile	Arg	Cys	Ala	Thr	Leu	
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20          25          30
gtc atc tca tgc ggt gaa tgc aag ttt act gtt cac agg aaa tgt gta      144
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Lys	Cys	His	Leu	Cys	Gly	Lys	Lys	Thr	Lys	Arg	Leu	Leu	Tyr	His	Cys	
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Cys	Ala	Arg	Ser	Pro	Leu	Lys	Leu	Pro	Trp	His	Asp	His	Pro	Leu	Ile	
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Lys	Val	Asp	Leu	Gly	Ala	Asn	Met	Pro	Cys	Asp	Phe	Cys	Asn	Glu	Ser	
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ggc	ata	gac	tat	tgt	tgc	cct	cgt	tgc	agg	ttc	atg	att	cat	gag	aga	480
Gly	Ile	Asp	Tyr	Cys	Cys	Pro	Arg	Cys	Arg	Phe	Met	Ile	His	Glu	Arg	
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			180					185					190			
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Leu	Asn	Cys	His	Ile	Cys	Gly	Asp	Ala	Thr	Gly	Asn	Leu	Leu	Tyr	His	
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Cys	Asp	Ile	Cys	Lys	Phe	Asn	Leu	Asn	Met	Arg	Cys	Ala	Ile	Arg	Glu	
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Phe	His	Gln	Glu	Cys	Ala	Lys	Leu	Pro	Arg	Val	Ile	His	Val	Asn	His	
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	305				310					315					320	
tca	tgc	tct	ctt	tgt	cct	aat	tat	gct	atg	cat	tca	ctg	tgt	gca	aca	1008
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Leu	Val	Leu	Cys	Leu	Gln	Asn	Gln	Arg	Asn	Thr	Glu	Thr	Cys	Asn	Ala	
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Cys	Gln	Gln	Val	Phe	Cys	Lys	Gly	Phe	Ile	Tyr	Ser	Ser	Phe	Pro	Lys	
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Trp	Cys	Asp	Ile	Cys	Glu	Arg	Glu	Thr	Asn	Pro	Lys	Ser	Trp	Phe	Tyr	
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Thr	Cys	Lys	Asp	Cys	Gly	Val	Thr	Phe	His	Ile	Phe	Cys	Val	Val	Trp	
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Tyr	Cys	Ser	Tyr	Tyr	Cys	Tyr	Ala	Arg	Leu	His	Ser	Leu	Arg	Tyr	Ile	
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<212> PRT

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Arg	His	Pro	Leu	Lys	Leu	Arg	Ser	Asn	Gly	Ala	Pro	Asp	Tyr	Thr	Asn
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Leu	Asn	Cys	His	Ile	Cys	Gly	Asp	Ala	Thr	Gly	Asn	Leu	Leu	Tyr	His
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Pro	Thr	Pro	Val	Ala	Leu	Ser	Asn	Met	Lys	Val	His	Glu	His	Thr	Leu
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Thr	Leu	Met	Pro	Arg	Leu	Ile	Ser	Phe	Val	Cys	Asp	Ala	Cys	Gly	Met
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Leu	Val	Leu	Cys	Leu	Gln	Asn	Gln	Arg	Asn	Thr	Glu	Thr	Cys	Asn	Ala
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Asn Val His Lys Gly Cys Leu Glu Ile Ile Asn Pro Ser Ser Pro Ala
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Ile Cys His Trp Val Phe His Arg Tyr Met Tyr Tyr Cys Ser Phe Ser
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Gly Leu Pro Val Cys Lys Gln Cys Val Arg Lys Pro Phe Ile Leu Asp
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Leu Cys Leu Cys Ile Pro Cys Arg Phe Thr Ile His Met Asp Cys Val
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Tyr Leu Pro Arg Val Ile Cys Val Asn Arg His Asp His Arg Ile Ser
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Gln	Phe	Gly	Glu	Met	Ala	Lys	Gly	Asp	Tyr	Trp	Cys	Asp	Ile	Cys	Glu	
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Lys	Ile	Leu	Asp	Pro	Gln	Lys	Trp	Phe	Tyr	Thr	Cys	Asp	Leu	Cys	Cys	
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Thr	Thr	Leu	His	Ile	Asp	Cys	Val	Leu	Gly	Met	Glu	Pro	Tyr	Met	Arg	
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<212> PRT

<213> Arabidopsis thaliana

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Gly	Glu	Glu	Thr	Ala	Gly	Lys	His	Ala	Cys	His	Ile	Cys	His	Glu	Ile	
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PF59082SeqList_PF59082.txt

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Tyr	Leu	Pro	Arg	Val	Ile	Cys	Val	Asn	Arg	His	Asp	His	Arg	Ile	Ser
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Ser	Leu	Thr	Gly	Gln	Asp	Asp	Leu	Phe	Met	Cys	Tyr	Lys	Cys	Ala	Thr
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Gln	Phe	Gly	Glu	Met	Ala	Lys	Gly	Asp	Tyr	Trp	Cys	Asp	Ile	Cys	Glu
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Thr	Thr	Leu	His	Ile	Asp	Cys	Val	Leu	Gly	Met	Glu	Pro	Tyr	Met	Arg
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Val	Gly	Ser	Thr	Phe	His	Leu	Lys	Arg	Phe	Val	Leu	Glu	Val	Leu	Ser
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Asn	Asp	Leu	Ile	Val	Tyr	Lys	Ser	Lys	Asp	Val	Tyr	Phe	Cys	Ser	Leu
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Pro Cys Val Gly Cys Asp Gly Asp Glu Thr Ala Gly Lys Cys Ser Cys	
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His Ile Cys Glu Ile Tyr Val His Lys Asp Cys Leu Glu Ile Ile Asn	
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Leu Cys Ser Phe Ser Gly Leu Pro Val Cys Glu Lys Cys Ala Arg Lys	
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Pro Phe Thr Ile Asp Pro Gly Arg Ala His Glu His Pro Leu Leu Val	
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Phe Leu Lys Gly Ser Phe Ser Phe Pro Cys Asp Ala Cys Gly Val Asn	
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cgg Arg	gaa Glu	gat Asp	tta Leu 420	ttt Phe	atg Met	tgc Cys	tac Tyr 425	aag Lys	tgt Cys	gct Ala	act Thr	atc Ile	cct Pro 430	gaa Glu	cta Leu	1296
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PF59082SeqList_PF59082.txt

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 385 390 395 400
 Cys Ser Arg Cys Gly Lys Gly Gly Asn Asp Val Trp Cys Leu Thr Gly
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Cys	Gly	Val	Cys	Arg	Lys	Thr	Ile	Asp	Cys	Val	Tyr	Gly	Ala	Phe	Ile		
		195				200						205					
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Ile	Val	His	Phe	Ser	His	Glu	Glu	His	Val	Leu	Arg	Leu	Asp	Val	Asn		
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tat	gtt	cat	gat	aat	gat	act	atg	tgc	tgt	gga	ggg	tgt	att	ctt	ccc		864
Tyr	Val	His	Asp	Asn	Asp	Thr	Met	Cys	Cys	Gly	Gly	Cys	Ile	Leu	Pro		
		275				280						285					
atc	aat	gat	gat	cca	tgc	tac	aag	tgc	gtg	gaa	tgt	gat	ttc	tgc	ctt		912
Ile	Asn	Asp	Asp	Pro	Cys	Tyr	Lys	Cys	Val	Glu	Cys	Asp	Phe	Cys	Leu		
	290					295					300						
cac	aaa	gga	tgt	gct	agt	ctt	cct	cga	aag	aaa	gcc	cat	ttt	ttg	cac		960
His	Lys	Gly	Cys	Ala	Ser	Leu	Pro	Arg	Lys	Lys	Ala	His	Phe	Leu	His		
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aac	cat	aaa	att	agc	cta	cgg	gct	cat	aag	gat	gac	gtt	tat	gta	gat		1008
Asn	His	Lys	Ile	Ser	Leu	Arg	Ala	His	Lys	Asp	Asp	Val	Tyr	Val	Asp		
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aaa	tgc	gga	gct	tgt	aaa	act	tat	tct	aat	ggg	ttc	aag	tac	gag	tgt		1056
Lys	Cys	Gly	Ala	Cys	Lys	Thr	Tyr	Ser	Asn	Gly	Phe	Lys	Tyr	Glu	Cys		
			340					345					350				
cac	gac	aaa	agc	agc	tgt	aga	ggg	aat	ata	aag	tat	gat	atc	cgt	tgt		1104
His	Asp	Lys	Ser	Ser	Cys	Arg	Gly	Asn	Ile	Lys	Tyr	Asp	Ile	Arg	Cys		
		355				360						365					
agc	tcc	ata	tca	gag	ccg	ttt	cac	cat	gat	gat	ctg	cat	cca	cat	cct		1152
Ser	Ser	Ile	Ser	Glu	Pro	Phe	His	His	Asp	Asp	Leu	His	Pro	His	Pro		
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tta	tat	tg	acc	ttg	gaa	acc	aaa	cag	tgt	aag	gct	tgt	ggc	aca			1200
Leu	Tyr	Trp	Thr	Leu	Glu	Glu	Thr	Lys	Gln	Cys	Lys	Ala	Cys	Gly	Thr		
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gag	ata	ctt	aag	cct	tta	agt	tgt	ttg	gtg	tgt	gag	tat	gct	cta	tgt		1248
Glu	Ile	Leu	Lys	Pro	Leu	Ser	Cys	Leu	Val	Cys	Glu	Tyr	Ala	Leu	Cys		

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cac His	ttc Phe	ttg Leu 435	tca Ser	cta Leu	tgc Cys	cat His	gat Asp 440	gct Ala	gga Gly	aac Asn	tcg Ser	agc Ser 445	ggg Gly	gac Asp	ttg Leu	1344
tgg Trp	tgt Cys 450	gat Asp	att Ile	tgt Cys	gag Glu 455	acc Thr	aag Lys	acc Thr	gat Asp	cca Pro	agt Ser 460	gta Val	tgt Cys	tac Tyr	tac Tyr	1392
act Thr 465	tgt Cys	gat Asp	aag Lys	tgt Cys 470	ggg Gly 470	gtc Val	agt Ser	ctc Leu	cat His	att Ile 475	aat Asn	tgt Cys	gta Val	cta Leu	gga Gly 480	1440
gat Asp	tta Leu	tat Tyr	tat Tyr	acg Thr 485	aag Lys	gta Val	gga Gly	ctc Leu 490	gtc Val	tat Tyr	cct Pro	ggg Gly	ctt Leu	gaa Glu 495	gta Val	1488
ctt Leu	ccc Pro	aac Asn	aat Asn 500	ggt Gly	gct Ala	act Thr	cga Arg	cct Pro 505	ttc Phe	tgc Cys	aac Asn	agc Ser 510	tgt Cys 510	aaa Lys	ggt Val	1536
cgt Arg	tgc Cys	aag Lys 515	ttc Phe	agc Ser	ttc Phe	ctt Leu	atg Met 520	aag Lys	caa Gln	act Thr	cta Leu	gga Gly 525	gac Asp	ctt Leu	ggt Val	1584
cgt Arg	tac Tyr 530	ttt Phe	tgt Cys	tca Ser	ata Ile	cgt Arg 535	tgt Cys	att Ile	cct Pro	aga Arg	gca Ala 540	agg Arg	taa			1626

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Gly	Thr	Ile	Phe	Phe	Cys	Glu	Lys	Cys	Asp	Leu	Asp	Leu	His	Lys	Gly
Cys	Ala	Gly	Lys	Phe	Leu	Asn	Asn	Ser	Ser	Arg	Cys	Asn	His	Ser	Leu
Lys	Ile	Phe	Gln	Gly	Arg	Phe	Gly	Gln	Phe	Gly	Glu	Asp	Asp	Asp	Tyr
Gln	Cys	His	Tyr	Cys	Gln	Gln	Asn	Val	Gly	Phe	His	Phe	Ala	Arg	Cys
Thr	Ile	Cys	Asn	Ile	Ser	Ile	Asp	Glu	Lys	Cys	Leu	Arg	Asn	Pro	Pro
Pro	Leu	Thr	Ile	Phe	Gln	Pro	Lys	His	His	Lys	His	Ser	Leu	Phe	Leu
Leu	Gly	Arg	Leu	Val	Ala	Phe	Thr	Cys	Asn	Ala	Cys	Gly	Val	Glu	Gly
Asp	Arg	Asn	Pro	Tyr	Ile	Cys	Ile	Glu	Cys	Asn	Leu	Met	Leu	His	Lys
Glu	Cys	Thr	Asp	Leu	Pro	Arg	Val	Ile	Ser	Ile	Asn	Arg	His	Glu	His
Arg	Ile	Ser	His	Thr	Phe	His	Leu	Gly	Lys	Gly	Glu	Gly	Val	Trp	Glu
Cys	Gly	Val	Cys	Arg	Lys	Thr	Ile	Asp	Cys	Val	Tyr	Gly	Ala	Phe	Ile
Cys	Ser	Arg	Cys	Pro	Ser	Ser	Tyr	Ala	Val	His	Ser	Arg	Cys	Ala	Thr
Arg	Lys	Glu	Val	Trp	Asp	Gly	Ile	Glu	Leu	Glu	Asp	Val	Pro	Glu	Glu
Asp	Glu	Glu	Leu	Glu	Asp	Pro	Phe	Lys	Val	Ile	Asn	Glu	Lys	Gly	Asp
Ile	Val	His	Phe	Ser	His	Glu	Glu	His	Val	Leu	Arg	Leu	Asp	Val	Asn
Tyr	Val	His	Asp	Asn	Asp	Thr	Met	Cys	Cys	Gly	Gly	Cys	Ile	Leu	Pro
Ile	Asn	Asp	Asp	Pro	Cys	Tyr	Lys	Cys	Val	Glu	Cys	Asp	Phe	Cys	Leu

PF59082SeqList_PF59082.txt

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305 Asn His Lys Ile Ser	310 Leu Arg Ala His Lys Asp Asp Val Tyr Val Asp	320
	325 Lys Thr Tyr Ser Asn Gly Phe Lys Tyr Ile Arg Cys	335
Lys Cys Gly Ala Cys	340 Lys Thr Tyr Ser Asn Gly Phe Lys Tyr Ile Arg Cys	350
His Asp Lys Ser Ser Cys Arg Gly Asn Ile Lys Tyr Asp Ile Arg Cys	355	365
Ser Ser Ile Ser Glu Pro Phe His His Asp Asp Leu His Pro His Pro	370	380
Leu Tyr Trp Thr Leu Glu Glu Thr Lys Gln Cys Lys Ala Cys Gly Thr	375	395
385 Glu Ile Leu Lys Pro Leu Ser Cys Leu Val Cys Glu Tyr Ala Leu Cys	405	415
Ile Arg Cys Ala Thr Leu Pro Lys Lys Val Lys His Arg Cys Asp Asp	420	430
His Phe Leu Ser Leu Cys His Asp Ala Gly Asn Ser Ser Gly Asp Leu	435	445
Trp Cys Asp Ile Cys Glu Thr Lys Thr Asp Pro Ser Val Cys Tyr Tyr	450	460
Thr Cys Asp Lys Cys Gly Val Ser Leu His Ile Asn Cys Val Leu Gly	465	475
Asp Leu Tyr Tyr Thr Lys Val Gly Leu Val Tyr Pro Gly Leu Glu Val	470	480
	485	495
Leu Pro Asn Asn Gly Ala Thr Arg Pro Phe Cys Asn Ser Cys Lys Val	500	510
Arg Cys Lys Phe Ser Phe Leu Met Lys Gln Thr Leu Gly Asp Leu Val	505	525
Arg Tyr Phe Cys Ser Ile Arg Cys Ile Pro Arg Ala Arg	515	540
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ttt ttg gta ttc aca tta gca caa aca aaa aac ctt acc tct tct agt	96
Phe Leu Val Phe Thr Leu Ala Gln Thr Lys Asn Leu Thr Ser Ser Ser	
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gga gca cta gcc ata aat tct ggt agc gac aac ctc cct ctt caa cct	144
Gly Ala Leu Ala Ile Asn Ser Gly Ser Asp Asn Leu Pro Leu Gln Pro	
35 40 45	
ctt ttt ttc tgc cct gct tcc cgt atc aat ttt cag aac ctc aac ctt	192
Leu Phe Phe Cys Pro Ala Ser Arg Ile Asn Phe Gln Asn Leu Asn Leu	
50 55 60	
acg gag gag gat aag gag aag ttt cgg cca ttt aat tct tct cct cat	240
Thr Glu Glu Asp Lys Glu Lys Phe Arg Pro Phe Asn Ser Ser Pro His	
65 70 75 80	
ttc cca aac aca aga agc ggt gat cag caa ggc gga tct ttg ctt gat	288
Phe Pro Asn Thr Arg Ser Gly Asp Gln Gln Gly Gly Ser Leu Leu Asp	
85 90 95	
tgc gac caa cat ggt ata tgt aag ctc cct gta gtc cct ctc ttt tgg	336
Cys Asp Gln His Gly Ile Cys Lys Leu Pro Val Val Pro Leu Phe Trp	
100 105 110	
tgc aac aat aaa agt cct agt tct gac gaa ttc atg tgc ggt gca tgc	384
Cys Asn Asn Lys Ser Pro Ser Ser Asp Glu Phe Met Cys Gly Ala Cys	
115 120 125	
gaa aaa ata gtg ctc agc aca aac tat ttt gca tgt ctc cag tgt caa	432
Glu Lys Ile Val Leu Ser Thr Asn Tyr Phe Ala Cys Leu Gln Cys Gln	
130 135 140	

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Pro	Ser	His	Pro	Phe	His	Ser	Leu	Arg	Leu	Tyr	Ser	Tyr	Leu	Lys	Asp	
				165					170					175		
ttc	aag	aca	tgc	ttt	tgt	tgt	aaa	gtt	ttt	aac	agt	atg	gtc	atg	ctt	576
Phe	Lys	Thr	Cys	Phe	Cys	Cys	Lys	Val	Phe	Asn	Ser	Met	Val	Met	Leu	
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Tyr	His	Cys	Thr	Thr	Trp	Asp	Leu	Ser	Met	His	Thr	Val	Cys	Ala	Met	
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aga	tca	ata	ccc	ttt	gtt	gtc	gac	cat	cca	aaa	agc	cat	tta	cat	cct	672
Arg	Ser	Ile	Pro	Phe	Val	Val	Asp	His	Pro	Lys	Ser	His	Leu	His	Pro	
						215					220					
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Leu	Thr	Phe	Phe	Pro	Ala	Gln	Ala	Ser	Leu	Ile	Cys	Ser	Phe	Cys	Ala	
225				230						235					240	
acg	att	aag	aag	ctt	gat	ccc	aca	tac	atc	tgt	atc	gaa	tgt	gtc	ttc	768
Thr	Ile	Lys	Lys	Leu	Asp	Pro	Thr	Tyr	Ile	Cys	Ile	Glu	Cys	Val	Phe	
				245					250					255		
gtg	atc	cat	gaa	cac	tgt	atg	ggc	ttc	cca	cat	gtc	ata	aga	ata	tcc	816
Val	Ile	His	Glu	His	Cys	Met	Gly	Phe	Pro	His	Val	Ile	Arg	Ile	Ser	
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Arg	His	Asn	His	Arg	Ile	Ser	Phe	Thr	Ser	Ser	Leu	Pro	Ser	Gly	Asn	
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Leu	Phe	Cys	Arg	Ala	Cys	His	Gln	Gln	Val	Asp	Asn	Asp	Tyr	Gly	Ala	
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Tyr																
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Gly	Ala	Leu	Ala	Ile	Asn	Ser	Gly	Ser	Asp	Asn	Leu	Pro	Leu	Gln	Pro	
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Leu	Phe	Phe	Cys	Pro	Ala	Ser	Arg	Ile	Asn	Phe	Gln	Asn	Leu	Asn	Leu	
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Thr	Glu	Glu	Asp	Lys	Glu	Lys	Phe	Arg	Pro	Phe	Asn	Ser	Ser	Pro	His	
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Cys	Asp	Gln	His	Gly	Ile	Cys	Lys	Leu	Pro	Val	Val	Pro	Leu	Phe	Trp	
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Glu	Lys	Ile	Val	Leu	Ser	Thr	Asn	Tyr	Phe	Ala	Cys	Leu	Gln	Cys	Gln	
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Lys	Asn	Phe	His	Lys	Glu	Cys	Val	Gln	Ser	Pro	Leu	Glu	Ile	Lys	His	
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Pro	Ser	His	Pro	Phe	His	Ser	Leu	Arg	Leu	Tyr	Ser	Tyr	Leu	Lys	Asp	
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Phe	Lys	Thr	Cys	Phe	Cys	Cys	Lys	Val	Phe	Asn	Ser	Met	Val	Met	Leu	
			180					185					190			
Tyr	His	Cys	Thr	Thr	Trp	Asp	Leu	Ser	Met	His	Thr	Val	Cys	Ala	Met	
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Arg	Ser	Ile	Pro	Phe	Val	Val	Asp	His	Pro	Lys	Ser	His	Leu	His	Pro	
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PF59082SeqList_PF59082.txt

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 Leu His Pro Phe His Ser His Gln Leu Gln Leu Glu Ile Phe Arg Asp
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 Tyr Asp Glu Lys Lys Tyr Cys Arg Gly Cys Ala Leu Pro Ile Tyr Glu
 35 40 45
 ggt caa ttc tat tca tgc atg gaa ttg gaa tgc cac tat atc ctc cat 192
 Gly Gln Phe Tyr Ser Cys Met Glu Leu Glu Cys His Tyr Ile Leu His
 50 55 60
 aaa agc tgt gca gaa gct cca cgt atg aaa cgg tat ccc tta ttt cca 240
 Lys Ser Cys Ala Glu Ala Pro Arg Met Lys Arg Tyr Pro Leu Phe Pro
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 cat cca ctt aca cta aaa gtt gcc acc aca cat gat agt ggc aga ggt 288
 His Pro Leu Thr Leu Lys Val Ala Thr Thr His Asp Ser Gly Arg Gly
 85 90 95
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 His Phe Cys Cys Ser Glu Cys Gly Arg Asp Gly Asn Gly Phe Phe Tyr
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 Glu Tyr Gln Lys Glu Gln Lys Ile Phe Arg Leu Asp Leu Arg Cys Ala
 115 120 125
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 Ser Ile Met Glu Pro Tyr Glu Tyr Gln Gly His Gln His Pro Leu Phe
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 Leu Pro Trp Tyr Thr Glu Glu Lys Thr Pro Cys Gln Val Cys Lys Tyr
 145 150 155 160
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 Lys Ser Tyr Asn Ser Lys Leu Ile Cys Met Glu Cys Asp Tyr Ser Ile
 165 170 175
 tgt ctc cgt tgt gct acc ttc cca tac aag gca agg tat aag cat gac 576
 Cys Leu Arg Cys Ala Thr Phe Pro Tyr Lys Ala Arg Tyr Lys His Asp
 180 185 190
 agt cat ttt ctc aca atc tgt gat ggg aaa gag gca aat gat caa cca 624
 Ser His Phe Leu Thr Ile Cys Asp Gly Lys Glu Ala Asn Asp Gln Pro
 195 200 205
 gac tgg tgt gag gtg tgc gaa tgc aaa ata gaa gat gta aag aag cct 672
 Asp Trp Cys Glu Val Cys Glu Cys Lys Ile Glu Asp Val Lys Lys Pro
 210 215 220
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 Gly Tyr Asn Lys Asn Met Gln Asn Val Glu Lys Arg Phe Tyr Lys Cys
 225 230 235 240
 aat gac tgc tgc acc act ctt cat att gat tgt tta ttt ggg gga gac 768
 Asn Asp Cys Cys Thr Thr Leu His Ile Asp Cys Leu Phe Gly Gly Asp

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Val	Tyr	Ser	Phe	Glu	Asp	Arg	Asp	Tyr	Asn	Trp	Ile	Asp	Val	Arg	Ala	
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Leu	Leu	Asn	Ser	Ser	Leu	Ser	Arg	Pro	Ile	Cys	Val	Gln	Cys	Met	Cys	
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cgt	tgt	cca	ttc	cca	ata	ttt	ttc	aag	ttg	aaa	ggg	aac	ggc	aga	ata	960
Arg	Cys	Pro	Phe	Pro	Ile	Phe	Phe	Lys	Leu	Lys	Gly	Asn	Gly	Arg	Ile	
305					310					315					320	
tac	tgt	tct	gtg	tat	tgt	ctt	ggg	ttt	gca	cgg	tta	tga				999
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Tyr	Asp	Glu	Lys	Lys	Tyr	Cys	Arg	Gly	Cys	Ala	Leu	Pro	Ile	Tyr	Glu	
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Gly	Gln	Phe	Tyr	Ser	Cys	Met	Glu	Leu	Glu	Cys	His	Tyr	Ile	Leu	His	
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Lys	Ser	Cys	Ala	Glu	Ala	Pro	Arg	Met	Lys	Arg	Tyr	Pro	Leu	Phe	Pro	
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Cys	Leu	Arg	Cys	Ala	Thr	Phe	Pro	Tyr	Lys	Ala	Arg	Tyr	Lys	His	Asp	
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Ser	His	Phe	Leu	Thr	Ile	Cys	Asp	Gly	Lys	Glu	Ala	Asn	Asp	Gln	Pro	
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Asp	Trp	Cys	Glu	Val	Cys	Glu	Cys	Lys	Ile	Glu	Asp	Val	Lys	Lys	Pro	
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Leu	Leu	Asn	Ser	Ser	Leu	Ser	Arg	Pro	Ile	Cys	Val	Gln	Cys	Met	Cys	
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<400> 1255

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caa ata tat agt ctg agc gtg ggt ttg aat ccg gat tca tat tta gat	96
Gln Ile Tyr Ser Leu Ser Val Gly Leu Asn Pro Asp Ser Tyr Leu Asp	
20 25 30	
ccg gac tgg gat tct att tct aag atg ata cca ctc att act caa aca	144
Pro Asp Trp Asp Ser Ile Ser Lys Met Ile Pro Leu Ile Thr Gln Thr	
35 40 45	
atc tct ctg gtc agc tca atg gat ttc gat tcg caa ccg ggg tcg agg	192
Ile Ser Leu Val Ser Ser Met Asp Phe Asp Ser Gln Pro Gly Ser Arg	
50 55 60	
ctc atg tca ctc act aat caa gca atc tat gtc ttc aac tct atg gat	240
Leu Met Ser Leu Thr Asn Gln Ala Ile Tyr Val Phe Asn Ser Met Asp	
65 70 75 80	
ttt gat tcc cag cca gat tcg tta agg aag ctc ata gct ctc ttt tca	288
Phe Asp Ser Gln Pro Asp Ser Leu Arg Lys Leu Ile Ala Leu Phe Ser	
85 90 95	
cac aag ctc tct ctc gtc aac tct acg gaa ttt att tcg gag cag gac	336
His Lys Leu Ser Leu Val Asn Ser Thr Glu Phe Ile Ser Glu Gln Asp	
100 105 110	
acg aat tca cag cca gac ttg gag ttt ttc gtg tta ctc att cga gaa	384
Thr Asn Ser Gln Pro Asp Leu Glu Phe Phe Val Leu Ile Arg Glu	
115 120 125	
tta tgt agt cca aca ccg gag ccg cca gag ctt ata tca ctc atc agt	432
Leu Cys Ser Pro Thr Pro Glu Pro Pro Glu Leu Ile Ser Leu Ile Ser	
130 135 140	
caa ata att gac gaa gtc gtc tgt tgg aag cca cag cca gag tta gtt	480
Gln Ile Ile Asp Glu Val Val Cys Trp Lys Pro Gln Pro Glu Leu Val	
145 150 155 160	
cgt gat ttg gag cca gag ccg gag ccg gag ccg gag ccg gag	528
Arg Asp Leu Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu	
165 170 175	
att aat ctt ggg ttg aaa atc ata tct ctc att act caa cta atc tcc	576
Ile Asn Leu Gly Leu Lys Ile Ile Ser Leu Ile Thr Gln Leu Ile Ser	
180 185 190	
caa cca ata tct tta tcc att aag aca tct ctc att cct caa ata ata	624
Gln Pro Ile Ser Leu Ser Ile Lys Thr Ser Leu Ile Pro Gln Ile Ile	
195 200 205	
tct atg gtc agt aaa att gat ttg gat gcg cag ccg gag acg gaa atg	672
Ser Met Val Ser Lys Ile Asp Leu Asp Ala Gln Pro Glu Thr Glu Met	
210 215 220	
atg tca ctc act act caa gca gtc tcg ctc ttc aac tct atg gat ttg	720
Met Ser Leu Thr Thr Gln Ala Val Ser Leu Phe Asn Ser Met Asp Leu	
225 230 235 240	
ggt tcc cag ccg gat ccg cta agg aag ctc ata tct ctc att tct gga	768
Gly Ser Gln Pro Asp Pro Leu Arg Lys Leu Ile Ser Leu Ile Ser Gly	
245 250 255	
gaa atc tct cat gtc aaa tct gtc agc gtt tta aag cgg gag caa gac	816
Glu Ile Ser His Val Lys Ser Val Ser Val Leu Lys Arg Glu Gln Asp	
260 265 270	
ccg gaa ttg cgt cat tct gct gga agt tta cta aga gtc cca cga ggc	864
Pro Glu Leu Arg His Ser Ala Gly Ser Leu Leu Arg Val Pro Arg Gly	
275 280 285	
tta tat cga aat tgc cat ccc gaa ata gat acc ggg aca aag tta ttg	912
Leu Tyr Arg Asn Cys His Pro Glu Ile Asp Thr Gly Thr Lys Leu Leu	
290 295 300	
aag cag gat tca aac tcg ggc aca tat tcg aac ata gag cat ttg gag	960
Lys Gln Asp Ser Asn Ser Gly Thr Tyr Ser Asn Ile Glu His Leu Glu	
305 310 315 320	
atg gat ttg aac ata gag cat ttg gag atg gat tcg aac tcg gac aca	1008
Met Asp Leu Asn Ile Glu His Leu Glu Met Asp Ser Asn Ser Asp Thr	

PF59082SeqList_PF59082.txt

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ttc Phe	gac Asp	ctg Leu 355	gag Glu	gca Ala	gat Asp	ccc Pro	gac Asp 360	ctc Leu	ttt Phe	ttc Phe	cgc Arg	tat Tyr 365	ttt Phe	aaa Lys	aga Arg	1104
gtg Val	agt Ser 370	ctc Leu	gat Asp	tcc Ser	tac Tyr	ctc Leu 375	att Ile	tcc Ser	ctc Leu	gtt Val	ggt Gly 380	gaa Glu	aca Thr	ttg Leu	agt Ser	1152
ctc Leu 385	gag Glu	cca Pro	cag Gln	ccg Pro	gag Glu 390	ctc Leu	ata Ile	tca Ser	ctc Leu	atc Ile 395	tat Tyr	caa Gln	ata Ile	ttc Phe	tca Ser 400	1200
ctc Leu	gtc Val	gtc Val	tct Ser	atg Met 405	tat Tyr	tca Ser	gag Glu	tgg Trp	aaa Lys 410	agg Arg	ctt Leu	att Ile	ttc Phe	ctt Leu 415	tac Tyr	1248
cct Pro	caa Gln	gta Val	caa Gln 420	gta Val	aaa Lys	ttg Leu	aaa Lys	aaa Lys 425	gga Gly	aaa Lys	ttt Phe	caa Gln	gtg Val 430	att Ile	gac Asp	1296
gaa Glu	gaa Glu	gtc Val 435	tcg Ser	tgg Trp	agc Ser	agc Ser	aat Asn 440	ggc Gly	aag Lys	tgg Trp	aag Lys	tgt Cys 445	ctc Leu	cct Pro	ttt Phe	1344
aac Asn	tgg Trp 450	gag Glu	aaa Lys	atc Ile	tgg Trp	ata Ile 455	tct Ser	gaa Glu	gaa Glu	ggc Gly	gtt Val 460	agt Ser	cat His	att Ile	cgc Arg	1392
tgc Cys 465	caa Gln	act Thr	tgc Cys	aat Asn 470	ggc Gly	gag Glu	aac Asn	cat His	gga Gly	gaa Glu 475	tat Tyr	gaa Glu	aag Lys	gct Ala	cca Pro 480	1440
gtt Val	gtg Val	atc Ile	aaa Lys	cat His 485	act Thr	ctt Leu	cat His	cca Pro	aaa Lys 490	cat His	tcc Ser	ctc Leu	caa Gln	ctt Leu 495	gtc Val	1488
ttg Leu	ttg Leu	aat Asn	ggg Gly 500	gac Asp	aca Thr	acc Thr	agg Arg	gaa Glu 505	tgt Cys	tat Tyr	tgt Cys	tgc Cys	gat Asp 510	aaa Lys	gat Asp	1536
ctc Leu	gaa Glu 515	gag Glu	gta Val	ttt Phe	tat Tyr	tat Tyr	tgc Cys 520	tcg Ser	gct Ala	tgc Cys	gat Asp	tat Tyr 525	gct Ala	atg Met	aat Asn	1584
att Ile	gct Ala 530	tgc Cys	ata Ile	aag Lys	aga Arg	aca Thr 535	aga Arg	gta Val	ttg Leu	tct Ser	ttg Leu 540	gac Asp	caa Gln	ccg Pro	aag Lys	1632
tgg Trp 545	cat His	gag Glu	cat His	aca Thr 550	ctt Leu	gct Ala	caa Gln	ttt Phe	cca Pro	aga Arg 555	aag Lys	act Thr	tct Ser	tta Leu	act Thr 560	1680
tgc Cys	aac Asn	gtt Val	tgt Cys	gcc Ala 565	ttg Leu	aca Thr	cat His	tca Ser	agc Ser 570	tgt Cys	cca Pro	ttt Phe	tat Tyr	atg Met 575	tgt Cys	1728
ccc Pro	cct Pro	tgc Cys	gac Asp 580	ttt Phe	gtg Val	gtc Val	cac His	caa Gln 585	aag Lys	tgt Cys	atc Ile	agc Ser	tta Leu 590	cca Pro	cgt Arg	1776
gtc Val	ata Ile 595	agg Arg	ata Ile	tct Ser	cgt Arg	cat His	ttc Phe 600	cat His	cgt Arg	atc Ile	cat His	ttt Phe 605	act Thr	cct Pro	tct Ser	1824
ttc Phe	gac Asp 610	caa Gln	gaa Glu	gtt Val	cga Arg	tgt Cys 615	tgt Cys	ggt Gly	gtt Val	tgt Cys	cgt Arg 620	aga Arg	aag Lys	atc Ile	gat Asp	1872
aat Asn 625	gat Asp	tat Tyr	ggg Gly	ggt Gly 630	tat Tyr	tct Ser	tgc Cys	aac Asn	aag Lys	gac Asp 635	ggt Gly	tgt Cys	tgg Trp	tat Tyr	gca Ala 640	1920
gca Ala	cat His	tca Ser	aaa Lys 645	tgt Cys	gcc Ala	aca Thr	cag Gln	agc Ser 650	aat Asn	gtg Val	tgg Trp	gat Asp	ggt Gly 655	aaa Lys	gaa Glu	1968
ctc Leu	gag Glu	gga Gly 660	gag Glu	ccc Pro	gaa Glu	gaa Glu	gac Asp	atc Ile 665	aaa Lys	aaa Lys	att Ile	gag Glu 670	ccg Pro	ttt Phe	gtg Val	2016
aca																

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Cys Gln Ala Cys Ile Thr Pro Ile Tyr Phe Gly Asn Phe Tyr Ser Cys			
705	710	715	720
atg caa tgt gat ttc att ctt cat gaa gaa tgt gca aaa ctg tct cgc			2208
Met Gln Cys Asp Phe Ile Leu His Glu Glu Cys Ala Lys Leu Ser Arg			
	725	730	735
aaa ata cat cac cca gta cat cca cat ctg ctt act cta gtg gga aga			2256
Lys Ile His His Pro Val His Pro His Leu Leu Thr Leu Val Gly Arg			
	740	745	750
tct gac ctt gtt atg gat gct acg aaa tca tgt tca att tgt tct tgg			2304
Ser Asp Leu Val Met Asp Ala Thr Lys Ser Cys Ser Ile Cys Ser Trp			
	755	760	765
agg tgc aca act ggt ttc ttc tat gag tgc agt gaa aga gaa tgt cgt			2352
Arg Cys Thr Thr Gly Phe Phe Tyr Glu Cys Ser Glu Arg Glu Cys Arg			
	770	775	780
ttt aag gta cac gtg cag tgt gcc aca att tcc gag cca ttg gtc cat			2400
Phe Lys Val His Val Gln Cys Ala Thr Ile Ser Glu Pro Leu Val His			
785	790	795	800
gca agt cat atg gat cct ttg ttc tta aca tcg aaa cca gga gag gaa			2448
Ala Ser His Met Asp Pro Leu Phe Leu Thr Ser Lys Pro Gly Glu Glu			
	805	810	815
cga aga tgt tgt gtt tgc aaa gag tta gga cat tgt tcc aca aat gaa			2496
Arg Arg Cys Cys Val Cys Lys Glu Leu Gly His Cys Ser Thr Asn Glu			
	820	825	830
aca ttc aat tgc att gag tgc gac ttc gct ttg tgt ttc aag tgt gct			2544
Thr Phe Asn Cys Ile Glu Cys Asp Phe Ala Leu Cys Phe Lys Cys Ala			
	835	840	845
act tta cct caa aag gtg agg tat aag cac gat aag cat atg ctt act			2592
Thr Leu Pro Gln Lys Val Arg Tyr Lys His Asp Lys His Met Leu Thr			
	850	855	860
ctt tct tat gga gag gaa aca agt acc atg acg tat tgg tgt gaa gtt			2640
Leu Ser Tyr Gly Glu Glu Thr Ser Thr Met Thr Tyr Trp Cys Glu Val			
865	870	875	880
tgc gag aaa aaa ata aac cca aag gag cgg ttt tat atg tgt gat gag			2688
Cys Glu Lys Lys Ile Asn Pro Lys Glu Arg Phe Tyr Met Cys Asp Glu			
	885	890	895
tat tgt tgt gtc acc ctt cac att gaa tgt atg ctt ggg gtg gac cta			2736
Tyr Cys Cys Val Thr Leu His Ile Glu Cys Met Leu Gly Val Asp Leu			
	900	905	910
tac atg aag tct ggt tca ttt tgg ctc tat tgc agt agc aag gta agc			2784
Tyr Met Lys Ser Gly Ser Phe Trp Leu Tyr Cys Ser Ser Lys Val Ser			
	915	920	925
gtt tta ccc aat aat cac cat atg tcc aga cct att tgc tcc ttt tgt			2832
Val Leu Pro Asn Asn His His Met Ser Arg Pro Ile Cys Ser Phe Cys			
	930	935	940
aag aag cgt tgt cca cac aac ata gtt ttc caa tgt tta gga tta ata			2880
Lys Lys Arg Cys Pro His Asn Ile Val Phe Gln Cys Leu Gly Leu Ile			
945	950	955	960
tcg tgt tcc act tct tgt att cgc gtt aag gat tct aaa aag atg acc			2928
Ser Cys Ser Thr Ser Cys Ile Arg Val Lys Asp Ser Lys Lys Met Thr			
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atg taa			2934
Met			

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Pro Asp Trp Asp Ser Ile Ser Lys Met Ile Pro Leu Ile Thr Gln Thr	
35 40 45	
Ile Ser Leu Val Ser Ser Met Asp Phe Asp Ser Gln Pro Gly Ser Arg	

PF59082SeqList_PF59082.txt

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				85					90					95	
His	Lys	Leu	Ser	Leu	Val	Asn	Ser	Thr	Glu	Phe	Ile	Ser	Glu	Gln	Asp
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Thr	Asn	Ser	Gln	Pro	Asp	Leu	Glu	Phe	Phe	Val	Leu	Leu	Ile	Arg	Glu
							120					125			
Leu	Cys	Ser	Pro	Thr	Pro	Glu	Pro	Pro	Glu	Leu	Ile	Ser	Leu	Ile	Ser
	130					135					140				
Gln	Ile	Ile	Asp	Glu	Val	Val	Cys	Trp	Lys	Pro	Gln	Pro	Glu	Leu	Val
145					150					155					160
Arg	Asp	Leu	Glu	Pro	Glu	Pro	Glu	Pro	Glu	Pro	Glu	Pro	Glu	Pro	Glu
				165					170					175	
Ile	Asn	Leu	Gly	Leu	Lys	Ile	Ile	Ser	Leu	Ile	Thr	Gln	Leu	Ile	Ser
			180					185					190		
Gln	Pro	Ile	Ser	Leu	Ser	Ile	Lys	Thr	Ser	Leu	Ile	Pro	Gln	Ile	Ile
		195					200					205			
Ser	Met	Val	Ser	Lys	Ile	Asp	Leu	Asp	Ala	Gln	Pro	Glu	Thr	Glu	Met
	210					215					220				
Met	Ser	Leu	Thr	Thr	Gln	Ala	Val	Ser	Leu	Phe	Asn	Ser	Met	Asp	Leu
225					230					235					240
Gly	Ser	Gln	Pro	Asp	Pro	Leu	Arg	Lys	Leu	Ile	Ser	Leu	Ile	Ser	Gly
				245					250					255	
Glu	Ile	Ser	His	Val	Lys	Ser	Val	Ser	Val	Leu	Lys	Arg	Glu	Gln	Asp
			260					265					270		
Pro	Glu	Leu	Arg	His	Ser	Ala	Gly	Ser	Leu	Leu	Arg	Val	Pro	Arg	Gly
		275					280					285			
Leu	Tyr	Arg	Asn	Cys	His	Pro	Glu	Ile	Asp	Thr	Gly	Thr	Lys	Leu	Leu
	290					295					300				
Lys	Gln	Asp	Ser	Asn	Ser	Gly	Thr	Tyr	Ser	Asn	Ile	Glu	His	Leu	Glu
305					310					315					320
Met	Asp	Leu	Asn	Ile	Glu	His	Leu	Glu	Met	Asp	Ser	Asn	Ser	Asp	Thr
				325					330					335	
Tyr	Val	Tyr	Ile	Lys	Leu	Ser	Glu	Leu	Asp	Ser	Asp	Leu	Asp	Ile	Glu
			340					345					350		
Phe	Asp	Leu	Glu	Ala	Asp	Pro	Asp	Leu	Phe	Phe	Arg	Tyr	Phe	Lys	Arg
		355					360					365			
Val	Ser	Leu	Asp	Ser	Tyr	Leu	Ile	Ser	Leu	Val	Gly	Glu	Thr	Leu	Ser
	370					375					380				
Leu	Glu	Pro	Gln	Pro	Glu	Leu	Ile	Ser	Leu	Ile	Tyr	Gln	Ile	Phe	Ser
385					390					395					400
Leu	Val	Val	Ser	Met	Tyr	Ser	Glu	Trp	Lys	Arg	Leu	Ile	Phe	Leu	Tyr
				405					410					415	
Pro	Gln	Val	Gln	Val	Lys	Leu	Lys	Lys	Gly	Lys	Phe	Gln	Val	Ile	Asp
			420					425					430		
Glu	Glu	Val	Ser	Trp	Ser	Ser	Asn	Gly	Lys	Trp	Lys	Cys	Leu	Pro	Phe
		435					440					445			
Asn	Trp	Glu	Lys	Ile	Trp	Ile	Ser	Glu	Glu	Gly	Val	Ser	His	Ile	Arg
	450					455					460				
Cys	Gln	Thr	Cys	Asn	Gly	Glu	Asn	His	Gly	Glu	Tyr	Glu	Lys	Ala	Pro
465					470					475					480
Val	Val	Ile	Lys	His	Thr	Leu	His	Pro	Lys	His	Ser	Leu	Gln	Leu	Val
				485					490					495	
Leu	Leu	Asn	Gly	Asp	Thr	Thr	Arg	Glu	Cys	Tyr	Cys	Cys	Asp	Lys	Asp
			500					505					510		
Leu	Glu	Glu	Val	Phe	Tyr	Tyr	Cys	Ser	Ala	Cys	Asp	Tyr	Ala	Met	Asn
		515					520					525			
Ile	Ala	Cys	Ile	Lys	Arg	Thr	Arg	Val	Leu	Ser	Leu	Asp	Gln	Pro	Lys
	530					535					540				
Trp	His	Glu	His	Thr	Leu	Ala	Gln	Phe	Pro	Arg	Lys	Thr	Ser	Leu	Thr
545					550					555					560
Cys	Asn	Val	Cys	Ala	Leu	Thr	His	Ser	Ser	Cys	Pro	Phe	Tyr	Met	Cys
				565					570					575	
Pro	Pro	Cys	Asp	Phe	Val	Val	His	Gln	Lys	Cys	Ile	Ser	Leu	Pro	Arg
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Val	Ile	Arg	Ile	Ser	Arg	His	Phe	His	Arg	Ile	His	Phe	Thr	Pro	Ser
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PF59082SeqList_PF59082.txt

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Asn Asp Tyr Gly Gly Tyr Ser Cys Asn Lys Asp Gly Cys Trp Tyr Ala
625 630 635 640
Ala His Ser Lys Cys Ala Thr Gln Ser Asn Val Trp Asp Gly Lys Glu
645 650 655
Leu Glu Gly Glu Pro Glu Glu Asp Ile Lys Lys Ile Glu Pro Phe Val
660 665 670
Thr Val Arg Asp Gly Ile Ile Arg His Phe Ser His Asp His His His
675 680 685
Leu Lys Leu Asp Glu Asn Ile Asp Arg Asp Tyr Asn Glu Asn Lys Leu
690 695 700
Cys Gln Ala Cys Ile Thr Pro Ile Tyr Phe Gly Asn Phe Tyr Ser Cys
705 710 715 720
Met Gln Cys Asp Phe Ile Leu His Glu Glu Cys Ala Lys Leu Ser Arg
725 730 735
Lys Ile His His Pro Val His Pro His Leu Leu Thr Leu Val Gly Arg
740 745 750
Ser Asp Leu Val Met Asp Ala Thr Lys Ser Cys Ser Ile Cys Ser Trp
755 760 765
Arg Cys Thr Thr Gly Phe Phe Tyr Glu Cys Ser Glu Arg Glu Cys Arg
770 775 780
Phe Lys Val His Val Gln Cys Ala Thr Ile Ser Glu Pro Leu Val His
785 790 795 800
Ala Ser His Met Asp Pro Leu Phe Leu Thr Ser Lys Pro Gly Glu Glu
805 810 815
Arg Arg Cys Cys Val Cys Lys Glu Leu Gly His Cys Ser Thr Asn Glu
820 825 830
Thr Phe Asn Cys Ile Glu Cys Asp Phe Ala Leu Cys Phe Lys Cys Ala
835 840 845
Thr Leu Pro Gln Lys Val Arg Tyr Lys His Asp Lys His Met Leu Thr
850 855 860
Leu Ser Tyr Gly Glu Glu Thr Ser Thr Met Thr Tyr Trp Cys Glu Val
865 870 875 880
Cys Glu Lys Lys Ile Asn Pro Lys Glu Arg Phe Tyr Met Cys Asp Glu
885 890 895
Tyr Cys Cys Val Thr Leu His Ile Glu Cys Met Leu Gly Val Asp Leu
900 905 910
Tyr Met Lys Ser Gly Ser Phe Trp Leu Tyr Cys Ser Ser Lys Val Ser
915 920 925
Val Leu Pro Asn Asn His His Met Ser Arg Pro Ile Cys Ser Phe Cys
930 935 940
Lys Lys Arg Cys Pro His Asn Ile Val Phe Gln Cys Leu Gly Leu Ile
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Met

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Pro Leu Ser Cys Gly Thr Phe Glu Ser Tyr Thr Phe Arg Ser Ile Leu
20 25 30
tct atc ccg aag cta aga aat ggc ata tac aac tgc tat cac tgc aag 144
Ser Ile Pro Lys Leu Arg Asn Gly Ile Tyr Asn Cys Tyr His Cys Lys
35 40 45
gag tgc agc ttg acg ttt cac aaa gaa tgg gct gac agc ttc ttc agc 192
50 55 60
Seite 1644

PF59082SeqList_PF59082.txt

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Gln	Gln	Phe	Ile	Cys	Asn	His	Val	Leu	Lys	Ile	Phe	Arg	Arg	Ala	Lys	
65	70	75														
aca	cca	tta	ggt	gac	agt	aca	gat	gac	cac	ttt	tgt	cat	ttt	tgt	cga	288
Thr	Pro	Leu	Val	Asp	Ser	Thr	Asp	Asp	His	Phe	Cys	His	Phe	Cys	Arg	
				85					90					95		
agc	aag	ctt	aag	tta	aag	cat	ttc	cgg	tgc	acg	ata	tgc	aac	ata	agc	336
Ser	Lys	Leu	Lys	Leu	Lys	His	Phe	Arg	Cys	Thr	Ile	Cys	Asn	Ile	Ser	
			100					105					110			
gtg	ggt	aga	gaa	tgt	gtg	aaa	gat	cca	cca	cca	ctc	aca	att	tat	caa	384
Val	Gly	Arg	Glu	Cys	Val	Lys	Asp	Pro	Pro	Pro	Leu	Thr	Ile	Tyr	Gln	
		115					120					125				
cca	aag	cac	cac	aag	cat	agc	ctc	acc	ctc	ttg	tta	agg	tta	gtc	acc	432
Pro	Lys	His	His	Lys	His	Ser	Leu	Thr	Leu	Leu	Leu	Arg	Leu	Val	Thr	
	130					135					140					
ttt	act	tgt	aat	gca	tgt	ggt	gtg	gaa	gac	gac	cgc	aat	cct	tat	gtt	480
Phe	Thr	Cys	Asn	Ala	Cys	Gly	Val	Glu	Asp	Asp	Arg	Asn	Pro	Tyr	Val	
145					150				155						160	
tgt	ctt	gaa	tgc	aat	ttg	atg	gtc	cat	aaa	tat	tgt	att	gag	aaa	cta	528
Cys	Leu	Glu	Cys	Asn	Leu	Met	Val	His	Lys	Tyr	Cys	Ile	Glu	Lys	Leu	
			165					170						175		
cca	cgc	gtc	ata	agc	ata	aac	cgt	cat	gac	cat	cgc	ata	aat	cat	acc	576
Pro	Arg	Val	Ile	Ser	Ile	Asn	Arg	His	Asp	His	Arg	Ile	Asn	His	Thr	
		180						185					190			
ttt	cat	ctt	ggt	caa	gga	gaa	gga	gat	aaa	gag	tgt	gga	ggt	tgt	cgg	624
Phe	His	Leu	Gly	Gln	Gly	Glu	Gly	Asp	Lys	Glu	Cys	Gly	Val	Cys	Arg	
		195					200					205				
aag	aag	att	aat	tgg	gcc	tac	gga	ggt	tat	gaa	tgc	tct	cgt	tgt	cct	672
Lys	Lys	Ile	Asn	Trp	Ala	Tyr	Gly	Gly	Tyr	Glu	Cys	Ser	Arg	Cys	Pro	
	210					215					220					
agt	tat	gcc	ggt	cat	tca	agg	tgt	gca	aca	aga	aga	gaa	gtg	tgg	gat	720
Ser	Tyr	Ala	Val	His	Ser	Arg	Cys	Ala	Thr	Arg	Arg	Glu	Val	Trp	Asp	
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ggg	tta	gag	ctc	gaa	gat	gtg	ccc	gaa	gaa	gaa	gaa	gaa	ata	gaa	gat	768
Gly	Leu	Glu	Leu	Glu	Asp	Val	Pro	Glu	Glu	Glu	Glu	Glu	Ile	Glu	Asp	
			245					250						255		
cca	ttc	aag	gta	ggt	aat	gaa	aag	gga	gat	atc	ggt	cat	ttt	tgt	cat	816
Pro	Phe	Lys	Val	Val	Asn	Glu	Lys	Gly	Asp	Ile	Val	His	Phe	Cys	His	
			260					265					270			
gaa	gag	cat	ggt	ctc	aga	ttg	gat	gag	aat	tat	ggt	aca	gat	aat	gtt	864
Glu	Glu	His	Val	Leu	Arg	Leu	Asp	Glu	Asn	Tyr	Val	Thr	Asp	Asn	Val	
		275					280					285				
aac	atg	cgt	tgt	cgg	tgt	tgt	ggt	ctt	gcc	atc	gac	ggg	gat	cca	tgc	912
Asn	Met	Arg	Cys	Arg	Cys	Cys	Val	Leu	Ala	Ile	Asp	Gly	Asp	Pro	Cys	
	290				295						300					
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Tyr	Arg	Cys	Leu	Glu	Cys	Asp	Phe	Ile	Leu	His	Glu	Lys	Cys	Ala	Asn	
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Leu	Pro	Arg	Lys	Met	Arg	His	Leu	Leu	His	Asn	His	Lys	Leu	Ser	Leu	
			325					330						335		
gag	ggt	tca	ttc	aca	cgt	ttt	cgt	cga	tca	gac	aat	ttc	ttt	tat	acg	1056
Glu	Val	Ser	Phe	Thr	Arg	Phe	Arg	Arg	Ser	Asp	Asn	Phe	Phe	Tyr	Thr	
			340					345					350			
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Cys	Ile	Ala	Cys	Gln	Thr	His	Thr	Asp	Gly	Phe	Ile	Tyr	Ala	Cys	His	
		355					360					365				
gat	ggg	ctt	tgt	aga	tac	ctc	ggt	aaa	agt	att	aag	tat	gat	gtt	cgg	1152
Asp	Gly	Leu	Cys	Arg	Tyr	Leu	Val	Lys	Ser	Ile	Lys	Tyr	Asp	Val	Arg	
	370					375					380					
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Cys	Ser	Ser	Val	Ser	Glu	Pro	Phe	His	His	Asp	Leu	His	Gln	His	Pro	
					390					395					400	
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Leu	Tyr	Phe	Thr	Leu	Gln	Ser	Ser	Arg	Gln	Cys	Gln	Ala	Cys	Gly	Thr	
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PF59082SeqList_PF59082.txt

Lys	Ile	Asp	His	Asp	Pro	Leu	Ser	Cys	Thr	Val	Cys	Asp	Tyr	Ser		
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Leu	Cys	Met	Arg	Cys	Thr	Thr	Leu	Pro	Arg	Lys	Val	Lys	His	Arg	Cys	
		435					440					445				
gat	gat	cat	ttt	ttg	tca	cta	tgt	caa	ggg	tct	tcc	gta	aac	gat	tcc	1392
Asp	Asp	His	Phe	Leu	Ser	Leu	Cys	Gln	Gly	Ser	Ser	Val	Asn	Asp	Ser	
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ggc	gac	ttg	tgg	tgc	gat	att	tgt	gag	acg	aag	aca	gat	ccg	agt	gta	1440
Gly	Asp	Leu	Trp	Cys	Asp	Ile	Cys	Glu	Thr	Lys	Thr	Asp	Pro	Ser	Val	
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Cys	Tyr	Tyr	Thr	Cys	Asp	Glu	Cys	Gly	Leu	Ser	Leu	His	Ile	Asp	Cys	
			485					490						495		
gta	ctt	gga	gat	tta	tat	tat	ttg	aag	cta	gga	atc	cca	gaa	cct	gat	1536
Val	Leu	Gly	Asp	Leu	Tyr	Tyr	Leu	Lys	Leu	Gly	Ile	Pro	Glu	Pro	Asp	
			500					505					510			
gtt	gaa	ata	tgt	cca	aac	aat	gag	gct	act	cga	cct	ctc	tgc	agt	ggt	1584
Val	Glu	Ile	Cys	Pro	Asn	Asn	Glu	Ala	Thr	Arg	Pro	Leu	Cys	Ser	Gly	
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Cys	Lys	Val	Arg	Cys	Lys	Asn	Pro	Phe	Phe	Ile	Arg	Ser	Thr	Glu	Glu	
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gaa	cct	gca	tca	cac	gct	tgt	tca	ata	gac	tgc	tca	taa				1671
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Ser	Ile	Pro	Lys	Leu	Arg	Asn	Gly	Ile	Tyr	Asn	Cys	Tyr	His	Cys	Lys	
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Thr	Pro	Leu	Val	Asp	Ser	Thr	Asp	Asp	His	Phe	Cys	His	Phe	Cys	Arg	
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Ser	Lys	Leu	Lys	Leu	Lys	His	Phe	Arg	Cys	Thr	Ile	Cys	Asn	Ile	Ser	
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Val	Gly	Arg	Glu	Cys	Val	Lys	Asp	Pro	Pro	Pro	Leu	Thr	Ile	Tyr	Gln	
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Pro	Lys	His	His	Lys	His	Ser	Leu	Thr	Leu	Leu	Leu	Arg	Leu	Val	Thr	
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Cys	Leu	Glu	Cys	Asn	Leu	Met	Val	His	Lys	Tyr	Cys	Ile	Glu	Lys	Leu	
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Lys	Lys	Ile	Asn	Trp	Ala	Tyr	Gly	Gly	Tyr	Glu	Cys	Ser	Arg	Cys	Pro	
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Ser	Tyr	Ala	Val	His	Ser	Arg	Cys	Ala	Thr	Arg	Arg	Glu	Val	Trp	Asp	
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Gly	Leu	Glu	Leu	Glu	Asp	Val	Pro	Glu	Glu	Glu	Glu	Glu	Ile	Glu	Asp	
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Pro	Phe	Lys	Val	Val	Asn	Glu	Lys	Gly	Asp	Ile	Val	His	Phe	Cys	His	
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 Tyr Arg Cys Leu Glu Cys Asp Phe Ile Leu His Glu Lys Cys Ala Asn
 305 310 315 320
 Leu Pro Arg Lys Met Arg His Leu Leu His Asn His Lys Leu Ser Leu
 325 330 335
 Glu Val Ser Phe Thr Arg Phe Arg Arg Ser Asp Asn Phe Phe Tyr Thr
 340 345 350
 Cys Ile Ala Cys Gln Thr His Thr Asp Gly Phe Ile Tyr Ala Cys His
 355 360 365
 Asp Gly Leu Cys Arg Tyr Leu Val Lys Ser Ile Lys Tyr Asp Val Arg
 370 375 380
 Cys Ser Ser Val Ser Glu Pro Phe His His Asp Leu His Gln His Pro
 385 390 395 400
 Leu Tyr Phe Thr Leu Gln Ser Ser Arg Gln Cys Gln Ala Cys Gly Thr
 405 410 415
 Lys Ile Asp His Asp Pro Leu Ser Cys Thr Val Cys Asp Asp Tyr Ser
 420 425 430
 Leu Cys Met Arg Cys Thr Thr Leu Pro Arg Lys Val Lys His Arg Cys
 435 440 445
 Asp Asp His Phe Leu Ser Leu Cys Gln Gly Ser Ser Val Asn Asp Ser
 450 455 460
 Gly Asp Leu Trp Cys Asp Ile Cys Glu Thr Lys Thr Asp Pro Ser Val
 465 470 475 480
 Cys Tyr Tyr Thr Cys Asp Glu Cys Gly Leu Ser Leu His Ile Asp Cys
 485 490 495
 Val Leu Gly Asp Leu Tyr Tyr Leu Lys Leu Gly Ile Pro Glu Pro Asp
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 Val Glu Ile Cys Pro Asn Asn Glu Ala Thr Arg Pro Leu Cys Ser Gly
 515 520 525
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<210> 1259

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<212> DNA

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<222> (1)..(1791)

<400> 1259

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cct ttt cat gat cat cct atg tca agt tct tat tgt att ttt ttg gaa	96
Pro Phe His Asp His Pro Met Ser Ser Tyr Cys Ile Phe Leu Glu	
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tct tgc tct ttg tgc tct ttc tct aag aac tct tca tgg cta aga aga	144
Ser Cys Ser Leu Cys Ser Phe Ser Lys Asn Ser Ser Trp Leu Arg Arg	
35 40 45	
agt gtt act tgt atc agt tac gag tgt acg gat tgt ggc ttg acg ttg	192
Ser Val Thr Cys Ile Ser Tyr Glu Cys Thr Asp Cys Gly Leu Thr Leu	
50 55 60	
cac aaa gaa tgc gtt gac cac ctc ttc ctc aac cgg cca ttt cta tgc	240
His Lys Glu Cys Val Asp His Leu Phe Leu Asn Arg Pro Phe Leu Cys	
65 70 75 80	
aat cac gtt ctc aag atc tac cgt aat acc ttc gcg tgg cct gac cct	288
Asn His Val Leu Lys Ile Tyr Arg Asn Thr Phe Ala Trp Pro Asp Pro	
85 90 95	
gac cgt aaa gac gac ctt tct tgt cat ttt tgt cga cgt aag ctt acg	336
Asp Arg Lys Asp Asp Leu Ser Cys His Phe Cys Arg Arg Lys Leu Thr	
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Ser Phe Phe Ala Arg Leu Arg Asn Leu Pro Ser Phe Phe Ala Arg Cys	
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PF59082SeqList_PF59082.txt

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cca Pro 145	cca Pro	ctc Leu	gca Ala	att Ile	ttc Phe 150	gaa Glu	cca Pro	aaa Lys	cac His	cac His 155	gag Glu	cat His	agt Ser	ctc Leu	acc Thr 160	480
ctc Leu	ttg Leu	tta Leu	agg Arg	tta Leu 165	gtc Val	acc Thr	ttt Phe	act Thr	tgt Cys 170	aat Asn	gct Ala	tgt Cys	ggg Gly	gtg Val 175	gta Val	528
gat Asp	gac Asp	cgc Arg	aat Asn 180	cct Pro	tac Tyr	gta Val	tgt Cys	ctt Leu 185	gaa Glu	tgc Cys	aat Asn	ttg Leu	atg Met 190	gtc Val	cac His	576
aaa Lys	gag Glu	tgt Cys 195	gtt Val	cag Gln	aat Asn	cta Leu 200	ccg Pro	cga Arg	gtc Val	ata Ile	agc Ser 205	ata Ile	aat Asn	cg Arg	cat His	624
gac Asp	cat His 210	cgc Arg	ata Ile	tct Ser	cat His	act Thr 215	ttt Phe	cac His	ctt Leu	ggg Gly 220	caa Gln	gga Gly	gaa Glu	gga Gly	gat Asp	672
tg Trp 225	gag Glu	tgt Cys	gga Gly	gtt Val	tgt Cys 230	cgg Arg	aag Lys	acg Thr	atc Ile	aat Asn 235	tg Trp	gtc Val	tat Tyr	gga Gly 240	ggg Gly	720
tat Tyr	aaa Lys	tgc Cys	tct Ser	cg Arg 245	tgt Cys	cct Pro	agt Ser	tat Tyr	gcc Ala 250	gtt Val	cat His	tca Ser	aga Arg	tgt Cys 255	gca Ala	768
aca Thr	aga Arg	tac Tyr	gaa Glu 260	gtg Val	tg Trp	gat Asp	ggg Gly	tta Leu 265	gag Glu	ctc Leu	gaa Glu	gat Asp	gtg Val 270	ccc Pro	gaa Glu	816
gaa Glu	gaa Glu 275	gaa Glu	gaa Glu	atc Ile	gaa Glu	gat Asp 280	cca Pro	ttc Phe	aag Lys	gta Val	att Ile 285	aat Asn	gaa Glu	aag Lys	gga Gly	864
gat Asp	atc Ile 290	att Ile	cat His	ttt Phe	agt Ser	cat His 295	gaa Glu	gag Glu	cat His	gtt Val 300	ctc Leu	aga Arg	ttg Leu	gac Asp	gag Glu	912
att Ile 305	tat Tyr	gta Val	acg Thr	gat Asp 310	gat Ala	gct Asn	aac Met	atg Arg	cg Cys 315	tgt Arg	cg Arg	tgt Cys	tgc Cys	gtt Val	ctt Leu 320	960
gct Ala	atc Ile	aac Asn	ggg Gly	gac Asp 325	cca Pro	tgc Cys	tac Tyr	aga Arg	tgc Cys 330	gtt Val	gaa Glu	tgt Cys	gat Asp	ttc Phe 335	atc Ile	1008
ctt Leu	cac His	aaa Lys	gcg Ala 340	tgt Cys	gc Ala	aat Asn	ctt Leu 345	cct Pro	cga Arg	aaa Lys	atg Met	cga Arg	cat His 350	tta Leu	ttg Leu	1056
cat His	aag Lys	cat His 355	aaa Lys	ctc Leu	act Thr	ctt Leu	tca Ser 360	tcg Ser	aca Thr	ggg Gly	aac Asn 365	cg Arg	ttt Phe	ttg Leu	aga Arg	1104
tgt Cys 370	aaa Lys	gct Ala	tgt Cys	gac Asp	ata Ile	aaa Lys 375	act Thr	aat Asn	ggg Gly	ttc Phe 380	att Ile	tac Tyr	gag Glu	tgt Cys	ctt Leu	1152
cat His 385	gaa Glu	ggg Gly	tgc Cys	aaa Lys	agt Ser 390	att Ile	agt Ser	ttt Phe	acg Thr	tac Tyr 395	gat Asp	gtt Val	cg Arg	tgt Cys	agt Ser 400	1200
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ttt Phe	acg Thr	ttg Leu	gag Glu 420	aaa Lys	acc Thr	aat Asn	aaa Lys	tgt Cys 425	cac His	gct Ala	tgt Cys	aaa Lys	aga Arg 430	aaa Lys	ata Ile	1296
gat Asp	tg Trp	aat Asn 435	ccc Pro	ttg Leu	aat Asn	tgt Cys	acg Thr 440	gtt Val	tgt Cys	gat Asp	gat Asp	tac Tyr 445	tct Ser	tta Leu	tgc Cys	1344
acg Thr 450	agg Arg	tgc Cys	gct Ala	gct Ala	tta Leu	cca Pro 455	aga Arg	aag Lys	gta Val	aaa Lys	cac His 460	aga Arg	tgt Cys	gat Asp	gat Asp	1392
cat His 465	tat Tyr	ctg Leu	tca Ser	cta Leu	tgt Cys 470	caa Gln	ggg Gly	gtg Val	gga Gly	agt Ser 475	gca Ala	agt Ser	ggg Gly	gac Asp	ttg Leu 480	1440
tg Trp	tgt Cys	gat Asp	att Ile	tgt Cys 485	gag Glu	aca Thr	aag Lys	aca Thr	gac Asp 490	ccg Pro	agt Ser	gta Val	ttt Phe	tac Tyr 495	tat Tyr	1488

PF59082SeqList_PF59082.txt

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Ile	Trp	Tyr	Cys	Ser	Lys	Asp	Leu	Cys	Pro	Lys	Glu	Phe	Asn	Phe	Ala	
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PF59082SeqList_PF59082.txt

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 Ser Val Ser Glu Pro Phe His His Asp Leu His Gln His Pro Leu Tyr
 405 410 415
 Phe Thr Leu Glu Lys Thr Asn Lys Cys His Ala Cys Lys Arg Lys Ile
 420 425 430
 Asp Trp Asn Pro Leu Asn Cys Thr Val Cys Asp Asp Tyr Ser Leu Cys
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 Thr Arg Cys Ala Ala Leu Pro Arg Lys Val Lys His Arg Cys Asp Asp
 450 455 460
 His Tyr Leu Ser Leu Cys Gln Gly Val Gly Ser Ala Ser Gly Asp Leu
 465 470 475
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 515 520 525
 His Pro Asn Asn Gly Ala Thr Arg Pro Ile Cys Thr Lys Cys Glu Leu
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<400> 1261

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Leu Cys Ser His Tyr His Ser Leu Ser Trp Gln Val Phe Arg Ser Gly	
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Val Trp Gln Asn Glu Val Glu Pro Trp Phe Arg Thr Ser Glu Tyr His	
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Gly Pro Ala Leu Arg Ile Ser Asn Asn Ile Asn Tyr His Cys Lys Glu	
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Cys Asp Ile Met Met His Lys Asp Cys Val Asp Arg Leu Phe Asn Gln	
85 90 95	
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Pro Phe Ile Cys Asn His Ile Leu Lys Ile Phe Val Ser Thr Ile Ser	
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Pro Leu Asp Ser Ile Val Asp Asp Leu Cys His Phe Cys Arg Phe Glu	

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 Asp Gly Asn Pro Tyr Phe Val Ile Leu Thr Glu Thr Lys Val Asp Gln
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 Lys Arg Arg Lys Lys Thr Tyr Phe Leu Cys Pro Ala Ala Arg Ile Lys
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 Tyr Leu Lys Phe Lys Arg Lys Met Leu Glu Asn Tyr Asp Tyr Gly Asp
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 Asp Asn Glu Asp Asp Asp Asn Asp Ala Asp Glu Asp Ala Lys Glu Asp
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 Gly Asp Gly His Asp Lys Leu Tyr Pro Phe Asn Ser Ser Ser His Phe
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 Pro Asn Thr Arg Arg Gly Asp Arg Gln Gly Lys Ser Leu Leu Asp Cys
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Lys	Gly	Leu	Arg	Leu	Ile	Tyr	Cys	Ser	Leu	Asp	Cys	Val	Arg	Asn	Leu	
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<213> Arabidopsis thaliana

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Asp	Gly	Asn	Pro	Tyr	Phe	Val	Ile	Leu	Thr	Glu	Thr	Lys	Val	Asp	Gln	
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Lys	Arg	Arg	Lys	Lys	Thr	Tyr	Phe	Leu	Cys	Pro	Ala	Ala	Arg	Ile	Lys	
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Tyr	Leu	Lys	Phe	Lys	Arg	Lys	Met	Leu	Glu	Asn	Tyr	Asp	Tyr	Gly	Asp	
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Asp	Asn	Glu	Asp	Asp	Asp	Asn	Asp	Ala	Asp	Glu	Asp	Ala	Lys	Glu	Asp	
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Gly	Asp	Gly	His	Asp	Lys	Leu	Tyr	Pro	Phe	Asn	Ser	Ser	Ser	His	Phe	
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Gly	Lys	Met	Leu	Asp	Thr	Ser	Lys	Asp	Tyr	Ala	Cys	Leu	Gln	Cys	Gln	
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PF59082SeqList_PF59082.txt

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Phe	Phe	Pro	Ala	Gln	Ala	Leu	Ile	Cys	His	Ile	Cys	Ala	Val	Ile	Lys
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	370					375					380				
Leu	His	Pro	Phe	His	Ser	His	His	Leu	Arg	Leu	Glu	Ile	Ser	Ile	Ala
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Tyr	Asp	Ala	Asn	Lys	Tyr	Cys	Arg	Gly	Cys	Ala	Leu	Pro	Ile	Tyr	Glu
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	530					535					540				
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545					550					555					560
Leu	Thr	Ile	Ser	Asn	Gly	Lys	Glu	Glu	Ser	Asp	Gln	Gln	Asp	Trp	Cys
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Leu	Trp	Asn	Gln	Lys	Glu	Ala	Leu	Arg	Tyr	Arg	Cys	Asn	Val	Cys	Cys
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Thr	Thr	Leu	His	Ile	Asp	Cys	Leu	His	Gly	Lys	Glu	Met	Tyr	Ile	Lys
	610					615					620				
Pro	Arg	Glu	Thr	Glu	Arg	Asp	His	Leu	Thr	Phe	His	Thr	Phe	Arg	Asp
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Met	Glu	Arg	Ile	Phe	Ile	Arg	Val	His	Leu	Asn	Ser	Ser	Leu	Ser	Arg
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Pro	Val	Cys	Ser	Arg	Cys	Asn	Arg	Arg	Cys	Pro	Phe	Pro	Ile	Phe	Phe
			660					665					670		
Lys	Gly	Leu	Arg	Leu	Ile	Tyr	Cys	Ser	Leu	Asp	Cys	Val	Arg	Asn	Leu
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Glu Ala Ala Ala Ala Lys Lys Ala Met Tyr Phe Gly Val Asp Asp	
35 40 45	
ctc cct ctt caa cct ctt ttt ttc tgt cct tct gtc cgc atc aaa ttt	192
Leu Pro Leu Gln Pro Leu Phe Phe Cys Pro Ser Val Arg Ile Lys Phe	
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Leu His Ser Lys Pro Lys Asn His Asp Asp Asp His His His Gly Gly	
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Ser His Asp Gln Gln Gly Glu Ser Leu Leu Asp Cys Asp Lys Asp Tyr	
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Ile Cys Lys Leu Pro Val Ile Pro Leu Phe Trp Cys Asn Asn Lys Glu	
115 120 125	
ttt cgc tat ggc aaa ttc gat tgt cgt gca tgt aat ggg aat att ttc	432
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130 135 140	
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165 170 175	
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His Ser Leu Arg Leu Phe Ser Gly Ser Ser Asn Gln Lys Cys Ser Cys	
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225 230 235 240	
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Thr Tyr Ile Cys Ile Gln Cys Val Phe Val Ile His Lys Gly Cys Met	
260 265 270	
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Phe Thr Ser Ser Leu Pro Cys Gly Asn Phe Ser Cys Gly Val Cys Arg	
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Gln Gln Val Asp Asn Asn Tyr Gly Ala Tyr Ser Cys Glu Ile Cys Asp	
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Asp Tyr Phe Val His Ser Lys Cys Ser Leu Leu Pro Arg Ile Trp Asp	
325 330 335	
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370	375	380	
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385	390	395	
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405	410	415	
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420	425	430	
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435	440	445	
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Phe Asp Tyr Gln Gly His Gln His Pro Leu Phe Leu Pro Trp Asp Thr			
485	490	495	
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Lys Lys Lys Thr Arg Cys Gln Met Cys Lys Tyr Glu Ser Lys Glu Ser			
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515	520	525	
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Gly Lys Lys Thr Glu Leu Arg Tyr Tyr Lys Cys Asn Asp Cys Cys Thr			
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660	665	670	
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Leu His Ser Lys Pro Lys Asn His Asp Asp Asp His His His Gly Gly
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Phe Met Pro His Pro Leu Asn Ser Thr Pro His Phe Pro Cys Thr Arg
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Glu Cys Val Glu Ser Pro Leu Glu Ile Lys His Pro Ser His Pro Phe
165     170     175
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Lys Lys Lys Thr Arg Cys Gln Met Cys Lys Tyr Glu Ser Lys Glu Ser
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 580 585 590
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 595 600 605
 Gly Glu Thr Glu Lys Glu Tyr Leu Ser Phe Ser Asp Phe Ser Phe Ser
 610 615 620
 Glu Asp Val Trp Lys Trp Met Asp Val Arg Ala Leu Leu Asn Ser Ser
 625 630 635 640
 Leu Ser Arg Pro Ile Cys Asn Gly Cys Lys Cys Arg Cys Pro Phe Pro
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Asn Pro Tyr Ile Cys Lys Leu Pro Val Val Leu Leu Phe Trp Cys Asn	
65 70 75 80	
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Pro Thr Leu Ser Ala Thr Tyr Tyr Ala Cys Leu Ile Cys Glu Lys Met	
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ttc cac aaa gaa tgc gta gag tct cca ttc gag atc ata cat cct tcc	384
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cac cct ttt cac tct ctt cga ctt acc agt tct cca cag agt caa aac	432
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130 135 140	
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Cys Ile Cys Cys His His Tyr Phe Asn Asp Ile Phe Tyr His Cys Ser	
145 150 155 160	
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Thr Cys Lys Leu Ile Met His Pro Ile Cys Ala Met Arg Ser Ile Pro	
165 170 175	
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Phe Ala Val Asp His Pro Lys Ser His Ser His Pro Leu Thr Phe Tyr	
180 185 190	
cct gca caa gct tct tta gtt tgc cat ttt tgt gcc tcg att aag aag	624
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195 200 205	

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Asp	Cys	Arg	Gly	Phe	Pro	His	Val	Ile	Arg	Ile	Ser	Arg	His	His	His	
225					230					235					240	
cgt	ata	tct	ttt	acc	tct	tct	ctt	cta	tct	gga	acc	ttt	tca	tgc	gga	768
Arg	Ile	Ser	Phe	Thr	Ser	Ser	Leu	Leu	Ser	Gly	Thr	Phe	Ser	Cys	Gly	
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Val	Cys	Arg	Glu	Gln	Val	Asp	Asn	Asn	Tyr	Gly	Ala	Tyr	Ala	Cys	Asn	
			260					265					270			
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His Asp Gly His Ile His Pro Leu Tyr Phe Ala Lys Lys Glu Glu His
                               485                               490                               495
Thr Cys Asp Gly Cys Gln Lys Ser Ile Glu Asp Tyr Met Leu Arg Cys
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Lys Ala Cys Asp Phe Asp Leu Cys Leu Tyr Cys Ala Thr Leu Pro Glu
                               515                               520                               525
Lys Ile Trp His Arg Asn Asp Gly His Pro Leu Thr Leu Cys Cys Gly
                               530                               535                               540
Glu Lys Glu Glu Ala Ser Gly Lys Tyr Trp Cys Asp Ile Cys Glu Lys
545                               550                               555                               560
Glu Leu Asp Pro Ser Ile Trp Phe Tyr Thr Cys Tyr Asp Cys Gly Val
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Thr Leu His Ala Gln Cys Val Leu Gly Asp Phe Ser Arg Leu Val Leu
                               580                               585                               590
Gly Gln Ile Tyr Ser Phe Gly Glu Lys Glu Ile Glu Phe Glu Ala Val
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Pro Asn Asn Ile Asn Thr Arg Pro Phe Cys Ile Gln Cys Asn Ser Arg
610                               615                               620
Cys Lys Val Ser Val Ile Leu Lys Ile Leu Lys Asp Ser Glu Asp Gly
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Ser Asp Asp Gly Ser Asp Asp Val Ser Asp Asp Val Ser Asp Asp Pro
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Ser Asn Asp Val Ser Asp Asp Thr Ser Asp Asp Asp Ser Asp Val Val
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Ser Asp Val Val Ser Asp Asp Ala Ser Asn Asp Asp Ser Asp Asp Thr
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Pro Ala Pro Arg Tyr Ile Asn Ala Arg Cys His Ile Cys Ser Val Thr
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His	Lys	Glu	Cys	Val	Glu	Leu	Pro	Ser	Glu	Ile	Asn	His	Leu	Phe	His	
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Pro	Gln	His	Pro	Leu	Leu	Leu	Thr	Tyr	Glu	Glu	Gly	Trp	Trp	Ser	Cys	
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Phe	Cys	Ala	Leu	Cys	Gly	Glu	Thr	Lys	Pro	Ala	Lys	Tyr	Phe	Tyr	Ser	
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Cys	Ser	Thr	Cys	Lys	Ile	Lys	Val	Asp	Leu	Thr	Cys	Gly	Met	Asn	Pro	
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cca	ccg	cca	gct	att	gaa	cat	ccc	atc	tgc	cat	gac	cat	cca	ctt	gtc	384
Pro	Pro	Pro	Ala	Ile	Glu	His	Pro	Ile	Cys	His	Asp	His	Pro	Leu	Val	
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Phe	Leu	Lys	Lys	Arg	Gln	Glu	Lys	Thr	Pro	Cys	Glu	Val	Cys	Lys	Asn	
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His	Val	Gly	Cys	Ile	His	Leu	Ser	Lys	Glu	Val	Asn	His	Pro	Cys	His	
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Ser	Asp	His	Pro	Leu	Met	Leu	Val	Glu	Ser	Glu	Ser	Leu	Thr	Asp	Asn	
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Asp	Lys	Lys	Thr	Cys	Phe	Leu	Cys	Gly	Gln	Gln	Pro	His	Gly	Ile	Leu	
		195					200					205				
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Tyr	His	Cys	Ser	Ile	Cys	Asn	Phe	Thr	Leu	Cys	Ile	Gly	Cys	Ile	Lys	
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Ser	Pro	Pro	Pro	Leu	Val	Val	Glu	Asn	Val	Lys	Thr	His	Lys	His	Pro	
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Leu	Thr	Phe	Phe	Pro	Arg	Gly	Val	Tyr	Cys	Thr	Cys	Asn	Val	Cys	Gly	
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gta	aaa	gga	ctt	ata	ctc	tct	tat	atg	tgt	ctt	cag	tgt	ggg	ttt	gcg	816
Val	Lys	Gly	Leu	Ile	Leu	Ser	Tyr	Met	Cys	Leu	Gln	Cys	Gly	Phe	Ala	
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gtc	cat	tgt	agt	tgt	gta	gac	tta	cct	caa	gtc	ata	aac	ata	aat	cgt	864
Val	His	Cys	Ser	Cys	Val	Asp	Leu	Pro	Gln	Val	Ile	Asn	Ile	Asn	Arg	
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His	Asp	His	Arg	Ile	Ser	Phe	Thr	Gln	His	Leu	Gly	Pro	Gly	Tyr	Leu	
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Asn	Cys	Gly	Val	Cys	Arg	Arg	Ser	Val	Cys	Gln	Phe	Asn	Gly	Ala	Tyr	
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Ser	Cys	Leu	Val	Cys	Pro	Asn	Tyr	Ala	Val	His	Ser	Arg	Cys	Ala	Thr	
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Arg	Tyr	Asp	Ile	Trp	Asp	Gly	Val	Glu	Leu	Glu	Gly	Lys	Ala	Glu	Asn	
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Ile	Glu	Asp	Ile	Ala	Pro	Phe	Lys	Val	Val	Gly	Asp	Asp	Leu	Ile	Arg	
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Ile	Tyr	Asp	Asp	Ser	Thr	Arg	Cys	Glu	Ala	Cys	Gly	His	Pro	Val	Glu	
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PF59082SeqList_PF59082.txt

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			420						425				430		
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Pro	Phe	Leu	Leu	Leu	Gly	Pro	Gly	Asn	Asp	Val	Cys	Lys	Val	Leu	Asp
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Gln	Lys	Glu	Leu	Pro	Cys	Asn	Ala	Cys	Gln	Lys	Thr	Ile	Arg	Asp	Tyr
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Met	Leu	Cys	Cys	Ala	Asp	Cys	Asp	Phe	Asn	Leu	Cys	Leu	Trp	Cys	Ala
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Ser	Leu	Pro	Lys	Lys	Ile	Arg	His	Ser	Asn	Asp	Glu	His	Ile	Leu	Thr
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Leu	Cys	Cys	Gly	Glu	Glu	Ala	Asn	Gly	Lys	Tyr	Trp	Cys	Asp	Ile	Cys
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Glu	Ala	Glu	Leu	Asp	Pro	Ser	Lys	Trp	Phe	Tyr	Thr	Cys	Phe	Gly	Cys
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Gly	Gly	Thr	Leu	His	Val	Glu	Cys	Val	Leu	Gly	Asp	Phe	Ser	Arg	Leu
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Met	Pro	Gly	Cys	Thr	Ile	Asp	Tyr	Arg	Val	Tyr	Thr	Val	Glu	Val	Val
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ttc	aat	aat	cac	aac	acg	cga	cca	atg	tgc	agc	cgg	tgt	cac	tct	cga
Phe	Asn	Asn	His	Asn	Thr	Arg	Pro	Met	Cys	Ser	Arg	Cys	His	Ser	Arg
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Cys	Lys	Val	Ser	Val	Ile	Leu	Lys	Phe	Arg	Glu	Gly	Asn	Ile	Val	Tyr
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Phe	Phe	Cys	Ser	Arg	Ser	Cys	Phe	Leu	Met	His	Phe	Ser	Tyr	Tyr	Leu
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 35 40 45
 His Lys Glu Cys Val Glu Leu Pro Ser Glu Ile Asn His Leu Phe His
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 Pro Gln His Pro Leu Leu Leu Thr Tyr Glu Glu Gly Trp Trp Ser Cys
 65 70 75 80
 Phe Cys Ala Leu Cys Gly Glu Thr Lys Pro Ala Lys Tyr Phe Tyr Ser
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PF59082SeqList_PF59082.txt

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Leu	Thr	Phe	Phe	Pro	Arg	Gly	Val	Tyr	Cys	Thr	Cys	Asn	Val	Cys	Gly
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Val	Lys	Gly	Leu	Ile	Leu	Ser	Tyr	Met	Cys	Leu	Gln	Cys	Gly	Phe	Ala
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Val	His	Cys	Ser	Cys	Val	Asp	Leu	Pro	Gln	Val	Ile	Asn	Ile	Asn	Arg
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Asn	Cys	Gly	Val	Cys	Arg	Arg	Ser	Val	Cys	Gln	Phe	Asn	Gly	Ala	Tyr
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Ser	Cys	Leu	Val	Cys	Pro	Asn	Tyr	Ala	Val	His	Ser	Arg	Cys	Ala	Thr
				325					330					335	
Arg	Tyr	Asp	Ile	Trp	Asp	Gly	Val	Glu	Leu	Glu	Gly	Lys	Ala	Glu	Asn
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Ile	Glu	Asp	Ile	Ala	Pro	Phe	Lys	Val	Val	Gly	Asp	Asp	Leu	Ile	Arg
		355					360					365			
His	Phe	Ser	His	Ser	Lys	His	Ser	Leu	Arg	Leu	His	Lys	Asn	Asn	Ile
	370					375					380				
Ile	Tyr	Asp	Asp	Ser	Thr	Arg	Cys	Glu	Ala	Cys	Gly	His	Pro	Val	Glu
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Phe	Gly	Arg	Ile	Tyr	Asn	Cys	Glu	Glu	Cys	Phe	Ile	Leu	His	Glu	
				405					410				415		
Lys	Cys	Ala	Asn	Leu	Pro	Met	Lys	Lys	Arg	Leu	Val	Phe	Ser	Thr	Leu
			420					425					430		
Pro	Phe	Leu	Leu	Leu	Gly	Pro	Gly	Asn	Asp	Val	Cys	Lys	Val	Leu	Asp
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Cys	Lys	Leu	Cys	Gly	Met	Phe	Phe	Thr	Gly	Phe	Glu	Tyr	Lys	Ser	Gln
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Pro	Phe	Val	His	Asp	Gly	His	Leu	His	Pro	Leu	Tyr	Phe	Asp	Gln	Lys
				485					490					495	
Gln	Lys	Glu	Leu	Pro	Cys	Asn	Ala	Cys	Gln	Lys	Thr	Ile	Arg	Asp	Tyr
			500					505					510		
Met	Leu	Cys	Cys	Ala	Asp	Cys	Asp	Phe	Asn	Leu	Cys	Leu	Trp	Cys	Ala
		515					520					525			
Ser	Leu	Pro	Lys	Lys	Ile	Arg	His	Ser	Asn	Asp	Glu	His	Ile	Leu	Thr
	530					535					540				
Leu	Cys	Cys	Gly	Glu	Glu	Ala	Asn	Gly	Lys	Tyr	Trp	Cys	Asp	Ile	Cys
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Glu	Ala	Glu	Leu	Asp	Pro	Ser	Lys	Trp	Phe	Tyr	Thr	Cys	Phe	Gly	Cys
				565					570					575	
Gly	Gly	Thr	Leu	His	Val	Glu	Cys	Val	Leu	Gly	Asp	Phe	Ser	Arg	Leu
				580				585					590		
Met	Pro	Gly	Cys	Thr	Ile	Asp	Tyr	Arg	Val	Tyr	Thr	Val	Glu	Val	Val
		595					600					605			
Phe	Asn	His	Asn	Thr	Arg	Pro	Met	Cys	Ser	Arg	Cys	His	Ser	Arg	
	610				615					620					
Cys	Lys	Val	Ser	Val	Ile	Leu	Lys	Phe	Arg	Glu	Gly	Asn	Ile	Val	Tyr
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Pro Ser Ala Arg Ile Val Phe Ser Thr Cys Lys Gly Cys Gly Val Glu
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Asp Phe Val Tyr Gly Gly Tyr Val Cys Asn Asp Ser Asp Cys Lys Ala
      35      40      45
cgg ttt cat aag gag tgc gct gag gcc cca tct gag atc agc cac tct     192
Arg Phe His Lys Glu Cys Ala Glu Ala Pro Ser Glu Ile Ser His Ser
      50      55      60
ttc cac caa caa cat cct ctc ttt ctc acc aat ggc ctg gga gat ctt     240
Phe His Gln Gln His Pro Leu Phe Leu Thr Asn Gly Leu Gly Asp Leu
      65      70      75
cca tgt gat ttg tgt gga caa aag cga ttg gaa gcc gct ggt tat agt     288
Pro Cys Asp Leu Cys Gly Gln Lys Arg Leu Glu Ala Ala Gly Tyr Ser
      85
tgt ccc aca tgt gag ttc aag ctg gat ttg act tgt ggg ata aac cca     336
Cys Pro Thr Cys Glu Phe Lys Leu Asp Leu Thr Cys Gly Ile Asn Pro
      100      105
tca ccg cct gct att gaa cat cct atc tgt cat gac cat cca ctt gtc     384
Ser Pro Pro Ala Ile Glu His Pro Ile Cys His Asp His Pro Leu Val
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Phe Leu Lys Lys Arg Glu Glu Lys Ala Pro Cys Glu Val Cys Lys Asp
      130      135      140
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Ser Ile Gly Gly Pro Ser Tyr Ser Cys Leu Gly Cys Asp Leu Tyr Phe
      145      150      155
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His Val Asp Cys Val His Leu Ser Lys Glu Val Asn His Pro Cys His
      165      170      175
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Pro Ser His Pro Leu Lys Leu Ile Ala Ser Glu Ser Leu Thr Asp Asn
      180      185      190
gct gag aag att tgt ctt tta tgt gaa caa caa cca gaa aat atg ctt     624
Ala Glu Lys Ile Cys Leu Leu Cys Glu Gln Gln Pro Glu Asn Met Leu
      195      200      205
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Tyr Tyr Cys Ser Val Cys Asn Phe Thr Ser Cys Leu Gly Cys Thr Lys
      210      215      220
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      245      250      255
tat aac agc aga gct tat atg tgc ctt cct tgt ggt ttc gtt gtc aat     816
Tyr Asn Ser Arg Ala Tyr Met Cys Leu Pro Cys Gly Phe Val Val Asn
      260      265      270
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Gly Asn Gly Ile Asn Leu Pro Gln Val Ile Asn Ile Asn Arg His Asp
      275      280      285
cat cgt atc tct tac act cat cag ctt ggc cct gga tat ttg aac tgc     912
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Ile	Ser	Thr	Arg	Phe	Val	Asn	Asp	Ser	Cys	Lys	Gly	Cys	Asn	Ile	Lys	
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Asn	Pro	Cys	Lys	Cys	Asn	Leu	Cys	Gly	Lys	Thr	Phe	Phe	Ala	Phe	Gly	
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Cys	Glu	Val	His	Phe	His	Val	Glu	Cys	Val	Asn	Leu	Ser	Gln	Glu	Val	
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Asn	His	Pro	Ser	His	Pro	Gln	His	Ser	Leu	Lys	Leu	Leu	Glu	Tyr	Glu	
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Ser	Leu	Thr	Ser	Asp	Ala	Glu	Glu	Thr	Cys	Leu	Leu	Cys	Gly	Glu	Arg	
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Pro	Asp	Lys	Val	Leu	Tyr	Arg	Cys	Ser	Ile	Cys	Asn	Phe	Ser	Val	Cys	
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Thr	His	Glu	His	Arg	Leu	Val	Leu	Leu	Ser	Arg	Leu	Ile	Ser	Phe	Glu	
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Cys	Asn	Ala	Cys	Gly	Met	Gln	Gly	Asp	Arg	Ser	Pro	Tyr	Met	Cys	Val	
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Gln	Cys	Gly	Phe	Val	Val	His	Arg	Thr	Cys	Ile	Asp	Leu	Pro	Arg	Val	
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Ser	Leu	Cys	Ala	Thr	Arg	Lys	Asp	Val	Trp	Asp	Gly	Val	Glu	Leu	Glu	
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Arg	Phe	Ile	Leu	His	Glu	Lys	Cys	Ala	Asn	His	Pro	Lys	Lys	Lys	Arg	
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His	Val	Phe	His	Thr	Lys	Pro	Phe	Thr	Leu	Trp	Ser	Arg	Pro	Pro	Arg	
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Thr	Phe	His	Ser	Lys	Asp	Phe	Arg	Phe	Tyr	Asp	Val	Phe	Arg	Cys	Tyr	
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Asp	Ala	Cys	Tyr	Lys	Glu	Ile	Asp	Gly	Tyr	Leu	Leu	Ser	Cys	Asp	Thr	
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Cys	Asp	Phe	Asp	Leu	Asp	Leu	His	Cys	Thr	Asp	Leu	Pro	Lys	Thr	Val	
	530				535					540						
aag	cac	agc	tgc	gac	aat	cat	cct	ctt	tcc	cta	tgc	tat	ggc	gaa	aat	1680
Lys	His	Ser	Cys	Asp	Asn	His	Pro	Leu	Ser	Leu	Cys	Tyr	Gly	Glu	Asn	
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gca	acc	gga	aaa	tat	tgg	tgt	gat	att	tgc	gag	gcg	gaa	aca	gat	cca	1728
Ala	Thr	Gly	Lys	Tyr	Trp	Cys	Asp	Ile	Cys	Glu	Ala	Glu	Thr	Asp	Pro	
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agt	aag	tgg	ttc	tac	act	tgc	tct	aaa	tgt	gtg	gtt	act	gca	cat	att	1776
Ser	Lys	Trp	Phe	Tyr	Thr	Cys	Ser	Lys	Cys	Val	Val	Thr	Ala	His	Ile	
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Glu	Cys	Val	Leu	Gly	Asp	Phe	Ser	Arg	Leu	Met	Pro	Gly	Arg	Ile	Ile	
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Asn	Tyr	Asn	Asn	Val	Arg	Val	Glu	Val	Val	Leu	Asn	Ser	Tyr	Ser	Ser	
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Leu	Lys	Leu	Cys	Asp	Pro	Tyr	Thr	Gly	Tyr	Ile	Cys	Ser	Asp	Ala	Cys	
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Asn	His	Pro	Ser	His	Pro	Gln	His	Ser	Leu	Lys	Leu	Leu	Glu	Tyr	Glu
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Thr	His	Glu	His	Arg	Leu	Val	Leu	Leu	Ser	Arg	Leu	Ile	Ser	Phe	Glu
				245					250					255	
Cys	Asn	Ala	Cys	Gly	Met	Gln	Gly	Asp	Arg	Ser	Pro	Tyr	Met	Cys	Val
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Gln	Cys	Gly	Phe	Val	Val	His	Arg	Thr	Cys	Ile	Asp	Leu	Pro	Arg	Val
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Ile	Asn	Ile	Asn	Arg	His	Asp	His	Arg	Ile	Ser	Phe	Thr	His	His	Leu
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Ser	Leu	Cys	Ala	Thr	Arg	Lys	Asp	Val	Trp	Asp	Gly	Val	Glu	Leu	Glu
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Leu	Asn	Lys	Asp	Asn	Ile	Asn	Arg	Asp	Glu	Gly	Ser	Arg	Cys	Glu	Ala
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Arg	Phe	Ile	Leu	His	Glu	Lys	Cys	Ala	Asn	His	Pro	Lys	Lys	Lys	Arg
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Val	Leu	Asp	Val	Arg	Cys	Gly	Ser	Arg	Ser	Glu	Pro	Val	Ile	His	Asp
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Cys	Asp	Phe	Asp	Leu	Asp	Leu	His	Cys	Thr	Asp	Leu	Pro	Lys	Thr	Val
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Lys	His	Ser	Cys	Asp	Asn	His	Pro	Leu	Ser	Leu	Cys	Tyr	Gly	Glu	Asn
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Ala	Thr	Gly	Lys	Tyr	Trp	Cys	Asp	Ile	Cys	Glu	Ala	Glu	Thr	Asp	Pro
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PF59082SeqList_PF59082.txt

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 Pro Pro Pro Pro Pro Pro Pro Pro Val Leu Pro His Ile Arg Ser
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 aga aaa aag atg gac atc aaa gaa gtg cat cta cct ctt cca cgt cac 192
 Arg Lys Lys Met Asp Ile Lys Glu Val His Leu Pro Leu Pro Arg His
 50 55 60
 tat cct cct cct cct ccg cct ctt ccg cct cct ccg cct tat gga ttc 240
 Tyr Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Tyr Gly Phe
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 aga cga cat cat aac caa agc ggc aac gag ctt gag aaa cga ata gca 288
 Arg Arg His His Asn Gln Ser Gly Asn Glu Leu Glu Lys Arg Ile Ala
 85 90 95
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 Arg Leu Gly Phe Pro Thr Leu Arg Pro Phe Gln Ser Lys Arg Tyr Asp
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 Asn Gln Thr Leu Pro Asn Pro Arg Cys Pro Leu Ser Asn Pro Thr Tyr
 115 120 125
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 Pro His Thr Leu Asn Pro Lys Phe Ser Val Asn Thr Thr Asn Gly Cys
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 Phe Thr Cys Gly Glu Asn Thr Ser Pro Trp Ile Asp His His Asn Val
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 His Phe Phe Cys Lys Arg Cys His Val Glu Phe His Phe Gly Cys His
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Arg Tyr Arg Asn Arg Tyr Gly Lys Lys Met Asp Lys Glu Glu Glu Glu	
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Glu Glu Asp Val Ala Pro Pro Gln Pro Pro Leu Gly Tyr Lys Gly Cys	
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Arg Asn Gln Cys Ser Ala Lys Met Asn Lys Glu Lys Val Ser Pro Pro	
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Pro	Gly	Phe	Arg	Phe	Lys	Tyr	Tyr	Ser	Ser	Lys	Val	Glu	Val	Arg	Arg	
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Gly	Tyr	Ile	Tyr	Tyr	Lys	Asn	Asp	Asn	Ser	Val	Thr	Val	Thr	Cys	Ser	
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 675 680 685
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Ser Thr Ile Val His Leu Lys Ala His Glu His Leu Leu Thr Leu Met	
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Leu	Ile	Gln	Lys	Phe	Thr	His	Val	Glu	Gly	Gly	Phe	Ser	Cys	Gln	Ala	
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Cys	Gly	Tyr	Asn	Leu	Asp	Val	Val	Cys	Ala	Ser	Ile	Ser	Glu	Pro	Phe	
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Asp	Tyr	Tyr	Phe	Cys	Asp	Lys	Cys	Asp	Lys	Arg	Phe	His	Lys	Glu	Cys	
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Gln	Pro	Lys	Arg	His	Asp	His	Thr	Leu	Thr	Leu	Phe	Pro	Arg	Gln	Ala	
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Val	Gly	Cys	Asp	Phe	Ile	Leu	His	Glu	Thr	Cys	Ala	Asp	Ala	Pro	Arg	
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Leu	His	Gly	Asp	Ser	Thr	Ser	Tyr	Tyr	His	Val	Val	Leu	Pro	Leu	Phe	
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tgg	tgc	aac	aat	aaa	gaa	gct	gat	cca	gac	atg	gat	tgc	ggg	ttt	tgc	384
Trp	Cys	Asn	Asn	Lys	Glu	Ala	Asp	Pro	Asp	Met	Asp	Cys	Gly	Phe	Cys	
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Pro	Ser	His	Pro	Gln	His	Ser	Leu	Gln	Ile	Tyr	Leu	Ser	Thr	Lys	Pro	
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Phe	Glu	His	Cys	Ile	Leu	Cys	Ser	Arg	Lys	Ala	His	Asn	Ile	Ile	Tyr	
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Cys	Thr	Tyr	Cys	Cys	Thr	Thr	Leu	His	Ile	Asn	Cys	Leu	Leu	Gly	Pro	
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Asp	Pro	Tyr	Leu	Lys	Pro	Asp	Gln	Thr	Ile	Pro	Thr	Asp	Gln	Ile	Glu	
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<213> Arabidopsis thaliana

<400> 1290

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Pro	Ser	His	Pro	Gln	His	Ser	Leu	Gln	Ile	Tyr	Leu	Ser	Thr	Lys	Pro
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Phe	Glu	His	Cys	Ile	Leu	Cys	Ser	Arg	Lys	Ala	His	Asn	Ile	Ile	Tyr
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Lys	Glu	Lys	Pro	Ile	Cys	Asn	Ile	Cys	Lys	Ser	Thr	Lys	Val	His	Lys
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<213> Arabidopsis thaliana

<400> 1294

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Thr	Ile	Cys	His	Lys	Gln	Leu	Asn	Cys	Ile	Lys	Cys	Asp	Phe	Ile	Val		
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Asp	Arg	Ser	Pro	Tyr	Ile	Cys	Val	Gln	Cys	Asn	Phe	Ile	Ile	His	Gln	
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Glu	Cys	Leu	Thr	Leu	Pro	Arg	Leu	Ile	Asn	Ile	Asn	Arg	His	Asp	His	
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Ser	Pro	Cys 35	Asn	Phe	Thr	Leu	Asp 40	Met	Arg	Cys	Ala	Leu 45	Asn	Pro	Pro
Ser	Ile 50	Ser	Phe	Glu	Asp	Ser 55	Lys	Thr	His	Asp	His 60	Gln	Leu	Thr	Leu
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Phe 225	Tyr	Gly	Cys	Met	Asp 230	Cys	Asp	Phe	Ile	Leu 235	His	Gln	Asn	Cys	Ala 240
Lys	Phe	Pro	Lys	Arg 245	Lys	Arg	His	Val	Leu 250	His	Asn	Glu	Arg	Leu 255	Thr
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 His Arg Val Asp Asp Tyr Pro Leu Leu Cys Tyr Gly Glu Lys Ala
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 Ala Glu Thr Gly Ser Tyr Glu Val Val Leu Asn Lys Asn Val Ser Arg
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Thr Asp Pro Lys Cys His Leu Cys Gly Asn Asn Thr Lys Arg Leu Leu	
85 90 95	
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Phe His Cys Ser Val Cys Gln Leu Asn Leu Asp Ile Phe Cys Ile Ala	
100 105 110	
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Asp His Leu Leu Gly Pro Glu Tyr Leu Asn Met Pro Trp His Pro His	
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Pro Leu Leu Cys Phe Asp Phe Gly Ser Arg Asn Trp Cys Asp Phe Cys	
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Pro	Gln	Pro	Leu	Thr	Leu	Ser	Tyr	His	Arg	Leu	Gln	Arg	Arg	Trp	Gly		
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Tyr Thr Cys Asn Asp Cys Gly Val Thr Leu His Val Leu Cys Val Val		
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Cys Tyr Ile Ile Thr Lys Ser Lys Lys Glu Tyr Ser Lys Ile Lys Leu		
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Phe	Ser	Leu	Thr	Ser	Arg	Glu	Trp	Phe	Cys	Gly	Val	Cys	Arg	Leu	Ser	
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Glu	Leu	Glu	Gly	Ile	Pro	Glu	Ile	Ile	Asp	Ile	Thr	Glu	Asn	Asp	Gly	
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Lys	Leu	Asp	Val	Arg	Cys	Ala	Leu	Ile	Ser	Glu	Pro	Phe	Asp	Tyr	Lys	
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 Arg Val Phe Cys Ser Cys Cys Gln Lys Arg Ile Asp Gly Leu Asn Tyr
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 Tyr Ser Pro Thr Asn Asn Phe Thr Leu His Leu Phe Cys Ala Phe Lys
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 Pro Ile Pro Phe Val Ile Asp His Pro Lys Arg His Pro His Pro Leu
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 Ile Lys Gly His Ile Pro Thr Tyr Val Cys Val Arg Cys Val Phe Val
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Gly	Gly	Tyr	Tyr	Ser	Cys	Met	Asp	Glu	Cys	Asp	Phe	Ile	Leu	His	Glu	
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Arg	Phe	Cys	Cys	Lys	Ala	Cys	Gln	Arg	Glu	Ser	Cys	Gly	Phe	Val	Tyr	
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Glu Arg Phe Tyr Phe Gly Arg Cys Ser Gly Cys Ser Arg Glu Gly Tyr	
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Phe Tyr Gly Gly Tyr Arg Cys Asn Glu Leu Ala Cys Phe Ala Val Phe	
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Phe	Tyr	Gly	Gly	Tyr	Arg	Cys	Asn	Glu	Leu	Ala	Cys	Phe	Ala	Val	Phe			
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Ala	Pro 370	Phe	Glu	Val	Val	Asp 375	Glu	Asn	Thr	Ile	Lys 380	His	Met	Ser	His
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Asp	Ala	Cys 595	Gly	Val	Thr	Leu	His 600	Val	Ser	Cys	Val	Val 605	Gly	Asp	Phe
Ser	Tyr 610	His	Met	Pro	Gly	Pro 615	Leu	Ser	Thr	Val	Val 620	Ser	Glu	Tyr	Lys
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Ser	Ile	Cys	Arg	Pro 645	Leu	Cys	Ser	Arg	Cys 650	His	Thr	Arg	Cys	Lys 655	Leu
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Phe Leu Val Tyr Arg Asn Val Ile Lys Pro Leu Pro Gln Thr Gln Thr	
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Ser Asn Ser Phe Asp Lys Gln Ser Ile Asp Ser Val Tyr Asp Leu Pro	
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Pro Gln Pro Leu Phe Leu Cys Pro Arg Leu Arg Thr Arg Ile Leu Leu	
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Asn Ser Leu Asp Asp Glu Val Glu Asp Glu Val Thr Asn His Ile Leu	
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Ser Lys Tyr Ser Ser Ser Pro Leu Phe Asp Glu Thr Ser Asn Asn His	
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His Val Leu Pro Leu Phe Trp Cys Asn Asn Lys Glu Val Asp Pro Glu	
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Ala Glu Gln Gly Asp Glu Cys Tyr Ser Cys Ser Ile Gln Thr Ile Gly	
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Thr Asp Tyr Tyr Phe Cys Ala Thr Cys Asp Lys Arg Phe His Lys Glu	
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Cys Val Glu Cys Pro Leu Glu Ile Ser Tyr Pro Thr His Thr Lys His	
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Cys Arg Lys Arg Ala Thr Tyr Met Ile Tyr Phe Cys Ala Leu Cys Asp	
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Ser Tyr Met His Val Leu Cys Ala Gln Ser Lys Ile Pro Phe Phe Ile	
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Tyr Ile Pro Gln Thr Ile Arg Ile Ser Arg His His His Arg Val Ser	
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Xaa Ile Ser Ser Leu Pro Phe Glu Glu Lys Ser Cys Gly Val Cys Arg	
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Gln Met Val Asp Ser Asp Tyr Gly Ala Tyr Thr Cys Asn Val Cys Ser	
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Gly Tyr Val Val His Val Arg Cys Ala Leu Arg Lys Asp Ile Trp Asp	
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Gly Lys Glu Leu Ala Glu Val Pro Glu Glu Leu Glu Asp Val Glu Ser	
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Phe	Ile	Ile	Cys	Phe	Glu	Cys	Ala	Thr	Leu	Pro	Tyr	Met	Val	Arg	Tyr	
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<223> The Xaa at location 273 stands for Phe, or Tyr.

<400> 1306

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PF59082SeqList_PF59082.txt

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Leu Thr Cys Asn Ile Cys Gly Leu Val Asn Lys Leu His Leu Thr Tyr	
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Ile Cys Pro Ile Cys Asp Phe Val Ala His Ser Asp Cys Ile Tyr Ile	
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Pro Gln Thr Ile Arg Ile Ser Arg His His Arg Val Ser Phe Ile	
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Val Ala His Ile Arg Cys Ala Leu Arg Ser Asp Ile Trp Asp Gly Lys	
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Phe Lys Arg Ile Ala Asp Gly Val Ile Leu His Phe Ser His Arg His	
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cat ctg tat ttt gag ata agt gga gtt tac aat gga aac aag ttt tgt	528
His Leu Tyr Phe Glu Ile Ser Gly Val Tyr Asn Gly Asn Lys Phe Cys	
165 170 175	
caa gct tgt gcc ctt cca gtc aat gaa ggg aat ttg tat gta tgt gtg	576
Gln Ala Cys Ala Leu Pro Val Asn Glu Gly Asn Leu Tyr Val Cys Val	
180 185 190	
gga tgt gat ttc atc cta cac gaa aca tgt gca gat gct cca cgt aga	624
Gly Cys Asp Phe Ile Leu His Glu Thr Cys Ala Asp Ala Pro Arg Arg	
195 200 205	
aag gtc cat cca tta cat ccc cat ccc ctt aaa cta att ttt tat gaa	672
Lys Val His Pro Leu His Pro His Pro Leu Lys Leu Ile Phe Tyr Glu	
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Asp Asn Cys Phe His Cys Lys Ala Cys Trp Arg Thr Ser Thr Ala Phe	
225 230 235 240	
gga tat agg tgt atc aac cac aat tgc aag tac atg ata gat ata gtg	768
Gly Tyr Arg Cys Ile Asn His Asn Cys Lys Tyr Met Ile Asp Ile Val	
245 250 255	

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Cys	Ala	Ser	Thr	Ala	Glu	Pro	Phe	Asp	Tyr	Gln	Gly	His	Arg	His	Pro	
			260				265						270			
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Leu	Phe	Leu	Ser	Leu	Asp	Pro	Lys	Glu	Lys	Pro	Met	Cys	His	Ile	Cys	
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agg	tca	aca	aaa	gat	aag	aag	gta	ctt	aac	tgc	att	gaa	tgt	gac	ttt	912
Arg	Ser	Thr	Lys	Asp	Lys	Lys	Val	Leu	Asn	Cys	Ile	Glu	Cys	Asp	Phe	
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att	gta	tgt	ttc	gaa	tgc	gcc	acc	tta	cca	tac	atg	ata	agg	tat	aag	960
Ile	Val	Cys	Phe	Glu	Cys	Ala	Thr	Leu	Pro	Tyr	Met	Ile	Arg	Tyr	Lys	
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cat	gat	gaa	cat	tac	ctc	aca	ttt	tgt	cat	gga	gat	gag	gca	agt	gac	1008
His	Asp	Glu	His	Tyr	Leu	Thr	Phe	Cys	His	Gly	Asp	Glu	Ala	Ser	Asp	
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tca	gat	tgg	tgt	gaa	tta	tgt	gag	gga	aag	tta	gca	att	gga	gga	aaa	1056
Ser	Asp	Trp	Cys	Glu	Leu	Cys	Glu	Gly	Lys	Leu	Ala	Ile	Gly	Gly	Lys	
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gaa	gga	ttc	tat	gag	tgc	aaa	gat	tgt	tgt	acg	aca	ctt	cat	att	aat	1104
Glu	Gly	Phe	Tyr	Glu	Cys	Lys	Asp	Cys	Cys	Thr	Thr	Leu	His	Ile	Asn	
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Cys	Leu	Leu	Gly	Pro	Asp	Pro	Tyr	Leu	Met	Val	Gly	Gln	Arg	Leu	Pro	
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Val	Pro	Asn	Gly	Glu	Ile	Phe	Phe	Arg	His	Asn	Asn	Tyr	Thr	Thr	Arg	
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cct	ttt	tgc	tcg	ata	tgc	aat	att	cgt	tgt	ccg	tat	cca	aca	ttt	gtt	1248
Pro	Phe	Cys	Ser	Ile	Cys	Asn	Ile	Arg	Cys	Pro	Tyr	Pro	Thr	Phe	Val	
				405					410					415		
tca	tac	ata	aag	gat	atg	ttt	ata	tct	tat	att	cta	tgt	tct	agt	aag	1296
Ser	Tyr	Ile	Lys	Asp	Met	Phe	Ile	Ser	Tyr	Ile	Leu	Cys	Ser	Ser	Lys	
			420				425					430				
cac	ttg	aag	acg	aga	tac	cat	cat	tga								1323
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Leu	Thr	Cys	Asn	Ile	Cys	Gly	Leu	Val	Asn	Lys	Leu	His	Leu	Thr	Tyr	
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Ile	Cys	Pro	Ile	Cys	Asp	Phe	Val	Ala	His	Ser	Asp	Cys	Ile	Tyr	Ile	
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Pro	Gln	Thr	Ile	Arg	Ile	Ser	Arg	His	His	His	Arg	Val	Ser	Phe	Ile	
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Ser	Ser	Leu	Pro	Phe	Glu	Glu	Lys	Ser	Cys	Gly	Val	Cys	Arg	Gln	Met	
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Leu	Asp	Ser	Asp	Tyr	Gly	Ala	Tyr	Ile	Cys	Lys	Gly	Cys	Ser	Gly	Phe	
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Val	Ala	His	Ile	Arg	Cys	Ala	Leu	Arg	Ser	Asp	Ile	Trp	Asp	Gly	Lys	
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Glu	Leu	Glu	Gly	Val	Pro	Glu	Glu	Val	Glu	Glu	Asp	Val	Glu	Ser		
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Phe	Lys	Arg	Ile	Ala	Asp	Gly	Val	Ile	Leu	His	Phe	Ser	His	Arg	His	
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His	Leu	Tyr	Phe	Glu	Ile	Ser	Gly	Val	Tyr	Asn	Gly	Asn	Lys	Phe	Cys	
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Gln	Ala	Cys	Ala	Leu	Pro	Val	Asn	Glu	Gly	Asn	Leu	Tyr	Val	Cys	Val	
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Gly	Cys	Asp	Phe	Ile	Leu	His	Glu	Thr	Cys	Ala	Asp	Ala	Pro	Arg	Arg	
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PF59082SeqList_PF59082.txt

Lys Val His Pro Leu His Pro His Pro Leu Lys Leu Ile Phe Tyr Glu
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 225 230 235 240
 Gly Tyr Arg Cys Ile Asn His Asn Cys Lys Tyr Met Ile Asp Ile Val
 245 250 255
 Cys Ala Ser Thr Ala Glu Pro Phe Asp Tyr Gln Gly His Arg His Pro
 260 265 270
 Leu Phe Leu Ser Leu Asp Pro Lys Glu Lys Pro Met Cys His Ile Cys
 275 280 285
 Arg Ser Thr Lys Asp Lys Lys Val Leu Asn Cys Ile Glu Cys Asp Phe
 290 295 300
 Ile Val Cys Phe Glu Cys Ala Thr Leu Pro Tyr Met Ile Arg Tyr Lys
 305 310 315 320
 His Asp Glu His Tyr Leu Thr Phe Cys His Gly Asp Glu Ala Ser Asp
 325 330 335
 Ser Asp Trp Cys Glu Leu Cys Glu Gly Lys Leu Ala Ile Gly Gly Lys
 340 345 350
 Glu Gly Phe Tyr Glu Cys Lys Asp Cys Cys Thr Thr Leu His Ile Asn
 355 360 365
 Cys Leu Leu Gly Pro Asp Pro Tyr Leu Met Val Gly Gln Arg Leu Pro
 370 375 380
 Val Pro Asn Gly Glu Ile Phe Phe Arg His Asn Asn Tyr Thr Thr Arg
 385 390 395 400
 Pro Phe Cys Ser Ile Cys Asn Ile Arg Cys Pro Tyr Pro Thr Phe Val
 405 410 415
 Ser Tyr Ile Lys Asp Met Phe Ile Ser Tyr Ile Leu Cys Ser Ser Lys
 420 425 430
 His Leu Lys Thr Arg Tyr His His
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 att act cgt ttt tct cgt gaa cat tgt aaa tgt aat gtg tgt ggg tct 96
 Ile Thr Arg Phe Ser Arg Glu His Cys Lys Cys Asn Val Cys Gly Ser
 20 25 30
 gtt ggt tac att tac gga ggc tac tgt tgc aat gag gtg gga tgt gaa 144
 Val Gly Tyr Ile Tyr Gly Gly Tyr Cys Cys Asn Glu Val Gly Cys Glu
 35 40 45
 tcc atg ttt cat aaa gag tgt gtt gag tct ttg tca gaa atc aag cac 192
 Ser Met Phe His Lys Glu Cys Val Glu Ser Leu Ser Glu Ile Lys His
 50 55 60
 act tct cat cct gat cat cct ctc aag ctg ctc ata agt gac aaa gca 240

PF59082SeqList_PF59082.txt

Thr 65	Ser	His	Pro	Asp	His 70	Pro	Leu	Lys	Leu	Leu 75	Ile	Ser	Asp	Lys	Ala 80	
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Ser	Phe	Cys	Ser	Arg 85	Cys	Glu	Gly	Arg	Phe 90	Glu	Asn	Gly	Tyr	Ile 95	Cys	
tct	att	tgc	gac	ttc	aag	ttg	gat	ttt	cgt	tgt	gct	aaa	gga	cct	gcc	336
Ser	Ile	Cys	Asp	Phe	Lys	Leu	Asp	Phe	Arg	Cys	Ala	Lys	Gly	Pro	Ala	
cca	ctc	ctt	att	ctt	gaa	aaa	tcc	aat	ctg	cac	gag	cat	cta	ctt	gar	384
Pro	Leu	Leu	Ile	Leu	Glu	Lys	Ser	Asn	Leu	His	Glu	His	Leu	Leu	Glu	
ttc	ttc	gtg	gga	tgg	cac	tct	tgg	aag	gga	cat	aga	gag	tgc	aaa	gcg	432
Phe	Phe	Val	Gly	Trp	His	Ser 135	Trp	Lys	Gly	His	Arg	Glu	Cys	Lys	Ala	
tgc	ggc	ggt	gcg	ggt	ttc	cgc	ggt	tat	cga	tgg	tat	gga	tgt	tat	caa	480
Cys 145	Gly	Gly	Ala	Gly	Phe 150	Arg	Gly	Tyr	Arg	Trp 155	Tyr	Gly	Cys	Tyr	Gln 160	
tgt	gat	aca	ctc	ttc	cat	gga	gaa	tgt	gct	gag	ttt	ttt	ccr	gaa	gca	528
Cys	Asp	Thr	Leu	Phe 165	His	Gly	Glu	Cys	Ala 170	Glu	Phe	Phe	Pro	Glu	Ala	
aaa	cac	act	tct	cac	ccg	caa	cac	aca	ctc	aaa	cac	atc	aca	tct	gaa	576
Lys	His	Thr	Ser 180	His	Pro	Gln	His	Thr 185	Leu	Lys	His	Ile	Thr 190	Ser	Glu	
gaa	gca	ccc	gat	tac	gcc	gac	aac	aag	tgt	ctt	ctt	tgc	gag	gag	gag	624
Glu	Ala	Pro 195	Asp	Tyr	Ala	Asp	Asn	Lys	Cys	Leu	Leu	Cys	Glu	Glu	Glu	
ttt	gat	caa	caa	cat	ccc	aaa	att	cac	cat	tgt	gat	gtt	tgt	aat	ttc	672
Phe	Asp 210	Gln	Gln	His	Pro	Lys 215	Ile	His	His	Cys	Asp 220	Val	Cys	Asn	Phe	
acc	ata	tgt	aga	gca	tgt	atg	aaa	aac	gca	cca	ccg	gtt	cgt	att	gaa	720
Thr 225	Ile	Cys	Arg	Ala	Cys 230	Met	Lys	Asn	Ala	Pro 235	Pro	Val	Arg	Ile	Glu 240	
agc	ctt	aca	acc	cat	gaa	cat	caa	cta	cat	ctc	gtt	cca	rga	cgc	att	768
Ser	Leu	Thr	Thr	His 245	Glu	His	Gln	Leu	His 250	Leu	Val	Pro	Xaa	Arg 255	Ile	
gat	ttc	act	tgc	aat	gct	tgc	ggg	acg	cta	ggt	gac	cga	agt	cct	tac	816
Asp	Phe	Thr	Cys 260	Asn	Ala	Cys	Gly	Thr 265	Leu	Gly	Asp	Arg	Ser 270	Pro	Tyr	
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Phe	Cys	Leu 275	Gln	Cys	Asn	Phe 280	Met	Ile	His	Arg	Gln	Cys 285	Ile	Asp	Leu	
cca	cgg	gtc	ata	aac	atc	aac	cgc	cac	gat	cac	cgc	atc	tct	tac	acc	912
Pro	Arg 290	Val	Ile	Asn	Ile	Asn 295	Arg	His	Asp	His	Arg 300	Ile	Ser	Tyr	Thr	
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Arg 305	Arg	Leu	Gly	His	Gly 310	Glu	Trp	Lys	Cys	Lys 315	Val	Cys	Arg	Lys	Lys 320	
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Val	Asp	Gly	Phe 325	Tyr	Gly	Ala	Tyr	Thr 330	Cys	Leu	Lys	Cys	Pro	Ser 335	Phe	
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Val	Val	His	Ser 340	Leu	Cys	Ala	Thr 345	Arg	Asn	Asp	Val	Trp 350	Asp	Met	Ile	
gag	cta	gaa	ggg	atg	caa	gaa	gaa	gag	gaa	att	gcg	cca	tac	gag	atg	1104
Glu	Leu	Glu 355	Gly	Met	Gln	Glu	Glu 360	Glu	Glu	Ile	Ala	Pro 365	Tyr	Glu	Met	
att	gat	gct	aac	acg	ata	aaa	cat	ttc	agc	cat	gat	cat	aac	cta	caa	1152
Ile	Asp 370	Ala	Asn	Thr	Ile	Lys 375	His	Phe	Ser	His	Asp 380	His	Asn	Leu	Gln	
atc	aac	aat	gat	ggc	cat	agg	att	caa	cct	gaa	aat	ata	gtt	tgt	Cys	1200
Ile 385	Asn	Asn	Asp	Gly	His 390	Gly	Arg	Ile	Gln	Pro 395	Glu	Asn	Ile	Val	400	
gaa	gcg	tgt	gtg	ttc	cag	atc	ttg	tca	gaa	ccg	ttc	tac	agt	tgc	aac	1248
Glu	Ala	Cys	Val 405	Phe	Gln	Ile	Leu	Ser 410	Glu	Pro	Phe	Tyr	Ser	Cys 415	Asn	
caa	tgt	agt	ttt	ata	ctc	cac	gaa	aaa	tgt	gca	aat	cat	cca	cgg	aag	1296
Gln	Cys	Ser	Phe 420	Ile	Leu	His	Glu	Lys 425	Cys	Ala	Asn	His	Pro 430	Arg	Lys	
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Cys	Asn	Lys	Ala	Asn	Ala	Ser	Cys	Gly	Leu	Cys	Lys	Gln	His	Phe	Thr	
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ggc	ttc	aga	tac	gaa	tca	ggc	cct	tat	gtt	act	ata	gat	gta	cga	tgc	1440
Gly	Phe	Arg	Tyr	Glu	Ser	Gly	Pro	Tyr	Val	Thr	Ile	Asp	Val	Arg	Cys	
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gct	gca	att	ttg	gat	aca	att	gag	cac	gga	agc	cat	caa	cat	cct	tta	1488
Ala	Ala	Ile	Leu	Asp	Thr	Ile	Glu	His	Gly	Ser	His	Gln	His	Pro	Leu	
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tat	tac	tac	act	aca	ttt	gac	tgg	aag	cct	tgt	agc	cga	tgc	aga	gag	1536
Tyr	Tyr	Tyr	Thr	Thr	Phe	Asp	Trp	Lys	Pro	Cys	Ser	Arg	Cys	Arg	Glu	
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gag	ggc	gcc	gtt	tta	ttt	cgt	tgt	gat	gag	tgt	gac	tac	att	ttg	gat	1584
Glu	Gly	Ala	Val	Leu	Phe	Arg	Cys	Asp	Glu	Cys	Asp	Tyr	Ile	Leu	Asp	
	515					520					525					
gga	aac	tgt	gct	ctt	ttt	cca	aaa	aag	gta	atg	aga	aat	aga	tac	gat	1632
Gly	Asn	Cys	Ala	Leu	Phe	Pro	Lys	Lys	Val	Met	Arg	Asn	Arg	Tyr	Asp	
	530					535				540						
gat	cat	ctt	ctc	ttc	ttg	tct	ttc	ggc	gac	aag	aat	gtg	agt	ggc	gac	1680
Asp	His	Leu	Leu	Phe	Leu	Ser	Phe	Gly	Asp	Lys	Asn	Val	Ser	Gly	Asp	
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Tyr	Trp	Cys	Glu	Ala	Cys	Glu	Thr	Lys	Val	Asn	Pro	Lys	Glu	Trp	Phe	
			565					570					575			
tat	aca	tgc	aac	gat	tgt	gga	acc	ata	tta	cat	ata	tct	tgt	gtt	gtg	1776
Tyr	Thr	Cys	Asn	Asp	Cys	Gly	Thr	Ile	Leu	His	Ile	Ser	Cys	Val	Val	
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gga	gat	ttc	tca	tat	atc	atg	cca	ggc	tct	cat	ata	aca	aca	tgg	aga	1824
Gly	Asp	Phe	Ser	Tyr	Ile	Met	Pro	Gly	Ser	His	Ile	Thr	Thr	Trp	Arg	
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Ala	Asn	Val	Val	Ser	Asn	Thr	Ser	Ile	Cys	Arg	Pro	Val	Cys	Tyr	Met	
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Cys	Asn	Ser	Arg	Cys	Lys	Leu	Pro	Ser	Val	Leu	Lys	Leu	Ser	Asp	Thr	
625				630					635					640		
aaa	gtt	gat	gta	tac	ctt	tgt	tct	ttc	aaa	tgt	gcc	tat	ttt	att	agg	1968
Lys	Val	Asp	Val	Tyr	Leu	Cys	Ser	Phe	Lys	Cys	Ala	Tyr	Phe	Ile	Arg	
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Lys																

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 Ser Met Phe His Lys Glu Cys Val Glu Ser Leu Ser Glu Ile Lys His
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 Thr Ser His Pro Asp His Pro Leu Lys Leu Leu Ile Ser Asp Lys Ala
 65 70 75 80
 Ser Phe Cys Ser Arg Cys Glu Gly Arg Phe Glu Asn Gly Tyr Ile Cys
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 Ser Ile Cys Asp Phe Lys Leu Asp Phe Arg Cys Ala Lys Gly Pro Ala
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Cys	Gly	Gly	Ala	Gly	Phe	Arg	Gly	Tyr	Arg	Trp	Tyr	Gly	Cys	Tyr	Gln
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Cys	Asp	Thr	Leu	Phe	His	Gly	Glu	Cys	Ala	Glu	Phe	Phe	Pro	Glu	Ala
				165					170					175	
Lys	His	Thr	Ser	His	Pro	Gln	His	Thr	Leu	Lys	His	Ile	Thr	Ser	Glu
			180					185					190		
Glu	Ala	Pro	Asp	Tyr	Ala	Asp	Asn	Lys	Cys	Leu	Leu	Cys	Glu	Glu	Glu
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Phe	Asp	Gln	Gln	His	Pro	Lys	Ile	His	His	Cys	Asp	Val	Cys	Asn	Phe
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Thr	Ile	Cys	Arg	Ala	Cys	Met	Lys	Asn	Ala	Pro	Pro	Val	Arg	Ile	Glu
225					230					235					240
Ser	Leu	Thr	Thr	His	Glu	His	Gln	Leu	His	Leu	Val	Pro	Xaa	Arg	Ile
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Asp	Phe	Thr	Cys	Asn	Ala	Cys	Gly	Thr	Leu	Gly	Asp	Arg	Ser	Pro	Tyr
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Phe	Cys	Leu	Gln	Cys	Asn	Phe	Met	Ile	His	Arg	Gln	Cys	Ile	Asp	Leu
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Pro	Arg	Val	Ile	Asn	Ile	Asn	Arg	His	Asp	His	Arg	Ile	Ser	Tyr	Thr
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Arg	Arg	Leu	Gly	His	Gly	Glu	Trp	Lys	Cys	Lys	Val	Cys	Arg	Lys	Lys
305					310					315					320
Val	Asp	Gly	Phe	Tyr	Gly	Ala	Tyr	Thr	Cys	Leu	Lys	Cys	Pro	Ser	Phe
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Val	Val	His	Ser	Leu	Cys	Ala	Thr	Arg	Asn	Asp	Val	Trp	Asp	Met	Ile
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Glu	Leu	Glu	Gly	Met	Gln	Glu	Glu	Glu	Glu	Ile	Ala	Pro	Tyr	Glu	Met
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Ile	Asp	Ala	Asn	Thr	Ile	Lys	His	Phe	Ser	His	Asp	His	Asn	Leu	Gln
	370					375					380				
Ile	Asn	Asn	Asp	Gly	His	Gly	Arg	Ile	Gln	Pro	Glu	Asn	Ile	Val	Cys
385					390					395					400
Glu	Ala	Cys	Val	Phe	Gln	Ile	Leu	Ser	Glu	Pro	Phe	Tyr	Ser	Cys	Asn
				405					410					415	
Gln	Cys	Ser	Phe	Ile	Leu	His	Glu	Lys	Cys	Ala	Asn	His	Pro	Arg	Lys
			420					425					430		
Lys	Arg	His	Val	Cys	Asn	Asn	Thr	Ser	Phe	Ile	Leu	Phe	Thr	Asp	Ser
		435					440					445			
Cys	Asn	Lys	Ala	Asn	Ala	Ser	Cys	Gly	Leu	Cys	Lys	Gln	His	Phe	Thr
	450					455					460				
Gly	Phe	Arg	Tyr	Glu	Ser	Gly	Pro	Tyr	Val	Thr	Ile	Asp	Val	Arg	Cys
465					470					475					480
Ala	Ala	Ile	Leu	Asp	Thr	Ile	Glu	His	Gly	Ser	His	Gln	His	Pro	Leu
				485					490					495	
Tyr	Tyr	Tyr	Thr	Phe	Asp	Trp	Lys	Pro	Cys	Ser	Arg	Cys	Arg	Glu	
			500				505					510			
Glu	Gly	Ala	Val	Leu	Phe	Arg	Cys	Asp	Glu	Cys	Asp	Tyr	Ile	Leu	Asp
		515					520				525				
Gly	Asn	Cys	Ala	Leu	Phe	Pro	Lys	Lys	Val	Met	Arg	Asn	Arg	Tyr	Asp
	530					535					540				
Asp	His	Leu	Leu	Phe	Leu	Ser	Phe	Gly	Asp	Lys	Asn	Val	Ser	Gly	Asp
545					550					555					560
Tyr	Trp	Cys	Glu	Ala	Cys	Glu	Thr	Lys	Val	Asn	Pro	Lys	Glu	Trp	Phe
				565					570					575	
Tyr	Thr	Cys	Asn	Asp	Cys	Gly	Thr	Ile	Leu	His	Ile	Ser	Cys	Val	Val
			580					585					590		
Gly	Asp	Phe	Ser	Tyr	Ile	Met	Pro	Gly	Ser	His	Ile	Thr	Thr	Trp	Arg
		595					600					605			
Ala	Asn	Val	Val	Ser	Asn	Thr	Ser	Ile	Cys	Arg	Pro	Val	Cys	Tyr	Met
	610					615					620				
Cys	Asn	Ser	Arg	Cys	Lys	Leu	Pro	Ser	Val	Leu	Lys	Leu	Ser	Asp	Thr
625					630					635					640
Lys	Val	Asp	Val	Tyr	Leu	Cys	Ser	Phe	Lys	Cys	Ala	Tyr	Phe	Ile	Arg
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PF59082SeqList_PF59082.txt

Lys

<210> 1311
<211> 1743
<212> DNA
<213> Arabidopsis thaliana

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<222> (138)..(138)
<223> r is g or a

<220>
<221> misc_feature
<222> (147)..(147)
<223> y is t or c

<220>
<221> misc_feature
<222> (977)..(977)
<223> y is t or c

<220>
<221> misc_feature
<222> (1562)..(1562)
<223> r is g or a

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Met Leu His Ser Asp Ser Cys Lys Leu Pro Leu Leu Pro Leu Phe Trp	
1 5 10 15	
tgc aac aat aaa aaa cct cat ctt ttc gat ttc att tgc cgt gca tgc	96
Cys Asn Asn Lys Lys Pro His Leu Phe Asp Phe Ile Cys Arg Ala Cys	
20 25 30	
aca acc cta gag cca gcc aca agc tat tac gtt tgt gtc acr tgt ggt	144
Thr Thr Leu Glu Pro Ala Thr Ser Tyr Tyr Val Cys Val Thr Cys Gly	
35 40 45	
gay cag ttc cac aaa gaa tgt att ggt tct cca ctt gag ttc aaa cac	192
Asp Gln Phe His Lys Glu Cys Ile Gly Ser Pro Leu Glu Phe Lys His	
50 55 60	
cct tca tat ccg tct ctt tct ctc caa ctt tac agt cct ccg tcc gac	240
Pro Ser Tyr Pro Ser Leu Ser Leu Gln Leu Tyr Ser Pro Pro Ser Asp	
65 70 75 80	
cgc gta ttc tgc tca tgt tgt caa aaa cgt atc gat ggc ctg aat tat	288
Arg Val Phe Cys Ser Cys Cys Gln Lys Arg Ile Asp Gly Leu Asn Tyr	
85 90 95	
tat agt cct acc aac aac ttc act ctg cat cta ttt tgt gca ttc aaa	336
Tyr Ser Pro Thr Asn Asn Phe Thr Leu His Leu Phe Cys Ala Phe Lys	
100 105 110	
cca ata ccc ttt gtt ata gat cac cca aaa agg cat ccc cat cct ctc	384
Pro Ile Pro Phe Val Ile Asp His Pro Lys Arg His Pro His Pro Leu	
115 120 125	
acc att ttc ccc aaa caa tct ttc tta cct tgc cat gtt tgt agc ctc	432
Thr Ile Phe Pro Lys Gln Ser Phe Leu Pro Cys His Val Cys Ser Leu	
130 135 140	
ata aaa gga cat att ccc acc tat gtt tgt gtt aga tgt gta ttt gta	480
Ile Lys Gly His Ile Pro Thr Tyr Val Cys Val Arg Cys Val Phe Val	
145 150 155 160	
gtt cat caa gat tgt atc tat ttc ccg tat gtc ata aaa ata tcc cgt	528
Val His Gln Asp Cys Ile Tyr Phe Pro Tyr Val Ile Lys Ile Ser Arg	
165 170 175	
cac cac cac cgt ata tct tat acc tcc tct ctt cca tct gga aaa tgg	576
His His His Arg Ile Ser Tyr Thr Ser Ser Leu Pro Ser Gly Lys Trp	
180 185 190	

PF59082SeqList_PF59082.txt																
tct	tgc	gga	gtc	tgt	cgt	caa	atg	ggt	gac	aac	gac	tat	ggt	gcc	tac	624
Ser	Cys	Gly	Val	Cys	Arg	Gln	Met	Val	Asp	Asn	Asp	Tyr	Gly	Ala	Tyr	
		195					200					205				
tct	tgc	aac	aag	tgt	gat	gac	tat	ttt	ggt	cat	tca	aga	tgc	gcg	ctg	672
Ser	Cys	Asn	Lys	Cys	Asp	Asp	Tyr	Phe	Val	His	Ser	Arg	Cys	Ala	Leu	
		210				215					220					
cgg	aga	gac	tta	tgg	gat	ggg	ata	gaa	ctc	gag	gga	gta	cct	gaa	gaa	720
Arg	Arg	Asp	Leu	Trp	Asp	Gly	Ile	Glu	Leu	Glu	Gly	Val	Pro	Glu	Glu	
225					230					235					240	
cct	gag	ata	gtt	gtt	gag	cca	ttt	atc	acg	att	tct	gat	ggt	ata	ata	768
Pro	Glu	Ile	Val	Val	Glu	Pro	Phe	Ile	Thr	Ile	Ser	Asp	Gly	Ile	Ile	
				245					250					255		
ctt	cat	ttt	tct	cat	ggc	cat	cat	ctg	aaa	ctc	aag	atc	agt	aga	gtc	816
Leu	His	Phe	Ser	His	Gly	His	His	Leu	Lys	Leu	Lys	Ile	Ser	Arg	Val	
			260					265					270			
tac	gac	gaa	aaa	atg	gtt	tgt	caa	gcg	tgc	atc	ctt	ccg	atc	tac	gag	864
Tyr	Asp	Glu	Lys	Met	Val	Cys	Gln	Ala	Cys	Ile	Leu	Pro	Ile	Tyr	Glu	
		275					280					285				
ggt	ggc	tat	tat	tca	tgt	atg	gat	gaa	tgt	gac	ttc	atc	ctc	cac	gaa	912
Gly	Gly	Tyr	Tyr	Ser	Cys	Met	Asp	Glu	Cys	Asp	Phe	Ile	Leu	His	Glu	
		290				295					300					
aca	tgt	gca	aat	gca	cct	tgc	aag	aaa	cat	cat	gct	ttg	cat	cct	cac	960
Thr	Cys	Ala	Asn	Ala	Pro	Cys	Lys	Lys	His	His	Ala	Leu	His	Pro	His	
305					310					315					320	
cca	ctt	acg	cta	acg	gyc	gtc	act	agt	gaa	tat	gaa	gac	aac	ata	gga	1008
Pro	Leu	Thr	Leu	Thr	Xaa	Val	Thr	Ser	Glu	Tyr	Glu	Asp	Asn	Ile	Gly	
				325					330					335		
cgt	ttt	tgt	tgt	aag	gct	tgt	cag	cgt	gaa	agt	tgt	ggt	ttc	gtc	tat	1056
Arg	Phe	Cys	Cys	Lys	Ala	Cys	Gln	Arg	Glu	Ser	Cys	Gly	Phe	Val	Tyr	
			340					345					350			
gag	gat	ctc	aga	gga	aag	att	ggt	aat	tat	aga	aga	aat	aaa	ttc	caa	1104
Glu	Asp	Leu	Arg	Gly	Lys	Ile	Gly	Asn	Tyr	Arg	Arg	Asn	Lys	Phe	Gln	
		355					360					365				
cta	gat	tta	cga	tgt	gcc	tca	ggt	tct	gaa	cca	ttt	gaa	tat	cta	ggc	1152
Leu	Asp	Leu	Arg	Cys	Ala	Ser	Val	Ser	Glu	Pro	Phe	Glu	Tyr	Leu	Gly	
		370				375					380					
cat	aag	cat	ctc	tta	tac	cta	gct	ttg	aat	cca	gaa	gaa	gaa	aag	tta	1200
His	Lys	His	Leu	Leu	Tyr	Leu	Ala	Leu	Asn	Pro	Glu	Glu	Glu	Lys	Leu	
385					390					395					400	
gca	ata	tgt	caa	atc	tgc	cac	gaa	agg	gaa	gat	gag	tct	tct	cat	tgc	1248
Ala	Ile	Cys	Gln	Ile	Cys	His	Glu	Arg	Glu	Asp	Glu	Ser	Ser	His	Cys	
				405					410					415		
aga	aaa	cta	aat	tgc	att	gaa	tgt	gat	ttt	gtg	ata	tgc	ttc	agg	tgt	1296
Arg	Lys	Leu	Asn	Cys	Ile	Glu	Cys	Asp	Phe	Val	Ile	Cys	Phe	Arg	Cys	
			420					425					430			
gct	acc	tta	cca	tat	aag	gca	ggg	tat	caa	cat	gac	aag	cat	ttc	ctc	1344
Ala	Thr	Leu	Pro	Tyr	Lys	Ala	Gly	Tyr	Gln	His	Asp	Lys	His	Phe	Leu	
		435					440					445				
aaa	ttt	tat	gag	acg	aaa	gag	gca	aat	gat	cat	tca	gag	tgg	tgt	gat	1392
Lys	Phe	Tyr	Glu	Thr	Lys	Glu	Ala	Asn	Asp	His	Ser	Glu	Trp	Cys	Asp	
		450				455					460					
gca	tgc	gaa	gga	aga	att	gca	gat	tta	aga	acg	aga	ggg	atc	tat	tcc	1440
Ala	Cys	Glu	Gly	Arg	Ile	Ala	Asp	Leu	Arg	Thr	Arg	Gly	Ile	Tyr	Ser	
465					470					475					480	
tgc	aac	gca	gat	tta	aga	acg	aaa	ggg	ttc	tat	tca	tgc	gac	gac	tgc	1488
Cys	Asn	Ala	Asp	Leu	Arg	Thr	Lys	Gly	Phe	Tyr	Ser	Cys	Asp	Asp	Cys	
				485					490					495		
tgc	acc	act	ctt	cat	att	gat	tgt	ttg	ctt	ggg	gaa	gac	atg	tat	atg	1536
Cys	Thr	Thr	Leu	His	Ile	Asp	Cys	Leu	Gly	Glu	Glu	Asp	Met	Tyr	Met	
			500					505					510			
aag	cct	ggt	cac	acc	ata	atg	tat	art	atg	acg	ggt	ttc	gac	gaa	cat	1584
Lys	Pro	Gly	His	Thr	Ile	Met	Tyr	Xaa	Met	Thr	Gly	Phe	Asp	Glu	His	
		515					520					525				
tat	gag	aag	aag	ctt	cgt	att	ctt	cgc	aac	aat	act	ttg	tct	cgg	cca	1632
Tyr	Glu	Lys	Lys	Leu	Arg	Ile	Leu	Arg	Asn	Asn	Thr	Leu	Ser	Arg	Pro	
		530				535					540					
tgt	tgc	agt	aca	tgc	ggg	cag	cgt	tgt	cga	cag	aaa	ata	gtt	ttc	aaa	1680
Cys	Cys	Ser	Thr	Cys	Gly	Gln	Arg	Cys	Arg	Gln	Lys	Ile	Val	Phe	Lys	
545					550					555					560	

PF59082SeqList_PF59082.txt

tac aaa gaa cac cat ata ttt tgt gct ata tct tgc cag aag cat gta 1728
Tyr Lys Glu His His Ile Phe Cys Ala Ile Ser Cys Gln Lys His Val
565 570 575

att aat tac tca tag 1743
Ile Asn Tyr Ser
580

<210> 1312

<211> 580

<212> PRT

<213> Arabidopsis thaliana

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<223> The Xaa at location 326 stands for Ala, or Val.

<220>

<221> misc_feature

<222> (521)..(521)

<223> The Xaa at location 521 stands for Asn, or Ser.

<400> 1312

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Thr Thr Leu Glu Pro Ala Thr Ser Tyr Tyr Val Cys Val Thr Cys Gly
35 40 45
Asp Gln Phe His Lys Glu Cys Ile Gly Ser Pro Leu Glu Phe Lys His
50 55 60
Pro Ser Tyr Pro Ser Leu Ser Leu Gln Leu Tyr Ser Pro Pro Ser Asp
65 70 75 80
Arg Val Phe Cys Ser Cys Cys Gln Lys Arg Ile Asp Gly Leu Asn Tyr
85 90 95
Tyr Ser Pro Thr Asn Asn Phe Thr Leu His Leu Phe Cys Ala Phe Lys
100 105 110
Pro Ile Pro Phe Val Ile Asp His Pro Lys Arg His Pro His Pro Leu
115 120 125
Thr Ile Phe Pro Lys Gln Ser Phe Leu Pro Cys His Val Cys Ser Leu
130 135 140
Ile Lys Gly His Ile Pro Thr Tyr Val Cys Val Arg Cys Val Phe Val
145 150 155 160
Val His Gln Asp Cys Ile Tyr Phe Pro Tyr Val Ile Lys Ile Ser Arg
165 170 175
His His His Arg Ile Ser Tyr Thr Ser Ser Leu Pro Ser Gly Lys Trp
180 185 190
Ser Cys Gly Val Cys Arg Gln Met Val Asp Asn Asp Tyr Gly Ala Tyr
195 200 205
Ser Cys Asn Lys Cys Asp Asp Tyr Phe Val His Ser Arg Cys Ala Leu
210 215 220
Arg Arg Asp Leu Trp Asp Gly Ile Glu Leu Glu Gly Val Pro Glu Glu
225 230 235 240
Pro Glu Ile Val Val Glu Pro Phe Ile Thr Ile Ser Asp Gly Ile Ile
245 250 255
Leu His Phe Ser His Gly His His Leu Lys Leu Lys Ile Ser Arg Val
260 265 270
Tyr Asp Glu Lys Met Val Cys Gln Ala Cys Ile Leu Pro Ile Tyr Glu
275 280 285
Gly Gly Tyr Tyr Ser Cys Met Asp Glu Cys Asp Phe Ile Leu His Glu
290 295 300
Thr Cys Ala Asn Ala Pro Cys Lys Lys His His Ala Leu His Pro His
305 310 315 320
Pro Leu Thr Leu Thr Xaa Val Thr Ser Glu Tyr Glu Asp Asn Ile Gly
325 330 335
Arg Phe Cys Cys Lys Ala Cys Gln Arg Glu Ser Cys Gly Phe Val Tyr
340 345 350
Glu Asp Leu Arg Gly Lys Ile Gly Asn Tyr Arg Arg Asn Lys Phe Gln
355 360 365

PF59082SeqList_PF59082.txt

Leu Asp Leu Arg Cys Ala Ser Val Ser Glu Pro Phe Glu Tyr Leu Gly
 370 375 380
 His Lys His Leu Leu Tyr Leu Ala Leu Asn Pro Glu Glu Glu Lys Leu
 385 390 400
 Ala Ile Cys Gln Ile Cys His Glu Arg Glu Asp Glu Ser Ser His Cys
 405 410 415
 Arg Lys Leu Asn Cys Ile Glu Cys Asp Phe Val Ile Cys Phe Arg Cys
 420 425 430
 Ala Thr Leu Pro Tyr Lys Ala Gly Tyr Gln His Asp Lys His Phe Leu
 435 440 445
 Lys Phe Tyr Glu Thr Lys Glu Ala Asn Asp His Ser Glu Trp Cys Asp
 450 455 460
 Ala Cys Glu Gly Arg Ile Ala Asp Leu Arg Thr Arg Gly Ile Tyr Ser
 465 470 475 480
 Cys Asn Ala Asp Leu Arg Thr Lys Gly Phe Tyr Ser Cys Asp Asp Cys
 485 490 495
 Cys Thr Thr Leu His Ile Asp Cys Leu Leu Gly Glu Asp Met Tyr Met
 500 505 510
 Lys Pro Gly His Thr Ile Met Tyr Xaa Met Thr Gly Phe Asp Glu His
 515 520 525
 Tyr Glu Lys Lys Leu Arg Ile Leu Arg Asn Asn Thr Leu Ser Arg Pro
 530 535 540
 Cys Cys Ser Thr Cys Gly Gln Arg Cys Arg Gln Lys Ile Val Phe Lys
 545 550 555 560
 Tyr Lys Glu His His Ile Phe Cys Ala Ile Ser Cys Gln Lys His Val
 565 570 575
 Ile Asn Tyr Ser
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 ttc atc aat gga aat cac gat tgt cat ttt tgt aaa att gat ctt tcg 96
 Phe Ile Asn Gly Asn His Asp Cys His Phe Cys Lys Ile Asp Leu Ser
 20 25 30
 acg acg tct ttg tat gct cgt tgc acg ata tgc aat gta aac atg gat 144
 Thr Thr Ser Leu Tyr Ala Arg Cys Thr Ile Cys Asn Val Asn Met Asp
 35 40 45
 cta gac tgt atg gtg art cta cca cca ctc act att ttc gag cca aag 192
 Leu Asp Cys Met Val Xaa Leu Pro Pro Leu Thr Ile Phe Glu Pro Lys
 50 55 60
 cac cat aag cat agc ttc aac ctc ttg tta cga gta gtc acc ttt act 240
 His His Lys His Ser Phe Asn Leu Leu Leu Arg Val Val Thr Phe Thr
 65 70 75 80
 tgt aat gca tgt gga ttg gaa ggt gac cgt aat cct tat gta tgt tat 288
 Cys Asn Ala Cys Gly Leu Glu Gly Asp Arg Asn Pro Tyr Val Cys Tyr
 85 90 95
 gaa tgc cat ctc atg gta cac aaa gat tgt att gaa ggt cta ccg gga 336
 Glu Cys His Leu Met Val His Lys Asp Cys Ile Glu Gly Leu Pro Gly

PF59082SeqList_PF59082.txt

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	115						120					125					
ctt	ggt	caa	gaa	gag	aga	gat	tgg	gag	tgt	gga	gtt	tgt	cgt	agg	acg		432
Leu	Gly	Gln	Glu	Glu	Arg	Asp	Trp	Glu	Cys	Gly	Val	Cys	Arg	Arg	Thr		
	130					135					140						
att	gat	tgg	gtc	tac	gga	gca	tat	aca	tgt	tct	ctt	tgt	cct	agt	tat		480
Ile	Asp	Trp	Val	Tyr	Gly	Ala	Tyr	Thr	Cys	Ser	Leu	Cys	Pro	Ser	Tyr		
	145				150					155					160		
gct	gtt	cat	tca	aaa	tgt	gca	acg	agg	aaa	gaa	gtg	tgg	gat	ggg	aga		528
Ala	Val	His	Ser	Lys	Cys	Ala	Thr	Arg	Lys	Glu	Val	Trp	Asp	Gly	Arg		
				165					170					175			
gaa	ctc	gaa	gat	gtg	tcc	gaa	gaa	gat	gaa	gaa	att	gaa	gat	cca	ttc		576
Glu	Leu	Glu	Asp	Val	Ser	Glu	Glu	Asp	Glu	Glu	Ile	Glu	Asp	Pro	Phe		
				180					185					190			
aaa	gta	att	aat	gaa	acg	gat	atc	ata	cat	ttt	agt	cat	gaa	gaa	cat		624
Lys	Val	Ile	Asn	Glu	Thr	Asp	Ile	Ile	His	Phe	Ser	His	Glu	Glu	His		
		195					200										
gta	ctt	aga	ttg	gat	gag	aat	tgt	cat	atg	gaa	aat	gac	gct	acg	cgt		672
Val	Leu	Arg	Leu	Asp	Glu	Asn	Cys	His	Met	Glu	Asn	Asp	Ala	Thr	Arg		
		210				215					220						
tgc	cgg	ggg	tgc	att	ctt	gct	att	aat	ggc	aat	cta	tcc	tac	aaa	tgt		720
Cys	Arg	Gly	Cys	Ile	Leu	Ala	Ile	Asn	Gly	Asn	Leu	Ser	Tyr	Lys	Cys		
				225		230				235					240		
ctg	gaa	tgc	gat	ttc	atc	att	cac	aaa	gta	tgt	gca	agt	ctt	ccg	cgg		768
Leu	Glu	Cys	Asp	Phe	Ile	Ile	His	Lys	Val	Cys	Ala	Ser	Leu	Pro	Arg		
				245					250					255			
aag	aga	cga	cat	ttt	ttg	cac	aac	cat	aaa	ctc	act	cta	cga	gtt	gac		816
Lys	Arg	Arg	His	Phe	Leu	His	Asn	His	Lys	Leu	Thr	Leu	Arg	Val	Asp		
				260				265					270				
aag	gct	tct	ata	ttt	tta	tgt	tct	act	tgt	gat	acc	act	cct	aat	ggg		864
Lys	Ala	Ser	Ile	Phe	Leu	Cys	Ser	Thr	Cys	Asp	Thr	Thr	Pro	Asn	Gly		
		275					280					285					
ttc	aga	tac	gag	tgt	gac	gaa	gac	cat	ggc	gat	gaa	gaa	ttt	gtc	ttt		912
Phe	Arg	Tyr	Glu	Cys	Asp	Glu	Asp	His	Gly	Asp	Glu	Glu	Phe	Val	Phe		
		290				295					300						
gat	ctt	cag	tgt	agt	tcc	ata	tca	gaa	ccc	ttt	cta	cac	gat	ttg	cat		960
Asp	Leu	Gln	Cys	Ser	Ser	Ile	Ser	Glu	Pro	Phe	Leu	His	Asp	Leu	His		
					310					315					320		
cca	cac	ccg	tta	tac	tgg	acc	ttg	gaa	cat	tcc	aaa	aag	tgt	aag	gct		1008
Pro	His	Pro	Leu	Tyr	Trp	Thr	Leu	Glu	His	Ser	Lys	Lys	Cys	Lys	Ala		
				325					330					335			
tgt	ggc	acc	aaa	gca	ggg	tat	gat	ctc	aac	tgt	ata	gtg	tgt	gat	gat		1056
Cys	Gly	Thr	Lys	Ala	Gly	Tyr	Asp	Leu	Asn	Cys	Ile	Val	Cys	Asp	Asp		
				340				345					350				
tac	tca	tta	tgc	atg	acg	tgc	gct	act	tta	cca	agt	aaa	gta	aaa	cat		1104
Tyr	Ser	Leu	Cys	Met	Thr	Cys	Ala	Thr	Leu	Pro	Ser	Lys	Val	Lys	His		
				355			360					365					
agg	tgt	gac	gat	cat	ctt	ctg	tca	cta	cgt	caa	ggg	gct	tct	gac	ttc		1152
Arg	Cys	Asp	Asp	His	Leu	Leu	Ser	Leu	Arg	Gln	Gly	Ala	Ser	Asp	Phe		
						375					380						
gat	act	ggg	cac	ttg	tgg	tgt	gat	att	tgt	gag	acc	aag	aca	gat	ccg		1200
Asp	Thr	Gly	His	Leu	Trp	Cys	Asp	Ile	Cys	Glu	Thr	Lys	Thr	Asp	Pro		
					390					395					400		
agt	gta	ttt	tac	tat	act	tgt	gat	gat	tgt	ggg	gtc	agc	ctt	cat	tta		1248
Ser	Val	Phe	Tyr	Tyr	Thr	Cys	Asp	Asp	Cys	Gly	Val	Ser	Leu	His	Leu		
				405					410					415			
aag	tgt	gta	ctt	gga	gat	tta	tat	aat	gcg	aag	cta	gga	cta	ata	gat		1296
Lys	Cys	Val	Leu	Gly	Asp	Leu	Tyr	Asn	Ala	Lys	Leu	Gly	Leu	Ile	Asp		
				420				425					430				
ccc	aga	gat	ccc	gct	cat	gaa	gta	ctt	ccc	aat	aat	ggg	ggt	act	cga		1344
Pro	Arg	Asp	Pro	Ala	His	Glu	Val	Leu	Pro	Asn	Asn	Gly	Val	Thr	Arg		
				435			440					445					
cct	ttc	tgc	ttc	cat	tgt	gaa	ctt	cgt	tgt	aag	ttc	ccc	ttc	ctt	ata		1392
Pro	Phe	Cys	Phe	His	Cys	Glu	Leu	Arg	Cys	Lys	Phe	Pro	Phe	Leu	Ile		
						455					460						
agg	aga	gct	aca	gaa	gaa	ttt	act	ctt	tac	tat	tgt	tcg	cta	aat	tgt		1440
Arg	Arg	Ala	Thr	Glu	Glu	Phe	Thr	Leu	Tyr	Tyr	Cys	Ser	Leu	Asn	Cys		

PF59082SeqList_PF59082.txt

465		470		475		480	
tgt tta gaa gca gcc ttc tat att ccm cct gta aca gat gaa ggg							1485
Cys Leu Glu Ala Ala Phe Tyr Ile Pro Pro Val Thr Asp Glu Gly							
		485		490		495	
tag							1488

<210> 1314
 <211> 495
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <221> misc_feature
 <222> (54)..(54)
 <223> The Xaa at location 54 stands for Asn, or Ser.

<400> 1314
 Met Arg Arg Asp Leu Arg Ala Leu Pro Cys Ser His Phe Pro Lys Ile
 1 5 10 15
 Phe Ile Asn Gly Asn His Asp Cys His Phe Cys Lys Ile Asp Leu Ser
 20 25 30
 Thr Thr Ser Leu Tyr Ala Arg Cys Thr Ile Cys Asn Val Asn Met Asp
 35 40 45
 Leu Asp Cys Met Val Xaa Leu Pro Pro Leu Thr Ile Phe Glu Pro Lys
 50 55 60
 His His Lys His Ser Phe Asn Leu Leu Leu Arg Val Val Thr Phe Thr
 65 70 75 80
 Cys Asn Ala Cys Gly Leu Glu Gly Asp Arg Asn Pro Tyr Val Cys Tyr
 85 90 95
 Glu Cys His Leu Met Val His Lys Asp Cys Ile Glu Gly Leu Pro Gly
 100 105 110
 Val Ile Tyr Ile Asn Arg His Asp His Arg Val Ser His Thr Phe His
 115 120 125
 Leu Gly Gln Glu Glu Arg Asp Trp Glu Cys Gly Val Cys Arg Arg Thr
 130 135 140
 Ile Asp Trp Val Tyr Gly Ala Tyr Thr Cys Ser Leu Cys Pro Ser Tyr
 145 150 155 160
 Ala Val His Ser Lys Cys Ala Thr Arg Lys Glu Val Trp Asp Gly Arg
 165 170 175
 Glu Leu Glu Asp Val Ser Glu Glu Asp Glu Glu Ile Glu Asp Pro Phe
 180 185 190
 Lys Val Ile Asn Glu Thr Asp Ile Ile His Phe Ser His Glu Glu His
 195 200 205
 Val Leu Arg Leu Asp Glu Asn Cys His Met Glu Asn Asp Ala Thr Arg
 210 215 220
 Cys Arg Gly Cys Ile Leu Ala Ile Asn Gly Asn Leu Ser Tyr Lys Cys
 225 230 235 240
 Leu Glu Cys Asp Phe Ile Ile His Lys Val Cys Ala Ser Leu Pro Arg
 245 250 255
 Lys Arg Arg His Phe Leu His Asn His Lys Leu Thr Leu Arg Val Asp
 260 265 270
 Lys Ala Ser Ile Phe Leu Cys Ser Thr Cys Asp Thr Thr Pro Asn Gly
 275 280 285
 Phe Arg Tyr Glu Cys Asp Glu Asp His Gly Asp Glu Glu Phe Val Phe
 290 295 300
 Asp Leu Gln Cys Ser Ser Ile Ser Glu Pro Phe Leu His Asp Leu His
 305 310 315 320
 Pro His Pro Leu Tyr Trp Thr Leu Glu His Ser Lys Lys Cys Lys Ala
 325 330 335
 Cys Gly Thr Lys Ala Gly Tyr Asp Leu Asn Cys Ile Val Cys Asp Asp
 340 345 350
 Tyr Ser Leu Cys Met Thr Cys Ala Thr Leu Pro Ser Lys Val Lys His
 355 360 365
 Arg Cys Asp Asp His Leu Leu Ser Leu Arg Gln Gly Ala Ser Asp Phe
 370 375 380
 Asp Thr Gly His Leu Trp Cys Asp Ile Cys Glu Thr Lys Thr Asp Pro
 385 390 395 400

PF59082SeqList_PF59082.txt

Ser Val Phe Tyr Tyr Thr Cys Asp Asp Cys Gly Val Ser Leu His Leu
 405 410 415
 Lys Cys Val Leu Gly Asp Leu Tyr Asn Ala Lys Leu Gly Leu Ile Asp
 420 425 430
 Pro Arg Asp Pro Ala His Glu Val Leu Pro Asn Asn Gly Val Thr Arg
 435 440 445
 Pro Phe Cys Phe His Cys Glu Leu Arg Cys Lys Phe Pro Phe Leu Ile
 450 455 460
 Arg Arg Ala Thr Glu Glu Phe Thr Leu Tyr Tyr Cys Ser Leu Asn Cys
 465 470 475 480
 Cys Leu Glu Ala Ala Phe Tyr Ile Pro Pro Val Thr Asp Glu Gly
 485 490 495

<210> 1315
 <211> 2115
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (1)..(2115)

<220>
 <221> misc_feature
 <222> (529)..(529)
 <223> y is t or c

<400> 1315
 atg tct ccc gca aaa caa ata aga ttt gat ctt gat tgg gtt ggt gaa 48
 Met Ser Pro Ala Lys Gln Ile Arg Phe Asp Leu Asp Trp Val Gly Glu
 1 5 10 15
 aag agg atg aat tct ttc att act aaa gta atg tct ctc gtc agc tca 96
 Lys Arg Met Asn Ser Phe Ile Thr Lys Val Met Ser Leu Val Ser Ser
 20 25 30
 atg gat ttg gat ttg cag ccg aag gag tgc gag ttc atg tca ctc 144
 Met Asp Leu Asp Leu Gln Pro Lys Pro Glu Ser Glu Phe Met Ser Leu
 35 40 45
 act act caa ata ttc tct cta ctc cac tct atg gat tgc gat tcc atg 192
 Thr Thr Gln Ile Phe Ser Leu Leu His Ser Met Asp Ser Asp Ser Met
 50 55 60
 ccg aag ccg ctc tca aat ctc atc tca ctc ctt tct caa gga aac ttt 240
 Pro Lys Pro Leu Ser Asn Leu Ile Ser Leu Leu Ser Gln Gly Asn Phe
 65 70 75 80
 gac cat aat acc gac ttc agg tta ttc ttt cgt caa act atg gca ctc 288
 Asp His Asn Thr Asp Phe Arg Leu Phe Phe Arg Gln Thr Met Ala Leu
 85 90 95
 gag cca gag cca ata ttt atg tca ctc atc tat caa ata ttc tcc cta 336
 Glu Pro Glu Pro Ile Phe Met Ser Leu Ile Tyr Gln Ile Phe Ser Leu
 100 105 110
 gta ata tct atg aat act aag agg gat aag ctt att tcc tta tgt cct 384
 Val Ile Ser Met Asn Thr Lys Arg Asp Lys Leu Ile Ser Leu Cys Pro
 115 120 125
 caa gca tgc gtg gtt ttg ggt aat aat ggg aat ttt gaa gtg atc gtt 432
 Gln Ala Cys Val Val Leu Gly Asn Asn Gly Asn Phe Glu Val Ile Val
 130 135 140
 aaa aaa caa gaa ggt caa gct cat aag ggc aaa gca atc ccg tgg agt 480
 Lys Lys Gln Glu Gly Gln Ala His Lys Gly Lys Ala Ile Pro Trp Ser
 145 150 155 160
 aga gat agc aag tgg gaa tgt ctt cct ttt aac tgg aag aca tat tgg 528
 Arg Asp Ser Lys Trp Glu Cys Leu Pro Phe Asn Trp Lys Thr Tyr Trp
 165 170 175
 yct agt gga gat gat gtt aca cat ttt cga tgc cga aac tgc gat ggc 576
 Xaa Ser Gly Asp Asp Val Thr His Phe Arg Cys Arg Asn Cys Asp Gly
 180 185 190
 gac aac cat aaa gaa tat gaa aag gct ccg gtt gag atc aaa cac tct 624
 Asp Asn His Lys Glu Tyr Glu Lys Ala Pro Val Glu Ile Lys His Ser
 195 200 205
 ctt cat cgg aaa cat tct ctt cag ctt gtc ttg ttg gat gag agt agt 672
 Leu His Arg Lys His Ser Leu Gln Leu Val Leu Asp Glu Ser Ser

PF59082SeqList_PF59082.txt

210	tat	acg	agg	gta	tgc	tat	tgt	tgc	gat	gaa	gat	ctc	aaa	agg	atg	ttt	720
	Tyr	Thr	Arg	Val	Cys	Tyr	Cys	Cys	Asp	Glu	Asp	Leu	Lys	Arg	Met	Phe	
225						230					235					240	
	tat	tat	tgt	cgg	act	tgc	gat	ttt	ggg	ctt	aat	ttc	ggt	tgt	gcg	aag	768
	Tyr	Tyr	Cys	Arg	Thr	Cys	Asp	Phe	Gly	Leu	Asn	Phe	Val	Cys	Ala	Lys	
						245				250						255	
	aaa	gaa	gca	atc	tta	tat	ata	gac	caa	ccg	aag	tgg	cat	gag	cat	aca	816
	Lys	Glu	Ala	Ile	Leu	Tyr	Ile	Asp	Gln	Pro	Lys	Trp	His	Glu	His	Thr	
						260				265				270			
	ctt	gcg	ttg	ttt	cta	aga	aag	act	tcg	tta	act	tgc	aac	gca	tgt	ggc	864
	Leu	Ala	Leu	Phe	Leu	Arg	Lys	Thr	Ser	Leu	Thr	Cys	Asn	Ala	Cys	Gly	
																285	
	tta	tca	cat	tca	agt	tgt	cct	ctc	tat	atg	tgt	ccc	cct	tgt	gac	ttt	912
	Leu	Ser	His	Ser	Ser	Cys	Pro	Leu	Tyr	Met	Cys	Pro	Pro	Cys	Asp	Phe	
																300	
	gtg	atc	cat	aag	agt	tgt	atc	agc	tta	cca	cgt	ctc	ata	agg	ata	tca	960
	Val	Ile	His	Lys	Ser	Cys	Ile	Ser	Leu	Pro	Arg	Leu	Ile	Arg	Ile	Ser	
						310					315					320	
	cga	cat	ttc	cat	cgt	ata	gct	tat	acc	cct	tct	ttt	gat	gaa	gga	gat	1008
	Arg	His	Phe	His	Arg	Ile	Ala	Tyr	Thr	Pro	Ser	Phe	Asp	Glu	Gly	Asp	
						325				330						335	
	tgg	tct	tgt	agt	ggt	tgt	cg	aag	aag	atc	gac	aat	gat	tac	gga	ggc	1056
	Trp	Ser	Cys	Ser	Val	Cys	Arg	Lys	Lys	Ile	Asp	Asn	Asp	Tyr	Gly	Gly	
																350	
	tat	gtt	tgt	acc	aaa	ggt	tgt	tcg	tat	gcg	gct	cat	tca	aaa	tgt	gcc	1104
	Tyr	Val	Cys	Thr	Lys	Gly	Cys	Ser	Tyr	Ala	Ala	His	Ser	Lys	Cys	Ala	
																365	
	act	cag	agc	aat	gtg	tgg	gat	ggg	ata	gaa	ctt	gag	gga	gag	cca	gaa	1152
	Thr	Gln	Ser	Asn	Val	Trp	Asp	Gly	Ile	Glu	Leu	Glu	Gly	Glu	Pro	Glu	
																380	
	gat	att	gaa	gaa	gaa	gtg	ctt	cct	ccg	ttt	ttg	gag	ata	agt	gat	gga	1200
	Asp	Ile	Glu	Glu	Glu	Val	Leu	Pro	Pro	Phe	Leu	Glu	Ile	Ser	Asp	Gly	
						390					395					400	
	atc	ata	caa	cat	ttt	agt	cat	cag	caa	cat	atg	aaa	ctt	gac	gag	gag	1248
	Ile	Ile	Gln	His	Phe	Ser	His	Gln	Gln	His	Met	Lys	Leu	Asp	Glu	Glu	
						405				410						415	
	aac	acg	ggc	aga	gat	tac	gac	gag	aat	aag	gag	tgt	gaa	gca	tgc	atc	1296
	Asn	Thr	Gly	Arg	Asp	Tyr	Asp	Glu	Asn	Lys	Glu	Cys	Glu	Ala	Cys	Ile	
																420	
	agg	cca	atc	tat	ttc	ggt	aat	ttc	tac	tct	tgt	ttg	gaa	tgt	gat	ttt	1344
	Arg	Pro	Ile	Tyr	Phe	Gly	Asn	Phe	Tyr	Ser	Cys	Leu	Glu	Cys	Asp	Phe	
																435	
	att	ctt	cac	gaa	gag	tgt	gca	aac	ctt	tct	cg	aag	ata	cat	cac	ccg	1392
	Ile	Leu	His	Glu	Glu	Cys	Ala	Asn	Leu	Ser	Arg	Lys	Ile	His	His	Pro	
																450	
	ata	cat	cca	cat	ctt	ctc	aat	cta	att	gga	gga	ttt	gat	ggg	ggt	ata	1440
	Ile	His	Pro	His	Leu	Leu	Asn	Leu	Ile	Gly	Gly	Phe	Asp	Gly	Val	Ile	
						470					475					480	
	aac	tat	tat	aac	gat	aaa	tgc	tca	gct	tgt	att	gga	ctg	tgc	aaa	ggt	1488
	Asn	Tyr	Tyr	Asn	Asp	Lys	Cys	Ser	Ala	Cys	Ile	Gly	Leu	Cys	Lys	Gly	
						485				490						495	
	ggg	ttc	ttc	tat	gat	tgt	ggg	aaa	caa	gga	tgt	aag	ttt	atg	cta	cat	1536
	Gly	Phe	Phe	Tyr	Glu	Cys	Gly	Lys	Gln	Gly	Cys	Lys	Phe	Met	Leu	His	
																500	
	gtg	cag	tgc	gcc	aca	act	tct	gag	cca	tta	gtt	cat	gaa	agt	cat	agg	1584
	Val	Gln	Cys	Ala	Thr	Thr	Ser	Glu	Pro	Leu	Val	His	Glu	Ser	His	Arg	
																515	
	cat	cca	cta	ttt	cta	aca	tcc	aaa	cca	gga	gag	aaa	ata	cgt	tgt	tca	1632
	His	Pro	Leu	Phe	Leu	Thr	Ser	Lys	Pro	Gly	Glu	Lys	Ile	Arg	Cys	Ser	
																530	
	gtt	tgc	aag	gat	tca	gaa	gag	aca	ttc	aat	tgc	att	gag	tgc	gac	ttt	1680
	Val	Cys	Lys	Asp	Ser	Glu	Glu	Thr	Phe	Asn	Cys	Ile	Glu	Cys	Asp	Phe	
						550					555					560	
	gct	ttg	tgt	ttc	tat	tgt	gct	att	ttc	cct	caa	aag	gtg	agg	tat	aag	1728
	Ala	Leu	Cys	Phe	Tyr	Cys	Ala	Ile	Phe	Pro	Gln	Lys	Val	Arg	Tyr	Lys	
						565				570						575	
	cat	gat	aag	cac	aca	ctc	act	ctt	tct	tac	ggg	aag	gag	aca	ggg	acg	1776
	His	Asp	Lys	His	Thr	Leu	Thr	Leu	Ser	Tyr	Gly	Lys	Glu	Thr	Gly	Thr	

PF59082SeqList_PF59082.txt

	580	585	590	
tct tgg tgt gaa gtt tgt gag gct aaa ata aat ctg aaa gga cgg ttt				1824
Ser Trp Cys Glu Val Cys Glu Ala Lys Ile Asn Leu Lys Gly Arg Phe				
tat atg tgt aat gag tat tgt tgt gtc ccc cta cac att aaa tgt acg				1872
Tyr Met Cys Asn Glu Tyr Cys Cys Val Pro Leu His Ile Lys Cys Thr				
cta ggg gac tta cac atg agg ccc ggt tca acg tgg atc acc ttt ggt				1920
Leu Gly Asp Leu His Met Arg Pro Gly Ser Thr Trp Ile Thr Phe Gly				
aac aag gta gat gtt cta cac aac agt aac cgt atg tct cga tct att				1968
Asn Lys Val Asp Val Leu His Asn Ser Asn Arg Met Ser Arg Ser Ile				
tgc tcc tat tgt gtg aaa cac tgt cca tat aag ata gtt tac atg tgt				2016
Cys Ser Tyr Cys Val Lys His Cys Pro Tyr Lys Ile Val Tyr Met Cys				
tct gga ttg ata tta tgt tcc caa ggt tgt gta gtg cgt agc ata ttg				2064
Ser Gly Leu Ile Leu Cys Ser Gln Gly Cys Val Val Arg Ser Ile Leu				
cag aaa cgt gga cgt tac aga gag tta gaa ttt ttg agt aga tat gct				2112
Gln Lys Arg Gly Arg Tyr Arg Glu Leu Glu Phe Leu Ser Arg Tyr Ala				
taa				2115

<210> 1316
 <211> 704
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <221> misc_feature
 <222> (177)..(177)
 <223> The Xaa at location 177 stands for Pro, or Ser.

<400> 1316
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 Lys Arg Met Asn Ser Phe Ile Thr Lys Val Met Ser Leu Val Ser Ser
 20 25 30
 Met Asp Leu Asp Leu Gln Pro Lys Pro Glu Ser Glu Phe Met Ser Leu
 35 40 45
 Thr Thr Gln Ile Phe Ser Leu Leu His Ser Met Asp Ser Asp Ser Met
 50 55 60
 Pro Lys Pro Leu Ser Asn Leu Ile Ser Leu Leu Ser Gln Gly Asn Phe
 65 70 75 80
 Asp His Asn Thr Asp Phe Arg Leu Phe Phe Arg Gln Thr Met Ala Leu
 85 90 95
 Glu Pro Glu Pro Ile Phe Met Ser Leu Ile Tyr Gln Ile Phe Ser Leu
 100 105 110
 Val Ile Ser Met Asn Thr Lys Arg Asp Lys Leu Ile Ser Leu Cys Pro
 115 120 125
 Gln Ala Cys Val Val Leu Gly Asn Asn Gly Asn Phe Glu Val Ile Val
 130 135 140
 Lys Lys Gln Glu Gly Gln Ala His Lys Gly Lys Ala Ile Pro Trp Ser
 145 150 155 160
 Arg Asp Ser Lys Trp Glu Cys Leu Pro Phe Asn Trp Lys Thr Tyr Trp
 165 170 175
 Xaa Ser Gly Asp Val Thr His Phe Arg Cys Arg Asn Cys Asp Gly
 180 185 190
 Asp Asn His Lys Glu Tyr Glu Lys Ala Pro Val Glu Ile Lys His Ser
 195 200 205
 Leu His Arg Lys His Ser Leu Gln Leu Val Leu Leu Asp Glu Ser Ser
 210 215 220
 Tyr Thr Arg Val Cys Tyr Cys Cys Asp Glu Asp Leu Lys Arg Met Phe
 225 230 235 240
 Tyr Tyr Cys Arg Thr Cys Asp Phe Gly Leu Asn Phe Val Cys Ala Lys
 245 250 255

PF59082SeqList_PF59082.txt

Lys Glu Ala Ile Leu Tyr Ile Asp Gln Pro Lys Trp His Glu His Thr
 260 265 270
 Leu Ala Leu Phe Leu Arg Lys Thr Ser Leu Thr Cys Asn Ala Cys Gly
 275 280 285
 Leu Ser His Ser Ser Cys Pro Leu Tyr Met Cys Pro Cys Asp Phe
 290 295 300
 Val Ile His Lys Ser Cys Ile Ser Leu Pro Arg Leu Ile Arg Ile Ser
 305 310 315 320
 Arg His Phe His Arg Ile Ala Tyr Thr Pro Ser Phe Asp Glu Gly Asp
 325 330 335
 Trp Ser Cys Ser Val Cys Arg Lys Lys Ile Asp Asn Asp Tyr Gly Gly
 340 345 350
 Tyr Val Cys Thr Lys Gly Cys Ser Tyr Ala Ala His Ser Lys Cys Ala
 355 360 365
 Thr Gln Ser Asn Val Trp Asp Gly Ile Glu Leu Glu Gly Glu Pro Glu
 370 375 380
 Asp Ile Glu Glu Glu Val Leu Pro Pro Phe Leu Glu Ile Ser Asp Gly
 385 390 395 400
 Ile Ile Gln His Phe Ser His Gln Gln His His Met Lys Leu Asp Glu
 405 410 415
 Asn Thr Gly Arg Asp Tyr Asp Glu Asn Lys Glu Cys Glu Ala Cys Ile
 420 425 430
 Arg Pro Ile Tyr Phe Gly Asn Phe Tyr Ser Cys Leu Glu Cys Asp Phe
 435 440 445
 Ile Leu His Glu Glu Cys Ala Asn Leu Ser Arg Lys Ile His His Pro
 450 455 460
 Ile His Pro His Leu Leu Asn Leu Ile Gly Gly Phe Asp Gly Val Ile
 465 470 475 480
 Asn Tyr Tyr Asn Asp Lys Cys Ser Ala Cys Ile Gly Leu Cys Lys Gly
 485 490 495
 Gly Phe Phe Tyr Glu Cys Gly Lys Gln Gly Cys Lys Phe Met Leu His
 500 505 510
 Val Gln Cys Ala Thr Thr Ser Glu Pro Leu Val His Glu Ser His Arg
 515 520 525
 His Pro Leu Phe Leu Thr Ser Lys Pro Gly Glu Lys Ile Arg Cys Ser
 530 535 540
 Val Cys Lys Asp Ser Glu Glu Thr Phe Asn Cys Ile Glu Cys Asp Phe
 545 550 555 560
 Ala Leu Cys Phe Tyr Cys Ala Ile Phe Pro Gln Lys Val Arg Tyr Lys
 565 570 575
 His Asp Lys His Thr Leu Thr Leu Ser Tyr Gly Lys Glu Thr Gly Thr
 580 585 590
 Ser Trp Cys Glu Val Cys Glu Ala Lys Ile Asn Leu Lys Gly Arg Phe
 595 600 605
 Tyr Met Cys Asn Glu Tyr Cys Cys Val Pro Leu His Ile Lys Cys Thr
 610 615 620
 Leu Gly Asp Leu His Met Arg Pro Gly Ser Thr Trp Ile Thr Phe Gly
 625 630 635 640
 Asn Lys Val Asp Val Leu His Asn Ser Asn Arg Met Ser Arg Ser Ile
 645 650 655
 Cys Ser Tyr Cys Val Lys His Cys Pro Tyr Lys Ile Val Tyr Met Cys
 660 665 670
 Ser Gly Leu Ile Leu Cys Ser Gln Gly Cys Val Val Arg Ser Ile Leu
 675 680 685
 Gln Lys Arg Gly Arg Tyr Arg Glu Leu Glu Phe Leu Ser Arg Tyr Ala
 690 695 700

<210> 1317

<211> 1299

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1299)

<220>

<221> misc_feature

<222> (255)..(255)

PF59082SeqList_PF59082.txt

<223> y is t or c

<220>

<221> misc_feature

<222> (951)..(951)

<223> m is a or c

<400> 1317

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Met His Pro Ile Cys 5 Ala Met Lys Pro Ile 10 Pro Phe Leu Ile Asp 15 Pro	
cca aaa aag cat atc cat cct ctc act ttt ttc ccc aga caa act tcc	96
Pro Lys Lys His 20 Ile His Pro Leu Thr 25 Phe Phe Pro Arg Gln Thr Ser	
ttg act tgt aat gtt tgt ggt ttg aga aaa att tat ccc acc tac	144
Leu Thr 35 Cys Asn Val Cys Gly 40 Leu Arg Lys Ile Tyr 45 Pro Thr Tyr	
gtt tgt ttc aga tgt aac ttt gta act cat aat gac tgt atg aat tcc	192
Val Cys 50 Phe Arg Cys Asn Phe 55 Val Thr His Asn Asp 60 Cys Met Asn Ser	
cca cac atc atc aag ata tca cgt cac cgt cat cgt atc tcg ttc act	240
Pro His Ile Ile Lys 70 Ile Ser Arg His Arg His Arg Ile Ser Phe Thr 80	
ttt tct ctt aca tcy aga gaa tgg ttt tgt gga gtt tgc cgt tta agt	288
Phe Ser Leu Thr 85 Ser Arg Glu Trp Phe Cys 90 Gly Val Cys Arg Leu Ser 95	
att aac gtt gat tat ggt gca tat act tgt gac acg tgt agc gat tat	336
Ile Asn Val 100 Asp Tyr Gly Ala Tyr Thr Cys Asp Thr Cys Ser Asp Tyr 110	
gtt gtt cat tca ata tgc gct ctt ggg aaa gat gtg tgg gat gga aaa	384
Val Val 115 His Ser Ile Cys Ala Leu Gly Lys Asp Val 125 Trp Asp Gly Lys 125	
gaa ctc gaa ggt ata cca gag ata atc gat ata aca gaa aat gat gga	432
Glu Leu 130 Glu Gly Ile Pro Glu 135 Ile Ile Asp Ile Thr 140 Glu Asn Asp Gly 140	
ccg ttc gag gtg ata tct gaa gga gtg ata ctt tat ttt cat cat aat	480
Pro Phe Glu Val 150 Ser Glu Gly Val Ile Leu Tyr Phe His His Asn 160	
cat cat ctc cga ctc gag gtc agc aac gtt tat gat gaa aac atg ctt	528
His His Leu Arg 165 Glu Val Ser Asn Val 170 Tyr Asp Glu Asn Met 175 Leu 175	
tgt caa gcg tgt gcc att cct atc tat gaa ggt aac tta tat gtt tgt	576
Cys Gln Ala Cys Ala Ile Pro Ile Tyr 185 Glu Gly Asn Leu Tyr Val Cys 190	
atg gag tgt gat ttc atc ctc cat gaa aca tgt gct aag gct ccc cgt	624
Met Glu Cys Asp Phe Ile Leu His Glu Thr Cys Ala Lys Ala Pro Arg 205	
aga atc caa cat gcc tta cat cct cac cca ctt gta ttg gag gtt atc	672
Arg Ile Gln His Ala Leu His 215 Pro His Pro Leu Val 220 Leu Glu Val Ile 220	
aat agc ttt act tac aat acc ttc cgt tgc aac gct tgt gat cgt ggt	720
Asn Ser Phe Thr Tyr Asn Thr Phe Arg Cys Asn Ala Cys Asp Arg Gly 240	
tct att ggc ttt gcc tat cac tgt agg atg gag gta tgc aac ttt ttc	768
Ser Ile Gly Phe Ala 245 Tyr His Cys Arg Met 250 Glu Val Cys Asn Phe Phe 255	
aag ctt gat gta agg tgc gct tta att tct gag ccg ttt gat tac aaa	816
Lys Leu Asp Val Arg Cys Ala Leu Ile Ser Glu Pro Phe Asp Tyr Lys 270	
ggt cat gaa gat ccc ttg ttc cta gct tta aac cca gaa ata aaa ccc	864
Gly His Glu Asp Pro Leu Phe Leu Ala Leu Asn Pro Glu Ile Lys Pro 285	
ata tgt cat ata tgc aaa aca gaa tgt tta aaa caa tta aat tgc atc	912
Ile Cys 290 His Ile Cys Lys Thr 295 Glu Cys Leu Lys 300 Gln Leu Asn Cys Ile 300	
aaa tgc aat ttc att gta tgt ttt aag tgt gtt acc ttm cca tac aaa	960
Lys Cys Asn Phe Ile Val Cys Phe Lys Cys Val Thr Xaa Pro Tyr Lys 320	
305 310 315 320	
ata aaa tat aag cat gac aca cac ttc ctc aca att tca ttt ggt gaa	1008

PF59082SeqList_PF59082.txt

Ile	Lys	Tyr	Lys	His 325	Asp	Thr	His	Phe	Leu 330	Thr	Ile	Ser	Phe	Gly 335	Glu		
gaa	gta	cgt	gag	caa	gaa	tgg	tgt	gaa	ata	tgt	gaa	cgt	agt	tta	aag	1056	
Glu	Val	Arg	Glu	Gln	Glu	Trp	Cys	Glu	Ile	Cys	Glu	Arg	Ser	Leu	Lys		
			340					345					350				
gat	aca	tgc	aca	aaa	gta	ttc	tac	tgg	tgc	aac	gag	tgt	tgc	acc	act	1104	
Asp	Thr	Cys	Thr	Lys	Val	Phe	Tyr	Trp	Cys	Asn	Glu	Cys	Cys	Thr	Thr		
		355					360					365					
ttt	cat	att	gaa	tgc	tta	att	ggg	gga	gac	cca	tat	atc	aag	ccc	ggg	1152	
Phe	His	Ile	Glu	Cys	Leu	Ile	Gly	Gly	Asp	Pro	Tyr	Ile	Lys	Pro	Gly		
	370					375					380						
caa	tat	ttc	aat	aaa	tgg	gta	tgc	agg	gtt	caa	gtt	ctt	ccc	aaa	tgt	1200	
Gln	Tyr	Phe	Asn	Lys	Trp	Val	Cys	Arg	Val	Gln	Val	Leu	Pro	Lys	Cys		
	385				390				395						400		
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aaa	ata	tat	gat	gta	ggc	tac	cgt	gtt	gaa	tgt	tca	tat	gaa	tgt	att	1296	
Lys	Ile	Tyr	Asp	Val	Gly	Tyr	Arg	Val	Glu	Cys	Ser	Tyr	Glu	Cys	Ile		
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 Val Cys Phe Arg Cys Asn Phe Val Thr His Asn Asp Cys Met Asn Ser
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 65 70 75 80
 Phe Ser Leu Thr Ser Arg Glu Trp Phe Cys Gly Val Cys Arg Leu Ser
 85 90 95
 Ile Asn Val Asp Tyr Gly Ala Tyr Thr Cys Asp Thr Cys Ser Asp Tyr
 100 105 110
 Val Val His Ser Ile Cys Ala Leu Gly Lys Asp Val Trp Asp Gly Lys
 115 120 125
 Glu Leu Glu Gly Ile Pro Glu Ile Ile Asp Ile Thr Glu Asn Asp Gly
 130 135 140
 Pro Phe Glu Val Ile Ser Glu Gly Val Ile Leu Tyr Phe His His Asn
 145 150 155 160
 His His Leu Arg Leu Glu Val Ser Asn Val Tyr Asp Glu Asn Met Leu
 165 170 175
 Cys Gln Ala Cys Ala Ile Pro Ile Tyr Glu Gly Asn Leu Tyr Val Cys
 180 185 190
 Met Glu Cys Asp Phe Ile Leu His Glu Thr Cys Ala Lys Ala Pro Arg
 195 200 205
 Arg Ile Gln His Ala Leu His Pro His Pro Leu Val Leu Glu Val Ile
 210 215 220
 Asn Ser Phe Thr Tyr Asn Thr Phe Arg Cys Asn Ala Cys Asp Arg Gly
 225 230 235 240
 Ser Ile Gly Phe Ala Tyr His Cys Arg Met Glu Val Cys Asn Phe Phe
 245 250 255
 Lys Leu Asp Val Arg Cys Ala Leu Ile Ser Glu Pro Phe Asp Tyr Lys
 260 265 270

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Gly His Glu Asp Pro Leu Phe Leu Ala Leu Asn Pro Glu Ile Lys Pro
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 Lys Cys Asn Phe Ile Val Cys Phe Lys Cys Val Thr Xaa Pro Tyr Lys
 305 310 315 320
 Ile Lys Tyr Lys His Asp Thr His Phe Leu Thr Ile Ser Phe Gly Glu
 325 330 335
 Glu Val Arg Glu Gln Glu Trp Cys Glu Ile Cys Glu Arg Ser Leu Lys
 340 345 350
 Asp Thr Cys Thr Lys Val Phe Tyr Trp Cys Asn Glu Cys Cys Thr Thr
 355 360 365
 Phe His Ile Glu Cys Leu Ile Gly Gly Asp Pro Tyr Ile Lys Pro Gly
 370 375 380
 Gln Tyr Phe Asn Lys Trp Val Cys Arg Val Gln Val Leu Pro Lys Cys
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 Ile Ser Thr Arg Phe Val Asn Asp Ser Cys Lys Gly Cys Asn Ile Lys
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 ggt ccc atc tat ggc ggc tac cgt tgc aac gag cct tcc tct act agt 144
 Gly Pro Ile Tyr Gly Gly Tyr Arg Cys Asn Glu Pro Ser Ser Thr Ser
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 ttg ttc ttc cac aaa gag tgc gca gag gct cca ccg gag att atc aac 192
 Leu Phe Phe His Lys Glu Cys Ala Glu Ala Pro Pro Glu Ile Ile Asn
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 His Pro Ser His Pro Gln His Thr Leu Lys His Asn Ser Leu Arg
 65 70 75 80
 aac cca tgt aaa tgt aat cta tgt ggc aag act ttt ttc gct ttt ggt 288
 Asn Pro Cys Lys Cys Asn Leu Cys Gly Lys Thr Phe Phe Ala Phe Gly
 85 90 95
 tat cgt tgt tca tca aaa tgt gac ttc atc gtg gat ctc act tgt ggg 336
 Tyr Arg Cys Ser Ser Lys Cys Asp Phe Ile Val Asp Leu Thr Cys Gly
 100 105 110
 ata aat cca ttg ccg gtt tct atc gaa cat cca aag tct cat cat cat 384
 Ile Asn Pro Leu Pro Val Ser Ile Glu His Pro Lys Ser His His His
 115 120 125
 cca gtt atc ttc ttg aaa gaa ccc gca aag ccg ggt agg cgc aga tgc 432
 Pro Val Ile Phe Leu Lys Glu Pro Ala Lys Pro Gly Arg Arg Arg Cys
 130 135 140
 gga att tgc aag ggc tat aat ggt gga tgt tct tat gca tgt ctt gaa 480
 Gly Ile Cys Lys Gly Tyr Asn Gly Gly Cys Ser Tyr Ala Cys Leu Glu
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 Cys Glu Val His Phe His Val Glu Cys Val Asn Leu Ser Gln Glu Val
 165 170 175
 aat cat cct tct cat cct caa cat tct ctc aag tta ctt gaa tat gaa 576
 Asn His Pro Ser His Pro Gln His Ser Leu Lys Leu Leu Glu Tyr Glu
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 Ser Leu Thr Ser Asp Ala Glu Glu Thr Cys Leu Cys Gly Glu Arg

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Arg	Phe	Cys	Thr	Lys	Asp	Pro	Pro	Pro	Leu	Ala	Ile	Glu	His	His	Lys		
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Thr	His	Glu	His	Arg	Leu	Val	Leu	Leu	Ser	Arg	Leu	Ile	Ser	Phe	Glu		
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tgt	aat	gct	tgt	ggg	atg	caa	ggt	gat	cga	agt	cct	tac	atg	tgt	gtt		816
Cys	Asn	Ala	Cys	Gly	Met	Gln	Gly	Asp	Arg	Ser	Pro	Tyr	Met	Cys	Val		
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Gln	Cys	Gly	Phe	Val	Val	His	Arg	Thr	Cys	Ile	Asp	Leu	Pro	Arg	Val		
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Gly	Val	Gly	Tyr	Ser	Arg	Cys	Gly	Ile	Cys	Arg	Lys	Asp	Ile	Ser	Gln		
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Gly	Thr	Pro	Asp	Asp	Asp	Asp	Glu	Asp	Ile	Val	Pro	Phe	Lys	Val	Val		
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Asp	Ala	Cys	Tyr	Lys	Glu	Ile	Asp	Gly	Tyr	Leu	Leu	Ser	Cys	Asp	Thr		
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Lys	His	Ser	Cys	Asp	Asn	His	Pro	Leu	Ser	Leu	Cys	Tyr	Gly	Glu	Asn		
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 405 410 415
 Arg Phe Ile Leu His Glu Lys Cys Ala Asn His Pro Lys Lys Arg
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 His Val Phe His Thr Lys Pro Phe Thr Leu Trp Ser Arg Pro Pro Arg
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 Gly His Arg His Pro Leu Tyr Tyr Glu His Lys Lys Asp His Cys Cys
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 Asp Ala Cys Tyr Lys Glu Ile Asp Gly Tyr Leu Leu Ser Cys Asp Thr
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 Cys Asp Phe Asp Leu Asp Leu His Cys Thr Asp Leu Pro Lys Thr Val
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 Asn Tyr Asn Asn Val Arg Val Glu Val Val Leu Asn Ser Tyr Ser Ser
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caa aac aaa aca aac tcc tcc gat gaa gta acc atc ggt gac gga gac	192
Gln Asn Lys Thr Asn Ser Ser Asp Glu Val Thr Ile Gly Asp Gly Asp	
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Asn Leu Pro Ile Ser Pro Ile Phe Ile Cys Leu Asn Leu Arg Leu Gln	
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His	Gly	Asp	Asn	Ile	Ser	Asp	Asp	His	Val	Val	Leu	Pro	Leu	Phe	Trp	
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Val	Gln	Lys	Ala	Gly	Thr	Asn	Tyr	Tyr	Tyr	Cys	Val	Glu	Cys	Asp	Val	
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Thr	Tyr	His	Lys	Glu	Cys	Ile	Glu	Ser	Pro	Leu	Glu	Ile	Ser	Tyr	Pro	
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Ala	Ile	Pro	Phe	Phe	Ile	Asp	Gln	Pro	Lys	Arg	His	Asp	His	Thr	Leu	
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Ser	Leu	Phe	Pro	Arg	Gln	Ala	Ser	Leu	Thr	Cys	Asn	Val	Cys	Ala	Leu	
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Val	Asn	Lys	Leu	His	Leu	Thr	Tyr	Val	Cys	Arg	Ser	Ile	Cys	Asp	Phe	
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Arg	His	His	His	Arg	Val	Ser	Phe	Thr	Ser	Ser	Leu	Pro	Leu	Glu	Lys	
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Trp	Ser	Cys	Gly	Val	Cys	Arg	Arg	Glu	Val	Asp	His	Asp	Tyr	Gly	Ala	
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Tyr	Thr	Cys	Cys	Val	Cys	Ser	Gly	Tyr	Ala	Val	His	Thr	Arg	Cys	Ala	
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Leu	Arg	Thr	Asp	Ile	Trp	Asp	Gly	Ile	Glu	Leu	Glu	Gly	Val	Gln	Glu	
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Cys	Val	Glu	Ala	Pro	Arg	Lys	Lys	Val	His	Pro	Leu	His	Pro	His	Pro	
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Phe Ala Gly Gln His Lys Phe Lys Arg Tyr Lys His Asp Glu His Tyr			
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Glu Pro Tyr Met Lys Ser Gly Glu Thr Pro Pro Lys Glu Gly Gly Gln			
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Ser His Cys Asn Asn Ser Ser Arg Gly Thr Gln Leu Ala Leu Gln His			
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Ile Asn Pro Asn Leu Phe His Thr Cys Asn Ser Ile Leu Lys Pro Arg			
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Ala	Ile	Pro	Phe	Phe	Ile	Asp	Gln	Pro	Lys	Arg	His	Asp	His	Thr	Leu
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Ser	Leu	Phe	Pro	Arg	Gln	Ala	Ser	Leu	Thr	Cys	Asn	Val	Cys	Ala	Leu

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 Tyr Thr Cys Cys Val Cys Ser Gly Tyr Ala Val His Thr Arg Cys Ala
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Pro Phe His Pro Ser His Pro Leu Thr Phe Ile Ser Leu Leu Leu Pro	
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Lys Phe Asp Val Thr Lys Ile Pro Lys Asn Trp Met Asp Ser Ser Ser	
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tta Leu 80	tcc Ser 80	gat Asp 80	gga Gly 80	aat Asn 80
gaa Glu 85	aag Lys 85	ata Ile 85	tat Tyr 85	cat His 85
gaa Glu 90	tgc Cys 90	tcg Ser 90	atg Met 90	aga Arg 90
cat His 95	gag Glu 95	cac His 95	atc Ile 95	ctc Leu 95
ggg Gly 100	gcg Ala 100	tgc Cys 100	ggc Gly 100	ttg Leu 100
tgt Cys 105	ctc Leu 105	cct Pro 105	tgc Cys 105	aac Asn 105
cgt Arg 110	gtc Val 110	att Ile 110	aag Lys 110	atc Ile 110
tcc Ser 115	ctt Leu 115	caa Gln 115	cct Pro 115	ggt Gly 115
gac Asp 120	gtc Val 120	aac Asn 120	tac Tyr 120	ggg Gly 120
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ctt Leu 165	gat Asp 165	gga Gly 165	gtg Val 165	agg Arg 165
ctt Leu 170	gat Asp 170	gga Gly 170	gtg Val 170	agg Arg 170
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ctt Leu 490	gat Asp 490	gga Gly 490	gtg Val 490	agg Arg 490
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Lys Phe Leu Leu Phe Ile Thr Arg Ile Ile Ser Ile Val Ser Ser Leu	
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PF59082SeqList_PF59082.txt

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gta gat ccg act ttt gat ttt tca ccc cga aac tgg aaa gac aag tcc      432
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130
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Gln Tyr Ser Cys Asn Lys Gly Cys His Tyr Ala Val His Ser Lys Cys
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 Pro Thr Cys Glu Phe Lys Val Asp Leu Thr Cys Gly Met Lys Pro Ser
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 Cys Ile Asn Ala Asn Leu Pro Ser Arg His Lys His Pro Leu Lys Val
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Gly	Ala	Tyr	Ala	Cys	Ser	Ile	Cys	Ser	Tyr	Phe	Phe	His	Ser	Lys	Cys	
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 385 390 395 400
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 405 410 415
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 420 425 430
 Gly Glu Lys Asn Val Asn Ala Arg Tyr Cys Cys Gly Ile Cys Glu Glu
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 Asp Val His Ser Lys Ser Trp Phe Tyr Lys Cys Asn Glu Cys Gly Ser
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Phe Glu Ser Phe Ala Tyr Tyr Cys Arg Glu Cys Arg Ser His Phe His	
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Lys Asp Cys Leu Thr Ile Ile Asn Ala Lys Ile His Glu His Thr Leu	
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Val His Arg Gln Cys Ile Phe Leu Pro Lys Val Ile Lys Leu Thr Arg	
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225      230      235      240
cat tct ctt cga ctt tgc agt ttt caa acg agg ctt act agc ggt tgt      768
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Leu Ser Met His Pro Val Cys Ala Met Arg Pro Val Pro Leu Val Val
275      280      285
gac cat cct aaa agc cat ccc cat cct ctc tcc ttt ttc cct aca caa      912
Asp His Pro Lys Ser His Pro His Pro Leu Ser Phe Phe Pro Thr Gln
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Ala Ser Thr Val Cys His Ile Cys Ala Lys Ile Lys His Leu Asp Pro
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aca tat atc tgt atc caa tgt gtc ttc gta atc cat aaa ggt tgt atg      1008
Thr Tyr Ile Cys Ile Gln Cys Val Phe Val Ile His Lys Gly Cys Met
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ggt ttc cca cat acc ata aga ata tct cgt cac cct cac cgt atc tct      1056
Gly Phe Pro His Thr Ile Arg Ile Ser Arg His Pro His Arg Ile Ser
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Pro	Arg	Met	Lys	Arg	Tyr	Pro	Leu	Tyr	Pro	His	Pro	Ile	Thr	Leu	Lys	
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Lys	Arg	Lys	Asp	Leu	Trp	Ile	Phe	Leu	Asn	Asn	Ser	Leu	Thr	Arg	Pro	
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      115      120      125
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Arg Ser Thr Val Gly Phe Glu Cys Gly Ala Cys Lys Met Thr Thr Leu
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Cys Glu Ser Tyr Phe Ala Cys Leu Gln Cys Gln Gly Lys Phe His Lys
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Cys Arg Lys Ile Thr Phe Gly Met Phe Tyr Gln Cys Thr Thr Cys Asn
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Val Thr Phe Pro Tyr Lys Val Arg Tyr Lys His Asp Ser His Phe Leu
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Ile Cys Glu Gly Lys Ile Glu Glu Glu Lys Glu Lys Glu Tyr Asn Trp
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Lys Arg Lys Asp Leu Trp Ile Phe Leu Asn Asn Ser Leu Thr Arg Pro
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20
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Ile Ile Ser Met Val Ser Ser Leu Asp Leu Asn Thr Gln Pro Lys Pro
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cag tcg aag ctc atg tca ctc att aca gaa aca atc tcc ctc ttc aac      192
Gln Ser Lys Leu Met Ser Leu Ile Thr Glu Thr Ile Ser Leu Phe Asn
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130
135

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Thr	Phe	Asn	Cys	Ile	Glu	Cys	Glu	Phe	Ala	Leu	Cys	Phe	Gly	Cys	Ala	
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Cys	Glu	Glu	Lys	Val	Asn	Pro	Lys	Asp	Arg	Phe	Tyr	Met	Cys	Asp	Asp	
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Tyr	Cys	Cys	Val	Thr	Leu	His	Met	Arg	Cys	Leu	Met	Ile	Ile	Arg	Ser	
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Ile	Ile	Ser	Met	Val	Ser	Ser	Leu	Asp	Leu	Asn	Thr	Gln	Pro	Lys	Pro	
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Gln	Ser	Lys	Leu	Met	Ser	Leu	Ile	Thr	Glu	Thr	Ile	Ser	Leu	Phe	Asn	
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Ser	Met	Asn	Leu	Asp	Ser	Gln	Pro	Glu	Pro	Leu	Arg	Lys	Leu	Val	Ser	
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Ser	Ile	Phe	Ala	Ile	Lys	Thr	Asn	Ala	Glu	Leu	Glu	Leu	Arg	Gly	Gly	
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Pro	Glu	Glu	Leu	Pro	Lys	Phe	Lys	Ser	Phe	Ile	Ser	Leu	Thr	Lys	Gln	
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Pro	Val	Leu	Phe	Ile	Asp	His	Pro	Lys	Trp	His	Ala	Asp	Thr	Leu	Ala	
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Gln	Lys	Asn	Val	Trp	Asp	Gly	Ile	Tyr	Leu	Glu	Gly	Val	Pro	Glu	Glu	
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Pro	Ile	Tyr	Phe	Gly	Asn	Phe	Phe	Ser	Cys	Met	Gln	Ser	Cys	Pro	Trp	
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675 680 685
Thr Phe Asn Cys Ile Glu Cys Glu Phe Ala Leu Cys Phe Gly Cys Ala
690 695 700
Thr Leu Pro Gln Lys Val Arg Tyr Lys His Asp Lys His Ile Leu Thr
705 710 715 720
Leu Ser Tyr Gly Lys Glu Thr Ser Thr Met Thr Tyr Trp Cys Glu Val
725 730 735
Cys Glu Glu Lys Val Asn Pro Lys Asp Arg Phe Tyr Met Cys Asp Asp
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Val Ser Arg Asn Asn Thr Asp Ser Glu Asn Ile Ser Cys Met Ile Gln	
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Thr Ile Ser Leu Val Ser Ser Met Asp Leu Lys Ser Gln Pro Lys Pro	
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Glu Ser Lys Leu Met Ser Leu Val Thr Gln Thr Ile Ser Leu Phe Asn	
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Ser Met Asp Leu Ser Ser Gln Pro Glu Pro Leu Arg Lys Leu Ile Ser	
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Leu Ile Ile Glu Lys Leu Ser His Leu Asn Ser Val Asp Ser Asp Tyr	
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Glu Pro Lys Pro Asp Ser Glu Phe Met Ser Thr Phe Tyr Glu Thr Tyr	
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Lys Leu Gln Pro Arg Pro Glu Ile Ile Ser Ile Ile His Gln Ile Tyr	
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Ala	Val	Val	Lys	Gln	Ile	Met	Ser	Phe	Ala	Asn	Ser	Ile	Ser	Asn	Ser	
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Glu	Pro	Glu	Trp	Gln	Phe	Ile	Ser	Ser	Met	Thr	Glu	Met	Ile	Arg	Leu	
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Val	Ala	Leu	Phe	Thr	His	Thr	Phe	Ser	Leu	Leu	Tyr	Tyr	Leu	Asp	Arg	
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Tyr	Thr	Asp	Ser	Glu	Pro	Glu	Ser	Glu	Trp	Gly	Leu	Asp	Gln	Leu	Met	
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Val	Thr	Gly	Lys	Ile	Glu	Arg	Lys	Asn	Lys	Glu	Lys	Gly	Lys	Cys	Gln	
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Gln	Leu	Val	Ser	Gln	Lys	Ser	Ser	Ile	Gln	Gln	Thr	Arg	Lys	Cys	Phe	
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Cys	Cys	Asp	Glu	Asp	Leu	Lys	Lys	Ile	Phe	Tyr	Tyr	Cys	Thr	Gly	Cys	
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Gln	Ala	Phe	Leu	Thr	Cys	Asn	Val	Cys	Ala	Val	Ala	Asp	Ser	Ser	Ser	
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Thr	Gly	Leu	Pro	Arg	Val	Ile	Arg	Ile	Ser	Arg	His	Arg	His	Arg	Ile	
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Ala	Thr	Leu	Pro	Gln	Lys	Val	Arg	Tyr	Lys	His	Asp	Lys	His	Ile	Leu	
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Thr	Leu	Ser	Tyr	Gly	Lys	Glu	Thr	Ser	Thr	Met	Thr	Tyr	Trp	Cys	Glu	
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Lys	Leu	Gln	Pro	Arg	Pro	Glu	Ile	Ile	Ser	Ile	Ile	His	Gln	Ile
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Leu	Asp	Tyr	Ser	Glu	Pro	Glu	Pro	Glu	Ser	Glu	Phe	Ile	Ser	Val
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805 810 815
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Gln Ile Ile Ser Leu Val Ser Ser Met Asp Leu Asp Ser Gln Pro Lys	
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Pro Glu Thr Lys Leu Met Ser Leu Ile Ala Gln Thr Ile Ser Leu Phe	
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Asn Ser Met Asp Leu Asp Ser Gln Pro Glu Pro Leu Arg Asn Leu Ile	
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 Gly Lys Asp Leu Tyr Met Lys Pro Gly Ser Leu Cys Ile Tyr Lys Asp
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Glu Lys Ile Tyr Asp Ser Leu Ile Tyr Ile Cys Asn Lys Cys Val Leu	
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gta cct ctg aga aaa gga aga ttt ggt tct tca tat ttc cat ttc aat	240
Val Pro Leu Arg Lys Gly Arg Phe Gly Ser Ser Tyr Phe His Phe Asn	
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Cys Ala Lys Tyr Pro Pro Ser Glu Val Ile Asp Val Pro Gln His His	
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Asp His Lys Leu Lys Leu Glu Met Val Lys Ser Cys Phe Ser Cys Ala	
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PF59082SeqList_PF59082.txt

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Asp	Leu	Lys	Phe	His	Val	Asn	Cys	Glu	Lys	His	Pro	Ala	Glu	Val	Thr	
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His	Phe	Ser	His	Pro	Leu	His	Pro	Leu	Lys	Leu	Val	Lys	Val	Glu	Pro	
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Pro	Ala	Tyr	Thr	Asp	Lys	Lys	Cys	Arg	Leu	Cys	Gly	Glu	Lys	Leu	Ala	
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Asn	Ser	Glu	Val	Phe	Tyr	His	Cys	Ser	Ala	Cys	Asn	Phe	Ser	Leu	Asp	
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Leu	Gln	Cys	Ile	Phe	Tyr	Pro	Pro	Lys	Gln	Asn	Pro	His	Asp	Pro	Asn	
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Ile	His	Gly	His	Gln	Leu	Thr	Leu	Met	Pro	Lys	Ser	Ile	Ser	Phe	Ser	
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ccc	tgt	gat	ttc	aca	agc	cac	aat	gat	tgc	tct	gga	ttt	cca	tgg	gtc	768
Pro	Cys	Asp	Phe	Thr	Ser	His	Asn	Asp	Cys	Ser	Gly	Phe	Pro	Trp	Val	
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Glu	Asn	Thr	Ile	Gln	His	Val	Ser	His	Lys	Glu	His	Asn	Leu	Arg	Leu	
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Arg	Ala	Ser	Leu	Asp	Leu	Arg	Cys	Ala	Ser	Ile	Thr	Glu	Pro	Phe	Val	
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Arg	Cys	Ile	Phe	Pro	Val	Ile	Leu	Lys	Thr	Trp	Asn	Glu	Ser	Ser	Leu		
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Arg	Asn	Glu	Tyr	Tyr	Cys	Ser	Glu	Leu	Leu	Asn	Ile	Cys	Met	Ile	Asp		
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Glu	Val	Lys	His	Asn	Gly	Lys	Tyr	Trp	Cys	Asp	Ile	Cys	Glu	Lys	Glu
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Val	Phe	Pro	Val	Ile	Ile	Thr	Thr	Val	Pro	Glu	Cys	Trp	Lys	Phe	Leu
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Ala Ser Ser Gln His Lys Ala Val Lys Gln Met Gly Phe Glu Asp Gly	
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Pro Arg Cys Leu Met Ser His Pro Ala His Pro Ser His Asn Leu Ser	
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Pro Glu Thr Arg Val Ile Ser Asn Ile Ile Pro Asp Ala Cys Pro Gly	
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Thr	Leu	Cys	Glu	Phe	Thr	Met	Cys	Tyr	Ser	Cys	Ala	Ile	Ile	Pro	Asp	
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Glu	Ser	Ala	Asp	Asn	Thr	Tyr	Trp	Cys	Glu	Val	Cys	Glu	Lys	Gln	Leu	
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Asp	Pro	Lys	Glu	Trp	Phe	Tyr	Thr	Cys	Asn	Lys	Cys	Cys	Ile	Thr	Ile	
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His	Leu	His	Cys	Ile	Phe	Gly	Ser	Ser	Val	Phe	Met	Lys	Pro	Gly	Ser	
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Ile	Phe	Arg	Asp	Tyr	Gly	Lys	Val	Gln	Val	Phe	Arg	Asn	Asn	Ser		
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aac	act	cga	caa	ctc	tgt	tat	atg	tgt	cac	aac	cgt	tgt	acc	ggg	ttg	1776
Asn	Thr	Arg	Gln	Leu	Cys	Tyr	Met	Cys	His	Asn	Arg	Cys	Thr	Gly	Leu	
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Ile	Phe	Tyr	Glu	Gly	Tyr	Arg	Arg	Asn	Ala	Thr	Tyr	Tyr	Tyr	Asn	His	
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Ser	Asn	Arg	Ser	Thr	His	Arg	Met	Ile	Phe	Cys	Ser	Leu	Glu	Cys	Glu	
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<211> 638

<212> PRT

<213> Arabidopsis thaliana

<400> 1346

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PF59082SeqList_PF59082.txt

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Cys Glu Val Thr Phe His Asn Gly Cys His Gln Arg Pro Arg Arg Ile
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Thr His Pro Tyr His Leu Gln His Pro Leu Thr Leu Phe Tyr Arg Asn
    100      105      110
Pro Glu Thr Arg Val Ile Ser Asn Ile Ile Pro Asp Ala Cys Pro Gly
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Lys Ile Glu Asp Thr Ser Gly Pro Glu Lys Tyr Glu Phe Val Asp Ile
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Val Pro Tyr Lys Ser Asp Ile Ile Phe Asn Lys Cys Thr Trp Cys Ala
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Lys Asp Phe Lys Gly Asp Trp Phe Tyr Arg Cys Leu Ile Cys Ser Phe
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Leu Val Pro Cys Asp Ala Cys Gly Leu Val Asp Gly Leu Glu Pro Ser
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Tyr Ala Cys Phe Gln Cys Asn Tyr Met Val His Gln Asn Cys Ile Asp
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Pro Ser Pro Gly Lys Phe Cys Cys Ser Ala Cys Ser Arg Glu Ser Thr
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Gly Phe Ser Tyr Ile Cys Ser Asn Lys Gly Cys Gln Asp Phe Val Leu
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Asp Val Arg Cys Ile Ser Val Leu Glu Tyr Phe Ile His Arg Ser His
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Glu His Pro Ile Phe Ile Ser Thr Ser Tyr Asn Ser Lys Asp Glu Ile
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Leu Cys Lys Val Cys Lys Lys Arg Cys Leu Gly Ala His Leu Gln Cys
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Glu Ser Ala Asp Asn Thr Tyr Trp Cys Glu Val Cys Glu Lys Gln Leu
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Ile Phe Arg Asp Tyr Tyr Gly Lys Val Gln Val Phe Arg Asn Asn Ser
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Phe Val 50 Phe Asn Ile Gln Glu 55 Ile Phe Asp His Pro Ser His Val Gly	
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cac gtc aat cac cat gac cac cgt gtt tct ttc aag tat cct ctt ggt	384
His Val Asn His His Asp His Arg Val Ser Phe Lys Tyr Pro Leu Gly	
cct gga gaa tgg cga tgt gga gtt tgt tgg gaa gag att gat tgg tca	432
Pro Gly Glu Trp Arg Cys Gly Val Cys Trp Glu Glu Ile Asp Trp Ser	
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Tyr Gly Ala Tyr Ser Cys Ser Phe Cys Pro Ser Tyr Ala Ile His Ser	
aga tgt gca aca agg aaa gat gtg tgg gat ggc aaa gag ctt gat ggg	528
Arg Cys Ala Thr Arg 165 Lys Asp Val Trp Asp Gly Lys Glu Leu Asp Gly	
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Val Pro Glu Glu Val Glu Asp Val Glu Pro Phe Lys Arg Asn Ala Asp	
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Asn Thr Ile Lys His Phe Ala His Gln His Asn Leu Met Ser Phe Ser	
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Lys Asp Ser Glu Glu Ser Asn 215 Phe Cys Gly Ala Cys Val Arg Pro Ile	
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Gly Ser Cys Thr Phe Tyr Lys Cys Ser Glu Ser 235 Asp Cys Ser Phe Ile	
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cgt	tgc	cca	ggg	ccc	ttc	att	ctt	cat	gat	cca	tat	aac	tat	cat	gga	1392
Arg	Cys	Pro	Gly	Pro	Phe	Ile	Leu	His	Asp	Pro	Tyr	Asn	Tyr	His	Gly	
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<212> PRT

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 Gly Ser Cys Thr Phe Tyr Lys Cys Ser Glu Ser Asp Cys Ser Phe Ile
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 260 265 270
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 Pro Leu Thr Leu Cys Tyr Gly Asp Glu Lys Ala Ser Gly Arg Tyr Trp
 370 375 380
 Cys Asp Ile Cys Glu Arg Glu Thr Asn Pro Lys Ile Trp Phe Tyr Thr
 385 390 395 400
 Cys Lys Asp Cys Gly Val Thr Ser His Ile Phe Cys Val Val Gly Asp
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 Gly Tyr Ser Cys Ser Glu Cys Lys Phe Asn Ile His Lys Lys Cys Val
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Asp	Gly	Glu	Glu	Asn	Ser	Leu	Cys	Gly	Ala	Cys	Val	Arg	Pro	Ile	Gly	
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Ser	Tyr	Thr	Phe	Tyr	Lys	Cys	Ser	Glu	Ser	Glu	Cys	Ile	Phe	Ile	Leu	
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Thr	Ala	450	Cys	Ser	Ala	Cys	Leu	455	Gln	Val	Cys	Ser	Glu	Gly	Phe	
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 His Val Ser Pro Thr Ala Gly Leu Phe Gly Ala Asp Trp Gly Tyr Tyr
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Lys	Trp	Lys	Lys	Leu	Ile	Ser	Phe	Cys	Pro	Ile	Phe	Glu	Val	Ser	Leu
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Asn	Leu	Leu	Lys	Leu	Pro	Gly	Glu	Asn	Asp	Phe	Thr	His	Phe	Arg	Cys
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Leu	Val	Leu	Ile	Glu	Ala	Ser	Tyr	Arg	Thr	Arg	Glu	Cys	Tyr	Cys	Cys	
	225				230					235				240		
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Phe	Tyr	Gly	Ala	His	Ser	Arg	Cys	Ala	Thr	Arg	Arg	Ser	Val	Trp	Asp	
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Asn	Met	Glu	Cys	Gln	Ala	Cys	Val	Arg	Pro	Ile	Tyr	Phe	Gly	Asn	Phe	
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Tyr	Ser	Cys	Met	Gln	Cys	Asp	Phe	Ile	Leu	His	Glu	Ala	Cys	Ala	Asn	
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Gln	Asp	Cys	Asp	Phe	Gln	Leu	His	Val	Gln	Cys	Ala	Val	Val	Ser	Glu	
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Cys	Ile	Phe	Ala	Met	Thr	Met	Lys	Pro	Tyr	Ser	Trp	Trp	Leu	Phe	Ser	
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cct Pro	acc Thr	aaa Lys	gat Asp	act Thr	aca Thr	cga Arg	cta Gln	tgc Leu	tcc Cys	cag Gln	tgt Cys	cac His	tct Ser	cga Arg	560	1680
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PF59082SeqList_PF59082.txt

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Gln	Ala	Ser	Leu	Val	Cys	His	Phe	Cys	Ala	Leu	Ile	Lys	Lys	Leu	Asp	
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Asp	Ala	Cys	His	Arg	Lys	Gly	Thr	Gly	Phe	Phe	Tyr	Glu	His	His	Thr	
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Asp	Gln	Glu	Asn	Ile	Phe	Met	Leu	Asp	Ile	His	Cys	Ala	Ser	Ile	Phe	
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Cys Ala Thr Leu Pro Tyr Lys Val Arg Tyr Lys His Asp Ser His Phe
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Pro	Lys	His	His	Lys	His	Ser	Phe	Asn	Leu	Leu	Leu	Arg	Val	Val	Thr	
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Phe	Thr	Cys	Asn	Ala	Cys	Gly	Leu	Glu	Gly	Asp	Arg	Asn	Pro	Tyr	Val	
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tgt	tat	gaa	tgc	cat	ctc	atg	gta	cac	aaa	gat	tgt	att	gaa	ggt	cta	192
Cys	Tyr	Glu	Cys	His	Leu	Met	Val	His	Lys	Asp	Cys	Ile	Glu	Gly	Leu	

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Phe His Leu Gly Gln Glu Glu Arg Asp Trp Glu Cys Gly Val Cys Arg				
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agg acg att gat tgg gtc tac gga gca tat aca tgt tct ctt tgt cct				336
Arg Thr Ile Asp Trp Val Tyr Gly Ala Tyr Thr Cys Ser Leu Cys Pro				
100	105	110		
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Ser Tyr Ala Val His Ser Lys Cys Ala Thr Arg Lys Glu Val Trp Asp				
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Gly Arg Glu Leu Glu Asp Val Ser Glu Glu Asp Glu Glu Ile Glu Asp				
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Glu His Val Leu Arg Leu Asp Glu Asn Cys His Met Glu Asn Asp Ala				
165	170	175		
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Thr Arg Cys Arg Gly Cys Ile Leu Ala Ile Asn Gly Asn Leu Ser Tyr				
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aaa tgt ctg gaa tgc gat ttc atc att cac aaa gta tgt gca agt ctt				624
Lys Cys Leu Glu Cys Asp Phe Ile Ile His Lys Val Cys Ala Ser Leu				
195	200	205		
ccg cgg aag aga cga cat ttt ttg cac aac cat aaa ctc act cta cga				672
Pro Arg Lys Arg Arg His Phe Leu His Asn His Lys Leu Thr Leu Arg				
210	215	220		
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Val Asp Lys Ala Ser Ile Phe Leu Cys Ser Thr Cys Asp Thr Thr Pro				
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Asn Gly Phe Arg Tyr Glu Cys Asp Glu Asp His Gly Asp Glu Glu Phe				
245	250	255		
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Val Phe Asp Leu Gln Cys Ser Ser Ile Ser Glu Pro Phe Leu His Asp				
260	265	270		
ttg cat cca cac ccg tta tac tgg acc ttg gaa cat tcc aaa aag tgt				864
Leu His Pro His Pro Leu Tyr Trp Thr Leu Glu His Ser Lys Lys Cys				
275	280	285		
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Lys Ala Cys Gly Thr Lys Ala Gly Tyr Asp Leu Asn Cys Ile Val Cys				
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Asp Asp Tyr Ser Leu Cys Met Thr Cys Ala Thr Leu Pro Ser Lys Val				
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aaa cat agg tgt gac gat cat ctt ctg tca cta cgt caa ggt gct tct				1008
Lys His Arg Cys Asp Asp His Leu Leu Ser Leu Arg Gln Gly Ala Ser				
325	330	335		
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Asp Phe Asp Thr Gly His Leu Trp Cys Asp Ile Cys Glu Thr Lys Thr				
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Asp Pro Ser Val Phe Tyr Tyr Thr Cys Asp Asp Cys Gly Val Ser Leu				
355	360	365		
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His Leu Lys Cys Val Leu Gly Asp Leu Tyr Asn Ala Lys Leu Gly Leu				
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Ile Asp Pro Arg Asp Pro Ala His Glu Val Leu Pro Asn Asn Gly Val				
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Thr Arg Pro Phe Cys Phe His Cys Glu Leu Arg Cys Lys Phe Pro Phe				
405	410	415		
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Leu Ile Arg Arg Ala Thr Glu Glu Phe Thr Leu Tyr Cys Ser Leu				

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Thr	Arg	Cys	Arg	Gly	Cys	Ile	Leu	Ala	Ile	Asn	Gly	Asn	Leu	Ser	Tyr
				180				185					190		
Lys	Cys	Leu	Glu	Cys	Asp	Phe	Ile	Ile	His	Lys	Val	Cys	Ala	Ser	Leu
				195			200					205			
Pro	Arg	Lys	Arg	Arg	His	Phe	Leu	His	Asn	His	Lys	Leu	Thr	Leu	Arg
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225					230					235					240
Asn	Gly	Phe	Arg	Tyr	Glu	Cys	Asp	Glu	Asp	His	Gly	Asp	Glu	Glu	Phe
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Ser Ser Arg Phe Ile Asn Gly Arg Cys Arg Gly Cys Lys Gln Thr Ser
          20          25          30
cct atc tat agt ggc tac cgt tgc aat gac tct gat tgt aac cat gtt      144
Pro Ile Tyr Ser Gly Tyr Arg Cys Asn Asp Ser Asp Cys Asn His Val
          35          40          45
tgg tat cac aaa gaa tgt ggc gaa tca tta ccg gag atc aat cat cct      192
Trp Tyr His Lys Glu Cys Gly Glu Ser Leu Pro Glu Ile Asn His Pro
          50          55          60
tcc cat ctc gag cat ccg ctc tgc tta atc gac tac agg gga agt ggt      240
Ser His Leu Glu His Pro Leu Cys Leu Ile Asp Tyr Arg Gly Ser Gly
  65          70          75          80
acg tgt gct ttt tgt gga gct ttc ttg ttt ggt cct acg tat cat tgt      288
Thr Cys Ala Phe Cys Gly Ala Phe Leu Phe Gly Pro Thr Tyr His Cys
          85          90          95
tgg ata tgc gcc ttt aat atc gat ata gct tgt gcg aga aaa caa cta      336
Trp Ile Cys Ala Phe Asn Ile Asp Ile Ala Cys Ala Arg Lys Gln Leu
          100          105          110
cct cca ctt gct gct att gaa aat ccc aaa tgt cat aac cat tca ctt      384
Pro Pro Leu Ala Ala Ile Glu Asn Pro Lys Cys His Asn His Ser Leu
          115          120          125
gtt ctt ttg gag aag caa gtg aag aaa gat cat tgt gga gtt tgc aag      432
Val Leu Leu Glu Lys Gln Val Lys Lys Asp His Cys Gly Val Cys Lys
          130          135          140
aaa aca gtt ttt ggt atg tat cct tac gtt tgt ctt gag tgt gat gtg      480
Lys Thr Val Phe Gly Met Tyr Pro Tyr Val Cys Leu Glu Cys Asp Val
  145          150          155          160
tat ttc cac gtc gaa tgc ata aat ata tcg cgg gag gtc cac cat tct      528
Tyr Phe His Val Glu Cys Ile Asn Ile Ser Arg Glu Val His His Ser
          165          170          175
tct cat act aat cac act ctc gag ctt ttc gga tct gag tcg cta cct      576
Ser His Thr Asn His Thr Leu Glu Leu Phe Gly Ser Glu Ser Leu Pro
          180          185          190
gat agc gct caa aag act tgt ctt ttg tgt gat gac gta tca gat cac      624
Asp Ser Ala Gln Lys Thr Cys Leu Leu Cys Asp Asp Val Ser Asp His
          195          200          205
ttg att tat cat tgt tcc gtt tgc aac ttc agc atc tgt gtt tat tgt      672
Leu Ile Tyr His Cys Ser Val Cys Asn Phe Ser Ile Cys Val Tyr Cys
          210          215          220
gcg ata aat cct cca ccg ctt gct ata gaa cat ctt aag act cac gag      720
Ala Ile Asn Pro Pro Pro Leu Ala Ile Glu His Leu Lys Thr His Glu
  225          230          235          240
cat acg cta act ctc ttg cct aga caa gtt aag ttt att tgc aat gct      768
His Thr Leu Thr Leu Leu Pro Arg Gln Val Lys Phe Ile Cys Asn Ala
          245          250          255
tgt gga atg aaa ggt gat gga tgt cct tac ttt tgt ctt gga tgt ggt      816
Cys Gly Met Lys Gly Asp Gly Cys Pro Tyr Phe Cys Leu Gly Cys Gly
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tac tta atc cat cgg aaa tgc atc gat tta cct cgc gtc att aac atc      864
Tyr Leu Ile His Arg Lys Cys Ile Asp Leu Pro Arg Val Ile Asn Ile
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Glu	Asp	Ser	Glu	Gln	Asp	Thr	Ala	Pro	Phe	Glu	Val	Val	Asp	Asp	Asn	
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Thr	Ile	Lys	His	Phe	Ser	His	Glu	Lys	His	Asn	Leu	Met	Leu	Asn	Lys	
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Tyr	Val	Leu	His	Glu	Thr	Cys	Ala	Asn	Leu	Pro	Arg	Lys	Lys	Arg	His	
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Val	Phe	Asn	Asn	Lys	Pro	Phe	Thr	Leu	His	Thr	Gly	Gly	Lys	Asp	Ser	
		435				440					445					
tct	agg	aat	tgg	ttt	gag	tgt	gat	gct	tgt	aga	aca	atc	tcc	aat	ggg	1392
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Phe	Arg	Tyr	Val	Ser	Gly	Asp	Trp	Ile	Leu	Asp	Val	His	Cys	Gly	Ser	
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Pro	Leu	Ser	Leu	Cys	His	Gly	Glu	Asp	Asp	Val	Ile	Lys	Asp	Asn	Lys	
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Tyr	Trp	Cys	Asp	Ile	Cys	Glu	Thr	Glu	Thr	Asp	Pro	Lys	Lys	Trp	Phe	
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Tyr	Thr	Cys	Tyr	Asp	Cys	Gly	Val	Thr	Leu	His	Val	Lys	Cys	Val	Leu	
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Ser His Leu Glu His Pro Leu Cys Leu Ile Asp Tyr Arg Gly Ser Gly
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Thr Cys Ala Phe Cys Gly Ala Phe Leu Phe Gly Pro Thr Tyr His Cys
85 90 95
Trp Ile Cys Ala Phe Asn Ile Asp Ile Ala Cys Ala Arg Lys Gln Leu
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Lys Thr Val Phe Gly Met Tyr Pro Tyr Val Cys Leu Glu Cys Asp Val
145 150 155 160
Tyr Phe His Val Glu Cys Ile Asn Ile Ser Arg Glu Val His His Ser
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180 185 190
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Ala Ile Asn Pro Pro Pro Leu Ala Ile Glu His Leu Lys Thr His Glu
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245 250 255
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260 265 270
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 515 520 525
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 545 550 555
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Ser Ser Gly Glu Val Leu Ala Met Asp Ser Thr Gly Asp Asp Gln Pro	
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Leu Asp Gln Pro Leu Phe Leu Cys Pro Asp Ala Arg Ile Lys Phe His	
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Lys Leu Lys Ile Gln Arg Glu Asp Gly Asp Ile Phe Asp Tyr Asp Phe	
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Gly Asp Gln Gln Gly Glu Ser Leu Leu Asp Cys Asp Glu Asp Gly Ile	
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Cys Lys Leu Pro Val Val Pro Leu Phe Trp Cys Asn Asn Lys Glu Ser	
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Ala Ser Tyr Tyr Ala Cys Leu Gln Cys Glu Lys Lys Phe His Lys Glu	
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PF59082SeqList_PF59082.txt

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Ser	Leu	Arg	Leu	Tyr	Tyr	His	Pro	Ala	Pro	Glu	Phe	Cys	Ile	Cys	Cys	
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Lys	Thr	Glu	Val	Phe	Met	Ile	Phe	Tyr	His	Cys	Leu	Thr	Cys	Asn	Leu	
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Ser	Met	His	Pro	Val	Cys	Ala	Met	Arg	Lys	Val	Pro	Phe	Phe	Ile	Asp	
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His	Pro	Lys	Ser	His	Pro	His	Pro	Leu	Thr	Phe	Phe	Pro	Thr	Gln	Ala	
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Ala	Thr	Arg	Gly	Pro	Gly	Asn	Glu	Glu	Gly	Thr	Phe	Gln	Cys	Asp	Ala	
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Glu	Asn	Ile	Phe	Met	Leu	Asp	Ile	His	Cys	Ala	Ser	Ile	Phe	Glu	Pro	
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Asn	Leu	Asn	Cys	Leu	Glu	Cys	Asp	Tyr	Ile	Leu	Cys	Phe	His	Cys	Ala	
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Cys	Glu	Gly	Lys	Ile	Glu	Glu	Gly	Thr 585	Glu	Arg	Ala	Phe	Tyr 590	Asn	Thr	
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Pro	Lys	Lys 595	Asp	Thr	Ser	Phe	Tyr 600	Lys	Cys	Asn	Ala	Cys 605	Cys	Thr	Thr	
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 Tyr Phe Val His 340 Ser Lys Cys Ala Leu Gln Arg His Val Trp Asp Gly
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 Glu Pro Phe Lys Arg Ile Ala 375 Asp Gly Ile Ile Leu His Pro Phe His
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 Tyr Cys Arg Gly Cys 405 Ala Leu Pro Ile Tyr 410 Glu Gly Gln Phe Tyr Ser
 Cys Ile Glu Ser Asp Phe Ile Leu His 425 Glu His Cys Ala Asn Ala Pro
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 Ala Thr Arg Gly Pro Gly Asn 455 Glu Glu Gly Thr Phe Gln Cys Asp Ala
 Cys 465 His Arg Lys Gly Thr 470 Gly Phe Phe Tyr Glu His His Thr Asp Gln
 Glu Asn Ile Phe Met 485 Leu Asp Ile His Cys 490 Ala Ser Ile Phe Glu Pro
 Phe Gln Tyr Gln Gly His Glu His Pro Leu Phe Leu Pro Ser Glu Pro
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20      25      30
atc tcc tgc aaa ggc caa caa tac act ggg aat agg cgt ggg tac tat      144
Ile Ser Cys Lys Gly Gln Gln Tyr Thr Gly Asn Arg Arg Gly Tyr Tyr
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Tyr Tyr Cys Ala Thr Cys Asp Leu Glu Phe His Lys Gly Cys Tyr Leu
50      55      60
ttt cct cca gaa atc aaa cac cct ttc cac ctc atc cac cct ctc acc      240
Phe Pro Pro Glu Ile Lys His Pro Phe His Leu Ile His Pro Leu Thr
65      70      75      80
ctc acc ttc tta gat cat aat ctt gtt agc tct gcg atc cct gaa att      288
Leu Thr Phe Leu Asp His Asn Leu Val Ser Ser Ala Ile Pro Glu Ile
85      90      95
tgg ttt ctg tta agc acg gaa tat cca tac aag cat atg ttt gga gat      336
Trp Phe Leu Leu Ser Thr Glu Tyr Pro Tyr Lys His Met Phe Gly Asp
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Glu Glu Glu Cys Ala Ser Asp Gly Asn His Lys Arg Cys Asn Ser Cys
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cgg aaa aag atc aca tac cgc gac cca gac tat cct tcg ttt ttt gat      432
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130      135      140
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Ile Thr Tyr Tyr His Cys Ser Ile Cys Asn Phe Ser Leu His Ser Ser
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tgc gta aag gat tca cca cct cat act att gaa aac cta aaa agc cat      528
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Glu His Thr Leu Thr Leu Phe Pro Arg Leu Leu Pro Leu Pro Cys Asp
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<213> Arabidopsis thaliana

<400> 1368

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Ile	Ser	Cys	Lys	Gly	Gln	Gln	Tyr	Thr	Gly	Asn	Arg	Arg	Gly	Tyr	Tyr	
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Tyr	Tyr	Cys	Ala	Thr	Cys	Asp	Leu	Glu	Phe	His	Lys	Gly	Cys	Tyr	Leu	
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Phe	Pro	Pro	Glu	Ile	Lys	His	Pro	Phe	His	Leu	Ile	His	Pro	Leu	Thr	
65					70					75					80	
Leu	Thr	Phe	Leu	Asp	His	Asn	Leu	Val	Ser	Ser	Ala	Ile	Pro	Glu	Ile	
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Glu	Glu	Glu	Cys	Ala	Ser	Asp	Gly	Asn	His	Lys	Arg	Cys	Asn	Ser	Cys	
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Ile Thr Tyr Tyr His Cys Ser Ile Cys Asn Phe Ser Leu His Ser Ser
145 150 155 160
Cys Val Lys Asp Ser Pro Pro His Thr Ile Glu Asn Leu Lys Ser His
165 170 175
Glu His Thr Leu Thr Leu Phe Pro Arg Asn Asp Ser Val Tyr Ser Phe
180 185 190
Ala Cys Gly Phe Ser Leu Asp Ala Arg Asn Asp Ser Val Tyr Ser Phe
195 200 205
Ala Val Pro Ser Gly Asp Glu Leu Ser Cys Gly Val Cys Arg Lys Leu
210 215 220
Val Asp Val Asn Tyr Gly Gln Tyr Ala Cys Lys Lys Gly Cys His Tyr
225 230 235 240
Ala Val His Ser Lys Cys Ala Thr Lys Asn Glu Val Trp Asp Gly Lys
245 250 255
Asp Leu Asp Gly Val Pro Glu Glu Glu Glu Glu Ile Glu Pro Phe
260 265 270
Val Arg Ile Asp Glu Glu Thr Ile Gln His Phe Ser His Asp His His
275 280 285
Tyr Leu Lys Ile His His Gly Asn Asp Asn His Glu Asn Lys Phe Cys
290 295 300
Gln Ala Cys Ile Leu Arg Ile Thr Val Ser Asp Ser Phe Tyr Ser Cys
305 310 315 320
Val Gln Cys Asp Phe Val Ile His Glu Thr Cys Ala Gly Leu Pro Arg
325 330 335
Ile Lys His His Pro Leu His Lys His Pro Leu Thr Leu Tyr His Leu
340 345 350
His Tyr Pro His Leu Asn Glu Val Gln Ser Lys Tyr Tyr Asp Leu Gly
355 360 365
Phe Phe Ala Cys Ser Gly Cys Ser Arg Glu Cys Cys Gly Phe Met Tyr
370 375 380
Lys Cys Cys Glu Lys Asp Cys Asp Phe Gln Leu Asp Ala Arg Cys Ala
385 390 395 400
Ser Leu Pro Asp Pro Ile Ile His Asp Cys His Pro His Asp His Pro
405 410 415
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420 425 430
Ser Gly Leu Arg Lys Tyr Leu Glu Cys Ile Glu Cys Arg Ser Phe Ser
435 440 445
Cys Leu Thr Cys Ala Thr Met Pro Leu Val Ala His Tyr Lys Tyr Asp
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Lys His Pro Leu Thr Leu Cys Cys Gly Glu Glu Lys Thr Lys Asp Leu
465 470 475 480
Gln Tyr Trp Cys Glu Ile Cys Glu Ser Glu Ile Asp Ala Gln Lys Trp
485 490 495
Phe Tyr Thr Cys Ser Tyr Cys Ser Val Thr Leu His Val Thr Cys Leu
500 505 510
Leu Gly Asp Lys Val Tyr Met Lys Pro Asn His Met Ile Lys Met Tyr
515 520 525
Glu Gly Ala Lys Thr Ser Ile Gly Ile Val Pro Asn Ser Gly Asn Ser
530 535 540
Arg Pro Met Cys Asp Gly Cys Arg Ser Arg Cys Val Asp Thr Leu Val
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<213> Arabidopsis thaliana

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seite 1825

PF59082SeqList_PF59082.txt

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cct tct tcc tct ggt gaa aca gcc att gat ggc gat cac gac ctc tct				144
Pro Ser Ser Ser Gly Glu Thr Ala Ile Asp Gly Asp His Asp Leu Ser				
ttt caa caa cct ctt ttc ctc tgt cct tct tta cgt ctt aaa gct gac				192
Phe Gln Gln Pro Leu Phe Leu Cys Pro Ser Leu Arg Leu Lys Ala Asp				
gag gaa aac tat tct tat agt gaa ctt ctc ccg ttc aat att tcc ccg				240
Glu Glu Asn Tyr Ser Tyr Ser Glu Leu Leu Pro Phe Asn Ile Ser Pro				
ctc ttc ccc agc ata agt agc gct gat caa caa gtc cag cat ttg ctt				288
Leu Phe Pro Ser Ile Ser Ser Ala Asp Gln Gln Val Gln His Leu Leu				
gat tcc gac agc cgt gat gct aat atc tgt aag ctc cct gtt gtc cct				336
Asp Ser Asp Ser Arg Asp Ala Asn Ile Cys Lys Leu Pro Val Val Pro				
atc tat tgg tgt aac aat aaa cac ggt gat tat gct caa ttc att tgc				384
Ile Tyr Trp Cys Asn Asn Lys His Gly Asp Tyr Ala Gln Phe Ile Cys				
cgt gca tgt gac aca ttc aag att gac aca gac tat tat ata tgt ctc				432
Arg Ala Cys Asp Thr Phe Lys Ile Asp Thr Asp Tyr Tyr Ile Cys Leu				
aca tgt gat caa atg ttc cac aaa gaa tgc gtg gag tct ccg ctt gag				480
Thr Cys Asp Gln Met Phe His Lys Glu Cys Val Glu Ser Pro Leu Glu				
ctc aaa aac cct tcg tat caa aaa cca tgc gtg agt tgc atg tgc tgt				528
Leu Lys Asn Pro Ser Tyr Gln Lys Pro Cys Val Ser Cys Met Cys Cys				
gat tta gct ctc ttt agc ttg ttt tat cat tgt ccc acc tac gaa ctt				576
Asp Leu Ala Leu Phe Ser Leu Phe Tyr His Cys Pro Thr Tyr Glu Leu				
agt atg cat ccc gtt tgt gcg atg aag cca ata ccc att ttc ata gac				624
Ser Met His Pro Val Cys Ala Met Lys Pro Ile Pro Ile Phe Ile Asp				
aac tca aaa agg cat ccc cac ctt ctc acc ttt ttt ccc aaa caa gct				672
Asn Ser Lys Arg His Pro His Leu Leu Thr Phe Phe Pro Lys Gln Ala				
tcc tta ctt tgc gat gtt tgt ggc ctc att aaa gaa gct ttc ccc acc				720
Ser Leu Leu Cys Asp Val Cys Gly Leu Ile Lys Glu Ala Phe Pro Thr				
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Tyr Val Cys Pro Arg Cys Ile Phe Val Ala His Gln Asp Cys Ile Tyr				
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Phe Pro Tyr Val Ile Lys Ile Tyr Arg His Gln His Arg Ile Ser Phe				
acc tct tct ctt cca tct gga aaa tgg tct tgt gga gtc tgt cgt agg				864
Thr Ser Ser Leu Pro Ser Gly Lys Trp Ser Cys Gly Val Cys Arg Arg				
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Lys Val Asp Asn Asn Cys Gly Ala Tyr Thr Cys Asn Lys Cys Ser His				
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Tyr Phe Val His Thr Arg Cys Ala Leu Arg Asn Asp Val Trp Asp Gly				
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Arg Asp Leu Glu Gly Val Pro Glu Glu Pro Glu Ile Ile Leu Glu Leu				
ttt gag acg ata gct gat gga ata ata ctc cat ttt tct cat gac cat				1056
Phe Glu Thr Ile Ala Asp Gly Ile Ile Leu His Phe Ser His Asp His				
cat caa ggc cat ttt tct gat gga aca att gtg cat cct tta ttc cta				1104
His Gln Gly His Phe Ser Asp Gly Thr Ile Val His Pro Leu Phe Leu				
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Val Ile Cys Phe Lys	Cys Ala Thr Leu Pro Tyr Glu Ala Lys Tyr Lys		
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His Asp Thr His Leu Leu	Thr Phe Trp Glu Gly Lys Glu Glu Ser Asp		
420	425	430	
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Glu Asp Gly Phe Tyr Ala	Cys Asp Asp Cys Cys Thr Thr Leu His Val		
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His Cys Leu Leu Gly Glu	Asp Met Tyr Met Leu Lys Pro Ser Gln Thr		
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Ile Thr Tyr Ile Lys Arg	Glu Val His Ile Leu Pro Asn Asn Thr Arg		
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<400> 1370

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Phe	Gln	Gln	Pro	Leu	Phe	Leu	Cys	Pro	Ser	Leu	Arg	Leu	Lys	Ala	Asp
	50					55					60				
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Leu	Phe	Pro	Ser	Ile	Ser	Ser	Ala	Asp	Gln	Gln	Val	Gln	His	Leu	Leu
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Arg	Ala	Cys	Asp	Thr	Phe	Lys	Ile	Asp	Thr	Asp	Tyr	Tyr	Ile	Cys	Leu
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Asp	Leu	Ala	Leu	Phe	Ser	Leu	Phe	Tyr	His	Cys	Pro	Thr	Tyr	Glu	Leu
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 Tyr Phe Val His Thr Arg Cys Ala Leu Arg Asn Asp Val Trp Asp Gly
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 Arg Asp Leu Glu Gly Val Pro Glu Glu Pro Glu Ile Ile Leu Glu Leu
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 Phe Glu Thr Ile Ala Asp Gly Ile Ile Leu His Phe Ser His Asp His
 340 345 350
 His Gln Gly His Phe Ser Asp Gly Thr Ile Val His Pro Leu Phe Leu
 355 360 365
 Ala Leu Asp Pro Asp Gln Glu Leu Glu Ala Thr Cys Gln Ile Cys Gln
 370 375 380
 Gln Lys Ala Thr Phe Leu Gln Lys Leu Asn Cys Ile Glu Cys Asp Tyr
 385 390 395 400
 Val Ile Cys Phe Lys Cys Ala Thr Leu Pro Tyr Glu Ala Lys Tyr Lys
 405 410 415
 His Asp Thr His Leu Leu Thr Phe Trp Glu Gly Lys Glu Glu Ser Asp
 420 425 430
 Gln Tyr Gly Trp Cys Glu Val Cys Glu Asn Gln Ile Val Tyr Ser Arg
 435 440 445
 Glu Asp Gly Phe Tyr Ala Cys Asp Asp Cys Cys Thr Thr Leu His Val
 450 455 460
 His Cys Leu Leu Gly Glu Asp Met Tyr Met Leu Lys Pro Ser Gln Thr
 465 470 475 480
 Ile Thr Tyr Ile Lys Arg Glu Val His Ile Leu Pro Asn Asn Thr Arg
 485 490 495
 Ser Arg Pro Leu Cys His Tyr His Val Asp Asn Arg Cys Pro Gln Lys
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<211> 1956

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<220>

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<400> 1371

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Ser Gly Glu Ala Ala Val Asp Ser Asp Gly Gly Asp Gly Leu Ser Leu	
35 40 45	
gag cct cgg atc ctc tgt cct act ttc cgt ctc aaa gtt aaa aag ttg	192
Glu Pro Arg Ile Leu Cys Pro Thr Phe Arg Leu Lys Val Lys Lys Leu	
50 55 60	
aaa cca tac acg aga gat tca gat cgt agc ttt ttc ccg ttg gtt gtt	240
Lys Pro Tyr Thr Arg Asp Ser Asp Arg Ser Phe Phe Pro Leu Val Val	
65 70 75 80	
tcc cct cac ttc ccc acc ata caa agt ggt cat gaa caa ccc gag tat	288
Ser Pro His Phe Thr Ile Gln Ser Gly His Glu Gln Pro Glu Tyr	
85 90 95	
atg ctt cat tcc gac agc tgt aag cta cct tta ctc cct ctc ttt tgg	336
Met Leu His Ser Asp Ser Cys Lys Leu Pro Leu Leu Pro Leu Phe Trp	
100 105 110	

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Thr	Thr	Leu	Glu	Pro	Ala	Thr	Ser	Tyr	Tyr	Val	Cys	Val	Thr	Cys	Gly		
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gac	cag	ttc	cac	aaa	gaa	tgt	att	ggg	tct	cca	ctt	gag	ttc	aaa	cac	480	
Asp	Gln	Phe	His	Lys	Glu	Cys	Ile	Gly	Ser	Pro	Leu	Glu	Phe	Lys	His		
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cct	tca	tat	ccg	tct	ctt	tct	ctc	caa	ctt	tac	agt	cct	ccg	tcc	gac	528	
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Tyr	Ser	Pro	Thr	Asn	Asn	Phe	Thr	Leu	His	Leu	Phe	Cys	Ala	Phe	Lys		
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Pro	Ile	Pro	Phe	Val	Ile	Asp	His	Pro	Lys	Arg	His	Pro	His	Pro	Leu		
		210				215					220						
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Thr	Ile	Phe	Pro	Lys	Gln	Ser	Phe	Leu	Pro	Cys	His	Val	Cys	Ser	Leu		
225					230					235					240		
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Val	His	Gln	Asp	Cys	Ile	Tyr	Phe	Pro	Tyr	Val	Ile	Lys	Ile	Ser	Arg		
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cac	cac	cac	cgt	ata	tct	tat	acc	tcc	tct	ctt	cca	tct	gga	aaa	tgg	864	
His	His	His	Arg	Ile	Ser	Tyr	Thr	Ser	Ser	Leu	Pro	Ser	Gly	Lys	Trp		
			275				280					285					
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Ser	Cys	Gly	Val	Cys	Arg	Gln	Met	Val	Asp	Asn	Asp	Tyr	Gly	Ala	Tyr		
		290				295					300						
tct	tgc	aac	aag	tgt	gat	gac	tat	ttt	gtt	cat	tca	aga	tgc	gcg	ctg	960	
Ser	Cys	Asn	Lys	Cys	Asp	Asp	Tyr	Phe	Val	His	Ser	Arg	Cys	Ala	Leu		
305					310					315					320		
cgg	aga	gac	tta	tgg	gat	ggg	ata	gaa	ctc	gga	gta	cct	gaa	gaa	gaa	1008	
Arg	Arg	Asp	Leu	Trp	Asp	Gly	Ile	Glu	Leu	Glu	Gly	Val	Pro	Glu	Glu		
				325					330					335			
cct	gag	ata	gtt	gtt	gag	cca	ttt	atc	acg	att	tct	gat	ggg	ata	ata	1056	
Pro	Glu	Ile	Val	Val	Glu	Pro	Phe	Ile	Thr	Ile	Ser	Asp	Gly	Ile	Ile		
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ctc	cat	ttt	tct	cat	ggc	cat	cat	ctg	aaa	ctc	aag	atc	agt	aga	gtc	1104	
Leu	His	Phe	Ser	His	Gly	His	His	Leu	Lys	Leu	Lys	Ile	Ser	Arg	Val		
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tac	gac	gaa	aaa	atg	gtt	tgt	caa	gcg	tgc	atc	ctt	ccg	atc	tac	gag	1152	
Tyr	Asp	Glu	Lys	Met	Val	Cys	Gln	Ala	Cys	Ile	Leu	Pro	Ile	Tyr	Glu		
		370				375						380					
ggg	ggc	tat	tat	tca	tgt	atg	gat	gaa	tgt	gac	ttc	atc	ctc	cac	gaa	1200	
Gly	Gly	Tyr	Tyr	Ser	Cys	Met	Asp	Glu	Cys	Asp	Phe	Ile	Leu	His	Glu		
385					390					395					400		
aca	tgt	gca	aat	gca	cct	tgc	aag	aaa	cat	cat	gct	ttg	cat	cct	cac	1248	
Thr	Cys	Ala	Asn	Ala	Pro	Cys	Lys	Lys	His	His	Ala	Leu	His	Pro	His		
				405					410					415			
cca	ctt	acg	cta	acg	gtc	gtc	act	agt	gaa	tat	gaa	gac	aac	ata	gga	1296	
Pro	Leu	Thr	Leu	Thr	Val	Val	Thr	Ser	Glu	Tyr	Glu	Asp	Asn	Ile	Gly		
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cgt	ttt	tgt	tgt	aag	gct	tgt	cag	cgt	gaa	agt	tgt	ggg	ttc	gtc	tat	1344	
Arg	Phe	Cys	Cys	Lys	Ala	Cys	Gln	Arg	Glu	Ser	Cys	Gly	Phe	Val	Tyr		
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gag	gat	ctc	aga	gga	aag	att	ggg	aat	tat	aga	aga	aat	aaa	ttc	caa	1392	
Glu	Asp	Leu	Arg	Gly	Lys	Ile	Gly	Asn	Tyr	Arg	Arg	Asn	Lys	Phe	Gln		
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cta	gat	tta	cga	tgt	gcc	tca	gtt	tct	gaa	cca	ttt	gaa	tat	cta	ggc	1440	
Leu	Asp	Leu	Arg	Cys	Ala	Ser	Val	Ser	Glu	Pro	Phe	Glu	Tyr	Leu	Gly		
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PF59082SeqList_PF59082.txt

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			485						490					495		
gca	ata	tgt	caa	atc	tgc	cac	gaa	agg	gaa	gat	gag	tct	tct	cat	tgc	1536
Ala	Ile	Cys	Gln	Ile	Cys	His	Glu	Arg	Glu	Asp	Glu	Ser	Ser	His	Cys	
			500						505					510		
aga	aaa	cta	aat	tgc	att	gaa	tgt	gat	ttt	gtg	ata	tgc	ttc	agg	tgt	1584
Arg	Lys	Leu	Asn	Cys	Ile	Glu	Cys	Asp	Phe	Val	Ile	Cys	Phe	Arg	Cys	
			515						520					525		
gct	acc	tta	cca	tat	aag	gca	agg	tat	caa	cat	gac	aag	cat	ttc	ctc	1632
Ala	Thr	Leu	Pro	Tyr	Lys	Ala	Arg	Tyr	Gln	His	Asp	Lys	His	Phe	Leu	
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PF59082SeqList_PF59082.txt

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Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
465					470					475					480
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	His	Xaa	Xaa	Cys	Xaa
				485				490						495	
Xaa	Gly	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			500					505					510		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			515				520					525			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asn	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
	530					535					540				

PF59082SeqList_PF59082.txt

Xaa 545	Xaa	Xaa	Xaa	Xaa	Xaa 550	Xaa	Xaa	Xaa	Xaa	Xaa 555		Xaa	Xaa	Xaa	Xaa	Xaa 560
Xaa	Xaa	Xaa	Xaa	Xaa 565	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Arg	Xaa	Xaa	Cys 575	Xaa	Xaa
Xaa	Xaa	Xaa	Xaa 580	Xaa	Xaa	Xaa	Cys									

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<223> protein pattern

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<220>
<221> variant
<222> (5)..(6)
<223> Xaa in position 5 to 6 is any amino acid
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<220>
<221> Variant
<222> (13)..(13)
<223> Xaa in position 13 is Ile, Leu or Val
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<220>
<221> Variant
<222> (15)..(15)
<223> Xaa in position 15 is Asp or Asn
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<220>
<221> variant
<222> (17)..(17)
<223> Xaa in position 17 is any amino acid
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<220>
<221> Variant
<222> (18)..(18)
<223> Xaa in position 18 is Asp or Glu
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<400> 1382
Tyr Xaa Xaa His Xaa Xaa Cys Ala Xaa Xaa Xaa Xaa Trp Xaa Gly
1 5 10 15
Xaa Xaa Leu

<220>
<223> protein pattern

<220>
<221> Variant
<222> (2)..(4)

<223> Xaa in position 2 to 4 is any amino acid

<220>

<221> Variant

<222> (5)..(5)

<223> Xaa in position 5 is Ala, Pro or Thr

<220>

<221> Variant

<222> (6)..(7)

<223> Xaa in position 6 to 7 is any amino acid

<220>

<221> Variant

<222> (9)..(9)

<223> Xaa in position 9 is any amino acid

<220>

<221> Variant

<222> (10)..(10)

<223> Xaa in position 10 is Ile, Met or Val

<220>

<221> Variant

<222> (11)..(11)

<223> Xaa in position 11 is any amino acid

<220>

<221> Variant

<222> (14)..(14)

<223> Xaa in position 14 is any amino acid

<220>

<221> Variant

<222> (17)..(17)

<223> Xaa in position 17 is Ile, Leu or Val

<400> 1383

Cys Xaa Xaa Xaa Xaa Xaa Ile Xaa Xaa Xaa Arg His Xaa His Arg
 1 5 10 15
 Xaa

<210> 1384

<211> 17

<212> PRT

<213> Artificial sequence

<220>

<223> protein pattern

<220>

<221> Variant

<222> (2)..(2)

<223> Xaa in position 2 is Asp, Glu or Gly

<220>

<221> Variant

<222> (3)..(3)

<223> Xaa in position 3 is Ile or Val

<220>

<221> Variant

<222> (5)..(5)

<223> Xaa in position 5 is Glu or Arg

<220>

<221> Variant

PF59082SeqList_PF59082.txt

<222> (6)..(8)
 <223> Xaa in position 6 to 8 is any amino acid
 <220>
 <221> Variant
 <222> (9)..(9)
 <223> Xaa in position 9 is Asp or Asn
 <220>
 <221> Variant
 <222> (10)..(14)
 <223> Xaa in position 10 to 14 is any amino acid
 <220>
 <221> Variant
 <222> (16)..(16)
 <223> Xaa in position 16 is any amino acid
 <220>
 <221> Variant
 <222> (17)..(17)
 <223> Xaa in position 17 is Cys, Gly or Ser
 <400> 1384
 Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa
 1 5 10 15
 Xaa

<210> 1385
 <211> 705
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (1)..(705)

<400> 1385
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 cgc ggt cac aaa tgc gaa gcc aaa gac gaa atc atc tgc tcc ggt tgt 96
 Arg Gly His Lys Cys Glu Ala Lys Asp Glu Ile Ile Cys Ser Gly Cys
 20 25 30
 gat ctc gat ctg gtt ggt gca gct ttc aaa tgc aca aag tca tca gat 144
 Asp Leu Asp Leu Val Gly Ala Ala Phe Lys Cys Thr Lys Ser Ser Asp
 35 40 45
 tgt gat tac ttc ttg cac aag tca tgt ttt gaa ctt cca cgt gaa acc 192
 Cys Asp Tyr Phe Leu His Lys Ser Cys Phe Glu Leu Pro Arg Glu Thr
 50 55 60
 aac cac aaa tct cac caa ccc cac act ttg act tta atc tat tcc cca 240
 Asn His Lys Ser His Gln Pro His Thr Leu Thr Leu Ile Tyr Ser Pro
 65 70 75 80
 aag tca acg tac acg tgt aat gct tgc ggc gaa tac gga tca agt ttc 288
 Lys Ser Thr Tyr Thr Cys Asn Ala Cys Gly Glu Tyr Gly Ser Ser Phe
 85 90 95
 acg tac aac tgt tca atc tgt cag tac gat gta cat gtc gga tgt gtt 336
 Thr Tyr Asn Cys Ser Ile Cys Gln Tyr Asp Val His Val Gly Cys Val
 100 105 110
 tca atg cct gaa aca gtg aag cgt gaa gat cac cca cat cca ctt act 384
 Ser Met Pro Glu Thr Val Lys Arg Glu Asp His Pro His Pro Leu Thr
 115 120 125
 ctt ctt tac ggt tct cct tat aac caa ccc ggt tta gtt tcc aaa tgc 432
 Leu Leu Tyr Gly Ser Pro Tyr Asn Gln Pro Gly Leu Val Ser Lys Cys
 130 135 140
 gat gtt tgt gaa gac att gta ccg gat aat ctc tgg tcg tat tat tgc 480
 Asp Val Cys Glu Asp Ile Val Pro Asp Asn Leu Trp Ser Tyr Tyr Cys
 145 150 155 160

PF59082SeqList_PF59082.txt

aag gaa tgt gat tac gct acg cat tta cac tca tgt aag aaa gag gaa	528
Lys Glu Cys Asp Tyr Ala Thr His Leu His Ser Cys Lys Lys Glu Glu	
165 170 175	
gag gca aag aaa gaa gat caa aaa gga gaa gga agt aaa aac tcg atg	576
Glu Ala Lys Lys Glu Asp Gln Lys Gly Glu Gly Ser Lys Asn Ser Met	
180 185 190	
aat tcg gag tta gct gca atg tta gag gct caa aga gaa gtg gag agg	624
Asn Ser Glu Leu Ala Ala Met Leu Glu Ala Gln Arg Glu Val Glu Arg	
195 200 205	
atg cag att gag atg cat ttg gcg atg caa agt gct ttg att tcg aaa	672
Met Gln Ile Glu Met His Leu Ala Met Gln Ser Ala Leu Ile Ser Lys	
210 215 220	
aag gcg aat aag gca gct ctc aat tgc atc taa	705
Lys Ala Asn Lys Ala Ala Leu Asn Cys Ile	
225 230	

<210> 1386
 <211> 234
 <212> PRT
 <213> Arabidopsis thaliana

<400> 1386

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20 25 30	
Asp Leu Asp Leu Val Gly Ala Ala Phe Lys Cys Thr Lys Ser Ser Asp	
35 40 45	
Cys Asp Tyr Phe Leu His Lys Ser Cys Phe Glu Leu Pro Arg Glu Thr	
50 55 60	
Asn His Lys Ser His Gln Pro His Thr Leu Thr Ile Tyr Ser Pro	
65 70 75 80	
Lys Ser Thr Tyr Thr Cys Asn Ala Cys Gly Glu Tyr Gly Ser Ser Phe	
85 90 95	
Thr Tyr Asn Cys Ser Ile Cys Gln Tyr Asp Val His Val Gly Cys Val	
100 105 110	
Ser Met Pro Glu Thr Val Lys Arg Glu Asp His Pro His Pro Leu Thr	
115 120 125	
Leu Leu Tyr Gly Ser Pro Tyr Asn Gln Pro Gly Leu Val Ser Lys Cys	
130 135 140	
Asp Val Cys Glu Asp Ile Val Pro Asp Asn Leu Trp Ser Tyr Tyr Cys	
145 150 155 160	
Lys Glu Cys Asp Tyr Ala Thr His Leu His Ser Cys Lys Lys Glu Glu	
165 170 175	
Glu Ala Lys Lys Glu Asp Gln Lys Gly Glu Gly Ser Lys Asn Ser Met	
180 185 190	
Asn Ser Glu Leu Ala Ala Met Leu Glu Ala Gln Arg Glu Val Glu Arg	
195 200 205	
Met Gln Ile Glu Met His Leu Ala Met Gln Ser Ala Leu Ile Ser Lys	
210 215 220	
Lys Ala Asn Lys Ala Ala Leu Asn Cys Ile	
225 230	

<210> 1387
 <211> 729
 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (1)..(729)

<400> 1387

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ttg cgt agt cac aaa gct caa gct gag gaa gag atc atc tgc tca ggc	96
Leu Arg Ser His Lys Ala Gln Ala Glu Glu Glu Ile Ile Cys Ser Gly	
20 25 30	

PF59082SeqList_PF59082.txt

tgt agc cta gac ctg ata ggc gca gct ttc aaa tgc aca aag tcc gaa	144
Cys Ser Leu Asp Leu Ile Gly Ala Ala Phe Lys Cys Thr Lys Ser Glu	
35 40 45	
tgc gat tac tta ttg cac aag tca tgt ttc gac ctt cca cgc gag aac	192
Cys Asp Tyr Leu Leu His Lys Ser Cys Phe Asp Leu Pro Arg Glu Asn	
50 55 60	
agt cac aag tct cac cag gaa cac cct ttg acc ctt ctg tac tct cca	240
Ser His Lys Ser His Gln Glu His Pro Leu Thr Leu Leu Tyr Ser Pro	
65 70 75 80	
acg tac gag tct tca gct ttc gcg tgc gac gca tgc ggt gag tat gga	288
Thr Tyr Glu Ser Ser Ala Phe Ala Cys Asp Ala Cys Gly Glu Tyr Gly	
85 90 95	
tcc ggg ttt tct tac aac tgt tct atc tgt aag tac gat gtg cat gtc	336
Ser Gly Phe Ser Tyr Asn Cys Ser Ile Cys Lys Tyr Asp Val His Val	
100 105 110	
gga tgt gtg tct atg ccc gag acc gtg gag cgt gaa gga cac gcg cat	384
Gly Cys Val Ser Met Pro Glu Thr Val Glu Arg Glu Gly His Ala His	
115 120 125	
ccg ctc acg ttg ctc tac cgt act cct tac cag aac ggt ctg atc ttt	432
Pro Leu Thr Leu Leu Tyr Arg Thr Pro Tyr Gln Asn Gly Leu Ile Phe	
130 135 140	
aac tgt gat gaa tgt cat gac act gtt ccg gat aat ctc tgg tct tat	480
Asn Cys Asp Glu Cys His Asp Thr Val Pro Asp Asn Leu Trp Ser Tyr	
145 150 155 160	
tac tgc aag aaa tgt gac tat ggg acg cat cta cac tct tgt gcg gtc	528
Tyr Cys Lys Lys Cys Asp Tyr Gly Thr His Leu His Ser Cys Ala Val	
165 170 175	
gag gaa gag cca aag aga gga gga gga gga agt ggg aat act agt agg	576
Glu Glu Glu Pro Lys Arg Gly Gly Gly Gly Ser Gly Asn Thr Ser Arg	
180 185 190	
aac aat ggt gga agg agc tct gcc gct tcg gac tta gct gca atg ctg	624
Asn Asn Gly Gly Arg Ser Ser Ala Ala Ser Asp Leu Ala Ala Met Leu	
195 200 205	
aaa gct caa agg gaa atg gag agg atg cag att gag tta cat atg gag	672
Lys Ala Gln Arg Glu Met Glu Arg Met Gln Ile Glu Leu His Met Glu	
210 215 220	
atg cag aga gct aag att gcg aag aaa gcg aga aag cat atg ctc aaa	720
Met Gln Arg Ala Lys Ile Ala Lys Lys Ala Arg Lys His Met Leu Lys	
225 230 235 240	
atg att taa	729
Met Ile	

<210> 1388
 <211> 242
 <212> PRT
 <213> Brassica napus

<400> 1388
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 Leu Arg Ser His Lys Ala Gln Ala Glu Glu Ile Ile Cys Ser Gly
 20 25 30
 Cys Ser Leu Asp Leu Ile Gly Ala Ala Phe Lys Cys Thr Lys Ser Glu
 35 40 45
 Cys Asp Tyr Leu Leu His Lys Ser Cys Phe Asp Leu Pro Arg Glu Asn
 50 55 60
 Ser His Lys Ser His Gln Glu His Pro Leu Thr Leu Leu Tyr Ser Pro
 65 70 75 80
 Thr Tyr Glu Ser Ser Ala Phe Ala Cys Asp Ala Cys Gly Glu Tyr Gly
 85 90 95
 Ser Gly Phe Ser Tyr Asn Cys Ser Ile Cys Lys Tyr Asp Val His Val
 100 105 110
 Gly Cys Val Ser Met Pro Glu Thr Val Glu Arg Glu Gly His Ala His
 115 120 125
 Pro Leu Thr Leu Leu Tyr Arg Thr Pro Tyr Gln Asn Gly Leu Ile Phe
 130 135 140
 Asn Cys Asp Glu Cys His Asp Thr Val Pro Asp Asn Leu Trp Ser Tyr
 145 150 155 160

PF59082SeqList_PF59082.txt

Tyr Cys Lys Lys Cys Asp Tyr Gly Thr His Leu His Ser Cys Ala Val
 165 170 175
 Glu Glu Glu Pro Lys Arg Gly Gly Gly Gly Ser Gly Asn Thr Ser Arg
 180 185 190
 Asn Asn Gly Gly Arg Ser Ser Ala Ala Ser Asp Leu Ala Met Leu
 195 200 205
 Lys Ala Gln Arg Glu Met Glu Arg Met Gln Ile Glu Leu His Met Glu
 210 215 220
 Met Gln Arg Ala Lys Ile Ala Lys Lys Ala Arg Lys His Met Leu Lys
 225 230 235 240
 Met Ile

<210> 1389
 <211> 729
 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (1)..(729)

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 1 5 10 15
 ttg cgt agt cac aaa gct caa gct gag gaa gag atc atc tgc tca ggc 96
 Leu Arg Ser His Lys Ala Gln Ala Glu Glu Glu Ile Ile Cys Ser Gly
 20 25 30
 tgt agc cta gac ctg ata ggc gca gct ttc aaa tgc acg aag tct gaa 144
 Cys Ser Leu Asp Leu Ile Gly Ala Ala Phe Lys Cys Thr Lys Ser Glu
 35 40 45
 tgc gat tac ttc ttg cac aag tca tgt ttc gag ctt cca cgc gag aac 192
 Cys Asp Tyr Phe Leu His Lys Ser Cys Phe Glu Leu Pro Arg Glu Asn
 50 55 60
 cgt cac aag tct cac ccg gaa cac cct ttg acc ctt ctg tac tct cca 240
 Arg His Lys Ser His Pro Glu His Pro Leu Thr Leu Leu Tyr Ser Pro
 65 70 75 80
 acg tac gag tct tca gct ttc gcg tgc gac gca tgc ggt gag tat gga 288
 Thr Tyr Glu Ser Ser Ala Phe Ala Cys Asp Ala Cys Gly Glu Tyr Gly
 85 90 95
 tcc ggg ttt tct tac aac tgt tct atc tgt aag tac gat gtg cat gtc 336
 Ser Gly Phe Ser Tyr Asn Cys Ser Ile Cys Lys Tyr Asp Val His Val
 100 105 110
 gga tgt gtg tct atg ccc gag acc gtg gag cgt gaa gga cac gcg cat 384
 Gly Cys Val Ser Met Pro Glu Thr Val Glu Arg Glu Gly His Ala His
 115 120 125
 ccg ctc acg ttg ctc tac cgt act cct tac cag aac ggt ctg atc ttt 432
 Pro Leu Thr Leu Leu Tyr Arg Thr Pro Tyr Gln Asn Gly Leu Ile Phe
 130 135 140
 aac tgt gat gaa tgt cat gac act gtt ccg gat aat ctc tgg tct tat 480
 Asn Cys Asp Glu Cys His Asp Thr Val Pro Asp Asn Leu Trp Ser Tyr
 145 150 155 160
 tac tgc aag aaa tgt gac tat ggg acg cat cta cac tct tgt gcg gtc 528
 Tyr Cys Lys Lys Cys Asp Tyr Gly Thr His Leu His Ser Cys Ala Val
 165 170 175
 gag gaa gag cca aag aga gga gga gga gga agt ggg aat act agt agg 576
 Glu Glu Glu Pro Lys Arg Gly Gly Gly Gly Ser Gly Asn Thr Ser Arg
 180 185 190
 aac aat ggt gga agg agc tct gcc gct tcg gac tta tct gca atg ttg 624
 Asn Asn Gly Gly Arg Ser Ser Ala Ala Ser Asp Leu Ser Ala Met Leu
 195 200 205
 aaa gct caa agg gaa atg gag agg atg cag att gag tta gat atg gcg 672
 Lys Ala Gln Arg Glu Met Glu Arg Met Gln Ile Glu Leu Asp Met Ala
 210 215 220
 atg cag agt gct aag att gcg aag aaa tcg aga aag cat atg ctc aaa 720
 Met Gln Ser Ala Lys Ile Ala Lys Lys Ser Arg Lys His Met Leu Lys
 225 230 235 240
 atg att taa 729

PF59082SeqList_PF59082.txt

Met Ile

<210> 1390
<211> 242
<212> PRT
<213> Brassica napus

<400> 1390
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20 25 30
Cys Ser Leu Asp Leu Ile Gly Ala Ala Phe Lys Cys Thr Lys Ser Glu
35 40 45
Cys Asp Tyr Phe Leu His Lys Ser Cys Phe Glu Leu Pro Arg Glu Asn
50 55 60
Arg His Lys Ser His Pro Glu His Pro Leu Thr Leu Leu Tyr Ser Pro
65 70 75 80
Thr Tyr Glu Ser Ser Ala Phe Ala Cys Asp Ala Cys Gly Glu Tyr Gly
85 90 95
Ser Gly Phe Ser Tyr Asn Cys Ser Ile Cys Lys Tyr Asp Val His Val
100 105 110
Gly Cys Val Ser Met Pro Glu Thr Val Glu Arg Glu Gly His Ala His
115 120 125
Pro Leu Thr Leu Leu Tyr Arg Thr Pro Tyr Gln Asn Gly Leu Ile Phe
130 135 140
Asn Cys Asp Glu Cys His Asp Thr Val Pro Asp Asn Leu Trp Ser Tyr
145 150 155 160
Tyr Cys Lys Lys Cys Asp Tyr Gly Thr His Leu His Ser Cys Ala Val
165 170 175
Glu Glu Glu Pro Lys Arg Gly Gly Gly Gly Ser Gly Asn Thr Ser Arg
180 185 190
Asn Asn Gly Gly Arg Ser Ser Ala Ala Ser Asp Leu Ser Ala Met Leu
195 200 205
Lys Ala Gln Arg Glu Met Glu Arg Met Gln Ile Glu Leu Asp Met Ala
210 215 220
Met Gln Ser Ala Lys Ile Ala Lys Lys Ser Arg Lys His Met Leu Lys
225 230 235 240
Met Ile

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<211> 747
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)..(747)

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1 5 10 15
cgc ggt cac aaa gcc caa gtt gaa gat gag atc atc tgc tct ggt tgc 96
Arg Gly His Lys Ala Gln Val Glu Asp Glu Ile Ile Cys Ser Gly Cys
20 25 30
gac cta gac cta ctc ggt gca tat ttc aag tgc aca aag tca gag tgt 144
Asp Leu Asp Leu Leu Gly Ala Tyr Phe Lys Cys Thr Lys Ser Glu Cys
35 40 45
gat tac ttc ttg cac aag tca tgt ttc gat ctc cca cgt gag atc cgt 192
Asp Tyr Phe Leu His Lys Ser Cys Phe Asp Leu Pro Arg Glu Ile Arg
50 55 60
cac aag tct cac cct gat cac cct ttg atc ctc ctc tat tcc cca cag 240
His Lys Ser His Pro Asp His Pro Leu Ile Leu Leu Tyr Ser Pro Gln
65 70 75 80
aat aat aat tca acg tat act tgt gac gca tgc ggt gag tat gga tcg 288
Asn Asn Asn Ser Thr Tyr Thr Cys Asp Ala Cys Gly Glu Tyr Gly Ser
seite 1847

PF59082SeqList_PF59082.txt

85	90	95	
ggg ttc act tac aat tgt tct atc tgc cag tac gat gtt cat gtt gga			336
Gly Phe Thr Tyr Asn Cys Ser Ile Cys Gln Tyr Asp Val His Val Gly			
100	105	110	
tgt gtg tct gtg cct gag acc atg aag cat gat gag cac gtt cac ccg			384
Cys Val Ser Val Pro Glu Thr Met Lys His Asp Glu His Val His Pro			
115	120	125	
ctc gct ttg atc tac aag gct cca tgc cca aag gat cat ata ttt acc			432
Leu Ala Leu Ile Tyr Lys Ala Pro Cys Pro Lys Asp His Ile Phe Thr			
130	135	140	
tgc gat gtt tgc gat gaa act atg ccg cat aat ctg tgg ttg tac tac			480
Cys Asp Val Cys Asp Glu Thr Met Pro His Asn Leu Trp Leu Tyr Tyr			
145	150	155	
tgc cag aaa tgt gac tac ggt gct cat tta cat tca tgc gtt gct gaa			528
Cys Gln Lys Cys Asp Tyr Gly Ala His Leu His Ser Cys Val Ala Glu			
165	170	175	
gaa gag gaa aag tca aag aaa gga gga aga gga aga gga gga gaa gga			576
Glu Glu Glu Lys Ser Lys Lys Gly Gly Arg Gly Arg Gly Gly Glu Gly			
180	185	190	
gga agt ggt gga aat gga gtg aac aga gga agg agc tcc gcg aat tca			624
Gly Ser Gly Gly Asn Gly Val Asn Arg Gly Arg Ser Ser Ala Asn Ser			
195	200	205	
gag cta gct gca atg tta aag gca caa aga gag atg gag cag atg caa			672
Glu Leu Ala Ala Met Leu Lys Ala Gln Arg Glu Met Glu Gln Met Gln			
210	215	220	
att gct ctt cac ttg gag atg caa aga gct aag att gat aag aaa tca			720
Ile Ala Leu His Leu Glu Met Gln Arg Ala Lys Ile Asp Lys Lys Ser			
225	230	235	
aga aag cat atg ctt aaa atg atc taa			747
Arg Lys His Met Leu Lys Met Ile			
245			

<210> 1392

<211> 248

<212> PRT

<213> Arabidopsis thaliana

<400> 1392

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Asp Leu Asp Leu Leu Gly Ala Tyr Phe Lys Cys Thr Lys Ser Glu Cys	
35 40 45	
Asp Tyr Phe Leu His Lys Ser Cys Phe Asp Leu Pro Arg Glu Ile Arg	
50 55 60	
His Lys Ser His Pro Asp His Pro Leu Ile Leu Leu Tyr Ser Pro Gln	
65 70 75 80	
Asn Asn Asn Ser Thr Tyr Thr Cys Asp Ala Cys Gly Glu Tyr Gly Ser	
85 90 95	
Gly Phe Thr Tyr Asn Cys Ser Ile Cys Gln Tyr Asp Val His Val Gly	
100 105 110	
Cys Val Ser Val Pro Glu Thr Met Lys His Asp Glu His Val His Pro	
115 120 125	
Leu Ala Leu Ile Tyr Lys Ala Pro Cys Pro Lys Asp His Ile Phe Thr	
130 135 140	
Cys Asp Val Cys Asp Glu Thr Met Pro His Asn Leu Trp Leu Tyr Tyr	
145 150 155 160	
Cys Gln Lys Cys Asp Tyr Gly Ala His Leu His Ser Cys Val Ala Glu	
165 170 175	
Glu Glu Glu Lys Ser Lys Lys Gly Gly Arg Gly Arg Gly Gly Glu Gly	
180 185 190	
Gly Ser Gly Gly Asn Gly Val Asn Arg Gly Arg Ser Ser Ala Asn Ser	
195 200 205	
Glu Leu Ala Ala Met Leu Lys Ala Gln Arg Glu Met Glu Gln Met Gln	
210 215 220	
Ile Ala Leu His Leu Glu Met Gln Arg Ala Lys Ile Asp Lys Lys Ser	
225 230 235 240	
Arg Lys His Met Leu Lys Met Ile	

<210> 1393
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 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (1)..(747)

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  1      5      10      15
aat cat ccg ttg cgg gtc ttc aac tcc aaa gaa gaa gat gag atc att      96
Asn His Pro Leu Arg Val Phe Asn Ser Lys Glu Glu Asp Glu Ile Ile
      20      25      30
tgc tcc gga tgc gaa cat gat cta att ggg caa gct ttc aag tgt aca      144
Cys Ser Gly Cys Glu His Asp Leu Ile Gly Gln Ala Phe Lys Cys Thr
      35      40      45
aag tca gag tgc gat tac ttc ttg cac aag tca tgt ttc gac ctt ccc      192
Lys Ser Glu Cys Asp Tyr Phe Leu His Lys Ser Cys Phe Asp Leu Pro
      50      55      60
ggg gag atc cat cac aag tct cac aca aat cac cct ttg acc ttg ctc      240
Gly Glu Ile His His Lys Ser His Thr Asn His Pro Leu Thr Leu Leu
      65      70      75
cat tct cca ccg aat ggc cta tcc act tac acg tgc gat gcg tgc ggt      288
His Ser Pro Pro Asn Gly Leu Ser Thr Tyr Thr Cys Asp Ala Cys Gly
      85      90      95
gag tat gga tct gct ttc act tac cat tgc tca gag tgc aaa tac cat      336
Glu Tyr Gly Ser Ala Phe Thr Tyr His Cys Ser Glu Cys Lys Tyr His
      100      105      110
gtt cac gtg gga tgt gcg ttt gtc ccc gag aac gtg aag cgt gaa gat      384
Val His Val Gly Cys Ala Phe Val Pro Glu Asn Val Lys Arg Glu Asp
      115      120      125
cac gaa cac cca ctc act cta ctt tac aac aca cca tgc aaa ggt cgt      432
His Glu His Pro Leu Thr Leu Leu Tyr Asn Thr Pro Cys Lys Gly Arg
      130      135      140
aag gac ggt gtg gtg ttc ata tgt gat gtt tgc gaa gta gat gtg tcg      480
Lys Asp Gly Val Val Phe Ile Cys Asp Val Cys Glu Val Asp Val Ser
      145      150      155
gag aat ctt tgg gtg tat tac tgc aaa gaa tgt gac tat ggg aca cat      528
Glu Asn Leu Trp Val Tyr Tyr Cys Lys Glu Cys Asp Tyr Gly Thr His
      160      165      170
gtt cat tca tgc acg aca aat gaa gac aat ggg cca aaa aaa gga gga      576
Val His Ser Cys Thr Thr Asn Glu Asp Asn Gly Pro Lys Lys Gly Gly
      175      180      185
gaa gaa gaa gga gaa tca agc tca tta tcg act tca agg ata aag tca      624
Glu Glu Glu Gly Glu Ser Ser Ser Leu Ser Thr Ser Arg Ile Lys Ser
      190      195      200
tta atg gag gct gaa aaa gag atg aga gag atg gcg ata ata cat caa      672
Leu Met Glu Ala Glu Lys Glu Met Arg Glu Met Ala Ile Ile His Gln
      205      210      215
cta cag tta gat gct ctt gac gca gca ggt agt tat gtc ggt tca tgg      720
Leu Gln Leu Asp Ala Leu Asp Ala Ala Gly Ser Tyr Val Gly Ser Trp
      220      225      230
gaa cca agg aga aaa gat tat tgg taa      747
Glu Pro Arg Arg Lys Asp Tyr Trp
      235      240      245

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<210> 1394
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 <212> PRT
 <213> Arabidopsis thaliana

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<400> 1394
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PF59082SeqList_PF59082.txt

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 20 25 30
 Cys Ser Gly Cys Glu His Asp Leu Ile Gly Gln Ala Phe Lys Cys Thr
 35 40 45
 Lys Ser Glu Cys Asp Tyr Phe Leu His Lys Ser Cys Phe Asp Leu Pro
 50 55 60
 Gly Glu Ile His His Lys Ser His Thr Asn His Pro Leu Thr Leu Leu
 65 70 75 80
 His Ser Pro Pro Asn Gly Leu Ser Thr Tyr Thr Cys Asp Ala Cys Gly
 85 90 95
 Glu Tyr Gly Ser Ala Phe Thr Tyr His Cys Ser Glu Cys Lys Tyr His
 100 105 110
 Val His Val Gly Cys Ala Phe Val Pro Glu Asn Val Lys Arg Glu Asp
 115 120 125
 His Glu His Pro Leu Thr Leu Tyr Asn Thr Pro Cys Lys Gly Arg
 130 135 140
 Lys Asp Gly Val Val Phe Ile Cys Asp Val Cys Glu Val Asp Val Ser
 145 150 155 160
 Glu Asn Leu Trp Val Tyr Tyr Cys Lys Glu Cys Asp Tyr Gly Thr His
 165 170 175
 Val His Ser Cys Thr Thr Asn Glu Asp Asn Gly Pro Lys Lys Gly Gly
 180 185 190
 Glu Glu Glu Gly Glu Ser Ser Ser Leu Ser Thr Ser Arg Ile Lys Ser
 195 200 205
 Leu Met Glu Ala Glu Lys Glu Met Arg Glu Met Ala Ile Ile His Gln
 210 215 220
 Leu Gln Leu Asp Ala Leu Asp Ala Ala Gly Ser Tyr Val Gly Ser Trp
 225 230 235 240
 Glu Pro Arg Arg Lys Asp Tyr Trp
 245

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<211> 753

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<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(753)

<400> 1395

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ttg cgc agt cac aag gcc caa gtt gaa gag atc att tgc tct ggt	96
Leu Arg Ser His Lys Ala Gln Val Glu Glu Glu Ile Ile Cys Ser Gly	
20 25 30	
tgc gac ctc gac ctg ata ggt gca gct ttc aaa tgc aca aag tca gaa	144
Cys Asp Leu Asp Leu Ile Gly Ala Ala Phe Lys Cys Thr Lys Ser Glu	
35 40 45	
tgc gat tac ttc ttg cac aag tca tgt ttt gag ctt cca cgt gag act	192
Cys Asp Tyr Phe Leu His Lys Ser Cys Phe Glu Leu Pro Arg Glu Thr	
50 55 60	
cgt cac aag gct cac ccg gat cac cct ttg ata ctg ctg tat tcc cca	240
Arg His Lys Ala His Pro Asp His Pro Leu Ile Leu Leu Tyr Ser Pro	
65 70 75 80	
cct tac gag tca act tac acg tgt gat gcg tgc ggt gag tat gga tcc	288
Pro Tyr Glu Ser Thr Tyr Thr Cys Asp Ala Cys Gly Glu Tyr Gly Ser	
85 90 95	
gga ttc act tac aac tgc tct atc tgc cag tac gat gtt cat gtt gga	336
Gly Phe Thr Tyr Asn Cys Ser Ile Cys Gln Tyr Asp Val His Val Gly	
100 105 110	
tgt gtg tcc atg cct gag tcc gtg gag cgt gaa gga cac gca cat cca	384
Cys Val Ser Met Pro Glu Ser Val Glu Arg Glu Gly His Ala His Pro	
115 120 125	
ctc aca ttg ctc tac cgt tct cct tac cag aac ggt ttg atc ttt aac	432
Leu Thr Leu Leu Tyr Arg Ser Pro Tyr Gln Asn Gly Leu Ile Phe Asn	
130 135 140	
tgt gat gtt tgc caa gag act gtt cca gat aat ctc tgg tcg tat tat	480

PF59082SeqList_PF59082.txt

Cys 145	Asp	Val	Cys	Gln	Glu 150	Thr	Val	Pro	Asp	Asn 155	Leu	Trp	Ser	Tyr	Tyr 160	
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Cys	Lys	Glu	Cys	Asp 165	Tyr	Gly	Thr	His	Leu 170	His	Ser	Cys	Ala	Val 175	Glu	
gaa	gaa	gaa	gca	gaa	gaa	gag	cca	aaa	aga	gga	gga	gga	agg	ggc	agt	576
Glu	Glu	Glu	Ala 180	Glu	Glu	Glu	Pro 185	Lys	Arg	Gly	Gly	Gly	Gly	Ser	Ala	
aga	gga	aac	aca	aag	agt	ggt	ggg	aat	aaa	gga	gga	agg	ggc	tca	gcg	624
Arg	Gly	Asn 195	Thr	Lys	Ser	Gly	Gly 200	Asn	Lys	Gly	Gly	Arg	Gly	Ser	Ala	
gca	tcg	gag	tta	gct	gca	atg	ttg	gaa	gct	caa	aga	gag	atg	gag	aag	672
Ala	Ser	Glu	Leu	Ala	Ala	Met 215	Leu	Glu	Ala	Gln 220	Arg	Glu	Met	Glu	Lys	
atg	cag	ata	gag	tta	cat	atg	gag	atg	caa	aga	gct	aag	att	gct	aag	720
Met	Gln	Ile	Glu	Leu	His 230	Met	Glu	Met	Gln	Arg 235	Ala	Lys	Ile	Ala	Lys 240	
aaa	gcg	aga	aag	gct	tgt	ctc	aag	ttg	atc	taa						753
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<211> 250

<212> PRT

<213> Arabidopsis thaliana

<400> 1396

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			20					25					30		
Cys	Asp	Leu	Asp	Leu	Ile	Gly	Ala	Ala	Phe	Lys	Cys	Thr	Lys	Ser	Glu
		35				40						45			
Cys	Asp	Tyr	Phe	Leu	His	Lys	Ser	Cys	Phe	Glu	Leu	Pro	Arg	Glu	Thr
	50					55					60				
Arg	His	Lys	Ala	His	Pro	Asp	His	Pro	Leu	Ile	Leu	Tyr	Ser	Pro	
65					70					75				80	
Pro	Tyr	Glu	Ser	Thr	Tyr	Thr	Cys	Asp	Ala	Cys	Gly	Glu	Tyr	Gly	Ser
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Gly	Phe	Thr	Tyr	Asn	Cys	Ser	Ile	Cys	Gln	Tyr	Asp	Val	His	Val	Gly
			100					105					110		
Cys	Val	Ser	Met	Pro	Glu	Ser	Val	Glu	Arg	Glu	Gly	His	Ala	His	Pro
		115					120					125			
Leu	Thr	Leu	Leu	Tyr	Arg	Ser	Pro	Tyr	Gln	Asn	Gly	Leu	Ile	Phe	Asn
	130					135					140				
Cys	Asp	Val	Cys	Gln	Glu	Thr	Val	Pro	Asp	Asn	Leu	Trp	Ser	Tyr	Tyr
145					150					155					160
Cys	Lys	Glu	Cys	Asp 165	Tyr	Gly	Thr	His	Leu 170	His	Ser	Cys	Ala	Val 175	Glu
Glu	Glu	Glu	Ala 180	Glu	Glu	Glu	Glu	Pro 185	Lys	Arg	Gly	Gly	Gly	Ser	Ala
												190			
Arg	Gly	Asn	Thr	Lys	Ser	Gly	Gly	Asn	Lys	Gly	Gly	Arg	Gly	Ser	Ala
		195					200					205			
Ala	Ser	Glu	Leu	Ala	Ala	Met	Leu	Glu	Ala	Gln	Arg	Glu	Met	Glu	Lys
	210					215					220				
Met	Gln	Ile	Glu	Leu	His	Met	Glu	Met	Gln	Arg	Ala	Lys	Ile	Ala	Lys
225					230					235					240
Lys	Ala	Arg	Lys	Ala 245	Cys	Leu	Lys	Leu	Ile 250						

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<211> 744

<212> DNA

<213> Arabidopsis thaliana

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<222> (1)..(744)

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1      5      10      15
cac aac cat ccg ctg cgt gtc ttt aaa gct cga gac gaa gat gag gtc      96
His Asn His Pro Leu Arg Val Phe Lys Ala Arg Asp Glu Asp Glu Val
20      25      30
gtt tgc tct gga tgc gag ctc gag cta acc gga caa gct ttc aag tgt      144
Val Cys Ser Gly Cys Glu Leu Glu Leu Thr Gly Gln Ala Phe Lys Cys
35      40      45
atg aag tca gat tgt gat tac ttc ttg cac aag tca tgt ttc gac cta      192
Met Lys Ser Asp Cys Asp Tyr Phe Leu His Lys Ser Cys Phe Asp Leu
50      55      60
cct cgt gaa acc aat cac aag tct cac cca aac cac tct ttg acc ctg      240
Pro Arg Glu Thr Asn His Lys Ser His Pro Asn His Ser Leu Thr Leu
65      70      75
ctt cat tcc cca ccg tac ggt cag tct tac aca tgc gac gca tgc ggt      288
Leu His Ser Pro Pro Tyr Gly Gln Ser Tyr Thr Cys Asp Ala Cys Gly
85      90      95
gag tac gga tct ggt ttc act tac aat tgt tct gaa tgt caa tat gat      336
Glu Tyr Gly Ser Gly Phe Thr Tyr Asn Cys Ser Glu Cys Gln Tyr Asp
100      105      110
gtt cat gtc gga tgt gct ttt atc cct gag acc gtg gag cgc gaa gat      384
Val His Val Gly Cys Ala Phe Ile Pro Glu Thr Val Glu Arg Glu Asp
115      120      125
cac gaa cac cca ctc acg ctt ctc tac aac aca cca tgc aaa ggt cgt      432
His Glu His Pro Leu Thr Leu Leu Tyr Asn Thr Pro Cys Lys Gly Arg
130      135      140
gag gac ggt gct aag ttc ata tgt gat gtt tgt gaa gaa aaa atg tcg      480
Glu Asp Gly Ala Lys Phe Ile Cys Asp Val Cys Glu Glu Lys Met Ser
145      150      155
gaa aat ctt tgg gtt tat tac tgc aaa gag tgt gat tat ggg acg cat      528
Glu Asn Leu Trp Val Tyr Tyr Cys Lys Glu Cys Asp Tyr Gly Thr His
165      170      175
gtg cat tct tgc gcg gtc tat gaa gat cat gag tca gag aaa aga gga      576
Val His Ser Cys Ala Val Tyr Glu Asp His Glu Ser Glu Lys Arg Gly
180      185      190
gga ggt agg gaa gaa gga gaa gcg agc tct gcg gtt tca agg atg aaa      624
Gly Gly Arg Glu Glu Gly Glu Ala Ser Ser Ala Val Ser Arg Met Lys
195      200      205
tcg ttg atg aag gct caa gat gag atg gcg gcg tta cag ctc gag gca      672
Ser Leu Met Lys Ala Gln Asp Glu Met Ala Ala Leu Gln Leu Glu Ala
210      215      220
cgt att aga aac gac act aat aat gct ata ctc gat tta tgg gat agt      720
Arg Ile Arg Asn Asp Thr Asn Asn Ala Ile Leu Asp Leu Trp Asp Ser
225      230      235      240
cca aag cgg aga tat tat tat tga
Pro Lys Arg Arg Tyr Tyr Tyr
245

<210> 1398
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<212> PRT
<213> Arabidopsis thaliana

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20      25      30
Val Cys Ser Gly Cys Glu Leu Glu Leu Thr Gly Gln Ala Phe Lys Cys
35      40      45
Met Lys Ser Asp Cys Asp Tyr Phe Leu His Lys Ser Cys Phe Asp Leu
50      55      60
Pro Arg Glu Thr Asn His Lys Ser His Pro Asn His Ser Leu Thr Leu
65      70      75
Leu His Ser Pro Pro Tyr Gly Gln Ser Tyr Thr Cys Asp Ala Cys Gly
85      90      95
Glu Tyr Gly Ser Gly Phe Thr Tyr Asn Cys Ser Glu Cys Gln Tyr Asp
200

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PF59082SeqList_PF59082.txt

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      100      105      110
Val His Val Gly Cys Ala Phe Ile Pro Glu Thr Val Glu Arg Glu Asp
      115      120      125
His Glu His Pro Leu Thr Leu Leu Tyr Asn Thr Pro Cys Lys Gly Arg
      130      135      140
Glu Asp Gly Ala Lys Phe Ile Cys Asp Val Cys Glu Glu Lys Met Ser
      145      150      155
Glu Asn Leu Trp Val Tyr Tyr Cys Lys Glu Cys Asp Tyr Gly Thr His
      160      165      170
Val His Ser Cys Ala Val Tyr Glu Asp His Glu Ser Glu Lys Arg Gly
      175      180      185
Gly Gly Arg Glu Glu Gly Glu Ala Ser Ser Ala Val Ser Arg Met Lys
      190      195      200
Ser Leu Met Lys Ala Gln Asp Glu Met Ala Ala Leu Gln Leu Glu Ala
      205      210      215
Arg Ile Arg Asn Asp Thr Asn Asn Ala Ile Leu Asp Leu Trp Asp Ser
      220      225      230
Pro Lys Arg Arg Tyr Tyr Tyr
      235      240
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<212> DNA

<213> Arabidopsis thaliana

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<222> (1)..(630)

<400> 1399

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      1      5      10
cat aac cat ccg ctg cgt gtc ttt aaa gct cga gac gaa gat gag gtc      96
His Asn His Pro Leu Arg Val Phe Lys Ala Arg Asp Glu Asp Glu Val
      15      20      25
gtc tgc tct gga tgt gag ctc gat cta acg gga caa gct ttc aag tgt      144
Val Cys Ser Gly Cys Glu Leu Asp Leu Thr Gly Gln Ala Phe Lys Cys
      30      35      40
ata aat gag act tac acg tgt gat gca tgc ggt gag tac gga tcc gga      192
Ile Asn Glu Thr Tyr Thr Cys Asp Ala Cys Gly Glu Tyr Gly Ser Gly
      45      50      55
ttc act tac aat tgt tct gaa tgt caa tat gat ctt cat gtc gga tgt      240
Phe Thr Tyr Asn Cys Ser Glu Cys Gln Tyr Asp Leu His Val Gly Cys
      60      65      70
gcg ttt atc ccg gag acc gtg gag cgg gaa gat cac gaa cac cca ctc      288
Ala Phe Ile Pro Glu Thr Val Glu Arg Glu Asp His Glu His Pro Leu
      75      80      85
act ctt ctc tac aat aca cca tgc aaa ggc tgt gag gac ggt gcg atg      336
Thr Leu Leu Tyr Asn Thr Pro Cys Lys Gly Cys Glu Asp Gly Ala Met
      90      95      100
ttc ata tgt aat gtt tgt gaa gaa gat atg tcg gag aat cta tgg gtt      384
Phe Ile Cys Asn Val Cys Glu Glu Asp Met Ser Glu Asn Leu Trp Val
      105      110      115
tat tat tgc aaa gaa tgt gat tat ggg acg cat gtg cat tct tgc gcg      432
Tyr Tyr Cys Lys Glu Cys Asp Tyr Gly Thr His Val His Ser Cys Ala
      120      125      130
gtt tat gaa gac gat gag cca aat aat aga gga gga gaa gaa gga gaa      480
Val Tyr Glu Asp Asp Glu Pro Asn Asn Arg Gly Gly Glu Glu Gly Glu
      135      140      145
gcg atg agc tcg gcg gtt tcg agg atg aag tcg ttg atg aag gct gag      528
Ala Met Ser Ser Ala Val Ser Arg Met Lys Ser Leu Met Lys Ala Glu
      150      155      160
gat gag ttg gcg gcg gta cag ctc gag gca cgt atg aag cga gac gct      576
Asp Glu Leu Ala Ala Val Gln Leu Glu Ala Arg Met Lys Arg Asp Ala
      165      170      175
aat aat gct ata ctc ggt tta tat gct gaa cca aag cgg aga tat tat      624
Asn Asn Ala Ile Leu Gly Leu Tyr Ala Glu Pro Lys Arg Arg Tyr Tyr
      180      185      190
      195      200

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tgg tga
Trp

<210> 1400
<211> 209
<212> PRT
<213> Arabidopsis thaliana

<400> 1400
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20 25 30
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35 40 45
Ile Asn Glu Thr Tyr Thr Cys Asp Ala Cys Gly Glu Tyr Gly Ser Gly
50 55 60
Phe Thr Tyr Asn Cys Ser Glu Cys Gln Tyr Asp Leu His Val Gly Cys
65 70 75 80
Ala Phe Ile Pro Glu Thr Val Glu Arg Glu Asp His Glu His Pro Leu
85 90 95
Thr Leu Leu Tyr Asn Thr Pro Cys Lys Gly Cys Glu Asp Gly Ala Met
100 105 110
Phe Ile Cys Asn Val Cys Glu Glu Asp Met Ser Glu Asn Leu Trp Val
115 120 125
Tyr Tyr Cys Lys Glu Cys Asp Tyr Gly Thr His Val His Ser Cys Ala
130 135 140
Val Tyr Glu Asp Asp Glu Pro Asn Asn Arg Gly Gly Glu Glu Gly Glu
145 150 155 160
Ala Met Ser Ser Ala Val Ser Arg Met Lys Ser Leu Met Lys Ala Glu
165 170 175
Asp Glu Leu Ala Ala Val Gln Leu Glu Ala Arg Met Lys Arg Asp Ala
180 185 190
Asn Asn Ala Ile Leu Gly Leu Tyr Ala Glu Pro Lys Arg Arg Tyr Tyr
195 200 205
Trp

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agg cac cca agt cac aac cat ccg ctg cgt gtc ttt aaa gcc aaa gaa 96
Arg His Pro Ser His Asn His Pro Leu Arg Val Phe Lys Ala Lys Glu 20 25 30
gag gat gag acc gca tgc tct ggc tgc gag cta gag ctg acc ggg caa 144
Glu Asp Glu Thr Ala Cys Ser Gly Cys Glu Leu Glu Leu Thr Gly Gln 35 40 45
gct ttc aaa tgt ata aag tca gag tgc gat tac ttc tta cac aag tca 192
Ala Phe Lys Cys Ile Lys Ser Glu Cys Asp Tyr Phe Leu His Lys Ser 50 55 60
tgt ttc gac ctt cct agt gag acc aat aac aag tct cac cag gac cac 240
Cys Phe Asp Leu Pro Ser Glu Thr Asn Asn Lys Ser His Gln Asp His 65 70 75 80
cct ctg acc ttg ctt cat tcc cca cca gat gat cgg tct gtc tac acg 288
Pro Leu Thr Leu Leu His Ser Pro Pro Asp Asp Arg Ser Val Tyr Thr 85 90 95
tgt gac gcg tgt gac caa tac gga tct gga ttt tct tac cat tgc tca 336
Cys Asp Ala Cys Asp Gln Tyr Gly Ser Gly Phe Ser Tyr His Cys Ser
1854

PF59082SeqList_PF59082.txt

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		115					120				125					
gta	gat	cgt	gaa	gat	cat	gaa	cat	cca	ctc	act	ctt	ctt	tat	tgc	aca	432
Val	Asp	Arg	Glu	Asp	His	Glu	His	Pro	Leu	Thr	Leu	Leu	Tyr	Cys	Thr	
		130				135					140					
ccg	tgt	aaa	gga	cgt	gaa	gac	acg	tac	ttc	act	tgc	agc	gct	tgt	gat	480
Pro	Cys	Lys	Gly	Arg	Glu	Asp	Thr	Tyr	Phe	Thr	Cys	Ser	Ala	Cys	Asp	
145					150					155					160	
gaa	act	att	tca	gaa	gat	cta	tgg	atg	tat	tac	tgt	aag	gat	tgt	gac	528
Glu	Thr	Ile	Ser	Glu	Asp	Leu	Trp	Met	Tyr	Tyr	Cys	Lys	Asp	Cys	Asp	
			165						170					175		
tat	gga	aca	cat	cta	cac	tca	tgt	gcg	gca	tat	gaa	gac	caa	ggg	aaa	576
Tyr	Gly	Thr	His	Leu	His	Ser	Cys	Ala	Ala	Tyr	Glu	Asp	Gln	Gly	Lys	
			180					185					190			
gaa	gaa	gaa	gat	gaa	gac	gaa	gaa	gga	gaa	gcg	agt	tct	cca	gct	tct	624
Glu	Glu	Glu	Asp	Glu	Asp	Glu	Glu	Gly	Glu	Ala	Ser	Ser	Pro	Ala	Ser	
		195				200						205				
agg	ata	aag	tcg	ttg	atg	aag	gcg	caa	gac	gag	atg	gcg	gct	atg	cag	672
Arg	Ile	Lys	Ser	Leu	Met	Lys	Ala	Gln	Asp	Glu	Met	Ala	Ala	Met	Gln	
		210				215					220					
cta	gag	gca	cgt	att	gag	aat	gat	gcg	agg	aat	gct	gca	ctt	gat	ctg	720
Leu	Glu	Ala	Arg	Ile	Glu	Asn	Asp	Ala	Arg	Asn	Ala	Ala	Leu	Asp	Leu	
					230					235					240	
tgg	gat	gaa	cca	aaa	cgt	aga	tac	tat	tgg	tga						753
Trp	Asp	Glu	Pro	Lys	Arg	Arg	Tyr	Tyr	Trp							
				245					250							

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<211> 250

<212> PRT

<213> Arabidopsis thaliana

<400> 1402

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			20					25					30			
Glu	Asp	Glu	Thr	Ala	Cys	Ser	Gly	Cys	Glu	Leu	Glu	Leu	Thr	Gly	Gln	
		35					40					45				
Ala	Phe	Lys	Cys	Ile	Lys	Ser	Glu	Cys	Asp	Tyr	Phe	Leu	His	Lys	Ser	
	50					55					60					
Cys	Phe	Asp	Leu	Pro	Ser	Glu	Thr	Asn	Asn	Lys	Ser	His	Gln	Asp	His	
65					70					75					80	
Pro	Leu	Thr	Leu	Leu	His	Ser	Pro	Pro	Asp	Asp	Arg	Ser	Val	Tyr	Thr	
				85					90					95		
Cys	Asp	Ala	Cys	Asp	Gln	Tyr	Gly	Ser	Gly	Phe	Ser	Tyr	His	Cys	Ser	
			100					105					110			
Asn	Cys	Asn	Tyr	Ser	Leu	His	Val	Gly	Cys	Ala	Phe	Ile	Pro	Glu	Thr	
		115					120					125				
Val	Asp	Arg	Glu	Asp	His	Glu	His	Pro	Leu	Thr	Leu	Leu	Tyr	Cys	Thr	
		130				135					140					
Pro	Cys	Lys	Gly	Arg	Glu	Asp	Thr	Tyr	Phe	Thr	Cys	Ser	Ala	Cys	Asp	
145					150				155						160	
Glu	Thr	Ile	Ser	Glu	Asp	Leu	Trp	Met	Tyr	Tyr	Cys	Lys	Asp	Cys	Asp	
			165						170					175		
Tyr	Gly	Thr	His	Leu	His	Ser	Cys	Ala	Ala	Tyr	Glu	Asp	Gln	Gly	Lys	
			180					185					190			
Glu	Glu	Glu	Asp	Glu	Asp	Glu	Glu	Gly	Glu	Ala	Ser	Ser	Pro	Ala	Ser	
		195				200						205				
Arg	Ile	Lys	Ser	Leu	Met	Lys	Ala	Gln	Asp	Glu	Met	Ala	Ala	Met	Gln	
		210				215					220					
Leu	Glu	Ala	Arg	Ile	Glu	Asn	Asp	Ala	Arg	Asn	Ala	Ala	Leu	Asp	Leu	
225					230					235					240	
Trp	Asp	Glu	Pro	Lys	Arg	Arg	Tyr	Tyr	Trp							
				245					250							

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 <223> primer

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 <210> 1404
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 <220>
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 <400> 1404
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 <210> 1405
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 <212> DNA
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 <220>
 <223> primer

 <400> 1405
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 <210> 1406
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 <400> 1406
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 <210> 1407
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 <220>
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 <400> 1407
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 <210> 1408
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<223> Xaa in position 147 to 152 is any amino acid

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PF59082SeqList_PF59082.txt

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 <223> Xaa in position 236 to 239 is any amino acid

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 1 5 10 15
 Arg His Xaa Ser His Asn His Pro Leu Arg Xaa Xaa Lys Xaa Xaa Xaa
 20 25 30
 Glu Xaa Glu Xaa Xaa Cys Ser Gly Cys Xaa Leu Xaa Leu Xaa Gly Xaa
 35 40 45
 Ala Phe Lys Cys Xaa Lys Ser Xaa Xaa Cys Asp Tyr Xaa Leu His Lys
 50 55 60
 Ser Cys Phe Xaa Leu Pro Xaa Glu Xaa Xaa Xaa Lys Xaa His Xaa Xaa
 65 70 75 80
 His Xaa Leu Xaa Leu Xaa Xaa Ser Pro Xaa Xaa Xaa Xaa Xaa Xaa
 85 90 95
 Xaa Cys Asp Ala Cys Gly Glu Tyr Gly Ser Xaa Phe Xaa Tyr Xaa Cys
 100 105 110
 Ser Xaa Cys Xaa Tyr Xaa Xaa His Val Gly Cys Xaa Xaa Xaa Pro Glu
 115 120 125
 Xaa Val Xaa Arg Glu Xaa His Xaa His Pro Leu Thr Leu Leu Tyr Xaa
 130 135 140
 Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Xaa Cys Xaa Xaa
 145 150 155 160
 Cys Xaa Xaa Xaa Xaa Xaa Xaa Asn Leu Trp Xaa Tyr Tyr Cys Lys Xaa
 165 170 175
 Cys Asp Tyr Gly Thr His Xaa His Ser Cys Xaa Xaa Xaa Glu Xaa Xaa
 180 185 190
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 195 200 205
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Ser Xaa Xaa Xaa Ser
 210 215 220
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala Xaa Xaa Glu Xaa Xaa Xaa Xaa Gln
 225 230 235 240

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<223> Xaa in position 12 is Ser or Thr

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<223> Xaa in position 14 is any amino acid

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<223> Xaa in position 17 is any amino acid

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<223> Xaa in position 19 is any amino acid

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<223> Xaa in position 21 is Asp or His

<220>
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<223> Xaa in position 22 is Leu or Val

<220>
<221> Variant
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<223> Xaa in position 27 is Ala or Val

<220>
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<223> Xaa in position 28 is any amino acid

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<223> Xaa in position 29 is Ile, Met or Val

<220>
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<223> Xaa in position 32 is Asn, Ser or Thr

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<220>
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<223> Xaa in position 34 is Glu or Lys

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<220>
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<223> Xaa in position 35 is His or Arg

<220>
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<223> Xaa in position 36 is Asp or Glu

<220>
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<223> Xaa in position 37 is Asp, Glu or Gly

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<223> Xaa in position 39 is any amino acid

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<223> Xaa in position 43 is Ala or Thr

<220>
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<223> Xaa in position 45 is Ile or Leu

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<223> Xaa in position 47 is any amino acid

<220>
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<222> (48)..(48)
<223> Xaa in position 48 is Ala, Ser or Thr

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Cys Xaa Ala Cys Gly Glu Tyr Gly Ser Xaa Phe Xaa Tyr Xaa Cys Ser
1          5          10          15
Xaa Cys Xaa Tyr Xaa Xaa His Val Gly Cys Xaa Xaa Xaa Pro Glu Xaa
          20          25          30
Xaa Xaa Xaa Xaa Xaa His Xaa His Pro Leu Xaa Leu Xaa Tyr Xaa Xaa
          35          40          45
Pro

<210> 1413
<211> 38
<212> PRT
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<220>
<223> protein pattern

<220>
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<220>
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<222> (12)..(12)
<223> Xaa in position 12 is Gly, Ser or Val

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<220>
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<222> (21)..(21)
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<223> Xaa in position 22 is Ala, Ile or Val

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<223> Xaa in position 27 is Asp, Glu or Ser

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<223> Xaa in position 29 is Asp or Glu

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<223> Xaa in position 31 is any amino acid

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<223> Xaa in position 33 is any or no amino acid

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<400> 1413
Val Arg His Xaa Ser His Asn His Pro Leu Arg Xaa Xaa Lys Xaa Xaa
1      5      10      15
Xaa Xaa Xaa Glu Xaa Xaa Cys Ser Gly Cys Xaa Leu Xaa Leu Xaa Gly
      20      25      30
Xaa Ala Xaa Phe Lys Cys
      35

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<223> Xaa in position 8 is Ile, Met or Val

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<222> (9)..(9)
<223> Xaa in position 9 is Pro or Ser

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<223> Xaa in position 23 is Ala or Gly

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<222> (34)..(34)
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1      5      10      15
Cys Lys Xaa Cys Asp Tyr Xaa Thr His Xaa His Ser Cys Xaa Xaa Xaa
      20      25      30
Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
      35      40

<210> 1415
<211> 20
<212> PRT
<213> Artificial sequence

<220>
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<220>
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<220>
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<220>
<221> Variant
<222> (8)..(8)
<223> Xaa in position 8 is any amino acid

<220>
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<222> (9)..(9)
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<220>
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<222> (11)..(11)
<223> Xaa in position 11 is Glu or Gln

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<222> (12)..(12)
<223> Xaa in position 12 is Asp or Arg

<220>
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<223> Xaa in position 14 is Leu, Met or Val

<220>
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 <222> (15)..(15)
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 1 5 10 15
 Xaa Gln Xaa Xaa
 20

<210> 1416
 <211> 16
 <212> PRT
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<220>
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 <223> Xaa in position 15 is Ala or Ser

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 1 5 10 15

<210> 1417

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<211> 9
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<220>
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<220>
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<220>
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<220>
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<220>
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His Xaa Leu Xaa Leu Xaa Xaa Ser Pro
1 5

<210> 1418
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<212> DNA
<213> Arabidopsis thaliana

<220>
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aac cag gat tct tcg ggt atc cgg gtc tgc ccc aaa tcc gat aac ctc 96
Asn Gln Asp Ser Ser Gly Ile Arg Val Cys Pro Lys Ser Asp Asn Leu
20 25 30
acc cga ctc acc gga acc att cct ggt cca atc ggt act cct tac gaa 144
Thr Arg Leu Thr Gly Thr Ile Pro Gly Pro Ile Gly Thr Pro Tyr Glu
35 40 45
ggc ggt aca ttt cag atc gat atc act atg cca gat ggg tat cca ttt 192
Gly Gly Thr Phe Gln Ile Asp Ile Thr Met Pro Asp Gly Tyr Pro Phe
50 55 60
gag cct cca aag atg cag ttt tca act aaa gtt tgg cat ccg aat att 240
Glu Pro Pro Lys Met Gln Phe Ser Thr Lys Val Trp His Pro Asn Ile
65 70 75 80
agt agc caa agc ggt gca ata tgc ttg gat atc ttg aaa gac cag tgg 288
Ser Ser Gln Ser Gly Ala Ile Cys Leu Asp Ile Leu Lys Asp Gln Trp
85 90 95
agt cca gct ctt act ctg aag aca gct ctt gtt tca att cag gct tta 336
Ser Pro Ala Leu Thr Leu Lys Thr Ala Leu Val Ser Ile Gln Ala Leu
100 105 110
ctc tct gca cct gag ccc aaa gac cct caa gat gct gtt gta gct gaa 384
Leu Ser Ala Pro Glu Pro Lys Asp Pro Gln Asp Ala Val Val Ala Glu
115 120 125
cag tac atg aag aac tat caa gtg ttt gta tca aca gct cgt tac tgg 432
Gln Tyr Met Lys Asn Tyr Gln Val Phe Val Ser Thr Ala Arg Tyr Trp
130 135 140
act gaa act ttc gcc aag aaa tct tct cta gag gaa aaa gtc aag aga 480

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Thr	Glu	Thr	Phe	Ala	Lys	Lys	Ser	Ser	Leu	Glu	Glu	Lys	Val	Lys	Arg	
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Leu	Val	Glu	Met	Gly	Phe	Gly	Asp	Ala	Gln	Val	Arg	Ser	Ala	Ile	Glu	
				165					170					175		
tca	agt	ggg	gat	gag	aat	ctg	gct	ctg	gaa	aag	ctc	tgt	tct	gct	576	
Ser	Ser	Gly	Gly	Asp	Glu	Asn	Leu	Ala	Leu	Glu	Lys	Leu	Cys	Ser	Ala	
			180					185					190			
tag															579	

<210> 1419
 <211> 192
 <212> PRT
 <213> Arabidopsis thaliana

Met	Ile	Asp	Phe	Ser	Arg	Ile	Gln	Lys	Glu	Leu	Gln	Asp	Cys	Glu	Arg	
1				5					10					15		
Asn	Gln	Asp	Ser	Ser	Gly	Ile	Arg	Val	Cys	Pro	Lys	Ser	Asp	Asn	Leu	
			20					25					30			
Thr	Arg	Leu	Thr	Gly	Thr	Ile	Pro	Gly	Pro	Ile	Gly	Thr	Pro	Tyr	Glu	
		35					40					45				
Gly	Gly	Thr	Phe	Gln	Ile	Asp	Ile	Thr	Met	Pro	Asp	Gly	Tyr	Pro	Phe	
	50					55					60					
Glu	Pro	Pro	Lys	Met	Gln	Phe	Ser	Thr	Lys	Val	Trp	His	Pro	Asn	Ile	
65					70				75					80		
Ser	Ser	Gln	Ser	Gly	Ala	Ile	Cys	Leu	Asp	Ile	Leu	Lys	Asp	Gln	Trp	
			85						90					95		
Ser	Pro	Ala	Leu	Thr	Leu	Lys	Thr	Ala	Leu	Val	Ser	Ile	Gln	Ala	Leu	
			100					105					110			
Leu	Ser	Ala	Pro	Glu	Pro	Lys	Asp	Pro	Gln	Asp	Ala	Val	Val	Ala	Glu	
		115					120				125					
Gln	Tyr	Met	Lys	Asn	Tyr	Gln	Val	Phe	Val	Ser	Thr	Ala	Arg	Tyr	Trp	
	130					135					140					
Thr	Glu	Thr	Phe	Ala	Lys	Lys	Ser	Ser	Leu	Glu	Glu	Lys	Val	Lys	Arg	
145					150					155					160	
Leu	Val	Glu	Met	Gly	Phe	Gly	Asp	Ala	Gln	Val	Arg	Ser	Ala	Ile	Glu	
			165					170						175		
Ser	Ser	Gly	Gly	Asp	Glu	Asn	Leu	Ala	Leu	Glu	Lys	Leu	Cys	Ser	Ala	
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 <213> Glycine max

<220>
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tacatatata atcagaaaaa gaaaactaac atacatcagt cactagtgtg tgaaaagcga	180
cacaacacaa cataagctth attctthtgtt gttctccccg tctgtgcagc actgtthttag	240
ggthtgggtca attgggtgaca agattgaag atg ata gac ctt gcg cgc gtg cag	293
Met Ile Asp Leu Ala Arg Val Gln	
1 5	
aag gag ctt gtg gaa tgc agc aag gac gcg gag gga tcg ggc atc aaa	341

PF59082SeqList_PF59082.txt

Lys	Glu	Leu	Val	Glu	Cys	Ser	Lys	Asp	Ala	Glu	Gly	Ser	Gly	Ile	Lys	
gtc	agc	ccc	aaa	aac	gac	aac	ctt	ggt	ctc	ttg	atc	ggc	acc	att	cct	389
Val	Ser	Pro	Lys	Asn	Asp	Asn	Leu	Val	Leu	Leu	Ile	Gly	Thr	Ile	Pro	
25					30					35					40	
ggc	ccc	gtc	gga	act	cca	tat	gaa	ggg	ggc	att	ttc	cag	att	gat	atc	437
Gly	Pro	Val	Gly	Thr	Pro	Tyr	Glu	Gly	Gly	Ile	Phe	Gln	Ile	Asp	Ile	
				45					50					55		
aca	ttg	cct	gat	ggg	tac	ccg	ttt	gaa	ccc	ccc	aag	atg	cag	ttt	aaa	485
Thr	Leu	Pro	Asp	Gly	Tyr	Pro	Phe	Glu	Pro	Pro	Lys	Met	Gln	Phe	Lys	
				60				65					70			
acc	aaa	ggt	tgg	cac	cct	aat	atc	agc	agc	caa	agt	gga	gct	att	tgc	533
Thr	Lys	Val	Trp	His	Pro	Asn	Ile	Ser	Ser	Gln	Ser	Gly	Ala	Ile	Cys	
		75				80						85				
ctg	gat	atc	ttg	aag	gac	cag	tgg	agc	cca	gca	ctc	act	ctg	aag	act	581
Leu	Asp	Ile	Leu	Lys	Asp	Gln	Trp	Ser	Pro	Ala	Leu	Thr	Leu	Lys	Thr	
	90					95					100					
gca	ctt	ctt	tct	gtg	caa	gca	ctt	ctc	tct	gct	cct	cag	cct	gat	gat	629
Ala	Leu	Leu	Ser	Val	Gln	Ala	Leu	Leu	Ser	Ala	Pro	Gln	Pro	Asp	Asp	
105					110					115					120	
cct	caa	gat	gcc	gtg	gtg	gca	cag	cag	tat	ctg	aaa	gac	tat	cag	aca	677
Pro	Gln	Asp	Ala	Val	Val	Ala	Gln	Gln	Tyr	Leu	Lys	Asp	Tyr	Gln	Thr	
				125					130					135		
ttt	ggt	aac	act	gct	cgc	tac	tgg	aca	gaa	agt	ttt	gcc	aag	gct	tcg	725
Phe	Val	Asn	Thr	Ala	Arg	Tyr	Trp	Thr	Glu	Ser	Phe	Ala	Lys	Ala	Ser	
				140				145					150			
tct	cgt	ggg	att	gaa	gat	aag	gta	cag	aaa	ctc	gtt	gag	atg	gga	ttt	773
Ser	Arg	Gly	Ile	Glu	Asp	Lys	Val	Gln	Lys	Leu	Val	Glu	Met	Gly	Phe	
		155				160						165				
cca	gaa	gct	cga	gta	agg	agc	att	ttg	gaa	gct	gtt	ggg	ggg	gat	gaa	821
Pro	Glu	Ala	Arg	Val	Arg	Ser	Ile	Leu	Glu	Ala	Val	Gly	Gly	Asp	Glu	
	170					175					180					
aac	atg	gcc	ctt	gaa	agg	ttg	ctg	tagatcatgg	tcaagtttag	gaagacgtgt						875
Asn	Met	Ala	Leu	Glu	Arg	Leu	Leu									
185					190											
ctccataata	tgatggaacc	atatagacaa	taggttttaa	attgaataga	gtcatataaa											935
tctacttggga	atatacgtata	gtccttttgt	tttacttttc	tcctccttgg	aaactacagt											995
tctcgactat	ttcctgatta	ttatatatat	cagctatgaa	attaaataacc	ttgttggcaa											1055
ggtttctgct	tc															1067

<210> 1421
 <211> 192
 <212> PRT
 <213> Glycine max

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 20 25 30
 Val Leu Leu Ile Gly Thr Ile Pro Gly Pro Val Gly Thr Pro Tyr Glu
 35 40 45
 Gly Gly Ile Phe Gln Ile Asp Ile Thr Leu Pro Asp Gly Tyr Pro Phe
 50 55 60
 Glu Pro Pro Lys Met Gln Phe Lys Thr Lys Val Trp His Pro Asn Ile
 65 70 75 80
 Ser Ser Gln Ser Gly Ala Ile Cys Leu Asp Ile Leu Lys Asp Gln Trp
 85 90 95
 Ser Pro Ala Leu Thr Leu Lys Thr Ala Leu Leu Ser Val Gln Ala Leu
 100 105 110
 Leu Ser Ala Pro Gln Pro Asp Asp Pro Gln Asp Ala Val Val Ala Gln
 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190
 Seite 1870

PF59082SeqList_PF59082.txt

atgggactcg agtgaaattc gacttcttca gagttcgttc gctttgtttg cttttttttt 926
tctcaacttt tgcttttgtg tctggtagcc tgaatcatca actctttgcc catggaactc 986
tggtaatatc tgatgcaaaa gaaacatcag attgacataa accccttgca acctggatgt 1046
gatggcctga tggataacat ctcatatattg attctc 1082

<210> 1423
<211> 195
<212> PRT
<213> Sorghum bicolor

<400> 1423
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Asp Arg Glu Val Ser Gly Val Ser Ile Ala Leu His Asp Gly Ala Asn
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Ile Ser His Leu Thr Gly Thr Ile Ala Gly Pro Ala Asp Ser Pro Tyr
35 40 45
Glu Gly Gly Thr Phe Val Ile Asp Ile Arg Leu Pro Gly Gly Tyr Pro
50 55 60
Phe Glu Pro Pro Lys Met Gln Phe Val Thr Lys Val Trp His Pro Asn
65 70 75 80
Ile Ser Ser Gln Asn Gly Ala Ile Cys Leu Asp Ile Leu Lys Asp Gln
85 90 95
Trp Ser Pro Ala Leu Thr Leu Lys Thr Ala Leu Leu Ser Leu Gln Ala
100 105 110
Leu Leu Ser Ser Pro Ala Pro Asp Asp Pro Gln Asp Ala Val Val Ala
115 120 125
Gln Gln Tyr Leu Arg Asp Tyr Pro Thr Phe Ala Ala Thr Ala Arg Tyr
130 135 140
Trp Thr Glu Ala Phe Ala Lys Ser Ala Ser Thr Gly Met Glu Glu Lys
145 150 155 160
Val Gln Lys Leu Val Glu Met Gly Phe Pro Glu Asp Leu Val Arg Ser
165 170 175
Thr Leu Lys Ser Val Asp Gly Asp Glu Asn Met Ala Leu Glu Lys Leu
180 185 190
Cys Ser Gly
195

<210> 1424
<211> 1043
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (175)..(768)

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<222> (1033)..(1033)
<223> n is a, g, c or t

<220>
<221> misc_feature
<222> (1034)..(1034)
<223> n is a, g, c or t

<220>
<221> misc_feature

PF59082SeqList_PF59082.txt

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<222> (1035)..(1035)
<223> n is a, g, c or t

<220>
<221> misc_feature
<222> (1036)..(1036)
<223> n is a, g, c or t

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agggaagtaa ctgccgcattc tcaagtctca accctcgcct ccaatcgcaa cgctcccag 120

gagagccagg aggaggtgac ggcggcgccg cgaggaagga gggatcgatc gagg atg 177
Met
1

gtg gac gtc tcg cgc gtg cag aag gag ctc acc gag tgc aac cgc gac 225
Val Asp Val Ser Arg Val Gln Lys Glu Leu Thr Glu Cys Asn Arg Asp
5 10 15

cgg gag gta tcg ggc gtc tcc atc gcg ctc cac gac ggc gcc aac atc 273
Arg Glu Val Ser Gly Val Ser Ile Ala Leu His Asp Gly Ala Asn Ile
20 25 30

tcc cac ctc acc ggc acc atc gcc ggg ccc gcc gac agc ccc tac gag 321
Ser His Leu Thr Gly Thr Ile Ala Gly Pro Ala Asp Ser Pro Tyr Glu
35 40 45

ggc ggc acg ttc gtc atc gat atc cgc ctg ccc ggt gga tat ccc ttt 369
Gly Gly Thr Phe Val Ile Asp Ile Arg Leu Pro Gly Gly Tyr Pro Phe
50 55 60

gag cct ccg aag atg cag ttc atc acc aaa gta tgg cac cct aac atc 417
Glu Pro Pro Lys Met Gln Phe Ile Thr Lys Val Trp His Pro Asn Ile
65 70 75 80

agc agc caa aat gga gca att tgc ttg gac att ctg aaa gat cag tgg 465
Ser Ser Gln Asn Gly Ala Ile Cys Leu Asp Ile Leu Lys Asp Gln Trp
85 90 95

agc cca gcc ctt acc ttg aag act gcg ctc ctt tcc ctt caa gct ctg 513
Ser Pro Ala Leu Thr Leu Lys Thr Ala Leu Leu Ser Leu Gln Ala Leu
100 105 110

ctt tct tct cct gca cct gat gat cct cag gat gct gtt gtt gcc caa 561
Leu Ser Ser Pro Ala Pro Asp Asp Pro Gln Asp Ala Val Val Ala Gln
115 120 125

cag tac ctg cgt gac tat cca aca ttt gcc gct acg gct cgc tac tgg 609
Gln Tyr Leu Arg Asp Tyr Pro Thr Phe Ala Ala Thr Ala Arg Tyr Trp
130 135 140 145

aca gag gcc ttt gcg aag agt gca tca acg ggc atg gaa gag aag gtg 657
Thr Glu Ala Phe Ala Lys Ser Ala Ser Thr Gly Met Glu Glu Lys Val
150 155 160

cag aag ctg gtt gag atg ggc ttc cca gag gat cag gtg aga agt gcc 705
Gln Lys Leu Val Glu Met Gly Phe Pro Glu Asp Gln Val Arg Ser Ala
165 170 175

ctg aag agc gtg gat ggc gac gag aac atg gct ctc gaa aag ctc tgc 753
Leu Lys Ser Val Asp Gly Asp Glu Asn Met Ala Leu Glu Lys Leu Cys
180 185 190

tct ggc tct ggg tgaaccattg tcttggggcc aatacatgag cagctgtaca 805
Ser Gly Ser Gly
195

tttcacagtg cctgctaattg ctctgctca gccatttcat ataggggccg tgccatggcc 865

catgggactg gagtgagact ctctaggac aacattcggt tctttaaact cttttgctgt 925

tgtgtctggt aggctgaatc gactcttgga ccatggaacc ctggtaatat ctgatgcaaa 985

ggaacatga ggttgacata aaaaaaaaaa aaaaaaaaaa aactcgannn ncttctag 1043

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PF59082SeqList_PF59082.txt

<210> 1425
 <211> 197
 <212> PRT
 <213> Zea mays

<400> 1425
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 20 25 30
 Ile Ser His Leu Thr Gly Thr Ile Ala Gly Pro Ala Asp Ser Pro Tyr
 35 40 45
 Glu Gly Gly Thr Phe Val Ile Asp Ile Arg Leu Pro Gly Gly Tyr Pro
 50 55 60
 Phe Glu Pro Pro Lys Met Gln Phe Ile Thr Lys Val Trp His Pro Asn
 65 70 75 80
 Ile Ser Ser Gln Asn Gly Ala Ile Cys Leu Asp Ile Leu Lys Asp Gln
 85 90 95
 Trp Ser Pro Ala Leu Thr Leu Lys Thr Ala Leu Leu Ser Leu Gln Ala
 100 105 110
 Leu Leu Ser Ser Pro Ala Pro Asp Asp Pro Gln Asp Ala Val Val Ala
 115 120 125
 Gln Gln Tyr Leu Arg Asp Tyr Pro Thr Phe Ala Ala Thr Ala Arg Tyr
 130 135 140
 Trp Thr Glu Ala Phe Ala Lys Ser Ala Ser Thr Gly Met Glu Glu Lys
 145 150 155 160
 Val Gln Lys Leu Val Glu Met Gly Phe Pro Glu Asp Gln Val Arg Ser
 165 170 175
 Ala Leu Lys Ser Val Asp Gly Asp Glu Asn Met Ala Leu Glu Lys Leu
 180 185 190
 Cys Ser Gly Ser Gly
 195

<210> 1426
 <211> 588
 <212> DNA
 <213> Oryza sativa (japonica cultivar-group)

<220>
 <221> CDS
 <222> (1)..(588)

<400> 1426	
atg gtg gac gtg tgc agg gtg cag aag gag ctg acg gag tgc aac cgg	48
Met Val Asp Val Ser Arg Val Gln Lys Glu Leu Thr Glu Cys Asn Arg	
1 5 10 15	
gac agg gag gtc tcc ggg gtg tcc atc gcg ctc cac gac ggc tcc acc	96
Asp Arg Glu Val Ser Gly Val Ser Ile Ala Leu His Asp Gly Ser Thr	
20 25 30	
atc tcc cac ctc acc ggc acc atc gcc ggg ccc caa ggc acg ccc tac	144
Ile Ser His Leu Thr Gly Thr Ile Ala Gly Pro Gln Gly Thr Pro Tyr	
35 40 45	
gag ggc ggc acc ttc gtc atc gac atc cgc ctc cca ggt ggt tac ccc	192
Glu Gly Gly Thr Phe Val Ile Asp Ile Arg Leu Pro Gly Gly Tyr Pro	
50 55 60	
ttt gag cct cct aag atg cag ttt atc acc aaa gta tgg cac cct aac	240
Phe Glu Pro Pro Lys Met Gln Phe Ile Thr Lys Val Trp His Pro Asn	
65 70 75 80	
att agc agc caa aac gga gca atc tgc ttg gac ata ctg aag gac caa	288
Ile Ser Ser Gln Asn Gly Ala Ile Cys Leu Asp Ile Leu Lys Asp Gln	
85 90 95	
tgg agc cca gcc ctt aca ttg aag acg gca ctg ctt tcc ctc caa gct	336
Trp Ser Pro Ala Leu Thr Leu Lys Thr Ala Leu Leu Ser Leu Gln Ala	
100 105 110	
ctg ctt tct gcc cct gca cct gat gat cct cag gat gct gtc gtt gca	384
Leu Leu Ser Ala Pro Ala Pro Asp Asp Pro Gln Asp Ala Val Val Ala	
115 120 125	
caa cag tac ttg cgt gac tat tcc aca ttt tct gct act gct cgc tac	432

PF59082SeqList_PF59082.txt

Gln	Gln	Tyr	Leu	Arg	Asp	Tyr	Ser	Thr	Phe	Ser	Ala	Thr	Ala	Arg	Tyr	
130						135					140					
tgg	acg	gag	gcc	ttt	gca	aag	aat	tcc	tcc	acc	ggc	atg	gaa	gaa	aag	480
Trp	Thr	Glu	Ala	Phe	Ala	Lys	Asn	Ser	Ser	Thr	Gly	Met	Glu	Glu	Lys	
145					150					155					160	
gtg	cag	aag	ctg	gtt	gag	atg	ggc	ttc	cct	gaa	gac	atg	gtg	aga	agt	528
Val	Gln	Lys	Leu	Val	Glu	Met	Gly	Phe	Pro	Glu	Asp	Met	Val	Arg	Ser	
				165					170					175		
gtt	ctg	aag	agt	gtc	aat	ggc	gac	gag	aac	atg	gct	ctt	gag	aag	ctc	576
Val	Leu	Lys	Ser	Val	Asn	Gly	Asp	Glu	Asn	Met	Ala	Leu	Glu	Lys	Leu	
			180					185					190			
tgc	tct	ggc	tga													588
Cys	Ser	Gly														
		195														

<210> 1427

<211> 195

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<400> 1427

Met	Val	Asp	Val	Ser	Arg	Val	Gln	Lys	Glu	Leu	Thr	Glu	Cys	Asn	Arg	
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Asp	Arg	Glu	Val	Ser	Gly	Val	Ser	Ile	Ala	Leu	His	Asp	Gly	Ser	Thr	
			20					25					30			
Ile	Ser	His	Leu	Thr	Gly	Thr	Ile	Ala	Gly	Pro	Gln	Gly	Thr	Pro	Tyr	
		35					40					45				
Glu	Gly	Gly	Thr	Phe	Val	Ile	Asp	Ile	Arg	Leu	Pro	Gly	Gly	Tyr	Pro	
	50					55				60						
Phe	Glu	Pro	Pro	Lys	Met	Gln	Phe	Ile	Thr	Lys	Val	Trp	His	Pro	Asn	
65				70					75						80	
Ile	Ser	Ser	Gln	Asn	Gly	Ala	Ile	Cys	Leu	Asp	Ile	Leu	Lys	Asp	Gln	
			85					90					95			
Trp	Ser	Pro	Ala	Leu	Thr	Leu	Lys	Thr	Ala	Leu	Leu	Ser	Leu	Gln	Ala	
			100					105					110			
Leu	Leu	Ser	Ala	Pro	Ala	Pro	Asp	Asp	Pro	Gln	Asp	Ala	Val	Val	Ala	
		115					120					125				
Gln	Gln	Tyr	Leu	Arg	Asp	Tyr	Ser	Thr	Phe	Ser	Ala	Thr	Ala	Arg	Tyr	
	130					135					140					
Trp	Thr	Glu	Ala	Phe	Ala	Lys	Asn	Ser	Ser	Thr	Gly	Met	Glu	Glu	Lys	
145					150				155						160	
Val	Gln	Lys	Leu	Val	Glu	Met	Gly	Phe	Pro	Glu	Asp	Met	Val	Arg	Ser	
			165					170						175		
Val	Leu	Lys	Ser	Val	Asn	Gly	Asp	Glu	Asn	Met	Ala	Leu	Glu	Lys	Leu	
			180					185					190			
Cys	Ser	Gly														
		195														

<210> 1428

<211> 585

<212> DNA

<213> Solanum tuberosum

<220>

<221> CDS

<222> (1)..(585)

<400> 1428

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1				5					10					15		
gat	gtt	cag	gtt	tct	gga	att	aat	gtt	acc	ctt	aaa	ggg	gac	agt	ctc	96
Asp	Val	Gln	Val	Ser	Gly	Ile	Asn	Val	Thr	Leu	Lys	Gly	Asp	Ser	Leu	
			20					25					30			
act	cac	ttg	att	ggg	aca	atc	cct	ggg	cct	gtt	ggg	act	cct	tat	gaa	144
Thr	His	Leu	Ile	Gly	Thr	Ile	Pro	Gly	Pro	Val	Gly	Thr	Pro	Tyr	Glu	
		35					40					45				
ggc	ggg	act	ttc	aag	atc	gat	atc	act	ctt	act	gat	ggg	tac	cca	ttt	192
Gly	Gly	Thr	Phe	Lys	Ile	Asp	Ile	Thr	Leu	Thr	Asp	Gly	Tyr	Pro	Phe	

PF59082SeqList_PF59082.txt

50	55	60	
gag cct cca aaa atg aaa ttc gcc aca aaa gtt tgg cat ccc aac ata			240
Glu Pro Pro Lys Met Lys Phe Ala Thr Lys Val Trp His Pro Asn Ile			
65	70	75	80
agt agt caa agt gga gca ata tgc cta gac atc ctg aag gac cag tgg			288
Ser Ser Gln Ser Gly Ala Ile Cys Leu Asp Ile Leu Lys Asp Gln Trp			
85	90	95	
agc cca gcg cta act ctc aag aca gct ctc ctt tct ata caa gca tta			336
Ser Pro Ala Leu Thr Leu Lys Thr Ala Leu Leu Ser Ile Gln Ala Leu			
100	105	110	
ctt tct gct cct gaa cct gat gat cca gat gca gtt gtt gca caa			384
Leu Ser Ala Pro Glu Pro Asp Asp Pro Gln Asp Ala Val Val Ala Gln			
115	120	125	
cag tat ctt aga gac cat cag acc ttt gtc ggc aca gct cgt tac tgg			432
Gln Tyr Leu Arg Asp His Gln Thr Phe Val Gly Thr Ala Arg Tyr Trp			
130	135	140	
act gaa act ttt gct aaa aca tcc aca ctt gct gca gat gag aag ata			480
Thr Glu Thr Phe Ala Lys Thr Ser Thr Leu Ala Ala Asp Glu Lys Ile			
145	150	155	160
caa aag ctt gtg gaa atg ggc ttt cct gaa gct caa gtt agg agt act			528
Gln Lys Leu Val Glu Met Gly Phe Pro Glu Ala Gln Val Arg Ser Thr			
165	170	175	
ttg gaa gca aat ggt tgg gat gaa aac atg gct ctt gaa aag ctg ttg			576
Leu Glu Ala Asn Gly Trp Asp Glu Asn Met Ala Leu Glu Lys Leu Leu			
180	185	190	
tcc agc tag			585
Ser Ser			

<210> 1429

<211> 194

<212> PRT

<213> Solanum tuberosum

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Thr His Leu Ile Gly Thr Ile Pro Gly Pro Val Gly Thr Pro Tyr Glu	
35 40 45	
Gly Gly Thr Phe Lys Ile Asp Ile Thr Leu Thr Asp Gly Tyr Pro Phe	
50 55 60	
Glu Pro Pro Lys Met Lys Phe Ala Thr Lys Val Trp His Pro Asn Ile	
65 70 75 80	
Ser Ser Gln Ser Gly Ala Ile Cys Leu Asp Ile Leu Lys Asp Gln Trp	
85 90 95	
Ser Pro Ala Leu Thr Leu Lys Thr Ala Leu Leu Ser Ile Gln Ala Leu	
100 105 110	
Leu Ser Ala Pro Glu Pro Asp Asp Pro Gln Asp Ala Val Val Ala Gln	
115 120 125	
Gln Tyr Leu Arg Asp His Gln Thr Phe Val Gly Thr Ala Arg Tyr Trp	
130 135 140	
Thr Glu Thr Phe Ala Lys Thr Ser Thr Leu Ala Ala Asp Glu Lys Ile	
145 150 155 160	
Gln Lys Leu Val Glu Met Gly Phe Pro Glu Ala Gln Val Arg Ser Thr	
165 170 175	
Leu Glu Ala Asn Gly Trp Asp Glu Asn Met Ala Leu Glu Lys Leu Leu	
180 185 190	
Ser Ser	

<210> 1430

<211> 923

<212> DNA

<213> Lycopersicon esculentum

<220>

<221> CDS

PF59082SeqList_PF59082.txt

<222> (60)..(644)

<400> 1430

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Met Val Asp Leu Ala Arg Val Gln Lys Glu Leu His Glu Cys Asn Arg
1 5 10 15
gat gtt cag gtt tct gga att aat gtt acc ctt aaa ggt gac agt ctc 155
Asp Val Gln Val Ser Gly Ile Asn Val Thr Leu Lys Gly Asp Ser Leu
20 25 30
act cac ttg att ggt aca atc cct ggt cct gtt ggt act cct tac gaa 203
Thr His Leu Ile Gly Thr Ile Pro Gly Pro Val Gly Thr Pro Tyr Glu
35 40 45
ggc ggt act ttc aag atc gat atc act ctt act gat ggc tac cca ttt 251
Gly Gly Thr Phe Lys Ile Asp Ile Thr Leu Thr Asp Gly Tyr Pro Phe
50 55 60
gag cct cca aaa atg aaa ttc gcc aca aaa gtt tgg cat ccc aac ata 299
Glu Pro Pro Lys Met Lys Phe Ala Thr Lys Val Trp His Pro Asn Ile
65 70 75 80
agt agt caa agt gga gca ata tgc cta gac atc ctg aag gac cag tgg 347
Ser Ser Gln Ser Gly Ala Ile Cys Leu Asp Ile Leu Lys Asp Gln Trp
85 90 95
agc cca gca cta act ctc aag aca gct ctc ctt tct ata caa gca tta 395
Ser Pro Ala Leu Thr Leu Lys Thr Ala Leu Leu Ser Ile Gln Ala Leu
100 105 110
ctt tct gct cct gaa cct gat gat cca caa gat gca gtt gtt gca cag 443
Leu Ser Ala Pro Glu Pro Asp Asp Pro Gln Asp Ala Val Val Ala Gln
115 120 125
cag tat ctt aga gaa cat cag acc ttt gtc ggc aca gct cgt tac tgg 491
Gln Tyr Leu Arg Glu His Gln Thr Phe Val Gly Thr Ala Arg Tyr Trp
130 135 140
act gag act ttt gca aaa aca tcc aca ctt gct gca gac gac aag ata 539
Thr Glu Thr Phe Ala Lys Thr Ser Thr Leu Ala Ala Asp Asp Lys Ile
145 150 155 160
caa aag ctt gtg gaa atg ggc ttt cct gaa gct caa gtg agg agt act 587
Gln Lys Leu Val Glu Met Gly Phe Pro Glu Ala Gln Val Arg Ser Thr
165 170 175
ttg gaa gca aat ggt tgg gat gaa aac atg gct ctt gaa aag ctg ttg 635
Leu Glu Ala Asn Gly Trp Asp Glu Asn Met Ala Leu Glu Lys Leu Leu
180 185 190
tcc agc taaaaccctt ctactgcaac tcatattttg ataagacaat tatatccttc 691
Ser Ser

cagcaaaaagc tgatgactag aatagagtca ctcggttata ctgttgcttg gcaatcttgt 751

ttctgtctcc tttatggttt gctgttgaca tctcttcata tcctgtgaag attctgatgt 811

tatttttaca atatcaagca aattgcatat gaatcatggg gaggaagtgg actttccggg 871

gtgaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 923
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<210> 1431

<211> 194

<212> PRT

<213> Lycopersicon esculentum

<400> 1431

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20 25 30
Thr His Leu Ile Gly Thr Ile Pro Gly Pro Val Gly Thr Pro Tyr Glu
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PF59082SeqList_PF59082.txt

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      35      40      45
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   50
Glu Pro Pro Lys Met Lys Phe Ala Thr Lys Val Trp His Pro Asn Ile
65
Ser Ser Gln Ser Gly Ala Ile Cys Leu Asp Ile Leu Lys Asp Gln Trp
   85
Ser Pro Ala Leu Thr Leu Lys Thr Ala Leu Leu Ser Ile Gln Ala Leu
   100
Leu Ser Ala Pro Glu Pro Asp Asp Pro Gln Asp Ala Val Val Ala Gln
   115
Gln Tyr Leu Arg Glu His Gln Thr Phe Val Gly Thr Ala Arg Tyr Trp
   130
Thr Glu Thr Phe Ala Lys Thr Ser Thr Leu Ala Ala Asp Asp Lys Ile
145
Gln Lys Leu Val Glu Met Gly Phe Pro Glu Ala Gln Val Arg Ser Thr
   165
Leu Glu Ala Asn Gly Trp Asp Glu Asn Met Ala Leu Glu Lys Leu Leu
   180
Ser Ser

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<210> 1432
 <211> 579
 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (1)..(579)

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<400> 1432
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Met Ile Asp Ile Ser Arg Val Gln Lys Glu Leu Gln Asp Cys Glu Lys
   1
gac aga gac tcc tcg ggc atc cgg gtc tgc ccg aaa tcc gat aac ctc      96
Asp Arg Asp Ser Ser Gly Ile Arg Val Cys Pro Lys Ser Asp Asn Leu
   20
acc cga ctc acc gga acc atc ccg ggt cca atc gga act cct tac gaa      144
Thr Arg Leu Thr Gly Thr Ile Pro Gly Pro Ile Gly Thr Pro Tyr Glu
   35
ggc gga acc ttt cag atc gat atc acc att cca gaa ggg tat ccc ttt      192
Gly Gly Thr Phe Gln Ile Asp Ile Thr Ile Pro Glu Gly Tyr Pro Phe
   50
gag cct cca aag atg caa ttt tca acc aaa gtt tgg cac ccg aac ata      240
Glu Pro Pro Lys Met Gln Phe Ser Thr Lys Val Trp His Pro Asn Ile
   65
agt agc caa agc ggg gca ata tgc ttg gat gtc ttg aaa gac cag tgg      288
Ser Ser Gln Ser Gly Ala Ile Cys Leu Asp Val Leu Lys Asp Gln Trp
   85
agt cca gct ctt act ttg aag aca gct ctt gtt tca gtc cag gca tta      336
Ser Pro Ala Leu Thr Leu Lys Thr Ala Leu Val Ser Val Gln Ala Leu
   100
ctc tct gca cca gag cct aaa gac cct caa gat gct gtt gtt gct gaa      384
Leu Ser Ala Pro Glu Pro Lys Asp Pro Gln Asp Ala Val Val Ala Glu
   115
cag tac atg aag aac tat caa gtg ttt gta tca aca gct cgt tac tgg      432
Gln Tyr Met Lys Asn Tyr Gln Val Phe Val Ser Thr Ala Arg Tyr Trp
   130
acc caa aca ttc gcc aag aac tct tct ctt gag gat aaa gtg aag aga      480
Thr Gln Thr Phe Ala Lys Asn Ser Ser Leu Glu Asp Lys Val Lys Arg
145
ctc gtc gag atg ggt ttt gga gat gct cag gct agg agt gca att gaa      528
Leu Val Glu Met Gly Phe Gly Asp Ala Gln Ala Arg Ser Ala Ile Glu
   165
tca agt ggt gga gat gag aat gtg gcg ctt gaa aag ctc tgt tct ggt      576
Ser Ser Gly Gly Asp Glu Asn Val Ala Leu Glu Lys Leu Cys Ser Gly
   180
tag

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PF59082SeqList_PF59082.txt

<210> 1433
 <211> 192
 <212> PRT
 <213> Brassica napus

<400> 1433
 Met Ile Asp Ile Ser Arg Val Gln Lys Glu Leu Gln Asp Cys Glu Lys
 1 5 10 15
 Asp Arg Asp Ser Ser Gly Ile Arg Val Cys Pro Lys Ser Asp Asn Leu
 20 25 30
 Thr Arg Leu Thr Gly Thr Ile Pro Gly Pro Ile Gly Thr Pro Tyr Glu
 35 40 45
 Gly Gly Thr Phe Gln Ile Asp Ile Thr Ile Pro Glu Gly Tyr Pro Phe
 50 55 60
 Glu Pro Pro Lys Met Gln Phe Ser Thr Lys Val Trp His Pro Asn Ile
 65 70 75 80
 Ser Ser Gln Ser Gly Ala Ile Cys Leu Asp Val Leu Lys Asp Gln Trp
 85 90 95
 Ser Pro Ala Leu Thr Leu Lys Thr Ala Leu Val Ser Val Gln Ala Leu
 100 105 110
 Leu Ser Ala Pro Glu Pro Lys Asp Pro Gln Asp Ala Val Val Ala Glu
 115 120 125
 Gln Tyr Met Lys Asn Tyr Gln Val Phe Val Ser Thr Ala Arg Tyr Trp
 130 135 140
 Thr Gln Thr Phe Ala Lys Asn Ser Ser Leu Glu Asp Lys Val Lys Arg
 145 150 155 160
 Leu Val Glu Met Gly Phe Gly Asp Ala Gln Ala Arg Ser Ala Ile Glu
 165 170 175
 Ser Ser Gly Gly Asp Glu Asn Val Ala Leu Glu Lys Leu Cys Ser Gly
 180 185 190

<210> 1434
 <211> 579
 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (1)..(579)

<400> 1434	
atg ata gat atc agt cga gtc cag aaa gag ctc caa gat tgc gag aaa	48
Met Ile Asp Ile Ser Arg Val Gln Lys Glu Leu Gln Asp Cys Glu Lys	
1 5 10 15	
gac aga gac tcc tcg ggc atc cgg gtc tgc ccg aaa tcc gat aac ctc	96
Asp Arg Asp Ser Ser Gly Ile Arg Val Cys Pro Lys Ser Asp Asn Leu	
20 25 30	
acc cga ctc acc gga acc atc ccg ggt cca atc gga act cct tac gaa	144
Thr Arg Leu Thr Gly Thr Ile Pro Gly Pro Ile Gly Thr Pro Tyr Glu	
35 40 45	
ggc gga acc ttt cag atc gat atc acc att cca gaa ggg tat ccc ttt	192
Gly Gly Thr Phe Gln Ile Asp Ile Thr Ile Pro Glu Gly Tyr Pro Phe	
50 55 60	
gag cct cca aag atg caa ttt tca acc aaa gtt tgg cac ccg aac ata	240
Glu Pro Pro Lys Met Gln Phe Ser Thr Lys Val Trp His Pro Asn Ile	
65 70 75 80	
agt agc caa agc ggg gca ata tgc ttg gat gtc ttg aaa gac cag tgg	288
Ser Ser Gln Ser Gly Ala Ile Cys Leu Asp Val Leu Lys Asp Gln Trp	
85 90 95	
agt cca gct ctt act ttg aag aca gct ctt gtt tca gtc cag gca tta	336
Ser Pro Ala Leu Thr Leu Lys Thr Ala Leu Val Ser Val Gln Ala Leu	
100 105 110	
ctc tct gca cca gag cct aaa gac cct caa gat gct gtt gtt gct gaa	384
Leu Ser Ala Pro Glu Pro Lys Asp Pro Gln Asp Ala Val Val Ala Glu	
115 120 125	
cag tac atg aag aac tat caa gtg ttt gta tca aca gct cgt tac tgg	432

PF59082SeqList_PF59082.txt

Gln	Tyr	Met	Lys	Asn	Tyr	Gln	Val	Phe	Val	Ser	Thr	Ala	Arg	Tyr	Trp	
130						135					140					
acc	caa	aca	ttc	gcc	aag	aac	tct	tct	ctt	gag	gat	aaa	gtg	aag	aga	480
Thr	Gln	Thr	Phe	Ala	Lys	Asn	Ser	Ser	Leu	Glu	Asp	Lys	Val	Lys	Arg	
145					150					155					160	
ctc	gtg	gag	atg	ggg	ttt	gga	gat	gct	cag	gtt	agg	agt	gca	att	gaa	528
Leu	Val	Glu	Met	Gly	Phe	Gly	Asp	Ala	Gln	Val	Arg	Ser	Ala	Ile	Glu	
				165					170					175		
tca	agt	ggg	gga	gat	gag	aat	gtg	gcg	ctt	gaa	aag	ctc	tgt	tct	ggg	576
Ser	Ser	Gly	Gly	Asp	Glu	Asn	Val	Ala	Leu	Glu	Lys	Leu	Cys	Ser	Gly	
			180					185					190			
tag																579

<210> 1435
 <211> 192
 <212> PRT
 <213> Brassica napus

<400> 1435
 Met Ile Asp Ile Ser Arg Val Gln Lys Glu Leu Gln Asp Cys Glu Lys
 1 5 10 15
 Asp Arg Asp Ser Gly Ile Arg Val Cys Pro Lys Ser Asp Asn Leu
 20 25 30
 Thr Arg Leu Thr Gly Thr Ile Pro Gly Pro Ile Gly Thr Pro Tyr Glu
 35 40 45
 Gly Gly Thr Phe Gln Ile Asp Ile Thr Ile Pro Glu Gly Tyr Pro Phe
 50 55 60
 Glu Pro Pro Lys Met Gln Phe Ser Thr Lys Val Trp His Pro Asn Ile
 65 70 75
 Ser Ser Gln Ser Gly Ala Ile Cys Leu Asp Val Leu Lys Asp Gln Trp
 80 85 90 95
 Ser Pro Ala Leu Thr Leu Lys Thr Ala Leu Val Ser Val Gln Ala Leu
 100 105 110
 Leu Ser Ala Pro Glu Pro Lys Asp Pro Gln Asp Ala Val Val Ala Glu
 115 120 125
 Gln Tyr Met Lys Asn Tyr Gln Val Phe Val Ser Thr Ala Arg Tyr Trp
 130 135 140
 Thr Gln Thr Phe Ala Lys Asn Ser Ser Leu Glu Asp Lys Val Lys Arg
 145 150 155 160
 Leu Val Glu Met Gly Phe Gly Asp Ala Gln Val Arg Ser Ala Ile Glu
 165 170 175
 Ser Ser Gly Gly Asp Glu Asn Val Ala Leu Glu Lys Leu Cys Ser Gly
 180 185 190

<210> 1436
 <211> 579
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (1)..(579)

atg	ata	gac	ctt	gcg	cgc	gtg	cag	aag	gag	ctc	gtg	gaa	tgc	agc	aag	48
Met	Ile	Asp	Leu	Ala	Arg	Val	Gln	Lys	Glu	Leu	Val	Glu	Cys	Ser	Lys	
1				5					10					15		
gac	gcg	gag	gga	tcg	ggc	atc	aaa	gtc	tgc	ccc	aaa	agc	gac	aac	ctt	96
Asp	Ala	Glu	Gly	Ser	Gly	Ile	Lys	Val	Cys	Pro	Lys	Ser	Asp	Asn	Leu	
			20				25						30			
gtt	ctc	ttg	atc	ggc	acc	att	cct	ggc	cct	gtc	gga	act	cct	tat	gaa	144
Val	Leu	Leu	Ile	Gly	Thr	Ile	Pro	Gly	Pro	Val	Gly	Thr	Pro	Tyr	Glu	
			35				40					45				
ggg	ggc	att	ttc	cag	att	gat	atc	aca	ttg	cca	gat	ggg	tac	ccg	ttt	192
Gly	Gly	Ile	Phe	Gln	Ile	Asp	Ile	Thr	Leu	Pro	Asp	Gly	Tyr	Pro	Phe	
			50			55					60					
gaa	ccc	ccc	aag	atg	aag	ttt	aaa	acc	aaa	gtt	tgg	cat	cct	aat	atc	240

PF59082SeqList_PF59082.txt

Glu 65	Pro	Pro	Lys	Met	Lys 70	Phe	Lys	Thr	Lys	Val 75	Trp	His	Pro	Asn	Ile 80	
agc	agc	caa	agt	gga	gct	att	tgc	ctg	gat	atc	ttg	aag	gac	cag	tgg	288
Ser	Ser	Gln	Ser	Gly 85	Ala	Ile	Cys	Leu	Asp 90	Ile	Leu	Lys	Asp	Gln 95	Trp	
agc	cca	gca	ctc	act	ctg	aag	act	gca	ctt	ctt	tct	gtg	caa	gca	ctt	336
Ser	Pro	Ala	Leu	Thr	Leu	Lys	Thr	Ala	Leu	Leu	Ser	Val	Gln	Ala	Leu	
ctc	tct	gct	cca	cag	cct	gat	gat	cct	caa	gat	gcc	gtg	gtg	gca	cag	384
Leu	Ser	Ala	Pro	Gln	Pro	Asp	Asp	Pro	Gln	Asp	Ala	Val	Val	Ala	Gln	
cag	tat	ctg	aaa	gac	tat	cag	aca	ttt	gtt	aac	act	gct	cgc	tac	tgg	432
Gln	Tyr	Leu	Lys	Asp	Tyr	Gln	Thr	Phe	Val	Asn	Thr	Ala	Arg	Tyr	Trp	
aca	gaa	agt	ttt	gcc	aag	gaa	tcg	tct	cgc	ggg	att	gaa	gac	aag	gta	480
Thr	Glu	Ser	Phe	Ala	Lys 150	Glu	Ser	Ser	Arg	Gly 155	Ile	Glu	Asp	Lys	Val 160	
cag	aaa	ctc	gtt	gag	atg	gga	ttt	cca	gaa	gct	caa	gta	agg	agc	att	528
Gln	Lys	Leu	Val	Glu 165	Met	Gly	Phe	Pro	Glu 170	Ala	Gln	Val	Arg	Ser 175	Ile	
ttg	gaa	gct	gtt	ggt	ggt	gat	gaa	aac	ttg	gct	ctt	gaa	agg	ttg	ctg	576
Leu	Glu	Ala	Val 180	Gly	Gly	Asp	Glu	Asn 185	Leu	Ala	Leu	Glu	Arg 190	Leu	Leu	
tag																579

<210> 1437
 <211> 192
 <212> PRT
 <213> Glycine max

<400> 1437

Met	Ile	Asp	Leu	Ala	Arg	Val	Gln	Lys	Glu	Leu	Val	Glu	Cys	Ser	Lys	
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Asp	Ala	Glu	Gly	Ser	Gly	Ile	Lys	Val	Cys	Pro	Lys	Ser	Asp	Asn	Leu	
			20					25					30			
Val	Leu	Leu	Ile	Gly	Thr	Ile	Pro	Gly	Pro	Val	Gly	Thr	Pro	Tyr	Glu	
		35					40					45				
Gly	Gly	Ile	Phe	Gln	Ile	Asp	Ile	Thr	Leu	Pro	Asp	Gly	Tyr	Pro	Phe	
	50					55					60					
Glu	Pro	Pro	Lys	Met	Lys	Phe	Lys	Thr	Lys	Val	Trp	His	Pro	Asn	Ile	
65					70					75					80	
Ser	Ser	Gln	Ser	Gly	Ala	Ile	Cys	Leu	Asp	Ile	Leu	Lys	Asp	Gln	Trp	
			85						90					95		
Ser	Pro	Ala	Leu	Thr	Leu	Lys	Thr	Ala	Leu	Leu	Ser	Val	Gln	Ala	Leu	
			100					105					110			
Leu	Ser	Ala	Pro	Gln	Pro	Asp	Asp	Pro	Gln	Asp	Ala	Val	Val	Ala	Gln	
		115					120					125				
Gln	Tyr	Leu	Lys	Asp	Tyr	Gln	Thr	Phe	Val	Asn	Thr	Ala	Arg	Tyr	Trp	
	130					135					140					
Thr	Glu	Ser	Phe	Ala	Lys	Glu	Ser	Ser	Arg	Gly	Ile	Glu	Asp	Lys	Val	
145					150					155					160	
Gln	Lys	Leu	Val	Glu	Met	Gly	Phe	Pro	Glu	Ala	Gln	Val	Arg	Ser	Ile	
			165						170					175		
Leu	Glu	Ala	Val	Gly	Gly	Asp	Glu	Asn	Leu	Ala	Leu	Glu	Arg	Leu	Leu	
			180					185					190			

<210> 1438
 <211> 579
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (1)..(579)

<400> 1438
 atg ata gac ctt gcg cgc gtg cag aag gag ctc gtg gaa tgc agc aag 48
 Seite 1881

PF59082SeqList_PF59082.txt

Met	Ile	Asp	Leu	Ala	Arg	Val	Gln	Lys	Glu	Leu	Val	Glu	Cys	Ser	Lys	
1				5					10					15		
gac	gcg	gag	gga	tcg	ggc	atc	aaa	gtc	tgc	ccc	aaa	agc	gac	aac	ctt	96
Asp	Ala	Glu	Gly	Ser	Gly	Ile	Lys	Val	Cys	Pro	Lys	Ser	Asp	Asn	Leu	
			20					25					30			
gtt	ctc	ttg	atc	ggc	acc	att	cct	ggc	cct	gtc	gga	act	cct	tat	gaa	144
Val	Leu	Leu	Ile	Gly	Thr	Ile	Pro	Gly	Pro	Val	Gly	Thr	Pro	Tyr	Glu	
		35					40					45				
ggg	ggc	att	ttc	cag	att	gat	atc	aca	ttg	cca	gat	ggg	tac	ccg	ttt	192
Gly	Gly	Ile	Phe	Gln	Ile	Asp	Ile	Thr	Leu	Pro	Asp	Gly	Tyr	Pro	Phe	
		50				55					60					
gaa	ccc	ccc	aag	atg	aag	ttt	aaa	acc	aaa	gtt	tgg	cat	cct	aat	atc	240
Glu	Pro	Pro	Lys	Met	Lys	Phe	Lys	Thr	Lys	Val	Trp	His	Pro	Asn	Ile	
65					70				75						80	
agc	agc	caa	agt	gga	gct	att	tgc	ctg	gat	atc	ttg	aag	gac	cag	tgg	288
Ser	Ser	Gln	Ser	Gly	Ala	Ile	Cys	Leu	Asp	Ile	Leu	Lys	Asp	Gln	Trp	
				85				90						95		
agc	cca	gca	ctc	act	ctg	aag	act	gca	ctt	ctt	tct	gtg	caa	gca	ctt	336
Ser	Pro	Ala	Leu	Thr	Leu	Lys	Thr	Ala	Leu	Leu	Ser	Val	Gln	Ala	Leu	
			100					105					110			
ctc	tct	gct	cca	cag	cct	gat	gat	cct	caa	gat	gcc	gtg	gtg	gca	cag	384
Leu	Ser	Ala	Pro	Gln	Pro	Asp	Asp	Pro	Gln	Asp	Ala	Val	Val	Ala	Gln	
		115					120					125				
cag	tat	ctg	aaa	gac	tat	cag	aca	ttt	gtt	aac	act	gct	cgc	tac	tgg	432
Gln	Tyr	Leu	Lys	Asp	Tyr	Gln	Thr	Phe	Val	Asn	Thr	Ala	Arg	Tyr	Trp	
		130				135					140					
aca	gaa	agt	ttt	gcc	aag	gct	tcg	tct	cgt	ggg	att	gaa	gat	aag	gta	480
Thr	Glu	Ser	Phe	Ala	Lys	Ala	Ser	Ser	Arg	Gly	Ile	Glu	Asp	Lys	Val	
145					150					155					160	
cag	aaa	ctc	gtt	gag	atg	gga	ttt	cca	gaa	gct	cga	gta	agg	agc	att	528
Gln	Lys	Leu	Val	Glu	Met	Gly	Phe	Pro	Glu	Ala	Arg	Val	Arg	Ser	Ile	
				165				170						175		
ttg	gaa	gct	gtt	ggt	ggt	gat	gaa	aac	atg	gcc	ctt	gaa	agg	ttg	ctg	576
Leu	Glu	Ala	Val	Gly	Gly	Asp	Glu	Asn	Met	Ala	Leu	Glu	Arg	Leu	Leu	
			180					185					190			
tag																579

<210> 1439
 <211> 192
 <212> PRT
 <213> Glycine max

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 Met Ile Asp Leu Ala Arg Val Gln Lys Glu Leu Val Glu Cys Ser Lys
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 Asp Ala Glu Gly Ser Gly Ile Lys Val Cys Pro Lys Ser Asp Asn Leu
 20 25 30
 Val Leu Leu Ile Gly Thr Ile Pro Gly Pro Val Gly Thr Pro Tyr Glu
 35 40 45
 Gly Gly Ile Phe Gln Ile Asp Ile Thr Leu Pro Asp Gly Tyr Pro Phe
 50 55 60
 Glu Pro Pro Lys Met Lys Phe Lys Thr Lys Val Trp His Pro Asn Ile
 65 70 75 80
 Ser Ser Gln Ser Gly Ala Ile Cys Leu Asp Ile Leu Lys Asp Gln Trp
 85 90 95
 Ser Pro Ala Leu Thr Leu Lys Thr Ala Leu Leu Ser Val Gln Ala Leu
 100 105 110
 Leu Ser Ala Pro Gln Pro Asp Asp Pro Gln Asp Ala Val Val Ala Gln
 115 120 125
 Gln Tyr Leu Lys Asp Tyr Gln Thr Phe Val Asn Thr Ala Arg Tyr Trp
 130 135 140
 Thr Glu Ser Phe Ala Lys Ala Ser Ser Arg Gly Ile Glu Asp Lys Val
 145 150 155 160
 Gln Lys Leu Val Glu Met Gly Phe Pro Glu Ala Arg Val Arg Ser Ile
 165 170 175
 Leu Glu Ala Val Gly Gly Asp Glu Asn Met Ala Leu Glu Arg Leu Leu
 180 185 190

PF59082SeqList_PF59082.txt

<210> 1440
 <211> 585
 <212> DNA
 <213> Helianthus annuus

<220>
 <221> CDS
 <222> (1)..(585)

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<400> 1440
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 1          5          10          15
gat caa agc ata gta ggc atg act tta act ccc gac gag aac gac att      96
Asp Gln Ser Ile Val Gly Met Thr Leu Thr Pro Asp Glu Asn Asp Ile
          20          25          30
cgc cac ctc acc gcc acc atc ccc ggc cct ctt tcc act ccc tac gaa      144
Arg His Leu Thr Ala Thr Ile Pro Gly Pro Leu Ser Thr Pro Tyr Glu
          35          40          45
ggc gga tta ttc ggt gtc gat att act tta cca gat ggg tat cct ttt      192
Gly Gly Leu Phe Gly Val Asp Ile Thr Leu Pro Asp Gly Tyr Pro Phe
          50          55          60
gtg cct cct aaa atg aag ttc act aca aaa gtt tgg cat cca aat atc      240
Val Pro Pro Lys Met Lys Phe Thr Thr Lys Val Trp His Pro Asn Ile
 65          70          75          80
agt agc caa act gga gct ata tgt ctt gat atc cta aag aac aac tgg      288
Ser Ser Gln Thr Gly Ala Ile Cys Leu Asp Ile Leu Lys Asn Asn Trp
          85          90          95
agt cca gct cta aac ctg aaa acc gct ctg att tcc tta caa gct ctg      336
Ser Pro Ala Leu Asn Leu Lys Thr Ala Leu Ile Ser Leu Gln Ala Leu
          100          105          110
tta tca acc ccg gaa cca aac gat ccc caa gat gct gtt gtt gcc aaa      384
Leu Ser Thr Pro Glu Pro Asn Asp Pro Gln Asp Ala Val Val Ala Lys
          115          120          125
cag tat ctt agc gat aat gct aca tat gtt gct aca gct cgg cgt tgg      432
Gln Tyr Leu Ser Asp Asn Ala Thr Tyr Val Ala Thr Ala Arg Arg Trp
          130          135          140
aca gag gac ttt gcc aag gct tca tcc agt ggg ttc agt ggg aag gtg      480
Thr Glu Asp Phe Ala Lys Ala Ser Ser Ser Gly Phe Ser Gly Lys Val
145          150          155          160
cag aag ctg gtt gaa atg ggg ttc cct gaa ggg ttg gta aaa aag acg      528
Gln Lys Leu Val Glu Met Gly Phe Pro Glu Gly Leu Val Lys Lys Thr
          165          170          175
ctg gaa gct ttt ggc ggt gat gaa aac atg gca ctt gaa cgg ttg tgt      576
Leu Glu Ala Phe Gly Gly Asp Glu Asn Met Ala Leu Glu Arg Leu Cys
          180          185          190
cgg aaa tag
Arg Lys
    
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<210> 1441
 <211> 194
 <212> PRT
 <213> Helianthus annuus

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          20          25          30
Arg His Leu Thr Ala Thr Ile Pro Gly Pro Leu Ser Thr Pro Tyr Glu
          35          40          45
Gly Gly Leu Phe Gly Val Asp Ile Thr Leu Pro Asp Gly Tyr Pro Phe
          50          55          60
Val Pro Pro Lys Met Lys Phe Thr Thr Lys Val Trp His Pro Asn Ile
 65          70          75          80
Ser Ser Gln Thr Gly Ala Ile Cys Leu Asp Ile Leu Lys Asn Asn Trp
          85          90          95
    
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PF59082SeqList_PF59082.txt

Ser Pro Ala Leu Asn Leu Lys Thr Ala Leu Ile Ser Leu Gln Ala Leu
 100 105 110
 Leu Ser Thr Pro Glu Pro Asn Asp Pro Gln Asp Ala Val Val Ala Lys
 115 120 125
 Gln Tyr Leu Ser Asp Asn Ala Thr Tyr Val Ala Thr Ala Arg Arg Trp
 130 135 140
 Thr Glu Asp Phe Ala Lys Ala Ser Ser Ser Gly Phe Ser Gly Lys Val
 145 150 155 160
 Gln Lys Leu Val Glu Met Gly Phe Pro Glu Gly Leu Val Lys Lys Thr
 165 170 175
 Leu Glu Ala Phe Gly Gly Asp Glu Asn Met Ala Leu Glu Arg Leu Cys
 180 185 190
 Arg Lys

<210> 1442
 <211> 594
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (1)..(594)

<400> 1442
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 Met Val Asp Val Ser Arg Val Gln Lys Glu Leu Thr Glu Cys Asn Arg
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 gac cgg gag gta tcg ggc gtc tcc atc gcg ctc cac gac ggc gcc aac 96
 Asp Arg Glu Val Ser Gly Val Ser Ile Ala Leu His Asp Gly Ala Asn
 20 25 30
 atc tcc cac ctc acc ggc acc atc gcc ggg ccc gcc gac agc ccc tac 144
 Ile Ser His Leu Thr Gly Thr Ile Ala Gly Pro Ala Asp Ser Pro Tyr
 35 40 45
 gag ggc ggc acg ttc gtc atc gat atc cgc ctg ccc ggt gga tat ccc 192
 Glu Gly Gly Thr Phe Val Ile Asp Ile Arg Leu Pro Gly Gly Tyr Pro
 50 55 60
 ttt gag cct ccg aag atg cag ttc atc acc aaa gta tgg cac cct aac 240
 Phe Glu Pro Pro Lys Met Gln Phe Ile Thr Lys Val Trp His Pro Asn
 65 70 75 80
 atc agc agc caa aat gga gca att tgc ttg gac att ctg aaa gat cag 288
 Ile Ser Ser Gln Asn Gly Ala Ile Cys Leu Asp Ile Leu Lys Asp Gln
 85 90 95
 tgg agc cca gcc ctt acc ttg aag act gcg ctc ctt tcc ctt caa gct 336
 Trp Ser Pro Ala Leu Thr Leu Lys Thr Ala Leu Leu Ser Leu Gln Ala
 100 105 110
 ctg ctt tct tct cct gca cct gat gat cct cag gat gct gtt gtt gca 384
 Leu Leu Ser Ser Pro Ala Pro Asp Asp Pro Gln Asp Ala Val Val Ala
 115 120 125
 caa cag tac ctg cgt gac tat cca aca ttt gcc gct acg gct cgc tac 432
 Gln Gln Tyr Leu Arg Asp Tyr Pro Thr Phe Ala Ala Thr Ala Arg Tyr
 130 135 140
 tgg aca gag gcc ttc gcg aag agt gca tca acg ggc atg gaa gag aag 480
 Trp Thr Glu Ala Phe Ala Lys Ser Ala Ser Thr Gly Met Glu Glu Lys
 145 150 155 160
 gtg cag aag ctg gtt gag atg ggc ttc cca gag gat cag gtg aga agt 528
 Val Gln Lys Leu Val Glu Met Gly Phe Pro Glu Asp Gln Val Arg Ser
 165 170 175
 gcc ctg aag agc gtg gat ggc gac gag aac atg gct ctc gaa aag ctc 576
 Ala Leu Lys Ser Val Asp Gly Asp Glu Asn Met Ala Leu Glu Lys Leu
 180 185 190
 tgc tct ggc tct ggg tga 594
 Cys Ser Gly Ser Gly

<210> 1443
 <211> 197
 <212> PRT
 <213> Zea mays

PF59082SeqList_PF59082.txt

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<400> 1443
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20      25      30
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35      40      45
Glu Gly Gly Thr Phe Val Ile Asp Ile Arg Leu Pro Gly Gly Tyr Pro
50      55      60
Phe Glu Pro Pro Lys Met Gln Phe Ile Thr Lys Val Trp His Pro Asn
65      70      75      80
Ile Ser Ser Gln Asn Gly Ala Ile Cys Leu Asp Ile Leu Lys Asp Gln
85      90      95
Trp Ser Pro Ala Leu Thr Leu Lys Thr Ala Leu Leu Ser Leu Gln Ala
100     105     110
Leu Leu Ser Ser Pro Ala Pro Asp Asp Pro Gln Asp Ala Val Val Ala
115     120     125
Gln Gln Tyr Leu Arg Asp Tyr Pro Thr Phe Ala Ala Thr Ala Arg Tyr
130     135     140
Trp Thr Glu Ala Phe Ala Lys Ser Ala Ser Thr Gly Met Glu Glu Lys
145     150     155     160
Val Gln Lys Leu Val Glu Met Gly Phe Pro Glu Asp Gln Val Arg Ser
165     170     175
Ala Leu Lys Ser Val Asp Gly Asp Glu Asn Met Ala Leu Glu Lys Leu
180     185     190
Cys Ser Gly Ser Gly
195

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<210> 1444
<211> 591
<212> DNA
<213> Triticum aestivum

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<220>
<221> CDS
<222> (1)..(591)

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gac tcg gac atc tcc ggc gtc tcc atc gcg ctc cac gac ggg ggc tcc      96
Asp Ser Asp Ile Ser Gly Val Ser Ile Ala Leu His Asp Gly Gly Ser
20      25
agc atc acc cac ctc acc ggc acc atc gcc ggg ccc cgc gac agc ccc      144
Ser Ile Thr His Leu Thr Gly Thr Ile Ala Gly Pro Arg Asp Ser Pro
35      40      45
tac gag ggc ggc acc ttc cgc atc gac atc cgc ctg cca ggt ggc tat      192
Tyr Glu Gly Gly Thr Phe Arg Ile Asp Ile Arg Leu Pro Gly Gly Tyr
50      55      60
ccc ttt gag cct cct aag atg cag ttc atc acc aaa gta tgg cac ccg      240
Pro Phe Glu Pro Pro Lys Met Gln Phe Ile Thr Lys Val Trp His Pro
65      70      75      80
aat att agc agc caa aat gga gca att tgc ttg gac ata ctg aaa gat      288
Asn Ile Ser Ser Gln Asn Gly Ala Ile Cys Leu Asp Ile Leu Lys Asp
85      90      95
cag tgg agc cca gcc ctt acc ttg aag aca gca ttg cta tcc ctt caa      336
Gln Trp Ser Pro Ala Leu Thr Leu Lys Thr Ala Leu Leu Ser Leu Gln
100     105     110
gct ctt ctt tct gct cct gcc cct gat gat cct cag gat gct gtt gtt      384
Ala Leu Leu Ser Ala Pro Ala Pro Asp Asp Pro Gln Asp Ala Val Val
115     120     125
gca caa cag tat ctg cgt gac aag gcc aca ttt gtc agt act gct cgc      432
Ala Gln Gln Tyr Leu Arg Asp Lys Ala Thr Phe Val Ser Thr Ala Arg
130     135     140
tat tgg acc gag gca ttt gca aag agc gac tcc acc ggc atg gaa gaa      480
Tyr Trp Thr Glu Ala Phe Ala Lys Ser Asp Ser Thr Gly Met Glu Glu
145     150     155     160

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PF59082SeqList_PF59082.txt

aag	gtg	cag	aag	ctg	gtc	gag	atg	ggc	ttc	ccc	gag	gat	atg	gtg	aga	528
Lys	Val	Gln	Lys	Leu	Val	Glu	Met	Gly	Phe	Pro	Glu	Asp	Met	Val	Arg	
				165					170					175		
agc	gcc	ctg	atg	agt	gtg	aac	ggc	gac	gag	aac	atg	gct	ctc	gag	aag	576
Ser	Ala	Leu	Met	Ser	Val	Asn	Gly	Asp	Glu	Asn	Met	Ala	Leu	Glu	Lys	
			180					185					190			
ctc	tgc	tct	ggc	tga												591
Leu	Cys	Ser	Gly													
			195													

<210> 1445
 <211> 196
 <212> PRT
 <213> Triticum aestivum

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			20					25					30				
Ser	Ile	Thr	His	Leu	Thr	Gly	Thr	Ile	Ala	Gly	Pro	Arg	Asp	Ser	Pro		
		35					40					45					
Tyr	Glu	Gly	Gly	Thr	Phe	Arg	Ile	Asp	Ile	Arg	Leu	Pro	Gly	Gly	Tyr		
	50					55					60						
Pro	Phe	Glu	Pro	Pro	Lys	Met	Gln	Phe	Ile	Thr	Lys	Val	Trp	His	Pro		
65					70					75					80		
Asn	Ile	Ser	Ser	Gln	Asn	Gly	Ala	Ile	Cys	Leu	Asp	Ile	Leu	Lys	Asp		
				85					90					95			
Gln	Trp	Ser	Pro	Ala	Leu	Thr	Leu	Lys	Thr	Ala	Leu	Leu	Ser	Leu	Gln		
			100					105					110				
Ala	Leu	Leu	Ser	Ala	Pro	Ala	Pro	Asp	Asp	Pro	Gln	Asp	Ala	Val	Val		
		115					120					125					
Ala	Gln	Gln	Tyr	Leu	Arg	Asp	Lys	Ala	Thr	Phe	Val	Ser	Thr	Ala	Arg		
	130					135					140						
Tyr	Trp	Thr	Glu	Ala	Phe	Ala	Lys	Ser	Asp	Ser	Thr	Gly	Met	Glu	Glu		
145					150					155					160		
Lys	Val	Gln	Lys	Leu	Val	Glu	Met	Gly	Phe	Pro	Glu	Asp	Met	Val	Arg		
				165					170					175			
Ser	Ala	Leu	Met	Ser	Val	Asn	Gly	Asp	Glu	Asn	Met	Ala	Leu	Glu	Lys		
			180					185					190				
Leu	Cys	Ser	Gly														
			195														

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 <211> 582
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (1)..(582)

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Met	Ile	Asp	Leu	Ala	Arg	Val	Gln	Lys	Glu	Leu	Val	Glu	Cys	Ser	Lys		
1				5					10					15			
gac	gcg	gag	gga	tcg	ggc	atc	aaa	gtc	tgc	ccc	aaa	agc	gac	aac	ctt		96
Asp	Ala	Glu	Gly	Ser	Gly	Ile	Lys	Val	Cys	Pro	Lys	Ser	Asp	Asn	Leu		
			20					25					30				
gtt	ctc	ttg	atc	ggc	acc	att	cct	ggc	cct	gtc	gga	act	cct	tat	gaa		144
Val	Leu	Leu	Ile	Gly	Thr	Ile	Pro	Gly	Pro	Val	Gly	Thr	Pro	Tyr	Glu		
		35					40					45					
ggg	ggc	att	ttc	cag	att	gat	atc	aca	ttg	cca	gat	ggg	tac	ccg	ttt		192
Gly	Gly	Ile	Phe	Gln	Ile	Asp	Ile	Thr	Leu	Pro	Asp	Gly	Tyr	Pro	Phe		
	50					55					60						
gaa	ccc	ccc	aag	atg	aag	ttt	aaa	acc	aaa	gtt	tgg	cat	cct	aat	atc		240
Glu	Pro	Pro	Lys	Met	Lys	Phe	Lys	Thr	Lys	Val	Trp	His	Pro	Asn	Ile		
	65				70					75					80		
agc	agc	caa	agt	gga	gct	att	tgc	ctg	gat	atc	ttg	aag	gac	cag	tgg		288

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Ser	Ser	Gln	Ser	Gly	Ala	Ile	Cys	Leu	Asp	Ile	Leu	Lys	Asp	Gln	Trp	
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agc	cca	gca	ctc	act	ctg	aag	act	gca	ctt	ctt	tct	gtg	caa	gca	ctt	336
Ser	Pro	Ala	Leu	Thr	Leu	Lys	Thr	Ala	Leu	Leu	Ser	Val	Gln	Ala	Leu	
			100					105					110			
ctc	tct	gct	cca	cag	cct	gat	gat	cct	caa	gtg	tcc	gtg	gtg	gca	cag	384
Leu	Ser	Ala	Pro	Gln	Pro	Asp	Asp	Pro	Gln	Val	Ser	Val	Val	Ala	Gln	
		115				120						125				
cag	tta	tct	gaa	aga	cta	tca	gac	att	tgt	tta	aca	ctg	ctc	gct	act	432
Gln	Leu	Ser	Glu	Arg	Leu	Ser	Asp	Ile	Cys	Leu	Thr	Leu	Leu	Ala	Thr	
		130				135					140					
gga	cag	aaa	gtt	ttg	cca	agg	ctt	cgt	ctc	gtg	agt	att	gaa	gat	aag	480
Gly	Gln	Lys	Val	Leu	Pro	Arg	Leu	Arg	Leu	Val	Ser	Ile	Glu	Asp	Lys	
145					150				155						160	
gta	gag	aaa	ctc	gtt	gcg	atg	gga	ttt	cca	gac	gct	cta	gta	agt	agc	528
Val	Glu	Lys	Leu	Val	Ala	Met	Gly	Phe	Pro	Asp	Ala	Leu	Val	Ser	Ser	
			165					170						175		
ata	cta	gaa	gct	gtt	agt	ggg	cat	gaa	aag	ctt	cac	tcc	aaa	aag	ttg	576
Ile	Leu	Glu	Ala	Val	Ser	Gly	His	Glu	Lys	Leu	His	Ser	Lys	Lys	Leu	
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ctg	tag															582
Leu																

<210> 1447
 <211> 193
 <212> PRT
 <213> Glycine max

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			20					25					30			
Val	Leu	Leu	Ile	Gly	Thr	Ile	Pro	Gly	Pro	Val	Gly	Thr	Pro	Tyr	Glu	
		35					40					45				
Gly	Gly	Ile	Phe	Gln	Ile	Asp	Ile	Thr	Leu	Pro	Asp	Gly	Tyr	Pro	Phe	
	50					55					60					
Glu	Pro	Pro	Lys	Met	Lys	Phe	Lys	Thr	Lys	Val	Trp	His	Pro	Asn	Ile	
65					70				75						80	
Ser	Ser	Gln	Ser	Gly	Ala	Ile	Cys	Leu	Asp	Ile	Leu	Lys	Asp	Gln	Trp	
				85					90					95		
Ser	Pro	Ala	Leu	Thr	Leu	Lys	Thr	Ala	Leu	Leu	Ser	Val	Gln	Ala	Leu	
			100					105					110			
Leu	Ser	Ala	Pro	Gln	Pro	Asp	Asp	Pro	Gln	Val	Ser	Val	Val	Ala	Gln	
		115				120						125				
Gln	Leu	Ser	Glu	Arg	Leu	Ser	Asp	Ile	Cys	Leu	Thr	Leu	Leu	Ala	Thr	
		130				135					140					
Gly	Gln	Lys	Val	Leu	Pro	Arg	Leu	Arg	Leu	Val	Ser	Ile	Glu	Asp	Lys	
145					150				155						160	
Val	Glu	Lys	Leu	Val	Ala	Met	Gly	Phe	Pro	Asp	Ala	Leu	Val	Ser	Ser	
			165					170						175		
Ile	Leu	Glu	Ala	Val	Ser	Gly	His	Glu	Lys	Leu	His	Ser	Lys	Lys	Leu	
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Leu																

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 <212> DNA
 <213> Zea mays

<220>
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1	5	10	15	
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Asp	Arg	Glu	Val	Ser
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atc	tcc	cac	ctc	acc
Ile	Ser	His	Leu	Thr
		35		
gag	ggc	ggc	acg	ttc
Glu	Gly	Gly	Thr	Phe
	50			
ttt	gag	ccg	ccg	aag
Phe	Glu	Pro	Pro	Lys
65				
atc	agc	agc	caa	aat
Ile	Ser	Ser	Gln	Asn
			85	
tgg	agc	cca	gcc	ctt
Trp	Ser	Pro	Ala	Leu
			100	
ctg	ctt	tct	tct	cct
Leu	Leu	Ser	Pro	Ala
		115		
caa	cag	tac	ctg	cgt
Gln	Gln	Tyr	Leu	Arg
	130			
tgg	aca	gag	gcc	ttc
Trp	Thr	Glu	Ala	Phe
145				
gtg	cag	aag	ctg	gtt
Val	Gln	Lys	Leu	Val
			165	
gcc	ctg	aag	agc	gtg
Ala	Leu	Lys	Ser	Val
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tgc	tct	ggc	tct	ggg
Cys	Ser	Gly	Ser	Gly
		195		

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 <211> 197
 <212> PRT
 <213> Zea mays

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 35 40 45
 Glu Gly Gly Thr Phe Val Ile Asp Ile Arg Leu Pro Gly Gly Tyr Pro
 50 55 60
 Phe Glu Pro Pro Lys Met Gln Phe Ile Thr Lys Val Trp His Pro Asn
 65 70 75 80
 Ile Ser Ser Gln Asn Gly Ala Ile Cys Leu Asp Ile Leu Lys Asp Gln
 85 90 95
 Trp Ser Pro Ala Leu Thr Leu Lys Thr Ala Leu Leu Ser Leu Gln Ala
 100 105 110
 Leu Leu Ser Pro Ala Pro Asp Pro Gln Asp Ala Val Val Ala
 115 120 125
 Gln Gln Tyr Leu Arg Asp Tyr Pro Thr Phe Ala Ala Thr Ala Arg Tyr
 130 135 140
 Trp Thr Glu Ala Phe Ala Lys Ser Ala Ser Thr Gly Met Glu Glu Lys
 145 150 155 160
 Val Gln Lys Leu Val Glu Met Gly Phe Pro Glu Asp Gln Val Arg Ser
 165 170 175
 Ala Leu Lys Ser Val Asp Gly Asp Glu Asn Met Ala Leu Glu Lys Leu
 180 185 190
 Cys Ser Gly Ser Gly

195

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 <220>
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 <400> 1452
 atgatatgatt tcagtcgaat ccag 24

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 <220>
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 <400> 1453
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 <210> 1454
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28

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<220>
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30

<210> 1458
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 <213> Artificial sequence

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<222> (119)..(119)
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<222> (130)..(130)
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<222> (133)..(138)
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<222> (140)..(141)
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<222> (145)..(145)
<223> Xaa in position 145 is any amino acid

<220>
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<222> (150)..(150)
<223> Xaa in position 150 is any amino acid

<220>
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<222> (154)..(155)
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<221> Variant

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<222> (189)..(189)

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<222> (193)..(193)

<223> Xaa in position 193 is any amino acid

<400> 1458

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20      25      30
Xaa Xaa Xaa Xaa Leu Xaa Gly Thr Ile Xaa Gly Pro Xaa Xaa Xaa Pro
35      40      45
Tyr Glu Gly Gly Xaa Phe Xaa Ile Asp Ile Xaa Leu Pro Xaa Gly Tyr
50      55      60
Pro Phe Glu Pro Pro Lys Met Xaa Phe Xaa Thr Lys Val Trp His Pro
65      70      75      80
Asn Ile Ser Ser Gln Xaa Gly Ala Ile Cys Leu Asp Ile Leu Lys Asp
85      90      95
Gln Trp Ser Pro Ala Leu Thr Leu Lys Thr Ala Leu Xaa Ser Xaa Gln
100     105     110
Ala Leu Leu Ser Xaa Pro Xaa Pro Xaa Asp Pro Gln Asp Ala Val Val
115     120     125
Ala Xaa Gln Tyr Xaa Xaa Xaa Xaa Xaa Phe Xaa Xaa Thr Ala Arg
130     135     140
Xaa Tyr Trp Thr Glu Xaa Phe Ala Lys Xaa Xaa Ser Xaa Xaa Xaa Glu
145     150     155     160
Xaa Lys Val Xaa Lys Leu Val Glu Met Gly Phe Pro Xaa Xaa Xaa Val
165     170     175
Arg Ser Xaa Leu Xaa Xaa Xaa Xaa Gly Asp Glu Asn Xaa Ala Leu Glu
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Xaa Leu

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<222> (8)..(8)

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<221> Variant

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<222> (13)..(13)

<223> Xaa in position 13 is Ile, Leu or Met

<220>

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<222> (15)..(15)

<223> Xaa in position 15 is any or no amino acid

PF59082SeqList_PF59082.txt

<220>
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 <223> Xaa in position 17 is any or no amino acid

<220>
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 <222> (26)..(26)
 <223> Xaa in position 26 is any amino acid

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 <222> (28)..(28)
 <223> Xaa in position 28 is any amino acid

<220>
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 <222> (40)..(40)
 <223> Xaa in position 40 is Asn or Ser

<220>
 <221> Variant
 <222> (47)..(47)
 <223> Xaa in position 47 is Ile or Val

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 His Pro Asn Ile Ser Ser Gln Xaa Gly Ala Ile Cys Leu Asp Xaa Leu
 35 40 45
 Lys Asp Gln Trp Ser Pro Ala Leu Thr Leu Lys Thr Ala
 50 55 60

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 <211> 20
 <212> PRT
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<220>
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 <222> (5)..(5)
 <223> Xaa in position 5 is Ala or Ser

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 <222> (7)..(7)
 <223> Xaa in position 7 is Ala, Glu or Gln

<220>
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 <222> (9)..(9)
 <223> Xaa in position 9 is Asp or Lys

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 <223> Xaa in position 18 is Glu or Gln

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 Ala Xaa Gln Tyr

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<223> Xaa in position 12 is Gly or Pro

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<223> Xaa in position 13 is Asp or Glu

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<223> Xaa in position 20 is Ile or Leu

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<223> Xaa in position 22 is Ala or Ser

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<222> (23)..(23)

<223> Xaa in position 23 is any amino acid

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<222> (24)..(24)

<223> Xaa in position 24 is Asp, Gly or Asn

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<222> (29)..(29)

<223> Xaa in position 29 is Leu, Met or Val

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<223> Xaa in position 33 is Lys or Arg

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<223> Xaa in position 2 is Ala or Val

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<220>

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<222> (10)..(10)

<223> Xaa in position 10 is Glu or Gln

<220>

<221> Variant

<222> (11)..(11)

<223> Xaa in position 11 is Ala, Ser or Thr

<400> 1462

Phe Xaa Xaa Thr Ala Arg Tyr Trp Thr Xaa Xaa Phe
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<210> 1463

<211> 11

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<213> Artificial sequence

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<222> (6)..(6)

<223> Xaa in position 6 is Ala or Pro

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<222> (9)..(9)

<223> Xaa in position 9 is Ala, Ile or Val

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<222> (10)..(10)

<223> Xaa in position 10 is Asp or Gly

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cat gga gtt aca gca aga gaa caa gtc ttc tct ttc tcc gtc gat gct	96
His Gly Val Thr Ala Arg Glu Gln Val Phe Ser Phe Ser Val Asp Ala	
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tcg tct caa aca gtc caa tca gac gat cca aca gct aaa ttc gcc ctt	144
Ser Ser Gln Thr Val Gln Ser Asp Asp Pro Thr Ala Lys Phe Ala Leu	
35 40 45	
ccg gtt gat tcc gaa cat cga gcc aaa gtg ttc aac cca ctc tct ttt	192
Pro Val Asp Ser Glu His Arg Ala Lys Val Phe Asn Pro Leu Ser Phe	
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gct aaa cct cac atg aga gcc ttc cac tta gga tgg ctc tca ttc ttc	240
Ala Lys Pro His Met Arg Ala Phe His Leu Gly Trp Leu Ser Phe Phe	
65 70 75 80	
aca tgc ttc atc tcc acc ttc gcg gca gca cca tta gtc ccc atc atc	288
Thr Cys Phe Ile Ser Thr Phe Ala Ala Ala Pro Leu Val Pro Ile Ile	
85 90 95	
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Arg Asp Asn Leu Asp Leu Thr Lys Thr Asp Ile Gly Asn Ala Gly Val	
100 105 110	
gca tcc gtc tct ggt gcc att ttc tca agg tta gcc atg gga gcg gtt	384
Ala Ser Val Ser Gly Ala Ile Phe Ser Arg Leu Ala Met Gly Ala Val	
115 120 125	
tgt gat ctc ctc ggt gca cga tat ggg act gcc ttc tcc ctc atg cta	432
Cys Asp Leu Leu Gly Ala Arg Tyr Gly Thr Ala Phe Ser Leu Met Leu	
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Tyr	Leu	Gly	Val	Arg	Phe	Met	Ile	Gly	Phe	Cys	Leu	Ala	Thr	Phe	Val	
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Ser	Cys	Gln	Tyr	Trp	Thr	Ser	Val	Met	Phe	Asn	Gly	Lys	Ile	Ile	Gly	
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Thr	Gln	Leu	Leu	Met	Pro	Met	Val	Phe	His	Val	Ile	Lys	Leu	Ala	Gly	
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cct	gac	ggt	aac	cta	agt	acc	ctt	cag	aag	agt	ggt	caa	gtc	tct	aaa	816
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Asp	Lys	Phe	Ser	Lys	Val	Phe	Trp	Phe	Ala	Val	Lys	Asn	Tyr	Arg	Thr	
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 Trp Leu Ser Leu Phe Ser Cys Phe Phe Ser Thr Phe Ser Ile Pro Pro
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 Ala Met Gly Pro Leu Cys Asp Leu Ile Gly Pro Arg Thr Ser Ser Ala
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 175 180 185
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 Phe Pro Ala Ile Phe Gln Val Thr Thr Ala Val Leu Val Leu Leu Tyr
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Thr	Thr	Asp	Asn	Val	Ile	Ala	Gly	Tyr	Phe	Tyr	Glu	Arg	Phe	Gly	Val	
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aat	ctg	gag	gcg	gcg	ggg	acg	atc	gcg	gcg	agt	ttc	ggg	ata	tcg	aac	1022
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Gly	Ser	Ile	Leu	Val	Met	Trp	Val	Phe	Ser	Val	Phe	Val	Gln	Ala	Ala	
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Ser	Gly	Leu	Val	Phe	Gly	Val	Val	Pro	Phe	Val	Ser	Lys	Arg	Ser	Leu	
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Gly	Val	Val	Ala	Gly	Ile	Thr	Gly	Ser	Gly	Gly	Thr	Val	Gly	Ala	Val	
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Val	Thr	Gln	Phe	Leu	Leu	Phe	Ser	Gly	Asp	Asp	Val	Arg	Lys	Gln	Arg	
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agc	att	tca	ctt	atg	ggg	ttg	atg	act	ttt	gtg	ttt	gct	ctt	tct	gtt	1406
Ser	Ile	Ser	Leu	Met	Gly	Leu	Met	Thr	Phe	Val	Phe	Ala	Leu	Ser	Val	
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Thr	Ser	Ile	Tyr	Phe	Pro	Gln	Trp	Gly	Gly	Met	Cys	Cys	Gly	Pro	Ser	
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Ser	Ser	Ser	Glu	Glu	Glu	Asp	Ile	Ser	Arg	Gly	Leu	Leu	Val	Glu	Asp	
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Glu	Asp	Glu	Glu	Gly	Lys	Val	Val	Ser	Gly	Ser	Leu	Arg	Pro	Val	Cys	
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<213> Arabidopsis thaliana

<400> 1467

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Leu Phe Ser Cys Phe Phe Ser Thr Phe Ser Ile Pro Leu Val Pro
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Val Ile Ser Ser Asp Leu Asn Leu Ser Ala Ser Thr Val Ser Ala Ala
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Thr Pro His Gly Asn Arg Lys Asn Ser Asn Gln Asn Lys Leu Thr Ile
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Pro Glu Glu Glu Val Leu Val Val Glu Asp Glu Arg Ser Ser
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Asn Val Ile Ala Gly Tyr Phe Tyr Glu Arg Phe Gly Val Asn Leu Glu
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Phe Leu Leu Phe Ser Gly Asp Asp Val Arg Lys Gln Arg Ser Ile Ser
      420      425      430
Leu Met Gly Leu Met Thr Phe Val Phe Ala Leu Ser Val Thr Ser Ile
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Tyr Phe Pro Gln Trp Gly Gly Met Cys Cys Gly Pro Ser Ser Ser
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<211> 1620

<212> DNA

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Lys Leu Gln Ser Pro His Val Arg Ala Phe His Leu Ser Trp Met Phe	
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260 265 270	
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Thr Trp Val Leu Thr Leu Asn Tyr Gly Tyr Cys Phe Gly Val Glu Leu	
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Seite 1904

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 Gln Val Asp Gly Lys Lys Thr Phe Leu Ala Gly Ile Arg Asn Tyr Arg
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 Ile Phe Cys Arg Ser Met Gly Gly Ile Ala Ser Asp Val Ala Gly Lys
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<213> Zea mays

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tcgaccgcgc cgcgccgct gccgcctccc agctcgctct atataaacac cacgtacgcg 180

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Gly Arg Glu Gln Ser Phe Ala Phe Ser Val Gln Ser Pro Ile Val His	
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Thr Asp Lys Thr Ala Lys Phe Asp Leu Pro Val Asp Thr Glu His Lys	
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Ala Thr Val Phe Lys Leu Phe Ser Phe Ala Lys Pro His Met Arg Thr	
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Phe His Leu Ser Trp Ile Ser Phe Ser Thr Cys Phe Val Ser Thr Phe	
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PF59082SeqList_PF59082.txt

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aaa Lys	caa Gln	gac Asp	att Ile 100	gga Gly	aac Asn	gcc Ala	gga Gly	ggt Val 105	gcc Ala	tct Ser	gtc Val	tct Ser	ggg Gly 110	agt Ser	atc Ile	336
ttc Phe	tct Ser	agg Arg 115	ctc Leu	gtg Val	atg Met	gga Gly	gcc Ala 120	gtg Val	tgt Cys	gat Asp	ctt Leu	ttg Leu 125	ggg Gly	ccc Pro	cgt Arg	384
tac Tyr	ggt Gly 130	tgt Cys	gcc Ala	ttc Phe	ctt Leu	gtg Val 135	atg Met	ttg Leu	tct Ser	gcc Ala 140	cca Pro	acg Thr	gtg Val	ttc Phe	tcc Ser	432
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gga Gly	tgg Trp	gga Gly 195	aac Asn	atg Met	ggt Gly	ggc Gly	ggc Gly 200	ata Ile	acg Thr	cag Gln	ttg Leu	ctc Leu 205	atg Met	ccc Pro	att Ile	624
gtg Val	tat Tyr 210	gaa Glu	atc Ile	att Ile	agg Arg	cgc Arg 215	tgc Cys	ggt Gly	tcc Ser	aca Thr	gcc Ala 220	ttc Phe	acg Thr	gcc Ala	tgg Trp	672
agg Arg 225	atc Ile	gcc Ala	ttc Phe	ttt Phe	gta Val 230	ccc Pro	ggt Gly	tgg Trp	ttg Leu	cac His 235	atc Ile	atc Ile	atg Met	gga Gly	atc Ile 240	720
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gct Ala	gga Gly	ggg Gly	aac Asn 420	ttt Phe	gga Gly	tca Ser	ggg Gly	ctc Leu 425	aca Thr	caa Gln	ctc Leu	ctc Leu	ttc Phe 430	ttc Phe	tcg Ser	1296
acc Thr	tca Ser	cac His 435	ttc Phe	aca Thr	act Thr	gaa Glu	caa Gln 440	ggg Gly	cta Leu	acg Thr	tgg Trp	atg Met 445	gga Gly	gtg Val	atg Met	1344

PF59082SeqList_PF59082.txt

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Trp	Tyr	Ala	Val	Thr	Asn	Tyr	Arg	Thr	Trp	Ile	Phe	Val	Leu	Leu	Tyr	
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 Thr Ser His Phe Thr Thr Glu Gln Gly Leu Thr Trp Met Gly Val Met
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 Gly Ser Met Phe Leu Pro Pro Ser Thr Asp Pro Val Lys Gly Thr Glu
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 485 490 495
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Thr Lys Lys Lys Tyr Asn Leu Pro Val Asp Ala Glu Asp Lys Ala Thr	
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gtt ttc aag ctc ttc tcc ttc gcc aaa cct cac atg aga acg ttc cac	192
Val Phe Lys Leu Phe Ser Phe Ala Lys Pro His Met Arg Thr Phe His	
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ctc tcg tgg atc tct ttc tcc aca tgt ttt gtt tcg acg ttc gca gct	240
Leu Ser Trp Ile Ser Phe Ser Thr Cys Phe Val Ser Thr Phe Ala Ala	
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Ala Pro Leu Ile Pro Ile Ile Arg Glu Asn Leu Asn Leu Thr Lys His	
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Asp Ile Gly Asn Ala Gly Val Ala Ser Val Ser Gly Ser Ile Phe Ser	
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agg ctc gtg atg gga gcc gtg tgt gat ctt ttg ggt cct cgt tac ggt	384
Arg Leu Val Met Gly Ala Val Cys Asp Leu Leu Gly Pro Arg Tyr Gly	
115 120 125	
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Cys Ala Phe Leu Val Met Leu Ser Ala Pro Thr Val Phe Ser Met Ser	
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PF59082SeqList_PF59082.txt

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Glu	Ile	Ile	Arg	Arg	Cys	Gly	Ser	Thr	Ala	Phe	Thr	Ala	Trp	Arg	Ile	
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Leu	Thr	Leu	Gly	Gln	Asp	Leu	Pro	Gly	Gly	Asn	Arg	Ala	Ala	Met	Glu	
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Met	Phe	Phe	Pro	Pro	Ser	Asn	Asp	Ser	Val	Asp	Ala	Thr	Glu	His	Tyr	
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Lys	Ser	Lys	Leu	Phe	Ala	Asp	Gly	Ala	Lys	Thr	Glu	Gly	Gly	Ser	Ser	
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gtc	cac	aaa	ggg	aac	gca	acc	aac	aat	gct	tga						1569
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Thr Phe Arg Leu Phe Ser Val Ala Lys Pro His Met Arg Ala Phe His
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Arg Ile Val Met Gly Thr Ala Cys Asp Leu Phe Gly Pro Arg Leu Ala
100      105      110
tcc gcc gct ttg acg ctc tcc acc gct ccc gcc gtc tat ttc acc gcc      384
Ser Ala Ala Leu Thr Leu Ser Thr Ala Pro Ala Val Tyr Phe Thr Ala
115      120      125
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Gly Ile Lys Ser Pro Ile Gly Phe Ile Met Val Arg Phe Phe Ala Gly
130      135      140
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Cys Phe Gly Val Glu Leu Thr Ile Asp Asn Ile Ile Ala Glu Tyr Phe
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Phe Asp Arg Phe His Leu Lys Leu Gln Thr Ala Gly Ile Ile Ala Ala
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295      300

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Gln	Ile	Ser 355	Ser	Leu	Thr	Val 360	Ser	Ile	Ile	Val	Met	Leu	Val 365	Phe	Ser	
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Ile	Ser	Arg	Arg	Ser	Leu 390	Gly	Val	Val	Ser	Gly 395	Met	Thr	Gly	Ala	Gly 400	
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Thr	Tyr	Thr	Arg 420	Glu	Thr	Gly	Ile	Thr 425	Leu	Met	Gly	Val	Met 430	Ser	Ile	
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Ala	Cys	Ser 435	Leu	Pro	Ile	Cys	Leu 440	Ile	Tyr	Phe	Pro	Gln	Trp 445	Gly	Gly	
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Met	Phe	Cys	Gly	Pro	Ser	Ser 455	Lys	Lys	Val	Thr	Glu 460	Glu	Asp	Tyr	Tyr	
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Leu	Ala	Glu	Trp	Asn	Asp 470	Glu	Glu	Lys	Glu	Lys 475	Asn	Leu	His	Ile	Gly 480	
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PF59082SeqList_PF59082.txt

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325 330 335
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Asp Val Pro Ser Ser Gln Ala Val Arg Thr Asn Asp Pro Thr Ala Lys	
35 40 45	
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Ala	Arg	Leu	Phe	Gly	Met	Arg	Gly	Arg	Leu	Trp	Ile	Leu	Trp	Ile	Leu	
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Ala Glu Gly Leu Ser Leu Met Gly Val Met Ala Val Val Cys Ser Leu
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Pro Val Ala Phe Ile His Phe Pro Gln Trp Gly Ser Met Phe Leu Arg
465          470          475          480
Pro Ser Gln Asp Gly Glu Lys Ser Lys Glu Glu His Tyr Tyr Gly Ala
          485          490          495
Glu Trp Thr Glu Glu Lys Ser Leu Gly Leu His Glu Gly Ser Ile
          500          505          510
Lys Phe Ala Glu Asn Ser Arg Ser Glu Arg Gly Arg Lys Ala Met Leu
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<210> 1480

<211> 1584

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1584)

<400> 1480

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ggc aga gaa caa agc tat gca ttc tct gtc gag tct ccg gca gtt cct      96
Gly Arg Glu Gln Ser Tyr Ala Phe Ser Val Glu Ser Pro Ala Val Pro
          20          25          30
tcc gac tca tca gca aaa ttt tct ctc ccc gtg gac acc gaa cac aaa      144
Ser Asp Ser Ser Ala Lys Phe Ser 40 Leu Pro Val Asp Thr Glu His Lys
          35          40          45
gcc aaa gtc ttc aaa ctc tta tcc ttt gaa gct cca cat atg aga act      192
Ala Lys Val Phe Lys Leu Leu Ser Phe Glu Ala Pro His Met Arg Thr
          50          55          60
ttc cat ctt gct tgg atc tca ttc ttc act tgc ttc att tcc act ttc      240
Phe His Leu Ala Trp Ile Ser Phe Phe Thr Cys Phe Ile Ser Thr Phe
          65          70          75
gct gct gct cct ctt gtc ccc atc att aga gat aac ctt aat ctc aca      288
Ala Ala Ala Pro Leu Val Pro Ile Ile Arg 90 Asp Asn Leu Asn Leu Thr
          85          90          95
aga caa gat gtc gga aat gct ggt gtt gct tct gtc tct ggc agt atc      336
Arg Gln Asp Val Gly Asn Ala Gly Val Ala Ser Val Ser Gly Ser Ile
          100          105          110
ttc tct agg ctt gtt atg gga gca gtt tgt gat ctc ctt ggg cca cgt      384
Phe Ser Arg Leu Val Met Gly Ala Val Cys Asp Leu 125 Gly Pro Arg
          115          120          125
tat ggc tgt gct ttc ctc gtc atg ctc tct gct cca acc gtc ttc tcc      432
Tyr Gly Cys Ala Phe Leu Val Met Leu Ser Ala Pro Thr Val Phe Ser
          130          135          140
atg tct ttc gtt ggt ggt gcc gga ggg tac ata acg gtg agg ttc atg      480
Met Ser Phe Val Gly Gly Ala Gly Gly Tyr Ile Thr Val Arg Phe Met
          145          150          155
atc ggg ttc tgc ctg gcg act ttc gtg tca tgc cag tat tgg atg agc      528
Ile Gly Phe Cys Leu Ala Thr Phe Val Ser Cys Gln Tyr Trp Met Ser
          165          170          175
aca atg ttc aat ggt cag atc ata ggt cta gtg aac ggg aca gcg gca      576
Thr Met Phe Asn Gly Gln Ile Ile Gly Leu Val Asn Gly Thr Ala Ala
          180          185          190
ggg tgg ggg aac atg ggc ggt ggg gtc act cag ttg ctc atg cca atg      624

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PF59082SeqList_PF59082.txt

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Val	Tyr	Glu	Ile	Ile	Arg	Arg	Leu	Gly	Ser	Thr	Ser	Phe	Thr	Ala	Trp	
agg	atg	gct	ttc	ttc	gtc	ccc	ggg	tgg	atg	cac	atc	atg	ggg	atc		720
Arg	Met	Ala	Phe	Phe	Val	Pro	Gly	Trp	Met	His	Ile	Ile	Met	Gly	Ile	
225					230					235					240	
ttg	gtc	ttg	act	cta	ggg	caa	gac	ctc	cct	gat	ggt	aat	aga	agc	aca	768
Leu	Val	Leu	Thr	Leu	Gly	Gln	Asp	Leu	Pro	Asp	Gly	Asn	Arg	Ser	Thr	
				245					250					255		
ctc	gag	aag	aaa	ggt	gca	gtt	act	aaa	gac	aag	ttc	tca	aag	gtt	tta	816
Leu	Glu	Lys	Lys	Gly	Ala	Val	Thr	Lys	Asp	Lys	Phe	Ser	Lys	Val	Leu	
			260					265					270			
tgg	tac	gcg	atc	acg	aac	tat	agg	aca	tgg	gtt	ttc	gtg	ctg	cta	tat	864
Trp	Tyr		Ile	Thr	Asn	Tyr	Arg	Thr	Trp	Val	Phe	Val	Leu	Leu	Tyr	
			275				280					285				
gga	tac	tcc	atg	gga	gta	gag	ctc	aca	acc	gat	aac	gtc	atc	gct	gag	912
Gly	Tyr	Ser	Met	Gly	Val	Glu	Leu	Thr	Thr	Asp	Asn	Val	Ile	Ala	Glu	
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tac	ttt	ttc	gac	agg	ttc	cat	ctt	aag	ctt	cat	acc	gcc	ggg	ata	atc	960
Tyr	Phe	Phe	Asp	Arg	Phe	His	Leu	Lys	Leu	His	Thr	Ala	Gly	Ile	Ile	
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gcg	gca	agc	ttt	ggg	atg	gca	aac	ttc	ttt	gcc	cgt	cct	att	ggg	ggg	1008
Ala	Ala	Ser	Phe	Gly	Met	Ala	Asn	Phe	Phe	Ala	Arg	Pro	Ile	Gly	Gly	
				325				330						335		
tgg	gcc	tca	gat	att	gcg	gct	aga	cgc	ttc	ggc	atg	aga	ggc	cgt	ctc	1056
Trp	Ala	Ser	Asp	Ile	Ala	Ala	Arg	Arg	Phe	Gly	Met	Arg	Gly	Arg	Leu	
			340				345						350			
tgg	acc	cta	tgg	atc	atc	caa	acc	tta	ggc	ggg	ttc	ttc	tgc	cta	tgg	1104
Trp	Thr	Leu	Trp	Ile	Ile	Gln	Thr	Leu	Gly	Gly	Phe	Phe	Cys	Leu	Trp	
			355			360						365				
cta	ggc	cga	gcc	acc	acg	ctc	ccg	acc	gcg	gtt	gtc	ttc	atg	atc	ctc	1152
Leu	Gly	Arg	Ala	Thr	Thr	Leu	Pro	Thr	Ala	Val	Val	Phe	Met	Ile	Leu	
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Phe	Ser	Leu	Gly	Ala	Gln	Ala	Ala	Cys	Gly	Ala	Thr	Phe	Ala	Ile	Ile	
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cct	ttc	atc	tca	cgc	cgc	tcc	tta	ggg	atc	atc	tct	ggg	ctt	act	gga	1248
Pro	Phe	Ile	Ser	Arg	Arg	Ser	Leu	Gly	Ile	Ile	Ser	Gly	Leu	Thr	Gly	
				405				410						415		
gct	ggg	gga	aac	ttc	ggc	tct	ggg	ttg	acc	caa	ctc	gta	ttc	ttc	tcg	1296
Ala	Gly	Gly	Asn	Phe	Gly	Ser	Gly	Leu	Thr	Gln	Leu	Val	Phe	Phe	Ser	
			420				425						430			
acc	tca	acg	ttc	tcc	acg	gaa	caa	ggg	ctg	aca	tgg	atg	ggg	gtg	atg	1344
Thr	Ser	Thr	Phe	Ser	Thr	Glu	Gln	Gly	Leu	Thr	Trp	Met	Gly	Val	Met	
			435			440						445				
att	atg	gcg	tgt	aca	tta	ccc	gtc	act	tta	gtg	cac	ttc	ccg	caa	tgg	1392
Ile	Met	Ala	Cys	Thr	Leu	Pro	Val	Thr	Leu	Val	His	Phe	Pro	Gln	Trp	
						455					460					
gga	agc	atg	ttt	ttg	cct	tcc	acg	gaa	gat	gaa	gtg	aag	tct	acg	gag	1440
Gly	Ser	Met	Phe	Leu	Pro	Ser	Thr	Glu	Asp	Glu	Val	Lys	Ser	Thr	Glu	
465					470					475					480	
gag	tat	tat	tac	atg	aaa	gag	tgg	aca	gag	acc	gag	aag	cga	aag	ggg	1488
Glu	Tyr	Tyr	Tyr	Met	Lys	Glu	Trp	Thr	Glu	Thr	Glu	Lys	Arg	Lys	Gly	
				485				490						495		
atg	cat	gaa	ggg	agt	ttg	aag	ttc	gcc	gtg	aat	agt	aga	tcg	gag	cgt	1536
Met	His	Glu	Gly	Ser	Leu	Lys	Phe	Ala	Val	Asn	Ser	Arg	Ser	Glu	Arg	
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gga	cgg	cgc	gtg	gct	tct	gca	ccg	tct	cct	ccg	ccg	gaa	cac	gtt		1581
Gly	Arg	Arg	Val	Ala	Ser	Ala	Pro	Ser	Pro	Pro	Pro	Glu	His	Val		
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 <212> PRT

<213> Arabidopsis thaliana

<400> 1481

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35      40      45
Ala Lys Val Phe Lys Leu Leu Ser Phe Glu Ala Pro His Met Arg Thr
50      55      60
Phe His Leu Ala Trp Ile Ser Phe Phe Thr Cys Phe Ile Ser Thr Phe
65      70      75      80
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85      90      95
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100     105
Phe Ser Arg Leu Val Met Gly Ala Val Cys Asp Leu Leu Gly Pro Arg
115     120     125
Tyr Gly Cys Ala Phe Leu Val Met Leu Ser Ala Pro Thr Val Phe Ser
130     135     140
Met Ser Phe Val Gly Gly Ala Gly Gly Tyr Ile Thr Val Arg Phe Met
145     150     155     160
Ile Gly Phe Cys Leu Ala Thr Phe Val Ser Cys Gln Tyr Trp Met Ser
165     170     175
Thr Met Phe Asn Gly Gln Ile Ile Gly Leu Val Asn Gly Thr Ala Ala
180     185     190
Gly Trp Gly Asn Met Gly Gly Gly Val Thr Gln Leu Leu Met Pro Met
195     200     205
Val Tyr Glu Ile Ile Arg Arg Leu Gly Ser Thr Ser Phe Thr Ala Trp
210     215     220
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225     230     235     240
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Leu Glu Lys Lys Gly Ala Val Thr Lys Asp Lys Phe Ser Lys Val Leu
260     265     270
Trp Tyr Ala Ile Thr Asn Tyr Arg Thr Trp Val Phe Val Leu Leu Tyr
275     280     285
Gly Tyr Ser Met Gly Val Glu Leu Thr Thr Asp Asn Val Ile Ala Glu
290     295     300
Tyr Phe Phe Asp Arg Phe His Leu Lys Leu His Thr Ala Gly Ile Ile
305     310     315     320
Ala Ala Ser Phe Gly Met Ala Asn Phe Phe Ala Arg Pro Ile Gly Gly
325     330     335
Trp Ala Ser Asp Ile Ala Ala Arg Arg Phe Gly Met Arg Gly Arg Leu
340     345     350
Trp Thr Leu Trp Ile Ile Gln Thr Leu Gly Gly Phe Phe Cys Leu Trp
355     360     365
Leu Gly Arg Ala Thr Thr Leu Pro Thr Ala Val Val Phe Met Ile Leu
370     375     380
Phe Ser Leu Gly Ala Gln Ala Ala Cys Gly Ala Thr Phe Ala Ile Ile
385     390     395     400
Pro Phe Ile Ser Arg Arg Ser Leu Gly Ile Ile Ser Gly Leu Thr Gly
405     410     415
Ala Gly Gly Asn Phe Gly Ser Gly Leu Thr Gln Leu Val Phe Phe Ser
420     425     430
Thr Ser Thr Phe Ser Thr Glu Gln Gly Leu Thr Trp Met Gly Val Met
435     440     445
Ile Met Ala Cys Thr Leu Pro Val Thr Leu Val His Phe Pro Gln Trp
450     455     460
Gly Ser Met Phe Leu Pro Ser Thr Glu Asp Glu Val Lys Ser Thr Glu
465     470     475     480
Glu Tyr Tyr Tyr Met Lys Glu Trp Thr Glu Thr Glu Lys Arg Lys Gly
485     490     495
Met His Glu Gly Ser Leu Lys Phe Ala Val Asn Ser Arg Ser Glu Arg
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PF59082SeqList_PF59082.txt

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 <213> Oryza sativa (japonica cultivar-group)

<220>
 <221> CDS
 <222> (1)..(1551)

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ggg ggc aag ccg cgg ttc agg atg ccg gtg gac tcc gac ctc aag gcg      96
Gly Gly Lys Pro Arg Phe Arg Met Pro Val Asp Ser Asp Leu Lys Ala
20      25      30
acg gag ttc tgg ctc ttc tcc ttc gcg agg cca cac atg gcc tcc ttc      144
Thr Glu Phe Trp Leu Phe Ser Phe Ala Arg Pro His Met Ala Ser Phe
35      40      45
cac atg gcg tgg ttc tcc ttc ttc tgc tgc ttc gtg tcc acg ttc gcc      192
His Met Ala Trp Phe Ser Phe Phe Cys Cys Phe Val Ser Thr Phe Ala
50      55      60
gcg ccg ccg ctg ctg ccg ctc atc cgc gac acc ctc ggg ctc acg gcc      240
Ala Pro Pro Leu Leu Pro Leu Ile Arg Asp Thr Leu Gly Leu Thr Ala
65      70      75
acg gac atc ggc aac gcc ggg atc gcg tcc gtg tcc ggc gcc gtg ttc      288
Thr Asp Ile Gly Asn Ala Gly Ile Ala Ser Val Ser Gly Ala Val Phe
85      90      95
gcg cgt ctg gcc atg ggc acg gcg tgc gac asp ctg gtc ggg ccc agg ctg      336
Ala Arg Leu Ala Met Gly Thr Ala Cys Asp Leu Val Gly Pro Arg Leu
100      105      110
gcc tcc gcg tct ctg atc ctc ctc acc aca ccg gcg gtg tac tgc tcc      384
Ala Ser Ala Ser Leu Ile Leu Leu Thr Thr Pro Ala Val Tyr Cys Ser
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tcc atc atc cag tcc ccg tcg ggg tac ctc ctc gtg cgc ttc ttc acg      432
Ser Ile Ile Gln Ser Pro Ser Gly Tyr Leu Leu Val Arg Phe Phe Thr
130      135      140
ggc atc tcg ctg gcg tcg ttc gtg tcg gcg cag ttc tgg atg agc tcc      480
Gly Ile Ser Leu Ala Ser Phe Val Ser Ala Gln Phe Trp Met Ser Ser
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tgg ggc aac ctc ggc ggc ggc gcc gtc atc ctg ctc atg ccg ctc gtg      576
Trp Gly Asn Leu Gly Gly Gly Ala Val Gln Leu Leu Met Pro Leu Val
180      185      190
tac gag gcc atc cac aag atc ggt agc acg ccg ttc acg gcg tgg cgc      624
Tyr Glu Ala Ile His Lys Ile Gly Ser Thr Pro Phe Thr Ala Trp Arg
195      200      205
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Ile Ala Phe Phe Ile Pro Gly Leu Met Gln Thr Phe Ser Ala Ile Ala
210      215      220
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Val Leu Ala Phe Gly Gln Asp Met Pro Gly Gly Asn Tyr Gly Lys Leu
225      230      235
cac aag act ggc gac atg cac aag gac agc ttc ggc aac gtg ctg cgc      768
His Lys Thr Gly Asp Met His Lys Asp Ser Phe Gly Asn Val Leu Arg
245      250      255
cac gcc ctc acc aac tac cgc ggc tgg atc ctg gcg ctc acc tac ggc      816
His Ala Leu Thr Asn Tyr Arg Gly Trp Ile Leu Ala Leu Thr Tyr Gly
260      265      270
tac agc ttc ggc gtc gag ctc acc atc gac aac gtc gtg cac cag tac      864
Tyr Ser Phe Gly Val Glu Leu Thr Ile Asp Asn Val Val His Gln Tyr
275      280      285
ttc tac gac cgc ttc gac gtc aac ctc cag acc gcc ggg ctc atc gcc      912
Phe Tyr Asp Arg Phe Asp Val Asn Leu Gln Thr Ala Gly Leu Ile Ala
290      295      300
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PF59082SeqList_PF59082.txt

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Leu	Ser	Asp	Trp	Leu 325	Ser	Ser	Arg	Tyr	Gly 330	Met	Arg	Gly	Arg	Leu 335	Trp	
ggg	ctg	tgg	act	gtg	cag	acc	atc	ggc	ggc	gtc	ctc	tgc	gtg	gtg	ctc	1056
Gly	Leu	Trp	Thr	Val	Gln	Thr	Ile	Gly 345	Gly	Val	Leu	Cys	Val	Val	Leu	
gga	atc	gtc	gac	ttc	tcc	ttc	gcc	gcg	tcc	gtc	gcc	gtg	atg	gtg	ctc	1104
Gly	Ile	Val 355	Asp	Phe	Ser	Phe	Ala 360	Ala	Ser	Val	Ala	Val 365	Met	Val	Leu	
ttc	tcc	ttc	ttc	gtc	cag	gcc	gcg	tgc	ggg	ctc	acc	ttc	ggc	atc	gtg	1152
Phe	Ser	Phe	Phe	Val	Gln	Ala 375	Ala	Cys	Gly	Leu	Thr	Phe	Gly	Ile	Val	
ccg	ttc	gtg	tcg	cgg	agg	tcg	ctg	ggg	ctc	atc	tcc	ggg	atg	acc	ggc	1200
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ggc	ggg	ggc	aac	gtg	ggc	gcc	gtg	ctg	acg	cag	tac	atc	ttc	ttc	cac	1248
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ggc	aca	aag	tac	aag	acg	gag	acc	ggg	atc	aag	tac	atg	ggg	ctc	atg	1296
Gly	Thr	Lys	Tyr	Lys	Thr	Glu	Thr	Gly 425	Ile	Lys	Tyr	Met	Gly 430	Leu	Met	
atc	atc	gcg	tgc	acg	ctg	ccc	gtc	atg	ctc	atc	tac	ttc	ccg	cag	tgg	1344
Ile	Ile	Ala 435	Cys	Thr	Leu	Pro	Val 440	Met	Leu	Ile	Tyr	Phe	Pro	Gln	Trp	
ggc	ggc	atg	ctc	gta	ggc	ccg	agg	aag	ggg	gcc	acg	gcg	gag	gag	tac	1392
Gly	Gly	Met	Leu	Val	Gly	Pro	Arg	Lys	Gly	Ala	Thr	Ala	Glu	Glu	Tyr	
tac	agc	cgg	gag	tgg	tcg	gat	cac	gag	cgc	gag	aag	ggt	ttc	aac	gcg	1440
Tyr	Ser	Arg	Glu	Trp	Ser 470	Asp	His	Glu	Arg	Glu 475	Lys	Gly	Phe	Asn	Ala	
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Ala	Ser	Val	Arg	Phe 485	Ala	Glu	Asn	Ser	Val 490	Arg	Glu	Gly	Gly	Arg	Ser	
tcg	gcg	aat	ggc	gga	cag	ccc	agg	cac	acc	gtc	ccc	gtc	gac	gcg	tcg	1536
Ser	Ala	Asn	Gly	Gly	Gln	Pro	Arg	His	Thr	Val	Pro	Val	Asp	Ala	Ser	
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<210> 1483

<211> 516

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<400> 1483

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Thr	Glu	Phe 35	Trp	Leu	Phe	Ser	Phe 40	Ala	Arg	Pro	His	Met 45	Ala	Ser	Phe
His	Met 50	Ala	Trp	Phe	Ser	Phe 55	Cys	Cys	Phe	Val 60	Ser	Thr	Phe	Ala	
Ala	Pro	Pro	Leu	Leu	Pro 70	Leu	Ile	Arg	Asp	Thr 75	Leu	Gly	Leu	Thr	Ala
Thr	Asp	Ile	Gly	Asn 85	Ala	Gly	Ile	Ala	Ser	Val 90	Ser	Gly	Ala	Val	Phe
Ala	Arg	Leu	Ala	Met	Gly	Thr	Ala	Cys	Asp	Leu	Val	Gly	Pro	Arg	Leu
Ala	Ser	Ala 115	Ser	Leu	Ile	Leu	Leu	Thr	Thr	Pro	Ala	Val	Tyr	Cys	Ser
Ser	Ile 130	Ile	Gln	Ser	Pro	Ser 135	Gly	Tyr	Leu	Leu	Val	Arg	Phe	Phe	Thr
Gly	Ile	Ser	Leu	Ala	Ser 150	Phe	Val	Ser	Ala	Gln 155	Phe	Trp	Met	Ser	Ser
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PF59082SeqList_PF59082.txt

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 Ile Ala Phe Phe Ile Pro Gly Leu Met Gln Thr Phe Ser Ala Ile Ala
 210 215 220
 Val Leu Ala Phe Gly Gln Asp Met Pro Gly Gly Asn Tyr Gly Lys Leu
 225 230 235 240
 His Lys Thr Gly Asp Met His Lys Asp Ser Phe Gly Asn Val Leu Arg
 245 250 255
 His Ala Leu Thr Asn Tyr Arg Gly Trp Ile Leu Ala Leu Thr Tyr Gly
 260 265 270
 Tyr Ser Phe Gly Val Glu Leu Thr Ile Asp Asn Val Val His Gln Tyr
 275 280 285
 Phe Tyr Asp Arg Phe Asp Val Asn Leu Gln Thr Ala Gly Leu Ile Ala
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 Ala Ser Phe Gly Met Ala Asn Ile Ile Ser Arg Pro Gly Gly Gly Leu
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 Leu Ser Asp Trp Leu Ser Ser Arg Tyr Gly Met Arg Gly Arg Leu Trp
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 Gly Leu Trp Thr Val Gln Thr Ile Gly Gly Val Leu Cys Val Val Leu
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 Gly Ile Val Asp Phe Ser Phe Ala Ala Ser Val Ala Val Met Val Leu
 355 360 365
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 370 375 380
 Pro Phe Val Ser Arg Arg Ser Leu Gly Leu Ile Ser Gly Met Thr Gly
 385 390 395 400
 Gly Gly Gly Asn Val Gly Ala Val Leu Thr Gln Tyr Ile Phe Phe His
 405 410 415
 Gly Thr Lys Tyr Lys Thr Glu Thr Gly Ile Lys Tyr Met Gly Leu Met
 420 425 430
 Ile Ile Ala Cys Thr Leu Pro Val Met Leu Ile Tyr Phe Pro Gln Trp
 435 440 445
 Gly Gly Met Leu Val Gly Pro Arg Lys Gly Ala Thr Ala Glu Glu Tyr
 450 455 460
 Tyr Ser Arg Glu Trp Ser Asp His Glu Arg Glu Lys Gly Phe Asn Ala
 465 470 475 480
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<211> 1602

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<400> 1484

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Thr Gly Arg Glu Pro Ala Phe Ala Phe Ser Thr Glu Val Gly Gly Glu	
20 25 30	
gac gcg gcg gcg gcg agc aag ttc gac ttg ccg gtg gac tcg gag cac	144
Asp Ala Ala Ala Ala Ser Lys Phe Asp Leu Pro Val Asp Ser Glu His	
35 40 45	
aag gcg aag acg atc agg ttg ctg tcg ttc gcg aac ccg cat atg agg	192
Lys Ala Lys Thr Ile Arg Leu Leu Ser Phe Ala Asn Pro His Met Arg	
50 55 60	
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PF59082SeqList_PF59082.txt

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Phe	Ala	Ala	Ala	Pro 85	Leu	Val	Pro	Ile	Ile 90	Arg	Asp	Asn	Leu	Asn 95	Leu	
acc	aag	gcc	gac	atc	ggc	aac	gcc	ggc	gtc	gcc	tcc	gtc	tcc	ggc	tcc	336
Thr	Lys	Ala	Asp	Ile	Gly	Asn	Ala	Gly	Val	Ala	Ser	Val	Ser	Gly	Ser	
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Arg	Tyr	Gly	Cys	Ala	Phe	Leu	Ile	Met	Leu	Ala	Ala	Pro	Thr	Val	Phe	
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Cys	Met	Ser	Leu	Ile	Asp	Ser	Ala	Ala	Gly	Tyr	Ile	Ala	Val	Arg	Phe	
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Ser	Thr	Met	Phe	Asn	Ser	Lys	Ile	Ile	Gly	Leu	Val	Asn	Gly	Leu	Ala	
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gcc	ggg	tgg	gga	aac	atg	ggc	ggc	ggc	gcg	acg	cag	ctc	atc	atg	ccg	624
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Trp	Arg	Leu	Ala	Tyr	Phe	Val	Pro	Gly	Thr	Leu	His	Val	Val	Met	Gly	
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Leu	Trp	Tyr	Ala	Val	Thr	Asn	Tyr	Arg	Thr	Trp	Ile	Phe	Val	Leu	Leu	
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Tyr	Gly	Tyr	Ser	Met	Gly	Val	Glu	Leu	Thr	Thr	Asp	Asn	Val	Ile	Ala	
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gag	tac	ttc	tac	gat	cgc	gtc	gac	ctc	gac	ctc	cgc	gtc	gcc	ggc	atc	960
Glu	Tyr	Phe	Tyr	Asp	Arg	Phe	Asp	Leu	Asp	Leu	Arg	Val	Ala	Gly	Ile	
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Gly	Leu	Leu	Ser	Asp	Leu	Gly	Ala	Arg	Tyr	Phe	Gly	Met	Arg	Ala	Arg	
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Leu	Trp	Asn	Ile	Trp	Ile	Leu	Gln	Thr	Ala	Gly	Gly	Ala	Phe	Cys	Leu	
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Ile	Pro	Phe	Val	Ser	Arg	Arg	Ser	Leu	Gly	Ile	Ile	Ser	Gly	Met	Thr	
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Gly	Ala	Gly	Gly	Asn	Phe	Gly	Ala	Gly	Leu	Thr	Gln	Leu	Leu	Phe	Phe	
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PF59082SeqList_PF59082.txt

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Trp	Gly	Ser	Met	Phe	Leu	Pro	Pro	Asn	Ala	Gly	Ala	Glu	Glu	Glu	His	
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tac	tac	ggc	tcc	gag	tgg	agc	gaa	cag	gag	aag	agc	aag	ggc	ctc	cac	1488
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ggg	gca	agt	ctc	aag	ttc	gcc	gag	aac	tcc	cgc	tcc	gag	cgt	ggc	cgc	1536
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Arg	Asn	Val	Ile	Asn	Ala	Ala	Ala	Ala	Ala	Ala	Thr	Pro	Pro	Asn	Asn	
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<211> 533

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<400> 1485

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Lys	Ala	Lys	Thr	Ile	Arg	Leu	Leu	Ser	Phe	Ala	Asn	Pro	His	Met	Arg	
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Thr	Phe	His	Leu	Ser	Trp	Ile	Ser	Phe	Phe	Ser	Cys	Phe	Val	Ser	Thr	
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Phe	Ala	Ala	Ala	Pro	Leu	Val	Pro	Ile	Ile	Arg	Asp	Asn	Leu	Asn	Leu	
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Thr	Lys	Ala	Asp	Ile	Gly	Asn	Ala	Gly	Val	Ala	Ser	Val	Ser	Gly	Ser	
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Ile	Phe	Ser	Arg	Leu	Ala	Met	Gly	Ala	Ile	Cys	Asp	Met	Leu	Gly	Pro	
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Arg	Tyr	Gly	Cys	Ala	Phe	Leu	Ile	Met	Leu	Ala	Ala	Pro	Thr	Val	Phe	
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Cys	Met	Ser	Leu	Ile	Asp	Ser	Ala	Ala	Gly	Tyr	Ile	Ala	Val	Arg	Phe	
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Ser	Leu	Gln	Lys	Gly	Asp	Val	Asn	Arg	Asp	Ser	Phe	Ser	Arg	Val		
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Tyr	Gly	Tyr	Ser	Met	Gly	Val	Glu	Leu	Thr	Thr	Asp	Asn	Val	Ile	Ala	
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 385 390 395 400
 Ile Pro Phe Val Ser Arg Arg Ser Leu Gly Ile Ile Ser Gly Met Thr
 405 410 415
 Gly Ala Gly Gly Asn Phe Gly Ala Gly Leu Thr Gln Leu Leu Phe Phe
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 Thr Ser Ser Arg Tyr Ser Thr Gly Thr Gly Leu Glu Tyr Met Gly Ile
 435 440 445
 Met Ile Met Ala Cys Thr Leu Pro Val Val Leu Val His Phe Pro Gln
 450 455 460
 Trp Gly Ser Met Phe Leu Pro Pro Asn Ala Gly Ala Glu Glu Glu His
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 Tyr Tyr Gly Ser Glu Trp Ser Glu Gln Glu Lys Ser Lys Gly Leu His
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<212> DNA

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<220>

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<400> 1486

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Met Ala Glu Ile Glu Gly Ser Pro Gly Ser Ser Met His Gly Val Thr
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gga aga gaa caa aca ttt gta gcc tca gtt gct tct cca att gtc cct 156

Gly Arg Glu Gln Thr Phe Val Ala Ser Val Ala Ser Pro Ile Val Pro
 20 25 30

aca gac acc aca gcc aaa ttt gct ctc cca gtg gat tca gaa cac aag 204

Thr Asp Thr Thr Ala Lys Phe Ala Leu Pro Val Asp Ser Glu His Lys
 35 40 45

gcc aag gtt ttc aaa ctc ttc tcc ctg gcc aat ccc cac atg aga acc 252

Ala Lys Val Phe Lys Leu Phe Ser Leu Ala Asn Pro His Met Arg Thr
 50 55 60

ttc cac ctt tct tgg atc tcc ttc ttc acc tgc ttc gtc tcg aca ttc 300

Phe His Leu Ser Trp Ile Ser Phe Phe Thr Cys Phe Val Ser Thr Phe
 65 70 75 80

gca gca gca cct ctt gtg ccc atc atc cgc gac aac ctt aac ctc acc 348

Ala Ala Ala Pro Leu Val Pro Ile Ile Arg Asp Asn Leu Asn Leu Thr
 85 90 95

aaa agc gac att gga aac gcc ggg gtt gct tct gtc tcc gga agc atc 396

Lys Ser Asp Ile Gly Asn Ala Gly Val Ala Ser Val Ser Gly Ser Ile
 100 105 110

ttc tca agg ctc gca atg ggt gca gtc tgt gac atg ttg ggt cca cgc 444

Phe Ser Arg Leu Ala Met Gly Ala Val Cys Asp Met Leu Gly Pro Arg
 115 120 125

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Tyr Gly Cys Ala Phe Leu Ile Met Leu Ser Ala Pro Thr Val Phe Cys
 130 135 140

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Met Ser Phe Val Lys Asp Ala Ala Gly Tyr Ile Ala Val Arg Phe Leu
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Thr	Met	Phe	Asn	Ser	Lys	Ile	Ile	Gly	Leu	Ala	Asn	Gly	Thr	Ala	Ala		
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Val	Tyr	Glu	Leu	Ile	Arg	Arg	Ala	Gly	Ala	Thr	Pro	Phe	Thr	Ala	Trp		
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Glu	Phe	Tyr	Tyr	Thr	Ser	Glu	Trp	Asn	Glu	Glu	Glu	Lys	Gln	Lys	Gly		
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      35      40      45
Ala Lys Val Phe Lys Leu Phe Ser Leu Ala Asn Pro His Met Arg Thr
      50      55      60
Phe His Leu Ser Trp Ile Ser Phe Phe Thr Cys Phe Val Ser Thr Phe
65      70      75      80
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Lys Ser Asp Ile Gly Asn Ala Gly Val Ala Ser Val Ser Gly Ser Ile
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Phe Ser Arg Leu Ala Met Gly Ala Val Cys Asp Met Leu Gly Pro Arg
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Tyr Gly Cys Ala Phe Leu Ile Met Leu Ser Ala Pro Thr Val Phe Cys
130      135      140
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145      150      155      160
Ile Gly Phe Ser Leu Ala Thr Phe Val Ser Cys Gln Tyr Trp Met Ser
      165      170      175
Thr Met Phe Asn Ser Lys Ile Ile Gly Leu Ala Asn Gly Thr Ala Ala
      180      185      190
Gly Trp Gly Asn Met Gly Gly Gly Ala Thr Gln Leu Ile Met Pro Leu
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Val Tyr Glu Leu Ile Arg Arg Ala Gly Ala Thr Pro Phe Thr Ala Trp
210      215      220
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225      230      235      240
Leu Val Leu Thr Leu Gly Gln Asp Leu Pro Asp Gly Asn Leu Gly Ala
      245      250      255
Leu Arg Lys Lys Gly Asp Val Ala Lys Asp Lys Phe Ser Lys Val Leu
      260      265      270
Trp Tyr Ala Ile Thr Asn Tyr Arg Thr Trp Ile Phe Ala Leu Leu Tyr
275      280      285
Gly Tyr Ser Met Gly Val Glu Leu Thr Thr Asp Asn Val Ile Ala Glu
290      295      300
Tyr Phe Tyr Asp Arg Phe Asn Leu Lys Leu His Thr Ala Gly Ile Ile
305      310      315      320
Ala Ala Ser Phe Gly Met Ala Asn Leu Val Ala Arg Pro Phe Gly Gly
      325      330      335
Tyr Ala Ser Asp Val Ala Ala Arg Leu Phe Gly Met Arg Gly Arg Leu
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PF59082SeqList_PF59082.txt

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 Pro Phe Ile Ser Arg Arg Ser Leu Gly Ile Ile Ser Gly Leu Thr Gly
 405 410 415
 Ala Gly Gly Asn Phe Gly Ser Gly Leu Thr Gln Leu Val Phe Phe Ser
 420 425 430
 Thr Ser Lys Phe Ser Thr Ala Thr Gly Leu Ser Leu Met Gly Val Met
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 Ile Val Ala Cys Thr Leu Pro Val Ser Val Val His Phe Pro Gln Trp
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 Gly Ser Met Phe Leu Pro Pro Ser Lys Asp Val Ser Lys Ser Thr Glu
 465 470 475 480
 Glu Phe Tyr Tyr Thr Ser Glu Trp Asn Glu Glu Lys Gln Lys Gly
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 His Val
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<211> 1709

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<222> (43)..(1611)

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Asp 5 Glu Pro Arg Ser Ser Met His Gly Val Thr 15 Gly Arg Glu Gln Ser 20	
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Tyr Ala Phe Ser Val Asp Gly Ser Glu Pro Thr Asn Thr Lys Lys Lys	
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Tyr Asn Leu Pro Val Asp Ala Glu Asp Lys Ala Thr Val Phe Lys Leu	
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Phe Ser Phe Ala Lys Pro His Met Arg Thr Phe His Leu Ser Trp Ile	
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gga gcc gtg tgt gat ctt ttg ggt cct cgt tac ggt tgt gcc ttc ctt	438
Gly Ala Val Cys Asp Leu Leu Gly Pro Arg Tyr Gly Cys Ala Phe Leu	
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Val Met Leu Ser Ala Pro Thr Val Phe Ser Met Ser Phe Val Ser Asp	
135 140 145	
gca gca ggc ttc ata acg gtg agg ttc atg att ggt ttt tgc ctg gcg	534
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PF59082SeqList_PF59082.txt

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ggc	ggc	ata	acg	cag	tgt	ctc	atg	ccc	att	gtg	tat	gaa	atc	att	agg	678
Gly	Gly	Ile	Thr	Gln	Leu	Leu	Met	Pro	Ile	Val	Tyr	Glu	Ile	Ile	Arg	
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cgc	tgc	gga	tca	aca	gcg	ttc	acg	gcc	tgg	agg	atc	gcc	ttc	ttt	gtc	726
Arg	Cys	Gly	Ser	Thr	Ala	Phe	Thr	Ala	Trp	Arg	Ile	Ala	Phe	Phe	Val	
		215					220					225				
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Pro	Gly	Trp	Leu	His	Ile	Ile	Met	Gly	Ile	Leu	Val	Leu	Thr	Leu	Gly	
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caa	gat	ctg	cca	ggt	gga	aac	aga	gct	gcc	atg	gag	aaa	gcg	gga	gaa	822
Gln	Asp	Leu	Pro	Gly	Gly	Asn	Arg	Ala	Ala	Met	Glu	Lys	Ala	Gly	Glu	
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ggt	gcc	aaa	gac	aaa	gga	aag	att	cta	tgg	tac	gcc	ggt	aca	aat		870
Val	Ala	Lys	Asp	Lys	Phe	Gly	Lys	Ile	Leu	Trp	Tyr	Ala	Val	Thr	Asn	
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tac	agg	act	tgg	att	ttc	gtt	ctt	ctg	tat	gga	tat	tcc	atg	gga	gtt	918
Tyr	Arg	Thr	Trp	Ile	Phe	Val	Leu	Leu	Tyr	Gly	Tyr	Ser	Met	Gly	Val	
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		295					300					305				
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His	Leu	Lys	Leu	His	Thr	Gly	Gly	Ile	Ile	Ala	Ala	Cys	Phe	Gly	Met	
	310					315					320					
gcc	aat	ttc	ttt	gct	cgt	cca	gca	gga	ggc	tgg	gca	tct	gac	att	gca	1062
Ala	Asn	Phe	Phe	Ala	Arg	Pro	Ala	Gly	Gly	Trp	Ala	Ser	Asp	Ile	Ala	
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gcc	aag	cgc	ttc	gga	atg	cga	ggg	agg	tgt	tgg	act	ttg	tgg	atc	att	1110
Ala	Lys	Arg	Phe	Gly	Met	Arg	Gly	Arg	Leu	Trp	Thr	Leu	Trp	Ile	Ile	
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cag	acg	tcc	ggt	ggt	ctc	ttt	tgt	gtg	tgg	ctc	gga	cgt	gcc	aac	acc	1158
Gln	Thr	Ser	Gly	Gly	Leu	Phe	Cys	Val	Trp	Leu	Gly	Arg	Ala	Asn	Thr	
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ctc	gtc	act	gcc	ggt	gta	tct	atg	gtc	ctc	ttc	tct	tta	gga	gca	caa	1206
Leu	Val	Thr	Ala	Val	Val	Ser	Met	Val	Leu	Phe	Ser	Leu	Gly	Ala	Gln	
		375					380					385				
gcc	gct	tgc	gga	gcc	acc	ttt	gct	atc	gtg	ccc	ttt	gtc	tcc	cgg	cga	1254
Ala	Ala	Cys	Gly	Ala	Thr	Phe	Ala	Ile	Val	Pro	Phe	Val	Ser	Arg	Arg	
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Ala	Leu	Gly	Ile	Ile	Ser	Gly	Leu	Thr	Gly	Ala	Gly	Gly	Asn	Phe	Gly	
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Ser	Gly	Leu	Thr	Gln	Leu	Val	Phe	Phe	Ser	Thr	Ser	Arg	Phe	Thr	Thr	
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Glu	Glu	Gly	Leu	Thr	Trp	Met	Gly	Val	Met	Ile	Val	Ala	Cys	Thr	Leu	
			440				445						450			
cct	gtt	acc	tta	atc	cac	ttt	cct	cag	tgg	gga	agc	atg	ttc	ttc	cct	1446
Pro	Val	Thr	Leu	Ile	His	Phe	Pro	Gln	Trp	Gly	Ser	Met	Phe	Phe	Pro	
		455					460					465				
cct	tcc	aac	gat	tcg	gtc	gac	gct	acg	gag	cac	tat	tat	gtt	ggc	gaa	1494
Pro	Ser	Asn	Asp	Ser	Val	Asp	Ala	Thr	Glu	His	Tyr	Tyr	Val	Gly	Glu	
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Tyr	Ser	Lys	Glu	Glu	Gln	Gln	Ile	Gly	Met	His	Leu	Lys	Ser	Lys	Leu	
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ttt	gct	gat	gga	gcc	aag	acc	gag	gga	ggc	agc	agc	gtc	cac	aaa	ggg	1590
Phe	Ala	Asp	Gly	Ala	Lys	Thr	Glu	Gly	Gly	Ser	Ser	Val	His	Lys	Gly	
				505					510					515		
aac	gca	acc	aac	aat	gct	tgatcatgtg	tcattgatata	caagaaatta								1638
Asn	Ala	Thr	Asn	Asn	Ala											
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1709

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<211> 522

<212> PRT

<213> *Arabidopsis thaliana*

<400> 1489

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Thr Lys Lys Lys Tyr Asn Leu Pro Val Asp Ala Glu Asp Lys Ala Thr
      35      40      45
Val Phe Lys Leu Phe Ser Phe Ala Lys Pro His Met Arg Thr Phe His
      50      55      60
Leu Ser Trp Ile Ser Phe Ser Thr Cys Phe Val Ser Thr Phe Ala Ala
65      70      75      80
Ala Pro Leu Ile Pro Ile Ile Arg Glu Asn Leu Asn Leu Thr Lys His
      85      90      95
Asp Ile Gly Asn Ala Gly Val Ala Ser Val Ser Gly Ser Ile Phe Ser
      100      105      110
Arg Leu Val Met Gly Ala Val Cys Asp Leu Leu Gly Pro Arg Tyr Gly
      115      120      125
Cys Ala Phe Leu Val Met Leu Ser Ala Pro Thr Val Phe Ser Met Ser
      130      135      140
Phe Val Ser Asp Ala Ala Gly Phe Ile Thr Val Arg Phe Met Ile Gly
145      150      155      160
Phe Cys Leu Ala Thr Phe Val Ser Cys Gln Tyr Trp Met Ser Thr Met
      165      170      175
Phe Asn Ser Gln Ile Ile Gly Leu Val Asn Gly Thr Ala Ala Gly Trp
      180      185      190
Gly Asn Met Gly Gly Gly Ile Thr Gln Leu Leu Met Pro Ile Val Tyr
      195      200      205
Glu Ile Ile Arg Arg Cys Gly Ser Thr Ala Phe Thr Ala Trp Arg Ile
      210      215      220
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Leu Thr Leu Gly Gln Asp Leu Pro Gly Gly Asn Arg Ala Ala Met Glu
      245      250      255
Lys Ala Gly Glu Val Ala Lys Asp Lys Phe Gly Lys Ile Leu Trp Tyr
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Ala Val Thr Asn Tyr Arg Thr Trp Ile Phe Val Leu Leu Tyr Gly Tyr
      275      280      285
Ser Met Gly Val Glu Leu Ser Thr Asp Asn Val Ile Ala Glu Tyr Phe
      290      295      300
Phe Asp Arg Phe His Leu Lys Leu His Thr Ala Gly Ile Ile Ala Ala
305      310      315      320
Cys Phe Gly Met Ala Asn Phe Phe Ala Arg Pro Ala Gly Gly Trp Ala
      325      330      335
Ser Asp Ile Ala Ala Lys Arg Phe Gly Met Arg Gly Arg Leu Trp Thr
      340      345      350
Leu Trp Ile Ile Gln Thr Ser Gly Gly Leu Phe Cys Val Trp Leu Gly
      355      360      365
Arg Ala Asn Thr Leu Val Thr Ala Val Val Ser Met Val Leu Phe Ser
      370      375      380
Leu Gly Ala Gln Ala Ala Cys Gly Ala Thr Phe Ala Ile Val Pro Phe
385      390      395      400
Val Ser Arg Arg Ala Leu Gly Ile Ile Ser Gly Leu Thr Gly Ala Gly
      405      410      415
Gly Asn Phe Gly Ser Gly Leu Thr Gln Leu Val Phe Phe Ser Thr Ser
      420      425      430
Arg Phe Thr Thr Glu Glu Gly Leu Thr Trp Met Gly Val Met Ile Val
      435      440      445
Ala Cys Thr Leu Pro Val Thr Leu Ile His Phe Pro Gln Trp Gly Ser
450      455      460
Met Phe Phe Pro Pro Ser Asn Asp Ser Val Asp Ala Thr Glu His Tyr

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PF59082SeqList_PF59082.txt

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<222> (91)..(1614)

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Met Glu Val Glu Ala Gly Ala His

ggc gac act gcc gcg agc aag ttc acg ctg ccg gta gac tcc gag cac 162
Gly Asp Thr Ala Ala Ser Lys Phe Thr Leu Pro Val Asp Ser Glu His
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aag gcc aag tcc ttc agg ctc ttc tcc ttc gcc aac ccg cac atg cgc 210
Lys Ala Lys Ser Phe Arg Leu Phe Ser Phe Ala Asn Pro His Met Arg
25 30 35 40

acc ttc cat ctc tcg tgg atc tcc ttc ttc act tgc ttc atc tcc acc 258
Thr Phe His Leu Ser Trp Ile Ser Phe Phe Thr Cys Phe Ile Ser Thr
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ttc gcc gca gcg ccc ctt gtc ccc atc att cgt gat aac ctc aac ctt 306
Phe Ala Ala Ala Pro Leu Val Pro Ile Arg Asp Asn Leu Asn Leu
60 65 70

gcc aag gcc gac atc gcc aat gcc ggt gtg gca tcc gtt tct ggg tcc 354
Ala Lys Ala Asp Ile Gly Asn Ala Gly Val Ala Ser Val Ser Gly Ser
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Ile Phe Ser Arg Leu Ala Met Gly Ala Ile Cys Asp Leu Leu Gly Pro
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Arg Tyr Gly Cys Ala Phe Leu Val Met Leu Ser Ala Pro Thr Val Phe
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Cys Met Ala Val Ile Asp Asp Ala Ser Gly Tyr Ile Ala Val Arg Phe
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Ser Thr Met Phe Asn Ser Lys Ile Ile Gly Thr Val Asn Gly Leu Ala
155 160 165

gct gga tgg ggc aac atg ggt ggt gcc acc cag ctc atc atg ccg 642
Ala Gly Trp Gly Asn Met Gly Gly Gly Ala Thr Gln Leu Ile Met Pro
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Leu Val Phe His Ala Ile Gln Lys Cys Gly Ala Thr Pro Phe Val Ala
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Trp Arg Ile Ala Tyr Phe Val Pro Gly Met Met His Ile Val Met Gly
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Leu Leu Val Leu Thr Met Gly Gln Asp Leu Pro Asp Gly Asn Leu Ala
220 225 230

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Ser Leu Gln Lys Lys Gly Asp Met Ala Lys Asp Lys Phe Ser Lys Val
235 240 245

PF59082SeqList_PF59082.txt

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Tyr	Gly	Tyr	Cys	Met	Gly	Val	Glu	Leu	Thr	Thr	Asp	Asn	Val	Ile	Ala	
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gag	tac	tac	ttc	gac	cac	ttc	cac	cta	gac	ctc	cgt	gcc	gcc	ggg	acc	978
Glu	Tyr	Tyr	Phe	Asp	His	Phe	His	Leu	Asp	Leu	Arg	Ala	Ala	Gly	Thr	
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Ile	Ala	Ala	Cys	Phe	Gly	Met	Ala	Asn	Ile	Val	Ala	Arg	Pro	Thr	Gly	
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Trp	Leu	Gly	Arg	Ala	Ser	Ala	Leu	Pro	Ala	Ser	Val	Thr	Ala	Met	Val	
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Leu	Phe	Ser	Ile	Cys	Ala	Gln	Ala	Ala	Cys	Gly	Ala	Ile	Phe	Gly	Val	
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			380					385					390			
ggg	gct	ggg	gga	aac	gtg	ggc	gca	ggg	ctc	aca	cag	ctt	ctc	ttc	ttc	1314
Gly	Ala	Gly	Gly	Asn	Val	Gly	Ala	Gly	Leu	Thr	Gln	Leu	Leu	Phe	Phe	
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Thr	Ser	Ser	Gln	Tyr	Ser	Thr	Gly	Arg	Gly	Leu	Glu	Tyr	Met	Gly	Ile	
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Met	Ile	Met	Ala	Cys	Thr	Leu	Pro	Val	Ala	Val	Val	His	Phe	Pro	Gln	
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tgg	gga	tcc	atg	ttc	ttc	cct	gcc	agc	gcc	gac	gcc	acg	gag	gag	gag	1458
Trp	Gly	Ser	Met	Phe	Phe	Pro	Ala	Ser	Ala	Asp	Ala	Thr	Glu	Glu	Glu	
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tac	tac	gcc	tcg	gag	tgg	tcc	gaa	gag	gag	aaa	gcc	aag	ggg	ctc	cat	1506
Tyr	Tyr	Ala	Ser	Glu	Trp	Ser	Glu	Glu	Glu	Lys	Ala	Lys	Gly	Leu	His	
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atc	gcc	ggc	caa	aaa	ttt	gct	gag	aat	tcc	cgc	tcg	gag	cgc	ggg	agg	1554
Ile	Ala	Gly	Gln	Lys	Phe	Ala	Glu	Asn	Ser	Arg	Ser	Glu	Arg	Gly	Arg	
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cgc	aac	gtc	atc	ctt	gcc	acg	tcc	gcc	aca	cca	ccc	aac	aat	acg	ccc	1602
Arg	Asn	Val	Ile	Leu	Ala	Thr	Ser	Ala	Thr	Pro	Pro	Asn	Asn	Thr	Pro	
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Gln	His	Val														
505																
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<213> Hordeum vulgare

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PF59082SeqList_PF59082.txt

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65      70      75      80
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      85      90      95
Ala Ile Cys Asp Leu Leu Gly Pro Arg Tyr Gly Cys Ala Phe Leu Val
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Met Leu Ser Ala Pro Thr Val Phe Cys Met Ala Val Ile Asp Asp Ala
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      130      135      140
Phe Val Ser Cys Gln Tyr Trp Met Ser Thr Met Phe Asn Ser Lys Ile
145      150      155      160
Ile Gly Thr Val Asn Gly Leu Ala Ala Gly Trp Gly Asn Met Gly Gly
      165      170      175
Gly Ala Thr Gln Leu Ile Met Pro Leu Val Phe His Ala Ile Gln Lys
      180      185      190
Cys Gly Ala Thr Pro Phe Val Ala Trp Arg Ile Ala Tyr Phe Val Pro
      195      200      205
Gly Met Met His Ile Val Met Gly Leu Leu Val Leu Thr Met Gly Gln
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Asp Leu Pro Asp Gly Asn Leu Ala Ser Leu Gln Lys Lys Gly Asp Met
225      230      235      240
Ala Lys Asp Lys Phe Ser Lys Val Leu Trp Gly Ala Val Thr Asn Tyr
      245      250      255
Arg Thr Trp Ile Phe Val Leu Leu Tyr Gly Tyr Cys Met Gly Val Glu
      260      265      270
Leu Thr Thr Asp Asn Val Ile Ala Glu Tyr Tyr Phe Asp His Phe His
      275      280      285
Leu Asp Leu Arg Ala Ala Gly Thr Ile Ala Ala Cys Phe Gly Met Ala
      290      295      300
Asn Ile Val Ala Arg Pro Thr Gly Gly Tyr Leu Ser Asp Leu Gly Ala
305      310      315      320
Arg Tyr Phe Gly Met Arg Ala Arg Leu Trp Asn Ile Trp Ile Leu Gln
      325      330      335
Thr Ala Gly Gly Ala Phe Cys Ile Trp Leu Gly Arg Ala Ser Ala Leu
      340      345      350
Pro Ala Ser Val Thr Ala Met Val Leu Phe Ser Ile Cys Ala Gln Ala
      355      360      365
Ala Cys Gly Ala Ile Phe Gly Val Ala Pro Phe Val Ser Arg Arg Ser
      370      375      380
Leu Gly Ile Ile Ser Gly Leu Thr Gly Ala Gly Gly Asn Val Gly Ala
385      390      395      400
Gly Leu Thr Gln Leu Phe Phe Thr Ser Ser Gln Tyr Ser Thr Gly
      405      410      415
Arg Gly Leu Glu Tyr Met Gly Ile Met Ile Met Ala Cys Thr Leu Pro
      420      425      430
Val Ala Leu Val His Phe Pro Gln Trp Gly Ser Met Phe Phe Pro Ala
      435      440      445
Ser Ala Asp Ala Thr Glu Glu Tyr Tyr Ala Ser Glu Trp Ser Glu
      450      455      460
Glu Glu Lys Ala Lys Gly Leu His Ile Ala Gly Gln Lys Phe Ala Glu
465      470      475      480
Asn Ser Arg Ser Glu Arg Gly Arg Arg Asn Val Ile Leu Ala Thr Ser
      485      490      495
Ala Thr Pro Pro Asn Asn Thr Pro Gln His Val
      500      505

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<210> 1492

<211> 1741

<212> DNA

<213> Hordeum vulgare

<220>

PF59082SeqList_PF59082.txt

<221> CDS

<222> (87)..(1616)

<400> 1492

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cgactaagct agctagctcg aggaag atg gag gtg gag tcg agc tcg cat ggc      113
                        Met Glu Val Glu Ser Ser Ser His Gly
                        1      5
gcc ggc gac gag gct gcg agc aag ttc tcg ctg ccc gtg gac tcg gag      161
Ala Gly Asp Glu Ala Ala Ser Lys Phe Ser Leu Pro Val Asp Ser Glu
10      15      20      25
cac aag gcc aag tcc atc agg ctc ttc tcc ttc gcc aac ccc cac atg      209
His Lys Ala Lys Ser Ile Arg Leu Phe Ser Phe Ala Asn Pro His Met
30      35      40
cgc acc ttc cac ctc tcc tgg atc tcc ttc ttc acc tgc ttc gtc tcc      257
Arg Thr Phe His Leu Ser Trp Ile Ser Phe Phe Thr Cys Phe Val Ser
45      50      55
acc ttc gct gcc gcg ccc ctc gtc cct atc atc cgc gac aac cta aac      305
Thr Phe Ala Ala Pro Leu Val Pro Ile Ile Arg Asp Asn Leu Asn
60      65      70
ctc gcc aag gcc gac atc ggc aac gcc ggt gtg gcg tcc gtg tcc ggg      353
Leu Ala Lys Ala Asp Ile Gly Asn Ala Gly Val Ala Ser Val Ser Gly
75      80      85
tct atc ttc tcg agg ctc gcc atg ggg gcc atc tgc gat ctc ctt ggc      401
Ser Ile Phe Ser Arg Leu Ala Met Gly Ala Ile Cys Asp Leu Leu Gly
90      95      100
cct cga tat gga tgc gcc ttc ctc gtc atg ctc gca gca ccc acc gtc      449
Pro Arg Tyr Gly Cys Ala Phe Leu Val Met Leu Ala Ala Pro Thr Val
110      115      120
ttc tgc atg tcc ctc atc gat gat gcg gcg ggc tac atc acg gtc cgc      497
Phe Cys Met Ser Leu Ile Asp Asp Ala Ala Gly Tyr Ile Thr Val Arg
125      130      135
ttc ctc atc ggc ttc tcc ctc gcg acg ttt gtg tcg tgc cag tat tgg      545
Phe Leu Ile Gly Phe Ser Leu Ala Thr Phe Val Ser Cys Gln Tyr Trp
140      145      150
atg agc acc atg ttc aac agc aag atc atc ggc acc gtc aac ggc ctg      593
Met Ser Thr Met Phe Asn Ser Lys Ile Ile Gly Thr Val Asn Gly Leu
155      160      165
gcg gcc ggc tgg ggc aac atg ggt ggt ggt gcc acc cag ctc att atg      641
Ala Ala Gly Trp Gly Asn Met Gly Gly Gly Ala Thr Gln Leu Ile Met
170      175      180
cca ctc gtc ttc cac gcc atc cag aag tgt ggt gcc acg ccc ttc gtc      689
Pro Leu Val Phe His Ala Ile Gln Lys Cys Gly Ala Thr Pro Phe Val
190      195      200
gca tgg cgc atc gcc tac ttc gtg cca gga atg atg cac gtg gtg atg      737
Ala Trp Arg Ile Ala Tyr Phe Val Pro Gly Met Met His Val Val Met
205      210      215
ggc ttg ctc gtg ctc acc atg gga cag gat ctc ccc gat ggt aac ctt      785
Gly Leu Leu Val Leu Thr Met Gly Gln Asp Leu Pro Asp Gly Asn Leu
220      225      230
gca agc ctc cag aag aag ggg gag atg gcc aag gac aag ttc tcc aag      833
Ala Ser Leu Gln Lys Lys Gly Glu Met Ala Lys Asp Lys Phe Ser Lys
235      240      245
gtt gtg tgg ggt gct gtt aca aac tac cgt aca tgg atc ttc gtt ctt      881
Val Val Trp Gly Ala Val Thr Asn Tyr Arg Thr Trp Ile Phe Val Leu
250      255      260
ctt tac gga tac tgc atg ggt gtt gag ctc acc acc gac aac gtc atc      929
Leu Tyr Gly Tyr Cys Met Gly Val Glu Leu Thr Thr Asp Asn Val Ile
270      275      280
gcc gag tac tac ttc gac cac ttt cac ctt gac ctt cga aca tcc ggc      977
Ala Glu Tyr Tyr Phe Asp His Phe His Leu Asp Leu Arg Thr Ser Gly
285      290      295
acc att gcc gcc tgt ttt ggc atg gcc aac atc gtt gct cgg cct gcg      1025
Thr Ile Ala Ala Cys Phe Gly Met Ala Asn Ile Val Ala Arg Pro Ala
300      305      310
ggg ggc tac ctc tcc gac ctc ggt gcc cgc tac ttc ggc atg cgt gcc      1073
Gly Gly Tyr Leu Ser Asp Leu Gly Ala Arg Tyr Phe Gly Met Arg Ala

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PF59082SeqList_PF59082.txt

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315          320          325
cgc ctc tgg aac atc tgg atc ctc cag acc gct ggt ggc gca ttc tgc 1121
Arg Leu Trp Asn Ile Trp Ile Leu Gln Thr Ala Gly Gly Ala Phe Cys
330          335          340
ctc tgg ctc ggc cgt gca aaa gcc ctc ccc gaa tcc atc act gcc atg 1169
Leu Trp Leu Gly Arg Ala Lys Ala Leu Pro Glu Ser Ile Thr Ala Met
          350          355          360
gtc ctc ttc tcc atc tgc gct cag gca gca tgt ggt gca gtc ttt ggt 1217
Val Leu Phe Ser Ile Cys Ala Gln Ala Ala Cys Gly Ala Val Phe Gly
          365          370          375
gtc atc ccc ttc gtc tcc cgc cgc tcc ctc ggc atc att tcg ggc ttg 1265
Val Ile Pro Phe Val Ser Arg Arg Ser Leu Gly Ile Ile Ser Gly Leu
          380          385          390
agt gga gcc ggt ggg aac ttt ggc gcc ggg ctg aca caa ttg ctc ttc 1313
Ser Gly Ala Gly Gly Asn Phe Gly Ala Gly Leu Thr Gln Leu Leu Phe
          395          400          405
ttc act tcg tcg aag tat ggc acc ggc agg ggg ctt gag tac atg ggt 1361
Phe Thr Ser Ser Lys Tyr Gly Thr Gly Arg Gly Leu Glu Tyr Met Gly
410          415          420
atc atg atc atg gcc tgc acg ctc cct gtg gcg ctt gtg cac ttc cca 1409
Ile Met Ile Met Ala Cys Thr Leu Pro Val Ala Leu Val His Phe Pro
          430          435          440
cag tgg ggt tcc atg ctc ttg ccg cca aac gcc aac gcc acc gag gag 1457
Gln Trp Gly Ser Met Leu Leu Pro Pro Asn Ala Asn Ala Thr Glu Glu
          445          450          455
gag ttc tat gcc gcc gaa tgg agc gag gag gag aag aag aag ggt ctc 1505
Glu Phe Tyr Ala Ala Glu Trp Ser Glu Glu Glu Lys Lys Lys Gly Leu
          460          465          470
cat atc cct ggc caa aag ttt gcc gag aat tcc cgc tcg gag cgt ggc 1553
His Ile Pro Gly Gln Lys Phe Ala Glu Asn Ser Arg Ser Glu Arg Gly
          475          480          485
agg cgc aac gtc atc ctt gcc aca gcc gcc aca ccc ccc aac aac act 1601
Arg Arg Asn Val Ile Leu Ala Thr Ala Ala Thr Pro Pro Asn Asn Thr
490          495          500          505
ccc caa cac gca taagactcga gcttttcttt acctgtgtac acgtacagtg 1653
Pro Gln His Ala

cgcgtattat acacacatcg atcgtgtata tacgcctgga atccgcaagc agtatgtttt 1713

ttgaaaaaaaa aaaagcggcc gcgaattc 1741

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<210> 1493
 <211> 509
 <212> PRT
 <213> Hordeum vulgare

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<400> 1493
Met Glu Val Glu Ser Ser Ser His Gly Ala Gly Asp Glu Ala Ala Ser
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Lys Phe Ser Leu Pro Val Asp Ser Glu His Lys Ala Lys Ser Ile Arg
20          25          30
Leu Phe Ser Phe Ala Asn Pro His Met Arg Thr Phe His Leu Ser Trp
35          40          45
Ile Ser Phe Phe Thr Cys Phe Val Ser Thr Phe Ala Ala Ala Pro Leu
50          55          60
Val Pro Ile Ile Arg Asp Asn Leu Asn Leu Ala Lys Ala Asp Ile Gly
65          70          75          80
Asn Ala Gly Val Ala Ser Val Ser Gly Ser Ile Phe Ser Arg Leu Ala
85          90          95
Met Gly Ala Ile Cys Asp Leu Leu Gly Pro Arg Tyr Gly Cys Ala Phe
100          105          110
Leu Val Met Leu Ala Ala Pro Thr Val Phe Cys Met Ser Leu Ile Asp
115          120          125
Asp Ala Ala Gly Tyr Ile Thr Val Arg Phe Leu Ile Gly Phe Ser Leu
130          135          140
Ala Thr Phe Val Ser Cys Gln Tyr Trp Met Ser Thr Met Phe Asn Ser

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PF59082SeqList_PF59082.txt

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145          150          155          160
Lys Ile Ile Gly Thr Val Asn Gly Leu Ala Ala Gly Trp Gly Asn Met
      165
Gly Gly Gly Ala Thr Gln Leu Ile Met Pro Leu Val Phe His Ala Ile
      180
Gln Lys Cys Gly Ala Thr Pro Phe Val Ala Trp Arg Ile Ala Tyr Phe
      195
Val Pro Gly Met Met His Val Val Met Gly Leu Leu Val Leu Thr Met
      210
Gly Gln Asp Leu Pro Asp Gly Asn Leu Ala Ser Leu Gln Lys Lys Gly
      225
Glu Met Ala Lys Asp Lys Phe Ser Lys Val Val Trp Gly Ala Val Thr
      245
Asn Tyr Arg Thr Trp Ile Phe Val Leu Leu Tyr Gly Tyr Cys Met Gly
      260
Val Glu Leu Thr Thr Asp Asn Val Ile Ala Glu Tyr Tyr Phe Asp His
      275
Phe His Leu Asp Leu Arg Thr Ser Gly Thr Ile Ala Ala Cys Phe Gly
      290
Met Ala Asn Ile Val Ala Arg Pro Ala Gly Gly Tyr Leu Ser Asp Leu
      305
Gly Ala Arg Tyr Phe Gly Met Arg Ala Arg Leu Trp Asn Ile Trp Ile
      325
Leu Gln Thr Ala Gly Gly Ala Phe Cys Leu Trp Leu Gly Arg Ala Lys
      340
Ala Leu Pro Glu Ser Ile Thr Ala Met Val Leu Phe Ser Ile Cys Ala
      355
Gln Ala Ala Cys Gly Ala Val Phe Gly Val Ile Pro Phe Val Ser Arg
      370
Arg Ser Leu Gly Ile Ile Ser Gly Leu Ser Gly Ala Gly Gly Asn Phe
      385
Gly Ala Gly Leu Thr Gln Leu Leu Phe Phe Thr Ser Ser Lys Tyr Gly
      405
Thr Gly Arg Gly Leu Glu Tyr Met Gly Ile Met Ile Met Ala Cys Thr
      420
Leu Pro Val Ala Leu Val His Phe Pro Gln Trp Gly Ser Met Leu Leu
      435
Pro Pro Asn Ala Asn Ala Thr Glu Glu Glu Phe Tyr Ala Ala Glu Trp
      450
Ser Glu Glu Glu Lys Lys Lys Gly Leu His Ile Pro Gly Gln Lys Phe
      465
Ala Glu Asn Ser Arg Ser Glu Arg Gly Arg Arg Asn Val Ile Leu Ala
      485
Thr Ala Ala Thr Pro Pro Asn Asn Thr Pro Gln His Ala
      500

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<210> 1494
 <211> 1691
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (62)..(1636)

<400> 1494
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60

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a atg gcg gcc gtc ggc gct ccg ggg agc tct ctg cac gga gtc acg ggg
  Met Ala Ala Val Gly Ala Pro Gly Ser Ser Leu His Gly Val Thr Gly
    1          5          10          15
cgc gag ccg gcg ttc gca ttc tcc acg gag cac gag gag gcg gcg agc
Arg Glu Pro Ala Phe Ala Phe Ser Thr Glu His Glu Glu Ala Ala Ser
    20          25          30
aat ggc ggc aag ttc gac ctg ccg gtg gac tcg gag cac aag gcg aag
Asn Gly Gly Lys Phe Asp Leu Pro Val Asp Ser Glu His Lys Ala Lys
    35          40          45
agc gtc cgg ctc ttc tcc gtg gcg aac ccg cac atg cgc acc ttc cac

```

109

157

205

253

PF59082SeqList_PF59082.txt

Ser	Val	Arg	Leu	Phe	Ser	Val	Ala	Asn	Pro	His	Met	Arg	Thr	Phe	His	
50	55	60														
ctc	tcc	tgg	atc	tcc	ttc	ttc	acc	tgc	ttc	gtg	tcc	acc	ttc	gcc	gcc	301
Leu	Ser	Trp	Ile	Ser	Phe	Phe	Thr	Cys	Phe	Val	Ser	Thr	Phe	Ala	Ala	
65	70	75	80													
gcg	ccg	ctg	gtc	ccc	atc	atc	cg	gac	aac	ctc	aac	ctc	acc	aag	gcc	349
Ala	Pro	Leu	Val	Pro	Ile	Ile	Arg	Asp	Asn	Leu	Asn	Leu	Thr	Lys	Ala	
				85					90					95		
gac	atc	ggc	aac	gcg	ggc	gtg	gcc	tcc	gtg	tcg	ggc	tcc	atc	ttc	tcc	397
Asp	Ile	Gly	Asn	Ala	Gly	Val	Ala	Ser	Val	Ser	Gly	Ser	Ile	Phe	Ser	
			100					105					110			
cg	ctc	acc	atg	ggc	gcc	gtc	tgc	gac	ctg	ctg	ggc	ccg	cg	tac	ggc	445
Arg	Leu	Thr	Met	Gly	Ala	Val	Cys	Asp	Leu	Leu	Gly	Pro	Arg	Tyr	Gly	
		115					120					125				
tgc	gcc	ttc	ctc	atc	atg	ctg	tcc	gcg	ccc	acc	gtg	ttc	tgc	atg	tcg	493
Cys	Ala	Phe	Leu	Ile	Met	Leu	Ser	Ala	Pro	Thr	Val	Phe	Cys	Met	Ser	
	130					135					140					
ctc	atc	gac	gac	gcc	gcg	ggc	tac	atc	acc	gtc	agg	ttc	ctc	atc	ggc	541
Leu	Ile	Asp	Asp	Ala	Ala	Gly	Tyr	Ile	Thr	Val	Arg	Phe	Leu	Ile	Gly	
145					150					155					160	
ttc	tcc	ctc	gcc	acc	ttc	gtc	tcc	tgc	cag	tac	tgg	atg	agc	acc	atg	589
Phe	Ser	Leu	Ala	Thr	Phe	Val	Ser	Cys	Gln	Tyr	Trp	Met	Ser	Thr	Met	
				165				170						175		
ttc	agc	agc	aag	atc	atc	ggc	acc	gtc	aac	ggg	ctc	gcc	gcc	gga	tgg	637
Phe	Ser	Ser	Lys	Ile	Ile	Gly	Thr	Val	Asn	Gly	Leu	Ala	Ala	Gly	Trp	
			180				185						190			
ggc	aac	atg	gga	ggc	ggc	gcc	acg	cag	ctc	atc	atg	ccg	ctc	gtc	tac	685
Gly	Asn	Met	Gly	Gly	Gly	Ala	Thr	Gln	Leu	Ile	Met	Pro	Leu	Val	Tyr	
		195				200						205				
gac	gtc	atc	cg	aag	tgc	ggc	gcc	acg	ccc	ttc	acg	gcg	tgg	cg	ctc	733
Asp	Val	Ile	Arg	Lys	Cys	Gly	Ala	Thr	Pro	Phe	Thr	Ala	Trp	Arg	Leu	
	210					215					220					
gcc	tac	ttc	gtg	ccg	ggc	ctc	atg	cac	gtc	gtc	atg	ggc	gtc	ctg	gtg	781
Ala	Tyr	Phe	Val	Pro	Gly	Leu	Met	His	Val	Val	Met	Gly	Val	Leu	Val	
225					230					235					240	
ctc	acg	ctg	ggg	cag	gac	ctc	ccc	gac	ggc	aac	ctc	agg	tcg	ctg	cag	829
Leu	Thr	Leu	Gly	Gln	Asp	Leu	Pro	Asp	Gly	Asn	Leu	Arg	Ser	Leu	Gln	
			245					250					255			
aag	aag	ggc	aac	gtc	aac	aag	gac	agc	ttc	tcc	aag	gtc	atg	tgg	tac	877
Lys	Lys	Gly	Asn	Val	Asn	Lys	Asp	Ser	Phe	Ser	Lys	Val	Met	Trp	Tyr	
			260				265						270			
gcc	gtc	atc	aac	tac	cg	acc	tgg	atc	ttc	gtc	ctc	ctc	tac	ggc	tac	925
Ala	Val	Ile	Asn	Tyr	Arg	Thr	Trp	Ile	Phe	Val	Leu	Leu	Tyr	Gly	Tyr	
	275					280						285				
tgc	atg	ggc	gtc	gag	ctc	acc	acc	gac	aac	gtc	atc	gcc	gag	tac	atg	973
Cys	Met	Gly	Val	Glu	Leu	Thr	Thr	Asp	Asn	Val	Ile	Ala	Glu	Tyr	Met	
	290					295				300						
tac	gac	cg	ttc	gac	ctc	gac	ctc	cg	gtc	gcc	ggg	acc	atc	gcc	gcc	1021
Tyr	Asp	Arg	Phe	Asp	Leu	Asp	Leu	Arg	Val	Ala	Gly	Thr	Ile	Ala	Ala	
305					310					315					320	
tgc	ttc	ggc	atg	gcc	aac	atc	gtc	gcg	cg	ccc	atg	ggc	ggc	atc	atg	1069
Cys	Phe	Gly	Met	Ala	Asn	Ile	Val	Ala	Arg	Pro	Met	Gly	Gly	Ile	Met	
			325					330					335			
tcc	gac	atg	ggc	gcg	cg	tac	tgg	ggc	atg	cg	gct	cg	ctc	tgg	aac	1117
Ser	Asp	Met	Gly	Ala	Arg	Tyr	Trp	Gly	Met	Arg	Ala	Arg	Leu	Trp	Asn	
			340				345						350			
atc	tgg	atc	ctc	cag	acc	gcc	ggc	ggc	gcc	ttc	tgc	ctc	tgg	ctg	gga	1165
Ile	Trp	Ile	Leu	Gln	Thr	Ala	Gly	Gly	Ala	Phe	Cys	Leu	Trp	Leu	Gly	
	355					360						365				
cg	gcc	agc	acc	ctc	ccc	gtc	tcc	gtc	gtc	gcc	atg	gtg	ctc	ttc	tcc	1213
Arg	Ala	Ser	Thr	Leu	Pro	Val	Ser	Val	Val	Ala	Met	Val	Leu	Phe	Ser	
	370					375					380					
ttc	tgc	gcg	cag	gcg	gcc	tgc	ggc	gcc	atc	ttc	ggg	gtc	atc	ccc	ttc	1261
Phe	Cys	Ala	Gln	Ala	Ala	Cys	Gly	Ala	Ile	Phe	Gly	Val	Ile	Pro	Phe	
385					390					395					400	
gtc	tcc	cg	cg	tcc	ctc	ggc	atc	atc	tcc	ggc	atg	acg	ggc	gcc	ggc	1309
Val	Ser	Arg	Arg	Ser	Leu	Gly	Ile	Ile	Ser	Gly	Met	Thr	Gly	Ala	Gly	
			405				410							415		
ggc	aac	ttc	ggc	gcg	ggg	ctc	acg	cag	ctg	ctc	ttc	ttc	acc	tcc	tca	1357

PF59082SeqList_PF59082.txt

Gly	Asn	Phe	Gly	Ala	Gly	Leu	Thr	Gln	Leu	Leu	Phe	Phe	Thr	Ser	Ser		
			420					425					430				
acc	tac	tcc	acg	ggc	agg	ggg	cta	gag	tac	atg	ggc	atc	atg	atc	atg		1405
Thr	Tyr	Ser	Thr	Gly	Arg	Gly	Leu	Glu	Tyr	Met	Gly	Ile	Met	Ile	Met		
		435					440					445					
gcg	tgc	acg	cta	cct	gtg	gtg	ttc	gtg	cac	ttc	ccg	cag	tggtgg	ggg	tcc		1453
Ala	Cys	Thr	Leu	Pro	Val	Val	Phe	Val	His	Phe	Pro	Gln	Trp	Gly	Ser		
	450					455					460						
atg	ttc	ttc	ccg	ccc	agc	gcc	acc	gcc	gac	gag	gag	ggc	tac	tac	gcc		1501
Met	Phe	Phe	Pro	Pro	Ser	Ala	Thr	Ala	Asp	Glu	Gly	Tyr	Tyr		480		
	465				470					475							
tcc	gag	tggtgg	aac	gac	gac	gag	aag	agc	aag	gga	ctc	cat	agc	gcc	agc		1549
Ser	Glu	Trp	Asn	Asp	Asp	Glu	Lys	Ser	Lys	Gly	Leu	His	Ser	Ala	Ser		
			485					490						495			
ctc	aag	ttt	gcc	gag	aac	agc	cgc	tca	gag	cgc	ggc	aag	cga	aac	gtc		1597
Leu	Lys	Phe	Ala	Glu	Asn	Ser	Arg	Ser	Glu	Arg	Gly	Lys	Arg	Asn	Val		
			500					505					510				
atc	cag	gcc	gat	gcc	gcc	gcc	acg	ccg	gag	cat	gtc	taagtctact					1643
Ile	Gln	Ala	Asp	Ala	Ala	Ala	Thr	Pro	Glu	His	Val						
		515					520										
actaataaga	tggtatcgatc	catcatccat	gttcacctgc	tacctacc													1691

<210> 1495
 <211> 524
 <212> PRT
 <213> Zea mays

<400> 1495

Met	Ala	Ala	Val	Gly	Ala	Pro	Gly	Ser	Ser	Leu	His	Gly	Val	Thr	Gly		
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Arg	Glu	Pro	Ala	Phe	Ala	Phe	Ser	Thr	Glu	His	Glu	Glu	Ala	Ala	Ser		
			20				25						30				
Asn	Gly	Gly	Lys	Phe	Asp	Leu	Pro	Val	Asp	Ser	Glu	His	Lys	Ala	Lys		
		35					40					45					
Ser	Val	Arg	Leu	Phe	Ser	Val	Ala	Asn	Pro	His	Met	Arg	Thr	Phe	His		
	50					55					60						
Leu	Ser	Trp	Ile	Ser	Phe	Thr	Cys	Phe	Val	Ser	Thr	Phe	Ala	Ala			
	65				70				75					80			
Ala	Pro	Leu	Val	Pro	Ile	Ile	Arg	Asp	Asn	Leu	Asn	Leu	Thr	Lys	Ala		
				85					90					95			
Asp	Ile	Gly	Asn	Ala	Gly	Val	Ala	Ser	Val	Ser	Gly	Ser	Ile	Phe	Ser		
			100					105					110				
Arg	Leu	Thr	Met	Gly	Ala	Val	Cys	Asp	Leu	Leu	Gly	Pro	Arg	Tyr	Gly		
		115					120					125					
Cys	Ala	Phe	Leu	Ile	Met	Leu	Ser	Ala	Pro	Thr	Val	Phe	Cys	Met	Ser		
	130					135					140						
Leu	Ile	Asp	Asp	Ala	Ala	Gly	Tyr	Ile	Thr	Val	Arg	Phe	Leu	Ile	Gly		
	145				150					155				160			
Phe	Ser	Leu	Ala	Thr	Phe	Val	Ser	Cys	Gln	Tyr	Trp	Met	Ser	Thr	Met		
			165					170						175			
Phe	Ser	Ser	Lys	Ile	Ile	Gly	Thr	Val	Asn	Gly	Leu	Ala	Ala	Gly	Trp		
			180					185					190				
Gly	Asn	Met	Gly	Gly	Gly	Ala	Thr	Gln	Leu	Ile	Met	Pro	Leu	Val	Tyr		
		195					200					205					
Asp	Val	Ile	Arg	Lys	Cys	Gly	Ala	Thr	Pro	Phe	Thr	Ala	Trp	Arg	Leu		
	210					215					220						
Ala	Tyr	Phe	Val	Pro	Gly	Leu	Met	His	Val	Val	Met	Gly	Val	Leu	Val		
	225				230					235					240		
Leu	Thr	Leu	Gly	Gln	Asp	Leu	Pro	Asp	Gly	Asn	Leu	Arg	Ser	Leu	Gln		
			245						250					255			
Lys	Lys	Gly	Asn	Val	Asn	Lys	Asp	Ser	Phe	Ser	Lys	Val	Met	Trp	Tyr		
			260					265					270				
Ala	Val	Ile	Asn	Tyr	Arg	Thr	Trp	Ile	Phe	Val	Leu	Leu	Tyr	Gly	Tyr		
		275					280					285					
Cys	Met	Gly	Val	Glu	Leu	Thr	Thr	Asp	Asn	Val	Ile	Ala	Glu	Tyr	Met		
	290					295					300						
Tyr	Asp	Arg	Phe	Asp	Leu	Asp	Leu	Arg	Val	Ala	Gly	Thr	Ile	Ala	Ala		

PF59082SeqList_PF59082.txt

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305          310          315          320
Cys Phe Gly Met Ala Asn Ile Val Ala Arg Pro Met Gly Gly Ile Met
          325          330          335
Ser Asp Met Gly Ala Arg Tyr Trp Gly Met Arg Ala Arg Leu Trp Asn
          340          345          350
Ile Trp Ile Leu Gln Thr Ala Gly Gly Ala Phe Cys Leu Trp Leu Gly
          355          360          365
Arg Ala Ser Thr Leu Pro Val Ser Val Val Ala Met Val Leu Phe Ser
          370          375          380
Phe Cys Ala Gln Ala Ala Cys Gly Ala Ile Phe Gly Val Ile Pro Phe
385          390          395
Val Ser Arg Arg Ser Leu Gly Ile Ile Ser Gly Met Thr Gly Ala Gly
          405          410          415
Gly Asn Phe Gly Ala Gly Leu Thr Gln Leu Leu Phe Phe Thr Ser Ser
          420          425          430
Thr Tyr Ser Thr Gly Arg Gly Leu Glu Tyr Met Gly Ile Met Ile Met
          435          440          445
Ala Cys Thr Leu Pro Val Val Phe Val His Phe Pro Gln Trp Gly Ser
          450          455          460
Met Phe Phe Pro Pro Ser Ala Thr Ala Asp Glu Gly Tyr Tyr Ala
465          470          475
Ser Glu Trp Asn Asp Asp Glu Lys Ser Lys Gly Leu His Ser Ala Ser
          485          490          495
Leu Lys Phe Ala Glu Asn Ser Arg Ser Glu Arg Gly Lys Arg Asn Val
          500          505          510
Ile Gln Ala Asp Ala Ala Ala Thr Pro Glu His Val
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<210> 1496

<211> 1527

<212> DNA

<213> Populus tremula x Populus tremuloides

<220>

<221> CDS

<222> (1)..(1527)

<400> 1496

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Met Glu Ile Glu Gly Gln Ala Thr Val Lys 10 Glu Ser Gln Pro 15 Lys
1          5
ttc gct ctt cca gtg gat tca gaa cac aag gca act gag ttc cgg ttg      96
Phe Ala Leu Pro Val Asp Ser Glu His Lys Ala Thr Glu Phe Arg Leu
          20          25          30
ttc tca gta gct gcc cct cac atg cgg gca ttc cat ctt tct tgg gtt      144
Phe Ser Val Ala Ala Pro His Met Arg Ala Phe His Leu Ser Trp Val
          35          40          45
tct ttc ttt gcc tgt ttt gtc tct tct ttt gct gct cca ccc ctt ctt      192
Ser Phe Phe Ala Cys Phe Val Ser Ser Phe Ala Pro Pro Leu Leu
          50          55          60
cct atc ata cgt gac aac ctc aac ctc act gcc tct gac att ggt aat      240
Pro Ile Ile Arg Asp Asn Leu Asn Leu Thr Ala Ser Asp Ile Gly Asn
          65          70          75
gcg ggc att gca tca gtg tca ggt gca gtt ttt gct cga gtt gct atg      288
Ala Gly Ile Ala Ser Val Ser Gly Ala Val Phe Ala Arg Val Ala Met
          80          85          90
ggg act gct tgt gac ctt ttc gga ccc cgt cta gcc tct gcc tca ttg      336
Gly Thr Ala Cys Asp Leu Phe Gly Pro Arg Leu Ala Ser Ala Ser Leu
          100          105          110
atc ctc ctc act gca cct gca gtt tac ttc act tcc atg gcc tca tct      384
Ile Leu Leu Thr Ala Pro Ala Val Tyr Phe Thr Ser Met Ala Ser Ser
          115          120          125
tct act tct ttt ctc ctg gtt cgt ttt ttc act ggc ttc tct ctg gcc      432
Ser Thr Ser Phe Leu Leu Val Arg Phe Phe Thr Gly Phe Ser Leu Ala
          130          135          140
act ttt gtc tcc act caa ttc tgg atg agc tct atg ttt tca gca ccg      480
Thr Phe Val Ser Thr Gln Phe Trp Met Ser Ser Met Phe Ser Ala Pro
          145          150          155
gta gtt gga acg gct aat ggc gtt gcg gga ggt tgg ggt aac ctt ggc      528
          160

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PF59082SeqList_PF59082.txt

Val	Val	Gly	Thr	Ala	Asn	Gly	Val	Ala	Gly	Gly	Trp	Gly	Asn	Leu	Gly	
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Gly	Gly	Ala	Thr	Gln	Leu	Ile	Met	Pro	Leu	Val	Phe	Gly	Leu	Ile	Arg	
			180					185					190			
gac	att	gga	gcc	atc	aaa	ttt	aca	gct	tgg	aga	att	gcg	ttt	ttc	att	624
Asp	Ile	Gly	Ala	Ile	Lys	Phe	Thr	Ala	Trp	Arg	Ile	Ala	Phe	Phe	Ile	
			195				200					205				
cct	gcc	ctg	ttt	cag	aca	cta	tcg	gca	ttt	gca	gtc	ttg	atc	ttt	ggc	672
Pro	Ala	Leu	Phe	Gln	Thr	Leu	Ser	Ala	Phe	Ala	Val	Leu	Ile	Phe	Gly	
			210				215				220					
aag	gac	ttg	ccg	gac	gga	aac	ttt	agg	cgg	ctg	cag	aaa	gca	ggg	gat	720
Lys	Asp	Leu	Pro	Asp	Gly	Asn	Phe	Arg	Arg	Leu	Gln	Lys	Ala	Gly	Asp	
225					230				235						240	
aaa	aca	aaa	gat	aaa	ttc	tca	aat	gtc	ttc	tat	cat	gga	ata	aaa	aat	768
Lys	Thr	Lys	Asp	Lys	Phe	Ser	Asn	Val	Phe	Tyr	His	Gly	Ile	Lys	Asn	
					245				250					255		
tac	aga	ggg	tgg	atc	ctg	gca	ctc	agt	tat	ggg	tac	tgt	ttt	ggg	gta	816
Tyr	Arg	Gly	Trp	Ile	Leu	Ala	Leu	Ser	Tyr	Gly	Tyr	Cys	Phe	Gly	Val	
			260					265					270			
gag	ctg	aca	ata	gac	aac	att	gtc	gca	gaa	tac	ttc	tat	gac	aga	ttt	864
Glu	Leu	Thr	Ile	Asp	Asn	Ile	Val	Ala	Glu	Tyr	Phe	Tyr	Asp	Arg	Phe	
			275				280					285				
gac	ctc	aaa	ctc	cat	aca	gca	gga	atg	att	gca	gca	agc	ttt	ggg	cta	912
Asp	Leu	Lys	Leu	His	Thr	Gly	Met	Ile	Ala	Ala	Ser	Phe	Gly	Leu		
			290			295				300						
gca	aac	att	gtt	tct	cga	cca	ggg	ggg	gga	atg	atc	tca	gat	gca	gta	960
Ala	Asn	Ile	Val	Ser	Arg	Pro	Gly	Gly	Gly	Met	Ile	Ser	Asp	Ala	Val	
305					310				315						320	
ggg	aag	agg	ttt	gga	atg	agg	ggg	aag	ttg	tgg	gct	ctg	tgg	gta	gtg	1008
Gly	Lys	Arg	Phe	Gly	Met	Arg	Gly	Lys	Leu	Trp	Ala	Leu	Trp	Val	Val	
					325				330					335		
cag	acc	ttg	gga	ggg	gtt	ttc	tgc	atc	ata	ctt	gga	cga	ggt	gga	tct	1056
Gln	Thr	Leu	Gly	Gly	Val	Phe	Cys	Ile	Ile	Leu	Gly	Arg	Val	Gly	Ser	
			340				345						350			
tta	ggc	gcg	tcc	att	gtg	gtg	atg	att	gtg	ttc	ttc	tta	ttc	tgc	caa	1104
Leu	Gly	Ala	Ser	Ile	Val	Val	Met	Ile	Val	Phe	Phe	Leu	Phe	Cys	Gln	
			355				360					365				
gca	gca	tgt	gga	cta	aca	ttt	ggg	gtg	gtg	cct	ttt	gtc	tca	cga	agg	1152
Ala	Ala	Cys	Gly	Leu	Thr	Phe	Gly	Val	Val	Pro	Phe	Val	Ser	Arg	Arg	
			370			375				380						
tca	ttg	ggg	ctc	ata	tct	ggg	atg	act	gga	ggg	ggg	gga	aac	gtg	ggg	1200
Ser	Leu	Gly	Leu	Ile	Ser	Gly	Met	Thr	Gly	Gly	Gly	Gly	Asn	Val	Gly	
385					390				395						400	
gca	gtt	cta	act	caa	cta	att	ttc	ttc	aga	gga	tcg	aaa	tac	tca	aaa	1248
Ala	Val	Leu	Thr	Gln	Leu	Ile	Phe	Phe	Arg	Gly	Ser	Lys	Tyr	Ser	Lys	
					405				410					415		
gag	aga	ggg	ata	atg	ctc	atg	ggg	gtc	atg	att	ata	tgc	tgc	act	ctt	1296
Glu	Arg	Gly	Ile	Met	Leu	Met	Gly	Val	Met	Ile	Ile	Cys	Cys	Thr	Leu	
			420				425						430			
cca	att	tgt	ctt	ata	cac	ttc	cca	caa	tgg	ggg	gga	atg	ttt	tgc	ggg	1344
Pro	Ile	Cys	Leu	Ile	His	Phe	Pro	Gln	Trp	Gly	Gly	Met	Phe	Cys	Gly	
			435				440					445				
cca	tca	tct	aca	aag	atc	gct	aca	gaa	gaa	gac	tac	tac	ttg	tcc	gaa	1392
Pro	Ser	Ser	Thr	Lys	Ile	Ala	Thr	Glu	Glu	Asp	Tyr	Tyr	Leu	Ser	Glu	
						455					460					
tgg	aat	tca	gag	gag	aag	gag	aaa	ggc	ctg	cat	cta	tca	agc	tta	aag	1440
Trp	Asn	Ser	Glu	Glu	Lys	Glu	Lys	Gly	Leu	His	Leu	Ser	Ser	Leu	Lys	
465					470					475					480	
ttt	gca	gat	aac	agc	aga	agt	gaa	aga	ggg	aga	aaa	gaa	gat	tct	gaa	1488
Phe	Ala	Asp	Asn	Ser	Arg	Ser	Glu	Arg	Gly	Arg	Lys	Glu	Asp	Ser	Glu	
					485				490					495		
acc	agg	cca	gta	gat	gaa	acc	cta	tca	aca	aaa	gtc	tag				1527
Thr	Arg	Pro	Val	Asp	Glu	Thr	Leu	Ser	Thr	Lys	Val					
			500				505									

<210> 1497

<211> 508

<212> PRT

<213> Populus tremula x Populus tremuloides

<400> 1497

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      20      25      30
Phe Ser Val Ala Ala Pro His Met Arg Ala Phe His Leu Ser Trp Val
      35      40      45
Ser Phe Phe Ala Cys Phe Val Ser Ser Phe Ala Ala Pro Pro Leu Leu
      50      55      60
Pro Ile Ile Arg Asp Asn Leu Asn Leu Thr Ala Ser Asp Ile Gly Asn
65      70      75      80
Ala Gly Ile Ala Ser Val Ser Gly Ala Val Phe Ala Arg Val Ala Met
      85      90      95
Gly Thr Ala Cys Asp Leu Phe Gly Pro Arg Leu Ala Ser Ala Ser Leu
      100      105      110
Ile Leu Leu Thr Ala Pro Ala Val Tyr Phe Thr Ser Met Ala Ser Ser
      115      120      125
Ser Thr Ser Phe Leu Leu Val Arg Phe Phe Thr Gly Phe Ser Leu Ala
      130      135      140
Thr Phe Val Ser Thr Gln Phe Trp Met Ser Ser Met Phe Ser Ala Pro
145      150      155      160
Val Val Gly Thr Ala Asn Gly Val Ala Gly Gly Trp Gly Asn Leu Gly
      165      170      175
Gly Gly Ala Thr Gln Leu Ile Met Pro Leu Val Phe Gly Leu Ile Arg
      180      185      190
Asp Ile Gly Ala Ile Lys Phe Thr Ala Trp Arg Ile Ala Phe Phe Ile
      195      200      205
Pro Ala Leu Phe Gln Thr Leu Ser Ala Phe Ala Val Leu Ile Phe Gly
      210      215      220
Lys Asp Leu Pro Asp Gly Asn Phe Arg Arg Leu Gln Lys Ala Gly Asp
225      230      235      240
Lys Thr Lys Asp Lys Phe Ser Asn Val Phe Tyr His Gly Ile Lys Asn
      245      250      255
Tyr Arg Gly Trp Ile Leu Ala Leu Ser Tyr Gly Tyr Cys Phe Gly Val
      260      265      270
Glu Leu Thr Ile Asp Asn Ile Val Ala Glu Tyr Phe Tyr Asp Arg Phe
      275      280      285
Asp Leu Lys Leu His Thr Ala Gly Met Ile Ala Ala Ser Phe Gly Leu
      290      295      300
Ala Asn Ile Val Ser Arg Pro Gly Gly Gly Met Ile Ser Asp Ala Val
305      310      315      320
Gly Lys Arg Phe Gly Met Arg Gly Lys Leu Trp Ala Leu Trp Val Val
      325      330      335
Gln Thr Leu Gly Gly Val Phe Cys Ile Ile Leu Gly Arg Val Gly Ser
      340      345      350
Leu Gly Ala Ser Ile Val Val Met Ile Val Phe Phe Leu Phe Cys Gln
      355      360      365
Ala Ala Cys Gly Leu Thr Phe Gly Val Val Pro Phe Val Ser Arg Arg
      370      375      380
Ser Leu Gly Leu Ile Ser Gly Met Thr Gly Gly Gly Asn Val Gly
385      390      395      400
Ala Val Leu Thr Gln Leu Ile Phe Phe Arg Gly Ser Lys Tyr Ser Lys
      405      410      415
Glu Arg Gly Ile Met Leu Met Gly Val Met Ile Ile Cys Cys Thr Leu
      420      425      430
Pro Ile Cys Leu Ile His Phe Pro Gln Trp Gly Gly Met Phe Cys Gly
      435      440      445
Pro Ser Ser Thr Lys Ile Ala Thr Glu Glu Asp Tyr Tyr Leu Ser Glu
      450      455      460
Trp Asn Ser Glu Glu Lys Glu Lys Gly Leu His Leu Ser Ser Leu Lys
465      470      475      480
Phe Ala Asp Asn Ser Arg Ser Glu Arg Gly Arg Lys Glu Asp Ser Glu
      485      490      495
Thr Arg Pro Val Asp Glu Thr Leu Ser Thr Lys Val
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<210> 1498

PF59082SeqList_PF59082.txt

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<213> Oryza sativa

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<221> CDS
<222> (224)..(1684)

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ccgcgctttc cgctatgcta taagagctga cgcgagggc acagcggatg tacgtacaca 180

cagtcactag ctaagctgct agccttgcta ccacgtgttg gag atg gag gct aag 235
               Met Glu Ala Lys
               1
ccg gtg gcg atg gag gtg gag ggg gtc gag gcg gcg ggg ggc aag ccg 283
Pro Val Ala Met Glu Val Glu Gly Val Glu Ala Ala Gly Gly Lys Pro
5 10 15 20
cgg ttc agg atg ccg gtg gac tcc gac ctc aag gcg acg gag ttc tgg 331
Arg Phe Arg Met Pro Val Asp Ser Asp Leu Lys Ala Thr Glu Phe Trp
25 30 35
ctc ttc tcc ttc gcg agg cca cac atg gcc tcc ttc cac atg gcg tgg 379
Leu Phe Ser Phe Ala Arg Pro His Met Ala Ser Phe His Met Ala Trp
40 45 50
ttc tcc ttc ttc tgc tgc ttc gtg tcc acg ttc gcc gtg ttc gcg cgt 427
Phe Ser Phe Phe Cys Cys Phe Val Ser Thr Phe Ala Val Phe Ala Arg
55 60 65
ctg gcc atg ggc acg gcg tgc gac ctg gtc ggg ccc agg ctg gcc tcc 475
Leu Ala Met Gly Thr Ala Cys Asp Leu Val Gly Pro Arg Leu Ala Ser
70 75 80
gcg tct ctg atc ctc ctc acc aca ccg gcg gtg tac tgc tcc tcc atc 523
Ala Ser Leu Ile Leu Leu Thr Thr Pro Ala Val Tyr Cys Ser Ser Ile
85 90 95
atc cag tcc ccg tcg ggg tac ctc ctc gtg cgc ttc ttc acg ggc atc 571
Ile Gln Ser Pro Ser Gly Tyr Leu Leu Val Arg Phe Phe Thr Gly Ile
100 105 110 115
tcg ctg gcg tcg ttc gtg tcg gcg cag ttc tgg atg agc tcc atg ttc 619
Ser Leu Ala Ser Phe Val Ser Ala Gln Phe Trp Met Ser Met Phe
120 125 130
tcg gcc ccc aaa gtg ggg ctg gcc aac ggc gtg gcc ggc ggc tgg ggc 667
Ser Ala Pro Lys Val Gly Leu Ala Asn Gly Val Ala Gly Gly Trp Gly
135 140 145
aac ctc ggc ggc ggc gcc gtc cag ctg ctc atg ccg ctc gtg tac gag 715
Asn Leu Gly Gly Gly Ala Val Gln Leu Leu Met Pro Leu Val Tyr Glu
150 155 160
gcc atc cac aag atc ggt agc acg ccg ttc acg gcg tgg cgc atc gcc 763
Ala Ile His Lys Ile Gly Ser Thr Pro Phe Thr Ala Trp Arg Ile Ala
165 170 175 180
ttc ttc atc ccg ggc ctg atg cag acg ttc tcg gcc atc gcc gtg ctg 811
Phe Phe Ile Pro Gly Leu Met Gln Thr Phe Ser Ala Ile Ala Val Leu
185 190 195
gcg ttc ggg cag gac atg ccc ggc ggc aac tac ggg aag ctc cac aag 859
Ala Phe Gly Gln Asp Met Pro Gly Gly Asn Tyr Gly Lys Leu His Lys
200 205 210
act ggc gac atg cac aag gac agc ttc ggc aac gtg ctg cgc cac gcc 907
Thr Gly Asp Met His Lys Asp Ser Phe Gly Asn Val Leu Arg His Ala
215 220 225
ctc acc aac tac cgc ggc tgg atc ctg gcg ctc acc tac ggc tac agc 955
Leu Thr Asn Tyr Arg Gly Trp Ile Leu Ala Leu Thr Tyr Gly Tyr Ser
230 235 240
ttc ggc gtc gag ctc acc atc gac aac gtc gtg cac cag tac ttc tac 1003
Phe Gly Val Glu Leu Thr Ile Asp Asn Val Val His Gln Tyr Phe Tyr
245 250 255 260

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[illegible]

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<210> 1499
<211> 486
<212> PRT
<213> Oryza sativa
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<400> 1499
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PF59082SeqList_PF59082.txt

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 Thr Glu Phe Trp Leu Phe Ser Phe Ala Arg Pro His Met Ala Ser Phe
 35 40 45
 His Met Ala Trp Phe Ser Phe Phe Cys Cys Phe Val Ser Thr Phe Ala
 50 55 60
 Val Phe Ala Arg Leu Ala Met Gly Thr Ala Cys Asp Leu Val Gly Pro
 65 70 75 80
 Arg Leu Ala Ser Ala Ser Leu Ile Leu Leu Thr Thr Pro Ala Val Tyr
 85 90 95
 Cys Ser Ser Ile Ile Gln Ser Pro Ser Gly Tyr Leu Leu Val Arg Phe
 100 105 110
 Phe Thr Gly Ile Ser Leu Ala Ser Phe Val Ser Ala Gln Phe Trp Met
 115 120 125
 Ser Ser Met Phe Ser Ala Pro Lys Val Gly Leu Ala Asn Gly Val Ala
 130 135 140
 Gly Gly Trp Gly Asn Leu Gly Gly Gly Ala Val Gln Leu Leu Met Pro
 145 150 155 160
 Leu Val Tyr Glu Ala Ile His Lys Ile Gly Ser Thr Pro Phe Thr Ala
 165 170 175
 Trp Arg Ile Ala Phe Phe Ile Pro Gly Leu Met Gln Thr Phe Ser Ala
 180 185 190
 Ile Ala Val Leu Ala Phe Gly Gln Asp Met Pro Gly Gly Asn Tyr Gly
 195 200 205
 Lys Leu His Lys Thr Gly Asp Met His Lys Asp Ser Phe Gly Asn Val
 210 215 220
 Leu Arg His Ala Leu Thr Asn Tyr Arg Gly Trp Ile Leu Ala Leu Thr
 225 230 235 240
 Tyr Gly Tyr Ser Phe Gly Val Glu Leu Thr Ile Asp Asn Val Val His
 245 250 255
 Gln Tyr Phe Tyr Asp Arg Phe Asp Val Asn Leu Gln Thr Ala Gly Leu
 260 265 270
 Ile Ala Ala Ser Phe Gly Met Ala Asn Ile Ile Ser Arg Pro Gly Gly
 275 280 285
 Gly Leu Leu Ser Asp Trp Leu Ser Ser Arg Tyr Gly Met Arg Gly Arg
 290 295 300
 Leu Trp Gly Leu Trp Thr Val Gln Thr Ile Gly Gly Val Leu Cys Val
 305 310 315 320
 Val Leu Gly Ile Val Asp Phe Ser Phe Ala Ser Val Ala Val Met
 325 330 335
 Val Leu Phe Ser Phe Phe Val Gln Ala Ala Cys Gly Leu Thr Phe Gly
 340 345 350
 Ile Val Pro Phe Val Ser Arg Arg Ser Leu Gly Leu Ile Ser Gly Met
 355 360 365
 Thr Gly Gly Gly Gly Asn Val Gly Ala Val Leu Thr Gln Tyr Ile Phe
 370 375 380
 Phe His Gly Thr Lys Tyr Lys Thr Glu Thr Gly Ile Lys Tyr Met Gly
 385 390 395 400
 Leu Met Ile Ile Ala Cys Thr Leu Pro Val Met Leu Ile Tyr Phe Pro
 405 410 415
 Gln Trp Gly Gly Met Leu Val Gly Pro Arg Lys Gly Ala Thr Ala Glu
 420 425 430
 Glu Tyr Tyr Ser Arg Glu Trp Ser Asp His Glu Arg Glu Lys Gly Phe
 435 440 445
 Asn Ala Ala Ser Val Arg Phe Ala Glu Asn Ser Val Arg Glu Gly Gly
 450 455 460
 Arg Ser Ser Ala Asn Gly Gly Gln Pro Arg His Thr Val Pro Val Asp
 465 470 475 480
 Ala Ser Pro Ala Gly Val
 485

<210> 1500

<211> 1650

<212> DNA

<213> Physcomitrella patens

<220>

<221> CDS

<222> (1)..(1650)

PF59082SeqList_PF59082.txt

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ccc ggc atg tcc atg cac ggt gtg aca gga aaa gag cct gtg tat gca      96
Pro Gly Met Ser Met His Gly Val Thr Gly Lys Glu Pro Val Tyr Ala
20      25      30
ttc tca gtg att caa gga act gta gag gac ccc gac gct gag aag ttt      144
Phe Ser Val Ile Gln Gly Thr Val Glu Asp Pro Asp Ala Glu Lys Phe
35      40      45
gcg ctc ccg gtg gac tct gag cac aag gcg aaa aca atc cga gtt tac      192
Ala Leu Pro Val Asp Ser Glu His Lys Ala Lys Thr Ile Arg Val Tyr
50      55      60
agt ttc gca aag cca cac atg cgc gcc ttt cat ctc gct tgg gtg tct      240
Ser Phe Ala Lys Pro His Met Arg Ala Phe His Leu Ala Trp Val Ser
65      70      75
ttc ttt aca tgt ttc ttg gca acc ttc gcg tcg ccg ccc ctg atg ccg      288
Phe Phe Thr Cys Phe Leu Ala Thr Phe Ala Ser Pro Pro Leu Met Pro
85      90      95
atc atc cgt gac aac ttg aat ttg acc aaa acc gac gtt gga cat gct      336
Ile Ile Arg Asp Asn Leu Asn Leu Thr Lys Thr Asp Val Gly His Ala
100      105      110
gcc atc gcc tca gta tct ggt tct atc ctg tct cgt ctg ctg atg gga      384
Ala Ile Ala Ser Val Ser Gly Ser Ile Leu Ser Arg Leu Leu Met Gly
115      120      125
acc gtg tgc gac gtg gtt gga ccc cga tat ggc tgt gca ttc ctg att      432
Thr Val Cys Asp Val Val Gly Pro Arg Tyr Gly Cys Ala Phe Leu Ile
130      135      140
atg ata att tcg cca gcc gtg tac tca atg gct ctt gtt tca gat gcc      480
Met Ile Ile Ser Pro Ala Val Tyr Ser Met Ala Leu Val Ser Asp Ala
145      150      155
gcg agc ttt ata ata gtc cga ttc ttt acc ggt ttc gct cta gcc acc      528
Ala Ser Phe Ile Ile Val Arg Phe Phe Thr Gly Phe Ala Leu Ala Thr
160      165      170
ttc gtc tct tgc caa ttt tgg atg agc tcc atg ttc aac agc aag atc      576
Phe Val Ser Cys Gln Phe Trp Met Ser Ser Met Phe Asn Ser Lys Ile
175      180      185
gtc ggc aca gct aat ggg ctg gcc gcg ggt tgg ggc aac ctc ggt ggt      624
Val Gly Thr Ala Asn Gly Leu Ala Gly Trp Gly Asn Leu Gly Gly
190      195      200
ggc gct act cag ctc atc atg cct ctg gtt ttc gcg tta atc cga gac      672
Gly Ala Thr Gln Leu Ile Met Pro Leu Val Phe Ala Leu Ile Arg Asp
205      210      215
agc ttc aac tct aca ccg gtt gca tgg cgc ctg gcc ttt ttc tta      720
Ser Phe Asn Ser Thr Pro Phe Val Ala Trp Arg Leu Ala Phe Phe Leu
220      225      230
ccc gga gcg atg cag aca att atg ggg ctc ctc gtt cta ttt ctc ggc      768
Pro Gly Ala Met Gln Thr Ile Met Gly Leu Leu Val Leu Phe Leu Gly
235      240      245
caa gat ctt ccc gac ggc aac tat tct cag ttg cag aaa caa ggc gtc      816
Gln Asp Leu Pro Asp Gly Asn Tyr Ser Gln Leu Gln Lys Gln Gly Val
250      255      260
aaa gtg aaa gat agc ttt cta aag gtc ttg atg tac gca att aca aat      864
Lys Val Lys Asp Ser Phe Leu Lys Val Leu Met Tyr Ala Ile Thr Asn
265      270      275
tac aga aca tgg gtg ttc ttt ctg ttg tat gga ttc acc ttc ggc gtt      912
Tyr Arg Thr Trp Val Phe Phe Leu Leu Tyr Gly Phe Thr Phe Gly Val
280      285      290
gag ctg aca gtc aac aac atc gct gag tac ttc tat gac cgc ttc      960
Glu Leu Thr Val Asn Asn Asn Ile Ala Glu Tyr Phe Tyr Asp Arg Phe
295      300      305
gat ttg aat ctc tcc aca gct gga ata atc gct tca tta ttc ggc ttg      1008
Asp Leu Asn Leu Ser Thr Ala Gly Ile Ile Ala Ser Leu Phe Gly Leu
310      315      320
atg aac ttt ttc gct cgt cca agt ggt gga atc atc tcc gat act gtt      1056
Met Asn Phe Phe Ala Arg Pro Ser Gly Gly Ile Ile Ser Asp Thr Val
325      330      335
gcg cgc cgt ttt gga atg aaa ggt cgc ctg tgc acg ctg tgg ata tgc      1104
340      345      350

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PF59082SeqList_PF59082.txt

Ala	Arg	Arg	Phe	Gly	Met	Lys	Gly	Arg	Leu	Cys	Thr	Leu	Trp	Ile	Cys	
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His	Ser	Leu	Gly	Ala	Val	Phe	Cys	Ile	Val	Leu	Gly	Arg	Met	Asp	Ser	
	370					375					380					
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Leu	Thr	Ala	Ala	Ile	Ala	Val	Leu	Ile	Val	Phe	Ala	Val	Phe	Ile	Gln	
	385				390					395					400	
gct	tct	agc	ggg	gct	ggt	ttt	ggc	ata	atc	cct	ttt	atc	tca	cgg	aga	1248
Ala	Ser	Ser	Gly	Ala	Val	Phe	Gly	Ile	Ile	Pro	Phe	Ile	Ser	Arg	Arg	
				405				410						415		
tca	ctt	ggt	gtg	att	tcg	gga	ttc	act	ggc	gca	gga	ggg	aat	gta	ggc	1296
Ser	Leu	Gly	Val	Ile	Ser	Gly	Phe	Thr	Gly	Ala	Gly	Gly	Asn	Val	Gly	
			420					425					430			
tcc	gtg	gta	ctg	caa	aca	gta	ttc	ttc	aca	tcg	ggt	tcg	tat	cga	acc	1344
Ser	Val	Val	Leu	Gln	Thr	Val	Phe	Phe	Thr	Ser	Gly	Ser	Tyr	Arg	Thr	
			435				440					445				
gaa	gaa	ggc	atc	cag	ttc	atg	ggg	gtg	atg	gtc	atc	tgt	gtc	gcc	gcg	1392
Glu	Glu	Gly	Ile	Gln	Phe	Met	Gly	Val	Met	Val	Ile	Cys	Val	Ala	Ala	
	450					455					460					
cta	aca	gta	ttt	atc	tat	ttc	ccc	cag	tgg	gga	ggg	atc	ttc	ttt	cct	1440
Leu	Thr	Val	Phe	Ile	Tyr	Phe	Pro	Gln	Trp	Gly	Gly	Ile	Phe	Phe	Pro	
	465				470					475					480	
cca	tcc	aaa	agc	acc	gaa	gaa	gat	tac	tac	gcc	tcc	gag	tgg	agt	gcc	1488
Pro	Ser	Lys	Ser	Thr	Glu	Glu	Asp	Tyr	Tyr	Ala	Ser	Glu	Trp	Ser	Ala	
				485				490						495		
gag	gag	cag	gag	caa	ggg	aag	cat	gca	aca	agc	atg	aaa	ttc	gcc	tct	1536
Glu	Glu	Gln	Glu	Gln	Gly	Lys	His	Ala	Thr	Ser	Met	Lys	Phe	Ala	Ser	
			500					505					510			
aat	gcg	aga	agc	gag	cgt	gga	aag	aga	ggg	ctg	aat	tct	ccc	gat	ttg	1584
Asn	Ala	Arg	Ser	Glu	Arg	Gly	Lys	Arg	Gly	Leu	Asn	Ser	Pro	Asp	Leu	
		515				520						525				
acc	atc	cat	ccc	ggt	act	gat	tcc	aag	gcc	acc	cca	ggt	tct	gac	gtt	1632
Thr	Ile	His	Pro	Val	Thr	Asp	Ser	Lys	Ala	Thr	Pro	Val	Ser	Asp	Val	
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Glu	Leu	Asn	Lys	Val												
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<210> 1501

<211> 549

<212> PRT

<213> Physcomitrella patens

<400> 1501

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Phe	Ser	Val	Ile	Gln	Gly	Thr	Val	Glu	Asp	Pro	Asp	Ala	Glu	Lys	Phe	
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Ala	Leu	Pro	Val	Asp	Ser	Glu	His	Lys	Ala	Lys	Thr	Ile	Arg	Val	Tyr	
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Ser	Phe	Ala	Lys	Pro	His	Met	Arg	Ala	Phe	His	Leu	Ala	Trp	Val	Ser	
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Phe	Phe	Thr	Cys	Phe	Leu	Ala	Thr	Phe	Ala	Ser	Pro	Pro	Leu	Met	Pro	
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Ile	Ile	Arg	Asp	Asn	Leu	Asn	Leu	Thr	Lys	Thr	Asp	Val	Gly	His	Ala	
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Ala	Ile	Ala	Ser	Val	Ser	Gly	Ser	Ile	Leu	Ser	Arg	Leu	Leu	Met	Gly	
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Thr	Val	Cys	Asp	Val	Val	Gly	Pro	Arg	Tyr	Gly	Cys	Ala	Phe	Leu	Ile	
	130					135					140					
Met	Ile	Ile	Ser	Pro	Ala	Val	Tyr	Ser	Met	Ala	Leu	Val	Ser	Asp	Ala	
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Ala	Ser	Phe	Ile	Ile	Val	Arg	Phe	Phe	Thr	Gly	Phe	Ala	Leu	Ala	Thr	
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Phe	Val	Ser	Cys	Gln	Phe	Trp	Met	Ser	Ser	Met	Phe	Asn	Ser	Lys	Ile	
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PF59082SeqList_PF59082.txt

Val Gly Thr Ala Asn Gly Leu 195
 Gly Ala Thr Gln Leu Ile Met 210
 Ser Phe Asn Ser Thr Pro Phe Val Ala Trp Arg Leu Ala Phe Phe Leu 225
 Pro Gly Ala Met Gln Thr Ile Met Gly Leu Leu Val Leu Phe Leu Gly 240
 Gln Asp Leu Pro Asp Gly Asn Tyr Ser Gln Leu Gln Lys Gln Gly Val 255
 Lys Val Lys Asp Ser Phe Leu Lys Val Leu Met Tyr Ala Ile Thr Asn 270
 Tyr Arg Thr Trp Val Phe Phe Leu Leu Tyr Gly Phe Thr Phe Gly Val 285
 Glu Leu Thr Val Asn Asn Ile Ala Glu Tyr Phe Tyr Asp Arg Phe 300
 Asp Leu Asn Leu Ser Thr Ala Gly Ile Ile Ala Ser Leu Phe Gly Leu 315
 Met Asn Phe Phe Ala Arg Pro Ser Gly Gly Ile Ile Ser Asp Thr Val 330
 Ala Arg Arg Phe Gly Met Lys Gly Arg Leu Cys Thr Leu Trp Ile Cys 345
 His Ser Leu Gly Ala Val Phe Cys Ile Val Leu Gly Arg Met Asp Ser 360
 Leu Thr Ala Ala Ile Ala Val Leu Ile Val Phe Ala Val Phe Ile Gln 375
 Ala Ser Ser Gly Ala Val Phe Gly Ile Ile Pro Phe Ile Ser Arg Arg 390
 Ser Leu Gly Val Ile Ser Gly Phe Thr Gly Ala Gly Gly Asn Val Gly 405
 Ser Val Val Leu Gln Thr Val Phe Phe Thr Ser Gly Ser Tyr Arg Thr 420
 Glu Glu Gly Ile Gln Phe Met Gly Val Met Val Ile Cys Val Ala Ala 435
 Leu Thr Val Phe Ile Tyr Phe Pro Gln Trp Gly Gly Ile Phe Phe Pro 450
 Pro Ser Lys Ser Thr Glu Glu Asp Tyr Tyr Ala Ser Glu Trp Ser Ala 465
 Glu Glu Gln Glu Gln Gly Lys His Ala Thr Ser Met Lys Phe Ala Ser 480
 Asn Ala Arg Ser Glu Arg Gly Lys Arg Gly Leu Asn Ser Pro Asp Leu 495
 Thr Ile His Pro Val Thr Asp Ser Lys Ala Thr Pro Val Ser Asp Val 510
 Glu Leu Asn Lys Val 535
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<210> 1502

<211> 1838

<212> DNA

<213> Nicotiana tabacum

<220>

<221> CDS

<222> (19)..(1611)

<400> 1502

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atg	cat	gga	gtt	aca	ggt	aga	gaa	cca	gtt	ctt	gct	ttc	99
Met	His	Gly	Val	Thr	Gly	Arg	Glu	Pro	Val	Leu	Ala	Phe	
		15				20				25			
tct	cca	atg	gta	caa	act	gat	acc	act	gca	cat	ttt	aaa	147
Ser	Pro	Met	Val	Gln	Thr	Asp	Thr	Ala	His	Phe	Lys	Val	
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gat	tct	gaa	cac	aag	gcc	aag	gtt	ttc	aaa	ttc	tac	tca	195
Asp	Ser	Glu	His	Lys	Ala	Lys	Val	Phe	Lys	Phe	Tyr	Ser	
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PF59082SeqList_PF59082.txt

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ttt	ggt	tct	act	ttt	gct	gct	gcc	cct	tta	ggt	cct	att	att	aga	gac	291
Phe	Val	Ser	Thr	Phe	Ala	Ala	Ala	Pro	Leu	Val	Pro	Ile	Ile	Arg	Asp	
				80					85					90		
aac	ctt	aac	ttg	acc	aaa	atg	gac	ggt	ggt	aat	gct	ggg	ggt	gcc	tct	339
Asn	Leu	Asn	Leu	Thr	Lys	Met	Asp	Val	Gly	Asn	Ala	Gly	Val	Ala	Ser	
			95					100					105			
ggt	tcc	gga	agt	att	cta	tct	agg	ctt	gca	atg	ggt	gcg	att	tgt	gac	387
Val	Ser	Gly	Ser	Ile	Leu	Ser	Arg	Leu	Ala	Met	Gly	Ala	Ile	Cys	Asp	
		110					115					120				
atg	ttg	gga	cca	aga	tat	gga	tgc	gcg	ttt	ctt	atc	atg	tta	tca	gct	435
Met	Leu	Gly	Pro	Arg	Tyr	Gly	Cys	Ala	Phe	Leu	Ile	Met	Leu	Ser	Ala	
	125					130					135					
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Pro	Thr	Val	Phe	Cys	Met	Ser	Phe	Val	Ser	Ser	Ala	Gly	Gly	Tyr	Val	
140				145						150					155	
gct	gtg	aga	ttc	atg	att	gga	ttc	tca	ctc	gcg	acg	ttt	gtg	tcg	tgt	531
Ala	Val	Arg	Phe	Met	Ile	Gly	Phe	Ser	Leu	Ala	Thr	Phe	Val	Ser	Cys	
				160				165						170		
caa	tat	tgg	atg	agt	acg	atg	ttt	aat	agt	cag	att	att	gga	ctt	ggt	579
Gln	Tyr	Trp	Met	Ser	Thr	Met	Phe	Asn	Ser	Gln	Ile	Ile	Gly	Leu	Val	
			175					180					185			
aat	gga	aca	gca	gca	gga	tgg	gga	aat	atg	ggg	ggt	gga	gct	act	cag	627
Asn	Gly	Thr	Ala	Ala	Gly	Trp	Gly	Asn	Met	Gly	Gly	Gly	Ala	Thr	Gln	
		190					195					200				
ctt	att	atg	cct	att	ctc	tat	gat	att	att	aga	aga	gca	gga	gcc	acc	675
Leu	Ile	Met	Pro	Ile	Leu	Tyr	Asp	Ile	Ile	Arg	Arg	Ala	Gly	Ala	Thr	
	205					210					215					
cct	ttt	act	gct	tgg	aga	att	gct	ttc	ttt	att	cct	ggg	tgg	ctt	cat	723
Pro	Phe	Thr	Ala	Trp	Arg	Ile	Ala	Phe	Phe	Ile	Pro	Gly	Trp	Leu	His	
220				225						230				235		
ggt	att	atg	gga	att	tta	gtg	tta	act	ctt	ggc	caa	gat	ttg	cct	gat	771
Val	Ile	Met	Gly	Ile	Leu	Val	Leu	Thr	Leu	Gly	Gln	Asp	Leu	Pro	Asp	
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ggt	aac	ctt	gct	tcc	cta	cag	aag	aaa	ggc	gat	ggt	tct	aaa	gat	aag	819
Gly	Asn	Leu	Ala	Ser	Leu	Gln	Lys	Lys	Gly	Asp	Val	Ser	Lys	Asp	Lys	
			255					260					265			
ttc	tct	aag	ata	ttg	tgg	tat	gct	gca	aca	aat	tac	agg	aca	tgg	atc	867
Phe	Ser	Lys	Ile	Leu	Trp	Tyr	Ala	Ala	Thr	Asn	Tyr	Arg	Thr	Trp	Ile	
		270					275					280				
ttt	gtc	ctg	ctc	tat	ggt	tac	tcc	atg	gga	ggt	gaa	ttg	act	aca	gat	915
Phe	Val	Leu	Leu	Tyr	Gly	Tyr	Ser	Met	Gly	Val	Glu	Leu	Thr	Thr	Asp	
	285					290					295					
aat	gtg	att	gct	gag	tac	ttc	ttt	gat	aga	ttt	gat	cta	aag	ctt	cac	963
Asn	Val	Ile	Ala	Glu	Tyr	Phe	Phe	Asp	Arg	Phe	Asp	Leu	Lys	Leu	His	
300				305						310				315		
acg	gct	gga	atc	att	gct	gcc	aca	ttt	ggt	atg	gct	aat	ctc	tta	gct	1011
Thr	Ala	Gly	Ile	Ile	Ala	Ala	Thr	Phe	Gly	Met	Ala	Asn	Leu	Leu	Ala	
				320				325						330		
cga	cct	ttt	gga	gga	tgg	tca	tca	gat	att	gca	gcc	aaa	cat	ttt	gga	1059
Arg	Pro	Phe	Gly	Gly	Trp	Ser	Ser	Asp	Ile	Ala	Ala	Lys	His	Phe	Gly	
			335					340					345			
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Met	Arg	Gly	Arg	Leu	Trp	Asn	Leu	Trp	Ile	Leu	Gln	Thr	Leu	Gly	Gly	
		350				355					360					
ggt	ttc	tgt	ttc	tta	ctt	gga	aaa	gca	aac	aca	ctt	cct	atg	gct	ata	1155
Val	Phe	Cys	Phe	Leu	Leu	Gly	Lys	Ala	Asn	Thr	Leu	Pro	Met	Ala	Ile	
	365					370					375					
gct	tgg	atg	atc	ata	ttc	tcc	tta	ggt	gct	caa	gca	gca	tgt	gga	gct	1203
Ala	Trp	Met	Ile	Ile	Phe	Ser	Leu	Gly	Ala	Gln	Ala	Ala	Cys	Gly	Ala	
380				385				390						395		
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Thr	Phe	Gly	Ile	Ile	Pro	Phe	Ile	Ser	Arg	Arg	Ser	Leu	Gly	Ile	Ile	
				400				405						410		
tca	ggt	atg	aca	gga	gct	gga	gga	aat	ttt	ggt	tct	gga	ttg	aca	caa	1299
Ser	Gly	Met	Thr	Gly	Ala	Gly	Gly	Asn	Phe	Gly	Ser	Gly	Leu	Thr	Gln	
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PF59082SeqList_PF59082.txt

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		430					435				440					
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Tyr	Met	Gly	Ile	Met	Ile	Ile	Ala	Cys	Thr	Leu	Pro	Val	Ser	Leu	Val	
	445					450					455					
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Val	Lys	Ser	Thr	Glu	Glu	His	Tyr	Phe	Thr	Ser	Glu	Tyr	Thr	Glu	Ala	
				480				485						490		
gag	aag	caa	aag	ggg	atg	cac	caa	aac	agc	atc	aag	ttt	gct	gaa	aac	1539
Glu	Lys	Gln	Lys	Gly	Met	His	Gln	Asn	Ser	Ile	Lys	Phe	Ala	Glu	Asn	
		495					500						505			
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Cys	Arg	Ser	Glu	Arg	Gly	Lys	Arg	Val	Gly	Ser	Ala	Leu	Thr	Pro	Pro	
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aat	gta	acg	cca	aac	cgt	gtc	tgagcttgag	tctcacggat	cagtacggag							1638
Asn	Val	Thr	Pro	Asn	Arg	Val										
	525					530										
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gtgatatgtg	tcttttaatg	agctttatat	taccaagtg	tgagtagtta	atttgtatta											1758
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<211> 530

<212> PRT

<213> Nicotiana tabacum

<400> 1503

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Thr	Asp	Thr	Thr	Ala	His	Phe	Lys	Val	Pro	Val	Asp	Ser	Glu	His	Lys
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Phe	Gln	Leu	Ser	Trp	Ile	Ser	Phe	Phe	Thr	Cys	Phe	Val	Ser	Thr	Phe
65					70				75						80
Ala	Ala	Ala	Pro	Leu	Val	Pro	Ile	Ile	Arg	Asp	Asn	Leu	Asn	Leu	Thr
			85					90					95		
Lys	Met	Asp	Val	Gly	Asn	Ala	Gly	Val	Ala	Ser	Val	Ser	Gly	Ser	Ile
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Leu	Ser	Arg	Leu	Ala	Met	Gly	Ala	Ile	Cys	Asp	Met	Leu	Gly	Pro	Arg
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Tyr	Gly	Cys	Ala	Phe	Leu	Ile	Met	Leu	Ser	Ala	Pro	Thr	Val	Phe	Cys
	130					135				140					
Met	Ser	Phe	Val	Ser	Ser	Ala	Gly	Gly	Tyr	Val	Ala	Val	Arg	Phe	Met
145					150				155						160
Ile	Gly	Phe	Ser	Leu	Ala	Thr	Phe	Val	Ser	Cys	Gln	Tyr	Trp	Met	Ser
			165					170					175		
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		180						185					190		
Gly	Trp	Gly	Asn	Met	Gly	Gly	Gly	Ala	Thr	Gln	Leu	Ile	Met	Pro	Ile
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 260 265 270
 Trp Tyr Ala Thr Asn Tyr Arg Thr Trp Ile Phe Val Leu Leu Tyr
 275 280 285
 Gly Tyr Ser Met Gly Val Glu Leu Thr Thr Asp Asn Val Ile Ala Glu
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 Tyr Phe Phe Asp Arg Phe Asp Leu Lys Leu His Thr Ala Gly Ile Ile
 305 310 315 320
 Ala Ala Thr Phe Gly Met Ala Asn Leu Leu Ala Arg Pro Phe Gly Gly
 325 330 335
 Trp Ser Ser Asp Ile Ala Ala Lys His Phe Gly Met Arg Gly Arg Leu
 340 345 350
 Trp Asn Leu Trp Ile Leu Gln Thr Leu Gly Gly Val Phe Cys Phe Leu
 355 360 365
 Leu Gly Lys Ala Asn Thr Leu Pro Met Ala Ile Ala Trp Met Ile Ile
 370 375 380
 Phe Ser Leu Gly Ala Gln Ala Ala Cys Gly Ala Thr Phe Gly Ile Ile
 385 390 395 400
 Pro Phe Ile Ser Arg Arg Ser Leu Gly Ile Ile Ser Gly Met Thr Gly
 405 410 415
 Ala Gly Gly Asn Phe Gly Ser Gly Leu Thr Gln Leu Leu Phe Thr
 420 425 430
 Thr Thr Lys Trp Ser Thr Glu Thr Gly Leu Ser Tyr Met Gly Ile Met
 435 440 445
 Ile Ile Ala Cys Thr Leu Pro Val Ser Leu Val His Phe Pro Gln Trp
 450 455 460
 Gly Ser Met Phe Leu Pro Thr Lys Asp Pro Val Lys Ser Thr Glu
 465 470 475 480
 Glu His Tyr Phe Thr Ser Glu Tyr Thr Glu Ala Glu Lys Gln Lys Gly
 485 490 495
 Met His Gln Asn Ser Ile Lys Phe Ala Glu Asn Cys Arg Ser Glu Arg
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 515 520 525
 Arg Val
 530

<210> 1504

<211> 1611

<212> DNA

<213> Nicotiana tabacum

<220>

<221> CDS

<222> (12)..(1604)

<400> 1504

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Gly	Val	Thr	Gly	Arg	Glu	Pro	Val	Leu	Ala	Phe	Ser	Val	Ala	Ser	Pro
	15				20					25					
atg	gtg	cca	act	gat	acc	act	gca	aaa	ttt	tca	gta	cca	gtt	gat	act
Met	Val	Pro	Thr	Asp	Thr	Thr	Ala	Lys	Phe	Ser	Val	Pro	Val	Asp	Thr
	30				35				40					45	
gaa	cac	aaa	gcc	aag	att	ttt	aag	ttc	tat	tca	ttt	tca	aag	cca	cat
Glu	His	Lys	Ala	Lys	Ile	Phe	Lys	Phe	Tyr	Ser	Phe	Ser	Lys	Pro	His
			50					55						60	
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Gly	Leu	Thr	Phe	Gln	Leu	Ser	Trp	Ile	Ser	Phe	Phe	Thr	Cys	Phe	Val
			65				70					75			
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Ser	Thr	Phe	Ala	Ala	Ala	Pro	Leu	Val	Pro	Ile	Ile	Arg	Asp	Asn	Leu
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PF59082SeqList_PF59082.txt

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Gly	Ser	Ile	Leu	Ser	Arg	Leu	Val	Met	Gly	Ala	Val	Cys	Asp	Met	Leu	
110					115					120					125	
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Val	Phe	Cys	Met	Ser	Phe	Val	Ser	Ser	Ala	Gly	Gly	Tyr	Val	Ala	Val	
				145				150					155			
cgg	ttc	atg	atc	gga	ttc	tcg	cta	gca	aca	ttt	gtg	tcg	tgc	caa	tat	530
Arg	Phe	Met	Ile	Gly	Phe	Ser	Leu	Ala	Thr	Phe	Val	Ser	Cys	Gln	Tyr	
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Trp	Met	Ser	Thr	Met	Phe	Asn	Ser	Gln	Ile	Ile	Gly	Leu	Val	Asn	Gly	
						180					185					
aca	gct	gca	gga	tgg	gga	aat	atg	ggt	ggt	ggt	gcg	act	caa	ctt	att	626
Thr	Ala	Ala	Gly	Trp	Gly	Asn	Met	Gly	Gly	Gly	Ala	Thr	Gln	Leu	Ile	
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Met	Pro	Ile	Val	Tyr	Asp	Ile	Ile	Arg	Arg	Ala	Gly	Ala	Thr	Pro	Phe	
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Thr	Ala	Trp	Arg	Ile	Ala	Phe	Phe	Ile	Pro	Gly	Trp	Leu	His	Ile	Val	
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cgt	ggt	gat	tta	cag	aag	aag	ggt	gat	ggt	tct	aaa	gat	aaa	ttc	tcc	818
Arg	Gly	Asp	Leu	Gln	Lys	Lys	Gly	Asp	Val	Ser	Lys	Asp	Lys	Phe	Ser	
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Asn	Ile	Leu	Trp	Tyr	Ala	Ala	Thr	Asn	Tyr	Arg	Thr	Trp	Ile	Phe	Val	
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Ile	Ala	Glu	Tyr	Phe	Phe	Asp	Arg	Phe	Asp	Leu	Lys	Leu	His	Thr	Ala	
				305			310						315			
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Gly	Ile	Ile	Ala	Ala	Thr	Phe	Gly	Met	Ala	Asn	Leu	Leu	Ala	Arg	Pro	
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ttc	gga	gga	ttt	tct	tca	gat	tac	gca	gcc	aaa	aga	ttc	ggc	atg	aga	1058
Phe	Gly	Gly	Phe	Ser	Ser	Asp	Tyr	Ala	Ala	Lys	Arg	Phe	Gly	Met	Arg	
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Gly	Arg	Leu	Trp	Val	Leu	Trp	Ile	Leu	Gln	Thr	Leu	Gly	Gly	Val	Phe	
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Cys	Val	Leu	Leu	Gly	Arg	Ser	Asn	Pro	Leu	Pro	Ile	Ala	Val	Thr	Phe	
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Met	Thr	Gly	Ala	Gly	Gly	Asn	Phe	Gly	Ser	Gly	Leu	Thr	Gln	Leu	Leu	
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Phe	Phe	Thr	Ser	Ser	Lys	Tyr	Ser	Thr	Ala	Thr	Gly	Leu	Thr	Tyr	Met	
430					435					440					445	
gga	cta	atg	atc	ata	gga	tgc	act	ctt	cca	gtg	act	ttc	tgt	cat	ttc	1394
Gly	Leu	Met	Ile	Ile	Gly	Cys	Thr	Leu	Pro	Val	Thr	Phe	Cys	His	Phe	
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Gly	Ser	Glu	Glu	His	Tyr	Tyr	Ala	Ala	Glu	Tyr	Thr	Glu	Ala	Glu	Arg
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Gln	Lys	Gly	Met	His	Gln	Asn	Ser	Leu	Lys	Phe	Ala	Glu	Asn	Cys	Arg
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<400> 1505

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Phe	Gln	Leu	Ser	Trp	Ile	Ser	Phe	Phe	Thr	Cys	Phe	Val	Ser	Thr	Phe
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Ala	Ala	Ala	Pro	Leu	Val	Pro	Ile	Ile	Arg	Asp	Asn	Leu	Asn	Leu	Thr
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Lys	Met	Asp	Val	Gly	Asn	Ala	Gly	Val	Ala	Ser	Val	Ser	Gly	Ser	Ile
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Leu	Ser	Arg	Leu	Val	Met	Gly	Ala	Val	Cys	Asp	Met	Leu	Gly	Pro	Arg
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Tyr	Gly	Cys	Ala	Phe	Leu	Ile	Met	Leu	Ser	Ala	Pro	Thr	Val	Phe	Cys
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Ile	Gly	Phe	Ser	Leu	Ala	Thr	Phe	Val	Ser	Cys	Gln	Tyr	Trp	Met	Ser
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Leu	Val	Leu	Thr	Leu	Gly	Gln	Asp	Leu	Pro	Asp	Gly	Asn	Arg	Gly	Asp
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Trp	Tyr	Ala	Ala	Thr	Asn	Tyr	Arg	Thr	Trp	Ile	Phe	Val	Leu	Leu	Tyr
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Tyr	Phe	Phe	Asp	Arg	Phe	Asp	Leu	Lys	Leu	His	Thr	Ala	Gly	Ile	Ile
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Ala	Ala	Thr	Phe	Gly	Met	Ala	Asn	Leu	Leu	Ala	Arg	Pro	Phe	Gly	Gly
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Phe	Ser	Ser	Asp	Tyr	Ala	Ala	Lys	Arg	Phe	Gly	Met	Arg	Gly	Arg	Leu
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Trp	Val	Leu	Trp	Ile	Leu	Gln	Thr	Leu	Gly	Gly	Val	Phe	Cys	Val	Leu
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 Ile Ile Gly Cys Thr Leu Pro Val Thr Phe Cys His Phe Pro Gln Trp
 450 455 460
 Gly Ser Met Phe Phe Pro Thr Lys Asp Pro Val Lys Gly Ser Glu
 465 470 475 480
 Glu His Tyr Tyr Ala Ala Glu Tyr Thr Glu Ala Glu Arg Gln Lys Gly
 485 490 495
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 Met Ala Ala Val Gly Ala Pro Gly Ser Ser Leu His Gly Val
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111

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 Thr Gly Arg Glu Pro Ala Phe Ala Phe Ser Thr Glu His Glu Glu Ala
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159

gcg agc aat ggt ggc aag ttc gac ctg ccg gtg gac tca gag cac aag
 Ala Ser Asn Gly Gly Lys Phe Asp Leu Pro Val Asp Ser Glu His Lys
 35 40 45

207

gcg aag agc gtc cgt ctc ttc tcc gtg gcg aac cca cac atg cgc acc
 Ala Lys Ser Val Arg Leu Phe Ser Val Ala Asn Pro His Met Arg Thr
 50 55 60

255

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303

gcc gcc gcg ccg ctg gtc ccc atc atc cgc gac aac ctc aac ctc acc
 Ala Ala Ala Pro Leu Val Pro Ile Ile Arg Asp Asn Leu Asn Leu Thr
 80 85 90

351

aag gcc gac atc ggc aac gcg ggc gtg gcc tcg gtg tcg ggc tcc atc
 Lys Ala Asp Ile Gly Asn Ala Gly Val Ala Ser Val Ser Gly Ser Ile
 95 100 105 110

399

ttc tcc cgc ctc acc atg ggc gcc gtc tgc gac ctg ctg ggc ccg cgc
 Phe Ser Arg Leu Thr Met Gly Ala Val Cys Asp Leu Leu Gly Pro Arg
 115 120 125

447

tac ggc tgc gcc ttc ctc atc atg ctg tcc gcg ccc acc gtg ttc tgc
 Tyr Gly Cys Ala Phe Leu Ile Met Ser Ala Pro Thr Val Phe Cys
 130 135 140

495

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 Met Ser Leu Ile Asp Asp Ala Ala Gly Tyr Ile Thr Val Arg Phe Leu
 145 150 155

543

atc gcc ttc tcc ctc gcc acc ttc gtc tcc tgc cag tac tgg atg agc
 Ile Gly Phe Ser Leu Ala Thr Phe Val Ser Cys Gln Tyr Trp Met Ser
 160 165 170

591

acc atg ttc agc agc aag atc atc ggc acc gtc aac ggg ctc gcc gcc
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639

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Gly	Trp	Gly	Thr	Met	Gly	Arg	Arg	Arg	His	Ala	Ala	His	Met	Pro	Leu	
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Val	Tyr	Asp	Val	Ile	Arg	Lys	Cys	Gly	Ala	Thr	Pro	Phe	Thr	Ala	Trp	
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cgc	ctc	gcc	tac	ttc	gtg	ccg	ggc	ctc	atg	cac	gtc	gtc	atg	ggc	gtc	783
Arg	Leu	Ala	Tyr	Phe	Val	Pro	Gly	Leu	Met	His	Val	Val	Met	Gly	Val	
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Leu	Val	Leu	Thr	Leu	Gly	Gln	Asp	Leu	Pro	Asp	Gly	Asn	Leu	Arg	Ser	
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ctg	cag	aag	aag	ggc	aac	gtc	aac	aag	gac	agc	ttc	tcc	aag	gtc	atg	879
Leu	Gln	Lys	Lys	Gly	Asn	Val	Asn	Lys	Asp	Ser	Phe	Ser	Lys	Val	Met	
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tgg	tac	gcc	gtc	atc	aac	tac	cgt	acc	tgg	atc	ttt	gtc	ctc	ctc	tac	927
Trp	Tyr	Ala	Val	Ile	Asn	Tyr	Arg	Thr	Trp	Ile	Phe	Val	Leu	Leu	Tyr	
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Tyr	Met	Tyr	Asp	Arg	Phe	Asp	Leu	Asp	Leu	Arg	Val	Ala	Gly	Thr	Ile	
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Ile	Met	Ser	Asp	Met	Gly	Ala	Arg	Tyr	Trp	Gly	Met	Arg	Ala	Arg	Leu	
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tgg	aac	atc	tgg	atc	ctc	cag	acc	gcc	ggc	ggc	gcc	ttc	tgc	ctc	tgg	1167
Trp	Asn	Ile	Trp	Ile	Leu	Gln	Thr	Ala	Gly	Gly	Ala	Phe	Cys	Leu	Trp	
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Leu	Gly	Arg	Ala	Ser	Thr	Leu	Pro	Val	Ser	Val	Val	Ala	Met	Val	Leu	
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Phe	Ser	Phe	Cys	Ala	Gln	Ala	Ala	Cys	Gly	Ala	Ile	Phe	Gly	Val	Ile	
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Pro	Phe	Val	Ser	Arg	Arg	Ser	Leu	Gly	Ile	Ile	Ser	Gly	Met	Thr	Gly	
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gcc	ggc	ggc	aac	ttc	ggc	gcc	ggg	ctc	acg	cag	ctg	ctc	ttc	ttt	acc	1359
Ala	Gly	Gly	Asn	Phe	Gly	Ala	Gly	Leu	Thr	Gln	Leu	Leu	Phe	Phe	Thr	
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tcc	tcg	acc	tac	tcc	acg	ggc	agg	ggg	ctg	gag	tac	atg	ggc	atc	atg	1407
Ser	Ser	Thr	Tyr	Ser	Thr	Gly	Arg	Gly	Leu	Glu	Tyr	Met	Gly	Ile	Met	
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atc	atg	gcg	tgc	acg	ctg	ccc	gtg	gtg	ttc	gtg	cac	ttc	cct	cag	tgg	1455
Ile	Met	Ala	Cys	Thr	Leu	Pro	Val	Val	Phe	Val	His	Phe	Pro	Gln	Trp	
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Gly	Ser	Met	Phe	Phe	Pro	Pro	Ser	Ala	Thr	Ala	Asp	Glu	Glu	Gly	Tyr	
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Tyr	Ala	Ser	Glu	Trp	Asn	Asp	Asp	Glu	Lys	Ser	Lys	Gly	Leu	His	Ser	
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Ala	Ser	Leu	Lys	Phe	Ala	Glu	Asn	Ser	Arg	Ser	Glu	Arg	Gly	Lys	Arg	
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 Phe Ser Leu Ala Thr Phe Val Ser Cys Gln Tyr Trp Met Ser Thr Met
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 Phe Ser Ser Lys Ile Ile Gly Thr Val Asn Gly Leu Ala Ala Gly Trp
 180 185 190
 Gly Thr Met Gly Arg Arg Arg His Ala Ala His Met Pro Leu Val Tyr
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 Asp Val Ile Arg Lys Cys Gly Ala Thr Pro Phe Thr Ala Trp Arg Leu
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 Ala Tyr Phe Val Pro Gly Leu Met His Val Val Met Gly Val Leu Val
 225 230 235 240
 Leu Thr Leu Gly Gln Asp Leu Pro Asp Gly Asn Leu Arg Ser Leu Gln
 245 250 255
 Lys Lys Gly Asn Val Asn Lys Asp Ser Phe Ser Lys Val Met Trp Tyr
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 Ala Val Ile Asn Tyr Arg Thr Trp Ile Phe Val Leu Leu Tyr Gly Tyr
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 Cys Met Gly Val Glu Leu Thr Thr Asp Asn Val Ile Ala Glu Tyr Met
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 Tyr Asp Arg Phe Asp Leu Asp Leu Arg Val Ala Gly Thr Ile Ala Ala
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 Cys Phe Gly Met Ala Asn Ile Val Ala Arg Pro Met Gly Gly Ile Met
 325 330 335
 Ser Asp Met Gly Ala Arg Tyr Trp Gly Met Arg Ala Arg Leu Trp Asn
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 Ile Trp Ile Leu Gln Thr Ala Gly Gly Ala Phe Cys Leu Trp Leu Gly
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 Arg Ala Ser Thr Leu Pro Val Ser Val Val Ala Met Val Leu Phe Ser
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 Val Ser Arg Arg Ser Leu Gly Ile Ile Ser Gly Met Thr Gly Ala Gly
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 Ser Glu Trp Asn Asp Asp Glu Lys Ser Lys Gly Leu His Ser Ala Ser
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 Leu Lys Phe Ala Glu Asn Ser Arg Ser Glu Arg Gly Lys Arg Asn Val
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 Ile Gln Ala Asp Ala Ala Ala Thr Pro Glu His Val
 515 520

<210> 1508

<211> 1646

<212> DNA

<213> Lycopersicon esculentum

<220>

<221> CDS

<222> (8)..(1603)

<400> 1508

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	Met	Gly	Asp	Ile	Glu	Gly	Ser	Pro	Gly	Ser	Ser	Met	His	Gly	
	1				5				10						
gtt	act	ggt	aga	gag	cca	gtt	ctt	gca	ttt	tca	gtt	gct	tca	cta	att
Val	Thr	Gly	Arg	Glu	Pro	Val	Leu	Ala	Phe	Ser	Val	Ala	Ser	Leu	Ile
15					20				25						30
gta	cca	act	gat	aca	tca	gcc	aat	ttc	aaa	gtc	cct	ggt	gat	tct	gaa
Val	Pro	Thr	Asp	Thr	Ser	Ala	Asn	Phe	Lys	Val	Pro	Val	Asp	Ser	Glu
				35				40						45	145
cat	aaa	gct	aaa	ggt	ttt	aaa	ttt	tat	tcg	ttt	tcg	aaa	cct	cat	gga
His	Lys	Ala	Lys	Val	Phe	Lys	Phe	Tyr	Ser	Phe	Ser	Lys	Pro	His	Gly
			50				55					60			193
cta	acg	ttt	caa	ctc	tca	tgg	att	tca	ttt	tgt	act	tgt	ttc	gta	tcg
Leu	Thr	Phe	Gln	Leu	Ser	Trp	Ile	Ser	Phe	Cys	Thr	Cys	Phe	Val	Ser
	65				70					75					241
act	ttt	gct	gca	gcc	cct	tta	gtc	cct	att	att	agg	gac	aat	ctt	aat
Thr	Phe	Ala	Ala	Ala	Pro	Leu	Val	Pro	Ile	Ile	Arg	Asp	Asn	Leu	Asn
	80				85			90							289
cta	act	aaa	atg	gat	gtt	ggt	aat	gct	gga	gtt	gcc	tct	ggt	tcg	ggt
Leu	Thr	Lys	Met	Asp	Val	Gly	Asn	Ala	Gly	Val	Ala	Ser	Val	Ser	Gly
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agt	atc	ttg	tct	agg	cta	gct	atg	ggc	gcg	att	tgt	gac	atg	tta	ggt
Ser	Ile	Leu	Ser	Arg	Leu	Ala	Met	Gly	Ala	Ile	Cys	Asp	Met	Leu	Gly
				115				120						125	385
cct	aga	tat	ggt	tgc	gcg	ttc	ctt	ata	atg	tta	tca	gcc	cca	act	gtt
Pro	Arg	Tyr	Gly	Cys	Ala	Phe	Leu	Ile	Met	Leu	Ser	Ala	Pro	Thr	Val
			130				135					140			433
tta	tgt	atg	tct	ttt	gtg	tca	tcg	gct	gga	ggg	tac	ggt	gct	gtg	agg
Leu	Cys	Met	Ser	Phe	Val	Ser	Ser	Ala	Gly	Gly	Tyr	Val	Ala	Val	Arg
	145					150					155				481
ttt	atg	att	ggg	ttt	tca	cta	gca	acg	ttt	gtg	tca	tgt	cag	tat	tgg
Phe	Met	Ile	Gly	Phe	Ser	Leu	Ala	Thr	Phe	Val	Ser	Cys	Gln	Tyr	Trp
	160				165					170					529
atg	agt	acg	atg	ttt	aat	agt	caa	atc	att	gga	ctt	gtg	aat	ggt	aca
Met	Ser	Thr	Met	Phe	Asn	Ser	Gln	Ile	Ile	Gly	Leu	Val	Asn	Gly	Thr
	175				180					185					190
gct	gct	gga	tgg	ggt	aat	atg	ggt	ggt	ggt	gct	act	caa	ctt	att	atg
Ala	Ala	Gly	Trp	Gly	Asn	Met	Gly	Gly	Gly	Ala	Thr	Gln	Leu	Ile	Met
				195				200						205	625
cct	ttg	ctc	tac	gat	ata	ata	cgt	aga	gca	ggg	gca	acc	ccg	ttc	act
Pro	Leu	Leu	Tyr	Asp	Ile	Ile	Arg	Arg	Ala	Gly	Ala	Thr	Pro	Phe	Thr
			210				215					220			673
gct	tgg	aga	atc	gca	ttt	ttt	att	cct	gga	tgg	ctt	cat	ggt	att	atg
Ala	Trp	Arg	Ile	Ala	Phe	Phe	Ile	Pro	Gly	Trp	Leu	His	Val	Ile	Met
	225						230					235			721
gga	att	tta	ggt	tta	act	ctt	gga	caa	gat	tta	cct	gat	ggt	aac	ctc
Gly	Ile	Leu	Val	Leu	Thr	Leu	Gly	Gln	Asp	Leu	Pro	Asp	Gly	Asn	Leu
	240					245					250				769
gct	tct	tta	cag	aag	aaa	ggc	gat	ggt	tct	aaa	gat	aaa	ttc	tca	aag
Ala	Ser	Leu	Gln	Lys	Lys	Gly	Asp	Val	Ser	Lys	Asp	Lys	Phe	Ser	Lys
															817

PF59082SeqList_PF59082.txt

255	ata tta tgg tat gct gca aca aat tac aga aca tgg atc ctt gtt ctg	260	265	270	
Ile Leu Trp Tyr Ala	Ala Thr Asn Tyr Arg Thr Trp Ile Leu Val Leu				865
ctc tat gga tac tca atg gga gtt gaa tta act aca gat aac gtg att	275	280	285		913
Leu Tyr Gly Tyr Ser Met Gly Val Glu Leu Thr Thr Asp Asn Val Ile	290	295	300		
gct gag tat ttc ttc gat aga ttt gat ttg aag ctt cat acg gct gga	305	310	315		961
Ala Glu Tyr Phe Phe Asp Arg Phe Asp Leu Lys Leu His Thr Ala Gly					
atc atc gct gca aca ttt ggc atg gct aac tta tta gcg cga cca ttt	320	325	330		1009
Ile Ile Ala Ala Thr Phe Gly Met Ala Asn Leu Leu Ala Arg Pro Phe					
gga gga tgg tca tca gat gtt gca gct aaa cat ttc ggg atg aga ggc	335	340	345		1057
Gly Gly Trp Ser Ser Asp Val Ala Ala Lys His Phe Gly Met Arg Gly					
aga tta tgg aat tca tgg att tta caa aca ctt ggt ggt gtg ttc tgt	355	360	365		1105
Arg Leu Trp Asn Ser Trp Ile Leu Gln Thr Leu Gly Gly Val Phe Cys					
tta cta ctt gga agg gct act aca ctt cct ctg gct att act tgg atg	370	375	380		1153
Leu Leu Leu Gly Arg Ala Thr Thr Leu Pro Leu Ala Ile Thr Trp Met					
atc ata ttc tca ata ggt gca caa gca gca tgt ggt gta acg ttt gga	385	390	395		1201
Ile Ile Phe Ser Ile Gly Ala Gln Ala Ala Cys Gly Val Thr Phe Gly					
att att ccc ttt att tcg cga aga tca tta ggt ata ata tca ggt atg	400	405	410		1249
Ile Ile Pro Phe Ile Ser Arg Arg Ser Leu Gly Ile Ile Ser Gly Met					
aca gga gct gga ggc aat ttt ggt tcc gga ttg aca caa cta ctg ttt	415	420	425		1297
Thr Gly Ala Gly Gly Asn Phe Gly Ser Gly Thr Thr Gln Leu Leu Phe					
ttc acg agt aca aag tac tcg aca gga aca gga cta acg tat atg ggg	435	440	445		1345
Phe Thr Ser Thr Lys Tyr Ser Thr Gly Thr Gly Leu Thr Tyr Met Gly					
atg atg atc atc gcg tgt aca ctt cca gta atg tta gtt cgt ttt cca	450	455	460		1393
Met Met Ile Ile Ala Cys Thr Leu Pro Val Met Leu Val Arg Phe Pro					
cag tgg ggt agt atg ttt ttg cct cca tct aaa gat cct att aag ggt	465	470	475		1441
Gln Trp Gly Ser Met Phe Leu Pro Pro Ser Lys Asp Pro Ile Lys Gly					
act gaa gaa cat tat ttt ggt tct gag tat act gag gat gag aaa caa	480	485	490		1489
Thr Glu Glu His Tyr Phe Gly Ser Glu Tyr Thr Glu Asp Glu Lys Gln					
aag gga atg cac cag aac agc atc aag ttc gcg gaa aac agc agg aca	495	500	505		1537
Lys Gly Met His Gln Asn Ser Ile Lys Phe Ala Glu Asn Ser Arg Thr					
gag cgt ggg aag aag cgc gtt ggt tca gca cct act ccg cct aat gta	515	520	525		1585
Glu Arg Gly Lys Lys Arg Val Gly Ser Ala Pro Thr Pro Pro Asn Val					
aca cca aat cgc gtc tgatggggaa aaaaattaaa atacttactt cgcagttcat	530				1640
Thr Pro Asn Arg Val					
gctcgt					1646

<210> 1509

<211> 531

<212> PRT

<213> Lycopersicon esculentum

<400> 1509

Met Gly Asp Ile Glu Gly Ser Pro Gly Ser Ser Met His Gly Val Thr	1	5	10	15
Gly Arg Glu Pro Val Leu Ala Phe Ser Val Ala Ser Leu Ile Val Pro	20	25	30	
Thr Asp Thr Ser Ala Asn Phe Lys Val Pro Val Asp Ser Glu His Lys	35	40	45	
Ala Lys Val Phe Lys Phe Tyr Ser Phe Ser Lys Pro His Gly Leu Thr				

PF59082SeqList_PF59082.txt

50	55	60																	
Phe	Gln	Leu	Ser	Trp	Ile	Ser	Phe	Cys	Thr	Cys	Phe	Val	Ser	Thr	Phe				
65					70					75					80				
Ala	Ala	Ala	Pro	Leu	Val	Pro	Ile	Ile	Arg	Asp	Asn	Leu	Asn	Leu	Thr				
				85					90					95					
Lys	Met	Asp	Val	Gly	Asn	Ala	Gly	Val	Ala	Ser	Val	Ser	Gly	Ser	Ile				
			100					105					110						
Leu	Ser	Arg	Leu	Ala	Met	Gly	Ala	Ile	Cys	Asp	Met	Leu	Gly	Pro	Arg				
		115					120					125							
Tyr	Gly	Cys	Ala	Phe	Leu	Ile	Met	Leu	Ser	Ala	Pro	Thr	Val	Leu	Cys				
	130					135					140								
Met	Ser	Phe	Val	Ser	Ser	Ala	Gly	Gly	Tyr	Val	Ala	Val	Arg	Phe	Met				
145					150					155					160				
Ile	Gly	Phe	Ser	Leu	Ala	Thr	Phe	Val	Ser	Cys	Gln	Tyr	Trp	Met	Ser				
				165					170					175					
Thr	Met	Phe	Asn	Ser	Gln	Ile	Ile	Gly	Leu	Val	Asn	Gly	Thr	Ala	Ala				
			180					185					190						
Gly	Trp	Gly	Asn	Met	Gly	Gly	Gly	Ala	Thr	Gln	Leu	Ile	Met	Pro	Leu				
		195					200					205							
Leu	Tyr	Asp	Ile	Ile	Arg	Arg	Ala	Gly	Ala	Thr	Pro	Phe	Thr	Ala	Trp				
	210					215					220								
Arg	Ile	Ala	Phe	Phe	Ile	Pro	Gly	Trp	Leu	His	Val	Ile	Met	Gly	Ile				
225					230					235				240					
Leu	Val	Leu	Thr	Leu	Gly	Gln	Asp	Leu	Pro	Asp	Gly	Asn	Leu	Ala	Ser				
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Leu	Gln	Lys	Lys	Gly	Asp	Val	Ser	Lys	Asp	Lys	Phe	Ser	Lys	Ile	Leu				
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Trp	Tyr	Ala	Ala	Thr	Asn	Tyr	Arg	Thr	Trp	Ile	Leu	Val	Leu	Leu	Tyr				
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Gly	Tyr	Ser	Met	Gly	Val	Glu	Leu	Thr	Thr	Asp	Asn	Val	Ile	Ala	Glu				
	290					295					300								
Tyr	Phe	Phe	Asp	Arg	Phe	Asp	Leu	Lys	Leu	His	Thr	Ala	Gly	Ile	Ile				
305					310					315				320					
Ala	Ala	Thr	Phe	Gly	Met	Ala	Asn	Leu	Leu	Ala	Arg	Pro	Phe	Gly	Gly				
				325					330					335					
Trp	Ser	Ser	Asp	Val	Ala	Ala	Lys	His	Phe	Gly	Met	Arg	Gly	Arg	Leu				
			340					345					350						
Trp	Asn	Ser	Trp	Ile	Leu	Gln	Thr	Leu	Gly	Gly	Val	Phe	Cys	Leu	Leu				
		355					360					365							
Leu	Gly	Arg	Ala	Thr	Thr	Leu	Pro	Leu	Ala	Ile	Thr	Trp	Met	Ile	Ile				
	370					375					380								
Phe	Ser	Ile	Gly	Ala	Gln	Ala	Ala	Cys	Gly	Val	Thr	Phe	Gly	Ile	Ile				
385					390					395				400					
Pro	Phe	Ile	Ser	Arg	Arg	Ser	Leu	Gly	Ile	Ile	Ser	Gly	Met	Thr	Gly				
				405					410					415					
Ala	Gly	Gly	Asn	Phe	Gly	Ser	Gly	Leu	Thr	Gln	Leu	Leu	Phe	Phe	Thr				
			420				425						430						
Ser	Thr	Lys	Tyr	Ser	Thr	Gly	Thr	Gly	Leu	Thr	Tyr	Met	Gly	Met	Met				
		435					440					445							
Ile	Ile	Ala	Cys	Thr	Leu	Pro	Val	Met	Leu	Val	Arg	Phe	Pro	Gln	Trp				
	450					455					460								
Gly	Ser	Met	Phe	Leu	Pro	Pro	Ser	Lys	Asp	Pro	Ile	Lys	Gly	Thr	Glu				
465					470					475				480					
Glu	His	Tyr	Phe	Gly	Ser	Glu	Tyr	Thr	Glu	Asp	Glu	Lys	Gln	Lys	Gly				
				485					490					495					
Met	His	Gln	Asn	Ser	Ile	Lys	Phe	Ala	Glu	Asn	Ser	Arg	Thr	Glu	Arg				
			500					505					510						
Gly	Lys	Lys	Arg	Val	Gly	Ser	Ala	Pro	Thr	Pro	Pro	Asn	Val	Thr	Pro				
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Asn	Arg	Val																	
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 <213> Triticum aestivum

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<222> (63)..(1586)

<400> 1510

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  Met Glu Val Glu Ser Ser Ala His Gly Asp Ala Ala Ala Ser Lys
    1          5          10          15
ttc acg ctg cct gtg gac tcc gag cac aag gcc aag tcc ttc agg ctc      155
  Phe Thr Leu Pro Val Asp Ser Glu His Lys Ala Lys Ser Phe Arg Leu
    20          25          30
ttc tcc ttc gcc aac ccc cac atg cgc acc ttc cac ctc tcc tgg ata      203
  Phe Ser Phe Ala Asn Pro His Met Arg Thr Phe His Leu Ser Trp Ile
    35          40          45
tcc ttc ttc acc tgc ttt gtc tcc acc ttc gcc gcc gcg ccg ttg gtg      251
  Ser Phe Phe Thr Cys Phe Val Ser Thr Phe Ala Ala Ala Pro Leu Val
    50          55          60
ccc atc atc cgt gac aac ctc aac ctc gcc aag gcc gac ata ggg aat      299
  Pro Ile Ile Arg Asp Asn Leu Asn Leu Ala Lys Ala Asp Ile Gly Asn
    65          70          75
gcc ggt gtg gca tct gtg tca ggg tcc atc ttc tcc agg ctt gcc atg      347
  Ala Gly Val Ala Ser Val Ser Gly Ser Ile Phe Ser Arg Leu Ala Met
    80          85          90
ggc gcc gtc tgc gac ctt ttg ggg ccg cgg tat ggc tgt gcc ttc ctc      395
  Gly Ala Val Cys Asp Leu Leu Gly Pro Arg Tyr Gly Cys Ala Phe Leu
    100          105          110
gtc atg ctc tca gcg cca acg gtc ttc tgc atg gcc gtc atc gat gac      443
  Val Met Leu Ser Ala Pro Thr Val Phe Cys Met Ala Val Ile Asp Asp
    115          120          125
gcc tcg ggg tac atc gct gta cgc ttc ctc att ggc ttc tcc ctc gcc      491
  Ala Ser Gly Tyr Ile Ala Val Arg Phe Leu Ile Gly Phe Ser Leu Ala
    130          135          140
gcc ttt gtg tcc tgc caa tac tgg atg agc acc atg ttc aac agt aag      539
  Ala Phe Val Ser Cys Gln Tyr Trp Met Ser Thr Met Phe Asn Ser Lys
    145          150          155
atc att ggc acg gtg aat ggc ctc gcg gcc ggc tgg ggc aac atg ggg      587
  Ile Ile Gly Thr Val Asn Gly Leu Ala Ala Gly Trp Gly Asn Met Gly
    160          165          170
ggc ggt gcc aca caa ctc att atg cca ctt gtt ttc cat gcc atc caa      635
  Gly Gly Ala Thr Gln Leu Ile Met Pro Leu Val Phe His Ala Ile Gln
    175          180          185
aag tgc ggt gcc aca ccc ttc gtg gca tgg cgt atc gcc tac ttc gtg      683
  Lys Cys Gly Ala Thr Pro Phe Val Ala Trp Arg Ile Ala Tyr Phe Val
    190          195          200
ccg gga atg atg cac atc gtc atg ggg ttg ctt gtc ctc aca atg ggc      731
  Pro Gly Met Met His Ile Val Met Gly Leu Leu Val Leu Thr Met Gly
    205          210          215
caa gat ctc ccc gac ggc aac ctt gcg agc ctc cag aag aag gga gac      779
  Gln Asp Leu Pro Asp Gly Asn Leu Ala Ser Leu Gln Lys Lys Gly Asp
    220          225          230
atg gcc aag gac aag ttc tcc aag gtc ctt tgg ggc gcc gtc acc aac      827
  Met Ala Lys Asp Lys Phe Ser Lys Val Leu Trp Gly Ala Val Thr Asn
    235          240          245
tac cgg aca tgg atc ttc gtc ctc ctc tac ggc tac tgc atg ggt gtc      875
  Tyr Arg Thr Trp Ile Phe Val Leu Leu Tyr Gly Tyr Cys Met Gly Val
    250          255          260
gag ctc acc act gac aac gtc atc gcc gag tac tac tac gac cat ttc      923
  Glu Leu Thr Thr Asp Asn Val Ile Ala Glu Tyr Tyr Tyr Asp His Phe
    265          270          275
cac cta cac ctt cgc gct gca ggc acc atc gcc gcc tgc ttt ggc atg      971
  His Leu His Leu Arg Ala Ala Gly Thr Ile Ala Ala Cys Phe Gly Met
    280          285          290
gcc aat atc gtc gca cgt cct atg gga ggt tac ctc tct gac ctt ggc      1019
  Ala Asn Ile Val Ala Arg Pro Met Gly Gly Tyr Leu Ser Asp Leu Gly
    295          300          305
gct cgc tac ttt ggt atg cgt gct cgc cta tgg aac atc tgg atc ctc      1067
  Ala Arg Tyr Phe Gly Met Arg Ala Arg Leu Trp Asn Ile Trp Ile Leu
    310          315          320          325          330          335

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PF59082SeqList_PF59082.txt

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Gln Thr Ala Gly Gly Ala Phe Cys Ile Trp Leu Gly Arg Ala Ser Ala	
ctc ccc gcc tca gtg act gcc atg gtt ctc ttc tcc atc tgc gcc caa	1163
Leu Pro Ala Ser Val Thr Ala Met Val Leu Phe Ser Ile Cys Ala Gln	
gct gca tgt ggc gct gtc ttt ggt gtt gca cca ttc gtt tcc agg cgt	1211
Ala Ala Cys Gly Ala Val Phe Gly Val Ala Pro Phe Val Ser Arg Arg	
tcc ctt ggc atc atc tct ggg tta acc ggc gct ggt ggc aat gtg ggc	1259
Ser Leu Gly Ile Ile Ser Gly Leu Thr Gly Ala Gly Asn Val Gly	
gcg ggg ctc aca caa ctt ctc ttc ttc act tcg tcg caa tac tcc acc	1307
Ala Gly Leu Thr Gln Leu Leu Phe Phe Thr Ser Ser Gln Tyr Ser Thr	
ggg agg ggt ctc gag tac atg ggc atc atg atg gca tgc aca tta	1355
Gly Arg Gly Leu Glu Tyr Met Gly Ile Met Ile Met Ala Cys Thr Leu	
cct atc act ctg gtg cac ttc cca caa tgg ggc tcc atg ttc ttc ccg	1403
Pro Ile Thr Leu Val His Phe Pro Gln Trp Gly Ser Met Phe Phe Pro	
gcc agt gct gat gct acg gag gag gag tac tac gct tcc gag tgg tca	1451
Ala Ser Ala Asp Ala Thr Glu Glu Glu Tyr Tyr Ala Ser Glu Trp Ser	
gag gag gag aag ggc aag ggt ctc cat atc gca ggc cag aag ttt gca	1499
Glu Glu Glu Lys Gly Lys Gly Leu His Ile Ala Gly Gln Lys Phe Ala	
gag aac tcc cgc tcg gag cgt ggt agg cgc aat gtt atc ctc gcc aca	1547
Glu Asn Ser Arg Ser Glu Arg Gly Arg Arg Asn Val Ile Leu Ala Thr	
tcc gcc acg ccg ccc aac aat aca ccc cag cat gta taaggccctt	1593
Ser Ala Thr Pro Pro Asn Asn Thr Pro Gln His Val	
gttttctgtc acctatgaat tgtacggttc gtcacgtaca tatacaaacc gtatatctac	1653
gtcggcagcc ccagcgtaat aagttgtatg gggatttatc tttctactag taaacttaag	1713
gaaacgctgg ttttgcgttc ctgctctgta c	1744

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<211> 507

<212> PRT

<213> Triticum aestivum

<400> 1511

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1 Thr Leu Pro Val Asp Ser Glu His Lys Ala Lys Ser Phe Arg Leu Phe	
20 Ser Phe Ala Asn Pro His Met Arg Thr Phe His Leu Ser Trp Ile Ser	
35 Phe Phe Thr Cys Phe Val Ser Thr Phe Ala Ala Ala Pro Leu Val Pro	
50 Ile Ile Arg Asp Asn Leu Asn Leu Ala Lys Ala Asp Ile Gly Asn Ala	
65 Gly Val Ala Ser Val Ser Gly Ser Ile Phe Ser Arg Leu Ala Met Gly	
85 Ala Val Cys Asp Leu Leu Gly Pro Arg Tyr Gly Cys Ala Phe Leu Val	
100 Met Leu Ser Ala Pro Thr Val Phe Cys Met Ala Val Ile Asp Asp Ala	
115 Ser Gly Tyr Ile Ala Val Arg Phe Leu Ile Gly Phe Ser Leu Ala Ala	
130 Phe Val Ser Cys Gln Tyr Trp Met Ser Thr Met Phe Asn Ser Lys Ile	
145 150 155 160	

PF59082SeqList_PF59082.txt

Ile Gly Thr Val Asn Gly Leu Ala Ala Gly Trp Gly Asn Met Gly Gly
165 170 175
Gly Ala Thr Gln Leu Ile Met Pro Leu Val Phe His Ala Ile Gln Lys
180 185 190
Cys Gly Ala Thr Pro Phe Val Ala Trp Arg Ile Ala Tyr Phe Val Pro
195 200 205
Gly Met Met His Ile Val Met Gly Leu Leu Val Leu Thr Met Gly Gln
210 215 220
Asp Leu Pro Asp Gly Asn Leu Ala Ser Leu Gln Lys Lys Gly Asp Met
225 230 235 240
Ala Lys Asp Lys Phe Ser Lys Val Leu Trp Gly Ala Val Thr Asn Tyr
245 250 255
Arg Thr Trp Ile Phe Val Leu Leu Tyr Gly Tyr Cys Met Gly Val Glu
260 265 270
Leu Thr Thr Asp Asn Val Ile Ala Glu Tyr Tyr Tyr Asp His Phe His
275 280 285
Leu His Leu Arg Ala Ala Gly Thr Ile Ala Ala Cys Phe Gly Met Ala
290 295 300
Asn Ile Val Ala Arg Pro Met Gly Gly Tyr Leu Ser Asp Leu Gly Ala
305 310 315 320
Arg Tyr Phe Gly Met Arg Ala Arg Leu Trp Asn Ile Trp Ile Leu Gln
325 330 335
Thr Ala Gly Gly Ala Phe Cys Ile Trp Leu Gly Arg Ala Ser Ala Leu
340 345 350
Pro Ala Ser Val Thr Ala Met Val Leu Phe Ser Ile Cys Ala Gln Ala
355 360 365
Ala Cys Gly Ala Val Phe Gly Val Ala Pro Phe Val Ser Arg Arg Ser
370 375 380
Leu Gly Ile Ile Ser Gly Leu Thr Gly Ala Gly Gly Asn Val Gly Ala
385 390 395 400
Gly Leu Thr Gln Leu Leu Phe Phe Thr Ser Ser Gln Tyr Ser Thr Gly
405 410 415
Arg Gly Leu Glu Tyr Met Gly Ile Met Ile Met Ala Cys Thr Leu Pro
420 425 430
Ile Thr Leu Val His Phe Pro Gln Trp Gly Ser Met Phe Phe Pro Ala
435 440 445
Ser Ala Asp Ala Thr Glu Glu Glu Tyr Tyr Ala Ser Glu Trp Ser Glu
450 455 460
Glu Glu Lys Gly Lys Gly Leu His Ile Ala Gly Gln Lys Phe Ala Glu
465 470 475 480
Asn Ser Arg Ser Glu Arg Gly Arg Arg Asn Val Ile Leu Ala Thr Ser
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Ala Thr Pro Pro Asn Asn Thr Pro Gln His Val
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<223> y is t or c

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<223> y is t or c

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<223> s is g or c

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<223> w is a or t

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<223> y is t or c

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His	Ala	Asp	Ala	Ala	Ala	Ser	Lys	Phe	Thr	Leu	
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cac	aag	gcc	aag	tcc	ttc	agg	ctc	ttc	tcc	ttc	151
His	Lys	Ala	Lys	Ser	Phe	Arg	Leu	Phe	Ser	Phe	
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cgc	acc	ttt	cac	ctc	tcg	tgg	atc	tcc	ttc	ttc	199
Arg	Thr	Phe	His	Leu	Ser	Trp	Ile	Ser	Phe	Phe	
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Thr	Phe	Ala	Ala	Ala	Pro	Leu	Val	Pro	Ile	Arg	
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Leu	Ala	Lys	Ala	Asp	Ile	Gly	Asn	Ala	Gly	Val	
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tcc	atc	ttc	tcc	agg	ctg	gcc	atg	ggc	gct	atc	343
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cca	cgg	tat	ggg	tgt	gcc	ttc	ctc	gtc	atg	ctc	391
Pro	Arg	Tyr	Gly	Cys	Ala	Phe	Leu	Val	Met	Leu	
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Phe	Cys	Met	Ala	Val	Ile	Asp	Asp	Ala	Ser	Gly	
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Phe	Leu	Ile	Gly	Phe	Ser	Leu	Ala	Thr	Phe	Val	
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ccg	ctt	gtc	ttc	cac	gca	atc	cag	aag	tgt	ggc	631
Pro	Leu	Val	Phe	His	Ala	Ile	Gln	Lys	Cys	Gly	
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Ala	Trp	Arg	Ile	Ala	Tyr	Phe	Val	Pro	Gly	Met	
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Gly	Leu	Leu	Val	Leu	Thr	Met	Gly	Gln	Asp	Leu	
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Ala	Ser	Leu	Gln	Lys	Lys	Gly	Asp	Met	Ala	Lys	
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Val	Leu	Trp	Gly	Ala	Val	Thr	Asn	Tyr	Arg	Thr	
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Leu	Tyr	Gly	Tyr	Cys	Met	Gly	Val	Glu	Leu	Thr	
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Ala	Glu	Tyr	Tyr	Tyr	Asp	His	Phe	His	Leu	Asp	
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Thr	Ile	Ala	Ala	Cys	Phe	Gly	Met	Ala	Asn	Ile	
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ggk	ggc	tac	ctc	tcy	gac	ctt	ggg	gcc	cgc	tac	1015
Gly	Gly	Tyr	Leu	Ser	Asp	Leu	Gly	Ala	Arg	Tyr	
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cgc	ctt	tgg	aac	atc	tgg	atc	ctm	caa	acy	gcc	1063
Arg	Leu	Trp	Asn	Ile	Trp	Ile	Leu	Gln	Thr	Ala	
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Val	Leu	Phe	Ser	Ile	Cys	Ala	Gln	Ala	Ala	Cys	Gly	Ala	Val	Phe	Gly	
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Val	Ala	Pro	Phe	Val	Ser	Arg	Arg	Ser	Leu	Gly	Ile	Ile	Ser	Gly	Leu	
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Phe	Thr	Ser	Ser	Gln	Tyr	Ser	Thr	Gly	Arg	Gly	Leu	Glu	Tyr	Met	Gly	
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Ile	Met	Ile	Met	Ala	Cys	Thr	Leu	Pro	Val	Ala	Leu	Val	His	Phe	Pro	
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Gln	Trp	Gly	Ser	Met	Phe	Phe	Pro	Ala	Ser	Ala	Asp	Ala	Thr	Glu	Glu	
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gaa	tac	tat	gcc	tct	gag	tgg	tcg	gag	gag	gag	aag	aac	aag	ggg	ctc	1447
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His	Ile	Ala	Gly	Gln	Lys	Phe	Ala	Glu	Asn	Ser	Arg	Ser	Glu	Arg	Gly	
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Arg	Arg	Asn	Val	Ile	Leu	Ala	Thr	Ser	Ala	Thr	Pro	Pro	Asn	Asn	Thr	
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Pro	Gln	His	Val													
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Phe	Val	Ser	Cys	Gln	Tyr	Trp	Met	Ser	Thr	Met	Phe	Asn	Ser	Lys	Ile	
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Cys	Gly	Ala	Thr	Pro	Phe	Val	Ala	Trp	Arg	Ile	Ala	Tyr	Phe	Val	Pro
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Gly	Met	Met	His	Ile	Val	Met	Gly	Leu	Leu	Val	Leu	Thr	Met	Gly	Gln
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Arg	Tyr	Phe	Gly	Met	Arg	Ala	Arg	Leu	Trp	Asn	Ile	Trp	Ile	Leu	Gln
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Thr	Ala	Gly	Gly	Ala	Phe	Cys	Ile	Trp	Leu	Gly	Arg	Ala	Ser	Ala	Leu
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Pro	Ala	Ser	Val	Thr	Ala	Met	Val	Leu	Phe	Ser	Ile	Cys	Ala	Gln	Ala
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Ala	Cys	Gly	Ala	Val	Phe	Gly	Val	Ala	Pro	Phe	Val	Ser	Arg	Arg	Ser
	370					375					380				
Leu	Gly	Ile	Ile	Ser	Gly	Leu	Thr	Gly	Ala	Gly	Gly	Asn	Val	Gly	Ala
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			405						410					415	
Arg	Gly	Leu	Glu	Tyr	Met	Gly	Ile	Met	Ile	Met	Ala	Cys	Thr	Leu	Pro
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Asn	Ser	Arg	Ser	Glu	Arg	Gly	Arg	Arg	Asn	Val	Ile	Leu	Ala	Thr	Ser
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Glu Pro Gly Ser Ser Met His Gly Val Thr Gly Arg Glu Gln Thr Phe																	
gct ttc tcg gtg gct tca ccg att gtc cca acc gac aag aca gca aag																	150
Ala Phe Ser Val Ala Ser Pro Ile Val Pro Thr Asp Lys Thr Ala Lys																	
ttc gac ctg ccg gtg gac tcg gag cat aag gca acg gtt ttc aag ctc																	198
Phe Asp Leu Pro Val Asp Ser Glu His Lys Ala Thr Val Phe Lys Leu																	
ttc tcc ttc gcc aaa cct cac atg cga acg ttc cat ctc tcg tgg atc																	246
Phe Ser Phe Ala Lys Pro His Met Arg Thr Phe His Leu Ser Trp Ile																	

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				75					80					85		
ccc	atc	atc	cga	gag	aat	ctc	aac	ctc	acg	aaa	caa	gac	atc	ggt	aac	342
Pro	Ile	Ile	Arg	Glu	Asn	Leu	Asn	Leu	Thr	Lys	Gln	Asp	Ile	Gly	Asn	
			90					95					100			
gca	gga	gtt	gcg	tcc	gtc	tcg	ggg	agt	atc	ttc	tct	agg	ctg	gtg	atg	390
Ala	Gly	Val	Ala	Ser	Val	Ser	Gly	Ser	Ile	Phe	Ser	Arg	Leu	Val	Met	
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gga	gca	gtg	tgt	gat	ctt	ctc	ggt	cca	cgt	tac	ggc	tgt	gcc	ttc	ctt	438
Gly	Ala	Val	Cys	Asp	Leu	Leu	Gly	Pro	Arg	Tyr	Gly	Cys	Ala	Phe	Leu	
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Val	Met	Leu	Ser	Ala	Pro	Thr	Val	Phe	Ser	Met	Ser	Phe	Val	Ser	Gly	
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Thr	Phe	Val	Ser	Cys	Gln	Tyr	Gly	Met	Ser	Thr	Met	Phe	Asn	Ser	Gln	
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		185				190						195				
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Arg	Cys	Gly	Ala	Thr	Ala	Phe	Thr	Ala	Trp	Arg	Leu	Ala	Phe	Phe	Val	
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caa	gat	ttg	cca	gat	ggt	aac	cga	agt	gcc	ttg	gag	aaa	aag	gga	gaa	822
Gln	Asp	Leu	Pro	Asp	Gly	Asn	Arg	Ser	Ala	Leu	Glu	Lys	Lys	Gly	Glu	
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Ala	Lys	Tyr	Phe	Gly	Met	Arg	Gly	Arg	Leu	Trp	Ala	Leu	Trp	Ile	Ile	
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Gln	Thr	Ala	Gly	Gly	Val	Phe	Cys	Val	Trp	Leu	Gly	Arg	Ala	Asn	Thr	
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ctc	gtt	act	gcc	gtt	gta	gct	atg	gtc	ctc	ttc	tct	tta	gga	gca	caa	1206
Leu	Val	Thr	Ala	Val	Val	Ala	Met	Val	Leu	Phe	Ser	Leu	Gly	Ala	Gln	
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gcc	gct	tgt	gga	gcc	acc	ttc	gca	atc	gtt	ccc	ttt	gtt	tct	cgg	cga	1254
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Ala	Leu	Gly	Ile	Ile	Ser	Gly	Leu	Thr	Gly	Ala	Gly	Gly	Asn	Phe	Gly	
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tca	ggg	ctc	aca	cag	ctc	atc	ttc	ttc	tcg	acc	tca	agg	ttc	aca	acc	1350
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Pro	Ser	Thr	Asp	Pro	Val	Lys	Gly	Pro	Lys	Glu	His	Tyr	Tyr	Ala	Ser		
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acaaatgcgt	atgttatcaa	tgcttgctgg	acgttatctg	ttgtgtatct	ttcttttttt												1756
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 <212> PRT
 <213> Brassica napus

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 Ala Thr Val Phe Lys Leu Phe Ser Phe Ala Lys Pro His Met Arg Thr
 50 55 60
 Phe His Leu Ser Trp Ile Ser Phe Ser Thr Cys Phe Val Ser Thr Phe
 65 70 75 80
 Ala Ala Ala Pro Leu Val Pro Ile Ile Arg Glu Asn Leu Asn Leu Thr
 85 90 95
 Lys Gln Asp Ile Gly Asn Ala Gly Val Ala Ser Val Ser Gly Ser Ile
 100 105 110
 Phe Ser Arg Leu Val Met Gly Ala Val Cys Asp Leu Leu Gly Pro Arg
 115 120 125
 Tyr Gly Cys Ala Phe Leu Val Met Leu Ser Ala Pro Thr Val Phe Ser
 130 135 140
 Met Ser Phe Val Ser Gly Ala Ala Gly Phe Ile Thr Val Arg Phe Met
 145 150 155 160
 Ile Gly Phe Cys Leu Ala Thr Phe Val Ser Cys Gln Tyr Gly Met Ser
 165 170 175
 Thr Met Phe Asn Ser Gln Ile Ile Gly Leu Val Asn Gly Thr Ala Ala
 180 185 190
 Gly Trp Gly Asn Met Gly Gly Gly Ile Thr Gln Leu Leu Met Pro Val
 195 200 205
 Val Tyr Glu Ile Ile Arg Arg Cys Gly Ala Thr Ala Phe Thr Ala Trp
 210 215 220
 Arg Leu Ala Phe Phe Val Pro Gly Trp Leu His Ile Ile Met Gly Val
 225 230 235 240
 Leu Val Leu Asn Leu Gly Gln Asp Leu Pro Asp Gly Asn Arg Ser Ala
 245 250 255

PF59082SeqList_PF59082.txt

Leu Glu Lys Lys Gly Glu Val Ala Lys Asp Lys Phe Gly Lys Ile Met
 260 265 270
 Trp Tyr Ala Val Thr Asn Tyr Arg Thr Trp Ile Phe Val Leu Leu Tyr
 275 280 285
 Gly Tyr Ser Met Gly Val Glu Leu Ser Thr Asp Asn Val Ile Ala Glu
 290 295 300
 Tyr Phe Phe Asp Arg Phe His Leu Lys Leu His Thr Ala Gly Ile Ile
 305 310 315 320
 Ala Ala Cys Phe Gly Met Ala Asn Phe Phe Ala Arg Pro Ala Gly Gly
 325 330 335
 Tyr Ala Ser Asp Leu Ala Lys Tyr Phe Gly Met Arg Gly Arg Leu
 340 345 350
 Trp Ala Leu Trp Ile Ile Gln Thr Ala Gly Gly Val Phe Cys Val Trp
 355 360 365
 Leu Gly Arg Ala Asn Thr Leu Val Thr Ala Val Val Ala Met Val Leu
 370 375 380
 Phe Ser Leu Gly Ala Gln Ala Ala Cys Gly Ala Thr Phe Ala Ile Val
 385 390 395 400
 Pro Phe Val Ser Arg Arg Ala Leu Gly Ile Ile Ser Gly Leu Thr Gly
 405 410 415
 Ala Gly Gly Asn Phe Gly Ser Gly Leu Thr Gln Leu Ile Phe Phe Ser
 420 425 430
 Thr Ser Arg Phe Thr Thr Glu Gln Gly Leu Thr Trp Met Gly Val Met
 435 440 445
 Ile Val Ala Cys Thr Leu Pro Val Thr Leu Ile His Phe Pro Gln Trp
 450 455 460
 Gly Ser Met Phe Leu Pro Pro Ser Thr Asp Pro Val Lys Gly Pro Lys
 465 470 475 480
 Glu His Tyr Tyr Ala Ser Glu Trp Asn Glu Gln Glu Lys Glu Lys Asn
 485 490 495
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 Asn Val
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<211> 1796

<212> DNA

<213> Triticum aestivum

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<222> (66)..(1589)

<400> 1516

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 Met Glu Val Glu Ala Ser Ala His Gly Asp Thr Ala Ala Ser Lys
 1 5 10 15

110

ttc acg ctg ccc gtg gac tcc gag cac aag gcc aag tcc ttc aga ctc
 Phe Thr Leu Pro Val Asp Ser Glu His Lys Ala Lys Ser Phe Arg Leu
 20 25 30

158

ttc tcc ttc gcc aac ccc cac atg cgt acc ttc cac ctc tcc tgg ata
 Phe Ser Phe Ala Asn Pro His Met Arg Thr Phe His Leu Ser Trp Ile
 35 40 45

206

tcc ttc ttc acc tgc ttc gtc tcc acc ttc gcg gcg gca ccg ttg gtg
 Ser Phe Phe Thr Cys Phe Val Ser Thr Phe Ala Ala Ala Pro Leu Val
 50 55 60

254

ccc atc atc cgt gac aac ctc aac ctc gct aag gcc gac ata ggg aat
 Pro Ile Ile Arg Asp Asn Leu Asn Leu Ala Lys Ala Asp Ile Gly Asn
 65 70 75

302

gcc ggt gtg gca tct gtg tct ggg tcc atc ttc tcc agg ctt gcc atg
 Ala Gly Val Ala Ser Val Ser Gly Ser Ile Phe Ser Arg Leu Ala Met
 80 85 90 95

350

ggg gcc atc tgc gac ctt tta ggg ccg cgg tat ggc tgc gcc ttc ctc

398

PF59082SeqList_PF59082.txt

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Val	Met	Leu	Ser	Ala	Pro	Thr	Val	Phe	Cys	Met	Ala	Ala	Ile	Asp	Asp	
			115					120					125			
gcg	tca	ggc	tac	atc	gcc	gta	cgc	ttc	ctc	att	ggc	ttc	tcc	ctc	gcc	494
Ala	Ser	Gly	Tyr	Ile	Ala	Val	Arg	Phe	Leu	Ile	Gly	Phe	Ser	Leu	Ala	
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Thr	Phe	Val	Ser	Cys	Gln	Tyr	Trp	Met	Ser	Thr	Met	Phe	Asn	Ser	Lys	
	145					150					155					
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Ile	Ile	Gly	Thr	Val	Asn	Gly	Leu	Ala	Ala	Gly	Trp	Gly	Asn	Met	Gly	
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ggt	ggt	gcc	aca	caa	ctc	atc	atg	ccg	ctt	ggt	ttc	cat	gcc	atc	caa	638
Gly	Gly	Ala	Thr	Gln	Leu	Ile	Met	Pro	Leu	Val	Phe	His	Ala	Ile	Gln	
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Lys	Cys	Gly	Ala	Thr	Pro	Phe	Val	Ala	Trp	Arg	Ile	Ala	Tyr	Phe	Val	
		195						200				205				
ccg	gga	atg	atg	cac	atc	gtc	atg	ggg	ttg	ctt	gtg	ctc	act	atg	ggc	734
Pro	Gly	Met	Met	His	Ile	Val	Met	Gly	Leu	Leu	Val	Leu	Thr	Met	Gly	
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Gln	Asp	Leu	Pro	Asp	Gly	Asn	Leu	Ala	Ser	Leu	Gln	Lys	Lys	Gly	Asp	
	225					230					235					
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Met	Ala	Lys	Asp	Lys	Phe	Ser	Lys	Val	Leu	Trp	Gly	Ala	Val	Thr	Asn	
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tac	cgg	aca	tgg	ata	ttc	gtc	ctc	ctc	tac	ggc	tac	tgc	atg	ggt	gtc	878
Tyr	Arg	Thr	Trp	Ile	Phe	Val	Leu	Leu	Tyr	Gly	Tyr	Cys	Met	Gly	Val	
			260						265					270		
gag	ctc	acc	acc	gac	aac	gtc	atc	gcc	gag	tac	tac	tac	gac	cac	ttc	926
Glu	Leu	Thr	Thr	Asp	Asn	Val	Ile	Ala	Glu	Tyr	Tyr	Tyr	Asp	His	Phe	
		275						280					285			
cac	ctt	gac	ctt	cgc	gcc	gct	ggc	acc	att	gcc	gct	tgc	ttc	ggc	atg	974
His	Leu	Asp	Leu	Arg	Ala	Ala	Gly	Thr	Ile	Ala	Ala	Cys	Phe	Gly	Met	
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Ala	Asn	Ile	Val	Ala	Arg	Pro	Met	Gly	Gly	Tyr	Leu	Ser	Asp	Leu	Gly	
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gcc	cgc	tac	ttc	ggc	atg	cgt	gct	cgg	ctc	tgg	aac	atc	tgg	atc	ctc	1070
Ala	Arg	Tyr	Phe	Gly	Met	Arg	Ala	Arg	Leu	Trp	Asn	Ile	Trp	Ile	Leu	
320					325					330					335	
cag	acc	gct	ggt	ggc	gct	ttc	tgc	atc	tgg	ctc	ggt	cgt	gca	tcg	gcc	1118
Gln	Thr	Ala	Gly	Gly	Ala	Phe	Cys	Ile	Trp	Leu	Gly	Arg	Ala	Ser	Ala	
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ctt	cct	gcc	tca	gtc	acg	gcc	atg	gtc	ctc	ttt	tcc	att	tgt	gca	caa	1166
Leu	Pro	Ala	Ser	Val	Thr	Ala	Met	Val	Leu	Phe	Ser	Ile	Cys	Ala	Gln	
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Ala	Ala	Cys	Gly	Ala	Val	Phe	Gly	Val	Ala	Pro	Phe	Val	Ser	Arg	Arg	
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Ser	Leu	Gly	Ile	Ile	Ser	Gly	Leu	Thr	Gly	Ala	Gly	Gly	Asn	Val	Gly	
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Ala	Gly	Leu	Thr	Gln	Leu	Leu	Phe	Phe	Thr	Ser	Ser	Gln	Tyr	Ser	Thr	
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Gly	Arg	Gly	Leu	Glu	Tyr	Met	Gly	Ile	Met	Ile	Met	Ala	Cys	Thr	Leu	
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ccc	gtc	gct	ctg	gtg	cac	ttc	ccc	caa	tgg	ggc	tcc	atg	ttc	ttc	ccg	1406
Pro	Val	Ala	Leu	Val	His	Phe	Pro	Gln	Trp	Gly	Ser	Met	Phe	Phe	Pro	
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gct	agc	gct	gat	gcc	acg	gaa	gag	gaa	tac	tat	gct	tct	gag	tgg	tcg	1454
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PF59082SeqList_PF59082.txt

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 480 485 490 495
 tcc gcc acg cca ccc aac aca ccc cag cac gta taaggccctt 1596
 Ser Ala Thr Pro Pro Asn Asn Thr Pro Gln His Val
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 cgtctgcagc cccagcgtaa taagttgtat ggggatttat gtttctacta gtaaaacttaa 1716

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 <213> Triticum aestivum

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 35 40 45
 Phe Phe Thr Cys Phe Val Ser Thr Phe Ala Ala Ala Pro Leu Val Pro
 50 55 60
 Ile Ile Arg Asp Asn Leu Asn Leu Ala Lys Ala Asp Ile Gly Asn Ala
 65 70 75 80
 Gly Val Ala Ser Val Ser Gly Ser Ile Phe Ser Arg Leu Ala Met Gly
 85 90 95
 Ala Ile Cys Asp Leu Leu Gly Pro Arg Tyr Gly Cys Ala Phe Leu Val
 100 105 110
 Met Leu Ser Ala Pro Thr Val Phe Cys Met Ala Ala Ile Asp Asp Ala
 115 120 125
 Ser Gly Tyr Ile Ala Val Arg Phe Leu Ile Gly Phe Ser Leu Ala Thr
 130 135 140
 Phe Val Ser Cys Gln Tyr Trp Met Ser Thr Met Phe Asn Ser Lys Ile
 145 150 155 160
 Ile Gly Thr Val Asn Gly Leu Ala Ala Gly Trp Gly Asn Met Gly Gly
 165 170 175
 Gly Ala Thr Gln Leu Ile Met Pro Leu Val Phe His Ala Ile Gln Lys
 180 185 190
 Cys Gly Ala Thr Pro Phe Val Ala Trp Arg Ile Ala Tyr Phe Val Pro
 195 200 205
 Gly Met Met His Ile Val Met Gly Leu Leu Val Leu Thr Met Gly Gln
 210 215 220
 Asp Leu Pro Asp Gly Asn Leu Ala Ser Leu Gln Lys Lys Gly Asp Met
 225 230 235 240
 Ala Lys Asp Lys Phe Ser Lys Val Leu Trp Gly Ala Val Thr Asn Tyr
 245 250 255
 Arg Thr Trp Ile Phe Val Leu Leu Tyr Gly Tyr Cys Met Gly Val Glu
 260 265 270
 Leu Thr Thr Asp Asn Val Ile Ala Glu Tyr Tyr Tyr Asp His Phe His
 275 280 285
 Leu Asp Leu Arg Ala Ala Gly Thr Ile Ala Ala Cys Phe Gly Met Ala
 290 295 300
 Asn Ile Val Ala Arg Pro Met Gly Gly Tyr Leu Ser Asp Leu Gly Ala
 305 310 315 320
 Arg Tyr Phe Gly Met Arg Ala Arg Leu Trp Asn Ile Trp Ile Leu Gln
 325 330 335

PF59082SeqList_PF59082.txt

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 355 360 365
 Ala Cys Gly Ala Val Phe Gly Val Ala Pro Phe Val Ser Arg Arg Ser
 370 375 380
 Leu Gly Ile Ile Ser Gly Leu Thr Gly Ala Gly Gly Asn Val Gly Ala
 385 390 395 400
 Gly Leu Thr Gln Leu Leu Phe Phe Thr Ser Gln Tyr Ser Thr Gly
 405 410 415
 Arg Gly Leu Glu Tyr Met Gly Ile Met Ile Met Ala Cys Thr Leu Pro
 420 425 430
 Val Ala Leu Val His Phe Pro Gln Trp Gly Ser Met Phe Phe Pro Ala
 435 440 445
 Ser Ala Asp Ala Thr Glu Glu Tyr Tyr Ala Ser Glu Trp Ser Glu
 450 455 460
 Glu Glu Lys Gly Lys Gly Leu His Ile Thr Gly Gln Lys Phe Ala Glu
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<211> 2060

<212> DNA

<213> Lycopersicon esculentum

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<222> (65)..(1657)

<400> 1518

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 Met Ala Asp Val Glu Gly Ser Pro Gly Ser Ser Met His Gly Val 15

acc gga aga gaa cct gtt ctc gct ttc tcc gtg gct tct cca atg gtg 157
 Thr Gly Arg Glu Pro Val Leu Ala Phe Ser Val Ala Ser Pro Met Val 20 25 30

cct acg gat acc tcc gcc aaa ttt tca gta ccg gtg gac act gaa cac 205
 Pro Thr Asp Thr Ser Ala Lys Phe Ser Val Pro Val Asp Thr Glu His 35 40 45

aag gct aaa caa ttt aag ttt tat tcg ttt tcg aag cct cat gga ctt 253
 Lys Ala Lys Gln Phe Lys Phe Tyr Ser Phe Ser Lys Pro His Gly Leu 50 55 60

acg ttc cag ctc tcc tgg atc tcc ttt ttc act tgt ttc gtt tcg act 301
 Thr Phe Gln Leu Ser Trp Ile Ser Phe Phe Thr Cys Phe Val Ser Thr 65 70 75

ttt gct gct gca cct tta gtt cct att att agg gac aat ctt aat ttg 349
 Phe Ala Ala Ala Pro Leu Val Pro Ile Ile Arg Asp Asn Leu Asn Leu 80 85 90 95

aca aaa atg gat gtt ggt aac gct ggg gtt gct tcc gta tcc gga agt 397
 Thr Lys Met Asp Val Gly Asn Ala Gly Val Ala Ser Val Ser Gly Ser 100 105 110

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 Ile Leu Ser Arg Leu Thr Met Gly Ala Val Cys Asp Leu Leu Gly Pro 115 120 125

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 Arg Tyr Gly Cys Ala Phe Leu Ile Met Leu Ser Ala Pro Thr Val Phe 130 135 140

tgt atg tct ttt gtt tca tcc gct ggt ggc tac gta gct gtc cgg ttc 541
 Cys Met Ser Phe Val Ser Ser Ala Gly Gly Tyr Val Ala Val Arg Phe 145 150 155

atg att ggg ttt tcg ctc gca acg ttt gtg tct tgt caa tat tgg atg 589
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Leu	Leu	Tyr	Asp	Ile	Ile	Arg	Arg	Ala	Gly	Ala	Thr	Pro	Phe	Thr	Ala	
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Trp	Arg	Ile	Ala	Phe	Phe	Ile	Pro	Gly	Trp	Leu	His	Val	Val	Met	Gly	
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Ile	Leu	Val	Leu	Thr	Leu	Gly	Gln	Asp	Leu	Pro	Asp	Gly	Asn	Arg	Gly	
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Thr	Leu	Gln	Lys	Thr	Gly	Thr	Val	Ala	Lys	Asp	Lys	Phe	Gly	Asn	Ile	
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Leu	Trp	Tyr	Ala	Ala	Thr	Asn	Tyr	Arg	Thr	Trp	Ile	Phe	Val	Leu	Leu	
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Tyr	Gly	Tyr	Ser	Met	Gly	Val	Glu	Leu	Ser	Thr	Asp	Asn	Val	Ile	Ala	
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Ile	Ala	Ala	Thr	Phe	Gly	Met	Ala	Asn	Leu	Leu	Ala	Arg	Pro	Phe	Gly	
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Gly	Phe	Ser	Ser	Asp	Tyr	Ala	Ala	Lys	Lys	Phe	Gly	Met	Arg	Gly	Arg	
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Leu	Trp	Val	Leu	Trp	Ile	Leu	Gln	Thr	Leu	Gly	Gly	Val	Phe	Cys	Val	
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ctt	ttg	ggt	cgt	tcg	aat	tct	cta	cca	ctt	gcg	gta	acc	ttt	atg	atc	1213
Leu	Leu	Gly	Arg	Ser	Asn	Ser	Leu	Pro	Leu	Ala	Val	Thr	Phe	Met	Ile	
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Leu	Phe	Ser	Ile	Gly	Ala	Gln	Ala	Ala	Cys	Gly	Ala	Thr	Phe	Gly	Ile	
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Ile	Pro	Phe	Ile	Ser	Arg	Arg	Ser	Leu	Gly	Ile	Ile	Ser	Gly	Met	Thr	
400					405					410					415	
ggg	gca	ggt	gga	aat	ttt	ggt	tct	gga	ttg	act	caa	ttg	ttg	ttt	ttc	1357
Gly	Ala	Gly	Gly	Asn	Phe	Gly	Ser	Gly	Leu	Thr	Gln	Leu	Leu	Phe	Phe	
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Thr	Ser	Ser	Lys	Tyr	Ser	Thr	Ala	Thr	Gly	Leu	Thr	Tyr	Met	Gly	Phe	
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Met	Ile	Ile	Gly	Cys	Thr	Leu	Pro	Val	Thr	Phe	Cys	His	Phe	Pro	Gln	
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Trp	Gly	Ser	Met	Phe	Leu	Pro	Pro	Thr	Lys	Asp	Pro	Val	Lys	Gly	Thr	
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gaa	gaa	cat	tat	tat	act	tca	gag	tac	aca	gag	gcc	gag	agg	caa	aaa	1549
Glu	Glu	His	Tyr	Tyr	Thr	Ser	Glu	Tyr	Thr	Glu	Ala	Glu	Arg	Gln	Lys	
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ggg	atg	cac	caa	aac	agc	ttg	aaa	ttc	gct	gaa	aat	tgc	cga	tca	gag	1597
Gly	Met	His	Gln	Asn	Ser	Leu	Lys	Phe	Ala	Glu	Asn	Cys	Arg	Ser	Glu	
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PF59082SeqList_PF59082.txt

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Phe	Gln	Leu	Ser	Trp	Ile	Ser	Phe	Phe	Thr	Cys	Phe	Val	Ser	Thr	Phe
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Lys	Met	Asp	Val	Gly	Asn	Ala	Gly	Val	Ala	Ser	Val	Ser	Gly	Ser	Ile
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Leu	Ser	Arg	Leu	Thr	Met	Gly	Ala	Val	Cys	Asp	Leu	Leu	Gly	Pro	Arg
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Tyr	Gly	Cys	Ala	Phe	Leu	Ile	Met	Leu	Ser	Ala	Pro	Thr	Val	Phe	Cys
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Ile	Gly	Phe	Ser	Leu	Ala	Thr	Phe	Val	Ser	Cys	Gln	Tyr	Trp	Met	Ser
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Trp	Tyr	Ala	Thr	Asn	Tyr	Arg	Thr	Trp	Ile	Phe	Val	Leu	Leu	Tyr	
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Gly	Tyr	Ser	Met	Gly	Val	Glu	Leu	Ser	Thr	Asp	Asn	Val	Ile	Ala	Glu
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Tyr	Phe	Phe	Asp	Arg	Phe	Asp	Leu	Lys	Leu	Ser	Thr	Ala	Gly	Ile	Ile
305					310					315					320
Ala	Ala	Thr	Phe	Gly	Met	Ala	Asn	Leu	Leu	Ala	Arg	Pro	Phe	Gly	Gly
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PF59082SeqList_PF59082.txt

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 385 390 395 400
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 405 410 415
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 Ser Ser Lys Tyr Ser Thr Ala Thr Gly Leu Thr Tyr Met Gly Phe Met
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 Ile Ile Gly Cys Thr Leu Pro Val Thr Phe Cys His Phe Pro Gln Trp
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 Gly Ser Met Phe Leu Pro Thr Lys Asp Pro Val Lys Gly Thr Glu
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 Glu His Tyr Tyr Thr Ser Glu Tyr Thr Glu Ala Glu Arg Gln Lys Gly
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<400> 1520

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Glu	Pro	Val	Leu	Ala	Phe	Ser	Val	Ala	Ser	Pro	Met	Val	Pro	Thr	Asp	
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Thr	Ser	Ala	Lys	Phe	Ser	Val	Pro	Val	Asp	Thr	Glu	His	Lys	Ala	Lys	
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Gln	Phe	Lys	Phe	Tyr	Ser	Phe	Ser	Lys	Pro	His	Gly	Leu	Thr	Phe	Gln	
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ctc	tcc	tgg	atc	tcc	ttt	ttc	act	tgt	ttc	gtt	tcg	act	ttt	gct	gct	297
Leu	Ser	Trp	Ile	Ser	Phe	Phe	Thr	Cys	Phe	Val	Ser	Thr	Phe	Ala	Ala	
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Cys	Ala	Phe	Leu	Ile	Met	Leu	Ser	Ala	Pro	Thr	Val	Phe	Cys	Met	Ser	
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PF59082SeqList_PF59082.txt

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Gly	Asn	Met	Gly	Gly	Gly	Ala	Thr	Gln	Leu	Ile	Met	Pro	Leu	Leu	Tyr	
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Ala	Phe	Phe	Ile	Pro	Gly	Trp	Leu	His	Val	Val	Met	Gly	Ile	Leu	Val	
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Lys	Thr	Gly	Thr	Val	Ala	Lys	Asp	Lys	Phe	Gly	Asn	Ile	Leu	Trp	Tyr	
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Ser	Met	Gly	Val	Glu	Leu	Ser	Thr	Asp	Asn	Val	Ile	Ala	Glu	Tyr	Phe	
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Ile	Ser	Arg	Arg	Ser	Leu	Gly	Ile	Ile	Ser	Gly	Met	Thr	Gly	Ala	Gly	
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Lys	Tyr	Ser	Thr	Ala	Thr	Gly	Leu	Thr	Tyr	Met	Gly	Phe	Met	Ile	Ile	
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Tyr	Tyr	Thr	Ser	Glu	Tyr	Thr	Glu	Ala	Glu	Arg	Gln	Lys	Gly	Met	His	
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Gln	Asn	Ser	Leu	Lys	Phe	Ala	Glu	Asn	Cys	Arg	Ser	Glu	Arg	Gly	Lys	
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Arg	Val	Gly	Ser	Ala	Pro	Thr	Pro	Pro	Asn	Leu	Thr	Pro	Asn	Arg	Val	
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Lys Met Asp Val Gly Asn Ala Gly Val Ala Ser Val Ser Gly Ser Ile
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Thr Met Phe Asn Ser Lys Ile Ile Gly Leu Val Asn Gly Thr Ala Ala
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Trp Tyr Ala Ala Thr Asn Tyr Arg Thr Trp Ile Phe Val Leu Leu Tyr
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Gly Tyr Ser Met Gly Val Glu Leu Ser Thr Asp Asn Val Ile Ala Glu
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Tyr Phe Phe Asp Arg Phe Asp Leu Lys Leu Ser Thr Ala Gly Ile Ile
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 Gly Ser Met Phe Leu Pro Pro Thr Lys Asp Pro Val Lys Gly Thr Glu
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114

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162

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His Lys Ala Lys Ser Phe Arg Leu Phe Ser Phe Ala Asn Pro His Met
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210

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258

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306

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Leu Ala Lys Ala Asp Ile Gly Asn Ala Gly Val Ala Ser Val Ser Gly
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354

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402

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450

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120 125 130 135

498

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546

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594

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Ala Ala Gly Trp Gly Asn Met Gly Gly Gly Ala Thr Gln Leu Ile Met
170 175 180

642

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185 190

690

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Gly Leu Leu Val Leu Thr	Met Gly Gln Asp Leu	Pro Asp Gly Asn Leu				
220	gcg agc ctc cag aag aga	225	gga gac atg gcc aag	230	gac aag ttc tcc aag	834
Ala Ser Leu Gln Lys Arg	Gly Asp Met Ala Lys	Asp Lys Phe Ser Lys				
235	gtc ctt tgg ggc gcc gtc	240	acc aac tac cgg aca	245	tgg atc ttt gtc ctc	882
Val Leu Trp Gly Ala Val	Thr Asn Tyr Arg Thr	Trp Ile Phe Val Leu				
250	cta tat ggc tac tgc atg	255	ggt gtc gaa ctc acc	260	act gac aat gtc att	930
Leu Tyr Gly Tyr Cys Met	Gly Val Glu Leu Thr	Thr Asp Asn Val Ile				
265	gcc gag tac tac ttc gac	270	cac ttc cac cta gac	275	ctt cgc gcc gct ggt	978
Ala Glu Tyr Tyr Phe Asp	His Phe His Leu Asp	Leu Arg Ala Ala Gly				
280	acc atc gcc gcc tgc ttc	285	ggt atg gcc aac ata	290	gtc gca cgt cct atg	1026
Thr Ile Ala Ala Cys Phe	Gly Met Ala Asn Ile	Val Ala Arg Pro Met				
300	ggc ggc tac ctc tct gac	305	ctt ggc gcc cgc tat	310	ttc ggc atg cgt gcc	1074
Gly Gly Tyr Leu Ser Asp	Leu Gly Ala Arg Tyr	Phe Gly Met Arg Ala				
315	ctt tgg aac atc tgg atc	320	ctc caa acc gct ggt	325	ggc gct ttc tgc atc	1122
Leu Trp Asn Ile Trp Ile	Leu Gln Thr Ala Gly	Gly Gly Ala Phe Cys Ile				
330	tgg ctc ggt cgt gca tcg	335	gcc ctc cct gcc tcg	340	gtg acc gcc atg gtc	1170
Trp Leu Gly Arg Ala Ser	Ala Leu Pro Ala Ser	Val Thr Ala Met Val				
345	ctc ttc tcc atc tgt gcc	350	cag gct gcc tgt ggt	355	gct atc ttt ggt gtc	1218
Leu Phe Ser Ile Cys Ala	Gln Ala Ala Cys Gly	Ala Ile Phe Gly Val				
360	gca ccc ttc gtc tcc agg	365	cgt tcc ctt ggc att	370	att tcc ggg ttg acc	1266
Ala Pro Phe Val Ser Arg	Arg Ser Leu Gly Ile	Ile Ser Gly Leu Thr				
380	ggt gcc ggt gga aac gtg	385	ggc gca gga ctc aca	390	caa ctt cta ttc ttc	1314
Gly Ala Gly Gln Asn Val	Gly Ala Gly Leu Thr	Gln Leu Leu Phe Phe				
395	acc tca tcg caa tac tcc	400	act ggt agg ggt ctc	405	gag tac atg ggc atc	1362
Thr Ser Ser Gln Tyr Ser	Thr Gly Arg Gly Leu	Glu Tyr Met Gly Ile				
410	atg atc atg gca tgc acg	415	ctg ccc gtc gct ctt	420	gtg cac ttt ccg caa	1410
Met Ile Met Ala Cys Thr	Leu Pro Val Ala Leu	Val His Phe Pro Gln				
425	tgg gga tcc atg ttc ttc	430	ccg gcc agc gct gat	435	gcc act gag gag gag	1458
Trp Gly Ser Met Phe Phe	Pro Ala Ser Ala Asp	Ala Thr Pro Asn Glu				
440	tac tat gct tcc gag tgg	445	tcg gag gag gag aag	450	ggc aag ggt ctc cat	1506
Tyr Tyr Ala Ser Glu Trp	Ser Glu Glu Glu Lys	Gly Lys Gly Leu His				
460	atc gca ggc caa aag ttc	465	gcc gag aac tcc cgc	470	tcg gag cgc gcc agg	1554
Ile Ala Gly Gln Lys Phe	Ala Glu Asn Ser Arg	Ser Glu Arg Gly Arg				
475	cgc aac gtc atc ttt gcc	480	aca tcc gcc acg ccg	485	ccc aac aac aca ccc	1602
Arg Asn Val Ile Phe Ala	Thr Ser Ala Thr Pro	Pro Asn Asn Thr Pro				
490	cag cag gta taaggcattt	495	ttttttgtta cctatgaatt	500	ttacagctca tggcgtatat	1661
Gln Gln Val						
505	atacaaacag tatattttacg		tttgcagccc cagcgtata		agttgtatgg gggtttatct	1721
	ttttactatg gtaaacctaa		ggacatgtat tgtcaaattg		agtccgaaat taatacatga	1781
	acagtgttga tgttttgtgta		tgcttgaaaa aaaaaaaaaa		aaaa	1825

PF59082SeqList_PF59082.txt

<210> 1523
 <211> 506
 <212> PRT
 <213> Hordeum vulgare

<400> 1523
 Met Glu Val Glu Ala Gly Ala His Gly Asp Thr Ala Ala Ser Lys Phe
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 Thr Leu Pro Val Asp Ser Glu His Lys Ala Lys Ser Phe Arg Leu Phe
 20 25 30
 Ser Phe Ala Asn Pro His Met Arg Thr Phe His Leu Ser Trp Ile Ser
 35 40 45
 Phe Phe Thr Cys Phe Val Ser Thr Phe Ala Ala Ala Pro Leu Val Pro
 50 55 60
 Ile Ile Arg Asp Asn Leu Asn Leu Ala Lys Ala Asp Ile Gly Asn Ala
 65 70 75 80
 Gly Val Ala Ser Val Ser Gly Ser Ile Phe Ser Arg Leu Ala Met Gly
 85 90 95
 Ala Ile Cys Asp Leu Leu Gly Pro Arg Tyr Gly Cys Ala Phe Leu Val
 100 105 110
 Met Leu Ser Ala Pro Thr Val Phe Cys Met Ala Val Ile Asp Asp Ala
 115 120 125
 Ser Gly Tyr Ile Ala Val Arg Phe Leu Ile Gly Phe Ser Leu Ala Thr
 130 135 140
 Phe Val Ser Cys Gln Tyr Trp Met Ser Thr Met Phe Asn Ser Lys Ile
 145 150 155 160
 Ile Gly Thr Val Asn Gly Leu Ala Ala Gly Trp Gly Asn Met Gly Gly
 165 170 175
 Gly Ala Thr Gln Leu Ile Met Pro Leu Val Phe His Ala Ile Gln Lys
 180 185 190
 Cys Gly Ala Thr Pro Phe Val Ala Trp Arg Ile Ala Tyr Phe Val Pro
 195 200 205
 Gly Met Met His Ile Val Met Gly Leu Leu Val Leu Thr Met Gly Gln
 210 215 220
 Asp Leu Pro Asp Gly Asn Leu Ala Ser Leu Gln Lys Arg Gly Asp Met
 225 230 235 240
 Ala Lys Asp Lys Phe Ser Lys Val Leu Trp Gly Ala Val Thr Asn Tyr
 245 250 255
 Arg Thr Trp Ile Phe Val Leu Leu Tyr Gly Tyr Cys Met Gly Val Glu
 260 265 270
 Leu Thr Thr Asp Asn Val Ile Ala Glu Tyr Tyr Phe Asp His Phe His
 275 280 285
 Leu Asp Leu Arg Ala Ala Gly Thr Ile Ala Ala Cys Phe Gly Met Ala
 290 295 300
 Asn Ile Val Ala Arg Pro Met Gly Gly Tyr Leu Ser Asp Leu Gly Ala
 305 310 315 320
 Arg Tyr Phe Gly Met Arg Ala Leu Trp Asn Ile Trp Ile Leu Gln Thr
 325 330 335
 Ala Gly Gly Ala Phe Cys Ile Trp Leu Gly Arg Ala Ser Ala Leu Pro
 340 345 350
 Ala Ser Val Thr Ala Met Val Leu Phe Ser Ile Cys Ala Gln Ala Ala
 355 360 365
 Cys Gly Ala Ile Phe Gly Val Ala Pro Phe Val Ser Arg Arg Ser Leu
 370 375 380
 Gly Ile Ile Ser Gly Leu Thr Gly Ala Gly Gly Asn Val Gly Ala Gly
 385 390 395 400
 Leu Thr Gln Leu Leu Phe Phe Thr Ser Ser Gln Tyr Ser Thr Gly Arg
 405 410 415
 Gly Leu Glu Tyr Met Gly Ile Met Ile Met Ala Cys Thr Leu Pro Val
 420 425 430
 Ala Leu Val His Phe Pro Gln Trp Gly Ser Met Phe Phe Pro Ala Ser
 435 440 445
 Ala Asp Ala Thr Glu Glu Glu Tyr Tyr Ala Ser Glu Trp Ser Glu Glu
 450 455 460
 Glu Lys Gly Lys Gly Leu His Ile Ala Gly Gln Lys Phe Ala Glu Asn
 465 470 475 480
 Ser Arg Ser Glu Arg Gly Arg Arg Asn Val Ile Phe Ala Thr Ser Ala

PF59082SeqList_PF59082.txt

485 490 495
Thr Pro Pro Asn Asn Thr Pro Gln Gln Val
500 505

<210> 1524
<211> 1704
<212> DNA
<213> Hordeum vulgare

<220>
<221> CDS
<222> (95)..(1618)

<400> 1524
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gctaggctag ctcgatccag ctagctcagt agat atg gag gtg gag gcc gga gct 115
Met Glu Val Glu Ala Gly Ala

cat ggc gat gcg gcg gcg agc aag ttc acg ctg ccc gtg gac tcc gag 163
His Gly Asp Ala Ala Ala Ser Lys Phe Thr Leu Pro Val Asp Ser Glu
10 15 20

cac aag gcc aag tcc ttc agg ctc ttc tcc ttc gcc aac ccg cac atg 211
His Lys Ala Lys Ser Phe Arg Leu Phe Ser Phe Ala Asn Pro His Met
25 30 35

cgc acc ttc cac ctc tcg tgg atc tcc ttc ttc acc tgc ttc gtc tcc 259
Arg Thr Phe His Leu Ser Trp Ile Ser Phe Phe Thr Cys Phe Val Ser
40 45 50 55

acc ttt gcc gct gct ccg ttg gtg ccc atc atc cgc gac aac ctc aac 307
Thr Phe Ala Ala Ala Pro Leu Val Pro Ile Ile Arg Asp Asn Leu Asn
60 65 70

ctc gcc aag gcc gac atc ggc aat gcc ggt gtg gcg tcc gtg tcc ggc 355
Leu Ala Lys Ala Asp Ile Gly Asn Ala Gly Val Ala Ser Val Ser Gly
75 80 85

tcc atc ttc tcg agg ctc gcc atg ggc gcc att tgt gac ctg ctt ggc 403
Ser Ile Phe Ser Arg Leu Ala Met Gly Ala Ile Cys Asp Leu Leu Gly
90 95 100

ccg cgg tac ggt tgt gcc ttt ctc gtc atg cta tcg gcg cca acc gtc 451
Pro Arg Tyr Gly Cys Ala Phe Leu Val Met Leu Ser Ala Pro Thr Val
105 110 115

ttc tgc atg gcc gtc atc gac gac gcg tcg gga tac atc gca gtc cgc 499
Phe Cys Met Ala Val Ile Asp Asp Ala Ser Gly Tyr Ile Ala Val Arg
120 125 130 135

ttc ctc atc ggc ttc tcc ctc gca acc ttc gtg tca tgc cag tac tgg 547
Phe Leu Ile Gly Phe Ser Leu Ala Thr Phe Val Ser Cys Gln Tyr Trp
140 145 150

atg agc aca atg ttc aac agt aaa atc atc ggc acg gtt aat ggc ctc 595
Met Ser Thr Met Phe Asn Ser Lys Ile Ile Gly Thr Val Asn Gly Leu
155 160 165

gca gcc ggg tgg ggc aac atg ggt ggc ggg gcc aca cag ctc atc atg 643
Ala Ala Gly Trp Gly Asn Met Gly Gly Gly Ala Thr Gln Leu Ile Met
170 175 180

ccc ctc gtc ttc cat gcc atc caa aag tgt ggt gcc aca ccc ttt gtg 691
Pro Leu Val Phe His Ala Ile Gln Lys Cys Gly Ala Thr Pro Phe Val
185 190 195

gca tgg cgt atc gcc tac ttc gtg ccg ggg atg atg cac atc gtg atg 739
Ala Trp Arg Ile Ala Tyr Phe Val Pro Gly Met Met His Ile Val Met
200 205 210 215

ggc cta ctc gtg ctc acc atg gga caa gac ctc cct gat ggg aac ctc 787
Gly Leu Leu Val Leu Thr Met Gly Gln Asp Leu Pro Asp Gly Asn Leu
220 225 230

gca agc ctg cag aag aag gga gac atg gcc aag gac aag ttc tcc aag 835
Ala Ser Leu Gln Lys Lys Gly Asp Met Ala Lys Asp Lys Phe Ser Lys
235 240 245

gtc ctt tgg ggc gcc gtt acc aac tac cgg aca tgg atc ttt gtc ctc 883
Val Leu Trp Gly Ala Val Thr Asn Tyr Arg Thr Trp Ile Phe Val Leu
250 255 260

ctc tat ggc tac tgc atg ggt gtc gag ctc acc act ggc aat gtc att 931

PF59082SeqList_PF59082.txt

Leu	Tyr	Gly	Tyr	Cys	Met	Gly	Val	Glu	Leu	Thr	Thr	Gly	Asn	Val	Ile	
265						270					275					
gcc	gag	tac	tac	ttc	gat	cac	ttc	cac	cta	aac	ctc	cgt	gcc	gcc	ggt	979
Ala	Glu	Tyr	Tyr	Phe	Asp	His	Phe	His	Leu	Asn	Leu	Arg	Ala	Ala	Gly	
280					285					290					295	
acc	atc	gcc	gct	tgc	ttc	ggc	atg	gcc	aac	atc	gtc	gca	cgt	cct	atg	1027
Thr	Ile	Ala	Ala	Cys	Phe	Gly	Met	Ala	Asn	Ile	Val	Ala	Arg	Pro	Met	
				300					305					310		
ggc	ggc	tac	ctc	tcc	gac	ctt	ggt	gct	cgc	tac	ttc	ggt	atg	cgt	gct	1075
Gly	Gly	Tyr	Leu	Ser	Asp	Leu	Gly	Ala	Arg	Tyr	Phe	Gly	Met	Arg	Ala	
			315					320					325			
cgc	ctt	tgg	aac	atc	tgg	atc	ctt	cag	aca	gct	ggc	ggc	gcc	ttt	tgc	1123
Arg	Leu	Trp	Asn	Ile	Trp	Ile	Leu	Gln	Thr	Ala	Gly	Gly	Ala	Phe	Cys	
		330				335						340				
atc	tgg	ctt	ggg	cgc	gcc	tcg	gcc	ctc	ccc	gcc	tca	gtg	act	gcc	atg	1171
Ile	Trp	Leu	Gly	Arg	Ala	Ser	Ala	Leu	Pro	Ala	Ser	Val	Thr	Ala	Met	
	345					350					355					
gtc	ctc	ttc	tcc	atc	tgc	gcc	cag	gct	gcg	tgt	ggt	gct	atc	ttt	ggt	1219
Val	Leu	Phe	Ser	Ile	Cys	Ala	Gln	Ala	Ala	Cys	Gly	Ala	Ile	Phe	Gly	
360					365					370					375	
gtc	gaa	ccc	ttc	gtc	tcc	agg	cgt	tcc	ctt	ggc	atc	att	tcc	ggg	ttg	1267
Val	Glu	Pro	Phe	Val	Ser	Arg	Arg	Ser	Leu	Gly	Ile	Ile	Ser	Gly	Leu	
				380				385						390		
acc	ggt	gct	ggt	gga	aac	gtg	ggc	gca	ggg	ctc	aca	cag	ctt	ctc	ttc	1315
Thr	Gly	Ala	Gly	Gly	Asn	Val	Gly	Ala	Gly	Leu	Thr	Gln	Leu	Leu	Phe	
			395					400					405			
ttc	act	tcg	tcg	caa	tac	tcc	act	ggc	agg	ggt	ctt	gag	tac	atg	ggc	1363
Phe	Thr	Ser	Ser	Gln	Tyr	Ser	Thr	Gly	Arg	Gly	Leu	Glu	Tyr	Met	Gly	
		410				415						420				
atc	atg	atc	atg	gca	tgc	acc	tta	ccc	gtc	gct	ctc	gtt	cac	ttc	cct	1411
Ile	Met	Ile	Met	Ala	Cys	Thr	Leu	Pro	Val	Ala	Leu	Val	His	Phe	Pro	
	425					430					435					
cag	tgg	ggc	tct	atg	ttc	ttg	gct	gcc	agt	gcc	gac	gcc	acg	gag	gag	1459
Gln	Trp	Gly	Ser	Met	Phe	Leu	Ala	Ala	Ser	Ala	Asp	Ala	Thr	Glu	Glu	
440					445					450					455	
gag	tac	tac	gcc	tca	gag	tgg	tca	gag	gag	gag	aag	agc	aag	ggt	ctc	1507
Glu	Tyr	Tyr	Ala	Ser	Glu	Trp	Ser	Glu	Glu	Glu	Lys	Ser	Lys	Gly	Leu	
			460					465						470		
cat	atc	gca	gga	caa	aag	ttt	gct	gag	aac	tcc	cgc	tcg	gaa	cgc	ggc	1555
His	Ile	Ala	Gly	Gln	Lys	Phe	Ala	Glu	Asn	Ser	Arg	Ser	Glu	Arg	Gly	
			475					480					485			
agg	cgc	aac	gtc	atc	ctt	gcc	aca	tcc	gcc	aca	cca	ccc	aac	aac	acg	1603
Arg	Arg	Asn	Val	Ile	Leu	Ala	Thr	Ser	Ala	Thr	Pro	Pro	Asn	Asn	Thr	
		490				495						500				
ccc	cta	cac	gta	taagtttcaa	attttgtgtt	acacaagaaa	tgtacatctt									1655
Pro	Leu	His	Val													
	505															
gctgagtata	tatacacatc	gtatatTTTta	gtaaaaaaaa	aaaaaaaaa												1704

<210> 1525
 <211> 507
 <212> PRT
 <213> Hordeum vulgare

<400> 1525
 Met Glu Val Glu Ala Gly Ala His Gly Asp Ala Ala Ala Ser Lys Phe
 1 5 10 15
 Thr Leu Pro Val Asp Ser Glu His Lys Ala Lys Ser Phe Arg Leu Phe
 20 25 30
 Ser Phe Ala Asn Pro His Met Arg Thr Phe His Leu Ser Trp Ile Ser
 35 40 45
 Phe Phe Thr Cys Phe Val Ser Thr Phe Ala Ala Ala Pro Leu Val Pro
 50 55 60
 Ile Ile Arg Asp Asn Leu Asn Leu Ala Lys Ala Asp Ile Gly Asn Ala
 65 70 75 80
 Gly Val Ala Ser Val Ser Gly Ser Ile Phe Ser Arg Leu Ala Met Gly
 85 90 95

PF59082SeqList_PF59082.txt

Ala Ile Cys Asp Leu Leu Gly Pro Arg Tyr Gly Cys Ala Phe Leu Val
 100 105 110
 Met Leu Ser Ala Pro Thr Val Phe Cys Met Ala Val Ile Asp Asp Ala
 115 120 125
 Ser Gly Tyr Ile Ala Val Arg Phe Leu Ile Gly Phe Ser Leu Ala Thr
 130 135 140
 Phe Val Ser Cys Gln Tyr Trp Met Ser Thr Met Phe Asn Ser Lys Ile
 145 150 155 160
 Ile Gly Thr Val Asn Gly Leu Ala Ala Gly Trp Gly Asn Met Gly Gly
 165 170 175
 Gly Ala Thr Gln Leu Ile Met Pro Leu Val Phe His Ala Ile Gln Lys
 180 185 190
 Cys Gly Ala Thr Pro Phe Val Ala Trp Arg Ile Ala Tyr Phe Val Pro
 195 200 205
 Gly Met Met His Ile Val Met Gly Leu Leu Val Leu Thr Met Gly Gln
 210 215 220
 Asp Leu Pro Asp Gly Asn Leu Ala Ser Leu Gln Lys Lys Gly Asp Met
 225 230 235 240
 Ala Lys Asp Lys Phe Ser Lys Val Leu Trp Gly Ala Val Thr Asn Tyr
 245 250 255
 Arg Thr Trp Ile Phe Val Leu Leu Tyr Gly Tyr Cys Met Gly Val Glu
 260 265 270
 Leu Thr Thr Gly Asn Val Ile Ala Glu Tyr Tyr Phe Asp His Phe His
 275 280 285
 Leu Asn Leu Arg Ala Ala Gly Thr Ile Ala Ala Cys Phe Gly Met Ala
 290 295 300
 Asn Ile Val Ala Arg Pro Met Gly Gly Tyr Leu Ser Asp Leu Gly Ala
 305 310 315 320
 Arg Tyr Phe Gly Met Arg Ala Arg Leu Trp Asn Ile Trp Ile Leu Gln
 325 330 335
 Thr Ala Gly Gly Ala Phe Cys Ile Trp Leu Gly Arg Ala Ser Ala Leu
 340 345 350
 Pro Ala Ser Val Thr Ala Met Val Leu Phe Ser Ile Cys Ala Gln Ala
 355 360 365
 Ala Cys Gly Ala Ile Phe Gly Val Glu Pro Phe Val Ser Arg Arg Ser
 370 375 380
 Leu Gly Ile Ile Ser Gly Leu Thr Gly Ala Gly Gly Asn Val Gly Ala
 385 390 395 400
 Gly Leu Thr Gln Leu Phe Phe Thr Ser Gln Tyr Ser Thr Gly
 405 410 415
 Arg Gly Leu Glu Tyr Met Gly Ile Met Ile Met Ala Cys Thr Leu Pro
 420 425 430
 Val Ala Leu Val His Phe Pro Gln Trp Gly Ser Met Phe Leu Ala Ala
 435 440 445
 Ser Ala Asp Ala Thr Glu Glu Tyr Tyr Ala Ser Glu Trp Ser Glu
 450 455 460
 Glu Glu Lys Ser Lys Gly Leu His Ile Ala Gly Gln Lys Phe Ala Glu
 465 470 475 480
 Asn Ser Arg Ser Glu Arg Gly Arg Arg Asn Val Ile Leu Ala Thr Ser
 485 490 495
 Ala Thr Pro Pro Asn Asn Thr Pro Leu His Val
 500 505

<210> 1526
 <211> 1593
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (1)..(1593)

<400> 1526
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 Met Ala Asp Ile Glu Gly Ser Pro Gly Ser Met His Gly Val Thr
 1 5 10 15
 gga agg gaa caa acc ttc ata gcc tca gtg gct tcc cct atg gtc cct
 Gly Arg Glu Gln Thr Phe Ile Ala Ser Val Ala Ser Pro Met Val Pro
 20 25 30

48

96

PF59082SeqList_PF59082.txt

aca	gac	acc	aca	gca	aat	ttc	gct	ttg	cca	gta	gat	tct	gag	cac	aag	144
Thr	Asp	Thr	Thr	Ala	Asn	Phe	Ala	Leu	Pro	Val	Asp	Ser	Glu	His	Lys	
		35					40					45				
gca	aaa	att	ttc	aag	ctt	ttt	tcc	tta	gcc	aac	cct	cac	atg	aga	acc	192
Ala	Lys	Ile	Phe	Lys	Leu	Phe	Ser	Leu	Ala	Asn	Pro	His	Met	Arg	Thr	
	50					55					60					
ttc	cac	ttg	tct	tgg	ata	tcc	ttc	ttc	act	tgc	ttt	gtc	tcg	acc	ttc	240
Phe	His	Leu	Ser	Trp	Ile	Ser	Phe	Phe	Thr	Cys	Phe	Val	Ser	Thr	Phe	
65					70					75					80	
gcg	gcg	gcg	cca	ctt	gtc	ccc	atc	att	cgc	gac	aac	ctt	aac	ctc	acc	288
Ala	Ala	Ala	Pro	Leu	Val	Pro	Ile	Ile	Arg	Asp	Asn	Leu	Asn	Leu	Thr	
				85					90					95		
aaa	ggc	gac	atc	ggg	aac	gcc	ggc	gtt	gcc	tct	gtc	tcc	ggc	agc	atc	336
Lys	Gly	Asp	Ile	Gly	Asn	Ala	Gly	Val	Ala	Ser	Val	Ser	Gly	Ser	Ile	
			100					105					110			
ttc	tcc	agg	ctc	aca	atg	ggc	gcg	gtt	gac	cta	ctt	gga	ccg	cgt		384
Phe	Ser	Arg	Leu	Thr	Met	Gly	Ala	Val	Cys	Asp	Leu	Leu	Gly	Pro	Arg	
		115					120					125				
tac	ggc	tgt	gcc	ttc	ctc	atc	atg	ctc	tct	gca	cca	acc	gtg	ttc	tgc	432
Tyr	Gly	Cys	Ala	Phe	Leu	Ile	Met	Leu	Ser	Ala	Pro	Thr	Val	Phe	Cys	
	130					135					140					
atg	tct	ttt	gtg	aat	gat	gct	gct	ggc	tac	ata	gca	gtg	agg	ttc	atg	480
Met	Ser	Phe	Val	Asn	Asp	Ala	Ala	Gly	Tyr	Ile	Ala	Val	Arg	Phe	Met	
145					150					155					160	
ata	ggg	ttt	tcg	ttg	gcc	act	ttt	gtt	tca	tgc	cag	tat	tgg	atg	agt	528
Ile	Gly	Phe	Ser	Leu	Ala	Thr	Phe	Val	Ser	Cys	Gln	Tyr	Trp	Met	Ser	
				165					170					175		
act	atg	ttt	aat	agt	aag	att	ata	ggg	ctt	gtg	aat	ggg	act	gct	gca	576
Thr	Met	Phe	Asn	Ser	Lys	Ile	Ile	Gly	Leu	Val	Asn	Gly	Thr	Ala	Ala	
			180					185					190			
ggg	tgg	ggg	aac	atg	ggt	ggt	ggg	gcc	act	cag	ctc	ata	atg	cct	atg	624
Gly	Trp	Gly	Asn	Met	Gly	Gly	Gly	Ala	Thr	Gln	Leu	Ile	Met	Pro	Met	
		195					200					205				
gtt	tat	gag	ttg	att	aga	aga	gct	ggg	gct	act	ccc	ttt	acg	gct	tgg	672
Val	Tyr	Glu	Leu	Ile	Arg	Arg	Ala	Gly	Ala	Thr	Pro	Phe	Thr	Ala	Trp	
	210					215					220					
agg	att	gct	ttc	ttc	gtc	cct	ggc	tgg	atg	cat	gtg	gtc	atg	ggg	atc	720
Arg	Ile	Ala	Phe	Phe	Val	Pro	Gly	Trp	Met	His	Val	Val	Met	Gly	Ile	
225					230					235					240	
ttg	gtc	cta	acc	cta	ggc	caa	gat	tta	cct	gat	gga	aac	ctt	ggc	gcc	768
Leu	Val	Leu	Thr	Leu	Gly	Gln	Asp	Leu	Pro	Asp	Gly	Asn	Leu	Gly	Ala	
				245					250					255		
ttg	cag	aag	aag	ggt	aat	gtt	gcc	aaa	gac	aaa	ttc	tcc	aag	gtg	cta	816
Leu	Gln	Lys	Lys	Gly	Asn	Val	Ala	Lys	Asp	Lys	Phe	Ser	Lys	Val	Leu	
		260						265					270			
tgg	tat	gcc	ata	aca	aat	tac	agg	aca	tgg	gtt	ttt	gcc	ctc	cta	tat	864
Trp	Tyr	Ala	Ile	Thr	Asn	Tyr	Arg	Thr	Trp	Val	Phe	Ala	Leu	Leu	Tyr	
		275					280					285				
ggg	tac	tcg	atg	gga	gtt	gaa	tta	acc	act	gac	aat	gtc	att	gct	gag	912
Gly	Tyr	Ser	Met	Gly	Val	Glu	Leu	Thr	Thr	Asp	Asn	Val	Ile	Ala	Glu	
	290					295					300					
tat	ttc	tat	gac	agg	ttt	aat	ctc	aag	cta	cac	act	gct	gga	atc	att	960
Tyr	Phe	Tyr	Asp	Arg	Phe	Asn	Leu	Lys	Leu	His	Thr	Ala	Gly	Ile	Ile	
305					310					315					320	
gct	gct	tca	ttt	gga	atg	gca	aat	ctc	cta	gct	cgt	ccc	ttt	ggc	gga	1008
Ala	Ala	Ser	Phe	Gly	Met	Ala	Asn	Leu	Leu	Ala	Arg	Pro	Phe	Gly	Gly	
				325					330					335		
tac	act	tct	gat	gtt	gca	gcc	agg	ttg	ttt	ggc	atg	agg	ggc	agg	ctt	1056
Tyr	Thr	Ser	Asp	Val	Ala	Ala	Arg	Leu	Phe	Gly	Met	Arg	Gly	Arg	Leu	
			340					345					350			
tgg	aac	ctg	tgg	atc	ctc	caa	acc	cta	gga	ggc	gtt	ttc	tgc	ata	tgg	1104
Trp	Asn	Leu	Trp	Ile	Leu	Gln	Thr	Leu	Gly	Gly	Val	Phe	Cys	Ile	Trp	
		355					360					365				
ctt	ggg	cgt	gcc	aat	tcc	ctt	ccc	att	gca	gtc	ttg	gcc	atg	atc	ctc	1152
Leu	Gly	Arg	Ala	Asn	Ser	Leu	Pro	Ile	Ala	Val	Leu	Ala	Met	Ile	Leu	
	370					375					380					
ttc	tcc	att	ggc	gct	caa	gct	gca	tgc	ggc	gca	act	ttt	ggc	atc	att	1200
Phe	Ser	Ile	Gly	Ala	Gln	Ala	Ala	Cys	Gly	Ala	Thr	Phe	Gly	Ile	Ile	
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Pro	Phe	Ile	Ser	Arg	Arg	Ser	Leu	Gly	Ile	Ile	Ser	Gly	Leu	Thr	Gly	
				405				410						415		
gca	ggt	gga	aac	ttt	ggt	tct	ggt	ttg	acc	caa	ttg	atc	ttc	ttt	tca	1296
Ala	Gly	Gly	Asn	Phe	Gly	Ser	Gly	Leu	Thr	Gln	Leu	Ile	Phe	Phe	Ser	
			420					425					430			
acc	tca	agg	ttt	tct	act	tcc	act	ggt	ctc	tcc	ctt	atg	ggt	gtc	atg	1344
Thr	Ser	Arg	Phe	Ser	Thr	Ser	Thr	Gly	Leu	Ser	Leu	Met	Gly	Val	Met	
		435				440					445					
att	gtg	tgt	tgc	act	ctt	cct	gtg	act	ctt	gtt	cac	ttc	cct	cag	tgg	1392
Ile	Val	Cys	Cys	Thr	Leu	Pro	Val	Thr	Leu	Val	His	Phe	Pro	Gln	Trp	
	450					455					460					
ggt	agc	atg	ttc	ctc	cct	cct	tca	aag	gat	gtc	aac	aag	tcc	act	gag	1440
Gly	Ser	Met	Phe	Leu	Pro	Pro	Ser	Lys	Asp	Val	Asn	Lys	Ser	Thr	Glu	
465					470					475					480	
gaa	tac	tat	tac	acc	gct	gag	tgg	aac	gag	gaa	gag	aag	caa	aaa	ggg	1488
Glu	Tyr	Tyr	Tyr	Thr	Ala	Glu	Trp	Asn	Glu	Glu	Glu	Lys	Gln	Lys	Gly	
				485				490						495		
ttg	cac	cag	aat	agt	ctc	aag	ttt	gct	gag	aat	agc	cgt	tca	gag	aga	1536
Leu	His	Gln	Asn	Ser	Leu	Lys	Phe	Ala	Glu	Asn	Ser	Arg	Ser	Glu	Arg	
			500					505					510			
ggt	aag	cgt	gtg	gcc	tca	gca	cca	aca	cca	cca	aac	aca	act	cca	act	1584
Gly	Lys	Arg	Val	Ala	Ser	Ala	Pro	Thr	Pro	Pro	Asn	Thr	Thr	Pro	Thr	
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cat	gcc	tag														1593
His	Ala															
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<400> 1527

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			20					25					30			
Thr	Asp	Thr	Thr	Ala	Asn	Phe	Ala	Leu	Pro	Val	Asp	Ser	Glu	His	Lys	
		35					40					45				
Ala	Lys	Ile	Phe	Lys	Leu	Phe	Ser	Leu	Ala	Asn	Pro	His	Met	Arg	Thr	
	50					55				60						
Phe	His	Leu	Ser	Trp	Ile	Ser	Phe	Phe	Thr	Cys	Phe	Val	Ser	Thr	Phe	
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Ala	Ala	Ala	Pro	Leu	Val	Pro	Ile	Ile	Arg	Asp	Asn	Leu	Asn	Leu	Thr	
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Lys	Gly	Asp	Ile	Gly	Asn	Ala	Gly	Val	Ala	Ser	Val	Ser	Gly	Ser	Ile	
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Phe	Ser	Arg	Leu	Thr	Met	Gly	Ala	Val	Cys	Asp	Leu	Leu	Gly	Pro	Arg	
		115				120						125				
Tyr	Gly	Cys	Ala	Phe	Leu	Ile	Met	Leu	Ser	Ala	Pro	Thr	Val	Phe	Cys	
	130				135					140						
Met	Ser	Phe	Val	Asn	Asp	Ala	Ala	Gly	Tyr	Ile	Ala	Val	Arg	Phe	Met	
145					150					155					160	
Ile	Gly	Phe	Ser	Leu	Ala	Thr	Phe	Val	Ser	Cys	Gln	Tyr	Trp	Met	Ser	
			165						170					175		
Thr	Met	Phe	Asn	Ser	Lys	Ile	Ile	Gly	Leu	Val	Asn	Gly	Thr	Ala	Ala	
			180					185					190			
Gly	Trp	Gly	Asn	Met	Gly	Gly	Gly	Ala	Thr	Gln	Leu	Ile	Met	Pro	Met	
		195				200						205				
Val	Tyr	Glu	Leu	Ile	Arg	Arg	Ala	Gly	Ala	Thr	Pro	Phe	Thr	Ala	Trp	
	210					215					220					
Arg	Ile	Ala	Phe	Phe	Val	Pro	Gly	Trp	Met	His	Val	Val	Met	Gly	Ile	
225					230					235					240	
Leu	Val	Leu	Thr	Leu	Gly	Gln	Asp	Leu	Pro	Asp	Gly	Asn	Leu	Gly	Ala	
				245					250					255		
Leu	Gln	Lys	Lys	Gly	Asn	Val	Ala	Lys	Asp	Lys	Phe	Ser	Lys	Val	Leu	
		260						265					270			
Trp	Tyr	Ala	Ile	Thr	Asn	Tyr	Arg	Thr	Trp	Val	Phe	Ala	Leu	Leu	Tyr	

PF59082SeqList_PF59082.txt

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 290 285
 Tyr Phe Tyr Asp Arg Phe Asn Leu Lys Leu His Thr Ala Gly Ile Ile
 305 315
 Ala Ala Ser Phe Gly Met Ala Asn Leu Leu Ala Arg Pro Phe Gly Gly
 325 335
 Tyr Thr Ser Asp Val Ala Ala Arg Leu Phe Gly Met Arg Gly Arg Leu
 340 350
 Trp Asn Leu Trp Ile Leu Gln Thr Leu Gly Gly Val Phe Cys Ile Trp
 355 365
 Leu Gly Arg Ala Asn Ser Leu Pro Ile Ala Val Leu Ala Met Ile Leu
 370 380
 Phe Ser Ile Gly Ala Gln Ala Ala Cys Gly Ala Thr Phe Gly Ile Ile
 385 395
 Pro Phe Ile Ser Arg Arg Ser Leu Gly Ile Ile Ser Gly Leu Thr Gly
 405 415
 Ala Gly Gly Asn Phe Gly Ser Gly Leu Thr Gln Leu Ile Phe Phe Ser
 420 430
 Thr Ser Arg Phe Ser Thr Ser Thr Gly Leu Ser Leu Met Gly Val Met
 435 445
 Ile Val Cys Cys Thr Leu Pro Val Thr Leu Val His Phe Pro Gln Trp
 450 460
 Gly Ser Met Phe Leu Pro Pro Ser Lys Asp Val Asn Lys Ser Thr Glu
 465 475
 Glu Tyr Tyr Tyr Thr Ala Glu Trp Asn Glu Glu Lys Gln Lys Gly
 485 495
 Leu His Gln Asn Ser Leu Lys Phe Ala Glu Asn Ser Arg Ser Glu Arg
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 Gly Lys Arg Val Ala Ser Ala Pro Thr Pro Pro Asn Thr Thr Pro Thr
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 His Ala
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 Gly Arg Glu Gln Thr Phe Val Ala Ser Val Ala Ser Pro Ile Val Pro
 20 25 30
 aca gac acc aca gcc aaa ttt gct ctc cca gtg gat tca gaa cac aag 144
 Thr Asp Thr Thr Ala Lys Phe Ala Leu Pro Val Asp Ser Glu His Lys
 35 40 45
 gcc aag gtt ttc aaa ctc ttc tcc ctg gcc aat ccc cac atg aga acc 192
 Ala Lys Val Phe Lys Leu Phe Ser Leu Ala Asn Pro His Met Arg Thr
 50 55 60
 ttc cac ctt tct tgg atc tcc ttc ttc acc tgc ttc gtc tcg aca ttc 240
 Phe His Leu Ser Trp Ile Ser Phe Phe Thr Cys Phe Val Ser Thr Phe
 65 70 75 80
 gca gca gca cct ctt gtg ccc atc atc cgc gac aac ctt aac ctc acc 288
 Ala Ala Ala Pro Leu Val Pro Ile Ile Arg Asp Asn Leu Asn Leu Thr
 85 90 95
 aaa agc gac att gga aac gcc ggg gtt gct tct gtc tcc gga agc atc 336
 Lys Ser Asp Ile Gly Asn Ala Gly Val Ala Ser Val Ser Gly Ser Ile
 100 105 110
 ttc tca agg ctc gca atg ggt gca gtc tgt gac atg ttg ggt cca cgc 384
 Phe Ser Arg Leu Ala Met Gly Ala Val Cys Asp Met Leu Gly Pro Arg
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 tat ggc tgc gcc ttc ctc atc atg ctt tcg gcc cct acg gtg ttc tgc 432

PF59082SeqList_PF59082.txt

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Met	Ser	Phe	Val	Lys	Asp	Ala	Ala	Gly	Tyr	Ile	Ala	Val	Arg	Phe	Leu	
145					150					155					160	
att	ggg	ttc	tcg	ttg	gcg	acg	ttt	gtg	tcg	tgc	cag	tac	tgg	atg	agc	528
Ile	Gly	Phe	Ser	Leu	Ala	Thr	Phe	Val	Ser	Cys	Gln	Tyr	Trp	Met	Ser	
				165				170						175		
acg	atg	ttc	aac	agt	aag	att	ata	ggg	ctt	gcg	aat	ggg	act	gct	gcg	576
Thr	Met	Phe	Asn	Ser	Lys	Ile	Ile	Gly	Leu	Ala	Asn	Gly	Thr	Ala	Ala	
			180					185					190			
ggg	tgg	ggg	aac	atg	ggt	ggt	gga	gcc	act	cag	ctc	ata	atg	cct	ttg	624
Gly	Trp	Gly	Asn	Met	Gly	Gly	Gly	Ala	Thr	Gln	Leu	Ile	Met	Pro	Leu	
		195				200						205				
gtg	tat	gag	ctt	atc	aga	aga	gct	ggg	gct	act	ccc	ttc	act	gct	tgg	672
Val	Tyr	Glu	Leu	Ile	Arg	Arg	Ala	Gly	Ala	Thr	Pro	Phe	Thr	Ala	Trp	
	210				215						220					
agg	att	gcc	ttc	ttt	gtt	ccg	ggt	ttc	atg	cat	gtc	atc	atg	ggg	att	720
Arg	Ile	Ala	Phe	Phe	Val	Pro	Gly	Phe	Met	His	Val	Ile	Met	Gly	Ile	
225					230					235					240	
ctt	gtc	ctc	act	cta	ggc	cag	gac	ttg	cct	gat	gga	aac	ctc	ggg	gcc	768
Leu	Val	Leu	Thr	Leu	Gly	Gln	Asp	Leu	Pro	Asp	Gly	Asn	Leu	Gly	Ala	
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Leu	Arg	Lys	Lys	Gly	Asp	Val	Ala	Lys	Asp	Lys	Phe	Ser	Lys	Val	Leu	
			260					265					270			
tgg	tat	gcc	ata	aca	aat	tac	agg	aca	tgg	att	ttt	gct	ctc	ctc	tat	864
Trp	Tyr	Ala	Ile	Thr	Asn	Tyr	Arg	Thr	Trp	Ile	Phe	Ala	Leu	Leu	Tyr	
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ggg	tac	tcc	atg	gga	gtt	gaa	tta	aca	act	gac	aat	gtc	att	gct	gag	912
Gly	Tyr	Ser	Met	Gly	Val	Glu	Leu	Thr	Thr	Asp	Asn	Val	Ile	Ala	Glu	
	290					295					300					
tat	ttc	tat	gac	aga	ttt	aat	ctc	aag	cta	cac	act	gct	gga	atc	att	960
Tyr	Phe	Tyr	Asp	Arg	Phe	Asn	Leu	Lys	Leu	His	Thr	Ala	Gly	Ile	Ile	
305					310					315					320	
gct	gct	tca	ttt	gga	atg	gca	aac	tta	gtt	gct	cga	cct	ttt	ggt	gga	1008
Ala	Ala	Ser	Phe	Gly	Met	Ala	Asn	Leu	Val	Ala	Arg	Pro	Phe	Gly	Gly	
				325				330						335		
tat	gct	tca	gat	gtt	gca	gcc	agg	ctg	ttt	ggc	atg	agg	gga	aga	ctc	1056
Tyr	Ala	Ser	Asp	Val	Ala	Ala	Arg	Phe	Gly	Met	Arg	Gly	Arg	Leu		
			340					345					350			
tgg	acc	ctt	tgg	atc	ctc	caa	acc	tta	gga	ggg	gtt	ttc	tgt	att	tgg	1104
Trp	Thr	Leu	Trp	Ile	Leu	Gln	Thr	Leu	Gly	Gly	Val	Phe	Cys	Ile	Trp	
		355				360						365				
ctt	ggc	cgt	gcc	aat	tct	ctt	cct	att	gct	gta	ttg	gcc	atg	atc	ctg	1152
Leu	Gly	Arg	Ala	Asn	Ser	Leu	Pro	Ile	Ala	Val	Leu	Ala	Met	Ile	Leu	
	370					375					380					
ttc	tct	ata	gga	gct	caa	gct	gca	tgt	ggt	gca	act	ttt	ggc	atc	att	1200
Phe	Ser	Ile	Gly	Ala	Gln	Ala	Ala	Cys	Gly	Ala	Thr	Phe	Gly	Ile	Ile	
385					390					395					400	
cct	ttc	atc	tca	aga	agg	tct	ttg	ggg	atc	ata	tca	ggt	cta	act	ggt	1248
Pro	Phe	Ile	Ser	Arg	Arg	Ser	Leu	Gly	Ile	Ile	Ser	Gly	Leu	Thr	Gly	
				405				410						415		
gca	ggt	gga	aac	ttt	ggg	tct	ggc	ctc	acc	caa	ttg	gtc	ttc	ttt	tca	1296
Ala	Gly	Gly	Asn	Phe	Gly	Ser	Gly	Leu	Thr	Gln	Leu	Val	Phe	Phe	Ser	
			420					425					430			
acc	tcc	aaa	ttc	tct	act	gcc	aca	ggt	ctc	tcc	ttg	atg	ggt	gta	atg	1344
Thr	Ser	Lys	Phe	Ser	Thr	Ala	Thr	Gly	Leu	Ser	Leu	Met	Gly	Val	Met	
		435				440						445				
ata	gtg	gct	tgc	act	cta	cca	gtg	agt	gtt	gtt	cac	ttc	cca	cag	tgg	1392
Ile	Val	Ala	Cys	Thr	Leu	Pro	Val	Ser	Val	Val	His	Phe	Pro	Gln	Trp	
	450					455					460					
ggt	agc	atg	ttt	cta	cca	ccc	tca	aaa	gat	gtc	agc	aaa	tcc	act	gaa	1440
Gly	Ser	Met	Phe	Leu	Pro	Pro	Ser	Lys	Asp	Val	Ser	Lys	Ser	Thr	Glu	
465					470					475					480	
gaa	ttc	tat	tac	acc	tct	gaa	tgg	aat	gag	gaa	gag	aag	cag	aag	ggt	1488
Glu	Phe	Tyr	Tyr	Thr	Ser	Glu	Trp	Asn	Glu	Glu	Glu	Lys	Gln	Lys	Gly	
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ttg	cac	cag	caa	agt	ctc	aaa	ttt	gct	gag	aat	agc	cga	tct	gag	aga	1536

PF59082SeqList_PF59082.txt

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Gly	Lys	Arg	Val	Ala	Ser	Ala	Pro	Thr	Pro	Pro	Asn	Ala	Thr	Pro	Thr		
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cat	gtc	tag															1593
His	Val																
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			20					25					30				
Thr	Asp	Thr	Thr	Ala	Lys	Phe	Ala	Leu	Pro	Val	Asp	Ser	Glu	His	Lys		
		35					40					45					
Ala	Lys	Val	Phe	Lys	Leu	Phe	Ser	Leu	Ala	Asn	Pro	His	Met	Arg	Thr		
	50					55					60						
Phe	His	Leu	Ser	Trp	Ile	Ser	Phe	Phe	Thr	Cys	Phe	Val	Ser	Thr	Phe		
65					70					75					80		
Ala	Ala	Ala	Pro	Leu	Val	Pro	Ile	Ile	Arg	Asp	Asn	Leu	Asn	Leu	Thr		
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Lys	Ser	Asp	Ile	Gly	Asn	Ala	Gly	Val	Ala	Ser	Val	Ser	Gly	Ser	Ile		
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Phe	Ser	Arg	Leu	Ala	Met	Gly	Ala	Val	Cys	Asp	Met	Leu	Gly	Pro	Arg		
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Tyr	Gly	Cys	Ala	Phe	Leu	Ile	Met	Leu	Ser	Ala	Pro	Thr	Val	Phe	Cys		
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Met	Ser	Phe	Val	Lys	Asp	Ala	Ala	Gly	Tyr	Ile	Ala	Val	Arg	Phe	Leu		
145					150					155					160		
Ile	Gly	Phe	Ser	Leu	Ala	Thr	Phe	Val	Ser	Cys	Gln	Tyr	Trp	Met	Ser		
				165					170					175			
Thr	Met	Phe	Asn	Ser	Lys	Ile	Ile	Gly	Leu	Ala	Asn	Gly	Thr	Ala	Ala		
			180					185					190				
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Val	Tyr	Glu	Leu	Ile	Arg	Arg	Ala	Gly	Ala	Thr	Pro	Phe	Thr	Ala	Trp		
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Leu	Val	Leu	Thr	Leu	Gly	Gln	Asp	Leu	Pro	Asp	Gly	Asn	Leu	Gly	Ala		
				245					250					255			
Leu	Arg	Lys	Lys	Gly	Asp	Val	Ala	Lys	Asp	Lys	Phe	Ser	Lys	Val	Leu		
			260					265					270				
Trp	Tyr	Ala	Ile	Thr	Asn	Tyr	Arg	Thr	Trp	Ile	Phe	Ala	Leu	Leu	Tyr		
		275					280					285					
Gly	Tyr	Ser	Met	Gly	Val	Glu	Leu	Thr	Thr	Asp	Asn	Val	Ile	Ala	Glu		
	290					295					300						
Tyr	Phe	Tyr	Asp	Arg	Phe	Asn	Leu	Lys	Leu	His	Thr	Ala	Gly	Ile	Ile		
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Ala	Ala	Ser	Phe	Gly	Met	Ala	Asn	Leu	Val	Ala	Arg	Pro	Phe	Gly	Gly		
				325					330					335			
Tyr	Ala	Ser	Asp	Val	Ala	Ala	Arg	Leu	Phe	Gly	Met	Arg	Gly	Arg	Leu		
			340					345					350				
Trp	Thr	Leu	Trp	Ile	Leu	Gln	Thr	Leu	Gly	Gly	Val	Phe	Cys	Ile	Trp		
		355					360					365					
Leu	Gly	Arg	Ala	Asn	Ser	Leu	Pro	Ile	Ala	Val	Leu	Ala	Met	Ile	Leu		
	370					375					380						
Phe	Ser	Ile	Gly	Ala	Gln	Ala	Ala	Cys	Gly	Ala	Thr	Phe	Gly	Ile	Ile		
385					390					395					400		
Pro	Phe	Ile	Ser	Arg	Arg	Ser	Leu	Gly	Ile	Ile	Ser	Gly	Leu	Thr	Gly		
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PF59082SeqList_PF59082.txt

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 465 470 475
 Glu Phe Tyr Tyr Thr Ser Glu Trp Asn Glu Glu Glu Lys Gln Lys Gly
 485 490 495
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 His Val
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Arg	Glu	Pro	Ala	Phe	Ala	Phe	Ser	Thr	Glu	His	Glu	Glu	Ala	Ala	Ser	
			20					25					30			
aat	ggc	ggc	aag	ttc	gac	ctg	ccg	gtg	gac	tcg	gag	cac	aag	gcg	aag	144
Asn	Gly	Gly	Lys	Phe	Asp	Leu	Pro	Val	Asp	Ser	Glu	His	Lys	Ala	Lys	
		35					40					45				
agc	gtc	cgg	ctc	ttc	tcc	gtg	gcg	aac	cca	cac	atg	cgc	acc	ttc	cac	192
Ser	Val	Arg	Leu	Phe	Ser	Val	Ala	Asn	Pro	His	Met	Arg	Thr	Phe	His	
	50					55					60					
ctc	tcc	tgg	atc	tcc	ttc	ttc	acc	tgc	ttc	gtg	tcc	acc	ttc	gcc	gcc	240
Leu	Ser	Trp	Ile	Ser	Phe	Phe	Thr	Cys	Phe	Val	Ser	Thr	Phe	Ala	Ala	
	65				70					75					80	
gcg	ccg	ctg	gtc	ccc	atc	atc	cg	gac	aac	ctc	aac	ctc	acc	aag	gcc	288
Ala	Pro	Leu	Val	Pro	Ile	Ile	Arg	Asp	Asn	Leu	Asn	Leu	Thr	Lys	Ala	
				85				90						95		
gac	atc	ggc	aac	gcg	ggc	gtg	gcc	tcc	gtg	tcg	ggc	tcc	atc	ttc	tcc	336
Asp	Ile	Gly	Asn	Ala	Gly	Val	Ala	Ser	Val	Ser	Gly	Ser	Ile	Phe	Ser	
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cgc	ctc	acc	atg	ggc	gcc	gtc	tgc	gac	ctg	ctg	ggc	ccg	cg	tac	ggc	384
Arg	Leu	Thr	Met	Gly	Ala	Val	Cys	Asp	Leu	Leu	Gly	Pro	Arg	Tyr	Gly	
		115					120					125				
tgc	gcc	ttc	ctc	atc	atg	ctg	tcc	gcg	ccc	acc	gtg	ttc	tgc	atg	tcg	432
Cys	Ala	Phe	Leu	Ile	Met	Leu	Ser	Ala	Pro	Thr	Val	Phe	Cys	Met	Ser	
	130					135					140					
ctc	atc	gac	gac	gcc	gcg	ggc	tac	atc	acc	gtc	agg	ttc	ctc	atc	ggc	480
Leu	Ile	Asp	Asp	Ala	Ala	Gly	Tyr	Ile	Thr	Val	Arg	Phe	Leu	Ile	Gly	
	145				150					155					160	
ttc	tcc	ctc	gcc	acc	ttc	gtc	tcc	tgc	cag	tac	tgg	atg	agc	acc	atg	528
Phe	Ser	Leu	Ala	Thr	Phe	Val	Ser	Cys	Gln	Tyr	Trp	Met	Ser	Thr	Met	
			165					170						175		
ttc	agc	agc	aag	atc	atc	ggc	acc	gtc	aac	ggg	ctc	gcc	gcc	gga	tgg	576
Phe	Ser	Ser	Lys	Ile	Ile	Gly	Thr	Val	Asn	Gly	Leu	Ala	Ala	Gly	Trp	
			180				185						190			
ggc	aac	atg	gga	ggc	ggc	gcc	acg	cag	ctc	atc	atg	ccg	ctc	gtc	tac	624
Gly	Asn	Met	Gly	Gly	Gly	Ala	Thr	Gln	Leu	Ile	Met	Pro	Leu	Val	Tyr	
		195				200						205				
gac	gtc	atc	cg	aag	tgc	ggc	gcc	acg	cca	ttc	acg	gcc	tgg	cg	ctc	672
Asp	Val	Ile	Arg	Lys	Cys	Gly	Ala	Thr	Pro	Phe	Thr	Ala	Trp	Arg	Leu	
	210					215					220					
gcc	tac	ttc	gtg	ccg	ggc	ctc	atg	cac	gtc	gtc	atg	ggc	gtc	ctg	gtg	720
Ala	Tyr	Phe	Val	Pro	Gly	Leu	Met	His	Val	Val	Met	Gly	Val	Leu	Val	

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	Leu	Thr	Leu	Gly	Gln	Asp	Leu	Pro	Asp	Gly	Asn	Leu	Arg	Ser	Leu	Gln	
				245						250					255		
aag	aag	ggc	aac	gtc	aac	aag	gac	agc	ttc	tcc	aag	gtc	atg	tgg	tac	816	
Lys	Lys	Gly	Asn	Val	Asn	Lys	Asp	Ser	Phe	Ser	Lys	Val	Met	Trp	Tyr		
			260					265					270				
gcc	gtc	atc	aac	tac	cgt	acc	tgg	atc	ttc	gtc	ctc	ctc	tac	ggc	tac	864	
Ala	Val	Ile	Asn	Tyr	Arg	Thr	Trp	Ile	Phe	Val	Leu	Leu	Tyr	Gly	Tyr		
		275					280					285					
tgc	atg	ggc	gtc	gag	ctc	acc	acc	gac	aac	gtc	atc	gcc	gag	tac	atg	912	
Cys	Met	Gly	Val	Glu	Leu	Thr	Thr	Asp	Asn	Val	Ile	Ala	Glu	Tyr	Met		
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tac	gac	cgc	ttc	gac	ctc	gac	ctc	cgc	gtc	gcc	ggg	acc	atc	gcc	gcc	960	
Tyr	Asp	Arg	Phe	Asp	Leu	Asp	Leu	Arg	Val	Ala	Gly	Thr	Ile	Ala	Ala		
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tgc	ttc	ggc	atg	gcc	aac	atc	gtc	gca	cgc	ccc	atg	ggc	ggc	atc	atg	1008	
Cys	Phe	Gly	Met	Ala	Asn	Ile	Val	Ala	Arg	Pro	Met	Gly	Gly	Ile	Met		
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Ser	Asp	Met	Gly	Ala	Arg	Tyr	Trp	Gly	Met	Arg	Ala	Arg	Leu	Trp	Asn		
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atc	tgg	atc	ctc	cag	acc	gcc	ggc	ggc	gcc	ttc	tgc	ctc	tgg	ctg	gga	1104	
Ile	Trp	Ile	Leu	Gln	Thr	Ala	Gly	Gly	Ala	Phe	Cys	Leu	Trp	Leu	Gly		
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cgc	gcc	agc	acc	ctc	ccc	gtc	tcc	gtc	gtc	gcc	atg	gtg	ctc	ttc	tcc	1152	
Arg	Ala	Ser	Thr	Leu	Pro	Val	Ser	Val	Val	Ala	Met	Val	Leu	Phe	Ser		
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Phe	Cys	Ala	Gln	Ala	Ala	Cys	Gly	Ala	Ile	Phe	Gly	Val	Ile	Pro	Phe		
385				390						395					400		
gtc	tcc	cgc	cgc	tcc	ctc	ggc	atc	atc	tcc	ggc	atg	acg	ggc	gcc	ggc	1248	
Val	Ser	Arg	Arg	Ser	Leu	Gly	Ile	Ile	Ser	Gly	Met	Thr	Gly	Ala	Gly		
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ggc	aac	ttc	ggc	ggc	ggg	ctc	acg	cag	ctg	ctc	ttc	ttt	acc	tcc	tcg	1296	
Gly	Asn	Phe	Gly	Ala	Gly	Leu	Thr	Gln	Leu	Leu	Phe	Phe	Thr	Ser	Ser		
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acc	tac	tcc	acg	ggc	agg	ggg	ctg	gag	tac	atg	ggc	atc	atg	atc	atg	1344	
Thr	Tyr	Ser	Thr	Gly	Arg	Gly	Leu	Glu	Tyr	Met	Gly	Ile	Met	Ile	Met		
		435					440					445					
gcg	tgc	acg	ctg	ccg	gtg	gtg	ttc	gtg	cac	ttc	ccg	cag	tgg	ggg	tcc	1392	
Ala	Cys	Thr	Leu	Pro	Val	Val	Phe	Val	His	Phe	Pro	Gln	Trp	Gly	Ser		
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atg	ttc	ttc	ccg	ccc	agc	gcc	acc	gcc	gac	gag	gag	ggc	tac	tac	gcc	1440	
Met	Phe	Phe	Pro	Pro	Ser	Ala	Thr	Ala	Asp	Glu	Glu	Gly	Tyr	Tyr	Ala		
465					470					475					480		
tcc	gag	tgg	aac	gac	gac	gag	aag	agc	aag	gga	ctc	cat	agc	gcc	agc	1488	
Ser	Glu	Trp	Asn	Asp	Asp	Glu	Lys	Ser	Lys	Gly	Leu	His	Ser	Ala	Ser		
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ctc	aag	ttc	gcc	gag	aac	agc	cgc	tca	gag	cgc	ggc	aag	cga	aac	gtc	1536	
Leu	Lys	Phe	Ala	Glu	Asn	Ser	Arg	Ser	Glu	Arg	Gly	Lys	Arg	Asn	Val		
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atc	cag	gcc	gac	gcc	gcc	gcc	acg	ccg	gag	cat	gtc	taa				1575	
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 <211> 524
 <212> PRT
 <213> Zea mays

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 Asn Gly Gly Lys Phe Asp Leu Pro Val Asp Ser Glu His Lys Ala Lys
 35 40 45
 Ser Val Arg Leu Phe Ser Val Ala Asn Pro His Met Arg Thr Phe His
 50 55 60
 Seite 1991

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50          55          60
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      85      90      95
Asp Ile Gly Asn Ala Gly Val Ala Ser Val Ser Gly Ser Ile Phe Ser
100      105      110
Arg Leu Thr Met Gly Ala Val Cys Asp Leu Leu Gly Pro Arg Tyr Gly
115      120      125
Cys Ala Phe Leu Ile Met Leu Ser Ala Pro Thr Val Phe Cys Met Ser
130      135      140
Leu Ile Asp Asp Ala Ala Gly Tyr Ile Thr Val Arg Phe Leu Ile Gly
145      150      155      160
Phe Ser Leu Ala Thr Phe Val Ser Cys Gln Tyr Trp Met Ser Thr Met
165      170      175
Phe Ser Ser Lys Ile Ile Gly Thr Val Asn Gly Leu Ala Ala Gly Trp
180      185      190
Gly Asn Met Gly Gly Gly Ala Thr Gln Leu Ile Met Pro Leu Val Tyr
195      200      205
Asp Val Ile Arg Lys Cys Gly Ala Thr Pro Phe Thr Ala Trp Arg Leu
210      215      220
Ala Tyr Phe Val Pro Gly Leu Met His Val Val Met Gly Val Leu Val
225      230      235      240
Leu Thr Leu Gly Gln Asp Leu Pro Asp Gly Asn Leu Arg Ser Leu Gln
245      250      255
Lys Lys Gly Asn Val Asn Lys Asp Ser Phe Ser Lys Val Met Trp Tyr
260      265      270
Ala Val Ile Asn Tyr Arg Thr Trp Ile Phe Val Leu Leu Tyr Gly Tyr
275      280      285
Cys Met Gly Val Glu Leu Thr Thr Asp Asn Val Ile Ala Glu Tyr Met
290      295      300
Tyr Asp Arg Phe Asp Leu Asp Leu Arg Val Ala Gly Thr Ile Ala Ala
305      310      315      320
Cys Phe Gly Met Ala Asn Ile Val Ala Arg Pro Met Gly Gly Ile Met
325      330      335
Ser Asp Met Gly Ala Arg Tyr Trp Gly Met Arg Ala Arg Leu Trp Asn
340      345      350
Ile Trp Ile Leu Gln Thr Ala Gly Gly Ala Phe Cys Leu Trp Leu Gly
355      360      365
Arg Ala Ser Thr Leu Pro Val Ser Val Val Ala Met Val Leu Phe Ser
370      375      380
Phe Cys Ala Gln Ala Ala Cys Gly Ala Ile Phe Gly Val Ile Pro Phe
385      390      395      400
Val Ser Arg Arg Ser Leu Gly Ile Ile Ser Gly Met Thr Gly Ala Gly
405      410      415
Gly Asn Phe Gly Ala Gly Leu Thr Gln Leu Leu Phe Phe Thr Ser Ser
420      425      430
Thr Tyr Ser Thr Gly Arg Gly Leu Glu Tyr Met Gly Ile Met Ile Met
435      440      445
Ala Cys Thr Leu Pro Val Val Phe Val His Phe Pro Gln Trp Gly Ser
450      455      460
Met Phe Phe Pro Pro Ser Ala Thr Ala Asp Glu Glu Gly Tyr Tyr Ala
465      470      475      480
Ser Glu Trp Asn Asp Asp Glu Lys Ser Lys Gly Leu His Ser Ala Ser
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500      505      510
Ile Gln Ala Asp Ala Ala Ala Thr Pro Glu His Val
515      520

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PF59082SeqList_PF59082.txt

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cgc gag ccg gcg ttc gcc ttc tcc acg gag cac gag gag gcg gcg agc      96
Arg Glu Pro Ala Phe Ala Phe Ser Thr Glu His Glu Glu Ala Ala Ser
20      25      30
aat ggc ggc aag ttc gac ctg ccg gtg gac tcg gag cac aag gcg aag      144
Asn Gly Gly Lys Phe Asp Leu Pro Val Asp Ser Glu His Lys Ala Lys
35      40      45
agc gtc ccg ctc ttc tcc gtg gcg aac cca cac atg cgc acc ttc cac      192
Ser Val Arg Leu Phe Ser Val Ala Asn Pro His Met Arg Thr Phe His
50      55      60
ctc tcc tgg atc tcc ttc ttc acc tgc ttc gtg tcc acc ttc gcc gcc      240
Leu Ser Trp Ile Ser Phe Phe Thr Cys Phe Val Ser Thr Phe Ala Ala
65      70      75
gcg ccg ctg gtc ccc atc atc cgc gac aac ctc aac ctc acc aag gcc      288
Ala Pro Leu Val Pro Ile Ile Arg Asp Asn Leu Asn Leu Thr Lys Ala
85      90      95
gac atc ggc aac gcg ggc gtg gcc tcc gtg tcg ggc tcc atc ttc tcc      336
Asp Ile Gly Asn Ala Gly Val Ala Ser Val Ser Gly Ser Ile Phe Ser
100      105      110
cgc ctc acc atg ggc gcc gtc tgc gac ctg ctg ggc ccg cgc tac ggc      384
Arg Leu Thr Met Gly Ala Val Cys Asp Leu Leu Gly Pro Arg Tyr Gly
115      120      125
tgc gcc ttc ctc atc atg ctg tcc gcg ccc acc gtg ttc tgc atg tcg      432
Cys Ala Phe Leu Ile Met Leu Ser Ala Pro Thr Val Phe Cys Met Ser
130      135      140
ctc atc gac gac gcc gcg ggc tac atc acc gtc agg ttc ctc atc ggc      480
Leu Ile Asp Asp Ala Gly Tyr Ile Thr Val Arg Phe Leu Ile Gly
145      150      155
ttc tcc ctc gcc acc ttc gtc tcc tgc cag tac tgg atg agc acc atg      528
Phe Ser Leu Ala Thr Phe Val Ser Cys Gln Tyr Trp Met Ser Thr Met
165      170      175
ttc agc agc aag atc atc ggc acc gtc ttc aac ggc ctc gcc gcc gga tgg      576
Phe Ser Ser Lys Ile Ile Gly Thr Val Asn Gly Leu Ala Ala Gly Trp
180      185      190
ggc aac atg gga ggc ggc gcc acg cag ctc atc atg ccg ctc gtc tac      624
Gly Asn Met Gly Gly Gly Ala Thr Gln Leu Ile Met Pro Leu Val Tyr
195      200      205
gac gtc atc cgc aag tgc ggc gcc acg cca ttc acg gcc tgg cgc ctc      672
Asp Val Ile Arg Lys Cys Gly Ala Thr Pro Phe Thr Ala Trp Arg Leu
210      215      220
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Ala Tyr Phe Val Pro Gly Leu Met His Val Val Met Gly Val Leu Val
225      230      235
ctc acg ctg ggc cag gac ctc ccc gac ggc aac ctc agg tcg ctg cag      768
Leu Thr Leu Gly Gln Asp Leu Pro Asp Gly Asn Leu Arg Ser Leu Gln
245      250      255
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Lys Lys Gly Asn Val Asn Lys Asp Ser Phe Ser Lys Val Met Trp Tyr
260      265      270
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Ala Val Ile Asn Tyr Arg Thr Trp Ile Phe Val Leu Leu Tyr Gly Tyr
275      280      285
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Cys Met Gly Val Glu Leu Thr Thr Asp Asn Val Ile Ala Glu Tyr Met
290      295      300
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Tyr Asp Arg Phe Asp Leu Asp Leu Arg Val Ala Gly Thr Ile Ala Ala
305      310      315
tgc ttc ggc atg gcc aac atc gtc gca cgc cct atg ggc ggc atc atg      1008
Cys Phe Gly Met Ala Asn Ile Val Ala Arg Pro Met Gly Gly Ile Met
325      330      335
tcg gac atg ggc gcg cgc tac tgg ggc atg cgc gct cgc ctc tgg aac      1056
Ser Asp Met Gly Ala Arg Tyr Trp Gly Met Arg Ala Arg Leu Trp Asn
340      345      350
atc tgg atc ctc cag acc gcc ggc ggc gcc ttc tgc ctc tgg ctg gga      1104
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PF59082SeqList_PF59082.txt

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Phe Cys Ala Gln Ala Ala Cys Gly Ala Ile Phe Gly Val Ile Pro Phe				
385	390	395		
gtc tcc cgc cgc tcc ctc ggc atc atc tcc ggc atg acg ggc gcc ggc	1248			
Val Ser Arg Arg Ser Leu Gly Ile Ile Ser Gly Met Thr Gly Ala Gly				
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420	425	430		
acc tac tcc acg ggc agg ggg ctg gag tac atg ggc atc atg atc atg	1344			
Thr Tyr Ser Thr Gly Arg Gly Leu Glu Tyr Met Gly Ile Met Ile Met				
435	440	445		
gcg tgc acg ctg ccg gtg gtg ttc gtg cac ttc ccg cag tgg ggg tcc	1392			
Ala Cys Thr Leu Pro Val Val Phe Val His Phe Pro Gln Trp Gly Ser				
450	455	460		
atg ttc ttc ccg ccc agc ggc acc gcc gac gag ggc tac tac gcc	1440			
Met Phe Phe Pro Pro Ser Ala Thr Ala Asp Glu Gly Tyr Tyr Ala				
465	470	475		
tcc gag tgg aac gac gac gag aag agc aag gga ctc cat agc gct agc	1488			
Ser Glu Trp Asn Asp Asp Glu Lys Ser Lys Gly Leu His Ser Ala Ser				
485	490	495		
ctc aag ttc gcc gag aac agc cgc tca gag cgc ggc aag cgc aac gtc	1536			
Leu Lys Phe Ala Glu Asn Ser Arg Ser Glu Arg Gly Lys Arg Asn Val				
500	505	510		
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Ile Gln Ala Asp Ala Ala Ala Thr				
515	520			

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Asn	Gly	Gly	Lys	Phe	Asp	Leu	Pro	Val	Asp	Ser	Glu	His	Lys	Ala	Lys
		35					40					45			
Ser	Val	Arg	Leu	Phe	Ser	Val	Ala	Asn	Pro	His	Met	Arg	Thr	Phe	His
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Leu	Ser	Trp	Ile	Ser	Phe	Phe	Thr	Cys	Phe	Val	Ser	Thr	Phe	Ala	Ala
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Ala	Pro	Leu	Val	Pro	Ile	Ile	Arg	Asp	Asn	Leu	Asn	Leu	Thr	Lys	Ala
				85					90					95	
Asp	Ile	Gly	Asn	Ala	Gly	Val	Ala	Ser	Val	Ser	Gly	Ser	Ile	Phe	Ser
			100				105						110		
Arg	Leu	Thr	Met	Gly	Ala	Val	Cys	Asp	Leu	Leu	Gly	Pro	Arg	Tyr	Gly
		115					120					125			
Cys	Ala	Phe	Leu	Ile	Met	Leu	Ser	Ala	Pro	Thr	Val	Phe	Cys	Met	Ser
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			180				185					190			
Gly	Asn	Met	Gly	Gly	Gly	Ala	Thr	Gln	Leu	Ile	Met	Pro	Leu	Val	Tyr
		195				200						205			
Asp	Val	Ile	Arg	Lys	Cys	Gly	Ala	Thr	Pro	Phe	Thr	Ala	Trp	Arg	Leu
	210					215					220				
Ala	Tyr	Phe	Val	Pro	Gly	Leu	Met	His	Val	Val	Met	Gly	Val	Leu	Val
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 Tyr Asp Arg Phe Asp Leu Asp Leu Arg Val Ala Gly Thr Ile Ala Ala
 305 310 315 320
 Cys Phe Gly Met Ala Asn Ile Val Ala Arg Pro Met Gly Gly Ile Met
 325 330 335
 Ser Asp Met Gly Ala Arg Tyr Trp Gly Met Arg Ala Arg Leu Trp Asn
 340 345 350
 Ile Trp Ile Leu Gln Thr Ala Gly Gly Ala Phe Cys Leu Trp Leu Gly
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 Arg Ala Ser Thr Leu Pro Val Ser Val Val Ala Met Val Leu Phe Ser
 370 375 380
 Phe Cys Ala Gln Ala Ala Cys Gly Ala Ile Phe Gly Val Ile Pro Phe
 385 390 395 400
 Val Ser Arg Arg Ser Leu Gly Ile Ile Ser Gly Met Thr Gly Ala Gly
 405 410 415
 Gly Asn Phe Gly Ala Gly Leu Thr Gln Leu Leu Phe Phe Thr Ser Ser
 420 425 430
 Thr Tyr Ser Thr Gly Arg Gly Leu Glu Tyr Met Gly Ile Met Ile Met
 435 440 445
 Ala Cys Thr Leu Pro Val Val Phe Val His Phe Pro Gln Trp Gly Ser
 450 455 460
 Met Phe Phe Pro Pro Ser Ala Thr Ala Asp Glu Glu Gly Tyr Tyr Ala
 465 470 475 480
 Ser Glu Trp Asn Asp Asp Glu Lys Ser Lys Gly Leu His Ser Ala Ser
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22

PF59082SeqList_PF59082.txt

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 Ser Phe Phe Xaa Cys Phe Val Ser Thr Phe Ala Ala Ala Pro Leu Xaa
 35 40 45

PF59082SeqList_PF59082.txt

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Xaa	Met	Leu	Xaa	Ala	Pro	Xaa	Val	Xaa	Xaa	Met	Xaa	Xaa	Xaa	Xaa	Xaa
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Thr	Trp	Ile	Xaa	Xaa	Leu	Leu	Tyr	Gly	Tyr	Xaa	Xaa	Gly	Val	Glu	Leu
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PF59082SeqList_PF59082.txt

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PF59082SeqList_PF59082.txt

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Ser Pro Arg Glu Ile Thr Ser Gln Ser Asn Ile Ile Gly Asp Thr Gly
20 25 30
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Ser Asn Gly Trp Leu Ile Arg Phe Phe Asp Ser Ala Phe Phe Cys Glu
35 40 45
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Trp Ile Ala Val Ser Tyr Leu Tyr Lys His Pro His Ala Gly Val Arg
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65 70 75 80
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Ser Tyr Leu Phe Gln Ile Cys Tyr Met Met Val His Lys Pro Ser Pro
85 90 95
tcg ctt gat aag ttt gtt ata gac atc tgt gga aag tca ctg aaa atc 336
Ser Leu Asp Lys Phe Val Ile Asp Ile Cys Gly Lys Ser Leu Lys Ile
100 105 110
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Ala Leu Lys Val His Trp Phe Leu Leu Ala Glu Leu Glu Asp Ala Asp
115 120 125
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145 150 155 160
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Ser Thr Pro Gly Ser Lys Asn Gln Val Leu Asn Arg Leu Leu Ser Ser
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Leu Ser Phe Ser Pro Ser Pro Gly Thr Asn Val Gln Asp Asp Gly Ser
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Gln Leu Pro Ala Glu Asp Asn Lys Ile Phe Lys Lys Leu Ile Pro Ser
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Pro Lys Val Arg Asp Ala Leu Met Phe Arg Lys Ser Ala Asp Lys Asp
225 230 235 240
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Phe Lys Arg Leu Leu Arg Glu Ser Lys Asn Glu Asp Glu Glu Ser Asn	360	365	
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Phe Leu Lys Lys Leu Phe Arg Glu Lys Asn Asp Asp Lys Arg His Gly	420	425	
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Gly Glu Glu Asp Glu Arg Glu Gly Phe Phe Lys Lys Phe Phe Lys Glu	460	465	
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 Ser Pro Arg Glu Ile Thr Ser Pro Ser Asn Leu Ile Ser Glu Ser Gly
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 Trp Ile Ala Val Ser Tyr Leu Tyr Lys His Gln His Ser Gly Val Arg
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 Asp Tyr Leu Cys Asn Arg Met Tyr Thr Leu Pro Leu Ser Gly Ile Glu
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 Ser Tyr Leu Phe Gln Ile Cys Tyr Leu Met Val His Lys Pro Ser Pro
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Lys	Leu	Phe	Ser	Leu	Thr	Leu	Ser	Pro	Pro	Thr	Gln	Lys	Ser	Leu	Leu	
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agt	act	gtt	gcc	atg	gag	gaa	gtt	agg	gct	gct	gca	gcg	aag	gga	gag	2400
Ser	Thr	Val	Ala	Met	Glu	Glu	Val	Arg	Ala	Ala	Ala	Ala	Lys	Gly	Glu	
785					790					795					800	
gca	cct	cca	ggc	ctt	cct	ctc	aaa	ggg	gcg	ggg	cag	gat	tcg	tcg	gat	2448
Ala	Pro	Pro	Gly	Leu	Pro	Leu	Lys	Gly	Ala	Gly	Gln	Asp	Ser	Ser	Asp	
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Ala	Gln	Pro	Arg	Ala	Asn	Gly	Gly	Met	Leu	Lys	Glu	Gly	Asp	Ala	Leu	
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Ser	Gly	Glu	Leu	Trp	Glu	Gly	Lys	Arg	Asp	Arg	Ile	Arg	Lys	Ala	Ser	
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Ile	Tyr	Gly	Lys	Leu	Pro	Gly	Trp	Asp	Leu	Arg	Ser	Ile	Ile	Val	Lys	
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agc	ggt	gac	gac	tgt	agg	cag	gag	cat	ctt	gct	gtg	caa	ctc	att	tct	2640
Ser	Gly	Asp	Asp	Cys	Arg	Gln	Glu	His	Leu	Ala	Val	Gln	Leu	Ile	Ser	
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cac	ttt	tat	gat	ata	ttc	cag	gaa	gca	ggt	cta	ccc	ctc	tgg	tta	cgt	2688
His	Phe	Tyr	Asp	Ile	Phe	Gln	Glu	Ala	Gly	Leu	Pro	Leu	Trp	Leu	Arg	
			885						890					895		
cct	tat	gaa	gtc	ttg	gtt	aca	tct	tct	tat	act	gcc	ctt	ata	gaa	aca	2736
Pro	Tyr	Glu	Val	Leu	Val	Thr	Ser	Ser	Tyr	Thr	Ala	Leu	Ile	Glu	Thr	
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Ile	Pro	Asp	Thr	Ala	Ser	Ile	His	Ser	Ile	Lys	Ser	Arg	Tyr	Pro	Asn	
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Tyr	Ser	Leu	Val	Cys	Tyr	Leu	Leu	Gln	Val	Lys	Asp	Arg	His	Asn	Gly	
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aat	ctt	ctc	ttg	gat	gaa	gag	ggt	cac	att	ata	cac	att	gat	ttt	ggt	2976
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Phe	Met	Leu	Ser	Asn	Ser	Pro	Gly	Gly	Val	Asn	Phe	Glu	Ser	Ala	Pro	
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Gly	Val	Pro	Ser	Glu	Phe	Phe	Asp	Tyr	Phe	Lys	Val	Leu	Cys	Ile	Gln	
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Gly	Phe	Leu	Thr	Cys	Arg	Lys	His	Ala	Glu	Arg	Ile	Ile	Leu	Leu	Val	
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gaa	atg	tta	cag	gat	tcg	ggt	ttc	cct	tgc	ttc	aaa	ggt	ggt	cca	cga	3216
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Gln	Cys	Val	Ser	Leu	Val	Leu	Ser	Leu	Ile	Ser	Ser	Ser	Leu	Asp	Ala	
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Trp	Arg	Thr	Arg	Gln	Tyr	Asp	Tyr	Tyr	Gln	Arg	Val	Leu	Asn	Gly	Ile	
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 Trp Ile Ala Val Ser Tyr Leu Tyr Lys His Pro His Ala Gly Val Arg
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 Asp Tyr Leu Cys Asn Arg Met Tyr Thr Leu Pro Leu Ser Gly Ile Glu
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 Ser Thr Pro Gly Ser Lys Asn Gln Val Leu Asn Arg Leu Leu Ser Ser
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 325 330 335
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 385 390 395 400
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Leu	Cys	Glu	Thr	Ser	Tyr	Gly	Leu	Val	Asp	Ile	Phe	Pro	Ile	Glu	Asp
Arg	Lys	Ile	Gly	Leu	Arg	Glu	Ser	Leu	Ala	Glu	Ile	Asn	Phe	His	Leu
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Val	Phe	Arg	Val	Val	His	Ile	Pro	Glu	Asp	Glu	Cys	Ile	Leu	Leu	Asn
Ser	Arg	Glu	Lys	Ala	Pro	Tyr	Met	Ile	Ser	Val	Glu	Val	Leu	Lys	Ala
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Pro	Trp	Ala	Tyr	Pro	Leu	Trp	Thr	Thr	Gln	Glu	Val	Tyr	Arg	Asn	Ser
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Thr	Pro	Lys	Ser	Glu	Val	Lys	Val	Lys	Leu	Val	Asn	Val	Ser	Leu	Ser
Val	Glu	Asp	Arg	Thr	Ser	Ala	Leu	Glu	Ser	Phe	Gly	Asp	Pro	Ile	Asp
Asp	Val	Leu	Gly	Glu	Ala	Pro	Arg	Thr	Gly	Leu	Asn	Asn	Asp	Leu	Glu
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Ile	Pro	Asp	Pro	Ser	Val	Pro	Arg	Lys	Lys	Glu	His	Arg	Arg	Val	Pro
Ser	Thr	Val	Ala	Met	Glu	Gln	Val	Arg	Ala	Ala	Ala	Ala	Lys	Gly	Glu
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Pro	Tyr	Glu	Val	Leu	Val	Thr	Ser	Ser	Tyr	Thr	Ala	Leu	Ile	Glu	Thr
Ile	Pro	Asp	Thr	Ala	Ser	Ile	His	Ser	Ile	Lys	Ser	Arg	Tyr	Pro	Asn
Ile	Thr	Ser	Leu	Arg	Asp	Phe	Phe	Val	Ala	Lys	Tyr	Lys	Glu	Asn	Ser
Pro	Ser	Phe	Lys	Leu	Ala	Gln	Arg	Asn	Phe	Val	Glu	Ser	Met	Ala	Gly
Tyr	Ser	Leu	Val	Cys	Tyr	Leu	Leu	Gln	Val	Lys	Asp	Arg	His	Asn	Gly
Asn	Leu	Leu	Leu	Asp	Glu	Glu	Gly	His	Ile	Ile	His	Ile	Asp	Phe	Gly
Phe	Met	Leu	Ser	Asn	Ser	Pro	Gly	Gly	Val	Asn	Phe	Glu	Ser	Ala	Pro
Phe	Lys	Leu	Thr	Arg	Glu	Leu	Leu	Glu	Val	Met	Asp	Ser	Asp	Ala	Asp
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1075 1080 1085
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Glu Ile Glu Ser Lys Ser Asn Leu Thr Ser Asp Ser Ser Glu Asn Gly
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tgg ctt att agg ttc ttt gat tca tcg ttt ttt tgc gaa tgg att gct 144
Trp Leu Ile Arg Phe Phe Asp Ser Ser Phe Phe Cys Glu Trp Ile Ala
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Val Ser Tyr Leu Tyr Lys His Asp His Ala Gly Val Arg Asp Tyr Leu
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Cys Asn Arg Met Tyr Thr Leu Pro Leu Thr Gly Leu Glu Ser Tyr Leu
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Phe Gln Ile Cys Tyr Met Met Ile His Lys Pro Ser Pro Ser Leu Asp
85 90 95
aag ttt gtc ata gat atg tgt tcc aag tcg ctt aag att gca ttg aaa 336
Lys Phe Val Ile Asp Met Cys Ser Lys Ser Leu Lys Ile Ala Leu Lys
100 105 110
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Val His Trp Phe Leu Met Ala Glu Leu Glu Asp Ser Asp Asp Asn Asp
115 120 125
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Gly Ile Ser Arg Ile Gln Glu Lys Cys Gln Ile Ala Ala Thr Leu Met
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Gly Glu Trp Pro Pro Leu Ile Arg Pro His Thr Glu Pro Pro Ser Ala
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Gly Gly Lys Ser Gln Val Leu Asn Arg Leu Ser Ser Lys Asn Arg
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Ser Pro Gly Asn Asn Leu Gln Glu Asp Gly Asn Pro Leu Ser Pro Asp
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Glu Asn Arg Ile Phe Lys Lys Phe Met Pro Ser Pro Lys Val Arg Asp
210 215 220
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Ala Leu Leu Phe Arg Lys Ser Ala Asp Lys Glu Asp Gly Asp Ser Glu
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Asp	Ser	Lys	Asn	Asp	Ser	Glu	Asp	Lys	Thr	Asp	Ser	Lys	Thr	Val	Glu	
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Asp	Glu	Glu	Lys	Asp	Gly	Leu	Phe	Arg	Lys	Phe	Phe	Arg	Glu	Lys	Phe	
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Val	Tyr	Arg	Asn	Ser	Asn	Asp	Arg	Met	Ser	Arg	Ser	Thr	Ala	Gln	Ala	
		675					680					685				
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Ile	Asp	Gln	Ala	Met	Thr	His	Val	Ser	Glu	Pro	Lys	Phe	Val	Ser	Leu	
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Ala	Asp	Pro	Gly	Val	Arg	Leu	Glu	Asp	Ile	Glu	Asp	Lys	Ala	Pro	Ser	
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cgg	aaa	aag	gaa	cat	cg	cgt	gtt	cca	agt	aca	gtg	gca	ata	gaa	gaa	2304
Arg	Lys	Lys	Glu	His	Arg	Arg	Val	Pro	Ser	Thr	Val	Ala	Ile	Glu	Glu	
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Val	Lys	Ala	Ala	Ala	Ala	Lys	Gly	Glu	Ala	Pro	Leu	Gly	Leu	Pro	Leu	
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Lys	Lys	Asp	Arg	Val	Arg	Lys	Ala	Ser	Ile	Tyr	Gly	Lys	Leu	Pro	Gly	
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Trp	Asp	Leu	Arg	Ser	Ile	Ile	Val	Lys	Ser	Gly	Asp	Asp	Cys	Arg	Gln	
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Glu	His	Leu	Ala	Val	Gln	Leu	Ile	Ser	His	Phe	Tyr	Asp	Ile	Phe	Gln	
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Glu	Ala	Gly	Leu	Pro	Leu	Trp	Leu	Arg	Pro	Tyr	Glu	Val	Leu	Cys	Thr	
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Ser	Ser	Tyr	Thr	Ala	Leu	Ile	Glu	Thr	Ile	Pro	Asp	Thr	Ala	Ser	Leu	
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<400> 1558

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Phe	Gln	Ile	Cys	Tyr	Met	Met	Ile	His	Lys	Pro	Ser	Pro	Ser	Leu	Asp	
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Lys	Phe	Val	Ile	Asp	Met	Cys	Ser	Lys	Ser	Leu	Lys	Ile	Ala	Leu	Lys	
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Pro	Ser	Glu	Leu	Ser	Leu	Phe	Lys	Arg	Leu	Phe	Arg	Val	His	Pro Glu
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Asp	Asp	Lys	Ser	Ser	Pro	Val	Asn	Glu	Asn	Ser	Asn	Asn	Gly	Gly Leu
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Asp	Arg	Asp	Arg	Ser	Ile	Glu	Asp	Ser	Glu	Leu	Leu	Gly	Ser	Lys Arg
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Pro	Thr	Glu	Asp	Arg	Lys	Ser	Ala	Leu	Gln	Glu	Ser	Leu	Arg	Glu Ile
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Ile	Asp	Gln	Ala	Met	Thr	His	Val	Ser	Glu	Pro	Lys	Phe	Val	Ser Leu
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His Ser Ile Lys Ser Arg Tyr Pro Asn Ile Ser Ser Leu Arg Glu Phe
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Asp Tyr Leu Cys Asn Arg Met Tyr Thr Leu Pro Leu Ser Gly Ile Glu	
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Ser Tyr Leu Phe Gln Ile Cys Tyr Leu Met Val His Lys Pro Ser Pro	
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Thr	Glu	Gly	Phe	Phe	Lys	Lys	Leu	Phe	His	Glu	Ser	Lys	Asn	Glu	Asp	
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Asp	Lys	Val	Ser	Asn	Ala	Val	Asp	Asp	Glu	Glu	Lys	Asp	Gly	Phe	Leu	
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Leu	Phe	Arg	Asp	Arg	Asp	Arg	Ser	Val	Glu	Asp	Ser	Glu	Leu	Phe	Gly	
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Asn	Thr	Pro	Ser	Lys	Lys	Pro	Pro	Leu	Pro	Asn	Asn	Thr	Ala	Ala	Gln	
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Cys	Glu	Thr	Ser	Tyr	Asp	Leu	Val	Asp	Ile	Phe	Pro	Ile	Glu	Asp	Arg	
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Gln	Ala	Glu	Thr	Thr	Gly	Gly	Ile	Cys	Phe	Pro	Met	Gly	Arg	Gly	Val	
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Gly	Gly	Ile	Pro	Leu	Ala	Asn	Gly	Asp	Ala	Phe	Leu	His	Lys	Pro	Pro	
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Pro	Trp	Ala	Tyr	Pro	Leu	Ser	Thr	Ala	Gln	Glu	Val	Tyr	Arg	Asn	Ser	
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Ala	Asp	Arg	Met	Ser	Leu	Ser	Thr	Val	Glu	Ala	Ile	Asp	Gln	Ala	Met	
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Thr	His	Lys	Ser	Glu	Val	Lys	Leu	Val	Asn	Ala	Cys	Leu	Ser	Val	Glu	
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acg	cat	agt	aat	tca	aat	acc	aaa	tca	gta	agc	agt	ggt	gtg	act	ggt	2208
Thr	His	Ser	Asn	Ser	Asn	Thr	Lys	Ser	Val	Ser	Ser	Gly	Val	Thr	Gly	
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Leu	Thr	Ala	Asp	Pro	Gly	Leu	Arg	Met	Glu	Ser	Ile	Thr	Asp	Pro	Lys	
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Thr	Pro	Arg	Arg	Lys	Glu	His	Arg	Arg	Val	Ser	Ser	Ile	Val	Ala	Tyr	
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Glu	Glu	Val	Arg	Ala	Ala	Ala	Ala	Lys	Gly	Glu	Ala	Pro	Pro	Gly	Leu	
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gag	ggg	aag	cga	cta	aga	att	cgt	aaa	gat	tca	ata	tat	ggc	aac	cta	2544
Glu	Gly	Lys	Arg	Leu	Arg	Ile	Arg	Lys	Asp	Ser	Ile	Tyr	Gly	Asn	Leu	
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Ser	Ile	His	Ser	Ile	Lys	Ser	Arg	Tyr	Pro	Asn	Ile	Thr	Ser	Leu	Arg	
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gct	cag	agg	aat	ttt	gtt	gag	agc	atg	gct	gga	tat	tct	ttg	gtc	tgt	2880
Ala	Gln	Arg	Asn	Phe	Val	Glu	Ser	Met	Ala	Gly	Tyr	Ser	Leu	Val	Cys	
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Glu	Leu	Leu	Glu	Val	Met	Asp	Ser	Asp	Ala	Glu	Gly	Leu	Pro	Ser	Glu	
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Arg	Lys	His	Ala	Glu	Arg	Ile	Ile	Leu	Leu	Val	Glu	Met	Leu	Gln	Asp	
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Arg	Lys	Arg	Phe	His	Leu	Ser	Leu	Thr	Glu	Glu	Ala	Met	Arg	Leu	Phe	
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ggg	gct	ctc	tct	aat	cag	cag	ctt	aga	tgc	ttg	gcg	aac	tcg	aca		3312
Gly	Ala	Leu	Ser	Asn	Gln	Gln	Leu	Arg	Cys	Leu	Ala	Asn	Ser	Thr		
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Trp	Ile	Ala	Val	Ser	Tyr	Leu	Tyr	Lys	His	Gln	His	Ser	Gly	Val	Arg	
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145	Leu	Val	Gly	Glu	150	Ser	Pro	Leu	Met	Arg	155	Pro	His	Asn	Glu
Ser	Thr	Pro	Gly	Ser	165	Val	Leu	Asn	Lys	Phe	Leu	Ser	Ser	Lys	160
Lys	Leu	Phe	Ser	Leu	Thr	Leu	Ser	Pro	Pro	Thr	Gln	Lys	Ser	Leu	Gln
Phe	Ser	Pro	180	Ser	Gly	Ser	Asn	Leu	Gln	Asp	Asp	Gly	Ser	Gln	Leu
Ser	Ala	Asp	195	Asn	Lys	Ile	Phe	Lys	Arg	Leu	Ile	Pro	Ser	Pro	Lys
Val	Arg	Asp	Ala	Leu	Leu	210	Phe	Arg	Lys	Ser	Ala	Asp	Lys	Glu	Glu
225	Cys	Glu	Lys	Asp	Gly	230	Phe	Phe	Lys	Arg	235	Leu	Arg	Asp	Arg
Gly	Glu	Asp	245	Glu	Gln	Arg	Ser	Asn	Ser	Glu	Gly	Phe	Phe	Lys	Arg
Leu	Leu	Lys	260	Asn	Lys	Ser	Glu	Glu	Glu	Glu	Ile	Ser	Asn	Asn	Ser
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Lys	Leu	Leu	Arg	Asp	Ser	Lys	Asn	Glu	Asp	Glu	Glu	Pro	Asn	Ala	Asn
Thr	Glu	Gly	340	Phe	Lys	Lys	Leu	Phe	His	Glu	Ser	Lys	Asn	Glu	Asp
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Gln	Ala	Glu	580	Thr	Thr	Gly	Gly	Ile	Cys	Phe	Pro	Met	Gly	Arg	Val
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725 730 735
Val Leu Arg Thr Gly Leu Glu Ser Asp Leu Glu Trp Val Arg Leu Val
740 745 750
Leu Thr Ala Asp Pro Gly Leu Arg Met Glu Ser Ile Thr Asp Pro Lys
755 760 765
Thr Pro Arg Arg Lys Glu His Arg Arg Val Ser Ser Ile Val Ala Tyr
770 775 780
Glu Glu Val Arg Ala Ala Ala Lys Gly Glu Ala Pro Pro Gly Leu
785 790 795 800
Pro Leu Lys Gly Ala Gly Gln Asp Ser Ser Asp Ala Gln Pro Met Ala
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Glu Gly Lys Arg Leu Arg Ile Arg Lys Asp Ser Ile Tyr Gly Asn Leu
835 840 845
Pro Gly Trp Asp Leu Arg Ser Ile Ile Val Lys Ser Gly Asp Asp Cys
850 855 860
Arg Gln Glu His Leu Ala Val Gln Leu Ile Ser His Phe Phe Asp Ile
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Phe Gln Glu Ala Gly Leu Pro Leu Trp Leu Arg Pro Tyr Glu Val Leu
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Val Thr Ser Ser Tyr Thr Ala Leu Ile Glu Thr Ile Pro Asp Thr Ala
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Ser Ile His Ser Ile Lys Ser Arg Tyr Pro Asn Ile Thr Ser Leu Arg
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Ala Gln Arg Asn Phe Val Glu Ser Met Ala Gly Tyr Ser Leu Val Cys
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Tyr Leu Leu Gln Ile Lys Asp Arg His Asn Gly Asn Leu Leu Met Asp
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Glu Glu Gly His Ile Ile His Ile Asp Phe Gly Phe Met Leu Ser Asn
980 985 990
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995 1000 1005
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His Lys Pro Ser Pro Ser Leu Asp Arg Phe Val Ile Asp Thr Cys Ser	
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Val Arg Pro Ala Pro Pro Ser Pro Ile Ala Ser Pro Arg Gly Asn Pro	
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 Tyr Thr Ala Leu Ile Glu Thr Ile Pro Asp Thr Ala Ser Ile His Ser
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 Ser Pro Arg Glu Ile Thr Ser Gln Ser Asn Ile Ile Gly Asp Thr Gly
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 Trp Ile Ala Val Ser Tyr Leu Tyr Lys His Pro His Ala Gly Val Arg
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Lys	Gln	Lys	Leu	Phe	Ser	Leu	Lys	Leu	Ser	Pro	Pro	Thr	Gln	Lys	Ser	
			180					185					190			
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Gln	Leu	Pro	Ala	Glu	Asp	Asn	Lys	Ile	Phe	Lys	Lys	Leu	Ile	Pro	Ser	
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Ser Gly Asp Asp Cys Arg Gln Glu His Leu Ala Val Gln Leu Ile Ser	
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Pro Tyr Glu Val Leu Val Thr Ser Ser Tyr Thr Ala Leu Ile Glu Thr	
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Gly Val Pro Ser Glu Phe Phe Asp Tyr Phe Lys Val Leu Cys Ile Gln	
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Ser Pro Arg Glu Ile Thr Val Ala Gly Gly Gly Gly Asp Ala Ala
      20      25      30
gcg cac ccc gtg ggg agc agc ggc tgg ctc gtt cgc ttc ttc gac tcc      144
Ala His Pro Val Gly Ser Ser Gly Trp Leu Val Arg Phe Phe Asp Ser
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gcc ttc ttc tgc gag tgg atc gcc gtc agc tac ctc tac aag cat gac      192
Ala Phe Phe Cys Glu Trp Ile Ala Val Ser Tyr Leu Tyr Lys His Asp
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Leu Leu Ser Lys Glu Lys Glu Asn Glu Glu Glu Glu Gly Asp Arg Asp
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	450					455					460				
Lys	Xaa	Lys	Xaa	Xaa	Xaa	Lys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
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Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Phe
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			500					505				510			
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		515					520					525			
Glu	Asn	Phe	Phe	Arg	Lys	Leu	Phe	Xaa	Asp	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
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	545				550					555					560
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PF59082SeqList_PF59082.txt

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Ala	Xaa	Glu	Glu	Val	Xaa	Ala	Ala	Ala	Xaa	Lys	Gly	Glu	Ala	Pro	Xaa	
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Ser	Leu	Arg	Xaa	Xaa	Xaa	Ala	Lys	Xaa	Xaa	Glu	Asn	Ser	Pro	Xaa	Xaa	
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Leu	Ser	Asn	Ser	Pro	Gly	Gly	Val	Asn	Phe	Glu	Ser	Ala	Pro	Phe	Lys	
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Leu	Thr	Arg	Glu	Leu	Leu	Glu	Val	Met	Asp	Ser	Asp	Ala	Xaa	Gly	Xaa	
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Pro	Ser	Glu	Phe	Phe	Asp	Tyr	Phe	Lys	Val	Leu	Cys	Ile	Gln	Gly	Phe	
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Leu	Thr	Cys	Arg	Lys	His	Ala	Glu	Arg	Ile	Ile	Leu	Leu	Val	Glu	Met	
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Gln	Asn	Leu	Arg	Lys	Arg	Phe	His	Leu	Ser	Leu	Thr	Glu	Glu	Xaa	Xaa	
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					1220				1225					1230		
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PF59082SeqList_PF59082.txt

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1250          1255          1260
Xaa Xaa Xaa Xaa Leu Xaa Ala Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1265          1270          1275          1280
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1285          1290          1295
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Leu
1300          1305          1310
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<210> 1578

<211> 61

<212> PRT

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<223> protein pattern

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<223> Xaa in position 27 is Ala, Gln or Ser

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<222> (43)..(43)

<223> Xaa in position 43 is Pro, Ser or Thr

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<223> Xaa in position 45 is Ile or Leu

<220>

<221> Variant

<222> (47)..(47)

<223> Xaa in position 47 is Ala or Ser

<220>

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<222> (52)..(52)

<223> Xaa in position 52 is Ile or Val

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<222> (57)..(57)

<223> Xaa in position 57 is any amino acid

PF59082SeqList_PF59082.txt

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 <223> Xaa in position 58 is any or no amino acid

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 Ala Val Ser Tyr Leu Tyr Lys His Xaa His Xaa Gly Val Arg Asp Tyr
 20 25 30
 Leu Cys Asn Arg Met Tyr Thr Leu Pro Leu Xaa Gly Xaa Glu Xaa Tyr
 35 40 45
 Leu Phe Gln Xaa Cys Tyr Xaa Met Xaa Xaa His Lys Pro
 50 55 60

<210> 1579
 <211> 59
 <212> PRT
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<220>
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 <223> Xaa in position 59 is Ala, Glu or Gln

<400> 1579
 Phe Asp Tyr Phe Lys Val Leu Cys Ile Gln Gly Phe Leu Thr Cys Arg
 1 5 10 15
 Lys His Ala Glu Arg Ile Ile Leu Leu Val Glu Met Leu Gln Asp Ser
 20 25 30
 Gly Phe Pro Cys Phe Lys Gly Gly Xaa Arg Thr Ile Gln Asn Leu Arg
 35 40 45
 Lys Arg Phe His Leu Ser Leu Thr Glu Glu Xaa
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<210> 1580
 <211> 56
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 <222> (9)..(9)
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<223> Xaa in position 12 is Phe or Tyr

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<223> Xaa in position 31 is Cys or Val
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<223> Xaa in position 48 is Ile or Leu
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<223> Xaa in position 55 is Phe or Tyr
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<400> 1580
Glu His Leu Ala Val Gln Leu Xaa Xaa His Xaa Xaa Asp Ile Xaa Gln
1 5 10 15
Glu Ala Gly Leu Pro Leu Trp Leu Arg Pro Tyr Glu Val Xaa Xaa Thr
 20 25 30
Ser Xaa Tyr Thr Ala Leu Ile Glu Thr Ile Pro Asp Thr Ala Ser Xaa
 35 40 45
His Ser Ile Lys Ser Arg Xaa Pro
 50 55

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<210> 1581
<211> 61
<212> PRT
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<222> (15)..(15)
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$\langle 220 \rangle$

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 <223> Xaa in position 22 is Ile or Val

 <220>
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 <223> Xaa in position 32 is Ile, Leu or Met

 <400> 1581
 Ala Gln Arg Asn Phe Val Glu Ser Met Ala Gly Tyr Ser Xaa Xaa Cys
 1 5 10 15
 Tyr Xaa Leu Xaa Gln Xaa Lys Asp Arg His Asn Gly Asn Leu Leu Xaa
 20 25 30
 Asp Glu Glu Gly His Ile Ile His Ile Asp Phe Gly Phe Met Leu Ser
 35 40 45
 Asn Ser Pro Gly Gly Val Asn Phe Glu Ser Ala Pro Phe
 50 55 60

 <210> 1582
 <211> 57
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 <222> (12)..(12)
 <223> Xaa in position 12 is Ala or Val

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 <223> Xaa in position 13 is any amino acid

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 <222> (15)..(15)
 <223> Xaa in position 15 is any amino acid

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 <222> (25)..(25)
 <223> Xaa in position 25 is any amino acid

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 <222> (26)..(26)
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<222> (31)..(31)
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<222> (32)..(32)
<223> Xaa in position 32 is Asn or Arg

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<223> Xaa in position 33 is any amino acid

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<223> Xaa in position 43 is Ala, Ser or Val

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<223> Xaa in position 44 is Glu or Gln

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<223> Xaa in position 45 is Ala or Val

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<222> (51)..(51)
<223> Xaa in position 51 is Ala or Thr

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<222> (52)..(54)
<223> Xaa in position 52 to 54 is any amino acid

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<223> Xaa in position 56 is Ala, Pro or Val

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Ser Xaa Gly Gly Ile Pro Leu Ala Asn Gly Asp Xaa Xaa Leu Xaa Lys
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Pro Pro Pro Trp Ala Tyr Pro Leu Xaa Xaa Xaa Xaa Glu Xaa Xaa Xaa
20          25          30

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 35 40 45
 Ala Met Xaa Xaa Xaa Xaa Glu Xaa Lys
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<210> 1583
 <211> 58
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 <223> Xaa in position 6 is Ile, Leu or Val

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 <223> Xaa in position 7 is Ala or Ser

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 <223> Xaa in position 8 is Glu, Gln or Ser

<220>
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 <222> (9)..(9)
 <223> Xaa in position 9 is Ala, Thr or Val

<220>
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 <223> Xaa in position 10 is Glu or Gln

<220>
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 <222> (11)..(11)
 <223> Xaa in position 11 is any amino acid

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 <222> (12)..(12)
 <223> Xaa in position 12 is Asn or Thr

<220>
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 <223> Xaa in position 15 is Ile or Val

<220>
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 <222> (19)..(19)
 <223> Xaa in position 19 is Leu or Met

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 <223> Xaa in position 21 is Lys or Arg

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 <223> Xaa in position 23 is Ile, Met or Val

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 <222> (24)..(24)
 <223> Xaa in position 24 is Phe or Tyr

<220>
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 <222> (27)..(27)
 <223> Xaa in position 27 is Leu or Val

<220>
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 <223> Xaa in position 28 is any amino acid

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 <222> (34)..(34)
 <223> Xaa in position 34 is any amino acid

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<220>
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 <222> (43)..(43)
 <223> Xaa in position 43 is Ala or Val

<220>
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 <222> (46)..(46)
 <223> Xaa in position 46 is Leu or Met

<220>
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 <222> (48)..(48)
 <223> Xaa in position 48 is Cys or Ser

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 <222> (53)..(53)
 <223> Xaa in position 53 is Lys or Arg

<220>
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<220>
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 <222> (56)..(56)
 <223> Xaa in position 56 is any amino acid

<220>
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 <222> (58)..(58)
 <223> Xaa in position 58 is Cys or Ser

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 Glu Ile Asn Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Gly Xaa Cys
 1 5 10 15
 Phe Pro Xaa Gly Xaa Gly Xaa Xaa Arg Val Xaa Xaa Ile Pro Glu Asp
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 35 40 45
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 50 55

<210> 1584

<211> 61

<212> PRT

<213> Artificial sequence

<220>

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<223> Xaa in position 2 is Lys or Arg

<220>

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<222> (3)..(3)

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<220>

<221> Variant

<222> (4)..(4)

<223> Xaa in position 4 is Thr or Val

<220>

<221> Variant

<222> (5)..(5)

<223> Xaa in position 5 is Leu or Val

<220>

<221> Variant

<222> (6)..(6)

<223> Xaa in position 6 is Ser or Thr

<220>

<221> Variant

<222> (8)..(8)

<223> Xaa in position 8 is Asp or Val

<220>

<221> Variant

<222> (11)..(11)

<223> Xaa in position 11 is Leu or Val

<220>

<221> Variant

<222> (12)..(12)

<223> Xaa in position 12 is Asn or Arg

<220>

<221> Variant

<222> (13)..(13)

<223> Xaa in position 13 is Leu or Met

<220>

<221> Variant

<222> (14)..(14)

<223> Xaa in position 14 is Asp or Glu

<220>

<221> Variant

<222> (15)..(15)

<223> Xaa in position 15 is Asp or Ser

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<220>
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<220>
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<222> (19)..(20)
<223> Xaa in position 19 to 20 is any or no amino acid

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<223> Xaa in position 22 is any amino acid

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<223> Xaa in position 23 to 24 is any or no amino acid

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<222> (26)..(26)
<223> Xaa in position 26 is Lys or Arg

<220>
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<222> (28)..(28)
<223> Xaa in position 28 is Asp or Glu

<220>
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<222> (33)..(33)
<223> Xaa in position 33 is Pro or Ser

<220>
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<222> (35)..(35)
<223> Xaa in position 35 is any amino acid

<220>
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<223> Xaa in position 36 is Ile or Val

<220>
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<223> Xaa in position 38 is any amino acid

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<223> Xaa in position 42 is Lys or Arg

<220>
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<222> (46)..(46)
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<223> Xaa in position 52 is Leu or Pro

<220>

<221> Variant

<222> (59)..(59)

<223> Xaa in position 59 is Ala or Val

<400> 1584

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Val Xaa Xaa Xaa Xaa Xaa Ala Xaa Pro Gly Xaa Xaa Xaa Xaa Xaa Xaa
1      5      10      15
Xaa Asp Xaa Xaa Pro Xaa Xaa Xaa Arg Xaa Lys Xaa His Arg Arg Val
      20      25      30
Xaa Ser Xaa Xaa Ala Xaa Glu Glu Val Xaa Ala Ala Ala Xaa Lys Gly
      35      40      45
Glu Ala Pro Xaa Gly Leu Pro Leu Lys Gly Xaa Gly Gln
      50      55      60

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<210> 1585

<211> 29

<212> PRT

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<223> protein pattern

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<222> (3)..(3)

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<220>

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<222> (7)..(7)

<223> Xaa in position 7 is Asp or Ser

<220>

<221> Variant

<222> (9)..(9)

<223> Xaa in position 9 is Ile or Val

<220>

<221> Variant

<222> (12)..(12)

<223> Xaa in position 12 is any amino acid

<220>

<221> Variant

<222> (15)..(15)

<223> Xaa in position 15 is Ala or Ile

<220>

<221> Variant

<222> (19)..(19)

<223> Xaa in position 19 is Leu or Val

<220>

<221> Variant

<222> (20)..(20)

<223> Xaa in position 20 is any amino acid

<220>

<221> Variant

<222> (24)..(24)

<223> Xaa in position 24 is Pro or Ser

<220>

<221> Variant

<222> (27)..(27)

<223> Xaa in position 27 is Ile, Met or Val

<400> 1585

Asp	Asp	Xaa	Xaa	Gly	Ile	Xaa	Arg	Xaa	Gln	Glu	Xaa	Cys	Gln	Xaa	Ala
1				5				10						15	
Ala	Thr	Xaa	Xaa	Gly	Glu	Trp	Xaa	Pro	Leu	Xaa	Arg	Pro			
			20				25								

<210> 1586

<211> 42

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<223> protein pattern

<220>

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<222> (4)..(4)

<223> Xaa in position 4 is any or no amino acid

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<222> (6)..(9)

<223> Xaa in position 6 to 9 is any amino acid

<220>

<221> Variant

<222> (10)..(11)

<223> Xaa in position 10 to 11 is any or no amino acid

<220>

<221> Variant

<222> (15)..(15)

<223> Xaa in position 15 is Ala, Cys or Ser

<220>

<221> Variant

<222> (17)..(17)

<223> Xaa in position 17 is His or Tyr

<220>

<221> Variant

<222> (18)..(18)

<223> Xaa in position 18 is Ala, Asp or Glu

<220>

<221> Variant

<222> (22)..(22)

<223> Xaa in position 22 is Phe or Leu

<220>

<221> Variant

<222> (24)..(24)

<223> Xaa in position 24 is any amino acid

<220>

<221> Variant

<222> (25)..(25)

<223> Xaa in position 25 is Ala or Ser

<220>

<221> Variant

<222> (28)..(28)

<223> Xaa in position 28 is Asp or Glu

<220>

<221> Variant

<222> (32)..(32)

<223> Xaa in position 32 is Asp or Gly

<220>

<221> Variant

<222> (36)..(36)

<223> Xaa in position 36 is Ile or Val

<220>

<221> Variant

<222> (39)..(39)

<223> Xaa in position 39 is any amino acid

<400> 1586

Pro	Leu	Pro	Xaa	Asn	Xaa	Xaa	Xaa	Xaa	Xaa	Arg	Lys	Gly	Xaa	Tyr
1				5				10					15	
Xaa	Xaa	Ser	Leu	Glu	Xaa	Val	Xaa	Xaa	Leu	Cys	Xaa	Thr	Ser	Tyr
			20				25					30		
Leu	Val	Asp	Xaa	Phe	Pro	Xaa	Glu	Asp	Arg					
		35					40							

<210> 1587

<211> 38

<212> PRT

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<220>

<223> protein pattern

<220>

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<222> (4)..(4)

<223> Xaa in position 4 is Ala or Ser

<220>

<221> Variant

<222> (7)..(7)

<223> Xaa in position 7 is Phe, Ile or Leu

<220>

<221> Variant

<222> (9)..(9)

<223> Xaa in position 9 is Ala or Glu

<220>

<221> Variant

<222> (10)..(10)

<223> Xaa in position 10 is Ala, Gly or Val

<220>

<221> Variant

<222> (12)..(13)

<223> Xaa in position 12 to 13 is any or no amino acid

<220>

<221> Variant

<222> (15)..(15)

<223> Xaa in position 15 is Ile, Leu or Val

<220>

<221> Variant

<222> (17)..(17)

<223> Xaa in position 17 is Lys or Arg

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<220>
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<222> (18)..(18)
<223> Xaa in position 18 is Ala, Asp or Ser

<220>
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<222> (20)..(20)
<223> Xaa in position 20 is Ile or Val

<220>
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<222> (21)..(21)
<223> Xaa in position 21 is His or Tyr

<220>
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<222> (23)..(23)
<223> Xaa in position 23 is any amino acid

<220>
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<222> (32)..(32)
<223> Xaa in position 32 is Ile or Val

<400> 1587
Asp Ala Leu Xaa Gly Glu Xaa Trp Xaa Xaa Lys Xaa Xaa Arg Xaa Arg
1      5      10      15
Xaa Xaa Ser Xaa Xaa Gly Xaa Leu Pro Gly Trp Asp Leu Arg Ser Xaa
      20      25      30
Ile Val Lys Ser Gly Asp
      35

<210> 1588
<211> 27
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<220>
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<220>
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<223> Xaa in position 3 is Lys or Arg

<220>
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<222> (8)..(8)
<223> Xaa in position 8 is any amino acid

<220>
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<222> (10)..(10)
<223> Xaa in position 10 is Ala, Gly or Ser

<220>
<221> Variant
<222> (14)..(14)
<223> Xaa in position 14 is Lys or Arg

<220>
<221> Variant
<222> (19)..(19)
<223> Xaa in position 19 is Ala or Val

<220>

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<221> Variant
<222> (20)..(20)
<223> Xaa in position 20 is any amino acid

<220>
<221> Variant
<222> (22)..(22)
<223> Xaa in position 22 is Phe or Leu

<220>
<221> Variant
<222> (24)..(24)
<223> Xaa in position 24 is any amino acid

<400> 1588
Leu Asp Xaa Phe Val Ile Asp Xaa Cys Xaa Lys Ser Leu Xaa Ile Ala
1          5          10          15
Leu Lys Xaa Xaa Trp Xaa Leu Xaa Ala Glu Leu
          20          25

<210> 1589
<211> 33
<212> PRT
<213> Artificial sequence

<220>
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<220>
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<222> (2)..(13)
<223> Xaa in position 2 to 13 is any amino acid

<220>
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<222> (14)..(14)
<223> Xaa in position 14 is any or no amino acid

<220>
<221> Variant
<222> (16)..(16)
<223> Xaa in position 16 is any or no amino acid

<220>
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<222> (19)..(19)
<223> Xaa in position 19 is Ile or Leu

<220>
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<222> (20)..(20)
<223> Xaa in position 20 is Phe or Leu

<220>
<221> Variant
<222> (22)..(22)
<223> Xaa in position 22 is Lys or Arg

<220>
<221> Variant
<222> (23)..(23)
<223> Xaa in position 23 is Phe or Leu

<220>
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<222> (24)..(24)
<223> Xaa in position 24 is any amino acid

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PF59082SeqList_PF59082.txt

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 <223> Xaa in position 25 is Ile or Pro

<220>
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 <222> (26)..(26)
 <223> Xaa in position 26 is Gly or Ser

<220>
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 <222> (33)..(33)
 <223> Xaa in position 33 is Ala or Leu

<400> 1589
 Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Xaa
 1 5 10 15
 Asn Lys Xaa Xaa Lys Xaa Xaa Xaa Xaa Xaa Pro Lys Val Arg Asp Ala
 20 25 30
 Xaa

<210> 1590
 <211> 38
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<220>
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 <223> Xaa in position 2 is Phe, Ile or Leu

<220>
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 <223> Xaa in position 3 is any amino acid

<220>
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 <223> Xaa in position 4 is Glu or Gln

<220>
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 <223> Xaa in position 5 is Gly or Ser

<220>
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 <222> (9)..(9)
 <223> Xaa in position 9 is Ser or Thr

<220>
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 <222> (11)..(11)
 <223> Xaa in position 11 is Asn or Ser

<220>
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 <222> (14)..(14)
 <223> Xaa in position 14 is any or no amino acid

<220>
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<222> (16)..(16)
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 <223> Xaa in position 19 is Lys or Arg

 <220>
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 <222> (23)..(23)
 <223> Xaa in position 23 is Gln or Arg

 <220>
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 <222> (25)..(25)
 <223> Xaa in position 25 is Ile, Leu or Val

 <220>
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 <222> (31)..(31)
 <223> Xaa in position 31 is Phe or Leu

 <220>
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 <223> Xaa in position 35 to 36 is any amino acid

 <400> 1590
 Gly Xaa Xaa Xaa Xaa Ser Pro Gly Xaa Glu Xaa Phe Phe Xaa Arg Xaa
 1 5 10 15
 Leu Phe Xaa Asp Arg Asp Xaa Ser Xaa Glu Asp Ser Glu Leu Xaa Gly
 20 25 30
 Ser Lys Xaa Xaa Lys Glu
 35

 <210> 1591
 <211> 53
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 <223> Xaa in position 3 is Cys, Gly or Ser

 <220>
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 <223> Xaa in position 4 is Asp or Glu

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 <222> (5)..(5)
 <223> Xaa in position 5 is Lys or Arg

 <220>
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 <222> (6)..(6)
 <223> Xaa in position 6 is Asp or Glu

 <220>
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 <222> (9)..(9)
 <223> Xaa in position 9 is Phe or Leu

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<220>
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<223> Xaa in position 10 is any amino acid

<220>
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<222> (12)..(12)
<223> Xaa in position 12 is any or no amino acid

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<223> Xaa in position 14 is any or no amino acid

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<222> (16)..(16)
<223> Xaa in position 16 is Asp or Glu

<220>
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<222> (18)..(18)
<223> Xaa in position 18 is Lys or Arg

<220>
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<223> Xaa in position 19 is Asp, Gly or Ser

<220>
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<222> (21)..(21)
<223> Xaa in position 21 is any or no amino acid

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<223> Xaa in position 24 is Asp, Glu, Pro or Gln

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<223> Xaa in position 26 is Pro, Ser or Thr

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<223> Xaa in position 27 is Asn, Pro or Ser

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<223> Xaa in position 29 is Glu or Ser

<220>
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<222> (30)..(30)

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<223> Xaa in position 30 is Glu or Gly

<220>
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<220>
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<222> (32)..(32)
<223> Xaa in position 32 is Phe or Leu

<220>
<221> Variant
<222> (33)..(33)
<223> Xaa in position 33 is any amino acid

<220>
<221> Variant
<222> (34)..(34)
<223> Xaa in position 34 is Lys or Arg

<220>
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<220>
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<223> Xaa in position 37 is any amino acid

<220>
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<223> Xaa in position 38 is Asp or Arg

<220>
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<223> Xaa in position 40 to 41 is any amino acid

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<223> Xaa in position 42 is Asp, Glu or Asn

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<223> Xaa in position 44 is Glu, Gln or Ser

<220>
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<223> Xaa in position 45 is Asp, Glu or Gly

<220>
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<222> (46)..(47)

<223> Xaa in position 46 to 47 is any amino acid

<220>

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<222> (48)..(48)

<223> Xaa in position 48 is Glu, Asn or Thr

<220>

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<223> Xaa in position 49 is Asp, Glu, Asn or Ser

<220>

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<223> Xaa in position 50 is any amino acid

<220>

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<222> (51)..(51)

<223> Xaa in position 51 is Glu or Lys

<220>

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<222> (52)..(52)

<223> Xaa in position 52 is Gly or Thr

<220>

<221> Variant

<222> (53)..(53)

<223> Xaa in position 53 is Phe or Val

<400> 1591

Glu	Glu	Xaa	Xaa	Xaa	Gly	Phe	Xaa	Xaa	Arg	Xaa	Leu	Xaa	Arg	Xaa
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Ser	Xaa	Xaa	Glu	Xaa	Asp	Xaa	Xaa	Xaa	Xaa	Ser	Xaa	Xaa	Xaa	Xaa
		20					25				30			
Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		35				40					45			
Xaa	Xaa	Xaa	Xaa	Xaa										
		50												

<210> 1592

<211> 26

<212> PRT

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<220>

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<220>

<221> Variant

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<223> Xaa in position 2 is Ile or Val

<220>

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<223> Xaa in position 3 is Glu or Ser

<220>

<221> Variant

<222> (4)..(4)

<223> Xaa in position 4 is Ser or Val

<220>

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<222> (5)..(5)
<223> Xaa in position 5 is any amino acid

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<222> (6)..(6)
<223> Xaa in position 6 is Leu or Met

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<222> (7)..(7)
<223> Xaa in position 7 is Asp or Gly

<220>
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<222> (10)..(12)
<223> Xaa in position 10 to 12 is any or no amino acid

<220>
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<223> Xaa in position 16 is Gly or Gln

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<223> Xaa in position 17 is Trp or Tyr

<220>
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<222> (18)..(18)
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<220>
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<223> Xaa in position 24 is Leu or Val

<220>
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<220>

PF59082SeqList_PF59082.txt

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<222> (26)..(26)

<223> Xaa in position 26 is Ala or Gly

<400> 1592

Leu Xaa Xaa Xaa Xaa Xaa Xaa Ala Trp Xaa Xaa Xaa Arg Xaa Arg Xaa
1 5 10 15
Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa Xaa Xaa
20 25

<210> 1593

<211> 933

<212> DNA

<213> Arabidopsis thaliana

<220>

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<222> (1)..(933)

<400> 1593

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Met Arg Leu Val Val Ser Ser Cys Leu Leu Val Ala Ala Pro Phe Leu	
1 5 10 15	
tcc tct ctg tta cga gtc tca ctc gcc act gtt gtc ctc aat tcc atc	96
Ser Ser Leu Leu Arg Val Ser Leu Ala Thr Val Val Leu Asn Ser Ile	
20 25 30	
tcc gcc tct ttt gcc gat ctc cca gcc aaa ttt gac ggc tcc gtg acc	144
Ser Ala Ser Phe Ala Asp Leu Pro Ala Lys Phe Asp Gly Ser Val Thr	
35 40 45	
aaa aac gga atc tgt gga gct cta tac gtc gca gat cct ctc gac ggt	192
Lys Asn Gly Ile Cys Gly Ala Leu Tyr Val Ala Asp Pro Leu Asp Gly	
50 55 60	
tgc tca ccg ctt ctc cac gcc gcc gca tcc aac tgg acg caa cac aga	240
Cys Ser Pro Leu Leu His Ala Ala Ala Ser Asn Trp Thr Gln His Arg	
65 70 75 80	
act act aag ttc gct ttg ata atc aga ggc gaa tgt tct ttt gag gat	288
Thr Thr Lys Phe Ala Leu Ile Ile Arg Gly Glu Cys Ser Phe Glu Asp	
85 90 95	
aag ctg ctc aat gcc cag aac tca ggt ttt caa gct gtg att gtc tat	336
Lys Leu Leu Asn Ala Gln Asn Ser Gly Phe Gln Ala Val Ile Val Tyr	
100 105 110	
gac aac att gac aac gaa gat ctc atc gtc atg aag gtg aac cct cag	384
Asp Asn Ile Asp Asn Glu Asp Leu Ile Val Met Lys Val Asn Pro Gln	
115 120 125	
gac att aca gtt gat gca gtc ttc gtt tca aat gtc gcc ggt gag att	432
Asp Ile Thr Val Asp Ala Val Phe Val Ser Asn Val Ala Gly Glu Ile	
130 135 140	
ttg aga aag tac gcg aga ggc cga gat ggt gaa tgc tgc ctt aat ccg	480
Leu Arg Lys Tyr Ala Arg Gly Arg Asp Gly Glu Cys Cys Leu Asn Pro	
145 150 155 160	
cca gac aga ggg agc gct tgg act gtg ttg gcc atc tcc ttc tct	528
Pro Asp Arg Gly Ser Ala Trp Thr Val Leu Ala Ile Ser Phe Phe Ser	
165 170 175	
ctc ctt ctt ata gtc act ttc ctg ttg att gcc ttc ttt gca ccc aga	576
Leu Leu Leu Ile Val Thr Phe Leu Leu Ile Ala Phe Phe Ala Pro Arg	
180 185 190	
cac tgg acc caa tgg cga ggg agg cac acc agg acc atc agg tta gat	624
His Trp Thr Gln Trp Arg Gly Arg His Thr Arg Thr Ile Arg Leu Asp	
195 200 205	
gca aag ctc gtc cac aca ctc ccc tgc ttc acc ttc act gat tct gct	672
Ala Lys Leu Val His Thr Leu Pro Cys Phe Thr Phe Thr Asp Ser Ala	
210 215 220	
cac cac aag gcc ggg gaa aca tgt gct ata tgt ctc gag gat tac aga	720
His His Lys Ala Gly Glu Thr Cys Ala Ile Cys Leu Glu Asp Tyr Arg	
225 230 235 240	
ttt gga gaa agc ctc aga ctt ctc ccc tgc caa cat gct ttt cac ttg	768
Phe Gly Glu Ser Leu Arg Leu Leu Pro Cys Gln His Ala Phe His Leu	
245 250 255	
aat tgc atc gac tct tgg ttg aca aaa tgg ggt aca tct tgc cct gtg	816

PF59082SeqList_PF59082.txt

Asn	Cys	Ile	Asp	Ser	Trp	Leu	Thr	Lys	Trp	Gly	Thr	Ser	Cys	Pro	Val		
			260					265					270				
tgc	aag	cat	gac	ata	aga	acc	gag	act	atg	tct	tct	gag	gta	cat	aaa		864
Cys	Lys	His	Asp	Ile	Arg	Thr	Glu	Thr	Met	Ser	Ser	Glu	Val	His	Lys		
		275					280					285					
cga	gag	agt	ccg	aga	aca	gat	aca	agt	acg	agt	aga	ttt	gcc	ttt	gcc		912
Arg	Glu	Ser	Pro	Arg	Thr	Asp	Thr	Ser	Thr	Ser	Arg	Phe	Ala	Phe	Ala		
		290				295					300						
caa	tcc	agt	caa	agc	cgt	tag											933
Gln	Ser	Ser	Gln	Ser	Arg												
305					310												

<210> 1594

<211> 310

<212> PRT

<213> Arabidopsis thaliana

<400> 1594

Met	Arg	Leu	Val	Val	Ser	Ser	Cys	Leu	Leu	Val	Ala	Ala	Pro	Phe	Leu		
1				5					10					15			
Ser	Ser	Leu	Leu	Arg	Val	Ser	Leu	Ala	Thr	Val	Val	Leu	Asn	Ser	Ile		
			20					25					30				
Ser	Ala	Ser	Phe	Ala	Asp	Leu	Pro	Ala	Lys	Phe	Asp	Gly	Ser	Val	Thr		
		35					40					45					
Lys	Asn	Gly	Ile	Cys	Gly	Ala	Leu	Tyr	Val	Ala	Asp	Pro	Leu	Asp	Gly		
	50					55					60						
Cys	Ser	Pro	Leu	Leu	His	Ala	Ala	Ala	Ser	Asn	Trp	Thr	Gln	His	Arg		
65					70					75					80		
Thr	Thr	Lys	Phe	Ala	Leu	Ile	Ile	Arg	Gly	Glu	Cys	Ser	Phe	Glu	Asp		
			85						90					95			
Lys	Leu	Leu	Asn	Ala	Gln	Asn	Ser	Gly	Phe	Gln	Ala	Val	Ile	Val	Tyr		
			100					105					110				
Asp	Asn	Ile	Asp	Asn	Glu	Asp	Leu	Ile	Val	Met	Lys	Val	Asn	Pro	Gln		
		115					120					125					
Asp	Ile	Thr	Val	Asp	Ala	Val	Phe	Val	Ser	Asn	Val	Ala	Gly	Glu	Ile		
	130					135					140						
Leu	Arg	Lys	Tyr	Ala	Arg	Gly	Arg	Asp	Gly	Glu	Cys	Cys	Leu	Asn	Pro		
145					150					155				160			
Pro	Asp	Arg	Gly	Ser	Ala	Trp	Thr	Val	Leu	Ala	Ile	Ser	Phe	Phe	Ser		
			165					170						175			
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PF59082SeqList_PF59082.txt

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Val	Gly	Ser	His	Leu	Ser	Pro	Pro	Ile	Ser	Ile	Arg	Tyr	Trp	Ser	Ser
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Cys Val Gly Glu Lys Leu Arg Ile Leu Pro Cys Cys His Lys Phe His	
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Ser Ala Ile Gln Ile Ser Arg Ala Ala Ser Gln Thr Pro Ser Val Ser	
370 375 380	
cgt aac cac tcc ata gcc agt aca cct tat gtt cag cca tct ctt agg	1669
Arg Asn His Ser Ile Ala Ser Thr Pro Tyr Val Gln Pro Ser Leu Arg	
400 405 410	
tcc tcc tac cat caa tcc ccc tcc cta agc atc agc cga agc tcc gta	1717
Ser Ser Tyr His Gln Ser Pro Ser Leu Ser Ile Ser Arg Ser Ser Val	
420 425 430	
gat ctt agg aat gca tcc caa aga tct cta gct tct cac ttg aat tca	1765
Asp Leu Arg Asn Ala Ser Gln Arg Ser Leu Ala Ser His Leu Asn Ser	
435 440 445	
cca tgt tcc atg gga tac cca tct ttg tca tct ctt aac tca agg tac	1813
Pro Cys Ser Met Gly Tyr Pro Ser Leu Ser Ser Leu Asn Ser Arg Tyr	
450 455 460	
atg tct cca cac att cca agt cca agc aat gct tca gta agc tat atg	1861
Met Ser Pro His Ile Pro Ser Pro Ser Asn Ala Ser Val Ser Tyr Met	
465 470 475	
ggg tca tcc agt cat caa caa cat cct ctc cgt tat agt gag tcg gct	1909
Gly Ser Ser Ser His Gln Gln His Pro Leu Arg Tyr Ser Glu Ser Ala	
480 485 490	
gca agc ttc tcc cca ttt gca tcg aca cac tcc ctt cca gaa tgt	1954
Ala Ser Phe Ser Pro Phe Ala Ser Thr His Ser Leu Pro Glu Cys	
500 505 510	
taaattgttc aattgattat atcatatgat tgagacgtcc acgcagttga actagtaatt	2014
gccaagtctt gaactaaaag gtggccatgt gatgaccggt ggtctagttg aatagtccta	2074
tgtgatgctt ggggcattcc ctacctctgt catttgactt ccgtcttggc acctggtgta	2134
cattgtagct tctctctggg gttagtttcg ttacatgtg ctggttgagg ttcttacatt	2194
tatagggttg agagcttgca tacagtaact tgtgcgtatt gtttgtactt tgaatgttga	2254
cgttttcatg gccttgatgt ccaagtatag tcaactgcta acaagagaaa tgttgggctg	2314
tattgacact agacacattg aagtaagaag agttctttat gctctgtcta gtggatttgt	2374
ccaactgaat catgagagat catgtgatgt atcactctag tgttatctat acttgatcat	2434
ctaattgcaa ctctgagtat caataatact tgtaaaattt tcgtaaaaaa aatagctaatt	2494
agataatgct ggtaagtgtt atcaatttta aaccatgggg gcaaattaga taccctatctt	2554
gatccgtgga aaattcatca tctagatatg ttaaatacct tctgtggcat cttcgattta	2614
tagnnnnnng natnnnt	2631

<210> 1598
 <211> 510
 <212> PRT
 <213> Glycine max

PF59082SeqList_PF59082.txt

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<400> 1598
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Gly Thr Ser Asn Leu Leu Leu Phe Phe Ser Leu Met Ser Leu Cys Ala
20      25      30
Met Ala Ala Ser Lys Val Val Leu Ile Gly Asn Asn Ile Thr Leu Ser
35      40      45
Phe Asp Asp Ile Glu Ala Asn Phe Ala Pro Ala Val Lys Gly Ser Gly
50      55      60
Lys Tyr Gly Val Leu Tyr Leu Ala Glu Pro Leu Asp Ala Cys Ala Glu
65      70      75      80
Leu Thr Asn Lys Val Glu Gln Leu Pro Asn Ala Ser Ser Pro Phe Ala
85      90      95
Leu Val Val Arg Gly Gly Cys Ser Phe Glu Glu Lys Val Gly Leu Ala
100      105      110
Gln Lys Ala Gly Phe Lys Ala Val Ile Val Tyr Asp Asn Glu Glu Gly
115      120      125
Gly Ile Leu Val Ala Met Ala Gly Asn Ser Ala Gly Ile Arg Ile His
130      135      140
Ala Val Phe Val Ser Lys Ala Ser Gly Glu Ile Leu Lys Lys Tyr Ala
145      150      155      160
Gly Leu Thr Asn Val Glu Ile Trp Leu Ile Pro Thr Phe Glu Asn Ser
165      170      175
Ala Trp Ser Ile Met Ala Ile Ser Phe Ile Ser Leu Leu Ala Met Ser
180      185      190
Ala Val Leu Ala Thr Cys Phe Phe Val Arg Lys His Arg Ile Arg Arg
195      200      205
Glu Arg Pro Arg Ala Ser Leu Val Arg Glu Phe His Gly Met Ser Ser
210      215      220
Arg Leu Val Lys Ala Met Pro Ser Leu Val Phe Thr Ser Val Leu Glu
225      230      235      240
Asp Asn Cys Thr Ser Arg Thr Cys Ala Ile Cys Leu Glu Asp Tyr Cys
245      250      255
Val Gly Glu Lys Leu Arg Ile Leu Pro Cys Cys His Lys Phe His Ala
260      265      270
Ala Cys Val Asp Ser Trp Leu Thr Ser Trp Arg Thr Phe Cys Pro Val
275      280      285
Cys Lys Arg Asp Ala Arg Thr Gly Leu Thr Asp Pro Pro Pro Ser Glu
290      295      300
Ser Thr Pro Leu Leu Ser Ser Thr Pro Ala Ser Met Ala Ser Ser Val
305      310      315      320
Leu Ser Ser Ala Arg Ser Ser Leu Ala Ser Ser Ser Ala Ile Gln Ile
325      330      335
Ala Arg Thr Ala Ser Met Ala Ser Ser Ala Leu Pro Ser Ala Arg Ser
340      345      350
Ser Leu Ala Ser Ser Ser Ala Ile Gln Ile Ala Arg Thr Ala Ser Met
355      360      365
Ala Ser Ser Ala Leu His Ser Ala Arg Ser Ser Leu Ala Ser Ser Ser
370      375      380
Ala Ile Gln Ile Ser Arg Ala Ala Ser Gln Thr Pro Ser Val Ser Arg
385      390      395      400
Asn His Ser Ile Ala Ser Thr Pro Tyr Val Gln Pro Ser Leu Arg Ser
405      410      415
Ser Tyr His Gln Ser Pro Ser Leu Ser Ile Ser Arg Ser Ser Val Asp
420      425      430
Leu Arg Asn Ala Ser Gln Arg Ser Leu Ala Ser His Leu Asn Ser Pro
435      440      445
Cys Ser Met Gly Tyr Pro Ser Leu Ser Ser Leu Asn Ser Arg Tyr Met
450      455      460
Ser Pro His Ile Pro Ser Pro Ser Asn Ala Ser Val Ser Tyr Met Gly
465      470      475      480
Ser Ser Ser His Gln Gln His Pro Leu Arg Tyr Ser Glu Ser Ala Ala
485      490      495
Ser Phe Ser Pro Phe Ala Ser Thr His Ser Leu Pro Glu Cys
500      505      510

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<210> 1599

<211> 1381

PF59082SeqList_PF59082.txt

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (69)..(899)

<400> 1599

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tcccggcg atg agc ccc cgt gtg gtc ctc ctc ttc ctc gcc gcc ctc cgc      110
      Met Ser Pro Arg Val Val Leu Leu Phe Leu Ala Ala Leu Arg
      1      5      10
ccc tgc gcc gcc ctc gtc cgc ctt cac tcc acc act ttt tcc ttc act      158
Pro Cys Ala Ala Leu Val Arg Leu His Ser Thr Thr Phe Ser Phe Thr
      15      20      25      30
ttc ctt gac gcc cca gcg cgc ttt ggc ccc cga gtg agc ggc gat ggg      206
Phe Leu Asp Ala Pro Ala Arg Phe Gly Pro Arg Val Ser Gly Asp Gly
      35      40      45
atc tgc ggc tcc ctg cgt gcc gct gac ccg gcc gag gcg tgt gag acc      254
Ile Cys Gly Ser Leu Arg Ala Ala Asp Pro Ala Glu Ala Cys Glu Thr
      50      55      60
atc aaa gac cgc ggc ggc cgc cgc ggc gcg ggc agg aag gct ttc gtg      302
Ile Lys Asp Arg Gly Gly Arg Arg Gly Ala Gly Arg Lys Ala Phe Val
      65      70      75
ctg atc gcg agg ggc aac tgc agc ttt gag gag aag gtg cgg gcg gcg      350
Leu Ile Ala Arg Gly Asn Cys Ser Phe Glu Glu Lys Val Arg Ala Ala
      80      85      90
cag caa gcg ggg ttc gac gcc tcc atc gtg tac gat gag gag aag      398
Gln Gln Ala Gly Phe Asp Ala Ser Ile Val Tyr Asp Asp Glu Glu Lys
      95      100      105      110
gcc agc ctt tac tcc atg gtt ggt gaa tct gat ggc ata cac ata cct      446
Ala Ser Leu Tyr Ser Met Val Gly Glu Ser Asp Gly Ile His Ile Pro
      115      120      125
gcg ata ttt gtt tcc aag atg gct ggt gaa aca cta aag aag ttt gcc      494
Ala Ile Phe Val Ser Lys Met Ala Gly Glu Thr Leu Lys Lys Phe Ala
      130      135      140
agg ggt gaa gat gaa gag tgc tgt att aac tcg tcg atg gat gag act      542
Arg Gly Glu Asp Glu Glu Cys Ile Asn Ser Ser Met Asp Glu Thr
      145      150      155
gca ggg aca gtg ttg gta atg tca ttt gtg tca ctt gtt gtc atc atg      590
Ala Gly Thr Val Leu Val Met Ser Phe Val Ser Leu Val Val Ile Met
      160      165      170
tca gtt ctt gct tct ttt cta ttt gct cga aac tgc cga ctt cta cgc      638
Ser Val Leu Ala Ser Phe Leu Phe Ala Arg Asn Cys Arg Leu Leu Arg
      175      180      185      190
cat gga gtt gat aat cac cca cct tac gtc aag aaa caa gtg gtg gaa      686
His Gly Val Asp Asn His Pro Pro Tyr Val Lys Lys Gln Val Val Glu
      195      200      205
aag ttt ccc tgc tca gcg tac agt gct ccc tgt tct agt gaa gat aat      734
Lys Phe Pro Cys Ser Ala Tyr Ser Ala Pro Cys Ser Ser Glu Asp Asn
      210      215      220
ttc cag gaa gct tgt gca att tgc tta gaa gac tac aat aat ggt gat      782
Phe Gln Glu Ala Cys Ala Ile Cys Leu Glu Asp Tyr Asn Asn Gly Asp
      225      230      235
atg ctt aga cat ctc cca tgc aag cat gaa ttt cac aag atc tgt att      830
Met Leu Arg His Leu Pro Cys Lys His Glu Phe His Lys Ile Cys Ile
      240      245      250
gat tct tgg ctc aca aaa ggc atc ttc tgc cct ata tgc aag cta      878
Asp Ser Trp Leu Thr Lys Trp Gly Ile Phe Cys Pro Ile Cys Lys Leu
      255      260      265      270
gaa gta aca ttg ggc ggg taggcacact tcattactgc atccaagtgc      926
Glu Val Thr Leu Gly
      275
tggcagttct attgaagatt gttgatcttt tgatccattg cgaggttcaa tattcatttt      986

aatgattgat ctttgagaat gaagtacaga tctcagttcc tcaggttggg ccttgtagtg      1046

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PF59082SeqList_PF59082.txt

tgctactaga ctactgcgtt caggttaata tttcgatcat ctgtttgata tccttgtttg 1106
 gtgtgtggaa gagctcaagg agctctgctg ctgataaatg tcagcacttc tgttgcagtg 1166
 tattgccctg ttttcctaga gaaattaggt gttgtgtgca agcaaagtgt aatcgtaagt 1226
 ccaatgtaaa ccccttttat accaggttac gttaccttgc tcattttatt ttgtgggcac 1286
 agataaatgc tcgttaatta ggcagggggt gatcttactc taaaaaattg tcctaaggct 1346
 cagaaataac gatgtttgaa gatgcatttg ttgcg 1381

<210> 1600
 <211> 276
 <212> PRT
 <213> Zea mays

<400> 1600
 Met Ser Pro Arg Val Val Leu Leu Phe Leu Ala Ala Leu Arg Pro Cys
 1 5 10 15
 Ala Ala Leu Val Arg Leu His Ser Thr Thr Phe Ser Phe Thr Phe Leu
 20 25 30
 Asp Ala Pro Ala Arg Phe Gly Pro Arg Val Ser Gly Asp Gly Ile Cys
 35 40 45
 Gly Ser Leu Arg Ala Ala Asp Pro Ala Glu Ala Cys Glu Thr Ile Lys
 50 55 60
 Asp Arg Gly Gly Arg Arg Gly Ala Gly Arg Lys Ala Phe Val Leu Ile
 65 70 75 80
 Ala Arg Gly Asn Cys Ser Phe Glu Glu Lys Val Arg Ala Ala Gln Gln
 85 90 95
 Ala Gly Phe Asp Ala Ser Ile Val Tyr Asp Asp Glu Glu Lys Ala Ser
 100 105 110
 Leu Tyr Ser Met Val Gly Glu Ser Asp Gly Ile His Ile Pro Ala Ile
 115 120 125
 Phe Val Ser Lys Met Ala Gly Thr Leu Lys Lys Phe Ala Arg Gly
 130 135 140
 Glu Asp Glu Glu Cys Cys Ile Asn Ser Ser Met Asp Glu Thr Ala Gly
 145 150 155 160
 Thr Val Leu Val Met Ser Phe Val Ser Leu Val Val Ile Met Ser Val
 165 170 175
 Leu Ala Ser Phe Leu Phe Ala Arg Asn Cys Arg Leu Leu Arg His Gly
 180 185 190
 Val Asp Asn His Pro Pro Tyr Val Lys Lys Gln Val Val Glu Lys Phe
 195 200 205
 Pro Cys Ser Ala Tyr Ser Ala Pro Cys Ser Ser Glu Asp Asn Phe Gln
 210 215 220
 Glu Ala Cys Ala Ile Cys Leu Glu Asp Tyr Asn Asn Gly Asp Met Leu
 225 230 235 240
 Arg His Leu Pro Cys Lys His Glu Phe His Lys Ile Cys Ile Asp Ser
 245 250 255
 Trp Leu Thr Lys Trp Gly Ile Phe Cys Pro Ile Cys Lys Leu Glu Val
 260 265 270
 Thr Leu Gly Gly
 275

<210> 1601
 <211> 1798
 <212> DNA
 <213> Zea mays

PF59082SeqList_PF59082.txt

<220>

<221> CDS

<222> (142)..(1512)

<400> 1601

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tcgtgtcact cccctgctgc tgctgctgcc gggaagatca aatcccgtca aaaggctcca 120

aaggatcaga gttctgtcaa g atg gca tgc cca aga gct cca gca gtg gaa 171
                        Met Ala Cys Pro Arg 5 Ala Pro Ala Val Glu 10
ggg tca ggt gta agt ggc gtt ctt tat gct gaa cct aag gat gca 219
Gly Ser Gly Val Ser Gly Val Leu Tyr Ala Val Glu Pro Lys Asp Ala 25
tgc agt cca ttg aga gcg aaa gcg att caa ggc tct gtc tca cct ttt 267
Cys Ser Pro Leu Arg Ala Lys Ala Ile Gln Gly Ser Val Ser Pro Phe 40
gcg ttg att ata aga ggc ggt tgc caa ttt gat gac aaa att aga aat 315
Ala Leu Ile Ile Arg Gly Gly Cys Gln Phe Asp Asp Lys Ile Arg Asn 55
gca cag aat gct gga ttc aag gct gct gta gta tat aat aat gaa gat 363
Ala Gln Asn Ala Gly Phe Lys Ala Ala Val Val Tyr Asn Asn Glu Asp 70
aat gac atc ctt gtt tca atg gct gga agc tcg ctt ggt gtc cag ata 411
Asn Asp Ile Leu Val Ser Met Ala Gly Ser Ser Leu Gly Val Gln Ile 90
tat gca gtg ttc atc tct aag gca tca ggg gag gag ctg aag aaa tat 459
Tyr Ala Val Phe Ile Ser Lys Ala Ser Gly Glu Glu Leu Lys Lys Tyr 105
tca ggc caa act gat gca gag tta tgg ata ata cca aca tat gag aac 507
Ser Gly Gln Thr Asp Ala Glu Leu Trp Ile Ile Pro Thr Tyr Glu Asn 120
tca gct tgg cca atc atg gca att tca ttc gta tca ctg ctt gct atg 555
Ser Ala Trp Pro Ile Met Ala Ile Ser Phe Val Ser Leu Leu Ala Met 135
tct gct atc cta gtt gca tgt ttc ttt gcg agg aga cac cag atc aga 603
Ser Ala Ile Leu Val Ala Cys Phe Phe Ala Arg Arg His Gln Ile Arg 150
cgg gac agg gca aga ctt ccc cga gct cag gag tcc cat gga atg agc 651
Arg Asp Arg Ala Arg Leu Pro Arg Ala Gln Glu Ser His Gly Met Ser 170
agt caa tta gtt aag gca ata cca agc ctt att ttc aca aaa gtg caa 699
Ser Gln Leu Val Lys Ala Ile Pro Ser Leu Ile Phe Thr Lys Val Gln 185
gaa gac aac tgt aca tca gca aca tgc gcc att tgc ttg gaa gac tac 747
Glu Asp Asn Cys Thr Ser Ala Thr Cys Ala Ile Cys Leu Glu Asp Tyr 200
agt gtt gga gaa aag ata aga gtg cta cct tgt cga cac aag ttc cat 795
Ser Val Gly Glu Lys Ile Arg Val Leu Pro Cys Arg His Lys Phe His 215
gcg gct tgt gtg gac cta tgg ctc acc tca tgg aga aca ttc tgc cct 843
Ala Ala Cys Val Asp Leu Trp Leu Thr Ser Trp Arg Thr Phe Cys Pro 230
gta tgc aag cgg gac gca agt gct gga acg tca gac ccc cct gta tca 891
Val Cys Lys Arg Asp Ala Ser Ala Gly Thr Ser Asp Pro Pro Val Ser 250
gag tct acc cct ttg ctt tca tca tcc gcc aca cgc ttg ccg gaa tca 939
Glu Ser Thr Pro Leu Leu Ser Ser Ser Ala Thr Arg Leu Pro Glu Ser 265
act gtg ttg gct tcc ttg cgg tct aca gca gca gcg tct ccc ccc agg 987
Thr Val Leu Ala Ser Leu Arg Ser Thr Ala Ala Ala Ser Pro Pro Arg 280
acg atc agc cgg cat cct ttg ttg cgg tca ata tcc cgc aat tac tct 1035
Thr Ile Ser Arg His Pro Leu Leu Arg Ser Ile Ser Arg Asn Tyr Ser 295
gtt tca ggt tcc agt atc ctt cgc acc ccc gac tct agg ttt gat gca 1083

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PF59082SeqList_PF59082.txt

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Val Ser Gly Ser Ser Ile Leu Arg Thr Pro Asp Ser Arg Phe Asp Ala
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Asn Ser Ser Ile Cys Thr Ser Gly Ser Asn Leu Asp Leu Ala Asn Val
315 320 325 330
cca tcc cca tgg tct ggc act tgg cac cgt gcg tct gct cac tct ttg 1179
Pro Ser Pro Trp Ser Gly Thr Trp His Arg Ala Ser Ala His Ser Leu
335 340 345
tgc agg ggc tac ttg tcc cca ccg atc ggc atc agg aat acc tca gca 1227
Cys Arg Gly Tyr Leu Ser Pro Pro Ile Gly Ile Arg Asn Thr Ser Ala
350 355 360
cat gtc tcg cgt tct gcc aat gga tct ccc agt cgt tac gta ggc tca 1275
His Val Ser Arg Ser Ala Asn Gly Ser Pro Ser Arg Tyr Val Gly Ser
365 370 375
tca cgc atg tcc cat gga tct tca ggg cag cag cat cct cac ctg agg 1323
Ser Arg Met Ser His Gly Ser Ser Gly Gln Gln His Pro His Leu Arg
380 385 390
cac tgc aca ttg tca ggc ccg agc ctg ttc acc atg gtg ccc cag tca 1371
His Cys Thr Leu Ser Gly Pro Ser Leu Phe Thr Met Val Pro Gln Ser
395 400 405 410
ccg caa cag aac cag ttg cag cat ggt gga tac tcg gaa aca aat ctg 1419
Pro Gln Gln Asn Gln Leu Gln His Gly Gly Tyr Ser Glu Thr Asn Leu
415 420 425
tcg gct gcc gca tcg gct caa tca ttc cgt cag ctc tac ctg cag cat 1467
Ser Ala Ala Ala Ser Ala Gln Ser Phe Arg Gln Leu Tyr Leu Gln His
430 435 440
tgc cct gat tct gac acg tcg tct cag tca ctt cca ggg tgc tgatctcttg 1519
Cys Pro Asp Ser Asp Thr Ser Ser Gln Ser Leu Pro Gly Cys
445 450 455
ctgcaatatt cactgattct tgcgcccatg agaaatcttg cctggtgctg aattgacatg 1579

tggattttga gctcgtcagc atagttcacc atgatgataa aaaaaagaga aagaagtttg 1639

gagtagtttt acatgtggaa acaaaaactgc ttgtaagaag agagaatgtg cagccccaga 1699

gtgtgagcaa ttttacatgc ttgagtgtac agggggtttgg agtagtcttg gacttgctta 1759

ttttgaggca tgtattgcag tcataggtta cttctgctc 1798

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<210> 1602
 <211> 456
 <212> PRT
 <213> Zea mays

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<400> 1602
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Lys Ala Ile Gln Gly Ser Val Ser Pro Phe Ala Leu Ile Ile Arg Gly
35 40 45
Gly Cys Gln Phe Asp Asp Lys Ile Arg Asn Ala Gln Asn Ala Gly Phe
50 55 60
Lys Ala Ala Val Val Tyr Asn Asn Glu Asp Asn Asp Ile Leu Val Ser
65 70 75 80
Met Ala Gly Ser Ser Leu Gly Val Gln Ile Tyr Ala Val Phe Ile Ser
85 90 95
Lys Ala Ser Gly Glu Glu Leu Lys Lys Tyr Ser Gly Gln Thr Asp Ala
100 105 110
Glu Leu Trp Ile Ile Pro Thr Tyr Glu Asn Ser Ala Trp Pro Ile Met
115 120 125
Ala Ile Ser Phe Val Ser Leu Leu Ala Met Ser Ala Ile Leu Val Ala
130 135 140

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PF59082SeqList_PF59082.txt

Cys Phe Phe Ala Arg Arg His Gln Ile Arg Arg Asp Arg Ala Arg Leu
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Pro Arg Ala Gln Glu Ser His Gly Met Ser Ser Gln Leu Val Lys Ala
165 170 175
Ile Pro Ser Leu Ile Phe Thr Lys Val Gln Glu Asp Asn Cys Thr Ser
180 185 190
Ala Thr Cys Ala Ile Cys Leu Glu Asp Tyr Ser Val Gly Glu Lys Ile
195 200 205
Arg Val Leu Pro Cys Arg His Lys Phe His Ala Ala Cys Val Asp Leu
210 215 220
Trp Leu Thr Ser Trp Arg Thr Phe Cys Pro Val Cys Lys Arg Asp Ala
225 230 235 240
Ser Ala Gly Thr Ser Asp Pro Pro Val Ser Glu Ser Thr Pro Leu Leu
245 250 255
Ser Ser Ser Ala Thr Arg Leu Pro Glu Ser Thr Val Leu Ala Ser Leu
260 265 270
Arg Ser Thr Ala Ala Ala Ser Pro Pro Arg Thr Ile Ser Arg His Pro
275 280 285
Leu Leu Arg Ser Ile Ser Arg Asn Tyr Ser Val Ser Gly Ser Ser Ile
290 295 300
Leu Arg Thr Pro Asp Ser Arg Phe Asp Ala Asn Ser Ser Ile Cys Thr
305 310 315 320
Ser Gly Ser Asn Leu Asp Leu Ala Asn Val Pro Ser Pro Trp Ser Gly
325 330 335
Thr Trp His Arg Ala Ser Ala His Ser Leu Cys Arg Gly Tyr Leu Ser
340 345 350
Pro Pro Ile Gly Ile Arg Asn Thr Ser Ala His Val Ser Arg Ser Ala
355 360 365
Asn Gly Ser Pro Ser Arg Tyr Val Gly Ser Ser Arg Met Ser His Gly
370 375 380
Ser Ser Gly Gln Gln His Pro His Leu Arg His Cys Thr Leu Ser Gly
385 390 395 400
Pro Ser Leu Phe Thr Met Val Pro Gln Ser Pro Gln Gln Asn Gln Leu
405 410 415
Gln His Gly Gly Tyr Ser Glu Thr Asn Leu Ser Ala Ala Ala Ser Ala
420 425 430
Gln Ser Phe Arg Gln Leu Tyr Leu Gln His Cys Pro Asp Ser Asp Thr
435 440 445
Ser Ser Gln Ser Leu Pro Gly Cys
450 455

<210> 1603
<211> 2295
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (429)..(1925)

<400> 1603
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aaattagaga ttcattcgat caattctgat tgtttccttc cattccaaac caccttcaat 180
tctgatttct gcgggtgtgg gatatcgccc ccccttgcca ttccaaatcc tcctctgcaa 240
ttttctcatg gcagctgacg tttccatccc aactcgatcc gcgtcaaccg cccgctaatt 300
cctcctagtt ctagtcccct ctctcctgcg ccgactcatc ttttccctcg tgtcactccc 360

PF59082SeqList_PF59082.txt

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ctgtcaag atg gca tgc cca aga gga agg aca cca ttt ccc ctt tgt ttc Met Ala Cys Pro Arg Gly Arg Thr Pro Phe Pro Leu Cys Phe	470
ttt ctg atg att tgc ctc atg gct cag ctg gga gct tcc aat gtt gta Phe Leu Met Ile Cys Leu Met Ala Gln Leu Gly Ala Ser Asn Val Val	518
ctc atg gcg aac aac act acc ttg tcg ttg gat gat gtc gag gca act Leu Met Ala Asn Asn Thr Thr Leu Ser Leu Asp Asp Val Glu Ala Thr	566
ttt act cca gca gtg gaa ggt tca ggt gta agt ggc gtt ctt tat gct Phe Thr Pro Ala Val Glu Gly Ser Gly Val Ser Gly Val Leu Tyr Ala	614
gtg gaa cct aag gat gca tgc agt cca ttg aga gcg aaa gcg att caa Val Glu Pro Lys Asp Ala Cys Ser Pro Leu Arg Ala Lys Ala Ile Gln	662
ggc tct gtc tca cct ttt gcg ttg att ata aga ggc ggt tgc caa ttt Gly Ser Val Ser Pro Phe Ala Leu Ile Ile Arg Gly Gly Cys Gln Phe	710
gat gac aaa att aga aat gca cag aat gct gga ttc aag gct gct gta Asp Asp Lys Ile Arg Asn Ala Gln Asn Ala Gly Phe Lys Ala Ala Val	758
gta tat aat aat gaa gat aat gac atc ctt gtt tca atg gct gga agc Val Tyr Asn Asn Glu Asp Asn Asp Ile Leu Val Ser Met Ala Gly Ser	806
tcg ctt ggt gtc cag ata tat gca gtg ttc atc tct aag gca tca ggg Ser Leu Gly Val Gln Ile Tyr Ala Val Phe Ile Ser Lys Ala Ser Gly	854
gag gag ctg aag aaa tat tca ggc caa act gat gca gag tta tgg ata Glu Glu Leu Lys Lys Tyr Ser Gly Gln Thr Asp Ala Glu Leu Trp Ile	902
ata cca aca tat gag aac tca gct tgg cca atc atg gca att tca ttc Ile Pro Thr Tyr Glu Asn Ser Ala Trp Pro Ile Met Ala Ile Ser Phe	950
gta tca ctg ctt gct atg tct gct atc cta gtt gca tgt ttc ttt gcg Val Ser Leu Leu Ala Met Ser Ala Ile Leu Val Ala Cys Phe Phe Ala	998
agg aga cac cag atc cgg gac agg gca aga ctt ccc cga gct cag Arg Arg His Gln Ile Arg Arg Asp Arg Ala Arg Leu Pro Arg Ala Gln	1046
gag tcc cat gga atg agc agt caa tta gtt aag gca ata cca agc ctt Glu Ser His Gly Met Ser Ser Gln Leu Val Lys Ala Ile Pro Ser Leu	1094
att ttc aca aaa gtg caa gaa gac aac tgt aca tca gca aca tgc gcc Ile Phe Thr Lys Val Gln Glu Asp Asn Cys Thr Ser Ala Thr Cys Ala	1142
att tgc ttg gaa gac tac agt gtt gga ggc acg aga aga gtg cta cct Ile Cys Leu Glu Asp Tyr Ser Val Gly Gly Thr Arg Arg Val Leu Pro	1190
tgt cga cac aag ttc cat gcg gct tgt gtg gac cta tgg ctc acc tca Cys Arg His Lys Phe His Ala Ala Cys Val Asp Leu Trp Leu Thr Ser	1238
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tca gac ccc cct gta tca gag tct acc cct ttg ctt tca tca tcc gcc Ser Asp Pro Val Ser Glu Ser Thr Pro Leu Leu Ser Ser Ser Ala	1334
aca cgc ttg ccg gaa tca act gtg ttg gct tcc ttg cgg tct aca gca Thr Arg Leu Pro Glu Ser Thr Val Leu Ala Ser Leu Arg Ser Thr Ala	1382
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Ala Ser Ala His Ser Leu Cys Arg Gly Tyr Leu Ser Pro Pro Ile Gly	
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Ile Arg Asn Thr Ser Ala His Val Ser Arg Ser Ala Asn Gly Ser Pro	
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Ser Arg Tyr Val Gly Ser Ser Arg Met Ser His Gly Ser Ser Gly Gln	
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Gln His Pro His Leu Arg His Cys Thr Leu Ser Gly Pro Ser Leu Phe	
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Thr Met Val Pro Gln Ser Pro Gln Asn Gln Leu Gln His Gly Gly	
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PF59082SeqList_PF59082.txt

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Thr Tyr Glu Asn Ser Ala Trp Pro Ile Met Ala Ile Ser Phe Val Ser
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His Gln Ile Arg Arg Asp Arg Ala Arg Leu Pro Arg Ala Gln Glu Ser
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His Gly Met Ser Ser Gln Leu Val Lys Ala Ile Pro Ser Leu Ile Phe
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225 230 235 240
Leu Glu Asp Tyr Ser Val Gly Gly Thr Arg Arg Val Leu Pro Cys Arg
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Arg Phe Asp Ala Asn Ser Ser Ile Cys Thr Ser Gly Ser Asn Leu Asp
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Tyr	Trp	Ser	Ser	His	Val	Ala	His	Ser	Gly	Tyr	Gly	Ser	Pro	Ser	Pro		
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His	Val	Ser	Ser	Ser	Tyr	Ile	Ser	Asn	Ser	Gly	Tyr	Gly	Ser	Ser	Ser		
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Tyr	Cys	Tyr	Leu	Gly	Leu	Gly	Gly	Ser	Ser	His	Ser	Gln	His	Gly	Thr		
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Tyr	Leu	Arg	Arg	Cys	Gly	Glu	Ser	Gly	Pro	Ser	Leu	Cys	Thr	Met	Val		
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Pro	Gln	Gln	Leu	Gln	Trp	Glu	Thr	Asn	Val	Ala	Ala	Gly	Ala	Ser	Ser		
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Ala	Lys	Ser	Leu	Arg	Gln	Ser	Ser	Tyr	Leu	Arg	His	Cys	Gly	Asp	Ser		
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Asp	Ala	Ser	Leu	Ser	Asp	Met	Thr	Ser	Ala	Gln	Ser	Leu	Pro	Arg	Cys		
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 Leu Ser Phe Asp Asp Ile Glu Ala Ser Phe Ser Pro Gly Val Lys Gly
 35 40 45
 Ser Gly Val Ser Gly Val Val Tyr Ala Ser Glu Pro Leu Asn Ala Cys
 50 55 60
 Ser Pro Leu Thr Ile Lys Thr Val Asn Gly Pro Pro Ser Pro Phe Ala
 Seite 2121

PF59082SeqList_PF59082.txt

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Gly Asn Met Asp Val Glu Val Trp Ile Leu Pro Thr Phe Glu Asn Ser
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Ala Val Leu Gly Thr Cys Phe Phe Val Arg Arg His Arg Ile Arg Arg
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Glu His Pro Arg Ile Ala Glu Asp Arg Glu Phe His Gly Met Ser Ser
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Gln Leu Val Lys Ala Ile Pro Ser Leu Ile Phe Thr Lys Val Gln Glu
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Asp Asn Cys Thr Ser Ser Met Cys Ala Ile Cys Leu Ala Asp Tyr Asn
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Val Gly Glu Lys Leu Arg Val Leu Pro Cys Arg His Lys Phe His Ala
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Ala Cys Val Asp Leu Trp Leu Thr Ser Trp Arg Thr Phe Cys Pro Ile
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Cys Lys Arg Asp Ala Arg Ser Gly Ala Ser Glu Val Val Ala Thr Glu
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Asn Pro Phe Ile Ser Ser His Ile Ser Ser Pro Gly Ile Arg Ala Ser
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Arg Ser Ile Thr Asp Leu Gly Asn Ile Ser Ser Leu His Pro Arg Ile
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Ser His Leu Ser Ser Thr His Ser Leu Val Gly Ser His Leu Ser Pro
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Pro Ile Ser Ile Arg Tyr Trp Ser Ser His Val Ala His Ser Gly Tyr
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Gly Ser Pro Ser Pro His Val Ser Ser Ser Tyr Ile Ser Asn Ser Gly
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Tyr Gly Ser Ser Tyr Cys Tyr Leu Gly Leu Gly Gly Ser Ser His
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Arg Phe Gly Pro Arg Val Thr Gly Asp Gly Ile Cys Gly Ser Leu Arg	
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Ala Ala Glu Pro Ala Asp Ala Cys Ala Pro Val Arg Gly Ala Pro Gly	
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Gly Ser Gly Gly Met Ala Phe Val Leu Ile Ala Arg Gly Asn Cys Ser	
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Phe Glu Gly Lys Val Arg Ala Ala Gln Arg Ala Gly Phe Asp Ala Ala	
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ctc gtc cac gac gac gag gac aag gcc agc ctc tac tcc atg gtt ggc	448
Leu Val His Asp Asp Glu Asp Lys Ala Ser Leu Tyr Ser Met Val Gly	
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Asp Pro Glu Gly Ile His Ile Pro Ala Val Phe Val Ser Lys Met Ala	
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Gly Glu Thr Leu Lys Lys Phe Ala Arg Gly Glu Asp Gly Glu Cys Cys	
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Ile Asn Ser Ser Met Asp Glu Thr Ala Gly Thr Val Leu Val Met Ser	
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Phe Val Ser Leu Val Val Ile Ile Ser Val Val Ala Ser Phe Leu Phe	
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Tyr Ile Lys Lys His Val Val Glu Lys Leu Pro Ser Val Val Tyr Lys	
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Ala Pro Cys Ser Ser Gly Asn Asn Cys Glu Glu Ala Cys Ala Ile Cys	
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Leu Glu Asp Tyr Asp Asn Gly Asp Met Leu Arg Leu Leu Pro Cys Lys	
240 245 250	
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His Glu Phe His Val Glu Cys Ile Asp Pro Trp Leu Thr Lys Trp Gly	
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Thr Phe Cys Pro Val Cys Lys Leu Glu Val Leu Thr Gly Gly	
270 275 280	
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atacatccat tccccgaca agtatattccg gatggaggga gtatatacaa gtagtgctcg	1112
gcggcatgac gggtatatcc aggcgtgctg aactggttga tctgttggtg gctgggtttg	1172
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 50 55 60
 Asp Ala Cys Ala Pro Val Arg Gly Ala Pro Gly Gly Ser Gly Gly Met
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 Ala Phe Val Leu Ile Ala Arg Gly Asn Cys Ser Phe Glu Gly Lys Val
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 Arg Ala Ala Gln Arg Ala Gly Phe Asp Ala Ala Leu Val His Asp Asp
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 Glu Asp Lys Ala Ser Leu Tyr Ser Met Val Gly Asp Pro Glu Gly Ile
 115 120 125
 His Ile Pro Ala Val Phe Val Ser Lys Met Ala Gly Glu Thr Leu Lys
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 Asp Glu Thr Ala Gly Thr Val Leu Val Met Ser Phe Val Ser Leu Val
 165 170 175
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 180 185 190
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 195 200 205
 Val Val Glu Lys Leu Pro Ser Val Val Tyr Lys Ala Pro Cys Ser Ser
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 Gly Asn Asn Cys Glu Glu Ala Cys Ala Ile Cys Leu Glu Asp Tyr Asp
 225 230 235 240
 Asn Gly Asp Met Leu Arg Leu Leu Pro Cys Lys His Glu Phe His Val
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 ggt act tca aat ctt ctc ttg ttt ttc tct ctg atg agc ctg tgt gct 96
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PF59082SeqList_PF59082.txt

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Phe	Asp	Asp	Ile	Glu	Ala	Asn	Phe	Ala	Pro	Ala	Val	Lys	Gly	Ser	Gly	
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Lys	Tyr	Gly	Val	Leu	Tyr	Leu	Ala	Glu	Pro	Leu	Asp	Ala	Cys	Ala	Glu	
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Leu	Thr	Asn	Lys	Val	Glu	Gln	Leu	Pro	Asn	Ala	Ser	Ser	Pro	Phe	Ala	
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Leu	Val	Val	Arg	Gly	Gly	Cys	Ser	Phe	Glu	Glu	Lys	Val	Arg	Ile	Ala	
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Gln	Lys	Ala	Gly	Phe	Lys	Ala	Val	Ile	Val	Tyr	Asp	Asn	Glu	Glu	Gly	
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Gly	Ile	Leu	Val	Ala	Met	Ala	Gly	Asn	Ser	Ala	Gly	Ile	Arg	Ile	His	
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Glu	Arg	Pro	Arg	Ala	Ser	Leu	Val	Arg	Glu	Phe	His	Gly	Met	Ser	Ser	
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cgc	cta	gtg	aaa	gca	atg	ccg	agt	ttg	gta	ttt	act	tct	gtt	ttg	gaa	720
Arg	Leu	Val	Lys	Ala	Met	Pro	Ser	Leu	Val	Phe	Thr	Ser	Val	Leu	Glu	
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Asp	Asn	Cys	Thr	Ser	Arg	Thr	Cys	Ala	Ile	Cys	Leu	Glu	Asp	Tyr	Cys	
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Val	Gly	Glu	Lys	Leu	Arg	Ile	Leu	Pro	Cys	Cys	His	Lys	Phe	His	Ala	
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Ala	Cys	Val	Asp	Ser	Trp	Leu	Thr	Ser	Trp	Arg	Thr	Phe	Cys	Pro	Val	
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Cys	Lys	Arg	Asp	Ala	Arg	Thr	Gly	Leu	Thr	Asp	Pro	Pro	Pro	Ser	Glu	
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Leu	Ser	Ser	Ala	Arg	Ser	Ser	Leu	Ala	Ser	Ser	Ser	Ala	Ile	Gln	Ile	
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gcc	cgg	aca	gca	tct	atg	gca	tcc	tct	gcc	tta	cct	tct	gcg	aga	tca	1056
Ala	Arg	Thr	Ala	Ser	Met	Ala	Ser	Ser	Ala	Leu	Pro	Ser	Ala	Arg	Ser	
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Ser	Leu	Ala	Ser	Ser	Ser	Ala	Ile	Gln	Ile	Ala	Arg	Thr	Ala	Ser	Met	
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Ser	Tyr	His	Gln	Ser	Pro	Ser	Leu	Ser	Ile	Ser	Arg	Ser	Ser	Val	Asp	
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Cys	Ser	Met	Gly	Tyr	Pro	Ser	Leu	Ser	Ser	Leu	Asn	Ser	Arg	Tyr	Met	
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Gln	Lys	Ala	Gly	Phe	Lys	Ala	Val	Ile	Val	Tyr	Asp	Asn	Glu	Glu	Gly	
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225				230										240		
Asp	Asn	Cys	Thr	Ser	Arg	Thr	Cys	Ala	Ile	Cys	Leu	Glu	Asp	Tyr	Cys	
			245						250					255		
Val	Gly	Glu	Lys	Leu	Arg	Ile	Leu	Pro	Cys	Cys	His	Lys	Phe	His	Ala	
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			275					280					285			
Cys	Lys	Arg	Asp	Ala	Arg	Thr	Gly	Leu	Thr	Asp	Pro	Pro	Pro	Ser	Glu	
			290					295					300			
Ser	Thr	Pro	Leu	Leu	Ser	Ser	Thr	Pro	Ala	Ser	Met	Ala	Ser	Ser	Val	
305				310											320	
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PF59082SeqList_PF59082.txt

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 Ser Leu Ala Ser Ser Ser Ala Ile Gln Ile Ala Arg Thr Ala Ser Met
 355 360 365
 Ala Ser Ser Ala Leu His Ser Ala Arg Ser Ser Leu Ala Ser Ser Ser
 370 375 380
 Ala Ile Gln Ile Ser Arg Ala Ala Ser Gln Thr Pro Ser Val Ser Arg
 385 390 400
 Asn His Ser Ile Ala Ser Thr Pro Tyr Val Gln Pro Ser Leu Arg Ser
 405 410 415
 Ser Tyr His Gln Ser Pro Ser Leu Ser Ile Ser Arg Ser Ser Val Asp
 420 425 430
 Leu Arg Asn Ala Ser Gln Arg Ser Leu Ala Ser His Leu Asn Ser Pro
 435 440 445
 Cys Ser Met Gly Tyr Pro Ser Leu Ser Ser Leu Asn Ser Arg Tyr Met
 450 455 460
 Ser Pro His Ile Pro Ser Pro Ser Asn Ala Ser Val Ser Tyr Met Gly
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 485 490 495
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 <212> DNA
 <213> Arabidopsis thaliana

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 Ser Tyr Val Val Asp Ala Gly Gln Val Ile Leu Val Asp Ser Asn Ile
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 act cgc tct ttt gtc gac atg gaa gct gat ttc tct cca tca gtg act 144
 Thr Arg Ser Phe Val Asp Met Glu Ala Asp Phe Ser Pro Ser Val Thr
 35 40 45
 acg gtg gaa acc gga gtg gtt tat gta gct gag cct ctc aac gct tgc 192
 Thr Val Glu Thr Gly Val Tyr Val Ala Glu Pro Leu Asn Ala Cys
 50 55 60
 cga aac ttg agg aat aaa ccg gag cag agc cct tat ggt act tcc cct 240
 Arg Asn Leu Arg Asn Lys Pro Glu Gln Ser Pro Tyr Gly Thr Ser Pro
 65 70 75 80
 ctt gtg ttg atc ata aga gga ggc tgc agt ttt gag tac aaa gtc aga 288
 Leu Val Leu Ile Ile Arg Gly Gly Cys Ser Phe Glu Tyr Lys Val Arg
 85 90 95
 aac gcg cag aga agc ggt ttc aag gct gcc att gtc tat gac aat gtg 336
 Asn Ala Gln Arg Ser Gly Phe Lys Ala Ile Val Tyr Asp Asn Val
 100 105 110
 gac cgc aac ttc tta tcc gca atg ggg gga gac tcg gac ggt ata aag 384
 Asp Arg Asn Phe Leu Ser Ala Met Gly Gly Asp Ser Asp Gly Ile Lys
 115 120 125
 att caa gcg gtt ttt gtg atg aag aga gcc gga gaa atg ctc aag aag 432
 Ile Gln Ala Val Phe Val Met Lys Arg Ala Gly Glu Met Leu Lys Lys
 130 135 140
 tac gcg ggt tcg gag gaa atg gaa gtc atg ttg gtt cct cct aat aca 480
 Tyr Ala Gly Ser Glu Glu Met Glu Val Met Leu Val Pro Pro Asn Thr
 145 150 155 160
 gag gac tcg gtg tgg tca ttg tac gct tcc ata gca ttg atc ttg tcg 528
 Glu Asp Ser Val Trp Ser Leu Tyr Ala Ser Ile Ala Leu Ile Leu Ser
 165 170 175
 ctg gct att ttt tgt gtt atg gtt act tgt gtc ttc ttc tat aga tat 576
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Thr	Arg	Ser	Phe	Val	Asp	Met	Glu	Ala	Asp	Phe	Ser	Pro	Ser	Val	Thr
		35					40					45			
Thr	Val	Glu	Thr	Gly	Val	Val	Tyr	Val	Ala	Glu	Pro	Leu	Asn	Ala	Cys
	50					55					60				
Arg	Asn	Leu	Arg	Asn	Lys	Pro	Glu	Gln	Ser	Pro	Tyr	Gly	Thr	Ser	Pro
65					70					75					80
Leu	Val	Leu	Ile	Ile	Arg	Gly	Gly	Cys	Ser	Phe	Glu	Tyr	Lys	Val	Arg
				85					90					95	
Asn	Ala	Gln	Arg	Ser	Gly	Phe	Lys	Ala	Ala	Ile	Val	Tyr	Asp	Asn	Val
			100					105					110		
Asp	Arg	Asn	Phe	Leu	Ser	Ala	Met	Gly	Gly	Asp	Ser	Asp	Gly	Ile	Lys
		115					120					125			

PF59082SeqList_PF59082.txt

Ile Gln Ala Val Phe Val Met Lys Arg Ala Gly Glu Met Leu Lys Lys
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 Tyr Ala Gly Ser Glu Glu Met Glu Val Met Leu Val Pro Pro Asn Thr
 145 150 155 160
 Glu Asp Ser Val Trp Ser Leu Tyr Ala Ser Ile Ala Leu Ile Leu Ser
 165 170 175
 Leu Ala Ile Phe Cys Val Met Val Thr Cys Val Phe Phe Tyr Arg Tyr
 180 185 190
 Cys Ser Thr Ile Arg Asn Ser Thr Ser Gln Phe Asn Gly Met Cys Arg
 195 200 205
 Arg Thr Val Lys Ala Met Pro Ser Val Thr Phe Thr Cys Ala Lys Ile
 210 215 220
 Asp Asn Thr Thr Gly Phe Ser Cys Ala Ile Cys Leu Glu Asp Tyr Ile
 225 230 235 240
 Val Gly Asp Lys Leu Arg Val Leu Pro Cys Ser His Lys Phe His Val
 245 250 255
 Ala Cys Val Asp Ser Trp Leu Ile Ser Trp Arg Thr Phe Cys Pro Val
 260 265 270
 Cys Lys Arg Asp Ala Arg Thr Thr Ala Asp Glu Pro Leu Ala Thr Glu
 275 280 285
 Ser Thr Pro Phe Leu Ser Ser Ile Ala Thr Ser Ser Leu Val Cys
 290 295 300
 Ile Asp Ser Pro Pro Leu Gly Ser Ser Val Ser Phe Ser Pro Ala His
 305 310 315 320
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 325 330 335
 Gly Ser Arg Ile Ser Glu Asn Leu Arg Arg Gln Ala Ser Pro Leu Gln
 340 345 350
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 355 360 365
 Gly Tyr Ser Thr Met Ser Pro Leu Asn Ala Met Gly Met Ser Pro Tyr
 370 375 380
 Arg Pro Tyr Pro Ser Asn Ala Ser Pro Gly Leu Phe Ser Ser Thr Asn
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 Tyr Ala Ala Glu Pro Leu Asp Ala Cys Ser Tyr Leu Thr Asn Met Ala
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 Glu Lys Gly Ser Lys Phe Arg Pro Ser Tyr Val Leu Ile Val Arg Gly
 35 40 45
 ggc tgt agt ttt gag gaa aaa ata aga aat gcg cag gaa gct gga tac 192
 Gly Cys Ser Phe Glu Glu Lys Ile Arg Asn Ala Gln Glu Ala Gly Tyr
 50 55 60
 aaa gct gcg atc gtc tat aac gat aga tat gag gag ctc tta gta cgt 240
 Lys Ala Ala Ile Val Tyr Asn Asp Arg Tyr Glu Glu Leu Leu Val Arg
 65 70 75 80
 aga aat tca tct ggt gtc tat ata cat ggt gtg ctt gtt aca aga aca 288
 Arg Asn Ser Ser Gly Val Tyr Ile His Gly Val Leu Val Thr Arg Thr
 85 90 95
 tca ggg gag gta ctt aaa gag tat acc agt cga gct gag atg gag ctc 336
 Ser Gly Glu Val Leu Lys Glu Tyr Thr Ser Arg Ala Glu Met Glu Leu

PF59082SeqList_PF59082.txt

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Thr	Phe	Val	Ser	Leu	Leu	Val	Ile	Ser	Ala	Val	Leu	Ala	Ser	Tyr	Phe	
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Gly	Gly	Gln	Gly	His	Ser	Arg	Met	Pro	Lys	Asp	Leu	Leu	Gln	Ser	Met	
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Pro	Thr	Glu	Val	Tyr	Thr	Gly	Val	Leu	Glu	Glu	Gly	Ser	Thr	Ser	Val	
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Thr	Cys	Ala	Ile	Cys	Ile	Asp	Asp	Tyr	Arg	Val	Gly	Glu	Ile	Leu	Arg	
atc	cta	cct	tgc	aaa	cac	aaa	tat	cat	gcg	gtg	tgt	atc	gat	tct	tgg	672
Ile	Leu	Pro	Cys	Lys	His	Lys	Tyr	His	Ala	Val	Cys	Ile	Asp	Ser	Trp	
ctc	gga	cgt	tgt	aga	tcc	ttt	tgt	ccg	gtt	tgt	aaa	caa	aat	cca	aga	720
Leu	Gly	Arg	Cys	Arg	Ser	Phe	Cys	Pro	Val	Cys	Lys	Gln	Asn	Pro	Arg	
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Thr	Gly	Asn	Asp	Val	Pro	Pro	Ala	Ser	Glu	Thr	Thr	Pro	Leu	Ile	Ser	
cct	ggg	ccg	aac	tct	att	act	tca	cta	caa	tcg	ttt	tat	gat	cta	cca	816
Pro	Gly	Pro	Asn	Ser	Ile	Thr	Ser	Leu	Gln	Ser	Phe	Tyr	Asp	Leu	Pro	
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<211> 279

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Glu	Lys	Gly	Ser	Lys	Phe	Arg	Pro	Ser	Tyr	Val	Leu	Ile	Val	Arg	Gly
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Gly	Cys	Ser	Phe	Glu	Glu	Lys	Ile	Arg	Asn	Ala	Gln	Glu	Ala	Gly	Tyr
	50					55					60				
Lys	Ala	Ala	Ile	Val	Tyr	Asn	Asp	Arg	Tyr	Glu	Glu	Leu	Leu	Val	Arg
65				70						75				80	
Arg	Asn	Ser	Ser	Gly	Val	Tyr	Ile	His	Gly	Val	Leu	Val	Thr	Arg	Thr
				85					90					95	
Ser	Gly	Glu	Val	Leu	Lys	Glu	Tyr	Thr	Ser	Arg	Ala	Glu	Met	Glu	Leu
			100					105					110		
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Thr	Phe	Val	Ser	Leu	Leu	Val	Ile	Ser	Ala	Val	Leu	Ala	Ser	Tyr	Phe
	130					135					140				
Ser	Val	Arg	Arg	His	Arg	Ile	Arg	Gln	His	Val	Arg	Asp	Leu	His	His
145				150						155				160	
Gly	Gly	Gln	Gly	His	Ser	Arg	Met	Pro	Lys	Asp	Leu	Leu	Gln	Ser	Met
				165					170					175	
Pro	Thr	Glu	Val	Tyr	Thr	Gly	Val	Leu	Glu	Glu	Gly	Ser	Thr	Ser	Val
			180					185					190		
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		195					200					205			
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	210					215					220				

PF59082SeqList_PF59082.txt

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 Thr Gly Asn Asp Val Pro Pro Ala Ser Glu Thr Thr Pro Leu Ile Ser
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 260 265 270
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 Leu Ala Ser Ala Lys Val Val Leu Ile Gly Lys Asn Thr Ile Leu Ser
 20 25 30
 ttt gat gat gtc gag gca act ttc act cca att gtt aga aac tcg ggg 144
 Phe Asp Asp Val Glu Ala Thr Phe Thr Pro Ile Val Arg Asn Ser Gly
 35 40 45
 gaa tgt gga att ttg tac gtt gca gag cct ctt gag gca tgc tcg gat 192
 Glu Cys Gly Ile Leu Tyr Val Ala Glu Pro Leu Glu Ala Cys Ser Asp
 50 55 60
 ata acc aac atg gcg gaa aaa aga tca aag tat agg tcc tct tat gta 240
 Ile Thr Asn Met Ala Glu Lys Arg Ser Lys Tyr Arg Ser Ser Tyr Val
 65 70 75 80
 ttg atc gtc ctt ggt ggc tgt agt ttt gag gaa aag gtt aga aag gcg 288
 Leu Ile Val Leu Gly Gly Cys Ser Phe Glu Glu Lys Val Arg Lys Ala
 85 90 95
 cag aaa gct gga tac aaa gct gcg att gtc tat aac gat gga tat gat 336
 Gln Lys Ala Gly Tyr Lys Ala Ala Ile Val Tyr Asn Asp Gly Tyr Asp
 100 105 110
 gag ctc tta gta cct atg gca gga aat tca tct ggt gtg gat ata cat 384
 Glu Leu Leu Val Pro Met Ala Gly Asn Ser Ser Gly Val Asp Ile His
 115 120 125
 ggc ttg ctt gtt aca aga gca tca ggg gag gtg ctt aaa ggg tac gcg 432
 Gly Leu Leu Val Thr Arg Ala Ser Gly Glu Val Leu Lys Gly Tyr Ala
 130 135 140
 gat caa gac gag atg aag ctt tgg ctc atc ccg gga ttc ggg att tca 480
 Asp Gln Asp Glu Met Lys Leu Trp Leu Ile Pro Gly Phe Gly Ile Ser
 145 150 155 160
 tct tgg tcc atc atg ggt att aca ttc ata tct tta ctc gcc atg tct 528
 Ser Trp Ser Ile Met Gly Ile Thr Phe Ile Ser Leu Leu Ala Met Ser
 165 170 175
 gct att cta gcc act tgt ttc gtt gtc cgt agg cat caa att aga cag 576
 Ala Ile Leu Ala Thr Cys Phe Val Val Arg Arg His Gln Ile Arg Gln
 180 185 190
 agt gtg agg gat tta cca cat ggt ggc caa gga ctt tct tgt atg cca 624
 Ser Val Arg Asp Leu Pro His Gly Gly Gln Gly Leu Ser Cys Met Pro
 195 200 205
 aga gac ttg ttg caa agc atg ccg act gaa gta tat agc ggt gtt ctt 672
 Arg Asp Leu Leu Gln Ser Met Pro Thr Glu Val Tyr Ser Gly Val Leu
 210 215 220
 gaa gaa agt tca act tcg gtt act tgt gct ata tgt atc gat gat tat 720
 Glu Glu Ser Ser Thr Ser Val Thr Cys Ala Ile Cys Ile Asp Asp Tyr
 225 230 235 240
 tgc gtt ggt gaa aaa ctc cga atc cta cct tgc aaa cac aaa tat cat 768
 Cys Val Gly Glu Lys Leu Arg Ile Leu Pro Cys Lys His Lys Tyr His
 245 250 255
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PF59082SeqList_PF59082.txt

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Val Cys Lys Gln Asn Pro Arg Thr Gly Asn Asp Val Pro Pro Ala Ser			
275	280	285	
gaa aca aca cct ctg att tct cct agc ccg aac tct att act tca cta	912		
Glu Thr Thr Pro Leu Ile Ser Pro Ser Pro Asn Ser Ile Thr Ser Leu			
290	295	300	
caa tcg ttt tat gat cta cca ata gtt gtc aga gta tat ctg taa	957		
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305	310	315	

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 35 40 45
 Glu Cys Gly Ile Leu Tyr Val Ala Glu Pro Leu Glu Ala Cys Ser Asp
 50 55 60
 Ile Thr Asn Met Ala Glu Lys Arg Ser Lys Tyr Arg Ser Ser Tyr Val
 65 70 75 80
 Leu Ile Val Leu Gly Gly Cys Ser Phe Glu Glu Lys Val Arg Lys Ala
 85 90 95
 Gln Lys Ala Gly Tyr Lys Ala Ala Ile Val Tyr Asn Asp Gly Tyr Asp
 100 105 110
 Glu Leu Leu Val Pro Met Ala Gly Asn Ser Ser Gly Val Asp Ile His
 115 120 125
 Gly Leu Leu Val Thr Arg Ala Ser Gly Glu Val Leu Lys Gly Tyr Ala
 130 135 140
 Asp Gln Asp Glu Met Lys Leu Trp Leu Ile Pro Gly Phe Gly Ile Ser
 145 150 155 160
 Ser Trp Ser Ile Met Gly Ile Thr Phe Ile Ser Leu Leu Ala Met Ser
 165 170 175
 Ala Ile Leu Ala Thr Cys Phe Val Val Arg Arg His Gln Ile Arg Gln
 180 185 190
 Ser Val Arg Asp Leu Pro His Gly Gly Gln Gly Leu Ser Cys Met Pro
 195 200 205
 Arg Asp Leu Leu Gln Ser Met Pro Thr Glu Val Tyr Ser Gly Val Leu
 210 215 220
 Glu Glu Ser Ser Thr Ser Val Thr Cys Ala Ile Cys Ile Asp Asp Tyr
 225 230 235 240
 Cys Val Gly Glu Lys Leu Arg Ile Leu Pro Cys Lys His Lys Tyr His
 245 250 255
 Ala Val Cys Ile Asp Ser Trp Leu Gly Arg Cys Arg Ser Phe Cys Pro
 260 265 270
 Val Cys Lys Gln Asn Pro Arg Thr Gly Asn Asp Val Pro Pro Ala Ser
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Leu	Ala	Ser	Ser	Lys	Val	Ile	Leu	Met	Arg	Asn	Asn	Ile	Thr	Leu	Ser	
			20					25					30			
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Phe	Asp	Asp	Ile	Glu	Ala	Asn	Phe	Ala	Pro	Ser	Val	Lys	Gly	Thr	Gly	
		35					40					45				
gaa	att	gga	gtg	gtt	tat	gtg	gct	gag	cct	ctt	gac	gct	tgt	caa	aat	192
Glu	Ile	Gly	Val	Val	Tyr	Val	Ala	Glu	Pro	Leu	Asp	Ala	Cys	Gln	Asn	
		50				55					60					
ctt	atg	aat	aaa	cca	gaa	cag	agc	tcc	aat	gaa	act	tct	cct	ttt	gtg	240
Leu	Met	Asn	Lys	Pro	Glu	Gln	Ser	Ser	Asn	Glu	Thr	Ser	Pro	Phe	Val	
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Leu	Ile	Val	Arg	Gly	Gly	Cys	Ser	Phe	Glu	Glu	Lys	Val	Arg	Lys	Ala	
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cag	aga	gct	ggg	ttc	aaa	gct	gct	att	atc	tat	gac	aat	gaa	gac	cgt	336
Gln	Arg	Ala	Gly	Phe	Lys	Ala	Ala	Ile	Ile	Tyr	Asp	Asn	Glu	Asp	Arg	
		100						105					110			
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Gly	Thr	Leu	Ile	Ala	Met	Ala	Gly	Asn	Ser	Gly	Gly	Ile	Arg	Ile	His	
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Ala	Val	Phe	Val	Thr	Lys	Glu	Thr	Gly	Glu	Val	Leu	Lys	Glu	Tyr	Ala	
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ggg	ttc	ccc	gat	acg	aaa	gtt	tgg	ttg	atc	cca	agt	ttt	gag	aac	tcg	480
Gly	Phe	Pro	Asp	Thr	Lys	Val	Trp	Leu	Ile	Pro	Ser	Phe	Glu	Asn	Ser	
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gcg	tgg	tct	att	atg	gcg	gtt	tcg	ttt	atc	tcg	ctg	ctt	gca	atg	tcg	528
Ala	Trp	Ser	Ile	Met	Ala	Val	Ser	Phe	Ile	Ser	Leu	Leu	Ala	Met	Ser	
			165					170						175		
gct	gtt	ctc	gct	act	tgt	ttc	ttt	gtg	cgt	agg	cat	cga	ata	aga	agg	576
Ala	Val	Leu	Ala	Thr	Cys	Phe	Phe	Val	Arg	Arg	His	Arg	Ile	Arg	Arg	
		180						185					190			
cgg	aca	tct	cgg	tcc	tct	cga	gtg	cgt	gag	ttt	cac	ggg	atg	agc	cgc	624
Arg	Thr	Ser	Arg	Ser	Ser	Arg	Val	Arg	Glu	Phe	His	Gly	Met	Ser	Arg	
		195					200					205				
cgc	ttg	gtg	aaa	gca	atg	ccg	agt	ctt	ata	ttc	agt	tcg	ttt	cat	gaa	672
Arg	Leu	Val	Lys	Ala	Met	Pro	Ser	Leu	Ile	Phe	Ser	Ser	Phe	His	Glu	
		210				215					220					
gat	aac	act	act	gca	ttc	act	tgt	gct	att	tgc	ctt	gaa	gac	tac	act	720
Asp	Asn	Thr	Thr	Ala	Phe	Thr	Cys	Ala	Ile	Cys	Leu	Glu	Asp	Tyr	Thr	
		225			230				235					240		
gtt	gga	gac	aag	ctc	agg	ctc	tta	cct	tgc	tgt	cac	aag	ttt	cat	gct	768
Val	Gly	Asp	Lys	Leu	Arg	Leu	Leu	Pro	Cys	Cys	His	Lys	Phe	His	Ala	
			245					250						255		
gcg	tgt	gtt	gac	tca	tgg	tta	acc	tct	tgg	aga	act	ttc	tgt	ccg	gtg	816
Ala	Cys	Val	Asp	Ser	Trp	Leu	Thr	Ser	Trp	Arg	Thr	Phe	Cys	Pro	Val	
		260						265					270			
tgc	aaa	cga	gat	gca	aga	acg	agc	acg	gga	gag	cct	cca	gct	tca	gag	864
Cys	Lys	Arg	Asp	Ala	Arg	Thr	Ser	Thr	Gly	Glu	Pro	Pro	Ala	Ser	Glu	
		275					280					285				
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Ser	Thr	Pro	Leu	Leu	Ser	Ser	Ala	Ala	Ser	Ser		Thr	Ser	Ser	Ser	
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ctg	cac	tct	tca	gtc	aga	tca	tct	gca	cta	ttg	att	ggg	cct	tcc	ttg	960
Leu	His	Ser	Ser	Val	Arg	Ser	Ser	Ala	Leu	Leu	Ile	Gly	Pro	Ser	Leu	
		305			310				315						320	
ggc	tca	tta	cca	act	tca	atc	tct	ttc	tct	ccc	gca	tac	gca	agc	tca	1008
Gly	Ser	Leu	Pro	Thr	Ser	Ile	Ser	Phe	Ser	Pro	Ala	Tyr	Ala	Ser	Ser	
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tcc	tat	att	aga	caa	tca	ttc	cag	tct	tcc	tct	aac	cgt	cga	tca	cct	1056
Ser	Tyr	Ile	Arg	Gln	Ser	Phe	Gln	Ser	Ser	Ser	Asn	Arg	Arg	Ser	Pro	
		340					345						350			
cca	ata	agc	gta	agt	cga	agc	tca	gtg	gat	ctc	aga	caa	caa	gca	gct	1104
Pro	Ile	Ser	Val	Ser	Arg	Ser	Ser	Val	Asp	Leu	Arg	Gln	Gln	Ala	Ala	
		355					360					365				
tct	cca	tct	cca	tca	cca	tca	cag	aga	tca	tac	att	tcc	cat	atg	gct	1152

PF59082SeqList_PF59082.txt

Ser	Pro	Ser	Pro	Ser	Pro	Ser	Gln	Arg	Ser	Tyr	Ile	Ser	His	Met	Ala	
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Ser	Pro	Gln	Ser	Leu	Gly	Tyr	Pro	Thr	Ile	Ser	Pro	Phe	Asn	Thr	Arg	
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tac	atg	tca	ccg	tat	aga	cct	agc	ccg	agc	aat	gca	tca	cct	gca	atg	1248
Tyr	Met	Ser	Pro	Tyr	Arg	Pro	Ser	Pro	Ser	Asn	Ala	Ser	Pro	Ala	Met	
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gct	gga	tca	tcg	aat	tat	ccg	ttg	aat	cca	ctg	cgt	tac	agt	gaa	tca	1296
Ala	Gly	Ser	Ser	Asn	Tyr	Pro	Leu	Asn	Pro	Leu	Arg	Tyr	Ser	Glu	Ser	
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gct	gga	act	ttc	tct	cca	tac	gcc	tct	gca	aac	tcg	ctt	cca	gac	tgt	1344
Ala	Gly	Thr	Phe	Ser	Pro	Tyr	Ala	Ser	Ala	Asn	Ser	Leu	Pro	Asp	Cys	
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 <211> 448
 <212> PRT
 <213> Arabidopsis thaliana

<400> 1620

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Phe	Asp	Asp	Ile	Glu	Ala	Asn	Phe	Ala	Pro	Ser	Val	Lys	Gly	Thr	Gly
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Glu	Ile	Gly	Val	Val	Tyr	Val	Ala	Glu	Pro	Leu	Asp	Ala	Cys	Gln	Asn
	50					55					60				
Leu	Met	Asn	Lys	Pro	Glu	Gln	Ser	Ser	Asn	Glu	Thr	Ser	Pro	Phe	Val
65					70					75				80	
Leu	Ile	Val	Arg	Gly	Gly	Cys	Ser	Phe	Glu	Glu	Lys	Val	Arg	Lys	Ala
				85					90					95	
Gln	Arg	Ala	Gly	Phe	Lys	Ala	Ala	Ile	Ile	Tyr	Asp	Asn	Glu	Asp	Arg
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Gly	Thr	Leu	Ile	Ala	Met	Ala	Gly	Asn	Ser	Gly	Gly	Ile	Arg	Ile	His
		115					120					125			
Ala	Val	Phe	Val	Thr	Lys	Glu	Thr	Gly	Glu	Val	Leu	Lys	Glu	Tyr	Ala
	130					135					140				
Gly	Phe	Pro	Asp	Thr	Lys	Val	Trp	Leu	Ile	Pro	Ser	Phe	Glu	Asn	Ser
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Ala	Trp	Ser	Ile	Met	Ala	Val	Ser	Phe	Ile	Ser	Leu	Leu	Ala	Met	Ser
				165					170					175	
Ala	Val	Leu	Ala	Thr	Cys	Phe	Phe	Val	Arg	Arg	His	Arg	Ile	Arg	Arg
			180					185					190		
Arg	Thr	Ser	Arg	Ser	Ser	Arg	Val	Arg	Glu	Phe	His	Gly	Met	Ser	Arg
		195					200					205			
Arg	Leu	Val	Lys	Ala	Met	Pro	Ser	Leu	Ile	Phe	Ser	Ser	Phe	His	Glu
	210					215					220				
Asp	Asn	Thr	Thr	Ala	Phe	Thr	Cys	Ala	Ile	Cys	Leu	Glu	Asp	Tyr	Thr
225					230					235				240	
Val	Gly	Asp	Lys	Leu	Arg	Leu	Leu	Pro	Cys	Cys	His	Lys	Phe	His	Ala
				245					250					255	
Ala	Cys	Val	Asp	Ser	Trp	Leu	Thr	Ser	Trp	Arg	Thr	Phe	Cys	Pro	Val
			260					265					270		
Cys	Lys	Arg	Asp	Ala	Arg	Thr	Ser	Thr	Gly	Glu	Pro	Pro	Ala	Ser	Glu
		275					280					285			
Ser	Thr	Pro	Leu	Leu	Ser	Ser	Ala	Ala	Ser	Ser	Phe	Thr	Ser	Ser	Ser
		290				295					300				
Leu	His	Ser	Ser	Val	Arg	Ser	Ser	Ala	Leu	Leu	Ile	Gly	Pro	Ser	Leu
305					310					315				320	
Gly	Ser	Leu	Pro	Thr	Ser	Ile	Ser	Phe	Ser	Pro	Ala	Tyr	Ala	Ser	Ser
				325					330					335	
Ser	Tyr	Ile	Arg	Gln	Ser	Phe	Gln	Ser	Ser	Ser	Asn	Arg	Arg	Ser	Pro
			340					345					350		
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seite 2134

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Tyr Met Ser Pro Tyr Arg Pro Ser Pro Ser Asn Ala Ser Pro Ala Met
          405          410          415
Ala Gly Ser Ser Asn Tyr Pro Leu Asn Pro Leu Arg Tyr Ser Glu Ser
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<211> 1296

<212> DNA

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<220>

<221> CDS

<222> (1)..(1296)

<400> 1621

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Leu Val Ser Ala Lys Val Leu Leu Ile Gly Asn Ser Thr Ser Leu Ser
          20          25          30
ttc gac gac gtc gaa gcc act ttc act ccg atg att aag aga tcg gat      144
Phe Asp Asp Val Glu Ala Thr Phe Thr Pro Met Ile Lys Arg Ser Asp
          35          40          45
caa ggc ggt gtg ttg tat gta gca gag cca ctc gat gct tgt tcg gat      192
Gln Gly Gly Val Leu Tyr Val Ala Glu Pro Leu Asp Ala Cys Ser Asp
          50          55          60
ttg gtg aat acg gtg aat gtg aaa aat gga act act gtg tct cct ccg      240
Leu Val Asn Thr Val Asn Val Lys Asn Gly Thr Thr Val Ser Pro Pro
          65          70          75          80
tat gtg ttg att atc cgc ggt ggt tgt agt ttc gaa gat aag att agg      288
Tyr Val Leu Ile Ile Arg Gly Gly Cys Ser Phe Glu Asp Lys Ile Arg
          85          90          95
aat gct caa aag gct ggt tat aaa gct gct att gtt tat gac tat gaa      336
Asn Ala Gln Lys Ala Gly Tyr Lys Ala Ala Ile Val Tyr Asp Tyr Glu
          100          105          110
gat ttt ggg ttc tta gta tca aca act ggg gaa gta ctt aaa gag tat      384
Asp Phe Gly Phe Leu Val Ser Thr Thr Gly Glu Val Leu Lys Glu Tyr
          115          120          125
gcg ggt cgt acc gat ttt gaa gtg tgg ctc atg cca agt ttc gag act      432
Ala Gly Arg Thr Asp Phe Glu Val Trp Leu Met Pro Ser Phe Glu Thr
          130          135          140          145
tca gca tgg tca atc atg gct att tct ttc ata tct ctc ctc gcc atg      480
Ser Ala Trp Ser Ile Met Ala Ile Ser Phe Ile Ser Leu Leu Ala Met
          150          155          160
tcg gct gtg ctc gct act tgc ttc ttt gtc cgt agg cat cga gtt agg      528
Ser Ala Val Leu Thr Cys Phe Phe Val Arg Arg His Arg Val Arg
          165          170          175
cgt cgg cgt att ctg gct ctt aat ggc aat gac ttt cat cgt atg ccc      576
Arg Arg Arg Ile Leu Ala Leu Asn Gly Asn Asp Phe His Arg Met Pro
          180          185          190
aaa agc atg ata ata cgt atg cct act acc ata ttt aac ggt att tgt      624
Lys Ser Met Ile Ile Arg Met Pro Thr Thr Ile Phe Asn Gly Ile Cys
          195          200          205
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          210          215          220
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Glu Lys Gly Asp Lys Leu Arg Ile Leu Pro Cys His His Lys Phe His
          225          230          235          240
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Glu	His	Thr	Pro	Phe	Leu	Ser	Arg	Thr	Pro	Ser	Met	Thr	Pro	Thr	Ser	
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Ser	Phe	Leu	Leu	Ser	Ser	Ser	Ser	Thr	Thr	Pro	Leu	Gln	Ser	Ser	His	
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Glu	Leu	Pro	Ile	Ser	Ile	Arg	Val	Asp	Pro	Ser	Leu	Pro	Ser	Thr	Ser	
					310					315					320	
atg	cag	cca	cac	aca	gtt	cct	atg	tat	ctc	tcc	cac	tct	cgc	tcc	cac	1008
Met	Gln	Pro	His	Thr	Val	Pro	Met	Tyr	Leu	Ser	His	Ser	Arg	Ser	His	
				325					330					335		
aca	agc	ttc	caa	aat	gga	tca	aac	cga	ttt	tcc	cgg	cct	ata	cca	gtt	1056
Thr	Ser	Phe	Gln	Asn	Gly	Ser	Asn	Arg	Phe	Ser	Arg	Pro	Ile	Pro	Val	
			340					345					350			
agc	cgg	agt	tca	gca	gat	ctc	agg	aac	gcc	gtt	tcc	caa	aga	tct	tac	1104
Ser	Arg	Ser	Ser	Ala	Asp	Leu	Arg	Asn	Ala	Val	Ser	Gln	Arg	Ser	Tyr	
			355				360					365				
aac	tca	ccc	cac	cag	gtt	tct	ttg	cct	cgt	ttc	ctc	cac	tca	aga	tat	1152
Asn	Ser	Pro	His	Gln	Val	Ser	Leu	Pro	Arg	Phe	Leu	His	Ser	Arg	Tyr	
			370			375					380					
acg	cac	ata	ctt	ggc	ccg	gga	aat	gca	tca	aga	agc	cag	gtt	gtt	ggg	1200
Thr	His	Ile	Leu	Gly	Pro	Gly	Asn	Ala	Ser	Arg	Ser	Gln	Val	Val	Gly	
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ttg	tta	aca	agc	cag	cgc	gag	cat	tca	ctt	cat	caa	aat	gac	tcg	cgc	1248
Leu	Leu	Thr	Ser	Gln	Arg	Glu	His	Ser	Leu	His	Gln	Asn	Asp	Ser	Arg	
				405				410						415		
agg	tct	ttc	att	cac	ttt	gca	tct	gcg	agc	tcc	tta	cca	ggc	tgg		1293
Arg	Ser	Phe	Ile	His	Phe	Ala	Ser	Ala	Ser	Ser	Leu	Pro	Gly	Trp		
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<211> 431

<212> PRT

<213> Arabidopsis thaliana

<400> 1622

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			20					25				30			
Phe	Asp	Asp	Val	Glu	Ala	Thr	Phe	Thr	Pro	Met	Ile	Lys	Arg	Ser	Asp
		35					40				45				
Gln	Gly	Gly	Val	Leu	Tyr	Val	Ala	Glu	Pro	Leu	Asp	Ala	Cys	Ser	Asp
	50				55					60					
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Tyr	Val	Leu	Ile	Ile	Arg	Gly	Gly	Cys	Ser	Phe	Glu	Asp	Lys	Ile	Arg
			85					90					95		
Asn	Ala	Gln	Lys	Ala	Gly	Tyr	Lys	Ala	Ala	Ile	Val	Tyr	Asp	Tyr	Glu
			100					105					110		
Asp	Phe	Gly	Phe	Leu	Val	Ser	Thr	Thr	Gly	Glu	Val	Leu	Lys	Glu	Tyr
		115					120				125				
Ala	Gly	Arg	Thr	Asp	Phe	Glu	Val	Trp	Leu	Met	Pro	Ser	Phe	Glu	Thr
	130				135					140					
Ser	Ala	Trp	Ser	Ile	Met	Ala	Ile	Ser	Phe	Ile	Ser	Leu	Leu	Ala	Met
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Ser	Ala	Val	Leu	Ala	Thr	Cys	Phe	Phe	Val	Arg	Arg	His	Arg	Val	Arg
			165					170						175	
Arg	Arg	Arg	Ile	Leu	Ala	Leu	Asn	Gly	Asn	Asp	Phe	His	Arg	Met	Pro
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Glu Lys Gly Asp Lys Leu Arg Ile Leu Pro Cys His His Lys Phe His
225 230 235
Val Ala Cys Val Asp Trp Leu Gly Gln Arg Lys Ser Phe Cys Pro
245 250 255
Val Cys Lys Arg Asp Ala Arg Ser Ile Ser Thr Asp Lys Pro Pro Ser
260 265 270
Glu His Thr Pro Phe Leu Ser Arg Thr Pro Ser Met Thr Pro Thr Ser
275 280 285
Ser Phe Leu Leu Ser Ser Ser Ser Thr Thr Pro Leu Gln Ser Ser His
290 295 300
Glu Leu Pro Ile Ser Ile Arg Val Asp Pro Ser Leu Pro Ser Thr Ser
305 310 315
Met Gln Pro His Thr Val Pro Met Tyr Leu Ser His Ser Arg Ser His
325 330 335
Thr Ser Phe Gln Asn Gly Ser Asn Arg Phe Ser Arg Pro Ile Pro Val
340 345 350
Ser Arg Ser Ser Ala Asp Leu Arg Asn Ala Val Ser Gln Arg Ser Tyr
355 360 365
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370 375 380
Thr His Ile Leu Gly Pro Gly Asn Ala Ser Arg Ser Gln Val Val Gly
385 390 395
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Ser Ser Leu Leu Arg Val Ser Leu Ala Thr Val Val Leu Asn Ser Ile
20      25      30
tcc gcc tct ttt gcc gat ctc cca gcc aaa ttt gac ggc tcc gtg acc      144
Ser Ala Ser Phe Ala Asp Leu Pro Ala Lys Phe Asp Gly Ser Val Thr
35      40      45
aaa aac gga atc tgt gga gct cta tac gtc gca gat cct ctc gac ggt      192
Lys Asn Gly Ile Cys Gly Ala Leu Tyr Val Ala Asp Pro Leu Asp Gly
50      55      60
tgc tca ccg ctt ctc cac gcc gcc gca tcc aac tgg acg caa cac aga      240
Cys Ser Pro Leu Leu His Ala Ala Ala Ser Asn Trp Thr Gln His Arg
65      70      75
act act aag ttc gct ttg ata atc aga ggc gaa tgt tct ttt gag gat      288
Thr Thr Lys Phe Ala Leu Ile Ile Arg Gly Glu Cys Ser Phe Glu Asp
85      90      95
aag ctg ctc aat gcc cag aac tca ggt ttt caa gct gtg att gtc tat      336
Lys Leu Leu Asn Ala Gln Asn Ser Gly Phe Gln Ala Val Ile Val Tyr
100      105      110
gac aac att gac aac gaa gat ctc atc gtc atg aag gtg aac cct cag      384
Asp Asn Ile Asp Asn Glu Asp Leu Ile Val Met Lys Val Asn Pro Gln
115      120      125
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Asp Ile Thr Val Asp Ala Val Phe Val Ser Asn Val Ala Gly Glu Ile
130      135      140
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Leu Arg Lys Tyr Ala Arg Gly Arg Asp Gly Glu Cys Cys Leu Asn Pro

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Leu Leu Leu Ile Val Thr Phe Leu Ile Ala Phe Phe Ala Pro Arg					
cac tgg acc caa tgg cga ggg agg cac acc agg acc atc agg tta gat		180	185	190	624
His Trp Thr Gln Trp Arg Gly Arg His Thr Arg Thr Ile Arg Leu Asp					
gca aag ctc gtc cac aca ctc ccc tgc ttc acc ttc act gat tct gct		195	200	205	672
Ala Lys Leu Val His Thr Leu Pro Cys Phe Thr Phe Thr Asp Ser Ala					
cac cac aag gcc ggg gaa aca tgt gct ata tgt ctc gag gat tac aga		210	215	220	720
His His Lys Ala Gly Glu Thr Cys Ala Ile Cys Leu Glu Asp Tyr Arg					
ttt gga gaa agc ctc aga ctt ctc ccc tgc caa cat gct ttt cac ttg		225	230	235	768
Phe Gly Glu Ser Leu Arg Leu Leu Pro Cys Gln His Ala Phe His Leu					
aat tgc atc gac tct tgg ttg aca aaa tgg ggt aca tct tgc cct gtg		245	250	255	816
Asn Cys Ile Asp Ser Trp Leu Thr Lys Trp Gly Thr Ser Cys Pro Val					
tgc aag cat gac ata aga acc gag act atg tct tct gag gtg atc ctg		260	265	270	864
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<400> 1624

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Lys Asn Gly Ile Cys Gly Ala Leu Tyr Val Ala Asp Pro Leu Asp Gly	
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65 70 75 80	
Thr Thr Lys Phe Ala Leu Ile Ile Arg Gly Glu Cys Ser Phe Glu Asp	
85 90 95	
Lys Leu Leu Asn Ala Gln Asn Ser Gly Phe Gln Ala Val Ile Val Tyr	
100 105 110	
Asp Asn Ile Asp Asn Glu Asp Leu Ile Val Met Lys Val Asn Pro Gln	
115 120 125	
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130 135 140	
Leu Arg Lys Tyr Ala Arg Gly Arg Asp Gly Glu Cys Cys Leu Asn Pro	
145 150 155 160	
Pro Asp Arg Gly Ser Ala Trp Thr Val Leu Ala Ile Ser Phe Phe Ser	
165 170 175	
Leu Leu Leu Ile Val Thr Phe Leu Leu Ile Ala Phe Phe Ala Pro Arg	
180 185 190	
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195 200 205	
Ala Lys Leu Val His Thr Leu Pro Cys Phe Thr Phe Thr Asp Ser Ala	
210 215 220	
His His Lys Ala Gly Glu Thr Cys Ala Ile Cys Leu Glu Asp Tyr Arg	
225 230 235 240	
Phe Gly Glu Ser Leu Arg Leu Leu Pro Cys Gln His Ala Phe His Leu	
245 250 255	
Asn Cys Ile Asp Ser Trp Leu Thr Lys Trp Gly Thr Ser Cys Pro Val	
260 265 270	

PF59082SeqList_PF59082.txt

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 Leu Asp
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 <213> Oryza sativa (japonica cultivar-group)

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 Phe Cys Leu Met Thr Gln Leu Gly Ala Ala Asn Val Val Leu Met Gly
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 Thr Asn Leu Thr Leu Ser Phe Asp Asp Val Glu Ala Ser Phe Ala Pro
 35 40 45
 gga gtg aaa ggt tca ggt ttt gaa ggc gtt gtt tat act gct gaa cct 192
 Gly Val Lys Gly Ser Gly Phe Glu Gly Val Val Tyr Thr Ala Glu Pro
 50 55 60
 ttg gac gcc tgc agt ccg tta aca agt aaa gca gaa aag ggt cca cca 240
 Leu Asp Ala Cys Ser Pro Leu Thr Ser Lys Ala Glu Lys Gly Pro Pro
 65 70 75 80
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 Ser Pro Phe Ala Leu Ile Ile Arg Gly Gly Cys Thr Phe Asp Glu Lys
 85 90 95
 gta aaa aat gca cag gat gct gga ttc aaa gct gca ata gta tac gac 336
 Val Lys Asn Ala Gln Asp Ala Gly Phe Lys Ala Ala Ile Val Tyr Asp
 100 105 110
 aat gaa aat agc ggg gtt ctg att tca agt aat ttt aca gtg gct gga 384
 Asn Glu Asn Ser Gly Val Leu Ile Ser Ser Asn Phe Thr Val Ala Gly
 115 120 125
 agc tca ggt ggt att cac att tat gcg gtg ttc atc tcg aag gcc tca 432
 Ser Ser Gly Gly Ile His Ile Tyr Ala Val Phe Ile Ser Lys Ala Ser
 130 135 140
 ggg gag gtg ttg aag aaa ttt tca ggc cat act gat gta gag gtg tgg 480
 Gly Glu Val Leu Lys Lys Phe Ser Gly His Thr Asp Val Glu Val Trp
 145 150 155 160
 ata cta cct gcg ttt gag aac tca gcc tgg tca atc atg gca att tca 528
 Ile Leu Pro Ala Phe Glu Asn Ser Ala Trp Ser Ile Met Ala Ile Ser
 165 170 175
 ttc ata tct ctg ctt gcc atg tct gcg gtt cta gct act tgt ttc ttt 576
 Phe Ile Ser Leu Leu Ala Met Ser Ala Val Leu Ala Thr Cys Phe Phe
 180 185 190
 gtg aga aga cat cat ata agg cgg gac cgg cct aga att cca gaa gcc 624
 Val Arg Arg His His Ile Arg Arg Asp Arg Pro Arg Ile Pro Glu Ala
 195 200 205
 cga gaa ttc cat gga atg agc agt caa tta gtc aag gca atg cca agc 672
 Arg Glu Phe His Gly Met Ser Ser Gln Leu Val Lys Ala Met Pro Ser
 210 215 220
 ctt atc ttc acg aag gtg caa gag gac aac tgc aca tca tca atg tgt 720
 Leu Ile Phe Thr Lys Val Gln Glu Asp Asn Cys Thr Ser Ser Met Cys
 225 230 235 240
 gcc att tgc ttg gaa gac tac aat gtc gga gaa aaa tta aga gtg ttg 768
 Ala Ile Cys Leu Glu Asp Tyr Asn Val Gly Glu Lys Leu Arg Val Leu
 245 250 255
 cct tgc cgt cac aag ttc cat gca gct tgt gtg gac ctt tgg ctc aca 816
 Pro Cys Arg His Lys Phe His Ala Ala Cys Val Asp Leu Trp Leu Thr
 260 265 270
 act tgg aga act ttt tgc cct gta tgc aaa cgt gat gca agt act gga 864
 Thr Trp Arg Thr Phe Cys Pro Val Cys Lys Arg Asp Ala Ser Thr Gly
 275 280 285

PF59082SeqList_PF59082.txt

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Ile	Pro	Asp	Pro	Pro	Ala	Ser	Glu	Thr	Thr	Pro	Leu	Leu	Ser	Ser	Ala	
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gtt	cgt	ttg	cct	tct	cag	tca	tct	tcg	ttc	cgg	tca	agc	gtg	gca	gca	960
Val	Arg	Leu	Pro	Ser	Gln	Ser	Ser	Ser	Phe	Arg	Ser	Ser	Val	Ala	Ala	
305					310					315					320	
tcg	cct	cca	aga	cca	ata	agt	cga	cga	cct	tca	tca	cag	tcc	ata	tct	1008
Ser	Pro	Pro	Arg	Pro	Ile	Ser	Arg	Arg	Pro	Ser	Ser	Gln	Ser	Ile	Ser	
				325					330					335		
cgg	att	tat	gct	gct	tct	ggt	acc	ccc	aac	tct	cct	aac	ccc	ata	agg	1056
Arg	Ile	Tyr	Ala	Ala	Ser	Gly	Thr	Pro	Asn	Ser	Pro	Asn	Pro	Ile	Arg	
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Ser	Phe	Thr	Asn	Ser	Thr	Ala	Met	Ser	Ile	Ser	Arg	Ser	Asn	Val	Asp	
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Leu	Ser	Asn	Met	Ser	Ser	Arg	Pro	Arg	Ala	Ser	His	Leu	Ala	Ser	Ala	
	370					375					380					
cat	tct	ttg	gtt	ggc	agt	cac	ttg	tct	cca	cca	atc	aat	ata	agg	tac	1200
His	Ser	Leu	Val	Gly	Ser	His	Leu	Ser	Pro	Pro	Ile	Asn	Ile	Arg	Tyr	
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gca	tcg	ccg	cat	atg	tcc	cac	tct	ggc	tat	gca	tca	cct	agt	cca	cat	1248
Ala	Ser	Pro	His	Met	Ser	His	Ser	Gly	Tyr	Ala	Ser	Pro	Ser	Pro	His	
			405					410						415		
gtt	agc	tca	tcc	tat	gtc	tcc	aac	tct	ggg	tat	gga	tct	tca	agc	tac	1296
Val	Ser	Ser	Ser	Tyr	Val	Ser	Asn	Ser	Gly	Tyr	Gly	Ser	Ser	Ser	Tyr	
			420					425					430			
tat	ctc	ggg	tca	tcc	agc	cag	cat	cgg	tca	tac	cta	agg	cgc	tgt	ggg	1344
Tyr	Leu	Gly	Ser	Ser	Ser	Gln	His	Arg	Ser	Tyr	Leu	Arg	Arg	Cys	Gly	
		435				440						445				
gaa	tca	ggg	cct	agc	ttg	tct	acc	atg	gcc	cct	cag	tcg	ccg	caa	cag	1392
Glu	Ser	Gly	Pro	Ser	Leu	Ser	Thr	Met	Ala	Pro	Gln	Ser	Pro	Gln	Gln	
	450					455					460					
tcc	cag	tta	cgt	cat	ggc	ggc	gaa	tcc	gac	tta	aat	cta	gca	gga	gca	1440
Ser	Gln	Leu	Arg	His	Gly	Gly	Glu	Ser	Asp	Leu	Asn	Leu	Ala	Gly	Ala	
465					470				475						480	
tcc	tca	ggc	cag	tct	ttc	cgg	caa	tcc	tac	ctg	aga	cac	tgt	gct	gat	1488
Ser	Ser	Gly	Gln	Ser	Phe	Arg	Gln	Ser	Tyr	Leu	Arg	His	Cys	Ala	Asp	
			485					490						495		
tca	gag	gta	aat	cta	gca	gga	gca	tcc	tca	ggc	cag	tct	ttc	cgg	caa	1536
Ser	Glu	Val	Asn	Leu	Ala	Gly	Ala	Ser	Ser	Gly	Gln	Ser	Phe	Arg	Gln	
			500					505					510			
tcc	tat	ctg	aga	cac	tgt	gct	gat	tca	gat	gca	agc	tta	tct	gcc	atg	1584
Ser	Tyr	Leu	Arg	His	Cys	Ala	Asp	Ser	Asp	Ala	Ser	Leu	Ser	Ala	Met	
		515				520						525				
gca	tca	gct	caa	tcc	ttg	cca	gga	tgc	tga							1614
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<210> 1626

<211> 537

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<400> 1626

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		20						25					30		
Thr	Asn	Leu	Thr	Leu	Ser	Phe	Asp	Asp	Val	Glu	Ala	Ser	Phe	Ala	Pro
		35					40					45			
Gly	Val	Lys	Gly	Ser	Gly	Phe	Glu	Gly	Val	Val	Tyr	Thr	Ala	Glu	Pro
	50					55					60				
Leu	Asp	Ala	Cys	Ser	Pro	Leu	Thr	Ser	Lys	Ala	Glu	Lys	Gly	Pro	Pro
65					70					75					80
Ser	Pro	Phe	Ala	Leu	Ile	Ile	Arg	Gly	Gly	Cys	Thr	Phe	Asp	Glu	Lys
				85					90					95	
Val	Lys	Asn	Ala	Gln	Asp	Ala	Gly	Phe	Lys	Ala	Ala	Ile	Val	Tyr	Asp
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PF59082SeqList_PF59082.txt

Asn Glu Asn Ser Gly Val Leu Ile Ser Ser Asn Phe Thr Val Ala Gly
 115 120 125
 Ser Ser Gly Gly Ile His Ile Tyr Ala Val Phe Ile Ser Lys Ala Ser
 130 135 140
 Gly Glu Val Leu Lys Lys Phe Ser Gly His Thr Asp Val Glu Val Trp
 145 150 155 160
 Ile Leu Pro Ala Phe Glu Asn Ser Ala Trp Ser Ile Met Ala Ile Ser
 165 170 175
 Phe Ile Ser Leu Leu Ala Met Ser Ala Val Leu Ala Thr Cys Phe Phe
 180 185 190
 Val Arg Arg His His Ile Arg Arg Asp Arg Pro Arg Ile Pro Glu Ala
 195 200 205
 Arg Glu Phe His Gly Met Ser Ser Gln Leu Val Lys Ala Met Pro Ser
 210 215 220
 Leu Ile Phe Thr Lys Val Gln Glu Asp Asn Cys Thr Ser Ser Met Cys
 225 230 235 240
 Ala Ile Cys Leu Glu Asp Tyr Asn Val Gly Glu Lys Leu Arg Val Leu
 245 250 255
 Pro Cys Arg His Lys Phe His Ala Ala Cys Val Asp Leu Trp Leu Thr
 260 265 270
 Thr Trp Arg Thr Phe Cys Pro Val Cys Lys Arg Asp Ala Ser Thr Gly
 275 280 285
 Ile Pro Asp Pro Pro Ala Ser Glu Thr Thr Pro Leu Leu Ser Ser Ala
 290 295 300
 Val Arg Leu Pro Ser Gln Ser Ser Ser Phe Arg Ser Ser Val Ala Ala
 305 310 315 320
 Ser Pro Pro Arg Pro Ile Ser Arg Arg Pro Ser Ser Gln Ser Ile Ser
 325 330 335
 Arg Ile Tyr Ala Ala Ser Gly Thr Pro Asn Ser Pro Asn Ile Arg
 340 345 350
 Ser Phe Thr Asn Ser Thr Ala Met Ser Ile Ser Arg Ser Asn Val Asp
 355 360 365
 Leu Ser Asn Met Ser Ser Arg Pro Arg Ala Ser His Leu Ala Ser Ala
 370 375 380
 His Ser Leu Val Gly Ser His Leu Ser Pro Pro Ile Asn Ile Arg Tyr
 385 390 395 400
 Ala Ser Pro His Met Ser His Ser Gly Tyr Ala Ser Pro Ser Pro His
 405 410 415
 Val Ser Ser Ser Tyr Val Ser Asn Ser Gly Tyr Gly Ser Ser Tyr
 420 425 430
 Tyr Leu Gly Ser Ser Ser Gln His Arg Ser Tyr Leu Arg Arg Cys Gly
 435 440 445
 Glu Ser Gly Pro Ser Leu Ser Thr Met Ala Pro Gln Ser Pro Gln Gln
 450 455 460
 Ser Gln Leu Arg His Gly Glu Ser Asp Leu Asn Leu Ala Gly Ala
 465 470 475 480
 Ser Ser Gly Gln Ser Phe Arg Gln Ser Tyr Leu Arg His Cys Ala Asp
 485 490 495
 Ser Glu Val Asn Leu Ala Gly Ala Ser Ser Gly Gln Ser Phe Arg Gln
 500 505 510
 Ser Tyr Leu Arg His Cys Ala Asp Ser Asp Ala Ser Leu Ser Ala Met
 515 520 525
 Ala Ser Ala Gln Ser Leu Pro Gly Cys
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<210> 1627

<211> 1488

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<221> CDS

<222> (1)..(1488)

<400> 1627

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 Met Asn Cys Cys Ser Ser Glu Ala Val Leu Ser Ser Lys Val Ala Leu
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 ctg aat tca ctc ttc tgt act ata gta ttg cca aag gag aat tgc tct
 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535

48

96

PF59082SeqList_PF59082.txt

Leu	Asn	Ser	Leu	Phe	Cys	Thr	Ile	Val	Leu	Pro	Lys	Glu	Asn	Cys	Ser	
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aat	aag	atg	aac	tgt	aca	aaa	gga	ggg	gga	ttt	ccc	ctt	ttg	ttt	tgc	144
Asn	Lys	Met	Asn	Cys	Thr	Lys	Gly	Gly	Gly	Phe	Pro	Leu	Leu	Phe	Cys	
		35					40					45				
gca	gtc	att	tgt	ctc	atg	gcc	caa	cag	ggg	gct	tgc	aat	gtg	gtg	cta	192
Ala	Val	Ile	Cys	Leu	Met	Ala	Gln	Gln	Gly	Ala	Cys	Asn	Val	Val	Leu	
	50					55				60						
ata	gcg	aat	aac	act	acc	ttg	tca	ttt	gat	gat	gtc	gag	gca	act	ttt	240
Ile	Ala	Asn	Asn	Thr	Thr	Leu	Ser	Phe	Asp	Asp	Val	Glu	Ala	Thr	Phe	
	65				70				75					80		
act	cca	gaa	gtg	aaa	gat	tca	ggg	gta	aat	ggg	gca	att	tac	gct	gtg	288
Thr	Pro	Glu	Val	Lys	Asp	Ser	Gly	Val	Asn	Gly	Ala	Ile	Tyr	Ala	Val	
			85				90						95			
gaa	cct	ctg	gat	gca	tgt	agt	cca	ttg	aga	aag	aaa	gca	gcc	aat	ggg	336
Glu	Pro	Leu	Asp	Ala	Cys	Ser	Pro	Leu	Arg	Lys	Lys	Ala	Ala	Asn	Gly	
			100				105						110			
cct	gtt	tca	cca	ttt	gca	ctg	gtc	ata	cga	ggg	ggg	tgc	caa	ttt	gac	384
Pro	Val	Ser	Pro	Phe	Ala	Leu	Val	Ile	Arg	Gly	Gly	Cys	Gln	Phe	Asp	
		115				120						125				
gat	aaa	gtt	aga	aat	gca	cag	gln	asn	ala	gga	ttt	aag	gct	gtg	ata	432
Asp	Lys	Val	Arg	Asn	Ala	Gln	Asn	Ala	Gly	Phe	Lys	Ala	Val	Ile	Val	
	130				135					140						
tat	gat	gat	gaa	gac	agt	ggg	gtc	ctg	gtt	tca	atg	gct	ggg	agc	tcg	480
Tyr	Asp	Asp	Glu	Asp	Ser	Gly	Val	Leu	Val	Ser	Met	Ala	Gly	Ser	Ser	
	145				150				155					160		
tcc	ggg	atc	tac	ata	tat	gcg	gta	ttc	ctc	tct	aag	gct	tca	gga	gag	528
Ser	Gly	Ile	Tyr	Ile	Tyr	Ala	Val	Phe	Leu	Ser	Lys	Ala	Ser	Gly	Glu	
			165				170						175			
gtt	ttg	aag	aaa	tat	tca	ggg	caa	agt	gat	gta	gag	gtg	tgg	ata	cta	576
Val	Leu	Lys	Lys	Tyr	Ser	Gly	Gln	Ser	Asp	Val	Glu	Val	Trp	Ile	Leu	
			180				185						190			
cca	gta	tat	gaa	aac	tca	gct	tgg	tct	atc	atg	gca	att	tct	ttc	aca	624
Pro	Val	Tyr	Glu	Asn	Ser	Ala	Trp	Ser	Ile	Met	Ala	Ile	Ser	Phe	Thr	
		195				200					205					
tca	ctg	ctt	gct	atg	gct	gct	gtt	cta	gct	act	tgt	ttc	ttt	gtg	agg	672
Ser	Leu	Leu	Ala	Met	Ala	Ala	Val	Leu	Ala	Thr	Cys	Phe	Phe	Val	Arg	
	210				215						220					
aga	cac	cag	ata	agg	cgg	gac	agg	gga	agg	att	cct	gta	acc	cgg	gaa	720
Arg	His	Gln	Ile	Arg	Arg	Asp	Arg	Gly	Arg	Ile	Pro	Val	Thr	Arg	Glu	
	225			230					235					240		
ttt	cat	gga	atg	agc	agt	caa	ttg	gtt	aaa	gca	atg	cca	agt	ctt	att	768
Phe	His	Gly	Met	Ser	Ser	Gln	Leu	Val	Lys	Ala	Met	Pro	Ser	Leu	Ile	
			245				250						255			
ttt	aca	aaa	gtg	caa	gaa	gac	aat	agt	aca	tca	tca	tct	tgt	gcc	att	816
Phe	Thr	Lys	Val	Gln	Glu	Asp	Asn	Ser	Thr	Ser	Ser	Ser	Cys	Ala	Ile	
		260				265						270				
tgc	ttg	gaa	gac	tac	agt	ttt	gga	gaa	aag	cta	aga	gtg	ttg	cct	tgt	864
Cys	Leu	Glu	Asp	Tyr	Ser	Phe	Gly	Glu	Lys	Leu	Arg	Val	Leu	Pro	Cys	
		275					280					285				
cgt	cac	aag	ttc	cat	gcg	act	tgt	gtg	gac	atg	tgg	ttg	acc	tcg	tgg	912
Arg	His	Lys	Phe	His	Ala	Thr	Cys	Val	Asp	Met	Trp	Leu	Thr	Ser	Trp	
	290				295					300						
aag	aca	ttc	tgc	cct	gtg	tgc	aag	cga	gat	gca	agt	gct	gga	acc	tca	960
Lys	Thr	Phe	Cys	Pro	Val	Cys	Lys	Arg	Asp	Ala	Ser	Ala	Gly	Thr	Ser	
	305			310					315					320		
aaa	ccc	cct	gca	tcg	gag	tcc	acc	cct	ttg	ctt	tct	tct	gtt	att	cat	1008
Lys	Pro	Pro	Ala	Ser	Glu	Ser	Thr	Pro	Leu	Leu	Ser	Ser	Val	Ile	His	
			325						330				335			
ctg	tct	gct	gaa	tca	aca	gct	ttg	tct	tct	ttt	cgg	tca	acg	gtg	gca	1056
Leu	Ser	Ala	Glu	Ser	Thr	Ala	Leu	Ser	Ser	Phe	Arg	Ser	Thr	Val	Ala	
		340				345						350				
gta	tct	ccc	cct	agg	cca	ata	aga	cgt	cat	cct	tca	tca	cag	tcc	aca	1104
Val	Ser	Pro	Pro	Arg	Pro	Ile	Arg	Arg	His	Pro	Ser	Ser	Gln	Ser	Thr	
		355				360						365				
tcc	cgc	gct	tac	tcc	att	tcc	agt	gcc	ccc	cgc	aat	tat	aac	ctt	caa	1152
Ser	Arg	Ala	Tyr	Ser	Ile	Ser	Ser	Ala	Pro	Arg	Asn	Tyr	Asn	Leu	Gln	
	370				375					380						
aga	tat	tac	act	aac	tca	cct	tat	att	agt	acg	aga	agc	aat	gta		1200

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Asp	Leu	Ala	Asn	Met 405	Ser	Ser	Gln	Trp	Ser 410	His	Thr	Pro	His	Gln	Ala	
tcc	atg	cat	tct	cta	aga	agt	ggc	cat	ttg	tct	cta	ccg	atc	aac	atc	1296
Ser	Met	His	Ser	Leu	Arg	Ser	Gly	His	Leu	Ser	Leu	Pro	Ile	Asn	Ile	
agg	tat	aca	ata	cca	cat	gtt	tct	cgt	tct	gac	tat	gga	tct	gcc	agc	1344
Arg	Tyr	Thr	Ile	Pro	His	Val	Ser	Arg	Ser	Asp	Tyr	Gly	Ser	Ala	Ser	
ctg	ggg	tta	tcc	cat	gat	tcc	tgt	tct	cac	cat	gga	tct	ccg	agt	tat	1392
Leu	Gly	Leu	Ser	His	Asp	Ser	Cys	Ser	His	His	Gly	Ser	Pro	Ser	Tyr	
tat	cat	agc	tct	ttg	ggc	cag	caa	cgt	tct	tac	ctg	atg	cac	cgc	acc	1440
Tyr	His	Ser	Ser	Leu	Gly 470	Gln	Gln	Arg	Ser	Tyr 475	Leu	Met	His	Arg	Thr 480	
gag	tca	ggg	cca	agc	ctg	tct	act	atg	gtg	ctc	cag	tcg	cca	caa		1485
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<210> 1628

<211> 495

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<400> 1628

Met	Asn	Cys	Cys	Ser	Ser	Glu	Ala	Val	Leu	Ser	Ser	Lys	Val	Ala	Leu	
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			20					25					30			
Asn	Lys	Met	Asn	Cys	Thr	Lys	Gly	Gly	Gly	Phe	Pro	Leu	Leu	Phe	Cys	
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Ala	Val	Ile	Cys	Leu	Met	Ala	Gln	Gln	Gly	Ala	Cys	Asn	Val	Val	Leu	
	50					55				60						
Ile	Ala	Asn	Asn	Thr	Thr	Leu	Ser	Phe	Asp	Asp	Val	Glu	Ala	Thr	Phe	
65				70					75					80		
Thr	Pro	Glu	Val	Lys	Asp	Ser	Gly	Val	Asn	Gly	Ala	Ile	Tyr	Ala	Val	
				85					90					95		
Glu	Pro	Leu	Asp	Ala	Cys	Ser	Pro	Leu	Arg	Lys	Lys	Ala	Ala	Asn	Gly	
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Pro	Val	Ser	Pro	Phe	Ala	Leu	Val	Ile	Arg	Gly	Gly	Cys	Gln	Phe	Asp	
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Asp	Lys	Val	Arg	Asn	Ala	Gln	Asn	Ala	Gly	Phe	Lys	Ala	Val	Ile	Val	
	130					135					140					
Tyr	Asp	Asp	Glu	Asp	Ser	Gly	Val	Leu	Val	Ser	Met	Ala	Gly	Ser	Ser	
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Ser	Gly	Ile	Tyr	Ile	Tyr	Ala	Val	Phe	Leu	Ser	Lys	Ala	Ser	Gly	Glu	
				165					170					175		
Val	Leu	Lys	Lys	Tyr	Ser	Gly	Gln	Ser	Asp	Val	Glu	Val	Trp	Ile	Leu	
			180					185					190			
Pro	Val	Tyr	Glu	Asn	Ser	Ala	Trp	Ser	Ile	Met	Ala	Ile	Ser	Phe	Thr	
		195					200					205				
Ser	Leu	Leu	Ala	Met	Ala	Ala	Val	Leu	Ala	Thr	Cys	Phe	Phe	Val	Arg	
	210					215					220					
Arg	His	Gln	Ile	Arg	Arg	Asp	Arg	Gly	Arg	Ile	Pro	Val	Thr	Arg	Glu	
225				230						235				240		
Phe	His	Gly	Met	Ser	Ser	Gln	Leu	Val	Lys	Ala	Met	Pro	Ser	Leu	Ile	
			245						250					255		
Phe	Thr	Lys	Val	Gln	Glu	Asp	Asn	Ser	Thr	Ser	Ser	Ser	Cys	Ala	Ile	
		260						265					270			
Cys	Leu	Glu	Asp	Tyr	Ser	Phe	Gly	Glu	Lys	Leu	Arg	Val	Leu	Pro	Cys	
		275					280					285				
Arg	His	Lys	Phe	His	Ala	Thr	Cys	Val	Asp	Met	Trp	Leu	Thr	Ser	Trp	
	290					295					300					
Lys	Thr	Phe	Cys	Pro	Val	Cys	Lys	Arg	Asp	Ala	Ser	Ala	Gly	Thr	Ser	

PF59082SeqList_PF59082.txt

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Leu Ser Ala Glu Ser Thr Ala Leu Ser Ser Phe Arg Ser Thr Val Ala
Val Ser Pro Arg Pro Ile Arg Arg His Pro Ser Ser Gln Ser Thr
Ser Arg Ala Tyr Ser Ile Ser Ser Ala Pro Arg Asn Tyr Asn Leu Gln
Arg Tyr Tyr Thr Asn Ser Pro Tyr Ile Ser Thr Ser Arg Ser Asn Val
Asp Leu Ala Asn Met Ser Ser Gln Trp Ser His Thr Pro His Gln Ala
Ser Met His Ser Leu Arg Ser Gly His Leu Ser Leu Pro Ile Asn Ile
Arg Tyr Thr Ile Pro His Val Ser Arg Ser Asp Tyr Gly Ser Ala Ser
Leu Gly Leu Ser His Asp Ser Cys Ser His His Gly Ser Pro Ser Tyr
Tyr His Ser Ser Leu Gly Gln Gln Arg Ser Tyr Leu Met His Arg Thr
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<210> 1629
 <211> 2146
 <212> DNA
 <213> Oryza sativa

<220>
 <221> CDS
 <222> (395)..(1900)

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cgcatcccgcc ccaccaccgc cgcgccaccg cctccgccgc cgacgagccc ccgcggccac      120

cgccaccgcc acctcatctt ctctcccacc accgctccac agccgccctc cttacatgg      180

aagtcgacgt ctccatcgcc acgcccgcac cgcaggaatc ttagctgatt ggtgctttgg      240

actgcaggtc tggacacggt gtccgtttcc tgcttgtgca gacgtagggt tggagtcttt      300

ctgagtgtta aggtggcttt cttttttgtc cttccatggt tgaaatttgt atgaacaacc      360

ttgactttct cgaagatctg tgttggtcga taag atg aat cga aga aga aca atg      415
          Met Asn Arg Arg Arg Thr Met
          1          5
cta ttg ctt atc tgt ctc tgt gca aca ttt tgc ctc atg act cag tta      463
Leu Leu Leu Ile Cys Leu Cys Ala Thr Phe Cys Leu Met Thr Gln Leu
          10          15          20
gga gct gca aat gta gtg ctg atg ggg aca aat ctg act ttg tcg ttt      511
Gly Ala Ala Asn Val Val Met Gly Thr Asn Leu Thr Leu Ser Phe
          25          30          35
gat gat gtt gag gca agt ttt gct cca gga gtg aaa ggt tca ggt ttt      559
Asp Asp Val Glu Ala Ser Phe Ala Pro Gly Val Lys Gly Ser Gly Phe
          40          45          50          55
gaa ggc gtt gtt tat act gct gaa cct ttg gac gcc tgc agt ccg tta      607
Glu Gly Val Val Tyr Thr Ala Glu Pro Leu Asp Ala Cys Ser Pro Leu
          60          65          70
aca agt aaa gca gaa aag ggt cca cca tct cca ttt gca ctg atc ata      655
Thr Ser Lys Ala Glu Lys Gly Pro Pro Ser Pro Phe Ala Leu Ile Ile
          75          80          85

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PF59082SeqList_PF59082.txt

	75	80	85	
aga ggc ggc tgc aca ttt gat gaa aaa gta aaa aat gca cag gat gct	703			
Arg Gly Gly Cys Thr Phe Asp Glu Lys Val Lys Asn Ala Gln Asp Ala				
gga ttc aaa gct gca ata gta tac gac aat gaa aat agc ggc gtt ctg	751			
Gly Phe 90 Lys Ala Ala Ile Val 95 Tyr Asp Asn Glu 100 Ser Gly Val Leu				
att tca atg gct gga agc tca ggt ggt att cac att tat gcg gtg ttc	799			
Ile Ser Met Ala Gly Ser 120 Ser Gly Gly Ile His 130 Ile Tyr Ala Val Phe				
atc tcg aag gcc tca ggg gag gtg ttg aag aaa ttt tca ggc cat act	847			
Ile Ser Lys Ala Ser 140 Gly Glu Val Leu Lys 145 Phe Ser Gly His Thr				
gat gta gag gtg tgg ata cta cct gcg ttt gag aac tca gcc tgg tca	895			
Asp Val Glu 155 Trp Ile Leu Pro Ala Phe Glu Asn Ser Ala Trp Ser				
atc atg gca att tca ttc ata tct ctg ctt gcc atg tct gcg gtt cta	943			
Ile Met Ala 170 Ile Ser Phe Ile Ser Leu Leu Ala Met 180 Ser Ala Val Leu				
gct act tgt ttc ttt gtg aga aga cat cat ata agg cgg gac cgg cct	991			
Ala Thr 185 Cys Phe Phe Val Arg 190 Arg His His Ile Arg 195 Asp Arg Pro				
aga att cca gaa gcc cga gaa ttc cat gga atg agc agt caa tta gtc	1039			
Arg Ile Pro Glu Ala Arg 205 Glu Phe His Gly Met Ser Ser Gln Leu Val				
aag gca atg cca agc ctt atc ttc acg aag gtg caa gag gac aac tgc	1087			
Lys Ala Met Pro Ser Leu Ile Phe Thr Lys Val Gln Glu Asp Asn Cys				
aca tca tca atg tgt gcc att tgc ttg gaa gac tac aat gtc gga gaa	1135			
Thr Ser Ser Met 235 Cys Ala Ile Cys Leu Glu Asp Tyr Asn Val Gly Glu				
aaa tta aga gtg ttg cct tgc cgt cac aag ttc cat gca gct tgt gtg	1183			
Lys Leu Arg Val Leu Pro Cys Arg His Lys Phe His Ala Ala Cys Val				
gac ctt tgg ctc aca act tgg aga act ttt tgc cct gta tgc aaa cgt	1231			
Asp Leu 265 Trp Leu Thr Thr Trp Arg Thr Phe Cys Pro Val Cys Lys Arg				
gat gca agt act gga ata cca gat cct cca gcc tca gag act aca cca	1279			
Asp Ala Ser Thr Gly Ile 285 Pro Asp Pro Pro Ala Ser Glu Thr Thr Pro				
ttg ctt tct tct gca gtt cgt ttg cct tct cag tca tct tcg ttc cgg	1327			
Leu Leu Ser Ser Ala Val Arg Leu Pro Ser Gln Ser Ser Ser Phe Arg				
tca agc gtg gca gca tcg cct cca aga cca ata agt cga cga cct tca	1375			
Ser Ser Val 315 Ala Ala Ser Pro Pro Arg Pro Ile Ser Arg Arg Pro Ser				
tca cag tcc ata tct cgg att tat gct gct tct ggt acc ccc aac tct	1423			
Ser Gln Ser Ile Ser Arg Ile Tyr Ala Ala Ser Gly Thr 340 Pro Asn Ser				
cct aac ccc ata agg tct ttc aca aac tca act gcc atg agc ata agt	1471			
Pro Asn Pro Ile Arg Ser Phe Thr Asn Ser Thr Ala Met Ser Ile Ser				
aga agc aat gtg gac tta tca aac atg tct tcc cgc cct cgc gcc tca	1519			
Arg Ser Asn Val Asp Leu 365 Ser Asn Met Ser Ser Arg Pro Arg Ala Ser				
cac ctc gcc tcc gca cat tct ttg gtt ggc agt cac ttg tct cca cca	1567			
His Leu Ala Ser Ala His Ser Leu Val Gly Ser His Leu Ser Pro Pro				
atc aat ata agc tac tat ctc ggt tca tcc agc cag cat cgg tca tac	1615			
Ile Asn Ile 395 Ser Tyr Tyr Leu Gly Ser Ser Gln His Arg 405 Ser Tyr				
cta agg cgc tgt ggg gaa tca ggg cct agc ttg tct acc atg gcc cct	1663			
Leu Arg Arg Cys Gly Glu Ser Gly 415 Pro Ser Leu Ser Thr Met Ala Pro				
cag tcg ccg caa cag tcc cag tta cgt cat ggc ggc gaa tcc gac tta	1711			
Gln Ser Pro Gln Gln Ser Gln Leu Arg His Gly Gly Glu Ser Asp Leu				
aat cta gca gga gca tcc tca ggc cag tct ttc cgg caa tcc tac ctg	1759			
Asn Leu Ala Gly Ala Ser Ser Gly Gln Ser Phe Arg Gln Ser Tyr Leu				

PF59082SeqList_PF59082.txt

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440          445          450          455
aga cac tgt gct gat tca gag gta aat cta gca gga gca tcc tca ggc      1807
Arg His Cys Ala Asp Ser Glu Val Asn Leu Ala Gly Ala Ser Ser Gly
          460          465          470
cag tct ttc cgg caa tcc tat ctg aga cac tgt gct gat tca gat gca      1855
Gln Ser Phe Arg Gln Ser Tyr Leu Arg His Cys Ala Asp Ser Asp Ala
          475          480          485
agc tta tct gcc atg gca tca gct caa tcc ttg cca gga tgc tgatttctct      1907
Ser Leu Ser Ala Met Ala Ser Ala Gln Ser Leu Pro Gly Cys
          490          495          500
gggatcagat cagcttctgt ctgtactaag acctggcgtg acttgtgtat acatttgagg      1967

catgtactat aggctattgg ttgagagaaa atggtcgtat ttgtttgtgt ttctcctgct      2027

gccctgccct tttggttgta gtgattgtta gcgctctatt tgtttcaccc tagagtgtat      2087

agtacaattg tacagcaact ttcttttaaa ctaagcaata tcatccgcgc gttgcccg      2146

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<210> 1630
 <211> 501
 <212> PRT
 <213> Oryza sativa

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Phe Cys Leu Met Thr Gln Leu Gly Ala Ala Asn Val Val Leu Met Gly
          20      25      30
Thr Asn Leu Thr Leu Ser Phe Asp Asp Val Glu Ala Ser Phe Ala Pro
          35      40      45
Gly Val Lys Gly Ser Gly Phe Glu Gly Val Val Tyr Thr Ala Glu Pro
          50      55      60
Leu Asp Ala Cys Ser Pro Leu Thr Ser Lys Ala Glu Lys Gly Pro Pro
65      70      75      80
Ser Pro Phe Ala Leu Ile Ile Arg Gly Gly Cys Thr Phe Asp Glu Lys
          85      90      95
Val Lys Asn Ala Gln Asp Ala Gly Phe Lys Ala Ala Ile Val Tyr Asp
          100      105      110
Asn Glu Asn Ser Gly Val Leu Ile Ser Met Ala Gly Ser Ser Gly Gly
          115      120      125
Ile His Ile Tyr Ala Val Phe Ile Ser Lys Ala Ser Gly Glu Val Leu
130      135      140
Lys Lys Phe Ser Gly His Thr Asp Val Glu Val Trp Ile Leu Pro Ala
145      150      155      160
Phe Glu Asn Ser Ala Trp Ser Ile Met Ala Ile Ser Phe Ile Ser Leu
          165      170      175
Leu Ala Met Ser Ala Val Leu Ala Thr Cys Phe Phe Val Arg Arg His
          180      185      190
His Ile Arg Arg Asp Arg Pro Arg Ile Pro Glu Ala Arg Glu Phe His
          195      200      205
Gly Met Ser Ser Gln Leu Val Lys Ala Met Pro Ser Leu Ile Phe Thr
          210      215      220
Lys Val Gln Glu Asp Asn Cys Thr Ser Ser Met Cys Ala Ile Cys Leu
225      230      235      240
Glu Asp Tyr Asn Val Gly Glu Lys Leu Arg Val Leu Pro Cys Arg His
          245      250      255
Lys Phe His Ala Ala Cys Val Asp Leu Trp Leu Thr Thr Trp Arg Thr
          260      265      270
Phe Cys Pro Val Cys Lys Arg Asp Ala Ser Thr Gly Ile Pro Asp Pro
          275      280      285
Pro Ala Ser Glu Thr Thr Pro Leu Leu Ser Ser Ala Val Arg Leu Pro
          290      295      300
Ser Gln Ser Ser Ser Phe Arg Ser Ser Val Ala Ser Pro Pro Arg
305      310      315      320

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PF59082SeqList_PF59082.txt

Pro Ile Ser Arg Arg Pro Ser Ser Gln Ser Ile Ser Arg Ile Tyr Ala
 325 330 335
 Ala Ser Gly Thr Pro Asn Ser Pro Asn Pro Ile Arg Ser Phe Thr Asn
 340 345 350
 Ser Thr Ala Met Ser Ile Ser Arg Ser Asn Val Asp Leu Ser Asn Met
 355 360 365
 Ser Ser Arg Pro Arg Ala Ser His Leu Ala Ser Ala His Ser Leu Val
 370 375 380
 Gly Ser His Leu Ser Pro Pro Ile Asn Ile Ser Tyr Tyr Leu Gly Ser
 385 390 400
 Ser Ser Gln His Arg Ser Tyr Leu Arg Arg Cys Gly Glu Ser Gly Pro
 405 410 415
 Ser Leu Ser Thr Met Ala Pro Gln Ser Pro Gln Gln Ser Gln Leu Arg
 420 425 430
 His Gly Gly Glu Ser Asp Leu Asn Leu Ala Gly Ala Ser Ser Gly Gln
 435 440 445
 Ser Phe Arg Gln Ser Tyr Leu Arg His Cys Ala Asp Ser Glu Val Asn
 450 455 460
 Leu Ala Gly Ala Ser Ser Gly Gln Ser Phe Arg Gln Ser Tyr Leu Arg
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<211> 1378

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<213> Arabidopsis thaliana

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Met Arg Asn Asn Ile Thr Leu Ser Phe Asp Asp Ile Glu
 1 5 10

gct aac ttc gct ccg tca gtg aag ggt aca ggt gaa att gga gtg gtt 159

Ala Asn Phe Ala Pro Ser Val Lys Gly Thr Gly Glu Ile Gly Val Val
 15 20 25

tat gtg gct gag cct ctt gac gct tgt caa aat ctt atg aat aaa cca 207

Tyr Val Ala Glu Pro Leu Asp Ala Cys Gln Asn Leu Met Asn Lys Pro
 30 35 40 45

gaa cag agc tcc aat gaa act tct cct ttt gtg ttg att gtt aga gga 255

Glu Gln Ser Ser Asn Glu Thr Ser Pro Phe Val Leu Ile Val Arg Gly
 50 55 60

ggc tgt agt ttt gaa gag aaa gtt aga aaa gct cag aga gct ggt ttc 303

Gly Cys Ser Phe Glu Glu Lys Val Arg Lys Ala Gln Arg Ala Gly Phe
 65 70 75

aaa gct gct att atc tat gac aat gaa gac cgt gga aca ttg ata gca 351

Lys Ala Ala Ile Ile Tyr Asp Asn Glu Asp Arg Gly Thr Leu Ile Ala
 80 85 90

atg gca ggt aac tct gga ggt ata agg att cat gcg gtc ttt gtt acg 399

Met Ala Gly Asn Ser Gly Gly Ile Arg Ile His Ala Val Phe Val Thr
 95 100 105

aaa gaa acg gga gaa gtt tta aag gag tat gcg ggt ttc ccc gat acg 447

Lys Glu Thr Gly Glu Val Leu Lys Glu Tyr Ala Gly Phe Pro Asp Thr
 110 115 120 125

aaa gtt tgg ttg atc cca agt ttt gag aac tcg gcg tgg tct att atg 495

Lys Val Trp Leu Ile Pro Ser Phe Glu Asn Ser Ala Trp Ser Ile Met
 130 135 140

gcg gtt tcg ttt atc tcg ctg ctt gca atg tcg gct gtt ctc gct act 543

Ala Val Ser Phe Ile Ser Leu Leu Ala Met Ser Ala Val Leu Ala Thr
 145 150 155

tgt ttc ttt gtg cgt agg cat cga ata aga agg cgg aca tct cgg tcc 591

PF59082SeqList_PF59082.txt

Cys	Phe	Phe	Val	Arg	Arg	His	Arg	Ile	Arg	Arg	Arg	Thr	Ser	Arg	Ser	
		160					165					170				
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Ser	Arg	Val	Arg	Glu	Phe	His	Gly	Met	Ser	Arg	Arg	Leu	Val	Lys	Ala	
	175					180					185					
atg	ccg	agt	ctt	ata	ttc	agt	tcg	ttt	cat	gaa	gat	aac	act	act	gca	687
Met	Pro	Ser	Leu	Ile	Phe	Ser	Ser	Phe	His	Glu	Asp	Asn	Thr	Thr	Ala	
	190				195					200					205	
ttc	act	tgt	gct	att	tgc	ctt	gaa	gac	tac	act	ggt	gga	gac	aag	ctc	735
Phe	Thr	Cys	Ala	Ile	Cys	Leu	Glu	Asp	Tyr	Thr	Val	Gly	Asp	Lys	Leu	
				210					215					220		
agg	ctc	tta	cct	tgc	tgt	cac	aag	ttt	cat	gct	gcg	tgt	ggt	gac	tca	783
Arg	Leu	Leu	Pro	Cys	Cys	His	Lys	Phe	His	Ala	Ala	Cys	Val	Asp	Ser	
			225					230					235			
tgg	tta	acc	tct	tgg	aga	act	ttc	tgt	ccg	gtg	tgc	aaa	cga	gat	gca	831
Trp	Leu	Thr	Ser	Trp	Arg	Thr	Phe	Cys	Pro	Val	Cys	Lys	Arg	Asp	Ala	
		240					245					250				
aga	acg	agc	acg	gga	gag	cct	cca	gct	tca	gag	agc	acg	cca	ttg	ctc	879
Arg	Thr	Ser	Thr	Gly	Glu	Pro	Pro	Ala	Ser	Glu	Ser	Thr	Pro	Leu	Leu	
	255					260					265					
tca	tct	gct	gca	tcg	tct	ttc	act	tct	tcc	tct	ctg	cac	tct	tca	gtc	927
Ser	Ser	Ala	Ala	Ser	Ser	Phe	Thr	Ser	Ser	Ser	Leu	His	Ser	Ser	Val	
	270				275					280					285	
aga	tca	tct	gca	cta	ttg	att	ggg	cct	tcc	ttg	ggc	tca	tta	cca	act	975
Arg	Ser	Ser	Ala	Leu	Ile	Gly	Pro	Ser	Leu	Gly	Ser	Leu		300	Thr	
				290				295								
tca	atc	tct	ttc	tct	ccc	gca	tac	gca	agc	tca	tcc	tat	att	aga	caa	1023
Ser	Ile	Ser	Phe	Ser	Pro	Ala	Tyr	Ala	Ser	Ser	Ser	Tyr	Ile	Arg	Gln	
			305					310					315			
tca	ttc	cag	tct	tcc	tct	aac	cgt	cga	tca	cct	cca	ata	agc	gta	agt	1071
Ser	Phe	Gln	Ser	Ser	Ser	Asn	Arg	Arg	Ser	Pro	Pro	Ile	Ser	Val	Ser	
		320					325					330				
cga	agc	tca	gtg	gat	ctc	aga	caa	caa	gca	gct	tct	cca	tct	cca	tca	1119
Arg	Ser	Ser	Val	Asp	Leu	Arg	Gln	Gln	Ala	Ala	Ser	Pro	Ser	Pro	Ser	
	335					340					345					
cca	tca	cag	aga	tca	tac	att	tcc	cat	atg	gct	tct	cca	cag	tca	cta	1167
Pro	Ser	Gln	Arg	Ser	Tyr	Ile	Ser	His	Met	Ala	Ser	Pro	Gln	Ser	Leu	
	350				355					360					365	
ggg	tac	cca	act	atc	tcc	cct	ttc	aac	acg	agg	tac	atg	tca	ccg	tat	1215
Gly	Tyr	Pro	Thr	Ile	Ser	Pro	Phe	Asn	Thr	Arg	Tyr	Met	Ser	Pro	Tyr	
				370				375						380		
aga	cct	agc	ccg	agc	aat	gca	tca	cct	gca	atg	gct	gga	tca	tcg	aat	1263
Arg	Pro	Ser	Pro	Ser	Asn	Ala	Ser	Pro	Ala	Met	Ala	Gly	Ser	Ser	Asn	
			385					390				395				
tat	ccg	ttg	aat	cca	ctg	cgt	tac	agt	gaa	tca	gct	gga	act	ttc	tct	1311
Tyr	Pro	Leu	Asn	Pro	Leu	Arg	Tyr	Ser	Glu	Ser	Ala	Gly	Thr	Phe	Ser	
		400				405					410					
cca	tac	gcc	tct	gca	aac	tcg	ctt	cca	gac	tgt	tagaa	agtct	acaga	accaa		1364
Pro	Tyr	Ala	Ser	Ala	Asn	Ser	Leu	Pro	Asp	Cys						
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<211> 424

<212> PRT

<213> Arabidopsis thaliana

<400> 1632

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			20					25					30		
Glu	Pro	Leu	Asp	Ala	Cys	Gln	Asn	Leu	Met	Asn	Lys	Pro	Glu	Gln	Ser
		35					40					45			
Ser	Asn	Glu	Thr	Ser	Pro	Phe	Val	Leu	Ile	Val	Arg	Gly	Gly	Cys	Ser
	50					55					60				
Phe	Glu	Glu	Lys	Val	Arg	Lys	Ala	Gln	Arg	Ala	Gly	Phe	Lys	Ala	Ala

PF59082SeqList_PF59082.txt

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Asn Ser Gly Gly Ile Arg Ile His Ala Val Phe Val Thr Lys Glu Thr
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Gly Glu Val Leu Lys Glu Tyr Ala Gly Phe Pro Asp Thr Lys Val Trp
      115
Leu Ile Pro Ser Phe Glu Asn Ser Ala Trp Ser Ile Met Ala Val Ser
      130
Phe Ile Ser Leu Leu Ala Met Ser Ala Val Leu Ala Thr Cys Phe Phe
      145
Val Arg Arg His Arg Ile Arg Arg Arg Thr Ser Arg Ser Ser Arg Val
      165
Arg Glu Phe His Gly Met Ser Arg Arg Leu Val Lys Ala Met Pro Ser
      180
Leu Ile Phe Ser Ser Phe His Glu Asp Asn Thr Thr Ala Phe Thr Cys
      195
Ala Ile Cys Leu Glu Asp Tyr Thr Val Gly Asp Lys Leu Arg Leu Leu
      210
Pro Cys Cys His Lys Phe His Ala Ala Cys Val Asp Ser Trp Leu Thr
      225
Ser Trp Arg Thr Phe Cys Pro Val Cys Lys Arg Asp Ala Arg Thr Ser
      245
Thr Gly Glu Pro Pro Ala Ser Glu Ser Thr Pro Leu Leu Ser Ser Ala
      260
Ala Ser Ser Phe Thr Ser Ser Ser Leu His Ser Ser Val Arg Ser Ser
      275
Ala Leu Leu Ile Gly Pro Ser Leu Gly Ser Leu Pro Thr Ser Ile Ser
      290
Phe Ser Pro Ala Tyr Ala Ser Ser Ser Tyr Ile Arg Gln Ser Phe Gln
      305
Ser Ser Ser Asn Arg Arg Ser Pro Pro Ile Ser Val Ser Arg Ser Ser
      325
Val Asp Leu Arg Gln Gln Ala Ala Ser Pro Ser Pro Ser Pro Ser Gln
      340
Arg Ser Tyr Ile Ser His Met Ala Ser Pro Gln Ser Leu Gly Tyr Pro
      355
Thr Ile Ser Pro Phe Asn Thr Arg Tyr Met Ser Pro Tyr Arg Pro Ser
      370
Pro Ser Asn Ala Ser Pro Ala Met Ala Gly Ser Ser Asn Tyr Pro Leu
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Asn Pro Leu Arg Tyr Ser Glu Ser Ala Gly Thr Phe Ser Pro Tyr Ala
      405
Ser Ala Asn Ser Leu Pro Asp Cys
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 <222> (161)..(161)
 <223> n is a, g, c or t

<220>
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 <222> (194)..(194)
 <223> n is a, g, c or t

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 1 5 10 15

PF59082SeqList_PF59082.txt

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gaa	gct	aac	atc	gct	ccg	tca	gtg	aag	ggt	aca	ggt	gaa	att	gga	gtg	145
Glu	Ala	Asn	Ile	Ala	Pro	Ser	Val	Lys	Gly	Thr	Gly	Glu	Ile	Gly	Val	
		35					40					45				
ggt	tat	gtg	gct	gag	nct	ctt	gac	gct	tgt	caa	aat	ctt	atg	aat	aaa	193
Val	Tyr	Val	Ala	Glu	Xaa	Leu	Asp	Ala	Cys	Gln	Asn	Leu	Met	Asn	Lys	
	50					55					60					
nca	gaa	cag	agc	tcc	aat	gaa	act	tct	cct	ttt	gtg	ttg	att	ggt	aga	241
Xaa	Glu	Gln	Ser	Ser	Asn	Glu	Thr	Ser	Pro	Phe	Val	Leu	Ile	Val	Arg	
	65				70					75					80	
gga	ggc	tgt	agt	ttt	gaa	gag	aaa	ggt	aga	aaa	gct	cag	aga	gct	ggt	289
Gly	Gly	Cys	Ser	Phe	Glu	Glu	Lys	Val	Arg	Lys	Ala	Gln	Arg	Ala	Gly	
			85					90						95		
ttc	aaa	gct	gct	att	atc	tat	gac	aat	gaa	gac	cgt	gga	aca	ttg	ata	337
Phe	Lys	Ala	Ala	Ile	Ile	Tyr	Asp	Asn	Glu	Asp	Arg	Gly	Thr	Leu	Ile	
		100						105					110			
gca	atg	gca	ggt	aac	tct	gga	ggt	ata	agg	att	cat	gcg	gtc	ttt	ggt	385
Ala	Met	Ala	Gly	Asn	Ser	Gly	Gly	Ile	Arg	Ile	His	Ala	Val	Phe	Val	
		115					120					125				
acg	aaa	gaa	acg	gga	gaa	ggt	tta	aag	gag	tat	gcg	ggt	ttc	ccc	gat	433
Thr	Lys	Glu	Thr	Gly	Glu	Val	Leu	Lys	Glu	Tyr	Ala	Gly	Phe	Pro	Asp	
	130					135					140					
acg	aaa	ggt	tgg	ttg	atc	cca	agt	ttt	gag	aac	tcg	gcg	tgg	tct	att	481
Thr	Lys	Val	Trp	Leu	Ile	Pro	Ser	Phe	Glu	Asn	Ser	Ala	Trp	Ser	Ile	
	145				150					155					160	
atg	gcg	ggt	tcg	ttt	atc	tcg	ctg	ctt	gca	atg	tcg	gct	ggt	ctc	gct	529
Met	Ala	Val	Ser	Phe	Ile	Ser	Leu	Leu	Ala	Met	Ser	Ala	Val	Leu	Ala	
			165					170						175		
act	tgt	ttc	ttt	gtg	cgt	agg	cat	cga	ata	aga	agg	cgg	aca	tct	cgg	577
Thr	Cys	Phe	Phe	Val	Arg	Arg	His	Arg	Ile	Arg	Arg	Arg	Thr	Ser	Arg	
		180						185					190			
tcc	tct	cga	gtg	cgt	gag	ttt	cac	ggt	atg	agc	cgc	cgc	ttg	gtg	aaa	625
Ser	Ser	Arg	Val	Arg	Glu	Phe	His	Gly	Met	Ser	Arg	Arg	Leu	Val	Lys	
		195					200					205				
gca	atg	ccg	agt	ctt	ata	ttc	agt	tcg	ttt	cat	gaa	gat	aac	act	act	673
Ala	Met	Pro	Ser	Leu	Ile	Phe	Ser	Ser	Phe	His	Glu	Asp	Asn	Thr	Thr	
	210					215					220					
gca	ttc	act	tgt	gct	att	gtc	ctt	gaa	gac	tac	act	ggt	gga	gac	aag	721
Ala	Phe	Thr	Cys	Ala	Ile	Cys	Leu	Glu	Asp	Tyr	Thr	Val	Gly	Asp	Lys	
	225				230					235					240	
ctc	agg	ctc	tta	cct	tgc	tgt	cac	aag	ttt	cat	gct	gcg	tgt	ggt	gac	769
Leu	Arg	Leu	Leu	Pro	Cys	Cys	His	Lys	Phe	His	Ala	Ala	Cys	Val	Asp	
			245						250					255		
tca	tgg	tta	acc	tct	tgg	aga	act	ttc	tgt	ccg	gtg	tgc	aaa	cga	gat	817
Ser	Trp	Leu	Thr	Ser	Trp	Arg	Thr	Phe	Cys	Pro	Val	Cys	Lys	Arg	Asp	
		260						265					270			
gca	aga	acg	agc	acg	gga	gag	cct	cca	gct	tca	gag	agc	acg	cca	ttg	865
Ala	Arg	Thr	Ser	Thr	Gly	Glu	Pro	Pro	Ala	Ser	Glu	Ser	Thr	Pro	Leu	
		275					280					285				
ctc	tca	tct	gct	gca	tcg	tct	ttc	act	tct	tcc	tct	ctg	cac	tct	tca	913
Leu	Ser	Ser	Ala	Ala	Ser	Ser	Phe	Thr	Ser	Ser	Ser	Leu	His	Ser	Ser	
	290					295					300					
gtc	aga	tca	tct	gca	cta	ttg	att	ggt	cct	tcc	ttg	ggc	tca	tta	cca	961
Val	Arg	Ser	Ser	Ala	Leu	Leu	Ile	Gly	Pro	Ser	Leu	Gly	Ser	Leu	Pro	
	305				310					315					320	
act	tca	atc	tct	ttc	tct	ccc	gca	tac	gca	agc	tca	tcc	tat	att	aga	1009
Thr	Ser	Ile	Ser	Phe	Ser	Pro	Ala	Tyr	Ala	Ser	Ser	Ser	Tyr	Ile	Arg	
			325						330					335		
caa	tca	ttc	cag	tct	tcc	tct	aac	cgt	cga	tca	cct	cca	ata	agc	gta	1057
Gln	Ser	Phe	Gln	Ser	Ser	Ser	Asn	Arg	Arg	Ser	Pro	Pro	Ile	Ser	Val	
		340						345					350			
agt	cga	agc	tca	gtg	gat	ctc	aga	caa	caa	gca	gct	tct	cca	tct	cca	1105
Ser	Arg	Ser	Ser	Val	Asp	Leu	Arg	Gln	Gln	Ala	Ala	Ser	Pro	Ser	Pro	
		355					360					365				
tca	cca	tca	cag	aga	tca	tac	att	tcc	cat	atg	gct	tct	cca	cag	tca	1153
Ser	Pro	Ser	Gln	Arg	Ser	Tyr	Ile	Ser	His	Met	Ala	Ser	Pro	Gln	Ser	
	370					375					380					

PF59082SeqList_PF59082.txt

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Leu Gly Tyr Pro Thr Ile Ser Pro Phe Asn Thr Arg Tyr Met Ser Pro	
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tat aga cct agc ccg agc aat gca tca cct gca atg gct gga tca tcg	1249
Tyr Arg Pro Ser Pro Ser Asn Ala Ser Pro Ala Met Ala Gly Ser Ser	
405 410 415	
aat tat ccg ttg aat cca ctg cgt tac agt gaa tca gct gga act ttc	1297
Asn Tyr Pro Leu Asn Pro Leu Arg Tyr Ser Glu Ser Ala Gly Thr Phe	
420 425 430	
tct cca tac gcc tct gca aac tcg ctt cca gac tgt tagaaagtct	1343
Ser Pro Tyr Ala Ser Ala Asn Ser Leu Pro Asp Cys	
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 Glu Ala Asn Ile Ala Pro Ser Val Lys Gly Thr Gly Glu Ile Gly Val
 35 40 45
 Val Tyr Val Ala Glu Xaa Leu Asp Ala Cys Gln Asn Leu Met Asn Lys
 50 55 60
 Xaa Glu Gln Ser Ser Asn Glu Thr Ser Pro Phe Val Leu Ile Val Arg
 65 70 75 80
 Gly Gly Cys Ser Phe Glu Glu Lys Val Arg Lys Ala Gln Arg Ala Gly
 85 90 95
 Phe Lys Ala Ala Ile Ile Tyr Asp Asn Glu Asp Arg Gly Thr Leu Ile
 100 105 110
 Ala Met Ala Gly Asn Ser Gly Gly Ile Arg Ile His Ala Val Phe Val
 115 120 125
 Thr Lys Glu Thr Gly Glu Val Leu Lys Glu Tyr Ala Gly Phe Pro Asp
 130 135 140
 Thr Lys Val Trp Leu Ile Pro Ser Phe Glu Asn Ser Ala Trp Ser Ile
 145 150 155 160
 Met Ala Val Ser Phe Ile Ser Leu Leu Ala Met Ser Ala Val Leu Ala
 165 170 175
 Thr Cys Phe Phe Val Arg Arg His Arg Ile Arg Arg Arg Thr Ser Arg
 180 185 190
 Ser Ser Arg Val Arg Glu Phe His Gly Met Ser Arg Arg Leu Val Lys
 195 200 205
 Ala Met Pro Ser Leu Ile Phe Ser Ser Phe His Glu Asp Asn Thr Thr
 210 215 220
 Ala Phe Thr Cys Ala Ile Cys Leu Glu Asp Tyr Thr Val Gly Asp Lys
 225 230 235 240
 Leu Arg Leu Leu Pro Cys Cys His Lys Phe His Ala Ala Cys Val Asp
 245 250 255
 Ser Trp Leu Thr Ser Trp Arg Thr Phe Cys Pro Val Cys Lys Arg Asp
 260 265 270

PF59082SeqList_PF59082.txt

Ala Arg Thr Ser Thr Gly Glu Pro Pro Ala Ser Glu Ser Thr Pro Leu
 275 280 285
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 290 295 300
 Val Arg Ser Ser Ala Leu Ile Gly Pro Ser Leu Gly Ser Leu Pro
 305 310 315 320
 Thr Ser Ile Ser Phe Ser Pro Ala Tyr Ala Ser Ser Ser Tyr Ile Arg
 325 330 335
 Gln Ser Phe Gln Ser Ser Ser Asn Arg Arg Ser Pro Pro Ile Ser Val
 340 345 350
 Ser Arg Ser Ser Val Asp Leu Arg Gln Gln Ala Ala Ser Pro Ser Pro
 355 360 365
 Ser Pro Ser Gln Arg Ser Tyr Ile Ser His Met Ala Ser Pro Gln Ser
 370 375 380
 Leu Gly Tyr Pro Thr Ile Ser Pro Phe Asn Thr Arg Tyr Met Ser Pro
 385 390 395 400
 Tyr Arg Pro Ser Pro Ser Asn Ala Ser Pro Ala Met Ala Gly Ser Ser
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acc tgc gcc gcc gcc cgc ccc tgc gcg gcc ctc gtc cgc ctc ggc gcc	96
Thr Cys Ala Ala Ala Arg Pro Cys Ala Ala Leu Val Arg Leu Gly Ala	
gcc acc ttc ctc gac gcc ccc gcg cgc ttc ggg ccc cgg gtg acc agc	144
Ala Thr Phe Leu Asp Ala Pro Ala Arg Phe Gly Pro Arg Val Thr Ser	
gac ggg ata tgc ggg tcg ctg cgc gcc gcg gac ccc gcc gac gcg tgc	192
Asp Gly Ile Cys Gly Ser Leu Arg Ala Ala Asp 60 Ala Asp Ala Cys	
acg ccc gtc agg gcc gcc cct ggc tcc ggc ggg atg gcg ttc gtg ctg	240
Thr Pro Val Arg Ala Ala Pro Gly Ser Gly Gly Met Ala Phe Val Leu	
atc gcg cgc ggg aac tgc agc ttc gag ggc aag gtg cgg gcg gcg cag	288
Ile Ala Arg Gly Asn Cys Ser Phe Glu Gly 90 Lys Val Arg Ala Ala Gln	
ctg gcc ggc ttc gac gcc gcc ctc gtc cac gac gac gag gac aag gcc	336
Leu Ala Gly Phe Asp Ala Ala Leu Val His Asp Asp Glu Asp Lys Ala	
agc ctc tac tcc atg gtt ggt gat cct gag ggc ata cac ata cct gcg	384
Ser Leu Tyr Ser Met Val Gly Asp Pro Glu Gly Ile His Ile Pro Ala	
gta ttc gta tcc aaa atg gct ggg caa act ttg aag aag ttt gct aga	432
Val Phe Val Ser Lys Met Ala Gly Gln Thr Leu Lys Lys Phe Ala Arg	
ggt gaa gat ggt gag tgc tgc ata aac tcc tcg atg gat gag act gca	480
Gly Glu Asp Gly Glu Cys Cys Ile Asn Ser Ser Met Asp Glu Thr Ala	
ggg aca gtg ttg gtg atg tcg ttc gta tca ctt gtt gtc atc ata tca	528
Gly Thr Val Leu Val Met Ser Phe Val Ser 170 Leu Val Val Ile Ile Ser	
gtt gta gct tca ttt ctt ttc gct cgg aac tgc cga ctt tta cgc cat	576
Val Val Ala Ser Phe Leu Phe Ala Arg Asn Cys Arg Leu Leu Arg His	

PF59082SeqList_PF59082.txt

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Gly Val Asp Asn His Pro Pro Cys Ile Lys Lys His Val Val Glu Lys	
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att cct tcc ttg gta tat aaa gct ccc tgc tca agt ggc aac aat tgt	672
Ile Pro Ser Leu Val Tyr Lys Ala Pro Cys Ser Ser Gly Asn Asn Cys	
210 215 220	
gaa gaa gcc tgt gcc att tgt tta gaa gac tat gat aat ggt gac atg	720
Glu Glu Ala Cys Ala Ile Cys Leu Glu Asp Tyr Asp Asn Gly Asp Met	
225 230 235 240	
ctt aga ctt ctc cca tgc aaa cat gaa ttt cat gtg gag tgt att gat	768
Leu Arg Leu Leu Pro Cys Lys His Glu Phe His Val Glu Cys Ile Asp	
245 250 255	
ccc tgg ctg aca aag tgg ggc aca ttt tgc cca gta tgt aaa ctt gaa	816
Pro Trp Leu Thr Lys Trp Gly Thr Phe Cys Pro Val Cys Lys Leu Glu	
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Val Thr Thr Gly Glu	
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Ala Thr Phe Leu Asp Ala Pro Ala Arg Phe Gly Pro Arg Val Thr Ser	
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Asp Gly Ile Cys Gly Ser Leu Arg Ala Ala Asp Pro Ala Asp Ala Cys	
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Thr Pro Val Arg Ala Ala Pro Gly Ser Gly Gly Met Ala Phe Val Leu	
65 70 75 80	
Ile Ala Arg Gly Asn Cys Ser Phe Glu Gly Lys Val Arg Ala Ala Gln	
85 90 95	
Leu Ala Gly Phe Asp Ala Ala Leu Val His Asp Asp Glu Asp Lys Ala	
100 105 110	
Ser Leu Tyr Ser Met Val Gly Asp Pro Glu Gly Ile His Ile Pro Ala	
115 120 125	
Val Phe Val Ser Lys Met Ala Gly Gln Thr Leu Lys Lys Phe Ala Arg	
130 135 140	
Gly Glu Asp Gly Glu Cys Ile Asn Ser Ser Met Asp Glu Thr Ala	
145 150 155 160	
Gly Thr Val Leu Val Met Ser Phe Val Ser Leu Val Val Ile Ile Ser	
165 170 175	
Val Val Ala Ser Phe Leu Phe Ala Arg Asn Cys Arg Leu Leu Arg His	
180 185 190	
Gly Val Asp Asn His Pro Pro Cys Ile Lys Lys His Val Val Glu Lys	
195 200 205	
Ile Pro Ser Leu Val Tyr Lys Ala Pro Cys Ser Ser Gly Asn Asn Cys	
210 215 220	
Glu Glu Ala Cys Ala Ile Cys Leu Glu Asp Tyr Asp Asn Gly Asp Met	
225 230 235 240	
Leu Arg Leu Leu Pro Cys Lys His Glu Phe His Val Glu Cys Ile Asp	
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PF59082SeqList_PF59082.txt

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PF59082SeqList_PF59082.txt

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Arg Gly Xaa Cys Xaa Phe Xaa Xaa Lys Xaa Xaa Xaa Ala Gln Xaa Ala
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Gly Phe Xaa Ala Xaa Ile Val Tyr Asp Xaa Xaa Xaa Xaa Xaa Xaa Leu
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Xaa Xaa Xaa Xaa Xaa Met Xaa Gly Xaa Xaa Xaa Gly Xaa Xaa Ile
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Xaa Ala Val Phe Xaa Xaa Xaa Xaa Xaa Gly Glu Xaa Leu Lys Xaa Xaa
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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
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Xaa Xaa Xaa Xaa Xaa Xaa Val Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa
      195      200      205
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Ala Ile Cys
      210      215      220
Leu Glu Asp Tyr Xaa Xaa Gly Xaa Xaa Leu Arg Xaa Leu Pro Cys Xaa
      225      230      235      240
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<222> (48)..(48)
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 <223> Xaa in position 49 is Asp or Asn

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 <223> Xaa in position 50 is Ala, Ile or Pro

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 <223> Xaa in position 52 is Ala, Ser or Thr

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 <223> Xaa in position 53 is Glu, Gly, Ser or Thr

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 Xaa Xaa Arg Xaa Leu Pro Cys Xaa His Xaa Xaa His Xaa Xaa Cys Xaa
 20 25 30
 Asp Xaa Trp Leu Xaa Xaa Xaa Xaa Xaa Cys Pro Xaa Cys Lys Xaa
 35 40 45
 Xaa Xaa Xaa Xaa
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<223> Xaa in position 27 is Ile, Leu or Val

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<223> Xaa in position 29 is His or Tyr

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<223> Xaa in position 35 is Ala, Asp, Glu or Gly

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Xaa Xaa Xaa Xaa Leu Xaa Xaa
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<223> Xaa in position 6 is Glu or Lys

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<223> Xaa in position 12 is Asp or Asn

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<223> Xaa in position 20 to 21 is any amino acid

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<223> Xaa in position 22 is Asp, Glu or Arg

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<223> Xaa in position 23 is Glu, Gly, Asn or Thr

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<223> Xaa in position 28 is Ile or Val

<220>
<221> Variant

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<222> (29)..(29)
<223> Xaa in position 29 is Leu or Met

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<222> (30)..(30)
<223> Xaa in position 30 is Ala or Val

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<223> Xaa in position 40 is any amino acid

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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala Xaa Xaa Xaa Xaa Xaa Xaa Ser
      20      25      30
Phe Xaa Ser Leu Xaa Xaa Xaa Xaa Xaa
      35      40

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<223> Xaa in position 2 is Ala, Gly, Ile or Val

<220>
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<223> Xaa in position 3 is Ala, Ser or Thr

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 <223> Xaa in position 7 is Ala, Pro or Val

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 <223> Xaa in position 9 is any or no amino acid

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 <223> Xaa in position 11 to 14 is any or no amino acid

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 <222> (16)..(19)
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<400> 1649
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 20

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 1 5 10 15
 atg aaa cag agg aag aac agt aat ctc tca atc ttc gtc gta gtc ttc 96
 Met Lys Gln Arg Lys Asn Ser Asn Leu Ser Ile Phe Val Val Val Phe
 20 25 30
 tct gtt ttc ctc ttc ggg atc ttc atg tac aat gaa gac gtc aag tcc 144
 Ser Val Phe Leu Phe Gly Ile Phe Met Tyr Asn Glu Asp Val Lys Ser
 35 40 45
 atc gca gag ttt cct ttc tcc acc tca aaa cct cac gac gtc cac gac 192
 Ile Ala Glu Phe Pro Phe Ser Thr Ser Lys Pro His Asp Val His Asp
 50 55 60
 gaa gcg aca ccg atc aca gag atc aca aca cta ccg gtt caa gag tcg 240
 Glu Ala Thr Pro Ile Thr Glu Ile Thr Thr Leu Pro Val Gln Glu Ser
 65 70 75 80
 atc aag aac tca gac cca att cag gaa tcg atc aaa aac gca gac tca 288
 Ile Lys Asn Ser Asp Pro Ile Gln Glu Ser Ile Lys Asn Ala Asp Ser

PF59082SeqList_PF59082.txt

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tcg	aaa	aca	gag	gaa	gtt	aaa	aag	att	gag	ctt	ttc	gct	gcg	acg	gag	384
Ser	Lys	Thr	Glu	Glu	Val	Lys	Lys	Ile	Glu	Leu	Phe	Ala	Ala	Thr	Glu	
		115					120					125				
gat	gaa	gaa	gac	gtg	gaa	ttg	ccg	ccg	gag	gaa	tgc	gat	ttg	ttc	acc	432
Asp	Glu	Glu	Asp	Val	Glu	Leu	Pro	Pro	Glu	Glu	Cys	Asp	Leu	Phe	Thr	
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Gly	Glu	Trp	Val	Phe	Asp	Asn	Glu	Thr	His	Pro	Leu	Tyr	Lys	Glu	Asp	
145				150						155				160		
caa	tgt	gag	ttc	ttg	acg	gcg	caa	gtc	act	tgc	atg	aga	aat	gga	aga	528
Gln	Cys	Glu	Phe	Leu	Thr	Ala	Gln	Val	Thr	Cys	Met	Arg	Asn	Gly	Arg	
			165					170						175		
aga	gat	tct	ctg	tat	cag	aac	tgg	aga	tgg	caa	cct	aga	gat	tgt	tct	576
Arg	Asp	Ser	Leu	Tyr	Gln	Asn	Trp	Arg	Trp	Gln	Pro	Arg	Asp	Cys	Ser	
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Leu	Pro	Lys	Phe	Lys	Ala	Lys	Leu	Leu	Glu	Lys	Lys	Leu	Arg	Asn	Lys	
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aga	atg	atg	ttc	gtt	gga	gat	tcc	cta	aac	cgg	aac	caa	tgg	gaa	tca	672
Arg	Met	Met	Phe	Val	Gly	Asp	Ser	Leu	Asn	Arg	Asn	Gln	Trp	Glu	Ser	
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Met	Val	Cys	Leu	Val	Gln	Ser	Val	Val	Pro	Pro	Gly	Arg	Lys	Ser	Leu	
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Asn	Lys	Thr	Gly	Ser	Leu	Ser	Val	Phe	Arg	Val	Glu	Asp	Tyr	Asn	Ala	
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Thr	Val	Glu	Phe	Tyr	Trp	Ala	Pro	Phe	Leu	Val	Glu	Ser	Asn	Ser	Asp	
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Ile	Glu	Lys	His	Gly	Val	Asn	Trp	Lys	Gly	Val	Asp	Phe	Leu	Val	Phe	
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Asn	Thr	Tyr	Ile	Trp	Trp	Met	Asn	Thr	Phe	Ala	Met	Lys	Val	Leu	Arg	
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gga	tcg	ttc	gat	aaa	gga	gac	acc	gag	tat	gag	gag	atc	gaa	cgg	cca	1008
Gly	Ser	Phe	Asp	Lys	Gly	Asp	Thr	Glu	Tyr	Glu	Glu	Ile	Glu	Arg	Pro	
			325					330					335			
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Val	Ala	Tyr	Arg	Arg	Val	Met	Arg	Thr	Trp	Gly	Asp	Trp	Val	Glu	Arg	
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aat	att	gat	cct	cta	cgt	acc	act	gtc	ttc	ttt	gct	agc	atg	tct	cct	1104
Asn	Ile	Asp	Pro	Leu	Arg	Thr	Thr	Val	Phe	Phe	Ala	Ser	Met	Ser	Pro	
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ctt	cac	atc	aag	agc	ttg	gat	tgg	gag	aat	cca	gat	ggg	atc	aag	tgt	1152
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Leu	Asn	Val	Pro	Val	Tyr	Phe	Leu	Asn	Ile	Thr	Lys	Leu	Ser	Glu	Tyr	
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Arg	Lys	Asp	Ala	His	Thr	Ser	Val	His	Thr	Ile	Arg	Gln	Gly	Lys	Met	
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ctg	acg	ccg	gag	caa	caa	gcc	gat	ccc	aac	act	tac	gcc	gat	tgt	atc	1392
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Glu	Ala	Thr	Pro	Ile	Thr	Glu	Ile	Thr	Thr	Leu	Pro	Val	Gln	Glu	Ser
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Leu	Pro	Lys	Phe	Lys	Ala	Lys	Leu	Leu	Glu	Lys	Leu	Arg	Asn	Lys	
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Ala	Leu	Glu	Thr	Thr	Pro	Ile	Leu	Asn	Met	Ser	Met	Pro	Phe	Ser	Val
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Gly	Thr	Asp	Tyr	Arg	Leu	Phe	Ser	Val	Ala	Glu	Asn	Val	Thr	His	Ser
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Leu	Asn	Val	Pro	Val	Tyr	Phe	Leu	Asn	Ile	Thr	Lys	Leu	Ser	Glu	Tyr
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 1 5 10 15

110

ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc
 Gly Gly Val Phe Asp Pro Phe Gly Thr Lys Gln Ala Val Ser Ser Leu
 20 25 30

158

cgg aag ggc ggc cgg ctg ccg gtg tac gtg gct ggc gtc ttc ttc gtc
 Arg Lys Gly Gly Arg Leu Pro Val Tyr Val Ala Gly Val Phe Phe Val
 35 40 45

206

atc ttc gtc atc atc atg tac ggc gag gac atc cgg tcg ctc acg ctg
 Ile Phe Val Ile Ile Met Tyr Gly Glu Asp Ile Arg Ser Leu Thr Leu
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254

gac ccg atc ggc cgc ggc ggc aca acg ccg gcg cgg atc gtg gag ccg
 Asp Pro Ile Ala Arg Ala Gly Thr Thr Pro Ala Arg Ile Val Glu Pro
 65 70 75

302

gta gtg acg gag gag cgc cac gtc gcc cgg gtc aac cct cct cgg cgc
 Val Val Thr Glu Glu Arg His Val Ala Arg Val Asn Pro Pro Arg Arg
 80 85 90 95

350

gag gtc tcg tcc ggc gag aag gcc gcc gcg ttg ccg ctc gac gtc gac
 Glu Val Ser Ser Ala Glu Lys Ala Ala Ala Leu Pro Leu Asp Val Asp
 100 105 110

398

gag agg ccg aag ctg ggc acg ccg acg ccg acg gag gcg ggc aag gag
 Glu Arg Pro Lys Leu Ala Thr Pro Thr Pro Thr Glu Ala Ala Lys Glu
 115 120 125

446

gtc ccg aag gtc gag aag atc agg aag ccg aag aaa ccc aag acg acg
 Val Pro Lys Val Glu Lys Ile Arg Lys Pro Lys Lys Pro Lys Thr Thr
 130 135 140

494

aag aag aag ccg agg aag ccg cgg ccg gcg aag aag acg gtg gcg gcg
 Lys Lys Lys Pro Arg Lys Pro Arg Pro Ala Lys Lys Thr Val Ala Ala
 145 150 155

542

gca gcc ggc ggc ctg ctc ggc gtg ccg gag acg tgc gac ctg tcc aag
 Ala Ala Gly Gly Leu Leu Gly Val Pro Glu Thr Cys Asp Leu Ser Lys
 160 165 170 175

590

ggc gag tgg gtg ttc gac aac acc agc tac cct ctg tac cgg gag gag
 Gly Glu Trp Val Phe Asp Asn Thr Ser Tyr Pro Leu Tyr Arg Glu Glu
 180 185 190

638

cag tgc gag ttc ctc acg tcg cag gtg acg tgc atg agg aac ggc cgc
 Gln Cys Glu Phe Leu Thr Ser Gln Val Thr Cys Met Arg Asn Gly Arg
 195 200 205

686

cgc gac gac acc tac cag aag tgg cgg tgg cag ccc aaa gac tgc tcc
 Arg Asp Asp Thr Tyr Gln Lys Trp Arg Trp Gln Pro Lys Asp Cys Ser
 210 215 220

734

atg ccc agg ttc gac gcg aag ctg ttc atg gag agg ctc cga ggc aag
 Met Pro Arg Phe Asp Ala Lys Leu Phe Met Glu Arg Leu Arg Gly Lys
 225 230 235

782

cgg ttc atg ttc gtg ggc gac tcg ctg aac cgg aac cag tgg gag tcc
 Arg Phe Met Phe Val Gly Asp Ser Leu Asn Arg Asn Gln Trp Glu Ser
 240 245 250 255

830

PF59082SeqList_PF59082.txt

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acc	tgg	gag	gac	cag	cgg	gtc	gtc	ttc	cac	gcc	gtg	gag	tac	aac	gcg	926
Thr	Trp	Glu	Asp	Gln	Arg	Val	Val	Phe	His	Ala	Val	Glu	Tyr	Asn	Ala	
			275					280					285			
acg	gtg	gag	ttc	tac	tgg	gcg	ccg	ttc	ctg	gtg	gag	tcc	aac	tcc	gac	974
Thr	Val	Glu	Phe	Tyr	Trp	Ala	Pro	Phe	Leu	Val	Glu	Ser	Asn	Ser	Asp	
			290				295					300				
gac	ccc	aag	atc	cac	agc	atc	cag	cac	cgg	atc	atc	aag	gcg	gac	gcg	1022
Asp	Pro	Lys	Ile	His	Ser	Ile	Gln	His	Arg	Ile	Ile	Lys	Ala	Asp	Ala	
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Ile	Ala	Ala	His	Ala	Gln	Asn	Trp	Arg	Gly	Val	Asp	Tyr	Leu	Val	Phe	
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aac	acc	tac	atc	tgg	atg	aac	acc	ctc	atg	aag	atc	atg	aga			1118
Asn	Thr	Tyr	Ile	Trp	Trp	Met	Asn	Thr	Leu	Asn	Met	Lys	Ile	Met	Arg	
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ccg	ggc	ggg	cag	agc	tgg	gag	gag	cat	gac	gag	gtc	gtg	agg	atc	gag	1166
Pro	Gly	Gly	Gln	Ser	Trp	Glu	Glu	His	Asp	Glu	Val	Val	Arg	Ile	Glu	
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gcg	tat	cgg	aag	gtg	ctg	acg	acg	tgg	gcg	agc	tgg	gtg	aac	gac	aac	1214
Ala	Tyr	Arg	Lys	Val	Leu	Thr	Thr	Trp	Ala	Ser	Trp	Val	Asn	Asp	Asn	
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Ile	Asp	Pro	Ala	Arg	Thr	Ser	Val	Phe	Phe	Met	Ser	Ile	Ser	Pro	Leu	
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cac	atc	agc	ccg	gag	gtg	tgg	ggg	aac	ccg	ggc	ggg	atc	cgg	tgc	gcc	1310
His	Ile	Ser	Pro	Glu	Val	Trp	Gly	Asn	Pro	Gly	Gly	Ile	Arg	Cys	Ala	
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aag	gag	acg	atg	ccg	ctg	ctc	aac	tgg	cac	ggg	ccg	atc	tgg	ctg	ggc	1358
Lys	Glu	Thr	Met	Pro	Leu	Leu	Asn	Trp	His	Gly	Pro	Ile	Trp	Leu	Gly	
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Thr	Asp	Trp	Asp	Met	Phe	His	Ala	Ala	Ala	Asn	Val	Ser	Arg	Thr	Ala	
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gcg	acg	cgg	gtg	ccc	atc	acc	ttc	gtc	gac	gtg	acc	acc	atg	tcg	gag	1454
Ala	Thr	Arg	Val	Pro	Ile	Thr	Phe	Val	Asp	Val	Thr	Thr	Met	Ser	Glu	
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cgg	cgc	aag	gac	ggg	cac	acc	tcc	gtg	cac	acc	atc	cgg	cag	ggc	aag	1502
Arg	Arg	Lys	Asp	Gly	His	Thr	Ser	Val	His	Thr	Ile	Arg	Gln	Gly	Lys	
				465		470					475					
gtg	ctg	acg	ccg	gag	cag	cag	gcc	gac	cct	ggc	acc	tac	gcc	gac	tgc	1550
Val	Leu	Thr	Pro	Glu	Gln	Gln	Ala	Asp	Pro	Gly	Thr	Tyr	Ala	Asp	Cys	
					485				490					495		
atc	cac	tgg	tgc	ctc	ccc	ggc	gtc	cct	gac	atc	tgg	aac	ctc	atc	ctc	1598
Ile	His	Trp	Cys	Leu	Pro	Gly	Val	Pro	Asp	Ile	Trp	Asn	Leu	Ile	Leu	
				500				505					510			
tac	acc	agg	ata	atg	tcc	agg	ccg	cag	ctg	gta	tagcaaattc	caagaattta				1651
Tyr	Thr	Arg	Ile	Met	Ser	Arg	Pro	Gln	Leu	Val						
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atgtctttca	tttgttcttt	ttcttcaggg	gttaggttaa	gtgggaagag	atcgatacag											1831
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 Lys Gly Gly Arg Leu Pro Val Tyr Val Ala Gly Val Phe Phe Val Ile
 35 40 45
 Phe Val Ile Ile Met Tyr Gly Glu Asp Ile Arg Ser Leu Thr Leu Asp
 50 55 60
 Pro Ile Ala Arg Ala Gly Thr Thr Pro Ala Arg Ile Val Glu Pro Val
 65 70 75 80
 Val Thr Glu Glu Arg His Val Ala Arg Val Asn Pro Pro Arg Arg Glu
 85 90 95
 Val Ser Ser Ala Glu Lys Ala Ala Ala Leu Pro Leu Asp Val Asp Glu
 100 105 110
 Arg Pro Lys Leu Ala Thr Pro Thr Pro Thr Glu Ala Ala Lys Glu Val
 115 120 125
 Pro Lys Val Glu Lys Ile Arg Lys Pro Lys Lys Pro Lys Thr Thr Lys
 130 135 140
 Lys Lys Pro Arg Lys Pro Arg Pro Ala Lys Lys Thr Val Ala Ala Ala
 145 150 155 160
 Ala Gly Gly Leu Leu Gly Val Pro Glu Thr Cys Asp Leu Ser Lys Gly
 165 170 175
 Glu Trp Val Phe Asp Asn Thr Ser Tyr Pro Leu Tyr Arg Glu Glu Gln
 180 185 190
 Cys Glu Phe Leu Thr Ser Gln Val Thr Cys Met Arg Asn Gly Arg Arg
 195 200 205
 Asp Asp Thr Tyr Gln Lys Trp Arg Trp Gln Pro Lys Asp Cys Ser Met
 210 215 220
 Pro Arg Phe Asp Ala Lys Leu Phe Met Glu Arg Leu Arg Gly Lys Arg
 225 230 235 240
 Phe Met Phe Val Gly Asp Ser Leu Asn Arg Asn Gln Trp Glu Ser Met
 245 250 255
 Val Cys Leu Val Gln Ser Val Met Ser Pro Gly Lys Lys Tyr Val Thr
 260 265 270
 Trp Glu Asp Gln Arg Val Val Phe His Ala Val Glu Tyr Asn Ala Thr
 275 280 285
 Val Glu Phe Tyr Trp Ala Pro Phe Leu Val Glu Ser Asn Ser Asp Asp
 290 295 300
 Pro Lys Ile His Ser Ile Gln His Arg Ile Ile Lys Ala Asp Ala Ile
 305 310 315 320
 Ala Ala His Ala Gln Asn Trp Arg Gly Val Asp Tyr Leu Val Phe Asn
 325 330 335
 Thr Tyr Ile Trp Trp Met Asn Thr Leu Asn Met Lys Ile Met Arg Pro
 340 345 350
 Gly Gly Gln Ser Trp Glu Glu His Asp Glu Val Val Arg Ile Glu Ala
 355 360 365
 Tyr Arg Lys Val Leu Thr Thr Trp Ala Ser Trp Val Asn Asp Asn Ile
 370 375 380
 Asp Pro Ala Arg Thr Ser Val Phe Phe Met Ser Ile Ser Pro Leu His
 385 390 395 400
 Ile Ser Pro Glu Val Trp Gly Asn Pro Gly Gly Ile Arg Cys Ala Lys
 405 410 415
 Glu Thr Met Pro Leu Leu Asn Trp His Gly Pro Ile Trp Leu Gly Thr
 420 425 430
 Asp Trp Asp Met Phe His Ala Ala Ala Asn Val Ser Arg Thr Ala Ala
 435 440 445
 Thr Arg Val Pro Ile Thr Phe Val Asp Val Thr Thr Met Ser Glu Arg
 450 455 460
 Arg Lys Asp Gly His Thr Ser Val His Thr Ile Arg Gln Gly Lys Val
 465 470 475 480
 Leu Thr Pro Glu Gln Gln Ala Asp Pro Gly Thr Tyr Ala Asp Cys Ile
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PF59082SeqList_PF59082.txt

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 Ser Thr Thr Met Lys Gly Lys Arg Asn Ser Ser Ile Ser Ile Ser Ile
 20 25 30
 gtt gtg gtg gtg ttc tcc ata ttc ctc ttt ggg gtc ttc atg tac aac 144
 Val Val Val Val Phe Ser Ile Phe Leu Phe Gly Val Phe Met Tyr Asn
 35 40 45
 gag gac gtt aag tca atg gcc gag ttc act ttc ttg agg cct aag gct 192
 Glu Asp Val Lys Ser Met Ala Glu Phe Thr Phe Leu Arg Pro Lys Ala
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 caa gaa atc caa gaa gaa acg gtt tcc aac aac aat tca aga act caa 240
 Gln Glu Ile Gln Glu Glu Thr Val Ser Asn Asn Asn Ser Arg Thr Gln
 65 70 75 80
 cca gag aga aac cgg gtc gag gac tcc gag gaa tct caa gaa ccg att 288
 Pro Glu Arg Asn Arg Val Glu Asp Ser Glu Glu Ser Gln Glu Pro Ile
 85 90 95
 gat ttg aaa gcc gtt gtg gca gaa gag aag ata gtg gaa gag tat gag 336
 Asp Leu Lys Ala Val Val Ala Glu Glu Lys Ile Val Glu Glu Tyr Glu
 100 105 110
 gaa gaa aat gaa gag gtt gtg ttg ccc cca gaa gag tgt gac ttg ttc 384
 Glu Glu Asn Glu Glu Val Val Leu Pro Pro Glu Glu Cys Asp Leu Phe
 115 120 125
 aca gga gag tgg gtt ttt gat aac ttg aca cac cct ttg tac aaa gaa 432
 Thr Gly Glu Trp Val Phe Asp Asn Leu Thr His Pro Leu Tyr Lys Glu
 130 135 140
 gac caa tgc gaa ttc ctc act tca caa gtc acc tgc atg agg aat gga 480
 Asp Gln Cys Glu Phe Leu Thr Ser Gln Val Thr Cys Met Arg Asn Gly
 145 150 155 160
 aga agt gat tct ctc tat cag aat tgg aga tgg cag ccc aga gat tgc 528
 Arg Ser Asp Ser Leu Tyr Gln Asn Trp Arg Trp Gln Pro Arg Asp Cys
 165 170 175
 tct ttg ccc aaa ggg agg agg ctt atg ttt gtt gga gac tca ctg aac 576
 Ser Leu Pro Lys Gly Arg Arg Leu Met Phe Val Gly Asp Ser Leu Asn
 180 185 190
 agg aac cag tgg gaa tca atg att tgt ctg gtc cag tct gtt gtt cct 624
 Arg Asn Gln Trp Glu Ser Met Ile Cys Leu Val Gln Ser Val Val Pro
 195 200 205
 caa ggc aaa aaa agt ttg agc aag aat ggt tct ctt tct atc ttc aca 672
 Gln Gly Lys Lys Ser Leu Ser Lys Asn Gly Ser Leu Ser Ile Phe Thr
 210 215 220
 att gag gat tac aat gct acg gtg gag ttc tac tgg gca ccg ttc ctt 720
 Ile Glu Asp Tyr Asn Ala Thr Val Glu Phe Tyr Trp Ala Pro Phe Leu
 225 230 235 240
 gtg gag tca aac tca gat gat cca aag atg cac agc ata ttg aac cgt 768
 Val Glu Ser Asn Ser Asp Asp Pro Lys Met His Ser Ile Leu Asn Arg
 245 250 255
 att atc atg ccg gaa tca att gag aag cat gct gtg aat tgg aag aat 816
 Ile Ile Met Pro Glu Ser Ile Glu Lys His Ala Val Asn Trp Lys Asn
 260 265 270 275
 gtg gac tat ctg atc ttc aac acc tac ata tgg tgg atg aat act gcc 864
 Val Asp Tyr Leu Ile Phe Asn Thr Tyr Ile Trp Trp Met Asn Thr Ala
 275 280 285

PF59082SeqList_PF59082.txt

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Asp	Glu	Val	Pro	Arg	Pro	Ile	Ala	Tyr	Gly	Arg	Val	Leu	Asn	Thr	Trp	
	305				310					315					320	
tct	aaa	tgg	gtg	gaa	gac	aac	att	aat	cca	aat	cgc	acc	aaa	gtt	ttc	1008
Ser	Lys	Trp	Val	Glu	Asp	Asn	Ile	Asn	Pro	Asn	Arg	Thr	Lys	Val	Phe	
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ttc	tcc	agc	atg	tct	cct	ctt	cat	att	aag	agt	gag	gct	tgg	aac	aat	1056
Phe	Ser	Ser	Met	Ser	Pro	Leu	His	Ile	Lys	Ser	Glu	Ala	Trp	Asn	Asn	
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cca	gat	ggg	ata	aaa	tgt	gct	aag	gag	acc	ata	cca	att	ctg	aat	atg	1104
Pro	Asp	Gly	Ile	Lys	Cys	Ala	Lys	Glu	Thr	Ile	Pro	Ile	Leu	Asn	Met	
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Ser	Thr	Thr	Leu	Gln	Val	Gly	Thr	Asp	Arg	Arg	Leu	Phe	Val	Val	Ala	
			370			375					380					
aac	aat	gtg	acg	caa	tca	atg	aag	gtg	gtg	cca	gtg	aac	ttc	ctt	aac	1200
Asn	Asn	Val	Thr	Gln	Ser	Met	Lys	Val	Val	Pro	Val	Asn	Phe	Leu	Asn	
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Ile	Thr	Thr	Leu	Ser	Glu	Phe	Arg	Lys	Asp	Ala	His	Thr	Ser	Val	Tyr	
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acc	ata	cgc	caa	ggc	aaa	atg	tta	act	cca	gaa	caa	caa	gct	gat	cct	1296
Thr	Ile	Arg	Gln	Gly	Lys	Met	Leu	Thr	Pro	Glu	Gln	Gln	Ala	Asp	Pro	
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act	act	tat	gcc	gat	tgc	att	cat	tgg	tgt	tta	cca	gga	tta	cct	gac	1344
Thr	Thr	Tyr	Ala	Asp	Cys	Ile	His	Trp	Cys	Leu	Pro	Gly	Leu	Pro	Asp	
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act	tgg	aat	gag	ttc	ctc	tat	aca	agg	atc	atc	tct	caa	tct	tgacctacaa		1396
Thr	Trp	Asn	Glu	Phe	Leu	Tyr	Thr	Arg	Ile	Ile	Ser	Gln	Ser			
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gcatttttcc	ctttttttcc	tttgттаagc	caatttagcc	aagcacggaa	gcacagcaag											1636
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 Glu Asp Val Lys Ser Met Ala Glu Phe Thr Phe Leu Arg Pro Lys Ala
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 Gln Glu Ile Gln Glu Glu Thr Val Ser Asn Asn Asn Ser Arg Thr Gln
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 Pro Glu Arg Asn Arg Val Glu Asp Ser Glu Ser Gln Glu Pro Ile
 85 90 95 100
 Seite 2174

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Asp	Gln	Cys	Glu	Phe	Leu	Thr	Ser	Gln	Val	Thr	Cys	Met	Arg	Asn	Gly
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Arg	Ser	Asp	Ser	Leu	Tyr	Gln	Asn	Trp	Arg	Trp	Gln	Pro	Arg	Asp	Cys
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Ser	Leu	Pro	Lys	Gly	Arg	Arg	Leu	Met	Phe	Val	Gly	Asp	Ser	Leu	Asn
			180					185					190		
Arg	Asn	Gln	Trp	Glu	Ser	Met	Ile	Cys	Leu	Val	Gln	Ser	Val	Val	Pro
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Val	Glu	Ser	Asn	Ser	Asp	Asp	Pro	Lys	Met	His	Ser	Ile	Leu	Asn	Arg
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Ser	Lys	Trp	Val	Glu	Asp	Asn	Ile	Asn	Pro	Asn	Arg	Thr	Lys	Val	Phe
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Phe	Ser	Ser	Met	Ser	Pro	Leu	His	Ile	Lys	Ser	Glu	Ala	Trp	Asn	Asn
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Ile	Thr	Thr	Leu	Ser	Glu	Phe	Arg	Lys	Asp	Ala	His	Thr	Ser	Val	Tyr
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Thr	Ile	Arg	Gln	Gly	Lys	Met	Leu	Thr	Pro	Glu	Gln	Gln	Ala	Asp	Pro
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180

cgatcgagtc gggtccgtcc cgcgccg atg cgg atc ccg cgg cgg aag ggc ggg
Met Arg Ile Pro Arg Arg Lys Gly Gly

234

PF59082SeqList_PF59082.txt

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Ala	Val	Phe	Ala	Leu	Ala	Ala	Leu	Leu	Gly	Val	Ser	Val	Leu	Tyr	Asp	
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Asn	Ala	His	Ile	Ala	Ala	Ser	Leu	Arg	Arg	His	Gly	Gly	Pro	Arg	Thr	
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tac	gcc	aag	ctc	tcc	tcc	ttc	gaa	ggc	gcc	acc	gct	gtc	ccc	agc	atc	426
Tyr	Ala	Lys	Leu	Ser	Ser	Phe	Glu	Gly	Ala	Thr	Ala	Val	Pro	Ser	Ile	
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gcc	aag	gaa	gag	gcg	gcg	gcg	gcg	gtg	gcg	cgg	gca	acg	gag	tcg	gtg	474
Ala	Lys	Glu	Glu	Ala	Ala	Ala	Ala	Val	Ala	Arg	Ala	Thr	Glu	Ser	Val	
	75					80					85					
ccg	gtg	cac	ggc	gcg	gat	cgg	gcc	gac	tcg	ccc	ccg	cac	gag	cgg	cag	522
Pro	Val	His	Gly	Ala	Asp	Arg	Ala	Asp	Ser	Pro	Pro	His	Glu	Arg	Gln	
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gag	gag	atc	gag	gag	cgc	gca	tcg	aag	cct	gga	gcg	acg	gcc	ggg	agc	570
Glu	Glu	Ile	Glu	Glu	Arg	Ala	Ser	Lys	Pro	Gly	Ala	Thr	Ala	Gly	Ser	
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Ser	Leu	Gln	Asp	Ala	Pro	Leu	Ile	Glu	Glu	Val	Val	Gln	Gly	Gly	Ser	
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Gly	Gly	His	Asp	Gly	Asp	Gly	Asp	Gly	Asp	Gly	Gly	Ala	Gln	Ala	Gln	
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gag	cag	ccc	ccg	gcc	ccg	ggg	acc	tgc	gac	ctg	tac	aag	ggc	cgc	tgg	714
Glu	Gln	Pro	Pro	Ala	Pro	Gly	Thr	Cys	Asp	Leu	Tyr	Lys	Gly	Arg	Trp	
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Val	Tyr	Asp	Glu	Ser	Arg	Ala	Pro	Leu	Tyr	Lys	Glu	Ser	Asp	Cys	Ser	
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Phe	Leu	Thr	Glu	Gln	Val	Thr	Cys	Met	Arg	Asn	Gly	Arg	Arg	Asp	Asp	
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Asp	Tyr	Gln	Lys	Trp	Arg	Trp	Gln	Pro	Asp	Gly	Cys	Asp	Leu	Pro	Arg	
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Phe	Glu	Ala	Lys	Leu	Leu	Leu	Glu	Lys	Leu	Arg	Asn	Lys	Arg	Leu	Met	
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Phe	Val	Gly	Asp	Ser	Leu	Asn	Arg	Asn	Gln	Trp	Glu	Ser	Met	Val	Cys	
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ctg	gtc	cag	tca	gag	gct	cca	tgg	gac	aaa	aag	tcc	ctt	gtc	aag	aat	1002
Leu	Val	Gln	Ser	Glu	Ala	Pro	Trp	Asp	Lys	Lys	Ser	Leu	Val	Lys	Asn	
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Phe	Tyr	Trp	Ser	Pro	Phe	Leu	Val	Glu	Ser	Asn	Ser	Asp	Asp	Pro	Asp	
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Ile	His	Ser	Ile	Ser	Asp	Arg	Met	Ile	Lys	Pro	Thr	Ser	Ile	Ala	Lys	
		300				305						310				
cat	gcg	aac	tgg	gaa	ggg	gtg	gac	tac	ctg	atc	ttc	aac	act	tac		1194
His	Ala	Asn	Trp	Glu	Gly	Val	Asp	Tyr	Leu	Ile	Phe	Asn	Thr	Tyr		
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Ile	Trp	Trp	Met	Asn	Thr	Pro	Gln	Met	Lys	Thr	Leu	His	Gly	Gly	Ser	
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Phe	Ser	Arg	Lys	His	Val	Lys	Tyr	Asp	Glu	Ile	Glu	Arg	Val	Glu	Ala	
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Tyr	Arg	Lys	Val	Leu	Lys	Thr	Trp	Ser	Arg	Trp	Val	Glu	Ala	His	Val	

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Asp	Trp	Asp	Leu	Phe	Ala	Thr	Ala	Gln	Arg	Val	Thr	Arg	Ser	Met	Lys		
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acg	ccg	gag	cag	aag	gcg	aac	ccg	agg	aag	ttc	gcg	gac	tgc	atc	cac	1674	
Thr	Pro	Glu	Gln	Lys	Ala	Asn	Pro	Arg	Lys	Phe	Ala	Asp	Cys	Ile	His		
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Leu	Leu	Gly ₃₅	Val	Ser	Val	Leu	Tyr ₄₀	Asp	Asn	Ala	His ₄₅	Ile	Ala	Ala	Ser	
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 Pro Leu Tyr Lys Glu Ser Asp Cys Ser Phe Leu Thr Glu Gln Val Thr
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 Cys Met Arg Asn Gly Arg Arg Asp Asp Asp Tyr Gln Lys Trp Arg Trp
 195 200 205
 Gln Pro Asp Gly Cys Asp Leu Pro Arg Phe Glu Ala Lys Leu Leu Leu
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 Glu Lys Leu Arg Asn Lys Arg Leu Met Phe Val Gly Asp Ser Leu Asn
 225 230 235 240
 Arg Asn Gln Trp Glu Ser Met Val Cys Leu Val Gln Ser Glu Ala Pro
 245 250 255
 Trp Asp Lys Lys Ser Leu Val Lys Asn Gly Ser Leu Asn Val Phe His
 260 265 270
 Leu Gln Glu Tyr Asn Ala Thr Val Glu Phe Tyr Trp Ser Pro Phe Leu
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 Val Glu Ser Asn Ser Asp Asp Pro Asp Ile His Ser Ile Ser Asp Arg
 290 295 300
 Met Ile Lys Pro Thr Ser Ile Ala Lys His Ala Ala Asn Trp Glu Gly
 305 310 315 320
 Val Asp Tyr Leu Ile Phe Asn Thr Tyr Ile Trp Trp Met Asn Thr Pro
 325 330 335
 Gln Met Lys Thr Leu His Gly Gly Ser Phe Ser Arg Lys His Val Lys
 340 345 350
 Tyr Asp Glu Ile Glu Arg Val Glu Ala Tyr Arg Lys Val Leu Lys Thr
 355 360 365
 Trp Ser Arg Trp Val Glu Ala His Val Asp Pro Lys Arg Thr Thr Val
 370 375 380
 Leu Phe Met Ser Val Ser Pro Val His Met Gln Ser Glu Gly Trp Gly
 385 390 395 400
 Ser Pro Asn Ala Val Lys Cys Phe Ser Glu Thr Gln Pro Ala Ile Ser
 405 410 415
 Tyr Asn Lys Lys Leu Glu Val Gly Thr Asp Trp Asp Leu Phe Ala Thr
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 Ala Gln Arg Val Thr Arg Ser Met Lys Lys Val Pro Val His Phe Val
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 Asn Ile Thr Ala Leu Ser Glu Ile Arg Lys Asp Ala His Thr Ser Val
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 Pro Arg Lys Phe Ala Asp Cys Ile His Trp Cys Leu Pro Gly Val Pro
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120

PF59082SeqList_PF59082.txt

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tccttcaact tgacatcaca gcaatcgttg aggaggagga ggacacctgg aactcgattc 300

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Ala Thr Gly Lys Lys Ser Thr Ser Ser Gln Arg Phe Gln Trp Arg Ala

act aca gta ccc cgc cga acc gac gcc gac agc tgc cgc ctg ccg gac 688
Thr Thr Val Pro Arg Arg Thr Asp Ala Asp Ser Cys Arg Leu Pro Asp

cca aca aga agg aac caa gcc tac aaa atc aca act cca cgt tcg tcg 736
Pro Thr Arg Arg Asn Gln Ala Tyr Lys Ile Thr Thr Pro Arg Ser Ser

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Pro Arg Glu Asp Arg Ala Gly Leu Ala Ser Pro Arg Leu Ala Ser Ala

gcc acc tgc cgc gcg gcc act atc cag cct cct tcg gtc ctt ccc ctt 832
Ala Thr Cys Arg Ala Ala Thr Ile Gln Pro Pro Ser Val Leu Pro Leu

ccc cag cag cag gct ccg gcc gca gcc atg ccc aag cca ccg ccg ccc 880
Pro Gln Gln Gln Ala Pro Ala Ala Ala Met Pro Lys Pro Pro Pro Pro

acc tcc gac ccc tcg ctc ccc acc acc acc acc acc tcg acc ccc aag 928
Thr Ser Asp Pro Ser Leu Pro Thr Thr Thr Thr Thr Ser Thr Pro Lys

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Ser Gly Arg Ser Leu Ala Ser Ala Arg Arg Ser Pro Val Thr Thr

ctc gcc ggc gcc ttc ttc ctc ctc gcg ctc gtc atg tac gga gag gac 1072
Leu Ala Gly Ala Phe Phe Leu Leu Ala Leu Val Met Tyr Gly Glu Asp

gcc cgc acc atc gcc gag ctc tcc atc gac gac tac ctc tac ccg gac 1120
Ala Arg Thr Ile Ala Glu Leu Ser Ile Asp Asp Tyr Leu Tyr Pro Asp

gcc gat ctc tac aac gtc tcc ggc ctg ccg ccc ctt gcg ttg ccc ccg 1168
Ala Asp Leu Tyr Asn Val Ser Gly Leu Pro Pro Leu Ala Leu Pro Pro

cct acc tgc gac ctc tcc agt ggc cgc tgg gtc ttc gac aac gcc tcc 1216
Pro Thr Cys Asp Leu Ser Ser Gly Arg Trp Val Phe Asp Asn Ala Ser

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Val Pro Ala Tyr Arg Glu Lys Asp Cys Thr Phe Leu Thr Lys Gln Val

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Asp	Val	Asp	Tyr	Leu	Ile	Phe	Asn	Thr	Tyr	Ile	Trp	Trp	Met	Asn	Thr	
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Val	Trp	Asn	Gln	Ile	Leu	Tyr	Thr	Arg	Ile	Leu	Ser	Lys	Ser	Pro	Trp	
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Gln																
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<400> 1659

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Asn Gln Ala Tyr Lys Ile⁵⁵ Thr Pro Arg Ser Ser⁶⁰ Pro Arg Glu Asp
Arg Ala Gly Leu Ala Ser⁷⁰ Pro Arg Leu Ala Ser⁷⁵ Ala Ala Thr Cys Arg
65 Ala Ala Thr Ile⁸⁵ Gln Pro Pro Ser Val⁹⁰ Leu Pro Leu Pro Gln Gln⁹⁵ Gln
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Ser Leu Pro¹¹⁵ Thr Thr Thr Thr Thr¹²⁰ Ser Thr Pro Lys Ser¹²⁵ Ser Ser Arg
Pro Ala¹³⁰ Pro Ala Gly Leu¹³⁵ Leu Asp Pro Leu Ala Ala¹⁴⁰ Ser Gly Arg Ser
Leu Leu Ala Ser Ala¹⁵⁰ Arg Arg Ser Pro Val¹⁵⁵ Thr Thr Leu Ala Gly Ala¹⁶⁰
145 Phe Phe Leu Leu¹⁶⁵ Ala Leu Val Met Tyr Gly¹⁷⁰ Glu Asp Ala Arg Thr Ile¹⁷⁵
Ala Glu Leu Ser¹⁸⁰ Ile Asp Asp Tyr Leu¹⁸⁵ Tyr Pro Asp Ala Asp¹⁹⁰ Leu Tyr
Asn Val¹⁹⁵ Ser Gly Leu Pro Pro²⁰⁰ Leu Ala Leu Pro Pro²⁰⁵ Thr Cys Asp
Leu Ser²¹⁰ Ser Gly Arg Trp Val²¹⁵ Phe Asp Asn Ala Ser²²⁰ Val Pro Ala Tyr
Arg Glu Lys Asp Cys²³⁰ Thr Phe Leu Thr Lys Gln²³⁵ Val Thr Cys Leu Ala²⁴⁰
225 Asn Gly Arg Pro Asp²⁴⁵ Met Trp Gln Tyr Trp Arg Trp Gln Pro Ser²⁵⁵
Asp Cys Ser²⁶⁰ Leu Pro Thr Phe Asp Ala²⁶⁵ Arg Arg Phe Met Glu Ala Met²⁷⁰
Arg Gly Lys²⁷⁵ Arg Leu Met Phe Val²⁸⁰ Gly Asp Ser Leu Asn Arg Asn Gln²⁸⁵
Trp Glu²⁹⁰ Ser Leu Val Cys Leu²⁹⁵ Val Gln Pro Ile Leu³⁰⁰ Ser Lys Gly Arg
Lys Lys Ile Val³¹⁰ Lys Arg Gly Ser Leu Asn Thr³¹⁵ Phe Tyr Ala Lys Glu³²⁰
305 Tyr Arg Ala Thr³²⁵ Leu Glu Phe Tyr Trp Ala³³⁰ Pro Phe Leu Val Glu Ser³³⁵
Asn Ser Asp Asn³⁴⁰ Pro Asn Phe His Ser³⁴⁵ Ile Lys Glu Arg Ile Ile Ser³⁵⁰
Pro Glu Arg³⁵⁵ Ile Glu Ala His Ala³⁶⁰ Lys His Trp Lys Asp Val Asp Tyr³⁶⁵
Leu Ile³⁷⁰ Phe Asn Thr Tyr Ile³⁷⁵ Trp Trp Met Asn Thr³⁸⁰ Ala Asp Ile Lys
Val Arg Arg Pro Asn³⁹⁰ Ser Arg Tyr Trp Ser Glu Asn Asp Glu Val Pro⁴⁰⁰
385 Arg Ile Glu Ala Tyr⁴⁰⁵ Gly Arg Val Phe Lys Thr Trp Ser Asp Trp Leu⁴¹⁵
Asn Asp Asn Ile Asp Pro Ala Arg Thr⁴²⁵ Ser Val Phe Phe Met Thr Ile⁴³⁰
Ser Pro Leu⁴³⁵ His Ile Ser Pro Gln⁴⁴⁰ Asn Trp Gly Asn Pro⁴⁴⁵ Asp Gly Ile

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Lys Cys Val Arg Glu Thr Leu Pro Tyr Gln Asn Tyr Ser Gln Pro Leu
 450 455 460
 Asp Leu Tyr His Asp Met Arg Leu Tyr Asp Leu Val Ile Lys Val Ala
 465 470 475 480
 Ser Ser Met Glu Lys Val Pro Val Ser Val Ile Asn Ile Thr Lys Met
 485 490 495
 Ser Asp Tyr Arg Lys Asp Ala His Ala Ser Val Tyr Thr Ile Arg Gln
 500 505 510
 Gly Lys Leu Leu Thr Pro Lys Gln Lys Ala Asp Pro Glu Lys Phe Ala
 515 520 525
 Asp Cys Ile His Trp Cys Leu Pro Gly Val Pro Asp Val Trp Asn Gln
 530 535 540
 Ile Leu Tyr Thr Arg Ile Leu Ser Lys Ser Pro Trp Arg Ser Asn Phe
 545 550 555 560
 Ser Pro Pro Pro Ser Gln Ser Thr Pro Leu Pro Pro Gln
 565 570

<210> 1660
 <211> 1804
 <212> DNA
 <213> Zea mays subsp. mays

<220>
 <221> CDS
 <222> (132)..(1568)

<400> 1660
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gagtcgccgc caccaccacc atccagccag ccaaggcttc cttccccag cagcagcttc 120

cagccgcagc c atg gcc aag cca ccg ccg ccc acc tcc acc tcc gac ccc 170
 Met Ala Lys Pro Pro Pro Thr Ser Thr Ser Asp Pro
 1 5 10

gcg ctc ccc acc act gct aca acc acc tcg tcg gcc ccc aag tcg tcg 218
 Ala Leu Pro Thr Thr Ala Thr Thr Thr Ser Ser Ala Pro Lys Ser Ser
 15 20 25

tct cgc ccc tcc ccc cgc ccc cgg ggc ctc ctc gat ccg ctc gca gcc 266
 Ser Arg Pro Ser Pro Arg Pro Arg Gly Leu Leu Asp Pro Leu Ala Ala
 30 35 40 45

tcc gcg cgc tcc ctc ctc gcc tcg gcg cgc cgc tcc ccg gtc acc acg 314
 Ser Ala Arg Ser Leu Leu Ala Ser Ala Arg Arg Ser Pro Val Thr Thr
 50 55 60

cta gcc gcc gcc ttc ttc ctc ctc gcg ctc gtc atg tac ggc gag gac 362
 Leu Ala Ala Ala Phe Phe Leu Leu Ala Leu Val Met Tyr Gly Glu Asp
 65 70 75

gcc cgc acc atc gcc gag ctc tcc atc gac gac tac ctc tac ccg gac 410
 Ala Arg Thr Ile Ala Glu Leu Ser Ile Asp Asp Tyr Leu Tyr Pro Asp
 80 85 90

gcc gac ctc tac aac gtc tcc ggc ctg ccg ccc ctc gcg ctg ccc ccg 458
 Ala Asp Leu Tyr Asn Val Ser Gly Leu Pro Pro Leu Ala Leu Pro Pro
 95 100 105

ctc acc tgc gac ctc tcc cgc ggc aga tgg gtc ttc gac aac gtc tcc 506
 Leu Thr Cys Asp Leu Ser Arg Gly Arg Trp Val Phe Asp Asn Val Ser
 110 115 120 125

gtt ccg gcg tac ccg gag aaa gac tgc acc ttc ctc acc aag cag gtc 554
 Val Pro Ala Tyr Arg Glu Lys Asp Cys Thr Phe Leu Thr Lys Gln Val
 130 135 140

tcc tgc ctc gcc aac ggc cgc ccc gac gac atg tgg cag tac tgg aga 602
 Ser Cys Leu Ala Asn Gly Arg Pro Asp Asp Met Trp Gln Tyr Trp Arg
 145 150 155

tgg cag ccc aac gag tgc tcc ctc ccc acg ttc gac gct ccg aga ttc 650
 Trp Gln Pro Asn Glu Cys Ser Leu Pro Thr Phe Asp Ala Arg Arg Phe
 160 165 170

atg gag gcg atg cgc ggc aag cgg ctc atg ttc gtg ggg gac tcg ctg 698
 Met Glu Ala Met Arg Gly Lys Arg Leu Met Phe Val Gly Asp Ser Leu
 175 180 185

PF59082SeqList_PF59082.txt

aac	cgc	aac	cag	tgg	gag	tcg	ctg	gtg	tgc	ctc	gtg	cag	ccc	atc	ctg	746
Asn	Arg	Asn	Gln	Trp	Glu	Ser	Leu	Val	Cys	Leu	Val	Gln	Pro	Ile	Leu	
190					195				200						205	
tct	aag	ggc	agg	aag	aag	atc	gtc	aag	cgg	ggc	tcc	ttc	aac	acc	ttc	794
Ser	Lys	Gly	Arg	Lys	Lys	Ile	Val	Lys	Arg	Gly	Ser	Phe	Asn	Thr	Phe	
				210					215						220	
tac	gct	aag	gag	tac	cgc	gcc	acg	ctc	gag	ttc	tac	tgg	gcg	ccc	ttc	842
Tyr	Ala	Lys	Glu	Tyr	Arg	Ala	Thr	Leu	Glu	Phe	Tyr	Trp	Ala	Pro	Phe	
			225					230					235			
ctc	gtc	gaa	tcc	aac	tct	gac	aac	ccc	aac	ttc	cac	agc	atc	aag	gaa	890
Leu	Val	Glu	Ser	Asn	Ser	Asp	Asn	Pro	Asn	Phe	His	Ser	Ile	Lys	Glu	
		240					245					250				
cgg	atc	atc	agt	ccc	gag	cgg	atc	gag	gcg	cac	gcc	aag	cac	tgg	aag	938
Arg	Ile	Ile	Ser	Pro	Glu	Arg	Ile	Glu	Ala	His	Ala	Lys	His	Trp	Lys	
	255					260					265					
gat	gct	gac	tac	ctc	atc	ttc	aac	acc	tac	atc	tgg	atg	aac	aac		986
Asp	Ala	Asp	Tyr	Leu	Ile	Phe	Asn	Thr	Tyr	Ile	Trp	Trp	Met	Asn	Asn	
270					275					280					285	
gcc	gac	atc	aaa	gtc	agg	aga	ccc	aat	tcg	agg	tac	tgg	tct	gac	aac	1034
Ala	Asp	Ile	Lys	Val	Arg	Arg	Pro	Asn	Ser	Arg	Tyr	Trp	Ser	Asp	Asn	
				290					295					300		
gat	gag	gtt	ccc	agg	att	gag	gcg	tat	ggc	cgt	gtg	ttc	aag	aca	tgg	1082
Asp	Glu	Val	Pro	Arg	Ile	Glu	Ala	Tyr	Gly	Arg	Val	Phe	Lys	Thr	Trp	
			305					310					315			
tct	gat	tgg	ctc	aat	gac	aac	atc	gat	cct	gcc	cga	acg	tcc	gtc	ttc	1130
Ser	Asp	Trp	Leu	Asn	Asp	Asn	Ile	Asp	Pro	Ala	Arg	Thr	Ser	Val	Phe	
		320					325					330				
ttc	atg	acg	att	tct	cct	cct	cac	ctc	agc	cca	cag	aat	tgg	gga	aac	1178
Phe	Met	Thr	Ile	Ser	Pro	Pro	His	Leu	Ser	Pro	Gln	Asn	Trp	Gly	Asn	
	335					340					345					
ccg	gac	ggt	atc	aaa	tgt	gta	aga	gag	acg	ctt	cca	tat	cag	aac	tac	1226
Pro	Asp	Gly	Ile	Lys	Cys	Val	Arg	Glu	Thr	Leu	Pro	Tyr	Gln	Asn	Tyr	
350					355				360						365	
agc	caa	cac	ctg	gat	ctt	tac	cat	gac	atg	cgg	ctg	tat	gac	tta	gtg	1274
Ser	Gln	His	Leu	Asp	Leu	Tyr	His	Asp	Met	Arg	Leu	Tyr	Asp	Leu	Val	
				370					375					380		
gtc	aat	gtg	gcc	agc	tcc	atg	gag	aag	gtc	cca	gtg	aca	gtg	atc	aat	1322
Val	Asn	Val	Ala	Ser	Ser	Met	Glu	Lys	Val	Pro	Val	Thr	Val	Ile	Asn	
			385					390					395			
atc	aca	agg	atg	tca	gat	tac	cgg	aag	gac	gcc	cac	acg	tcc	ctg	tac	1370
Ile	Thr	Arg	Met	Ser	Asp	Tyr	Arg	Lys	Asp	Ala	His	Thr	Ser	Leu	Tyr	
		400					405					410				
acc	atc	cgg	caa	ggg	aag	ctg	ctg	acg	cct	aag	cag	aag	gca	gac	ccc	1418
Thr	Ile	Arg	Gln	Gly	Lys	Leu	Leu	Thr	Pro	Lys	Gln	Lys	Ala	Asp	Pro	
						420					425					
gag	aag	ttc	gcg	gat	tgc	atc	cac	tgg	tgc	ctt	cct	ggc	gtg	ccg	gac	1466
Glu	Lys	Phe	Ala	Asp	Cys	Ile	His	Trp	Cys	Leu	Pro	Gly	Val	Pro	Asp	
430					435				440						445	
gtg	tgg	aac	caa	ata	ctc	tac	acg	agg	att	ctt	tcg	aaa	tca	tcg	tgg	1514
Val	Trp	Asn	Gln	Ile	Leu	Tyr	Thr	Arg	Ile	Leu	Ser	Lys	Ser	Ser	Trp	
				450					455					460		
cat	tct	aat	ttt	agc	ccc	cct	cca	tcc	cag	tct	ctg	cct	ctt	cct	ccc	1562
His	Ser	Asn	Phe	Ser	Pro	Pro	Pro	Ser	Gln	Ser	Leu	Pro	Leu	Pro	Pro	
		465					470					475				
caa	tgagaatcag	aagtgggggc	ttggtttttg	tcggagaatg	tatgatTTTT											1615
Gln																
cattctTTTT	ccttcctTTTT	tgggtagatt	gagtaaaatg	atagcacgaa	aaggaaaatg											1675
aatgttctga	ttactgatgg	tatagcatgt	aagaagattc	agctgaagtg	taaattagtt											1735
gtgagttagc	caattgagaa	aacaacagcg	acctagtata	aagtgcatat	acatatactg											1795
ctggttcac																1804

PF59082SeqList_PF59082.txt

<210> 1661
 <211> 478
 <212> PRT
 <213> Zea mays subsp. mays

<400> 1661
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 Thr Thr Ala Thr Thr Ser Ser Ala Pro Lys Ser Ser Ser Arg Pro
 20 25 30
 Ser Pro Arg Pro Arg Gly Leu Leu Asp Pro Leu Ala Ala Ser Ala Arg
 35 40 45
 Ser Leu Leu Ala Ser Ala Arg Arg Ser Pro Val Thr Thr Leu Ala Ala
 50 55 60
 Ala Phe Phe Leu Leu Ala Leu Val Met Tyr Gly Glu Asp Ala Arg Thr
 65 70 75 80
 Ile Ala Glu Leu Ser Ile Asp Asp Tyr Leu Tyr Pro Asp Ala Asp Leu
 85 90 95
 Tyr Asn Val Ser Gly Leu Pro Pro Leu Ala Leu Pro Pro Leu Thr Cys
 100 105 110
 Asp Leu Ser Arg Gly Arg Trp Val Phe Asp Asn Val Ser Val Pro Ala
 115 120 125
 Tyr Arg Glu Lys Asp Cys Thr Phe Leu Thr Lys Gln Val Ser Cys Leu
 130 135 140
 Ala Asn Gly Arg Pro Asp Asp Met Trp Gln Tyr Trp Arg Trp Gln Pro
 145 150 155 160
 Asn Glu Cys Ser Leu Pro Thr Phe Asp Ala Arg Arg Phe Met Glu Ala
 165 170 175
 Met Arg Gly Lys Arg Leu Met Phe Val Gly Asp Ser Leu Asn Arg Asn
 180 185 190
 Gln Trp Glu Ser Leu Val Cys Leu Val Gln Pro Ile Leu Ser Lys Gly
 195 200 205
 Arg Lys Lys Ile Val Lys Arg Gly Ser Phe Asn Thr Phe Tyr Ala Lys
 210 215 220
 Glu Tyr Arg Ala Thr Leu Glu Phe Tyr Trp Ala Pro Phe Leu Val Glu
 225 230 235 240
 Ser Asn Ser Asp Asn Pro Asn Phe His Ser Ile Lys Glu Arg Ile Ile
 245 250 255
 Ser Pro Glu Arg Ile Glu Ala His Ala Lys His Trp Lys Asp Ala Asp
 260 265 270
 Tyr Leu Ile Phe Asn Thr Tyr Ile Trp Trp Met Asn Asn Ala Asp Ile
 275 280 285
 Lys Val Arg Arg Pro Asn Ser Arg Tyr Trp Ser Asp Asn Asp Glu Val
 290 295 300
 Pro Arg Ile Glu Ala Tyr Gly Arg Val Phe Lys Thr Trp Ser Asp Trp
 305 310 315 320
 Leu Asn Asp Asn Ile Asp Pro Ala Arg Thr Ser Val Phe Phe Met Thr
 325 330 335
 Ile Ser Pro Pro His Leu Ser Pro Gln Asn Trp Gly Asn Pro Asp Gly
 340 345 350
 Ile Lys Cys Val Arg Glu Thr Leu Pro Tyr Gln Asn Tyr Ser Gln His
 355 360 365
 Leu Asp Leu Tyr His Asp Met Arg Leu Tyr Asp Leu Val Val Asn Val
 370 375 380
 Ala Ser Ser Met Glu Lys Val Pro Val Thr Val Ile Asn Ile Thr Arg
 385 390 395 400
 Met Ser Asp Tyr Arg Lys Asp Ala His Thr Ser Leu Tyr Thr Ile Arg
 405 410 415
 Gln Gly Lys Leu Thr Pro Lys Gln Lys Ala Asp Pro Glu Lys Phe
 420 425 430
 Ala Asp Cys Ile His Trp Cys Leu Pro Gly Val Pro Asp Val Trp Asn
 435 440 445
 Gln Ile Leu Tyr Thr Arg Ile Leu Ser Lys Ser Ser Trp His Ser Asn
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 Phe Ser Pro Pro Pro Ser Gln Ser Leu Pro Leu Pro Pro Gln
 465 470 475

<210> 1662

PF59082SeqList_PF59082.txt

<211> 1804
<212> DNA
<213> Zea mays subsp. mays

<220>
<221> CDS
<222> (348)..(1568)

<400> 1662
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cagccgcagc catggccaag ccaccgccgc ccacctccac ctccgacccc gcgctcccca 180

ccactgctac aaccacctcg tcggcccca agtcgtcgtc tcgcccctcc ccccgccccc 240

ggggcctcct cgatccgctc gcagcctccg cgcgctccct cctcgccctg gcgcgccgct 300

ccccggtcac cagcctagcc gccgccttct tcctcctcgc gctcgtc atg tac ggc 356
Met Tyr Gly
1
gag gac gcc cgc acc atc gcc gag ctc tcc atc gac gac tac ctc tac 404
Glu Asp Ala Arg Thr Ile Ala Glu Leu Ser Ile Asp Asp Tyr Leu Tyr
5 10
ccg gac gcc gac ctc tac aac gtc tcc ggc ctg ccg ccc ctc gcg ctg 452
Pro Asp Ala Asp Leu Tyr Asn Val Ser Gly Leu Pro Pro Leu Ala Leu
20 25 30 35
ccc ccg ctc acc tgc gac ctc tcc cgc ggc aga tgg gtc ttc gac aac 500
Pro Pro Leu Thr Cys Asp Leu Ser Arg Gly Arg Trp Val Phe Asp Asn
40 45 50
gtc tcc gtt ccg gcg tac cgg gag aaa gac tgc acc ttc ctc acc aag 548
Val Ser Val Pro Ala Tyr Arg Glu Lys Asp Cys Thr Phe Leu Thr Lys
55 60 65
cag gtc tcc tgc ctc gcc aac ggc cgc gcc gac gac atg tgg cag tac 596
Gln Val Ser Cys Leu Ala Asn Gly Arg Pro Asp Asp Met Trp Gln Tyr
70 75 80
tgg aga tgg cag ccc aac gag tgc tcc ctc ccc acg ttc gac gct cgg 644
Trp Arg Trp Gln Pro Asn Glu Cys Ser Leu Pro Thr Phe Asp Ala Arg
85 90 95
aga ttc atg gag gcg atg cgc ggg aag cgg ctc atg ttc gtg ggg gac 692
Arg Phe Met Glu Ala Met Arg Gly Lys Arg Leu Met Phe Val Gly Asp
100 105 110 115
tcg ctg aac cgc aac cag tgg gag tcg ctg gtg tgc ctc gtg cag ccc 740
Ser Leu Asn Arg Asn Gln Trp Glu Ser Leu Val Cys Leu Val Gln Pro
120 125 130
atc ctg tct aag ggc agg aag aag atc gtc aag cgg ggc tcc ttc aac 788
Ile Leu Ser Lys Gly Arg Lys Lys Ile Val Lys Arg Gly Ser Phe Asn
135 140 145
acc ttc tac gct aag gag tac cgc gcc acg ctc gag ttc tac tgg gcg 836
Thr Phe Tyr Ala Lys Glu Tyr Arg Ala Thr Leu Glu Phe Tyr Trp Ala
150 155 160
ccc ttc ctc gtc gaa tcc aac tct gac aac ccc aac ttc cac agc atc 884
Pro Phe Leu Val Glu Ser Asn Ser Asp Asn Pro Asn Phe His Ser Ile
165 170 175
aag gaa cgg atc atc agt ccc gag cgg atc gag gcg cac gcc aag cac 932
Lys Glu Arg Ile Ile Ser Pro Glu Arg Ile Glu Ala His Ala Lys His
180 185 190 195
tgg aag gat gct gac tac ctc atc ttc aac acc tac atc tgg tgg atg 980
Trp Lys Asp Ala Asp Tyr Leu Ile Phe Asn Thr Tyr Ile Trp Trp Met
200 205 210
aac aac gcc gac atc aaa gtc agg aga ccc aat tcg agg tac tgg tct 1028
Asn Asn Ala Asp Ile Lys Val Arg Arg Pro Asn Ser Arg Tyr Trp Ser
215 220 225

PF59082SeqList_PF59082.txt

gac aac gat gag gtt ccc agg att gag gcg tat ggc cgt gtg ttc aag	1076
Asp Asn Asp Glu Val Pro Arg Ile Glu Ala Tyr Gly Arg Val Phe Lys	
230 235 240	
aca tgg tct gat tgg ctc aat gac aac atc gat cct gcc cga acg tcc	1124
Thr Trp Ser Asp Trp Leu Asn Asp Asn Ile Asp Pro Ala Arg Thr Ser	
245 250 255	
gtc ttc ttc atg acg att tct cct cct cac ctc agc cca cag aat tgg	1172
Val Phe Phe Met Thr Ile Ser Pro Pro His Leu Ser Pro Gln Asn Trp	
260 265 270 275	
gga aac ccg gac ggt atc aaa tgt gta aga gag acg ctt cca tat cag	1220
Gly Asn Pro Asp Gly Ile Lys Cys Val Arg Glu Thr Leu Pro Tyr Gln	
280 285 290	
aac tac agc caa cac ctg gat ctt tac cat gac atg cgg ctg tat gac	1268
Asn Tyr Ser Gln His Leu Asp Leu Tyr His Asp Met Arg Leu Tyr Asp	
295 300 305	
tta gtg gtc aat gtg gcc agc tcc atg gag aag gtc cca gtg aca gtg	1316
Leu Val Val Asn Val Ala Ser Ser Met Glu Lys Val Pro Val Thr Val	
310 315 320	
atc aat atc aca agg atg tca gat tac cgg aag gac gcc cac acg tcc	1364
Ile Asn Ile Thr Arg Met Ser Asp Tyr Arg Lys Asp Ala His Thr Ser	
325 330 335	
ctg tac acc atc cgg caa ggg aag ctg ctg acg cct aag cag aag gca	1412
Leu Tyr Thr Ile Arg Gln Gly Lys Leu Leu Thr Pro Lys Gln Lys Ala	
340 345 350 355	
gac ccc gag aag ttc gcg gat tgc atc cac tgg tgc ctt cct gcc gtg	1460
Asp Pro Glu Lys Phe Ala Asp Cys Ile His Trp Cys Leu Pro Gly Val	
360 365 370	
ccg gac gtg tgg aac caa ata ctc tac acg agg att ctt tcg aaa tca	1508
Pro Asp Val Trp Asn Gln Ile Leu Tyr Thr Arg Ile Leu Ser Lys Ser	
375 380 385	
tcg tgg cat tct aat ttt agc ccc cct cca tcc cag tct ctg cct ctt	1556
Ser Trp His Ser Asn Phe Ser Pro Pro Pro Ser Gln Ser Leu Pro Leu	
390 395 400	
cct ccc caa tgagaatcag aagtgggggc ttggtttttg tcggagaatg tatgatTTTT	1615
Pro Pro Gln	
405	
cattctTTTT ccttcTTTT tgggtagatt gagtaaaatg atagcacgaa aaggaaaatg	1675
aatgttctga ttactgatgg tatagcatgt aagaagattc agctgaagtg taaattagtt	1735
gtgagttagc caattgagaa aacaacagcg acctagtata aagtgcatat acatatactg	1795
ctggttcac	1804

<210> 1663

<211> 406

<212> PRT

<213> Zea mays subsp. mays

<400> 1663

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Tyr Leu Tyr Pro Asp Ala Asp Leu Tyr Asn Val Ser Gly Leu Pro Pro	
20 25 30	
Leu Ala Leu Pro Pro Leu Thr Cys Asp Leu Ser Arg Gly Arg Trp Val	
35 40 45	
Phe Asp Asn Val Ser Val Pro Ala Tyr Arg Glu Lys Asp Cys Thr Phe	
50 55 60	
Leu Thr Lys Gln Val Ser Cys Leu Ala Asn Gly Arg Pro Asp Asp Met	
65 70 75 80	
Trp Gln Tyr Trp Arg Trp Gln Pro Asn Glu Cys Ser Leu Pro Thr Phe	
85 90 95	
Asp Ala Arg Arg Phe Met Glu Ala Met Arg Gly Lys Arg Leu Met Phe	
100 105 110	

PF59082SeqList_PF59082.txt

Val Gly Asp Ser Leu Asn Arg Asn Gln Trp Glu Ser Leu Val Cys Leu
115 120 125
Val Gln Pro Ile Leu Ser Lys Gly Arg Lys Lys Ile Val Lys Arg Gly
130 135 140
Ser Phe Asn Thr Phe Tyr Ala Lys Glu Tyr Arg Ala Thr Leu Glu Phe
145 150 155 160
Tyr Trp Ala Pro Phe Leu Val Glu Ser Asn Ser Asp Asn Pro Asn Phe
165 170 175
His Ser Ile Lys Glu Arg Ile Ile Ser Pro Glu Arg Ile Glu Ala His
180 185 190
Ala Lys His Trp Lys Asp Ala Asp Tyr Leu Ile Phe Asn Thr Tyr Ile
195 200 205
Trp Trp Met Asn Asn Ala Asp Ile Lys Val Arg Arg Pro Asn Ser Arg
210 215 220
Tyr Trp Ser Asp Asn Asp Glu Val Pro Arg Ile Glu Ala Tyr Gly Arg
225 230 235 240
Val Phe Lys Thr Trp Ser Asp Trp Leu Asn Asp Asn Ile Asp Pro Ala
245 250 255
Arg Thr Ser Val Phe Phe Met Thr Ile Ser Pro Pro His Leu Ser Pro
260 265 270
Gln Asn Trp Gly Asn Pro Asp Gly Ile Lys Cys Val Arg Glu Thr Leu
275 280 285
Pro Tyr Gln Asn Tyr Ser Gln His Leu Asp Leu Tyr His Asp Met Arg
290 295 300
Leu Tyr Asp Leu Val Val Asn Val Ala Ser Ser Met Glu Lys Val Pro
305 310 315 320
Val Thr Val Ile Asn Ile Thr Arg Met Ser Asp Tyr Arg Lys Asp Ala
325 330 335
His Thr Ser Leu Tyr Thr Ile Arg Gln Gly Lys Leu Leu Thr Pro Lys
340 345 350
Gln Lys Ala Asp Pro Glu Lys Phe Ala Asp Cys Ile His Trp Cys Leu
355 360 365
Pro Gly Val Pro Asp Val Trp Asn Gln Ile Leu Tyr Thr Arg Ile Leu
370 375 380
Ser Lys Ser Ser Trp His Ser Asn Phe Ser Pro Pro Ser Gln Ser
385 390 395 400
Leu Pro Leu Pro Pro Gln
405

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<211> 1539
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (1)..(1539)

<400> 1664
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Met Gln Pro Leu Arg Arg Lys Thr Pro Leu Phe Thr Ser Glu Met Gly
1 5 10 15
aca atg aag ggt cgc aag aac aac aac ctc tcc atc ttc gtg gtg gtg 96
Thr Met Lys Gly Arg Lys Asn Asn Asn Leu Ser Ile Phe Val Val Val
20 25 30
ttc tcc atc ttc ctc ttt ggg ctc ttc atg tac aac gag gat gtt aag 144
Phe Ser Ile Phe Leu Phe Gly Leu Phe Met Tyr Asn Glu Asp Val Lys
35 40 45
tcc att gct gaa ttc cca ttc tcg agt ccc aaa gcg cat gag aca caa 192
Ser Ile Ala Glu Phe Pro Phe Ser Ser Pro Lys Ala His Glu Thr Gln
50 55 60
gaa gga gga gaa cct aat aaa cat gtt gat tct gtt caa gac agt gtt 240
Glu Gly Gly Glu Pro Asn Lys His Val Asp Ser Val Gln Asp Ser Val
65 70 75 80
gtt gtt caa agg gag agt gag aag aag gat gtg gaa gac act gtc aca 288
Val Val Gln Arg Glu Ser Glu Lys Lys Asp Val Glu Asp Thr Val Thr
85 90 95
gta aaa att tct tct aag agg agt act tca agg gct cag cta gag aag 336
Val Lys Ile Ser Ser Lys Arg Ser Thr Ser Arg Ala Gln Leu Glu Lys
100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405
seite 2187

PF59082SeqList_PF59082.txt

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agt ggt gct gag gat gag gat tct gat gag cgt gtt gat ttg aaa act	115	120	125	384
Ser Gly Ala Glu Asp Glu Asp Ser Asp Glu Arg Val Asp Leu Lys Thr				
gtt gtg gag aaa gag aag aag att gaa atg cca cgt gcg gag gaa gag	130	135	140	432
Val Val Glu Lys Glu Lys Lys Ile Glu Met Pro Arg Ala Glu Glu Glu				
gaa gag gtg gaa gaa gaa gaa gaa gat gag aaa gtt gag ttg cca cca	145	150	155	480
Glu Glu Val Glu Glu Glu Glu Glu Glu Asp Glu Lys Val Glu Leu Pro Pro				
gaa gat tgt gac ttg ttc act ggg gag tgg gtt ttg gat aac gtg aca	165	170	175	528
Glu Asp Cys Asp Leu Phe Thr Gly Glu Trp Val Leu Asp Asn Val Thr				
cac cct ttg tac aaa gaa gac aag tgt gag ttt ctc act tcg caa gtg	180	185	190	576
His Pro Leu Tyr Lys Glu Asp Lys Cys Glu Phe Leu Thr Ser Gln Val				
aca tgc atg aag aat gga cga cct gat tct ttg tat cag aat tgg aag	195	200	205	624
Thr Cys Met Lys Asn Gly Arg Pro Asp Ser Leu Tyr Gln Asn Trp Lys				
tgg aag cca aga gat tgt tct ctg cca aag ttc aaa ccg aag ctt ttg	210	215	220	672
Trp Lys Pro Arg Asp Cys Ser Leu Pro Lys Phe Lys Pro Lys Leu Leu				
ttt cag aag att aga ggg aag agg ctt atg ttt gtt gga gat tca ctg	225	230	235	720
Phe Gln Lys Ile Arg Gly Lys Arg Leu Met Phe Val Gly Asp Ser Leu				
aat agg aac cag tgg gaa tcc atg gtt tgt atg gtc aat tct gcg gtt	245	250	255	768
Asn Arg Asn Gln Trp Glu Ser Met Val Cys Met Val Asn Ser Ala Val				
cct tca cat aac aag acc tgg tac aag act ggt tct ctt gcc atc ttc	260	265	270	816
Pro Ser His Asn Lys Thr Trp Tyr Lys Thr Gly Ser Leu Ala Ile Phe				
aaa atc gag gag ccg gag cac gtt acc acg gtg gaa ttc tat tgg gca	275	280	285	864
Lys Ile Glu Glu Pro Glu His Val Thr Thr Val Glu Phe Tyr Trp Ala				
cca ttc ctt gta gag tca aat tca gat gat cca aac atg cac agc ata	290	295	300	912
Pro Phe Leu Val Glu Ser Asn Ser Asp Asp Pro Asn Met His Ser Ile				
tta aac cgt ata atc atg cct gaa tca ata gaa aaa cat gga gtg aat	305	310	315	960
Leu Asn Arg Ile Ile Met Pro Glu Ser Ile Glu Lys His Gly Val Asn				
tgg aag gat gtg gac tac ttg atc ttt aac acc tac ata tgg tgg atg	325	330	335	1008
Trp Lys Asp Val Asp Tyr Leu Ile Phe Asn Thr Tyr Ile Trp Trp Met				
aac act ttc tct atg aaa gtc cta cga ggg tca ttt gat gaa gga tcc	340	345	350	1056
Asn Thr Phe Ser Met Lys Val Leu Arg Gly Ser Phe Asp Glu Gly Ser				
acg gaa tat gat gaa gtt cct cgg cca ata gca tat ggg aga gtc att	355	360	365	1104
Thr Glu Tyr Asp Glu Val Pro Arg Pro Ile Ala Tyr Gly Arg Val Ile				
aac aca tgg tca aaa tgg ata gat gac aac att gac cca aat cga acc	370	375	380	1152
Asn Thr Trp Ser Lys Trp Ile Asp Asp Asn Ile Asp Pro Asn Arg Thr				
aaa gtt ttc ttc agc agc acg tcc cct ctt cat atc aag agt gag aat	385	390	395	1200
Lys Val Phe Phe Ser Ser Thr Ser Pro Leu His Ile Lys Ser Glu Asn				
tgg aac aac cca aat ggt ata aaa tgt gcc aag gag atc act ccg gtt	405	410	415	1248
Trp Asn Asn Pro Asn Gly Ile Lys Cys Ala Lys Glu Ile Thr Pro Val				
ctc aac atg tca acc cca ttg gat gta ggg aca gat cgt cgc ctt ttt	420	425	430	1296
Leu Asn Met Ser Thr Pro Leu Asp Val Gly Thr Asp Arg Leu Phe				
aca att gcc aac aat gtg act cag tca atg aag gtg cca gtg tac ttc	435	440	445	1344
Thr Ile Ala Asn Asn Val Thr Gln Ser Met Lys Val Pro Val Tyr Phe				
att aac atc act tct ttg tca gaa ttg aga aaa gat gca cac act tct	450	455	460	1392
Ile Asn Ile Thr Ser Leu Ser Glu Leu Arg Lys Asp Ala His Thr Ser				
gtt tac acc ata cgc caa ggc aaa atg cta act cca gaa caa caa gct				1440
Val Tyr Thr Ile Arg Gln Gly Lys Met Leu Thr Pro Glu Gln Gln Ala				

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465					470					475					480	
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Asp	Pro	Thr	Thr	Tyr	Ala	Asp	Cys	Ile	His	Trp	Cys	Leu	Pro	Gly	Leu	1488
				485					490					495		
cct	gac	act	tgg	aac	gag	ttc	ctc	tat	aca	agg	atc	atc	tct	caa	tct	
Pro	Asp	Thr	Trp	Asn	Glu	Phe	Leu	Tyr	Thr	Arg	Ile	Ile	Ser	Gln	Ser	1536
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tga																1539

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 <211> 512
 <212> PRT
 <213> Glycine max

<400> 1665

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Thr	Met	Lys	Gly	Arg	Lys	Asn	Asn	Asn	Leu	Ser	Ile	Phe	Val	Val	Val
			20					25					30		
Phe	Ser	Ile	Phe	Leu	Phe	Gly	Leu	Phe	Met	Tyr	Asn	Glu	Asp	Val	Lys
		35				40					45				
Ser	Ile	Ala	Glu	Phe	Pro	Phe	Ser	Ser	Pro	Lys	Ala	His	Glu	Thr	Gln
	50					55					60				
Glu	Gly	Gly	Glu	Pro	Asn	Lys	His	Val	Asp	Ser	Val	Gln	Asp	Ser	Val
65					70				75						80
Val	Val	Gln	Arg	Glu	Ser	Glu	Lys	Lys	Asp	Val	Glu	Asp	Thr	Val	Thr
			85					90					95		
Val	Lys	Ile	Ser	Lys	Arg	Ser	Thr	Ser	Arg	Ala	Gln	Leu	Glu	Lys	
		100					105					110			
Ser	Gly	Ala	Glu	Asp	Glu	Asp	Ser	Asp	Glu	Arg	Val	Asp	Leu	Lys	Thr
		115					120				125				
Val	Val	Glu	Lys	Glu	Lys	Lys	Ile	Glu	Met	Pro	Arg	Ala	Glu	Glu	Glu
	130					135					140				
Glu	Glu	Val	Glu	Glu	Glu	Glu	Glu	Asp	Glu	Lys	Val	Glu	Leu	Pro	Pro
145					150				155						160
Glu	Asp	Cys	Asp	Leu	Phe	Thr	Gly	Glu	Trp	Val	Leu	Asp	Asn	Val	Thr
			165						170					175	
His	Pro	Leu	Tyr	Lys	Glu	Asp	Lys	Cys	Glu	Phe	Leu	Thr	Ser	Gln	Val
		180						185					190		
Thr	Cys	Met	Lys	Asn	Gly	Arg	Pro	Asp	Ser	Leu	Tyr	Gln	Asn	Trp	Lys
		195					200					205			
Trp	Lys	Pro	Arg	Asp	Cys	Ser	Leu	Pro	Lys	Phe	Lys	Pro	Lys	Leu	Leu
	210					215					220				
Phe	Gln	Lys	Ile	Arg	Gly	Lys	Arg	Leu	Met	Phe	Val	Gly	Asp	Ser	Leu
225					230				235						240
Asn	Arg	Asn	Gln	Trp	Glu	Ser	Met	Val	Cys	Met	Val	Asn	Ser	Ala	Val
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Pro	Ser	His	Asn	Lys	Thr	Trp	Tyr	Lys	Thr	Gly	Ser	Leu	Ala	Ile	Phe
		260						265					270		
Lys	Ile	Glu	Glu	Pro	Glu	His	Val	Thr	Thr	Val	Glu	Phe	Tyr	Trp	Ala
		275					280					285			
Pro	Phe	Leu	Val	Glu	Ser	Asn	Ser	Asp	Asp	Pro	Asn	Met	His	Ser	Ile
	290					295					300				
Leu	Asn	Arg	Ile	Ile	Met	Pro	Glu	Ser	Ile	Glu	Lys	His	Gly	Val	Asn
305					310					315					320
Trp	Lys	Asp	Val	Asp	Tyr	Leu	Ile	Phe	Asn	Thr	Tyr	Ile	Trp	Trp	Met
			325						330					335	
Asn	Thr	Phe	Ser	Met	Lys	Val	Leu	Arg	Gly	Ser	Phe	Asp	Glu	Gly	Ser
		340						345					350		
Thr	Glu	Tyr	Asp	Glu	Val	Pro	Arg	Pro	Ile	Ala	Tyr	Gly	Arg	Val	Ile
		355					360					365			
Asn	Thr	Trp	Ser	Lys	Trp	Ile	Asp	Asp	Asn	Ile	Asp	Pro	Asn	Arg	Thr
	370					375					380				
Lys	Val	Phe	Phe	Ser	Ser	Thr	Ser	Pro	Leu	His	Ile	Lys	Ser	Glu	Asn
385					390					395					400
Trp	Asn	Asn	Pro	Asn	Gly	Ile	Lys	Cys	Ala	Lys	Glu	Ile	Thr	Pro	Val
				405					410					415	

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Leu Asn Met Ser Thr Pro Leu Asp Val Gly Thr Asp Arg Arg Leu Phe
 420 425 430
 Thr Ile Ala Asn Asn Val Thr Gln Ser Met Lys Val Pro Val Tyr Phe
 435 440 445
 Ile Asn Ile Thr Ser Leu Ser Gln Leu Arg Lys Asp Ala His Thr Ser
 450 455 460
 Val Tyr Thr Ile Arg Gln Gly Lys Met Leu Thr Pro Glu Gln Gln Ala
 465 470 475 480
 Asp Pro Thr Thr Tyr Ala Asp Cys Ile His Trp Cys Leu Pro Gly Leu
 485 490 495
 Pro Asp Thr Trp Asn Glu Phe Leu Tyr Thr Arg Ile Ile Ser Ser
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 ggg gca atg aag ggt cgc aag aac aac aac ctc tcc atc ttc gtg gtg 96
 Gly Ala Met Lys Gly Arg Lys Asn Asn Asn Leu Ser Ile Phe Val Val
 20 25 30
 gtg ttc tcc ata ttc ctc ttt ggg ctc ttc atg tac aac gag gac gtt 144
 Val Phe Ser Ile Phe Leu Phe Gly Leu Phe Met Tyr Asn Glu Asp Val
 35 40 45
 aag tca atg gcc gag ttc act ttc ttg agg cct aag gct caa gaa atc 192
 Lys Ser Met Ala Glu Phe Thr Phe Leu Arg Pro Lys Ala Gln Glu Ile
 50 55 60
 caa gaa gaa acg gtt tcc aac aac aat tca aga act caa cca gag aga 240
 Gln Glu Glu Thr Val Ser Asn Asn Asn Ser Arg Thr Gln Pro Glu Arg
 65 70 75 80
 aac cgg gtc gag gac tcc gag gaa tct caa gaa ccg att gat ttg aaa 288
 Asn Arg Val Glu Asp Ser Glu Glu Ser Gln Glu Pro Ile Asp Leu Lys
 85 90 95
 gcc gtt gtg gca gaa gag aag ata gtg gaa gag tat gag gaa gaa aat 336
 Ala Val Val Ala Glu Glu Lys Ile Val Glu Glu Tyr Glu Glu Glu Asn
 100 105 110
 gaa gag gtt gtg ttg ccc cca gaa gag tgt gac ttg ttc aca gga gag 384
 Glu Glu Val Val Leu Pro Pro Glu Glu Cys Asp Leu Phe Thr Gly Glu
 115 120 125
 tgg gtt ttt gat aac ttg aca cac cct ttg tac aaa gaa gac caa tgc 432
 Trp Val Phe Asp Asn Leu Thr His Pro Leu Tyr Lys Glu Asp Gln Cys
 130 135 140
 gaa ttc ctc act tca caa gtc acc tgc atg agg aat gga aga agt gat 480
 Glu Phe Leu Thr Ser Gln Val Thr Cys Met Arg Asn Gly Arg Ser Asp
 145 150 155 160
 tct ctc tat cag aat tgg aga tgg cag ccc aga gat tgc tct ttg ccc 528
 Ser Leu Tyr Gln Asn Trp Arg Trp Gln Pro Arg Asp Cys Ser Leu Pro
 165 170 175
 aaa ggg agg agg ctt atg ttt gtt gga gac tca ctg aac agg aac cag 576
 Lys Gly Arg Arg Leu Met Phe Val Gly Asp Ser Leu Asn Arg Asn Gln
 180 185 190
 tgg gaa tca atg att tgt ctg gtc cag tct gtt gtt cct caa cga aaa 624
 Trp Glu Ser Met Ile Cys Leu Val Gln Ser Val Val Pro Gln Arg Lys
 195 200 205
 aaa agt ttg agc aac aat ggt tct ctt tct atc ttc aca att gag gat 672
 Lys Ser Leu Ser Asn Asn Gly Ser Leu Ser Ile Phe Thr Ile Glu Asp
 210 215 220
 tac aat gct acg gtg gag ttc tac tgg gca ccg ttc ctt gag gag tca 720
 Tyr Asn Ala Thr Val Glu Phe Tyr Trp Ala Pro Phe Leu Glu Glu Ser
 225 230 235 240
 aac tca gat gat cca aag atg cac agc ata ttg aac cga att atc atg 768

PF59082SeqList_PF59082.txt

Asn	Ser	Asp	Asp	Pro	Lys	Met	His	Ser	Ile	Leu	Asn	Arg	Ile	Ile	Met	
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Pro	Glu	Ser	Ile	Glu	Lys	His	Ala	Val	Asn	Trp	Lys	Asn	Val	Asp	Tyr	
			260					265					270			
ctg	atc	ttc	aac	acc	tac	ata	tgg	tgg	atg	aat	act	gac	act	atg	aaa	864
Leu	Ile	Phe	Asn	Thr	Tyr	Ile	Trp	Trp	Met	Asn	Thr	Asp	Thr	Met	Lys	
			275				280					285				
gtc	tta	cga	ggg	tcg	ttt	gat	gaa	gga	tcc	acg	gag	tac	gat	gaa	gtc	912
Val	Leu	Arg	Gly	Ser	Phe	Asp	Glu	Gly	Ser	Thr	Glu	Tyr	Asp	Glu	Val	
			290			295					300					
cct	cgg	cca	ata	gca	tat	gga	aga	gtc	ctc	aac	aca	tgg	tct	aaa	tgg	960
Pro	Arg	Pro	Ile	Ala	Tyr	Gly	Arg	Val	Leu	Asn	Thr	Trp	Ser	Lys	Trp	
305					310					315					320	
gtg	gaa	gac	aac	att	aat	cca	aat	cgc	acc	aaa	gtt	ttc	ttc	tcc	agc	1008
Val	Glu	Asp	Asn	Ile	Asn	Pro	Asn	Arg	Thr	Lys	Val	Phe	Phe	Ser	Ser	
				325				330						335		
atg	tct	cct	ctt	cat	att	aag	agt	gag	gct	tgg	aac	aat	cca	gat	ggt	1056
Met	Ser	Pro	Leu	His	Ile	Lys	Ser	Glu	Ala	Trp	Asn	Asn	Pro	Asp	Gly	
			340					345					350			
ata	aaa	tgt	gct	aag	gag	acc	ata	cca	att	ctg	aat	atg	tca	aca	aca	1104
Ile	Lys	Cys	Ala	Lys	Glu	Thr	Ile	Pro	Ile	Leu	Asn	Met	Ser	Thr	Thr	
			355				360					365				
tta	caa	gtt	ggc	aca	gat	cgt	cga	ctg	ttt	gtg	gtt	gcc	aac	aat	gtg	1152
Leu	Gln	Val	Gly	Thr	Asp	Arg	Arg	Leu	Phe	Val	Val	Ala	Asn	Asn	Val	
			370			375					380					
acg	caa	tca	atg	aag	gtg	gtg	cca	gtg	aac	ttc	ctt	aac	atc	aca	acc	1200
Thr	Gln	Ser	Met	Lys	Val	Val	Pro	Val	Asn	Phe	Leu	Asn	Ile	Thr	Thr	
385					390					395					400	
tta	tca	gaa	ttt	aga	aaa	gat	gca	cat	aca	tct	gtt	tac	acc	ata	cgc	1248
Leu	Ser	Glu	Phe	Arg	Lys	Asp	Ala	His	Thr	Ser	Val	Tyr	Thr	Ile	Arg	
				405				410						415		
caa	ggc	aaa	atg	tta	act	cca	gaa	caa	caa	gct	gat	cct	act	act	tat	1296
Gln	Gly	Lys	Met	Leu	Thr	Pro	Glu	Gln	Gln	Ala	Asp	Pro	Thr	Thr	Tyr	
			420					425					430			
gcc	gat	tgc	att	cat	tgg	tgt	tta	cca	gga	tta	cct	gac	act	tgg	aat	1344
Ala	Asp	Cys	Ile	His	Trp	Cys	Leu	Pro	Gly	Leu	Pro	Asp	Thr	Trp	Asn	
			435			440						445				
gag	ttc	ctc	tat	aca	agg	atc	atc	tct	caa	tct	tga					1380
Glu	Phe	Leu	Tyr	Thr	Arg	Ile	Ile	Ser	Gln	Ser						
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<400> 1667

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			20					25					30			
Val	Phe	Ser	Ile	Phe	Leu	Phe	Gly	Leu	Phe	Met	Tyr	Asn	Glu	Asp	Val	
		35					40					45				
Lys	Ser	Met	Ala	Glu	Phe	Thr	Phe	Leu	Arg	Pro	Lys	Ala	Gln	Glu	Ile	
	50					55					60					
Gln	Glu	Glu	Thr	Val	Ser	Asn	Asn	Asn	Ser	Arg	Thr	Gln	Pro	Glu	Arg	
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Asn	Arg	Val	Glu	Asp	Ser	Glu	Glu	Ser	Gln	Glu	Pro	Ile	Asp	Leu	Lys	
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Ala	Val	Val	Ala	Glu	Glu	Lys	Ile	Val	Glu	Glu	Tyr	Glu	Glu	Glu	Asn	
			100					105					110			
Glu	Glu	Val	Val	Leu	Pro	Pro	Glu	Glu	Cys	Asp	Leu	Phe	Thr	Gly	Glu	
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Trp	Val	Phe	Asp	Asn	Leu	Thr	His	Pro	Leu	Tyr	Lys	Glu	Asp	Gln	Cys	
	130					135					140					
Glu	Phe	Leu	Thr	Ser	Gln	Val	Thr	Cys	Met	Arg	Asn	Gly	Arg	Ser	Asp	
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Ser	Leu	Tyr	Gln	Asn	Trp	Arg	Trp	Gln	Pro	Arg	Asp	Cys	Ser	Leu	Pro	

PF59082SeqList_PF59082.txt

165 170 175
 Lys Gly Arg Arg Leu Met Phe Val Gly Asp Ser Leu Asn Arg Asn Gln
 180 185 190
 Trp Glu Ser Met Ile Cys Leu Val Gln Ser Val Val Pro Gln Arg Lys
 195 200 205
 Lys Ser Leu Ser Asn Asn Gly Ser Leu Ser Ile Phe Thr Ile Glu Asp
 210 215 220
 Tyr Asn Ala Thr Val Glu Phe Tyr Trp Ala Pro Phe Leu Glu Glu Ser
 225 230 235 240
 Asn Ser Asp Asp Pro Lys Met His Ser Ile Leu Asn Arg Ile Ile Met
 245 250 255
 Pro Glu Ser Ile Glu Lys His Ala Val Asn Trp Lys Asn Val Asp Tyr
 260 265 270
 Leu Ile Phe Asn Thr Tyr Ile Trp Trp Met Asn Thr Asp Thr Met Lys
 275 280 285
 Val Leu Arg Gly Ser Phe Asp Glu Gly Ser Thr Glu Tyr Asp Glu Val
 290 295 300
 Pro Arg Pro Ile Ala Tyr Gly Arg Val Leu Asn Thr Trp Ser Lys Trp
 305 310 315 320
 Val Glu Asp Asn Ile Asn Pro Asn Arg Thr Lys Val Phe Phe Ser Ser
 325 330 335
 Met Ser Pro Leu His Ile Lys Ser Glu Ala Trp Asn Asn Pro Asp Gly
 340 345 350
 Ile Lys Cys Ala Lys Glu Thr Ile Pro Ile Leu Asn Met Ser Thr Thr
 355 360 365
 Leu Gln Val Gly Thr Asp Arg Arg Leu Phe Val Val Ala Asn Asn Val
 370 375 380
 Thr Gln Ser Met Lys Val Val Pro Val Asn Phe Leu Asn Ile Thr Thr
 385 390 395 400
 Leu Ser Glu Phe Arg Lys Asp Ala His Thr Ser Val Tyr Thr Ile Arg
 405 410 415
 Gln Gly Lys Met Leu Thr Pro Glu Gln Gln Ala Asp Pro Thr Thr Tyr
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<211> 1275

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

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<400> 1668

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atg	aag	caa	aga	aag	aag	agt	tat	ctc	tca	atc	ttc	gtg	atc	ttc	ttc	96
Met	Lys	Gln	Arg	Lys	Lys	Ser	Tyr	Leu	Ser	Ile	Phe	Val	Ile	Phe	Phe	
			20					25					30			
tct	ctt	ttc	ttc	ttc	ggg	atc	ttc	atg	tac	aat	gac	aac	ctc	aaa	tcc	144
Ser	Leu	Phe	Phe	Phe	Gly	Ile	Phe	Met	Tyr	Asn	Asp	Asn	Leu	Lys	Ser	
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tcc	att	gct	gac	ttc	aca	tct	tcg	aac	cca	ttc	tct	agt	tca	ttt	gtg	192
Ser	Ile	Ala	Asp	Phe	Thr	Ser	Ser	Asn	Pro	Phe	Ser	Ser	Ser	Phe	Val	
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gag	ttg	ccg	ccg	gat	gag	tgt	gat	ctg	ttc	acc	ggg	caa	tgg	gtt	ttc	240
Glu	Leu	Pro	Pro	Asp	Glu	Cys	Asp	Leu	Phe	Thr	Gly	Gln	Trp	Val	Phe	
65				70			75							80		
gac	aac	aag	aca	tat	cca	ttg	tat	aaa	gaa	gaa	gag	tgt	gag	ttc	ttg	288
Asp	Asn	Lys	Thr	Tyr	Pro	Leu	Tyr	Lys	Glu	Glu	Glu	Cys	Glu	Phe	Leu	
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acg	gag	caa	gtg	act	tgt	tta	aga	aac	gga	agg	aaa	gat	tct	ttg	ttt	336
Thr	Glu	Gln	Val	Thr	Cys	Leu	Arg	Asn	Gly	Arg	Lys	Asp	Ser	Leu	Phe	
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PF59082SeqList_PF59082.txt

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Gln	Asn	Trp	Arg	Trp	Gln	Pro	Arg	Asp	Cys	Ser	Leu	Pro	Lys	Phe	Asn	
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gca	aga	gtg	ttg	tta	gag	aag	ctg	agg	aac	aag	aga	ttg	atg	ttt	gtc	432
Ala	Arg	Val	Leu	Leu	Glu	Lys	Leu	Arg	Asn	Lys	Arg	Leu	Met	Phe	Val	
		130				135					140					
ggg	gac	tcg	tta	aac	cgg	aac	caa	tgg	gaa	tca	atg	gtt	tgt	ttg	gtt	480
Gly	Asp	Ser	Leu	Asn	Arg	Asn	Gln	Trp	Glu	Ser	Met	Val	Cys	Leu	Val	
		145			150				155					160		
caa	tca	gtg	att	cct	ccc	ggg	aga	aaa	agc	tta	aac	cag	acc	ggg	tca	528
Gln	Ser	Val	Ile	Pro	Pro	Gly	Arg	Lys	Ser	Leu	Asn	Gln	Thr	Gly	Ser	
				165					170					175		
ctc	act	gtt	ttc	aaa	atc	cag	gac	tat	aac	gcg	acg	gtg	gag	ttt	tat	576
Leu	Thr	Val	Phe	Lys	Ile	Gln	Asp	Tyr	Asn	Ala	Thr	Val	Glu	Phe	Tyr	
			180					185					190			
tgg	gcg	cca	ttt	ttg	gtg	gaa	tca	aat	tca	gac	gat	ccg	gaa	aag	cac	624
Trp	Ala	Pro	Phe	Leu	Val	Glu	Ser	Asn	Ser	Asp	Asp	Pro	Glu	Lys	His	
		195				200						205				
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Gly	Asp	Thr	Glu	Tyr	Asp	Glu	Ile	Lys	Arg	Pro	Ile	Ala	Tyr	Glu	Arg	
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Leu	Leu	Thr	Arg	Glu	Gln	Gln	Asn	Asp	Pro	Ala	Asn	Phe	Ala	Asp	Cys	
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Ile	His	Trp	Cys	Leu	Pro	Gly	Leu	Pro	Asp	Thr	Trp	Asn	Glu	Phe	Leu	
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<212> PRT

<213> Arabidopsis thaliana

<400> 1669

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 50 55 60
 Glu Leu Pro Pro Asp Glu Cys Asp Leu Phe Thr Gly Gln Trp Val Phe
 65 70 75 80
 Asp Asn Lys Thr Tyr Pro Leu Tyr Lys Glu Glu Cys Glu Phe Leu
 85 90 95
 Thr Glu Gln Val Thr Cys Leu Arg Asn Gly Arg Lys Asp Ser Leu Phe
 100 105 110
 Gln Asn Trp Arg Trp Gln Pro Arg Asp Cys Ser Leu Pro Lys Phe Asn
 115 120 125
 Ala Arg Val Leu Leu Glu Lys Leu Arg Asn Lys Arg Leu Met Phe Val
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 Gly Asp Ser Leu Asn Arg Asn Gln Trp Glu Ser Met Val Cys Leu Val
 145 150 155 160
 Gln Ser Val Ile Pro Pro Gly Arg Lys Ser Leu Asn Gln Thr Gly Ser
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 Leu Thr Val Phe Lys Ile Gln Asp Tyr Asn Ala Thr Val Glu Phe Tyr
 180 185 190
 Trp Ala Pro Phe Leu Val Glu Ser Asn Ser Asp Asp Pro Glu Lys His
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 Ser Ile Ile Asp Arg Ile Ile Met Pro Glu Ser Ile Glu Lys His Gly
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 Val Asn Trp Ile Gly Val Asp Phe Leu Val Phe Asn Ser Tyr Ile Trp
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 Trp Met Asn Thr Val Ser Ile Lys Val Leu Arg Gly Ser Phe Asp Asp
 245 250 255
 Gly Asp Thr Glu Tyr Asp Glu Ile Lys Arg Pro Ile Ala Tyr Glu Arg
 260 265 270
 Val Leu Arg Thr Leu Gly Asp Trp Val Asp His Asn Ile Asp Pro Leu
 275 280 285
 Ser Thr Thr Val Phe Phe Met Ser Met Ser Pro Leu His Ile Lys Ser
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 Ser Asp Trp Ala Asn Pro Glu Gly Ile Arg Cys Ala Leu Glu Thr Thr
 305 310 315 320
 Pro Ile Leu Asn Met Ser Phe Asn Val Ala Tyr Gly Gln Phe Ser Ala
 325 330 335
 Val Gly Thr Asp Tyr Arg Leu Phe Pro Val Ala Glu Asn Val Thr Gln
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 Ser Leu Lys Val Pro Ile His Phe Leu Asn Ile Thr Ala Leu Ser Glu
 355 360 365
 Tyr Arg Lys Asp Ala His Thr Ser Val Tyr Thr Ile Lys Gln Gly Lys
 370 375 380
 Leu Leu Thr Arg Glu Gln Gln Asn Asp Pro Ala Asn Phe Ala Asp Cys
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<212> DNA

<213> Arabidopsis thaliana

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<222> (1)..(1356)

<400> 1670

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 aca cac ttc ttc ttc acc gta ctc gct ttc atc tta ctc gcc gcc ttc
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48

96

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Pro	Thr	Ile	Val	His	Gln	Ser	Ala	Ile	Val	Val	Val	Val	Asp	Glu	Pro	
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Pro	Pro	Pro	Pro	Pro	Thr	Ser	Pro	Pro	Pro	Pro	Ser	Pro	Pro	Pro	Pro	
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Ser	Pro	Pro	Pro	Pro	Ser	Pro	Pro	Pro	Pro	Ser	Pro	Pro	Pro	Pro	Ala	
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Phe	Ala	Val	Gly	Lys	Thr	Pro	Glu	Gly	Cys	Asp	Val	Phe	Lys	Gly	Asn	
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Trp	Val	Lys	Asp	Trp	Ser	Thr	Arg	Pro	Leu	Tyr	Arg	Glu	Ser	Glu	Cys	
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Pro	Tyr	Ile	Gln	Pro	Gln	Leu	Thr	Cys	Arg	Thr	His	Gly	Arg	Pro	Asp	
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Ser	Asp	Tyr	Gln	Ser	Trp	Arg	Trp	Arg	Pro	Asp	Ser	Cys	Ser	Leu	Pro	
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Ser	Phe	Asn	Ala	Thr	Val	Met	Leu	Glu	Ser	Leu	Arg	Gly	Lys	Lys	Met	
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Met	Phe	Val	Gly	Asp	Ser	Leu	Asn	Arg	Gly	Met	Tyr	Val	Ser	Leu	Ile	
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Cys	Leu	Leu	His	Ser	Gln	Ile	Pro	Glu	Asn	Ser	Lys	Ser	Met	Asp	Thr	
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Phe	Gly	Ser	Leu	Thr	Val	Phe	Ser	Leu	Lys	Asp	Tyr	Asn	Ala	Thr	Ile	
		210				215					220					
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Glu	Phe	Tyr	Trp	Ala	Pro	Phe	Leu	Leu	Glu	Ser	Asn	Ser	Asp	Asn	Ala	
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Thr	Val	His	Arg	Val	Ser	Asp	Arg	Ile	Val	Arg	Lys	Gly	Ser	Ile	Asn	
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Lys	His	Gly	Arg	His	Trp	Arg	Gly	Ala	Asp	Ile	Val	Val	Phe	Asn	Thr	
			260					265					270			
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Tyr	Leu	Trp	Trp	Arg	Thr	Gly	Phe	Lys	Met	Lys	Ile	Leu	Glu	Gly	Ser	
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Phe	Lys	Asp	Glu	Lys	Lys	Arg	Ile	Val	Glu	Met	Glu	Ser	Glu	Asp	Ala	
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Gln	Thr	Thr	Pro	Ile	Gln	Asp	Met	Asn	His	Trp	Pro	Ser	Asp	Cys	Ser	
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Lys	Thr	Leu	Met	Lys	Val	Ile	Gly	Glu	Glu	Leu	Asp	Gln	Arg	Ala	Glu	
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Phe	Pro	Val	Thr	Val	Leu	Asn	Ile	Thr	Gln	Leu	Ser	Gly	Tyr	Arg	Lys	
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gag	cag	cta	gca	aat	ccg	gct	agc	tac	tca	gac	tgt	ata	cat	tgg	tgc	1296
Glu	Gln	Leu	Ala	Asn	Pro	Ala	Ser	Tyr	Ser	Asp	Cys	Ile	His	Trp	Cys	
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<212> PRT

<213> Arabidopsis thaliana

<400> 1671

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Pro	Tyr	Ile	Gln	Pro	Gln	Leu	Thr	Cys	Arg	Thr	His	Gly	Arg	Pro	Asp	
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Ser	Asp	Tyr	Gln	Ser	Trp	Arg	Trp	Arg	Pro	Asp	Ser	Cys	Ser	Leu	Pro	
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Phe	Gly	Ser	Leu	Thr	Val	Phe	Ser	Leu	Lys	Asp	Tyr	Asn	Ala	Thr	Ile	
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			340					345					350			
Gln	Thr	Thr	Pro	Ile	Gln	Asp	Met	Asn	His	Trp	Pro	Ser	Asp	Cys	Ser	
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Lys	Thr	Leu	Met	Lys	Val	Ile	Gly	Glu	Glu	Leu	Asp	Gln	Arg	Ala	Glu	
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PF59082SeqList_PF59082.txt

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 Phe Tyr Pro
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<211> 1284

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<400> 1672

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Tyr Asn Glu Lys Gln Leu Arg Val Gly Gln Phe Gln Glu Phe Asn Thr	
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aaa gac aag aag act gat ctt gtt cca tta gaa ttc tgt gat gtt ttc	240
Lys Asp Lys Lys Thr Asp Leu Val Pro Leu Glu Phe Cys Asp Val Phe	
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aca gga aaa tgg gtt ctt gat aac gtc aca cat cct tta tac aaa gaa	288
Thr Gly Lys Trp Val Leu Asp Asn Val Thr His Pro Leu Tyr Lys Glu	
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gat gaa tgt gag ttt cta tca gag tgg gtg gct tgt aca aga aac ggg	336
Asp Glu Cys Glu Phe Leu Ser Glu Trp Val Ala Cys Thr Arg Asn Gly	
100 105 110	
agg cca gac tct aag tac cag aaa tgg aga tgg caa cct caa gat tgc	384
Arg Pro Asp Ser Lys Tyr Gln Lys Trp Arg Trp Gln Pro Gln Asp Cys	
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tct ttg cca agg ttc gac agt aag ctg ctg cta gag aaa ctc agg gga	432
Ser Leu Pro Arg Phe Asp Ser Lys Leu Leu Leu Glu Lys Leu Arg Gly	
130 135 140	
aag aaa cta atg ttc att ggt gat tca ata cat tac aat cag tgg caa	480
Lys Lys Leu Met Phe Ile Gly Asp Ser Ile His Tyr Asn Gln Trp Gln	
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tcc atg gtt tgt atg gtt caa tcc gtg att ccc tca ggc aaa aag acc	528
Ser Met Val Cys Met Val Gln Ser Val Ile Pro Ser Gly Lys Lys Thr	
165 170 175	
tta aaa cac aca gca caa atg tcc atc ttc aac ata gag gag tac aat	576
Leu Lys His Thr Ala Gln Met Ser Ile Phe Asn Ile Glu Glu Tyr Asn	
180 185 190	
gca acc ata tca ttt tac tgg gca cct ttc cta gtc gaa tca aat gct	624
Ala Thr Ile Ser Phe Tyr Trp Ala Pro Phe Leu Val Glu Ser Asn Ala	
195 200 205	
gat cct cca gac aag aga gac ggg aag acc gat cca gta atc att cct	672
Asp Pro Pro Asp Lys Arg Asp Gly Lys Thr Asp Pro Val Ile Ile Pro	
210 215 220	
aat tca atc tcg aaa cac ggc gag aac tgg aaa gac gca gac tac ctc	720
Asn Ser Ile Ser Lys His Gly Glu Asn Trp Lys Asp Ala Asp Tyr Leu	
225 230 235 240	
ata ttc aac acc tac ata tgg tgg act aga cat tcc acg atc aaa gtt	768
Ile Phe Asn Thr Tyr Ile Trp Trp Thr Arg His Ser Thr Ile Lys Val	
245 250 255	
cta aaa caa gaa tct ttc aac aaa gga gac tca aaa gag tac aat gaa	816
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Trp	Leu	Glu	Gln	Asn	Ile	Asn	Pro	Ser	Gln	Thr	Ser	Ile	Phe	Phe	Ser	
		290				295					300					
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Ser	Met	Ser	Pro	Thr	His	Ile	Arg	Ser	Ser	Asp	Trp	Gly	Phe	Asn	Glu	
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gga	agc	aaa	tgt	gaa	aaa	gag	aca	gaa	cca	ata	cta	aac	atg	tca	aaa	1008
Gly	Ser	Lys	Cys	Glu	Lys	Glu	Thr	Glu	Pro	Ile	Leu	Asn	Met	Ser	Lys	
			325						330					335		
cca	ata	aat	ggt	gga	aca	aat	cga	aga	ctt	tac	gaa	atc	gca	ctg	aat	1056
Pro	Ile	Asn	Val	Gly	Thr	Asn	Arg	Arg	Leu	Tyr	Glu	Ile	Ala	Leu	Asn	
			340						345					350		
gcg	acc	aaa	tct	aca	aaa	gtg	ccg	att	cat	ttc	ctc	aac	ata	acg	act	1104
Ala	Thr	Lys	Ser	Thr	Lys	Val	Pro	Ile	His	Phe	Leu	Asn	Ile	Thr	Thr	
		355				360								365		
atg	tca	gag	tat	aga	aaa	gat	ggg	cat	acc	tca	ttt	tac	ggt	tcg	ata	1152
Met	Ser	Glu	Tyr	Arg	Lys	Asp	Gly	His	Thr	Ser	Phe	Tyr	Gly	Ser	Ile	
		370				375					380					
aat	ggg	aaa	ctc	atg	acg	ccg	gag	cag	aag	tta	gat	ccg	aga	act	ttt	1200
Asn	Gly	Lys	Leu	Met	Thr	Pro	Glu	Gln	Lys	Leu	Asp	Pro	Arg	Thr	Phe	
		385			390					395				400		
gct	gat	tgt	tat	cat	tgg	tgt	ctt	ccg	gga	ttg	cct	gat	tca	tgg	aac	1248
Ala	Asp	Cys	Tyr	His	Trp	Cys	Leu	Pro	Gly	Leu	Pro	Asp	Ser	Trp	Asn	
			405						410					415		
gag	ttg	ctc	tct	ctg	tat	atc	atc	tac	aaa	att	taa					1284
Glu	Leu	Leu	Ser	Leu	Tyr	Ile	Ile	Tyr	Lys	Ile						
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<210> 1673

<211> 427

<212> PRT

<213> Arabidopsis thaliana

<400> 1673

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Tyr	Phe	Ala	Val	Ile	Leu	Leu	Pro	Val	Phe	Leu	Leu	Gly	Cys	Tyr	Leu	
			20					25					30			
Tyr	Asn	Glu	Lys	Gln	Leu	Arg	Val	Gly	Gln	Phe	Gln	Glu	Phe	Asn	Thr	
		35					40					45				
His	Asn	Leu	Gln	Glu	His	Ile	Thr	Pro	Leu	Gln	Gln	Ser	Lys	Glu	Asp	
	50				55					60						
Lys	Asp	Lys	Lys	Thr	Asp	Leu	Val	Pro	Leu	Glu	Phe	Cys	Asp	Val	Phe	
65				70					75					80		
Thr	Gly	Lys	Trp	Val	Leu	Asp	Asn	Val	Thr	His	Pro	Leu	Tyr	Lys	Glu	
			85					90						95		
Asp	Glu	Cys	Glu	Phe	Leu	Ser	Glu	Trp	Val	Ala	Cys	Thr	Arg	Asn	Gly	
			100				105					110				
Arg	Pro	Asp	Ser	Lys	Tyr	Gln	Lys	Trp	Arg	Trp	Gln	Pro	Gln	Asp	Cys	
		115				120					125					
Ser	Leu	Pro	Arg	Phe	Asp	Ser	Lys	Leu	Leu	Leu	Glu	Lys	Leu	Arg	Gly	
	130				135						140					
Lys	Lys	Leu	Met	Phe	Ile	Gly	Asp	Ser	Ile	His	Tyr	Asn	Gln	Trp	Gln	
145				150					155					160		
Ser	Met	Val	Cys	Met	Val	Gln	Ser	Val	Ile	Pro	Ser	Gly	Lys	Lys	Thr	
			165					170					175			
Leu	Lys	His	Thr	Ala	Gln	Met	Ser	Ile	Phe	Asn	Ile	Glu	Glu	Tyr	Asn	
			180				185						190			
Ala	Thr	Ile	Ser	Phe	Tyr	Trp	Ala	Pro	Phe	Leu	Val	Glu	Ser	Asn	Ala	
		195				200					205					
Asp	Pro	Pro	Asp	Lys	Arg	Asp	Gly	Lys	Thr	Asp	Pro	Val	Ile	Ile	Pro	
	210				215						220					
Asn	Ser	Ile	Ser	Lys	His	Gly	Glu	Asn	Trp	Lys	Asp	Ala	Asp	Tyr	Leu	
225				230					235					240		
Ile	Phe	Asn	Thr	Tyr	Ile	Trp	Trp	Thr	Arg	His	Ser	Thr	Ile	Lys	Val	

PF59082SeqList_PF59082.txt

245 250 255
 Leu Lys Gln Glu Ser Phe Asn Lys Gly Asp Ser Lys Glu Tyr Asn Glu
 Ile Gly Ile Tyr Ile Val Tyr Lys Gln Val Leu Ser Thr Trp Thr Lys
 Trp Leu 275 Gln Asn Ile Asn 280 Ser Gln Thr Ser 285 Phe Phe Ser
 Ser Met Ser Pro Thr His Ile Arg Ser Ser Asp Trp Gly Phe Asn Glu
 Gly Ser Lys Cys Glu Lys Glu Thr Glu Pro Ile Leu Asn Met Ser Lys
 Pro Ile Asn Val Gly Thr Asn Arg Arg Leu Tyr Glu Ile Ala Leu Asn
 Ala Thr Lys Ser Thr Lys Val Pro Ile His Phe Leu Asn Ile Thr Thr
 Met Ser 355 Tyr Arg Lys Asp 360 His Thr Ser Phe 365 Tyr Gly Ser Ile
 Asn Gly Lys Leu Met Thr Pro Glu Gln Lys Leu Asp Pro Arg Thr Phe
 Ala Asp Cys Tyr His Trp Cys Leu Pro Gly Leu Pro Asp Ser Trp Asn
 Glu Leu Leu Ser Leu Tyr Ile Ile Tyr Lys Ile
 420 425

<210> 1674

<211> 1527

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<221> CDS

<222> (1)..(1527)

<400> 1674

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Met	Gln	Met	Gln	Gln	Arg	Arg	Lys	Pro	Pro	Pro	Ala	Ala	Ala	Pro	Val	
1				5				10						15		
gcc	gcc	aag	cag	cct	tcc	ccg	cgc	agg	acg	ccc	ggg	cct	ctc	tcc	ttc	96
Ala	Ala	Lys	Gln	Pro	Ser	Pro	Arg	Arg	Thr	Pro	Gly	Pro	Leu	Ser	Phe	
			20					25					30			
gcc	ggc	gcc	ctg	ctc	tcc	ctc	ctc	gtc	gtc	gcc	acc	ttc	ctc	tac	atc	144
Ala	Gly	Ala	Leu	Leu	Ser	Leu	Leu	Val	Val	Ala	Thr	Phe	Leu	Tyr	Ile	
		35					40				45					
aac	gac	cac	ggc	aac	atg	atg	cca	ccc	cac	gcg	tcc	ccc	gac	ccc	gac	192
Asn	Asp	His	Gly	Asn	Met	Met	Pro	Pro	His	Ala	Ser	Pro	Asp	Pro	Asp	
		50			55					60						
ctc	cgc	ctc	ctg	cag	gag	gcc	gcg	cac	caa	aag	gtc	aac	tcc	atc	ctc	240
Leu	Arg	Leu	Leu	Gln	Glu	Ala	Ala	His	Gln	Lys	Val	Asn	Ser	Ile	Leu	
	65				70					75				80		
ctc	tcc	cgc	cac	gcc	cct	gcc	cct	ccc	ccg	cgc	acc	aac	acc	aac	acg	288
Leu	Ser	Arg	His	Ala	Pro	Ala	Pro	Pro	Pro	Arg	Thr	Asn	Thr	Asn	Thr	
			85					90						95		
tct	tca	tcc	gac	caa	cac	ctc	cgc	ctc	atc	aac	atc	ccc	atg	tcc	tcc	336
Ser	Ser	Ser	Asp	Gln	His	Leu	Arg	Leu	Ile	Asn	Ile	Pro	Met	Ser	Ser	
			100					105					110			
gac	ttg	gac	ttg	gag	ttg	ggg	ggt	aac	agc	aca	agc	agc	agc	ggc	gtg	384
Asp	Leu	Asp	Leu	Glu	Leu	Gly	Gly	Asn	Ser	Thr	Ser	Ser	Ser	Gly	Val	
		115				120					125					
gag	att	caa	ttt	gag	cag	cag	cag	cag	cag	gag	gag	aag	aat	ctg	aga	432
Glu	Ile	Gln	Phe	Glu	Gln	Gln	Gln	Gln	Gln	Glu	Glu	Lys	Asn	Leu	Arg	
	130				135					140						
ggg	tgc	gag	cta	tac	aag	ggg	cgg	tgg	gtg	tac	gac	gcg	gcg	ggg	agg	480
Gly	Cys	Glu	Leu	Tyr	Lys	Gly	Arg	Trp	Val	Tyr	Asp	Ala	Ala	Gly	Arg	
	145				150					155					160	
gag	gcg	ccg	ctg	tac	agg	gag	tcg	gag	tgc	ggg	ttc	ctg	acg	gag	cag	528
Glu	Ala	Pro	Leu	Tyr	Arg	Glu	Ser	Glu	Cys	Gly	Phe	Leu	Thr	Glu	Gln	
			165					170						175		
gtg	acg	tgc	atg	cgc	aac	ggc	cgg	cgg	gac	gac	tcg	tac	cag	cgg	tgg	576
Val	Thr	Cys	Met	Arg	Asn	Gly	Arg	Arg	Asp	Asp	Ser	Tyr	Gln	Arg	Trp	

PF59082SeqList_PF59082.txt

<220>

<221> CDS

<222> (1)..(1569)

<400> 1676

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ggg gtg ttc gac ccg ttc ggc acg aaa cag gcc gtg tcg tcg ctg ccg	96
Gly Val Phe Asp Pro Phe Gly Thr Lys Gln Ala Val Ser Ser Leu Arg	
20 25 30	
aag ggc ggg cgg ctg ccg gtg tac gtg gct ggc gtc ttc ttc gtc atc	144
Lys Gly Gly Arg Leu Pro Val Tyr Val Ala Gly Val Phe Phe Val Ile	
35 40 45	
ttc gtc atc atc atg tac ggc gag gac atc ccg tcg ctc acg ctg gac	192
Phe Val Ile Ile Met Tyr Gly Glu Asp Ile Arg Ser Leu Thr Leu Asp	
50 55 60	
ccg atc gcg cgc gcg ggg aca acg ccg gcg ccg atc gtg gag ccg gta	240
Pro Ile Ala Arg Ala Gly Thr Thr Pro Ala Arg Ile Val Glu Pro Val	
65 70 75 80	
gtg acg gag gag cgc cac gtc gcc ccg gtc aac cct cct ccg cgc gag	288
Val Thr Glu Glu Arg His Val Ala Arg Val Asn Pro Pro Arg Arg Glu	
85 90 95	
gtc tcg tcc gcg gag aag gcc gcc gcg ttg ccg ctc gac gtc gac gag	336
Val Ser Ser Ala Glu Lys Ala Ala Leu Pro Leu Asp Val Asp Glu	
100 105 110	
agg ccg aag ctg gcg acg ccg acg ccg acg gag gcg gcg aag gag gtc	384
Arg Pro Lys Leu Ala Thr Pro Thr Pro Thr Glu Ala Ala Lys Glu Val	
115 120 125	
ccg aag gtc gag aag atc agg aag ccg aag aaa ccc aag acg acg aag	432
Pro Lys Val Glu Lys Ile Arg Lys Pro Lys Lys Pro Lys Thr Thr Lys	
130 135 140	
aag aag ccg agg aag ccg ccg gcg aag aag acg gtg gcg gcg gca	480
Lys Lys Pro Arg Lys Pro Arg Pro Ala Lys Lys Thr Val Ala Ala Ala	
145 150 155 160	
gcc ggg ggc ctg ctc ggc gtg ccg gag acg tgc gac ctg tcc aag ggc	528
Ala Gly Gly Leu Leu Gly Val Pro Glu Thr Cys Asp Leu Ser Lys Gly	
165 170 175	
gag tgg gtg ttc gac aac acc agc tac cct ctg tac ccg gag gag cag	576
Glu Trp Val Phe Asp Asn Thr Ser Tyr Pro Leu Tyr Arg Glu Glu Gln	
180 185 190	
tgc gag ttc ctc acg tcg cag gtg acg tgc atg agg aac ggc cgc cgc	624
Cys Glu Phe Leu Thr Ser Gln Val Thr Cys Met Arg Asn Gly Arg Arg	
195 200 205	
gac gac acc tac cag aag tgg ccg tgg cag ccc aaa gac tgc tcc atg	672
Asp Asp Thr Tyr Gln Lys Trp Arg Trp Gln Pro Lys Asp Cys Ser Met	
210 215 220	
ccc agg ttc gac gcg aag ctg ttc atg gag agg ctc cga ggg aag ccg	720
Pro Arg Phe Asp Ala Lys Leu Phe Met Glu Arg Leu Arg Gly Lys Arg	
225 230 235 240	
ttc atg ttc gtg ggg gac tcg ctg aac ccg aac cag tgg gag tcc atg	768
Phe Met Phe Val Gly Asp Ser Leu Asn Arg Asn Gln Trp Glu Ser Met	
245 250 255	
gtg tgc ctg gtg cag tcg gcg atg tcg ccg ggg aag aaa tac gtc acc	816
Val Cys Leu Val Gln Ser Ala Met Ser Pro Gly Lys Lys Tyr Val Thr	
260 265 270	
tgg gag gac cag ccg gtc gtc ttc cac gcc gtg gag tac aac gcg acg	864
Trp Glu Asp Gln Arg Val Val Phe His Ala Val Glu Tyr Asn Ala Thr	
275 280 285	
gtg gag ttc tac tgg gcg ccg ttc ctg gtg gag tcc aac tcc gac gac	912
Val Glu Phe Tyr Trp Ala Pro Phe Leu Val Glu Ser Asn Ser Asp Asp	
290 295 300	
ccc aag atc cac agc atc cag cac ccg atc atc aag gcg gac gcg atc	960
Pro Lys Ile His Ser Ile Gln His Arg Ile Ile Lys Ala Asp Ala Ile	
305 310 315 320	
gcg gcg cac gca cag aac tgg cgc ggc gtc gac tac ctc gtc ttc aac	1008
Ala Ala His Ala Gln Asn Trp Arg Gly Val Asp Tyr Leu Val Phe Asn	
325 330 335	
acc tac atc tgg tgg atg aac acc ctc aac atg aag atc atg aga ccg	1056

PF59082SeqList_PF59082.txt

Thr	Tyr	Ile	Trp	Trp	Met	Asn	Thr	Leu	Asn	Met	Lys	Ile	Met	Arg	Pro		
ggc	ggg	cag	agc	tgg	gag	gag	cat	gac	gag	gtc	gtg	agg	atc	gag	gcg	1104	
Gly	Gly	Gln	Ser	Trp	Glu	Glu	His	Asp	Glu	Val	Val	Arg	Ile	Glu	Ala		
		355					360					365					
tat	cgg	aag	gtg	ctg	acg	acg	tgg	gcg	agc	tgg	gtg	aac	gac	aac	atc	1152	
Tyr	Arg	Lys	Val	Leu	Thr	Thr	Trp	Ala	Ser	Trp	Val	Asn	Asp	Asn	Ile		
	370					375					380						
gac	ccg	gcg	cg	acg	tcc	gtc	ttc	ttc	atg	agc	atc	tcc	cct	ctt	cac	1200	
Asp	Pro	Ala	Arg	Thr	Ser	Val	Phe	Phe	Met	Ser	Ile	Ser	Pro	Leu	His		
	385				390					395					400		
atc	agc	ccg	gag	gtg	tgg	ggg	aac	ccg	ggc	ggg	atc	cg	tgc	gcc	aag	1248	
Ile	Ser	Pro	Glu	Val	Trp	Gly	Asn	Pro	Gly	Gly	Ile	Arg	Cys	Ala	Lys		
			405					410						415			
gag	acg	atg	ccg	ctg	ctc	aac	tgg	cac	ggg	ccg	atc	tgg	ctg	ggc	acg	1296	
Glu	Thr	Met	Pro	Leu	Leu	Asn	Trp	His	Gly	Pro	Ile	Trp	Leu	Gly	Thr		
			420				425						430				
gac	tgg	gac	atg	ttc	cac	gcg	gcg	gcc	aac	gtg	tcc	cg	acg	gcg	gcg	1344	
Asp	Trp	Asp	Met	Phe	His	Ala	Ala	Ala	Asn	Val	Ser	Arg	Thr	Ala	Ala		
		435				440						445					
acg	cgg	gtg	ccc	atc	acc	ttc	gtc	gac	gtg	acc	acc	atg	tcg	gag	cg	1392	
Thr	Arg	Val	Pro	Ile	Thr	Phe	Val	Asp	Val	Thr	Thr	Met	Ser	Glu	Arg		
	450					455					460						
cg	aag	gac	ggg	cac	acc	tcc	gtg	cac	acc	atc	cg	cag	ggc	aag	gtg	1440	
Arg	Lys	Asp	Gly	His	Thr	Ser	Val	His	Thr	Ile	Arg	Gln	Gly	Lys	Val		
	465				470					475					480		
ctg	acg	ccg	gag	cag	cag	gcc	gac	cct	ggc	acc	tac	gcc	gac	tgc	atc	1488	
Leu	Thr	Pro	Glu	Gln	Gln	Ala	Asp	Pro	Gly	Thr	Tyr	Ala	Asp	Cys	Ile		
			485					490						495			
cac	tgg	tgc	ctc	ccc	ggc	gtc	cct	gac	atc	tgg	aac	ctc	atc	ctc	tac	1536	
His	Trp	Cys	Leu	Pro	Gly	Val	Pro	Asp	Ile	Trp	Asn	Leu	Ile	Leu	Tyr		
			500					505					510				
acc	agg	ata	atg	tcc	agg	ccg	cag	ctg	gta	tag						1569	
Thr	Arg	Ile	Met	Ser	Arg	Pro	Gln	Leu	Val								
		515					520										

<210> 1677

<211> 522

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<400> 1677

Met	Ala	Asn	Arg	Arg	Lys	Phe	Ser	Gln	Ala	Gly	Gly	Gly	Gly	Gly	Gly		
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Gly	Val	Phe	Asp	Pro	Phe	Gly	Thr	Lys	Gln	Ala	Val	Ser	Ser	Leu	Arg		
			20					25					30				
Lys	Gly	Gly	Arg	Leu	Pro	Val	Tyr	Val	Ala	Gly	Val	Phe	Phe	Val	Ile		
		35					40					45					
Phe	Val	Ile	Ile	Met	Tyr	Gly	Glu	Asp	Ile	Arg	Ser	Leu	Thr	Leu	Asp		
	50					55					60						
Pro	Ile	Ala	Arg	Ala	Gly	Thr	Thr	Pro	Ala	Arg	Ile	Val	Glu	Pro	Val		
	65				70				75					80			
Val	Thr	Glu	Glu	Arg	His	Val	Ala	Arg	Val	Asn	Pro	Pro	Arg	Arg	Glu		
			85					90					95				
Val	Ser	Ser	Ala	Glu	Lys	Ala	Ala	Ala	Leu	Pro	Leu	Asp	Val	Asp	Glu		
			100					105					110				
Arg	Pro	Lys	Leu	Ala	Thr	Pro	Thr	Pro	Thr	Glu	Ala	Ala	Lys	Glu	Val		
		115				120						125					
Pro	Lys	Val	Glu	Lys	Ile	Arg	Lys	Pro	Lys	Lys	Pro	Lys	Thr	Thr	Lys		
	130					135					140						
Lys	Lys	Pro	Arg	Lys	Pro	Arg	Pro	Ala	Lys	Lys	Thr	Val	Ala	Ala	Ala		
	145				150					155				160			
Ala	Gly	Gly	Leu	Leu	Gly	Val	Pro	Glu	Thr	Cys	Asp	Leu	Ser	Lys	Gly		
			165					170						175			
Glu	Trp	Val	Phe	Asp	Asn	Thr	Ser	Tyr	Pro	Leu	Tyr	Arg	Glu	Glu	Gln		
			180					185					190				
Cys	Glu	Phe	Leu	Thr	Ser	Gln	Val	Thr	Cys	Met	Arg	Asn	Gly	Arg	Arg		
		195				200						205					
Asp	Asp	Thr	Tyr	Gln	Lys	Trp	Arg	Trp	Gln	Pro	Lys	Asp	Cys	Ser	Met		

PF59082SeqList_PF59082.txt

210 215 220
Pro Arg Phe Asp Ala Lys Leu Phe Met Glu Arg Leu Arg Gly Lys Arg
225 230 235 240
Phe Met Phe Val Gly Asp Ser Leu Asn Arg Asn Gln Trp Glu Ser Met
245 250 255
Val Cys Leu Val Gln Ser Ala Met Ser Pro Gly Lys Lys Tyr Val Thr
260 265 270
Trp Glu Asp Gln Arg Val Val Phe His Ala Val Glu Tyr Asn Ala Thr
275 280 285
Val Glu Phe Tyr Trp Ala Pro Phe Leu Val Glu Ser Asn Ser Asp Asp
290 295 300
Pro Lys Ile His Ser Ile Gln His Arg Ile Ile Lys Ala Asp Ala Ile
305 310 315 320
Ala Ala His Ala Gln Asn Trp Arg Gly Val Asp Tyr Leu Val Phe Asn
325 330 335
Thr Tyr Ile Trp Trp Met Asn Thr Leu Asn Met Lys Ile Met Arg Pro
340 345 350
Gly Gly Gln Ser Trp Glu Glu His Asp Glu Val Val Arg Ile Glu Ala
355 360 365
Tyr Arg Lys Val Leu Thr Thr Trp Ala Ser Trp Val Asn Asp Asn Ile
370 375 380
Asp Pro Ala Arg Thr Ser Val Phe Phe Met Ser Ile Ser Pro Leu His
385 390 395 400
Ile Ser Pro Glu Val Trp Gly Asn Pro Gly Gly Ile Arg Cys Ala Lys
405 410 415
Glu Thr Met Pro Leu Leu Asn Trp His Gly Pro Ile Trp Leu Gly Thr
420 425 430
Asp Trp Asp Met Phe His Ala Ala Ala Asn Val Ser Arg Thr Ala Ala
435 440 445
Thr Arg Val Pro Ile Thr Phe Val Asp Val Thr Thr Met Ser Glu Arg
450 455 460
Arg Lys Asp Gly His Thr Ser Val His Thr Ile Arg Gln Gly Lys Val
465 470 475 480
Leu Thr Pro Glu Gln Ala Asp Pro Gly Thr Tyr Ala Asp Cys Ile
485 490 495
His Trp Cys Leu Pro Gly Val Pro Asp Ile Trp Asn Leu Ile Leu Tyr
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Thr Arg Ile Met Ser Arg Pro Gln Leu Val
515 520

<210> 1678
<211> 1626
<212> DNA
<213> Oryza sativa

<220>
<221> CDS
<222> (50)..(1417)

<400> 1678
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Met Ser Lys

58

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Pro Gln Gln Gln Ser Pro Pro Ser Thr Thr Thr Thr Ser Pro Pro Pro
5 10 15

106

cca ccg ccc tcc act ccg ccc ccc gcc tcc tcc tcc cgc tcc ctc ctc
Pro Pro Pro Ser Thr Pro Pro Pro Ala Ser Ser Ser Ser Arg Ser Leu Leu
20 25 30 35

154

tcc gcg ctg cgc cgc tcc ccg gtc acc acc ctc gtc gcc gcc ttc ttc
Ser Ala Leu Arg Arg Ser Pro Val Thr Thr Leu Val Ala Ala Phe Phe
40 45 50

202

ctc ctc gcc ctc ttc atg tac ggc gag gac gtc cgc acc ctc gcc gag
Leu Leu Ala Leu Phe Met Tyr Gly Glu Asp Val Arg Thr Leu Ala Glu
55 60 65

250

ctc tcc atc gac gac tac ctc tac ccc gac gcc gat ttc tac aac gtc
Leu Ser Ile Asp Asp Tyr Leu Tyr Pro Asp Ala Asp Phe Tyr Asn Val
70 75 80

298

tcc gcc ctt ccc cct ctc ctc ctc ccc ccg ccc acc tgc gac ctc tcc

346

PF59082SeqList_PF59082.txt

Ser	Ala	Leu	Pro	Pro	Leu	Leu	Leu	Pro	Pro	Pro	Thr	Cys	Asp	Leu	Ser	
85						90					95					
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Arg	Gly	Arg	Trp	Val	Phe	Asp	Asn	Thr	Ser	Leu	Pro	Ala	Tyr	Arg	Glu	
100					105					110					115	
aag	gaa	tgc	acc	ttc	ctc	acc	aag	cag	gtc	tcc	tgc	ctc	gcc	aat	ggc	442
Lys	Glu	Cys	Thr	Phe	Leu	Thr	Lys	Gln	Val	Ser	Cys	Leu	Ala	Asn	Gly	
				120					125					130		
cgc	ccc	gac	gac	cta	tgg	cag	tac	tgg	cgc	tgg	caa	ccc	aac	aac	tgc	490
Arg	Pro	Asp	Asp	Leu	Trp	Gln	Tyr	Trp	Arg	Trp	Gln	Pro	Asn	Asn	Cys	
			135					140					145			
tcg	ctc	ccc	acg	ttc	gac	gcg	cgg	cgg	ttc	atg	gag	aag	atg	cgg	ggg	538
Ser	Leu	Pro	Thr	Phe	Asp	Ala	Arg	Arg	Phe	Met	Glu	Lys	Met	Arg	Gly	
		150				155					160					
aag	agg	atg	atg	ttc	gtg	ggg	gac	tcg	ctg	aat	cgg	aac	cag	tgg	gag	586
Lys	Arg	Met	Met	Phe	Val	Gly	Asp	Ser	Leu	Asn	Arg	Asn	Gln	Trp	Glu	
		165				170					175					
tcg	ctg	gtg	tgc	ctg	gtg	cag	ccc	atc	cta	tcc	aag	ggc	agg	aag	aag	634
Ser	Leu	Val	Cys	Leu	Val	Gln	Pro	Ile	Leu	Ser	Lys	Gly	Arg	Lys	Lys	
180					185					190					195	
atc	gtc	aag	cgc	ggc	tcc	ttc	aac	atc	ttc	tac	gcc	aag	gag	tat	cgc	682
Ile	Val	Lys	Arg	Gly	Ser	Phe	Asn	Ile	Phe	Tyr	Ala	Lys	Glu	Tyr	Arg	
			200					205						210		
gcc	acc	ctc	gag	ttc	tac	tgg	gct	cca	ttc	ctc	gtc	gag	tcc	aac	tcc	730
Ala	Thr	Leu	Glu	Phe	Tyr	Trp	Ala	Pro	Phe	Leu	Val	Glu	Ser	Asn	Ser	
			215					220					225			
gac	aac	ccc	aat	ttc	cac	cac	atc	gac	cag	cgc	atc	atc	agc	cct	gag	778
Asp	Asn	Pro	Asn	Phe	His	His	Ile	Asp	Gln	Arg	Ile	Ile	Ser	Pro	Glu	
		230					235				240					
cgg	atc	gag	agc	cat	gcc	aac	aac	tgg	aag	gac	gtt	gat	tac	ctc	atc	826
Arg	Ile	Glu	Ser	His	Ala	Asn	Asn	Trp	Lys	Asp	Val	Asp	Tyr	Leu	Ile	
		245				250					255					
ttc	aac	acc	tac	atc	tgg	tgg	atg	aac	aac	gaa	gac	atc	aaa	gtc	agg	874
Phe	Asn	Thr	Tyr	Ile	Trp	Trp	Met	Asn	Asn	Glu	Asp	Ile	Lys	Val	Arg	
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agg	cca	aat	tca	act	tct	tgg	tca	gat	cac	gac	gag	gtg	cca	agg	atc	922
Arg	Pro	Asn	Ser	Thr	Ser	Trp	Ser	Asp	His	Asp	Glu	Val	Pro	Arg	Ile	
			280					285					290			
gag	acc	tat	ggc	cgt	gtg	ttc	aag	act	tgg	tcg	acc	tgg	ctg	gaa	cag	970
Glu	Thr	Tyr	Gly	Arg	Val	Phe	Lys	Thr	Trp	Ser	Thr	Trp	Leu	Glu	Gln	
			295				300						305			
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Asn	Val	Asp	Pro	Ala	Arg	Thr	Ser	Val	Phe	Phe	Met	Thr	Ile	Ser	Pro	
		310				315					320					
ctt	cac	aac	agc	cca	gca	caa	tgg	ggg	aac	ccg	aac	ggg	atc	aaa	tgc	1066
Leu	His	Asn	Ser	Pro	Ala	Gln	Trp	Gly	Asn	Pro	Asn	Gly	Ile	Lys	Cys	
		325				330					335					
gta	aag	gag	aca	ctt	cca	gtc	ctc	aac	tac	acc	aag	cca	ctg	gat	ctc	1114
Val	Lys	Glu	Thr	Leu	Pro	Val	Leu	Asn	Tyr	Thr	Lys	Pro	Leu	Asp	Leu	
340					345					350					355	
aac	cat	gac	atg	cgg	atg	tac	gac	ctg	gta	gca	aaa	gtt	gct	aaa	aac	1162
Asn	His	Asp	Met	Arg	Met	Tyr	Asp	Leu	Val	Ala	Lys	Val	Ala	Lys	Asn	
			360					365					370			
atg	aag	aat	gtt	cca	gtg	tcg	ttg	atc	gac	atc	aca	agg	atg	tca	gat	1210
Met	Lys	Asn	Val	Pro	Val	Ser	Leu	Ile	Asp	Ile	Thr	Arg	Met	Ser	Asp	
			375					380					385			
tac	agg	aag	gat	gcc	cac	aca	tca	ttg	tat	tcc	atc	cgt	cag	ggc	aaa	1258
Tyr	Arg	Lys	Asp	Ala	His	Thr	Ser	Leu	Tyr	Ser	Ile	Arg	Gln	Gly	Lys	
		390					395					400				
ctg	ttg	aca	ccg	gag	cag	aag	gct	gac	cca	cag	aag	tac	gct	gac	tgc	1306
Leu	Leu	Thr	Pro	Glu	Gln	Lys	Ala	Asp	Pro	Gln	Lys	Tyr	Ala	Asp	Cys	
		405				410					415					
atc	cat	tgg	tgc	ctt	cct	ggg	gta	cca	gac	gtc	tgg	aac	cag	ata	ctc	1354
Ile	His	Trp	Cys	Leu	Pro	Gly	Val	Pro	Asp	Val	Trp	Asn	Gln	Ile	Leu	
				425						430					435	
tac	acc	agg	atc	ctc	tcc	aaa	tcc	tcc	cct	cca	tcc	aca	cat	ccc	tct	1402
Tyr	Thr	Arg	Ile	Leu	Ser	Lys	Ser	Ser	Pro	Pro	Ser	Thr	His	Pro	Ser	
			440						445					450		
ctc	cct	cca	caa	tgacaagcag	ggagcatgat	tttttttttt	gccccatcgt									1454

PF59082SeqList_PF59082.txt

Leu Pro Pro Gln
 455
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 caagctagag agagaaagga tggagtgggc tgtttactgg tggcatgtaa aatcgttcaa 1574
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 35 40 45
 Ala Phe Phe Leu Leu Ala Leu Phe Met Tyr Gly Glu Asp Val Arg Thr
 50 55 60
 Leu Ala Glu Leu Ser Ile Asp Asp Tyr Leu Tyr Pro Asp Ala Asp Phe
 65 70 75 80
 Tyr Asn Val Ser Ala Leu Pro Pro Leu Leu Pro Pro Pro Thr Cys
 85 90 95
 Asp Leu Ser Arg Gly Arg Trp Val Phe Asp Asn Thr Ser Leu Pro Ala
 100 105 110
 Tyr Arg Glu Lys Glu Cys Thr Phe Leu Thr Lys Gln Val Ser Cys Leu
 115 120 125
 Ala Asn Gly Arg Pro Asp Asp Leu Trp Gln Tyr Trp Arg Trp Gln Pro
 130 135 140
 Asn Asn Cys Ser Leu Pro Thr Phe Asp Ala Arg Arg Phe Met Glu Lys
 145 150 155 160
 Met Arg Gly Lys Arg Met Met Phe Val Gly Asp Ser Leu Asn Arg Asn
 165 170 175
 Gln Trp Glu Ser Leu Val Cys Leu Val Gln Pro Ile Leu Ser Lys Gly
 180 185 190
 Arg Lys Lys Ile Val Lys Arg Gly Ser Phe Asn Ile Phe Tyr Ala Lys
 195 200 205
 Glu Tyr Arg Ala Thr Leu Glu Phe Tyr Trp Ala Pro Phe Leu Val Glu
 210 215 220
 Ser Asn Ser Asp Asn Pro Asn Phe His His Ile Asp Gln Arg Ile Ile
 225 230 235 240
 Ser Pro Glu Arg Ile Glu Ser His Ala Asn Trp Lys Asp Val Asp
 245 250 255
 Tyr Leu Ile Phe Asn Thr Tyr Ile Trp Trp Met Asn Asn Glu Asp Ile
 260 265 270
 Lys Val Arg Arg Pro Asn Ser Thr Ser Trp Ser Asp His Asp Glu Val
 275 280 285
 Pro Arg Ile Glu Thr Tyr Gly Arg Val Phe Lys Thr Trp Ser Thr Trp
 290 295 300
 Leu Glu Gln Asn Val Asp Pro Ala Arg Thr Ser Val Phe Phe Met Thr
 305 310 315 320
 Ile Ser Pro Leu His Asn Ser Pro Ala Gln Trp Gly Asn Pro Asn Gly
 325 330 335
 Ile Lys Cys Val Lys Glu Thr Leu Pro Val Leu Asn Tyr Thr Lys Pro
 340 345 350
 Leu Asp Leu Asn His Asp Met Arg Met Tyr Asp Leu Val Ala Lys Val
 355 360 365
 Ala Lys Asn Met Lys Asn Val Pro Val Ser Leu Ile Asp Ile Thr Arg
 370 375 380
 Met Ser Asp Tyr Arg Lys Asp Ala His Thr Ser Leu Tyr Ser Ile Arg
 385 390 395 400
 Gln Gly Lys Leu Leu Thr Pro Glu Gln Lys Ala Asp Pro Gln Lys Tyr

PF59082SeqList_PF59082.txt

Ala Asp Cys Ile His Trp Cys Leu Pro Gly Val Pro Asp Val Trp Asn
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 His Pro Ser Leu Pro Pro Gln
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<220>
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 ccg agc agg agg gcg cag gtg gcg gcg gtg ttc gcg ctc gcg ctg ctg 96
 Pro Ser Arg Arg Ala Gln Val Ala Ala Val Phe Ala Leu Ala Leu Leu
 20 25 30
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 Leu Gly Val Ser Val Leu Tyr Asp Ser Ala His Ile Ala Ala Ser Leu
 35 40 45
 cgc cgc cac ggc gtc ggc ggc ggc ggg agt agc ggc ggc gga gga gga 192
 Arg Arg His Gly Val Gly Gly Gly Gly Ser Ser Gly Gly Gly Gly Gly
 50 55 60
 gga gga gga gac ggc gcc cgc gcc tac aca aac acc aag ctc tcc gcc 240
 Gly Gly Gly Asp Gly Ala Arg Ala Tyr Thr Asn Thr Lys Leu Ser Ala
 65 70 75 80
 acg acg gag gag gcg gag gcg gag gcg gcc gag gtg cgc tcc cca ccg 288
 Thr Thr Glu Glu Ala Glu Ala Glu Ala Glu Val Arg Ser Pro Pro
 85 90 95
 gcg cag ggg gtc gaa tcg gcg gtg gag gcg acg gat cgg ggc gag gct 336
 Ala Gln Gly Val Glu Ser Ala Val Glu Ala Thr Asp Arg Gly Glu Ala
 100 105 110
 cca ccg gag cag ccg gtg gcc gcg gac tcc gga gcg tcg tca gcc gag 384
 Pro Pro Glu Gln Pro Val Ala Ala Asp Ser Gly Ala Ser Ser Ala Glu
 115 120 125
 acc ccg ccg tct ctg ctg gag cag gtg acg gag acg ccg ccg ccg tcg 432
 Thr Pro Pro Ser Leu Leu Glu Gln Val Thr Glu Thr Pro Pro Pro Ser
 130 135 140
 ccg tcg tcg tcg tcg gcg gcg gcg gcg gcg gcg gag gcg cag gtg gga 480
 Pro Ser Ser Ser Ser Ala Ala Ala Ala Ala Ala Glu Ala Gln Val Gly
 145 150 155 160
 ggg gat cac ggt ggc gag agc tgc gac gtg tac aag ggg agg tgg gtg 528
 Gly Asp His Gly Gly Glu Ser Cys Asp Val Tyr Lys Gly Arg Trp Val
 165 170 175
 tac gac gag gcg aac gcg ccg ctg tac aag gag tcc gcc tgc gag ttc 576
 Tyr Asp Glu Ala Asn Ala Pro Leu Tyr Lys Glu Ser Ala Cys Glu Phe
 180 185 190
 ctc acc gag cag gtc acc tgc atg cgc aac ggc cgc gcg gac gac 624
 Leu Thr Glu Gln Val Thr Cys Met Arg Asn Gly Arg Arg Asp Asp Asp
 195 200 205
 tac cag aaa tgg cgg tgg cag ccc gac ggc tgc gac ctc ccc aga ttt 672
 Tyr Gln Lys Trp Arg Trp Gln Pro Asp Gly Cys Asp Leu Pro Arg Phe
 210 215 220
 gac gct aag ttg ctc ctg gag aaa ctg agg aac aaa cga ctg atg ttt 720
 Asp Ala Lys Leu Leu Leu Glu Lys Leu Arg Asn Lys Arg Leu Met Phe
 225 230 235 240
 gtg ggg gat tcg ctg aat cgg aac caa tgg gag tcc atg gtg tgc ctt 768
 Val Gly Asp Ser Leu Asn Arg Asn Gln Trp Glu Ser Met Val Cys Leu
 245 250 255
 gtc caa tct gag gct ccc tgg gag aag aaa tca ctt gtc aag aat gac 816
 Val Gln Ser Glu Ala Pro Trp Glu Lys Lys Ser Leu Val Lys Asn Asp
 260 265 270

PF59082SeqList_PF59082.txt

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		275					280					285				
tat	tgg	tca	cct	ttt	cta	gtt	gag	tca	aac	tca	gat	gat	cca	aac	atg	912
Tyr	Trp	Ser	Pro	Phe	Leu	Val	Glu	Ser	Asn	Ser	Asp	Asp	Pro	Asn	Met	
	290					295					300					
cat	agc	atc	gtt	gac	cgc	ata	atc	aag	cca	aca	tca	att	gca	aaa	cat	960
His	Ser	Ile	Val	Asp	Arg	Ile	Ile	Lys	Pro	Thr	Ser	Ile	Ala	Lys	His	
	305				310					315					320	
gca	gcg	aat	tgg	gaa	ggg	gtg	gac	tac	ttg	att	ttc	aac	act	tat	att	1008
Ala	Ala	Asn	Trp	Glu	Gly	Val	Asp	Tyr	Leu	Ile	Phe	Asn	Thr	Tyr	Ile	
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Trp	Trp	Met	Asn	Thr	Pro	Glu	Met	Lys	Ile	Leu	His	Gly	Gly	Ser	Phe	
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Ser	Lys	Lys	Pro	Val	Lys	Tyr	Asp	Glu	Met	Glu	Arg	Val	Ala	Ala	Tyr	
		355					360					365				
cgg	aag	gtc	ctc	aag	aca	tgg	tct	aga	tgg	gta	gaa	aag	cat	gta	gat	1152
Arg	Lys	Val	Leu	Lys	Thr	Trp	Ser	Arg	Trp	Val	Glu	Lys	His	Val	Asp	
	370					375					380					
ccg	aaa	aga	agt	aca	gtc	ttc	ttc	atg	agt	gtc	tca	cct	gtg	cat	atg	1200
Pro	Lys	Arg	Ser	Thr	Val	Phe	Phe	Met	Ser	Val	Ser	Pro	Val	His	Met	
	385				390					395					400	
cag	agc	gag	ggc	tgg	gga	aaa	cca	gat	gcc	ata	aaa	tgc	ttc	tct	gag	1248
Gln	Ser	Glu	Gly	Trp	Gly	Lys	Pro	Asp	Ala	Ile	Lys	Cys	Phe	Ser	Glu	
				405					410					415		
acg	cag	cca	gct	atc	aat	tac	aca	aag	aaa	ttg	gag	gtg	ggc	acg	gac	1296
Thr	Gln	Pro	Ala	Ile	Asn	Tyr	Thr	Lys	Lys	Leu	Glu	Val	Gly	Thr	Asp	
			420					425					430			
tgg	gat	ctg	ttc	tcg	aca	gct	cat	cac	gta	acg	aag	gct	atg	aag	agg	1344
Trp	Asp	Leu	Phe	Ser	Thr	Ala	His	His	Val	Thr	Lys	Ala	Met	Lys	Arg	
		435					440					445				
gtg	cca	gtg	cac	ttc	atc	aac	ata	acg	gcg	ttg	tca	gag	atc	cgc	aag	1392
Val	Pro	Val	His	Phe	Ile	Asn	Ile	Thr	Ala	Leu	Ser	Glu	Ile	Arg	Lys	
	450					455					460					
gac	gcg	cac	aca	tcg	aag	gcg	aac	ccc	cg	aag	ttc	gcg	gac	tgc	atc	1440
Asp	Ala	His	Thr	Ser	Lys	Ala	Asn	Pro	Arg	Lys	Phe	Ala	Asp	Cys	Ile	
	465				470					475					480	
cac	tgg	tgc	cta	cct	ggg	ttg	cca	gac	aca	tgg	aac	gag	ttc	att	tac	1488
His	Trp	Cys	Leu	Pro	Gly	Leu	Pro	Asp	Thr	Trp	Asn	Glu	Phe	Ile	Tyr	
				485					490					495		
ggg	cac	atc	gtc	tcg	agc	cct	caa	agg	agg	ccg	gtt	gag	ccg	att	gag	1536
Gly	His	Ile	Val	Ser	Ser	Pro	Gln	Arg	Arg	Pro	Val	Glu	Pro	Ile	Glu	
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Asn	Gln	Pro	Gln	Arg												
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<211> 517

<212> PRT

<213> Oryza sativa

<400> 1681

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Pro	Ser	Arg	Arg	Ala	Gln	Val	Ala	Ala	Val	Phe	Ala	Leu	Ala	Leu	Leu	
			20					25					30			
Leu	Gly	Val	Ser	Val	Leu	Tyr	Asp	Ser	Ala	His	Ile	Ala	Ala	Ser	Leu	
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Arg	Arg	His	Gly	Val	Gly	Gly	Gly	Gly	Ser	Ser	Gly	Gly	Gly	Gly	Gly	
	50				55					60						
Gly	Gly	Gly	Asp	Gly	Ala	Arg	Ala	Tyr	Thr	Asn	Thr	Lys	Leu	Ser	Ala	
	65				70					75					80	
Thr	Thr	Glu	Glu	Ala	Glu	Ala	Glu	Ala	Ala	Glu	Val	Arg	Ser	Pro	Pro	
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Ala	Gln	Gly	Val	Glu	Ser	Ala	Val	Glu	Ala	Thr	Asp	Arg	Gly	Glu	Ala	
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PF59082SeqList_PF59082.txt

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 Thr Pro Pro Ser Leu Leu Glu Gln Val Thr Glu Thr Pro Pro Pro Ser
 130 135 140
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 145 150 155 160
 Gly Asp His Gly Gly Glu Ser Cys Asp Val Tyr Lys Gly Arg Trp Val
 165 170 175
 Tyr Asp Glu Ala Asn Ala Pro Leu Tyr Lys Glu Ser Ala Cys Glu Phe
 180 185 190
 Leu Thr Glu Gln Val Thr Cys Met Arg Asn Gly Arg Arg Asp Asp Asp
 195 200 205
 Tyr Gln Lys Trp Arg Trp Gln Pro Asp Gly Cys Asp Leu Pro Arg Phe
 210 215 220
 Asp Ala Lys Leu Leu Leu Glu Lys Leu Arg Asn Lys Arg Leu Met Phe
 225 230 235 240
 Val Gly Asp Ser Leu Asn Arg Asn Gln Trp Glu Ser Met Val Cys Leu
 245 250 255
 Val Gln Ser Glu Ala Pro Trp Glu Lys Lys Ser Leu Val Lys Asn Asp
 260 265 270
 Ser Leu Asn Val Phe Arg Leu Glu Glu Tyr Asn Ala Thr Ile Glu Phe
 275 280 285
 Tyr Trp Ser Pro Phe Leu Val Glu Ser Asn Ser Asp Asp Pro Asn Met
 290 295 300
 His Ser Ile Val Asp Arg Ile Ile Lys Pro Thr Ser Ile Ala Lys His
 305 310 315 320
 Ala Ala Asn Trp Glu Gly Val Asp Tyr Leu Ile Phe Asn Thr Tyr Ile
 325 330 335
 Trp Trp Met Asn Thr Pro Glu Met Lys Ile Leu His Gly Gly Ser Phe
 340 345 350
 Ser Lys Lys Pro Val Lys Tyr Asp Glu Met Glu Arg Val Ala Ala Tyr
 355 360 365
 Arg Lys Val Leu Lys Thr Trp Ser Arg Trp Val Glu Lys His Val Asp
 370 375 380
 Pro Lys Arg Ser Thr Val Phe Phe Met Ser Val Ser Pro Val His Met
 385 390 395 400
 Gln Ser Glu Gly Trp Gly Lys Pro Asp Ala Ile Lys Cys Phe Ser Glu
 405 410 415
 Thr Gln Pro Ala Ile Asn Tyr Thr Lys Lys Leu Glu Val Gly Thr Asp
 420 425 430
 Trp Asp Leu Phe Ser Thr Ala His His Val Thr Lys Ala Met Lys Arg
 435 440 445
 Val Pro Val His Phe Ile Asn Ile Thr Ala Leu Ser Glu Ile Arg Lys
 450 455 460
 Asp Ala His Thr Ser Lys Ala Asn Pro Arg Lys Phe Ala Asp Cys Ile
 465 470 475 480
 His Trp Cys Leu Pro Gly Leu Pro Asp Thr Trp Asn Glu Phe Ile Tyr
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 Gly His Ile Val Ser Ser Pro Gln Arg Arg Pro Val Glu Pro Ile Glu
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 Asn Gln Pro Gln Arg
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 <212> DNA
 <213> Arabidopsis thaliana

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 <222> (49)..(1275)

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57

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105

PF59082SeqList_PF59082.txt

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gac	ttc	aca	tct	tcg	aac	cca	ttc	tct	agt	tca	ttt	gtg	gag	ttg	ccg	201
Asp	Phe	Thr	Ser	Ser	Asn	Pro	Phe	Ser	Ser	Ser	Phe	Val	Glu	Leu	Pro	
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ccg	gat	gag	tgt	gat	ctg	ttc	acc	ggg	caa	tgg	gtt	ttc	gac	aac	aag	249
Pro	Asp	Glu	Cys	Asp	Leu	Phe	Thr	Gly	Gln	Trp	Val	Phe	Asp	Asn	Lys	
			55					60					65			
aca	tat	cca	ttg	tat	aaa	gaa	gaa	gag	tgt	gag	ttc	ttg	acg	gag	caa	297
Thr	Tyr	Pro	Leu	Tyr	Lys	Glu	Glu	Glu	Cys	Glu	Phe	Leu	Thr	Glu	Gln	
			70				75					80				
gtg	act	tgt	tta	aga	aac	gga	agg	aaa	gat	tct	ttg	ttt	cag	aat	tgg	345
Val	Thr	Cys	Leu	Arg	Asn	Gly	Arg	Lys	Asp	Ser	Leu	Phe	Gln	Asn	Trp	
	85					90					95					
aga	ttg	caa	cct	agg	gac	tgt	tct	tta	cca	aaa	ttc	aat	gca	aga	gtg	393
Arg	Trp	Gln	Pro	Arg	Asp	Cys	Ser	Leu	Pro	Lys	Phe	Asn	Ala	Arg	Val	
100					105					110					115	
ttg	tta	gag	aag	ctg	agg	aac	aag	aga	ttg	atg	ttt	gtc	ggg	gac	tcg	441
Leu	Leu	Glu	Lys	Leu	Arg	Asn	Lys	Arg	Leu	Met	Phe	Val	Gly	Asp	Ser	
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tta	aac	cgg	aac	caa	tgg	gaa	tca	atg	gtt	tgt	ttg	gtt	caa	tca	gtg	489
Leu	Asn	Arg	Asn	Gln	Trp	Glu	Ser	Met	Val	Cys	Leu	Val	Gln	Ser	Val	
			135					140					145			
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Ile	Pro	Pro	Gly	Arg	Lys	Ser	Leu	Asn	Gln	Thr	Gly	Ser	Leu	Thr	Val	
		150					155					160				
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Phe	Lys	Ile	Gln	Asp	Tyr	Asn	Ala	Thr	Val	Glu	Phe	Tyr	Trp	Ala	Pro	
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Phe	Leu	Val	Glu	Ser	Asn	Ser	Asp	Asp	Pro	Glu	Lys	His	Ser	Ile	Ile	
180					185					190					195	
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Asp	Arg	Ile	Ile	Met	Pro	Glu	Ser	Ile	Glu	Lys	His	Gly	Val	Asn	Trp	
				200					205					210		
ata	ggc	gtt	gac	ttt	ctt	gtc	ttc	aat	agt	tac	atc	tgg	tgg	atg	aat	729
Ile	Gly	Val	Asp	Phe	Leu	Val	Phe	Asn	Ser	Tyr	Ile	Trp	Trp	Met	Asn	
			215					220					225			
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Thr	Val	Ser	Ile	Lys	Val	Leu	Arg	Gly	Ser	Phe	Asp	Asp	Gly	Asp	Thr	
		230					235					240				
gag	tat	gat	gag	atc	aaa	cgg	cca	ata	gcg	tac	gag	agg	gtg	ttg	agg	825
Glu	Tyr	Asp	Glu	Ile	Lys	Arg	Pro	Ile	Ala	Tyr	Glu	Arg	Val	Leu	Arg	
	245					250					255					
aca	ttg	gga	gat	tgg	gtg	gac	cat	aac	att	gat	cct	cta	agt	aca	act	873
Thr	Leu	Gly	Asp	Trp	Val	Asp	His	Asn	Ile	Asp	Pro	Leu	Ser	Thr	Thr	
260					265					270					275	
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Val	Phe	Phe	Met	Ser	Met	Ser	Pro	Leu	His	Ile	Lys	Ser	Ser	Asp	Trp	
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Ala	Asn	Pro	Glu	Gly	Ile	Arg	Cys	Ala	Leu	Glu	Thr	Thr	Pro	Ile	Leu	
			295					300					305			
aac	atg	tct	ttc	aac	gtg	gct	tac	ggg	cag	ttt	tcc	gcg	gtg	ggg	acg	1017
Asn	Met	Ser	Phe	Asn	Val	Ala	Tyr	Gly	Gln	Phe	Ser	Ala	Val	Gly	Thr	
		310					315					320				
gat	tac	agg	ctg	ttt	ccg	gtg	gcg	gaa	aac	gtt	aca	cag	tct	cta	aaa	1065
Asp	Tyr	Arg	Leu	Phe	Pro	Val	Ala	Glu	Asn	Val	Thr	Gln	Ser	Leu	Lys	
	325					330					335					
gtt	cct	att	cat	ttc	ctc	aac	att	act	gca	ttg	tct	gag	tat	cgt	aaa	1113
Val	Pro	Ile	His	Phe	Leu	Asn	Ile	Thr	Ala	Leu	Ser	Glu	Tyr	Arg	Lys	
340					345					350					355	
gat	gca	cat	act	tcg	gtt	tac	acg	atc	aag	caa	ggc	aag	ttg	ctg	acg	1161
Asp	Ala	His	Thr	Ser	Val	Tyr	Thr	Ile	Lys	Gln	Gly	Lys	Leu	Leu	Thr	
				360					365					370		
cgg	gag	cag	caa	aac	gat	cca	gcc	aat	ttt	gct	gat	tgc	ata	cac	tgg	1209
Arg	Glu	Gln	Gln	Asn	Asp	Pro	Ala	Asn	Phe	Ala	Asp	Cys	Ile	His	Trp	
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PF59082SeqList_PF59082.txt
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 Cys Leu Pro Gly Leu Pro Asp Thr Trp Asn Glu Phe Leu Tyr Thr His
 390 395 400
 att att tct cga aga tgagattcctt tcatacctctt ttttggttta aaaaaattct 1312
 Ile Ile Ser Arg Arg
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 <212> PRT
 <213> Arabidopsis thaliana

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 Ser Ile Ala Asp Phe Thr Ser Ser Asn Pro Phe Ser Ser Phe Val
 35 40 45
 Glu Leu Pro Pro Asp Glu Cys Asp Leu Phe Thr Gly Gln Trp Val Phe
 50 55 60
 Asp Asn Lys Thr Tyr Pro Leu Tyr Lys Glu Glu Cys Glu Phe Leu
 65 70 75 80
 Thr Glu Gln Val Thr Cys Leu Arg Asn Gly Arg Lys Asp Ser Leu Phe
 85 90 95
 Gln Asn Trp Arg Trp Gln Pro Arg Asp Cys Ser Leu Pro Lys Phe Asn
 100 105 110
 Ala Arg Val Leu Leu Glu Lys Leu Arg Asn Lys Arg Leu Met Phe Val
 115 120 125
 Gly Asp Ser Leu Asn Arg Asn Gln Trp Glu Ser Met Val Cys Leu Val
 130 135 140
 Gln Ser Val Ile Pro Pro Gly Arg Lys Ser Leu Asn Gln Thr Gly Ser
 145 150 155 160
 Leu Thr Val Phe Lys Ile Gln Asp Tyr Asn Ala Thr Val Glu Phe Tyr
 165 170 175
 Trp Ala Pro Phe Leu Val Glu Ser Asn Ser Asp Asp Pro Glu Lys His
 180 185 190
 Ser Ile Ile Asp Arg Ile Ile Met Pro Glu Ser Ile Glu Lys His Gly
 195 200 205
 Val Asn Trp Ile Gly Val Asp Phe Leu Val Phe Asn Ser Tyr Ile Trp
 210 215 220
 Trp Met Asn Thr Val Ser Ile Lys Val Leu Arg Gly Ser Phe Asp Asp
 225 230 235 240
 Gly Asp Thr Glu Tyr Asp Glu Ile Lys Arg Pro Ile Ala Tyr Glu Arg
 245 250 255
 Val Leu Arg Thr Leu Gly Asp Trp Val Asp His Asn Ile Asp Pro Leu
 260 265 270
 Ser Thr Thr Val Phe Phe Met Ser Met Ser Pro Leu His Ile Lys Ser
 275 280 285
 Ser Asp Trp Ala Asn Pro Glu Gly Ile Arg Cys Ala Leu Glu Thr Thr
 290 295 300
 Pro Ile Leu Asn Met Ser Phe Asn Val Ala Tyr Gly Gln Phe Ser Ala
 305 310 315 320
 Val Gly Thr Asp Tyr Arg Leu Phe Pro Val Ala Glu Asn Val Thr Gln
 325 330 335
 Ser Leu Lys Val Pro Ile His Phe Leu Asn Ile Thr Ala Leu Ser Glu
 340 345 350
 Tyr Arg Lys Asp Ala His Thr Ser Val Tyr Thr Ile Lys Gln Gly Lys
 355 360 365
 Leu Leu Thr Arg Glu Gln Gln Asn Asp Pro Ala Asn Phe Ala Asp Cys
 370 375 380
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PF59082SeqList_PF59082.txt

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<211> 1590
<212> DNA
<213> Zea mays

<220>
<221> CDS
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<400> 1684

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aag	cag	ccg	gcc	gcg	cgc	agg	ccc	acg	gcg	cgg	ctg	tcg	ctc	gcg	ggc	96
Lys	Gln	Pro	Ala	Ala	Arg	Arg	Pro	Thr	Ala	Arg	Leu	Ser	Leu	Ala	Gly	
			20					25					30			
ctc	gtc	gtc	tcc	atc	ttc	ctc	gtc	gcc	acc	ttc	ctg	tac	aac	gag	gac	144
Leu	Val	Val	Ser	Ile	Phe	Leu	Val	Ala	Thr	Phe	Leu	Tyr	Asn	Glu	Asp	
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gtg	gtg	aag	gcg	gcc	tcc	ggc	tcc	tcc	agc	tca	gca	aca	gac	gac		192
Val	Val	Lys	Ala	Ala	Ser	Gly	Ser	Ser	Ser	Ser	Ala	Thr	Thr	Ala	Asp	
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gcc	gct	gag	gta	ggc	gtc	tcc	ggg	cgg	gcg	agg	tca	ccc	gac	cta	agg	240
Ala	Ala	Glu	Val	Gly	Val	Ser	Gly	Arg	Ala	Arg	Ser	Pro	Asp	Leu	Arg	
65				70						75				80		
gtg	ctg	cag	gag	gcg	gcg	cac	cag	ggg	gtg	gaa	gct	gag	gag	cgg	gag	288
Val	Leu	Gln	Glu	Ala	Ala	His	Gln	Gly	Val	Glu	Ala	Glu	Glu	Arg	Glu	
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Val	Gly	Asp	Arg	Thr	Glu	Ala	Glu	Gln	Lys	Gln	Lys	Pro	Leu	Thr	Leu	
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ccc	atc	ccc	atc	ccc	gtg	gtg	gcg	ctg	gcg	gag	gag	gaa	ctc	gtg	gag	384
Pro	Ile	Pro	Ile	Pro	Val	Val	Ala	Leu	Ala	Glu	Glu	Glu	Leu	Val	Glu	
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aat	act	aag	gga	agg	cag	aag	cag	cag	cag	cag	gag	gag	gag	caa	acc	432
Asn	Thr	Lys	Gly	Arg	Gln	Lys	Gln	Gln	Gln	Gln	Glu	Glu	Glu	Gln	Thr	
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Gln	Lys	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Gln	Val	Ala	Gly	Cys	
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gac	ctg	tac	cgg	ggt	cgg	tgg	acg	ttc	gac	gcg	gcc	ggc	gag	cag	gcg	528
Asp	Leu	Tyr	Arg	Gly	Arg	Trp	Thr	Phe	Asp	Ala	Ala	Gly	Glu	Gln	Ala	
			165				170						175			
ccg	ctg	tac	cgc	gag	tcg	gag	tgc	gag	ttc	ctg	acg	gag	cag	gtg	acg	576
Pro	Leu	Tyr	Arg	Glu	Ser	Glu	Cys	Glu	Phe	Leu	Thr	Glu	Gln	Val	Thr	
			180				185						190			
tgc	atg	cgc	aac	ggc	cgc	cgc	gac	gac	tcg	tac	cag	aag	tgg	cgg	tgg	624
Cys	Met	Arg	Asn	Gly	Arg	Arg	Asp	Asp	Ser	Tyr	Gln	Lys	Trp	Arg	Trp	
			195				200					205				
cag	ccc	gat	gga	tgc	gac	ctg	ccc	agg	tac	gat	gct	cgg	ttg	ctg	ctt	672
Gln	Pro	Asp	Gly	Cys	Asp	Leu	Pro	Arg	Tyr	Asp	Ala	Arg	Leu	Leu	Leu	
			210			215					220					
gag	cgg	ctg	cgc	aac	aag	cgg	ctc	atg	ttc	gtg	ggt	gac	tcg	ctg	aac	720
Glu	Arg	Leu	Arg	Asn	Lys	Arg	Leu	Met	Phe	Val	Gly	Asp	Ser	Leu	Asn	
225					230					235				240		
cgc	aac	cag	tgg	gag	tcc	atg	gtg	tgc	ctg	gtg	cag	tct	gtg	gtg	ccc	768
Arg	Asn	Gln	Trp	Glu	Ser	Met	Val	Cys	Leu	Val	Gln	Ser	Val	Val	Pro	
			245				250						255			
tgg	ggc	cac	aag	acg	ctg	cac	aag	ttc	gtc	aac	aac	gga	tcg	ctc	aac	816
Trp	Gly	His	Lys	Thr	Leu	His	Lys	Phe	Val	Asn	Asn	Gly	Ser	Leu	Asn	
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Val	Phe	Thr	Ala	His	Asp	Tyr	Asn	Ala	Thr	Val	Glu	Phe	Tyr	Trp	Ala	
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Pro	Phe	Leu	Val	Glu	Ser	Asn	Ser	Asp	Asp	Pro	Gln	Ala	His	Ser	Val	
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Met	Asn	Arg	Val	Ile	Ala	Trp	Arg	Ala	Ile	Ala	Lys	His	Ala	Lys	Asn	

PF59082SeqList_PF59082.txt

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Trp Lys Gly Val Asp		325		330		335	
aac aca ttc gag atg aaa gtc att cgc cgt cat cag cat cag ctt gaa		Asn Thr Phe Glu Met Lys Val Ile Arg His Gln His Gln Leu Glu					1056
340		345		350			
aag gag gag gag ggg gtg agg tgg agc aag tac gcc ctt gtg gac cgg		Lys Glu Glu Glu Gly Val Arg Trp Ser Lys Tyr Ala Leu Val Asp Arg					1104
355		360		365			
ccg gtg gcg tac cgg gag gtg ctc aag acg tgg gcc agg tgg gtg gac		Pro Val Ala Tyr Arg Glu Val Leu Lys Thr Trp Ala Arg Trp Val Asp					1152
370		375		380			
cgc cac atc gac ccc aac cga aca aga gtc ttc ttc atg ggc atg tcg		Arg His Ile Asp Pro Asn Arg Thr Arg Val Phe Phe Met Gly Met Ser					1200
385		390		395		400	
ccc aac cac gtc acg ccg tgg gcg tgg ggt aac gac ggc ggc atc aag		Pro Asn His Val Thr Pro Trp Ala Trp Gly Asn Asp Gly Gly Ile Lys					1248
405		410		415			
tgc gcc atg gag acg cag ccc atc agc aac aac cgg acg ggg cga ctg		Cys Ala Met Glu Thr Gln Pro Ile Ser Asn Asn Arg Thr Gly Arg Leu					1296
420		425		430			
gac atc ggc acg gat tgg cgc ctg cac ggc gtg gcg cgc ggg gtg ctg		Asp Ile Gly Thr Asp Trp Arg Leu His Gly Val Ala Arg Gly Val Leu					1344
435		440		445			
gcg cgc tac ctc cgc cgc gtg ccg gtg cac ttc gtc gac atc acg ggg		Ala Arg Tyr Leu Arg Arg Val Pro Val His Phe Val Asp Ile Thr Gly					1392
450		455		460			
ctg tcg gag ctg cgc aag gac gcg cac acc tcc gtg cac acg ctg cgg		Leu Ser Glu Leu Arg Lys Asp Ala His Thr Ser Val His Thr Leu Arg					1440
465		470		475		480	
cag ggg aag ctg ctc aca ccg gag cag cag gcc gac ccc aag acc tac		Gln Gly Lys Leu Leu Thr Pro Glu Gln Gln Ala Asp Pro Lys Thr Tyr					1488
485		490		495			
gcc gac tgc atc cag tgg tgc ctc ccg gga ctc ccc gac acc tgg aac		Ala Asp Cys Ile His Trp Cys Leu Pro Gly Leu Pro Asp Thr Trp Asn					1536
500		505		510			
cac ttc ctc tac gcg cac atc ctc tcg ctc tcc tcg tcc gcc cag gat		His Phe Leu Tyr Ala His Ile Leu Ser Leu Ser Ser Ser Ala Gln Asp					1584
515		520		525			
cac taa							1590
His							

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 <213> Zea mays

<400> 1685
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 35 40 45
 Val Val Lys Ala Ala Ser Gly Ser Ser Ser Ser Ala Thr Thr Ala Asp
 50 55 60
 Ala Ala Glu Val Gly Val Ser Gly Arg Ala Arg Ser Pro Asp Leu Arg
 65 70 75 80
 Val Leu Gln Glu Ala Ala His Gln Gly Val Glu Ala Glu Glu Arg Glu
 85 90 95
 Val Gly Asp Arg Thr Glu Ala Glu Gln Lys Gln Lys Pro Leu Thr Leu
 100 105 110
 Pro Ile Pro Ile Pro Val Val Ala Leu Ala Glu Glu Glu Leu Val Glu
 115 120 125
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 130 135 140
 Gln Lys Pro Pro Pro Pro Pro Pro Pro Pro Pro Val Ala Gly Cys

PF59082SeqList_PF59082.txt

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 165 170 175
 Pro Leu Tyr Arg Glu Ser Glu Cys Glu Phe Leu Thr Glu Gln Val Thr
 180 185 190
 Cys Met Arg Asn Gly Arg Arg Asp Ser Tyr Gln Lys Trp Arg Trp
 195 200 205
 Gln Pro Asp Gly Cys Asp Leu Pro Arg Tyr Asp Ala Arg Leu Leu Leu
 210 215 220
 Glu Arg Leu Arg Asn Lys Arg Leu Met Phe Val Gly Asp Ser Leu Asn
 225 230 235 240
 Arg Asn Gln Trp Glu Ser Met Val Cys Leu Val Gln Ser Val Val Pro
 245 250 255
 Trp Gly His Lys Thr Leu His Lys Phe Val Asn Asn Gly Ser Leu Asn
 260 265 270
 Val Phe Thr Ala His Asp Tyr Asn Ala Thr Val Glu Phe Tyr Trp Ala
 275 280 285
 Pro Phe Leu Val Glu Ser Asn Ser Asp Asp Pro Gln Ala His Ser Val
 290 295 300
 Met Asn Arg Val Ile Ala Trp Arg Ala Ile Ala Lys His Ala Lys Asn
 305 310 315 320
 Trp Lys Gly Val Asp Tyr Leu Val Phe Asn Ser Tyr Ile Trp Trp Leu
 325 330 335
 Asn Thr Phe Glu Met Lys Val Ile Arg Arg His Gln His Gln Leu Glu
 340 345 350
 Lys Glu Glu Glu Gly Val Arg Trp Ser Lys Tyr Ala Leu Val Asp Arg
 355 360 365
 Pro Val Ala Tyr Arg Glu Val Leu Lys Thr Trp Ala Arg Trp Val Asp
 370 375 380
 Arg His Ile Asp Pro Asn Arg Thr Arg Val Phe Phe Met Gly Met Ser
 385 390 395 400
 Pro Asn His Val Thr Pro Trp Ala Trp Gly Asn Asp Gly Gly Ile Lys
 405 410 415
 Cys Ala Met Glu Thr Gln Pro Ile Ser Asn Asn Arg Thr Gly Arg Leu
 420 425 430
 Asp Ile Gly Thr Asp Trp Arg Leu His Gly Val Ala Arg Gly Val Leu
 435 440 445
 Ala Arg Tyr Leu Arg Arg Val Pro Val His Phe Val Asp Ile Thr Gly
 450 455 460
 Leu Ser Glu Leu Arg Lys Asp Ala His Thr Ser Val His Thr Leu Arg
 465 470 475 480
 Gln Gly Lys Leu Leu Thr Pro Glu Gln Gln Ala Asp Pro Lys Thr Tyr
 485 490 495
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 515 520 525
 His

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 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (1)..(1545)

<400> 1686
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 Val Pro Ser Arg Ala Gln Val Ala Val Phe Ala Leu Ala Thr
 20 25 30
 ctg ctg ggg gtc tcc gtg ctc tac gac gcc gcc cac atc gcc gcc tcg 144
 Leu Leu Gly Val Ser Val Leu Tyr Asp Ala Ala His Ile Ala Ala Ser
 35 40 45

PF59082SeqList_PF59082.txt																	
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gac	ggc	gcc	gcc	tcc	gtc	tcc	ggc	gtc	gcg	agg	gag	gag	gtg	gcg	gcc	240	
Asp	Gly	Ala	Ala	Ser	Val	Ser	Gly	Val	Ala	Arg	Glu	Glu	Val	Ala	Ala		
65					70					75					80		
gta	gag	acg	ctc	gcg	ccg	ccg	gcg	agg	gca	gtg	ggg	tct	gac	ggc	gcg	288	
Val	Glu	Thr	Leu	Ala	Pro	Pro	Ala	Arg	Ala	Val	Gly	Ser	Asp	Gly	Ala		
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gat	cgg	acc	gac	ccg	ccc	ccg	cac	gag	cag	cag	gag	gag	gcc	gag	gag	336	
Asp	Arg	Thr	Asp	Pro	Pro	Pro	His	Glu	Gln	Gln	Glu	Glu	Ala	Glu	Glu		
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Gly	Ala	Ala	Lys	Pro	Gly	Ala	Ser	Leu	Gln	Gln	Asp	Ala	Pro	Leu	Thr		
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Glu	Glu	Val	Val	Glu	Gly	Gly	Ser	Gly	Gly	His	Gly	Gly	Gly	Gly	Ser		
	130				135						140						
cag	gag	cag	gag	cag	gat	cag	gcc	cag	ggg	acc	tgc	gac	ctg	tac	aag	480	
Gln	Glu	Gln	Glu	Gln	Asp	Gln	Ala	Gln	Gly	Thr	Cys	Asp	Leu	Tyr	Lys		
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Gly	Arg	Trp	Val	Tyr	Asp	Glu	Ser	Arg	Ala	Pro	Leu	Tyr	Lys	Glu	Ser		
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gag	tgc	agc	ttc	ctc	acg	gag	cag	gtc	acc	tgc	acg	cgc	aac	ggc	cgc	576	
Glu	Cys	Ser	Phe	Leu	Thr	Glu	Gln	Val	Thr	Cys	Thr	Arg	Asn	Gly	Arg		
			180					185					190				
cgc	gac	gac	gac	tac	cag	aag	tgg	cgc	tgg	cag	ccc	gac	ggc	tgc	gac	624	
Arg	Asp	Asp	Asp	Tyr	Gln	Lys	Trp	Arg	Trp	Gln	Pro	Asp	Gly	Cys	Asp		
		195					200				205						
ctc	ccc	aga	ttt	gag	gct	aag	ttg	ctt	ctg	gag	aag	cta	agg	aac	aaa	672	
Leu	Pro	Arg	Phe	Glu	Ala	Lys	Leu	Leu	Leu	Glu	Lys	Leu	Arg	Asn	Lys		
	210					215					220						
agg	ctg	atg	ttt	gtg	ggt	gat	tct	ctg	aat	cgg	aac	cag	tgg	gag	tcc	720	
Arg	Leu	Met	Phe	Val	Gly	Asp	Ser	Leu	Asn	Arg	Asn	Gln	Trp	Glu	Ser		
225					230				235						240		
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Met	Val	Cys	Leu	Val	Gln	Ser	Glu	Ala	Pro	Trp	Asp	Lys	Lys	Ser	Leu		
				245					250					255			
gtc	aag	aat	ggt	tct	ctt	aat	gtc	ttc	cat	ctt	cag	gag	tac	aat	gca	816	
Val	Lys	Asn	Gly	Ser	Leu	Asn	Val	Phe	His	Leu	Gln	Glu	Tyr	Asn	Ala		
			260					265					270				
aca	gtt	gag	ttc	tac	tgg	gct	ccg	ttc	cta	gtg	gag	tca	aac	tca	gac	864	
Thr	Val	Glu	Phe	Tyr	Trp	Ala	Pro	Phe	Leu	Val	Glu	Ser	Asn	Ser	Asp		
		275					280					285					
gac	cca	gac	att	cac	agc	atc	agc	gac	cgc	atg	atc	aag	ccg	aca	tcg	912	
Asp	Pro	Asp	Ile	His	Ser	Ile	Ser	Asp	Arg	Met	Ile	Lys	Pro	Thr	Ser		
	290					295					300						
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Ile	Ala	Lys	His	Ala	Ala	Asn	Trp	Glu	Gly	Val	Asp	Tyr	Leu	Ile	Phe		
305					310					315					320		
aac	act	tac	att	tgg	tgg	atg	aac	aca	ccg	cag	atg	aaa	acc	gtg	cac	1008	
Asn	Thr	Tyr	Ile	Trp	Trp	Met	Asn	Thr	Pro	Gln	Met	Lys	Thr	Val	His		
				325					330					335			
ggt	gga	tct	ttc	tca	agg	aaa	cac	gta	aag	tac	gat	gaa	ata	gag	cgt	1056	
Gly	Gly	Ser	Phe	Ser	Arg	Lys	His	Val	Lys	Tyr	Asp	Glu	Ile	Glu	Arg		
			340					345					350				
gtg	gag	gca	tac	ccg	aag	gtc	ctc	aag	acg	tgg	tcc	aga	tgg	gta	gag	1104	
Val	Glu	Ala	Tyr	Arg	Lys	Val	Leu	Lys	Thr	Trp	Ser	Arg	Trp	Val	Glu		
		355					360					365					
gcg	cac	att	gat	ccc	aag	aga	agc	acg	gtc	cta	ttc	atg	agc	gtg	tca	1152	
Ala	His	Ile	Asp	Pro	Lys	Arg	Ser	Thr	Val	Leu	Phe	Met	Ser	Val	Ser		
				370		375					380						
ccg	gta	cat	atg	cag	agt	gaa	ggc	tgg	ggc	agc	ccc	aac	gcc	gta	aaa	1200	
Pro	Val	His	Met	Gln	Ser	Glu	Gly	Trp	Gly	Ser	Pro	Asn	Ala	Val	Lys		
					390				395						400		
tgc	ttc	tcc	gag	acg	cag	ccg	gcg	atc	aac	tac	acg	aag	aaa	ctg	gag	1248	
Cys	Phe	Ser	Glu	Thr	Gln	Pro	Ala	Ile	Asn	Tyr	Thr	Lys	Lys	Leu	Glu		
				405					410					415			

PF59082SeqList_PF59082.txt

gtg ggc acg gac tgg gac ctc ttc gcg gcc gcc cag cgc gtg acg agg	1296
Val Gly Thr Asp Trp Asp Leu Phe Ala Ala Ala Gln Arg Val Thr Arg	
	420
tcg atg gag aag gtg ccg gtg cgc ttc gtc gac gtg acc gcg ctg tcg	1344
Ser Met Glu Lys Val Pro Val Arg Phe Val Asp Val Thr Ala Leu Ser	
	435
gag atc cgc aag gac gcg cac acc tcc gtg cac acg ctg cgg cag ggg	1392
Glu Ile Arg Lys Asp Ala His Thr Ser Val His Thr Leu Arg Gln Gly	
	450
aag ctc ctg acg ccc gag cag aag gcg aac ccg agg aag ttc gcg gat	1440
Lys Leu Leu Thr Pro Glu Gln Lys Ala Asn Pro Arg Lys Phe Ala Asp	
	465
tgc atc cac tgg tgc ctc ccc ggc gtg ccg gac acg tgg aac cag ttc	1488
Cys Ile His Trp Cys Leu Pro Gly Val Pro Asp Thr Trp Asn Gln Phe	
	485
gtt tat ggt cac atc gtg tgc agc ccg ccg ccg cag gat caa cct	1536
Val Tyr Gly His Ile Val Ser Ser Pro Pro Pro Gln Asp Gln Pro	
	500
cac aga taa	1545
His Arg	

<210> 1687
 <211> 514
 <212> PRT
 <213> Zea mays

<400> 1687

Met Arg Ile Pro Arg Arg Lys Gly Gly Ala Gly Pro Leu Ala Val Gly	1	5	10	15
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Leu Leu Gly Val Ser Val Leu Tyr Asp Ala Ala His Ile Ala Ala Ser	35	40	45	
Leu Arg Arg His Gly Gly Pro Thr Ala Tyr Ala Lys Leu Ser Ser Ser	50	55	60	
Asp Gly Ala Ala Ser Val Ser Gly Val Ala Arg Glu Glu Val Ala Ala	65	70	75	80
Val Glu Thr Leu Ala Pro Pro Ala Arg Ala Val Gly Ser Asp Gly Ala	85	90	95	
Asp Arg Thr Asp Pro Pro Pro His Glu Gln Gln Glu Glu Ala Glu Glu	100	105	110	
Gly Ala Ala Lys Pro Gly Ala Ser Leu Gln Gln Asp Ala Pro Leu Thr	115	120	125	
Glu Glu Val Val Glu Gly Gly Ser Gly Gly His Gly Gly Gly Ser	130	135	140	
Gln Glu Gln Glu Gln Asp Gln Ala Gln Gly Thr Cys Asp Leu Tyr Lys	145	150	155	160
Gly Arg Trp Val Tyr Asp Glu Ser Arg Ala Pro Leu Tyr Lys Glu Ser	165	170	175	
Glu Cys Ser Phe Leu Thr Glu Gln Val Thr Cys Thr Arg Asn Gly Arg	180	185	190	
Arg Asp Asp Asp Tyr Gln Lys Trp Arg Trp Gln Pro Asp Gly Cys Asp	195	200	205	
Leu Pro Arg Phe Glu Ala Lys Leu Leu Leu Glu Lys Leu Arg Asn Lys	210	215	220	
Arg Leu Met Phe Val Gly Asp Ser Leu Asn Arg Asn Gln Trp Glu Ser	225	230	235	240
Met Val Cys Leu Val Gln Ser Glu Ala Pro Trp Asp Lys Lys Ser Leu	245	250	255	
Val Lys Asn Gly Ser Leu Asn Val Phe His Leu Gln Glu Tyr Asn Ala	260	265	270	
Thr Val Glu Phe Tyr Trp Ala Pro Phe Leu Val Glu Ser Asn Ser Asp	275	280	285	
Asp Pro Asp Ile His Ser Ile Ser Asp Arg Met Ile Lys Pro Thr Ser	290	295	300	
Ile Ala Lys His Ala Ala Asn Trp Glu Gly Val Asp Tyr Leu Ile Phe	305	310	315	320
Asn Thr Tyr Ile Trp Trp Met Asn Thr Pro Gln Met Lys Thr Val His				

PF59082SeqList_PF59082.txt

325 330 335
 Gly Gly Ser Phe Ser Arg Lys His Val Lys Tyr Asp Glu Ile Glu Arg
 340 345 350
 Val Glu Ala Tyr Arg Lys Val Leu Lys Thr Trp Ser Arg Trp Val Glu
 355 360 365
 Ala His Ile Asp Pro Lys Arg Ser Thr Val Leu Phe Met Ser Val Ser
 370 375 380
 Pro Val His Met Gln Ser Glu Gly Trp Gly Ser Pro Asn Ala Val Lys
 385 390 400
 Cys Phe Ser Glu Thr Gln Pro Ala Ile Asn Tyr Thr Lys Lys Leu Glu
 405 410 415
 Val Gly Thr Asp Trp Asp Leu Phe Ala Ala Ala Gln Arg Val Thr Arg
 420 425 430
 Ser Met Glu Lys Val Pro Val Arg Phe Val Asp Val Thr Ala Leu Ser
 435 440 445
 Glu Ile Arg Lys Asp Ala His Thr Ser Val His Thr Leu Arg Gln Gly
 450 455 460
 Lys Leu Leu Thr Pro Glu Gln Lys Ala Asn Pro Arg Lys Phe Ala Asp
 465 470 475
 Cys Ile His Trp Cys Leu Pro Gly Val Pro Asp Thr Trp Asn Gln Phe
 485 490 495
 Val Tyr Gly His Ile Val Ser Ser Pro Pro Pro Pro Gln Asp Gln Pro
 500 505 510
 His Arg

<210> 1688
 <211> 1464
 <212> DNA
 <213> Hordeum vulgare

<220>
 <221> CDS
 <222> (1)..(1464)

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 cgc cgg gcg cag atc gcc gcc gtc ttc gcg ctc gcc gtg ctg ctc ggc 96
 Arg Arg Ala Gln Ile Ala Ala Val Phe Ala Leu Ala Val Leu Leu Gly
 20 25 30
 gtc tcc gtc ctc tac gac agc gcc cac atc gcc gcc tcg ctg cgt cgc 144
 Val Ser Val Leu Tyr Asp Ser Ala His Ile Ala Ala Ser Leu Arg Arg
 35 40 45
 cac agc gga tac aac agg ccc tcc gcc acc acg gag ccg gcg gcg ggg 192
 His Ser Gly Tyr Asn Arg Pro Ser Ala Thr Thr Glu Pro Ala Ala Gly
 50 55 60
 gct ggc ccg cgt gct acg ccg gcg cag gcg gtg gaa tct gcg ggg ccg 240
 Ala Gly Pro Arg Ala Thr Pro Ala Gln Ala Val Glu Ser Ala Gly Pro
 65 70 75 80
 gcc gtg gat cgg acc gac ccg ccc ccg cgg ctc ggg gcg gag gag gcg 288
 Ala Val Asp Arg Thr Asp Pro Pro Pro Arg Leu Gly Ala Glu Glu Ala
 85 90 95
 tcc aag tct aac ccc ggg acg gcg gcg gac ggg tcc gag ccg gag acg 336
 Ser Lys Ser Asn Pro Gly Thr Ala Ala Asp Gly Ser Glu Pro Glu Thr
 100 105 110
 cgg gtc ctg aag gag gtg gtg gcg caa ggg ggg gag ccc acc tgc gac 384
 Arg Val Leu Lys Glu Val Val Ala Gln Gly Gly Glu Pro Thr Cys Asp
 115 120 125
 atg tac aag ggg agg tgg gtg cac gac cag gag aac gcg ccg ctc tac 432
 Met Tyr Lys Gly Arg Trp Val His Asp Gln Glu Asn Ala Pro Leu Tyr
 130 135 140
 aag gag tcc gac tgc gag ttc ctc acg gag cag gtc acc tgc atg cgc 480
 Lys Glu Ser Asp Cys Glu Phe Leu Thr Glu Gln Val Thr Cys Met Arg
 145 150 155 160
 aac ggc cgc cgc agc gac gag tac cag aag tgg cgg tgg cag cct gat 528
 Asn Gly Arg Arg Ser Asp Glu Tyr Gln Lys Trp Arg Trp Gln Pro Asp
 165 170 175

PF59082SeqList_PF59082.txt

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Ala	Cys	Asp	Leu	Pro	Arg	Phe	Glu	Ala	Lys	Leu	Leu	Leu	Glu	Lys	Leu	
			180					185					190			
agg	aac	aaa	aga	atg	atg	ttt	gtt	ggg	gat	tca	ctg	aac	cgg	aac	cag	624
Arg	Asn	Lys	Arg	Met	Met	Phe	Val	Gly	Asp	Ser	Leu	Asn	Arg	Asn	Gln	
		195					200					205				
tggt	gag	tcc	atg	gtg	tgc	ctg	gtt	cag	tct	gtg	gct	cca	tggt	gat	aag	672
Trp	Glu	Ser	Met	Val	Cys	Leu	Val	Gln	Ser	Val	Ala	Pro	Trp	Asp	Lys	
	210					215					220					
aaa	aag	ctt	gtc	aag	aat	gga	tct	cta	aat	gtg	ttc	cgc	ctt	atg	gag	720
Lys	Lys	Leu	Val	Lys	Asn	Gly	Ser	Leu	Asn	Val	Phe	Arg	Leu	Met	Glu	
225					230					235					240	
tac	aat	gca	aca	att	gag	ttc	tat	tggt	gct	cct	ttc	cta	gtt	gag	tcg	768
Tyr	Asn	Ala	Thr	Ile	Glu	Phe	Tyr	Trp	Ala	Pro	Phe	Leu	Val	Glu	Ser	
			245						250					255		
aac	tca	gat	gat	cca	gac	atc	cat	agc	atc	acg	gac	cga	atg	atc	acg	816
Asn	Ser	Asp	Asp	Pro	Asp	Ile	His	Ser	Ile	Thr	Asp	Arg	Met	Ile	Thr	
			260					265					270			
cca	aca	tcg	atc	gcc	aag	cat	gca	gca	aac	tggt	ata	gggt	gtgt	gac	tat	864
Pro	Thr	Ser	Ile	Ala	Lys	His	Ala	Ala	Asn	Trp	Ile	Gly	Val	Asp	Tyr	
		275					280					285				
ttgt	atc	ttc	aac	act	tac	att	tggt	tggt	atgt	aac	acc	cca	aag	atgt	aaa	912
Leu	Ile	Phe	Asn	Thr	Tyr	Ile	Trp	Trp	Met	Asn	Thr	Pro	Lys	Met	Lys	
	290					295					300					
att	gtgt	cct	gac	gggt	tcc	ttc	aca	aag	aaa	ccgt	gtgt	aag	tac	gat	gaa	960
Ile	Val	Pro	Asp	Gly	Ser	Phe	Thr	Lys	Lys	Pro	Val	Lys	Tyr	Asp	Glu	
305					310					315					320	
ttgt	gat	cgt	gtgt	gtt	gca	tac	cga	cag	atc	ctc	gag	aca	tggt	tct	gga	1008
Leu	Asp	Arg	Val	Val	Ala	Tyr	Arg	Gln	Ile	Leu	Glu	Thr	Trp	Ser	Gly	
				325					330					335		
tggt	gta	gaa	gag	aat	gta	gac	ccc	aaa	aga	aca	atgt	gtc	tta	ttc	atgt	1056
Trp	Val	Glu	Glu	Asn	Val	Asp	Pro	Lys	Arg	Thr	Met	Val	Leu	Phe	Met	
			340					345					350			
agtt	gtgt	tca	cca	gta	cat	atgt	cag	agtt	gaa	ggc	tggt	ggc	agc	cct	aac	1104
Ser	Val	Ser	Pro	Val	His	Met	Gln	Ser	Glu	Gly	Trp	Gly	Ser	Pro	Asn	
		355					360					365				
aac	ata	aaa	tgc	ttt	tct	gag	aca	caa	cca	gca	cta	aat	tac	tct	aaa	1152
Asn	Ile	Lys	Cys	Phe	Ser	Glu	Thr	Gln	Pro	Ala	Leu	Asn	Tyr	Ser	Lys	
	370					375					380					
cca	ttgt	gat	gtc	ggc	act	gac	tggt	gat	ctt	ttc	acgt	gaa	tct	cat	gaa	1200
Pro	Leu	Asp	Val	Gly	Thr	Asp	Trp	Asp	Leu	Phe	Thr	Glu	Ser	His	Glu	
385					390					395					400	
gtgt	acgt	aag	gct	atgt	aag	aag	gta	ccc	gtgt	cac	ttc	atc	aac	ata	acc	1248
Val	Thr	Lys	Ala	Met	Lys	Lys	Val	Pro	Val	His	Phe	Ile	Asn	Ile	Thr	
			405						410					415		
gca	ttgt	tcgt	gag	atc	cgt	aag	gac	gca	cac	aca	tct	gtgt	cac	act	ctgt	1296
Ala	Leu	Ser	Glu	Ile	Arg	Lys	Asp	Ala	His	Thr	Ser	Val	His	Thr	Leu	
			420				425						430			
cgt	cag	gggt	aag	ctc	ctgt	acgt	aag	gag	cag	cag	gcc	aac	cca	cgt	aag	1344
Arg	Gln	Gly	Lys	Leu	Leu	Thr	Lys	Glu	Gln	Gln	Ala	Asn	Pro	Arg	Lys	
		435					440					445				
ttc	gcc	gac	tgc	atc	cac	tggt	tgt	ctc	cct	ggc	ttgt	ccgt	gac	aca	tggt	1392
Phe	Ala	Asp	Cys	Ile	His	Trp	Cys	Leu	Pro	Gly	Leu	Pro	Asp	Thr	Trp	
	450					455					460					
aat	gag	ttc	att	tac	ggc	cac	att	gtgt	tcgt	agc	cct	ata	cag	cgt	cag	1440
Asn	Glu	Phe	Ile	Tyr	Gly	His	Ile	Val	Ser	Ser	Pro	Ile	Gln	Arg	Gln	
465					470					475					480	
att	gag	aat	caa	tct	gaa	aga	tga									1464
Ile	Glu	Asn	Gln	Ser	Glu	Arg										
			485													

<210> 1689

<211> 487

<212> PRT

<213> Hordeum vulgare

<400> 1689

Met Arg Ile Pro Arg Arg Lys Ala Gly Ala Ala Leu Gly Val Pro Ser
1 5 10 15

PF59082SeqList_PF59082.txt

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Arg Arg Ala Gln Ile Ala Ala Val Phe Ala Leu Ala Val Leu Gly
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Val Ser Val Leu Tyr Asp Ser Ala His Ile Ala Ala Ser Leu Arg Arg
      35      40      45
His Ser Gly Tyr Asn Arg Pro Ser Ala Thr Thr Glu Pro Ala Ala Gly
      50      55      60
Ala Gly Pro Arg Ala Thr Pro Ala Gln Ala Val Glu Ser Ala Gly Pro
      65      70      75      80
Ala Val Asp Arg Thr Asp Pro Pro Pro Arg Leu Gly Ala Glu Glu Ala
      85      90      95
Ser Lys Ser Asn Pro Gly Thr Ala Ala Asp Gly Ser Glu Pro Glu Thr
      100      105
Arg Val Leu Lys Glu Val Val Ala Gln Gly Gly Glu Pro Thr Cys Asp
      115      120      125
Met Tyr Lys Gly Arg Trp Val His Asp Gln Glu Asn Ala Pro Leu Tyr
      130      135      140
Lys Glu Ser Asp Cys Glu Phe Leu Thr Glu Gln Val Thr Cys Met Arg
      145      150      155      160
Asn Gly Arg Arg Ser Asp Glu Tyr Gln Lys Trp Arg Trp Gln Pro Asp
      165      170      175
Ala Cys Asp Leu Pro Arg Phe Glu Ala Lys Leu Leu Leu Glu Lys Leu
      180      185      190
Arg Asn Lys Arg Met Met Phe Val Gly Asp Ser Leu Asn Arg Asn Gln
      195      200      205
Trp Glu Ser Met Val Cys Leu Val Gln Ser Val Ala Pro Trp Asp Lys
      210      215      220
Lys Lys Leu Val Lys Asn Gly Ser Leu Asn Val Phe Arg Leu Met Glu
      225      230      235      240
Tyr Asn Ala Thr Ile Glu Phe Tyr Trp Ala Pro Phe Leu Val Glu Ser
      245      250      255
Asn Ser Asp Asp Pro Asp Ile His Ser Ile Thr Asp Arg Met Ile Thr
      260      265      270
Pro Thr Ser Ile Ala Lys His Ala Ala Asn Trp Ile Gly Val Asp Tyr
      275      280      285
Leu Ile Phe Asn Thr Tyr Ile Trp Trp Met Asn Thr Pro Lys Met Lys
      290      295      300
Ile Val Pro Asp Gly Ser Phe Thr Lys Lys Pro Val Lys Tyr Asp Glu
      305      310      315      320
Leu Asp Arg Val Val Ala Tyr Arg Gln Ile Leu Glu Thr Trp Ser Gly
      325      330      335
Trp Val Glu Glu Asn Val Asp Pro Lys Arg Thr Met Val Leu Phe Met
      340      345      350
Ser Val Ser Pro Val His Met Gln Ser Glu Gly Trp Gly Ser Pro Asn
      355      360      365
Asn Ile Lys Cys Phe Ser Glu Thr Gln Pro Ala Leu Asn Tyr Ser Lys
      370      375      380
Pro Leu Asp Val Gly Thr Asp Trp Asp Leu Phe Thr Glu Ser His Glu
      385      390      395      400
Val Thr Lys Ala Met Lys Lys Val Pro Val His Phe Ile Asn Ile Thr
      405      410      415
Ala Leu Ser Glu Ile Arg Lys Asp Ala His Thr Ser Val His Thr Leu
      420      425      430
Arg Gln Gly Lys Leu Leu Thr Lys Glu Gln Gln Ala Asn Pro Arg Lys
      435      440      445
Phe Ala Asp Cys Ile His Trp Cys Leu Pro Gly Leu Pro Asp Thr Trp
      450      455      460
Asn Glu Phe Ile Tyr Gly His Ile Val Ser Ser Pro Ile Gln Arg Gln
      465      470      475      480
Ile Glu Asn Gln Ser Glu Arg
      485

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<211> 1590

<212> DNA

<213> Zea mays

<220>

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<222> (1)..(1590)

PF59082SeqList_PF59082.txt

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1      5      10      15
gtg ccc agc agg cgg gcg cag gtc gcc gcg gtc ttc gcg ctc gcc gca      96
Val Pro Ser Arg Arg Ala Gln Val Ala Ala Val Phe Ala Leu Ala Ala
20      25      30
ctg ctg ggg gtc tcc gtg ctc tac gac aac gcc cac atc gcc gcc tcg      144
Leu Leu Gly Val Ser Val Leu Tyr Asp Asn Ala His Ile Ala Ala Ser
35      40      45
ctg cgg agg cac ggc ggc ccg agg acg tac gcc aag ctc tcc tcc ttc      192
Leu Arg Arg His Gly Gly Pro Arg Thr Tyr Ala Lys Leu Ser Ser Phe
50      55      60
gaa ggc gcc acc gct gtc ccc agc atc gcc aag gaa gag gcg gcg gcg      240
Glu Gly Ala Thr Ala Val Pro Ser Ile Ala Lys Glu Glu Ala Ala Ala
65      70      75      80
gcg gtg gcg cgg gca acg gag tcg gtg ccg gtg cac ggc gcg gat cgg      288
Ala Val Ala Arg Ala Thr Glu Ser Val Pro Val His Gly Ala Asp Arg
85      90      95
gcc gac tcg ccc ccg cac gag cgg cag gag gag atc gag gag cgc gca      336
Ala Asp Ser Pro Pro His Glu Arg Gln Glu Glu Ile Glu Glu Arg Ala
100      105      110
tcg aag cct gga gcg acg gcc ggg agc tcc ctg cag gac gcg ccg cta      384
Ser Lys Pro Gly Ala Thr Ala Gly Ser Ser Leu Gln Asp Ala Pro Leu
115      120      125
atc gag gag gtg gtg caa gga gga agc gga ggc cac gac ggc gac ggc      432
Ile Glu Glu Val Val Gln Gly Gly Ser Gly Gly His Asp Gly Asp Gly
130      135      140
gac ggc gac ggc ggc gcg cag gcg cag gag cag ccc ccg gcc ccg ggg      480
Asp Gly Asp Gly Gly Ala Gln Ala Gln Glu Gln Pro Pro Ala Pro Gly
145      150      155      160
acc tgc gac ctg tac aag ggc cgc tgg gtg tac gac gag tcc cgc gcg      528
Thr Cys Asp Leu Tyr Lys Gly Arg Trp Val Tyr Asp Glu Ser Arg Ala
165      170      175
ccg ctg tac aag gag tcc gac tgc agc ttc ctc acg gag cag gtc acc      576
Pro Leu Tyr Lys Glu Ser Asp Cys Ser Phe Leu Thr Glu Gln Val Thr
180      185      190
tgt atg cgc aac ggc cga cgc gac gac gac tat cag aag tgg cgc tgg      624
Cys Met Arg Asn Gly Arg Arg Asp Asp Tyr Gln Lys Trp Arg Trp
195      200      205
cag ccc gac ggc tgc gat ctc ccc aga ttt gaa gct aag ttg ctt ctg      672
Gln Pro Asp Gly Cys Asp Leu Pro Arg Phe Glu Ala Lys Leu Leu Leu
210      215      220
gag aag cta agg aac aaa agg ctg atg ttt gtg ggg gat tcc ctg aat      720
Glu Lys Leu Arg Asn Lys Arg Leu Met Phe Val Gly Asp Ser Leu Asn
225      230      235      240
cgg aac cag tgg gag tcc atg gtg tgc ctg gtc cag tca gag gct cca      768
Arg Asn Gln Trp Glu Ser Met Val Cys Leu Val Gln Ser Glu Ala Pro
245      250      255
tgg gac aaa aag tcc ctt gtc aag aat ggt tct ctt aat gtg ttc cat      816
Trp Asp Lys Lys Ser Leu Val Lys Asn Gly Ser Leu Asn Val Phe His
260      265      270
ctt cag gag tac aat gca acg gtt gag ttc tat tgg tct cct ttc cta      864
Leu Gln Glu Tyr Asn Ala Thr Val Glu Phe Tyr Trp Ser Pro Phe Leu
275      280      285
gtg gag tcg aac tca gat gac cca gac att cat agc atc agt gac cgc      912
Val Glu Ser Asn Ser Asp Asp Pro Asp Ile His Ser Ile Ser Asp Arg
290      295      300
atg atc aag ccg aca tcg atc gct aag cat gcg ggc aac tgg gaa ggg      960
Met Ile Lys Pro Thr Ser Ile Ala Lys His Ala Ala Asn Trp Glu Gly
305      310      315      320
gtg gac tac ctg atc ttc aac act tac atc tgg tgg atg aac acg cca      1008
Val Asp Tyr Leu Ile Phe Asn Thr Tyr Ile Trp Trp Met Asn Thr Pro
325      330      335
cag atg aaa act ctg cac ggt gga tct ttt tcg agg aaa cat gtc aag      1056
Gln Met Lys Thr Leu His Gly Gly Ser Phe Ser Arg Lys His Val Lys
340      345      350
tat gac gaa atc gaa cgt gtg gag gcg tac ccg aag gtc ctc aag aca      1104

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PF59082SeqList_PF59082.txt

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Trp	Ser	Arg	Trp	Val	Glu	Ala	His	Val	Asp	Pro	Lys	Arg	Thr	Thr	Val	
tta	ttc	atg	agc	gtg	tca	cca	gta	cat	atg	cag	agc	gaa	ggg	tgg	ggc	1200
Leu	Phe	Met	Ser	Val	Ser	Pro	Val	His	Met	Gln	Ser	Glu	Gly	Trp	Gly	
385					390					395					400	
agc	ccc	aac	gcc	gta	aaa	tgc	ttc	tcc	gag	aca	cag	ccg	gcg	atc	agc	1248
Ser	Pro	Asn	Ala	Val	Lys	Cys	Phe	Ser	Glu	Thr	Gln	Pro	Ala	Ile	Ser	
tac	aat	aag	aaa	ctg	gag	gtg	ggc	acg	gac	tgg	gac	ctc	ttc	gcg	acc	1296
Tyr	Asn	Lys	Lys	Leu	Glu	Val	Gly	Thr	Asp	Trp	Asp	Leu	Phe	Ala	Thr	
gcc	cag	cg	gtg	acg	agg	tcg	atg	aag	aag	gta	ccc	gtg	cac	ttc	gtc	1344
Ala	Gln	Arg	Val	Thr	Arg	Ser	Met	Lys	Lys	Val	Pro	Val	His	Phe	Val	
aac	ata	act	gcg	ctg	tcg	gag	atc	cg	aag	gac	gcg	cac	acc	tcc	gtg	1392
Asn	Ile	Thr	Ala	Leu	Ser	Glu	Ile	Arg	Lys	Asp	Ala	His	Thr	Ser	Val	
450					455					460						
cac	acg	ctg	cg	cag	ggg	aag	ctc	ctg	acg	ccg	gag	cag	aag	gcg	aac	1440
His	Thr	Leu	Arg	Gln	Gly	Lys	Leu	Leu	Thr	Pro	Glu	Gln	Lys	Ala	Asn	
465					470					475					480	
ccg	agg	aag	ttc	gcg	gac	tgc	atc	cac	tgg	tgc	ctc	ccc	ggg	gtg	ccg	1488
Pro	Arg	Lys	Phe	Ala	Asp	Cys	Ile	His	Trp	Cys	Leu	Pro	Gly	Val	Pro	
gac	acg	tgg	aac	gag	ttt	gtt	tat	ggc	cat	atc	gtg	tcg	agc	acc	ccg	1536
Asp	Thr	Trp	Asn	Glu	Phe	Val	Tyr	Gly	His	Ile	Val	Ser	Ser	Thr	Pro	
ccg	ccg	cag	cag	cag	cag	cag	cag	aag	ata	acc	gag	gat	gaa	cct	cac	1584
Pro	Pro	Gln	Gln	Gln	Gln	Gln	Gln	Lys	Ile	Thr	Glu	Asp	Glu	Pro	His	
aga	tga															1590
Arg																

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 35 40 45
 Leu Arg Arg His Gly Gly Pro Arg Thr Tyr Ala Lys Leu Ser Ser Phe
 50 55 60
 Glu Gly Ala Thr Ala Val Pro Ser Ile Ala Lys Glu Glu Ala Ala Ala
 65 70 75 80
 Ala Val Ala Arg Ala Thr Glu Ser Val Val His Gly Ala Asp Arg
 85 90 95
 Ala Asp Ser Pro Pro His Glu Arg Gln Glu Glu Ile Glu Glu Arg Ala
 100 105 110
 Ser Lys Pro Gly Ala Thr Ala Gly Ser Ser Leu Gln Asp Ala Pro Leu
 115 120 125
 Ile Glu Glu Val Val Gln Gly Ser Gly Gly His Asp Gly Asp Gly
 130 135 140
 Asp Gly Asp Gly Gly Ala Gln Ala Gln Glu Gln Pro Pro Ala Pro Gly
 145 150 155 160
 Thr Cys Asp Leu Tyr Lys Gly Arg Trp Val Tyr Asp Glu Ser Arg Ala
 165 170 175
 Pro Leu Tyr Lys Glu Ser Asp Cys Ser Phe Leu Thr Glu Gln Val Thr
 180 185 190
 Cys Met Arg Asn Gly Arg Arg Asp Asp Asp Tyr Gln Lys Trp Arg Trp
 195 200 205
 Gln Pro Asp Gly Cys Asp Leu Pro Arg Phe Glu Ala Lys Leu Leu Leu

PF59082SeqList_PF59082.txt

210 215 220
 Glu Lys Leu Arg Asn Lys Arg Leu Met Phe Val Gly Asp Ser Leu Asn
 225 230 235 240
 Arg Asn Gln Trp Glu Ser Met Val Cys Leu Val Gln Ser Glu Ala Pro
 245 250 255
 Trp Asp Lys Lys Ser Leu Val Lys Asn Gly Ser Leu Asn Val Phe His
 260 265 270
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<220>

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<222> (344)..(346)

<223> Xaa in position 344 to 346 is any amino acid

<220>

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<222> (357)..(357)

<223> Xaa in position 357 is any amino acid

<220>

<221> Variant

<222> (360)..(360)

<223> Xaa in position 360 is any amino acid

<220>

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<222> (363)..(365)

<223> Xaa in position 363 to 365 is any amino acid

<220>

<221> Variant

<222> (367)..(368)

<223> Xaa in position 367 to 368 is any amino acid

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<222> (370)..(370)

<223> Xaa in position 370 is any amino acid

<400> 1702

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Xaa	Pro	Leu	Tyr	Xaa	Glu	Xaa	Xaa	Cys	Xaa	Phe	Leu	Thr	Xaa	Gln	Val
		20						25				30			
Thr	Cys	Xaa	Xaa	Asn	Gly	Arg	Xaa	Asp	Xaa	Xaa	Xaa	Gln	Xaa	Trp	Arg
		35					40					45			
Trp	Gln	Pro	Xaa	Xaa	Cys	Xaa	Leu	Pro	Xaa	Phe	Xaa	Ala	Xaa	Xaa	Xaa
	50				55					60					
Xaa	Glu	Xaa	Xaa	Arg	Xaa	Lys	Arg	Xaa	Met	Phe	Val	Gly	Asp	Ser	Leu
65				70					75					80	
Asn	Arg	Asn	Gln	Trp	Glu	Ser	Xaa	Val	Cys	Leu	Val	Gln	Ser	Xaa	Xaa
		85						90					95		
Xaa	Xaa	Xaa	Xaa	Lys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Ser	Xaa	
		100					105					110			
Xaa	Xaa	Phe	Xaa	Xaa	Xaa	Xaa	Xaa	Tyr	Xaa	Ala	Thr	Xaa	Glu	Phe	
	115					120					125				

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Tyr	Trp	Ala	Pro	Phe	Leu	Val	Glu	Ser	Asn	Ser	Asp	Xaa	Pro	Xaa	Xaa
130						135					140				
Xaa	His	Ser	Ile	Xaa	Xaa	Arg	Xaa	Ile	Xaa	Xaa	Xaa	Xaa	Ile	Xaa	Xaa
145					150					155					160
His	Xaa	Xaa	Asn	Trp	Xaa	Xaa	Val	Asp	Tyr	Leu	Xaa	Phe	Asn	Thr	Tyr
			165					170						175	
Ile	Trp	Trp	Met	Asn	Xaa	Xaa	Xaa	Xaa	Lys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			180					185					190		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		195					200					205			
Glu	Xaa	Xaa	Arg	Xaa	Xaa	Ala	Tyr	Xaa	Xaa	Val	Xaa	Xaa	Thr	Trp	Xaa
210						215					220				
Xaa	Trp	Xaa	Xaa	Xaa	Xaa	Xaa	Asp	Pro	Xaa	Xaa	Thr	Xaa	Val	Xaa	Phe
225					230					235					240
Xaa	Xaa	Xaa	Ser	Pro	Xaa	His	Xaa	Xaa	Xaa	Xaa	Xaa	Trp	Xaa	Xaa	Xaa
			245					250					255		
Pro	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Glu	Thr	Xaa	Pro	Xaa	Xaa	Asn	Xaa
			260					265					270		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asp	Xaa
		275						280					285		
Xaa	Leu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Val	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
290						295					300				
Val	Pro	Xaa	Xaa	Xaa	Xaa	Xaa	Ile	Thr	Xaa	Xaa	Ser	Xaa	Xaa	Arg	Lys
305					310					315					320
Asp	Ala	His	Thr	Ser	Xaa	Xaa	Thr	Xaa	Xaa	Gln	Gly	Lys	Xaa	Leu	Thr
				325				330					335		
Xaa	Glu	Gln	Xaa	Ala	Xaa	Pro	Xaa	Xaa	Xaa	Ala	Asp	Cys	Ile	His	Trp
			340					345					350		
Cys	Leu	Pro	Gly	Xaa	Pro	Asp	Xaa	Trp	Asn	Xaa	Xaa	Xaa	Tyr	Xaa	Xaa
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Ile	Xaa	Ser													
370															

<210> 1703

<211> 33

<212> PRT

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<220>

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<220>

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<222> (8)..(8)

<223> Xaa in position 8 is any amino acid

<220>

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<222> (9)..(9)

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<220>

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<222> (11)..(11)

<223> Xaa in position 11 is any amino acid

<220>

<221> Variant

<222> (12)..(12)
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 <220>
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 <223> Xaa in position 13 is Asp or Asn

 <220>
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 <222> (15)..(16)
 <223> Xaa in position 15 to 16 is any amino acid

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 <222> (17)..(17)
 <223> Xaa in position 17 is Phe or Tyr

 <220>
 <221> Variant
 <222> (28)..(28)
 <223> Xaa in position 28 is Leu or Val

 <220>
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 <223> Xaa in position 31 is any amino acid

 <400> 1703
 Gln Gly Lys Xaa Leu Xaa Thr Xaa Xaa Gln Xaa Xaa Xaa Pro Xaa Xaa
 1 5 10 15
 Xaa Ala Asp Cys Ile His Trp Cys Leu Pro Gly Xaa Pro Asp Xaa Trp
 20 25 30
 Asn

 <210> 1704
 <211> 40
 <212> PRT
 <213> Artificial sequence

 <220>
 <223> protein pattern

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 <223> Xaa in position 3 to 4 is any or no amino acid

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 <222> (6)..(7)
 <223> Xaa in position 6 to 7 is any or no amino acid

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 <222> (9)..(9)
 <223> Xaa in position 9 is Glu, Gly, Ser or Thr

 <220>
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 <223> Xaa in position 13 is any amino acid
 Seite 2234

PF59082SeqList_PF59082.txt

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<223> Xaa in position 16 is Ser or Thr

<220>
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<223> Xaa in position 18 to 19 is any amino acid

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<223> Xaa in position 23 is any amino acid

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<223> Xaa in position 27 is Phe, Trp or Tyr

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<223> Xaa in position 29 is any amino acid

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<223> Xaa in position 35 is any amino acid

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<223> Xaa in position 38 is Asp or Ser

<220>
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<223> Xaa in position 39 is Leu or Met

<400> 1704
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1      5      10      15
Cys Xaa Xaa Asn Gly Arg Xaa Asp Xaa Xaa Gln Xaa Trp Arg Trp
      20      25      30
Gln Pro Xaa Xaa Cys Xaa Xaa Pro
      35      40

<210> 1705
<211> 42
<212> PRT
<213> Artificial sequence

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<222> (4)..(5)
<223> Xaa in position 4 to 5 is any amino acid

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<222> (8)..(8)
<223> Xaa in position 8 is Ile or Val

<220>
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<222> (9)..(10)
<223> Xaa in position 9 to 10 is any amino acid

<220>
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<222> (12)..(12)
<223> Xaa in position 12 is any or no amino acid

<220>
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<222> (18)..(18)
<223> Xaa in position 18 is any or no amino acid

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<223> Xaa in position 20 is Ala or Glu

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<223> Xaa in position 21 is any amino acid

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<223> Xaa in position 23 is Ala or Gly

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<222> (24)..(25)
<223> Xaa in position 24 to 25 is any amino acid

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<222> (27)..(27)
<223> Xaa in position 27 is any amino acid

<220>
<221> Variant
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<223> Xaa in position 28 is Asp, Gly or Asn

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PF59082SeqList_PF59082.txt

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<223> Xaa in position 29 is Ala or Val

<220>
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<223> Xaa in position 31 is Phe or Tyr

<220>
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<223> Xaa in position 33 is Ile or Val

<220>
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<222> (36)..(36)
<223> Xaa in position 36 is Ser or Thr

<220>
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<223> Xaa in position 41 is Leu or Met

<400> 1705
Asp Xaa Pro Xaa Xaa His Ser Xaa Xaa Xaa Arg Xaa Ile Xaa Xaa Xaa
1          5          10          15
Xaa Xaa Ile Xaa Xaa His Xaa Xaa Xaa Trp Xaa Xaa Xaa Asp Xaa Leu
          20          25          30
Xaa Phe Asn Xaa Tyr Ile Trp Trp Xaa Asn
          35          40

<210> 1706
<211> 28
<212> PRT
<213> Artificial sequence

<220>
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<223> Xaa in position 2 is Phe, Leu or Met

<220>
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<222> (17)..(17)
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<220>
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<222> (20)..(20)
<223> Xaa in position 20 is Leu or Met

<220>
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<222> (22)..(22)
<223> Xaa in position 22 is any amino acid

<220>
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<222> (23)..(25)
<223> Xaa in position 23 to 25 is any or no amino acid

<220>
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<222> (27)..(27)

<223> Xaa in position 27 is any amino acid

<220>

<221> Variant

<222> (28)..(28)

<223> Xaa in position 28 is Ala, Gly, Ile or Val

<400> 1706

Arg	Xaa	Met	Phe	Val	Gly	Asp	Ser	Leu	Asn	Arg	Asn	Gln	Trp	Glu	Ser
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Xaa	Val	Cys	Xaa	Val	Xaa	Xaa	Xaa	Xaa	Ser	Xaa	Xaa				
			20				25								

<210> 1707

<211> 44

<212> PRT

<213> Artificial sequence

<220>

<223> protein pattern

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<220>

<221> Variant

<222> (6)..(6)

<223> Xaa in position 6 is any or no amino acid

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<222> (8)..(8)

<223> Xaa in position 8 is any or no amino acid

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<222> (10)..(10)

<223> Xaa in position 10 is Phe, Ile, Leu or Met

<220>

<221> Variant

<222> (11)..(11)

<223> Xaa in position 11 is any amino acid

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<221> Variant

<222> (13)..(13)

<223> Xaa in position 13 is any amino acid

<220>

<221> Variant

<222> (14)..(14)

<223> Xaa in position 14 is Ala, Gly or Ser

<220>

<221> Variant

<222> (15)..(15)

<223> Xaa in position 15 is any amino acid

<220>

<221> Variant

<222> (17)..(17)

<223> Xaa in position 17 is Ile, Leu or Val

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<223> Xaa in position 18 is Asp, Glu or Asn

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<222> (19)..(20)
<223> Xaa in position 19 to 20 is any amino acid

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<223> Xaa in position 21 is Ile or Val

<220>
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<223> Xaa in position 22 is Asp or Asn

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<223> Xaa in position 24 to 25 is any amino acid

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<223> Xaa in position 26 is Ser or Thr

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<223> Xaa in position 38 is Phe, Ile, Leu, Met or Val

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<223> Xaa in position 39 is any amino acid

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PF59082SeqList_PF59082.txt

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<223> Xaa in position 40 is Pro or Ser

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<223> Xaa in position 41 is any amino acid

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<223> Xaa in position 42 is Ala, Asp, Gly, Asn or Val

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<223> Xaa in position 44 is Ala, Glu, Gly or Asn

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1          5          10          15
Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Val Xaa Phe Xaa Xaa
          20          25          30
Xaa Ser Pro Xaa His Xaa Xaa Xaa Xaa Trp Xaa
          35          40

<210> 1708
<211> 18
<212> PRT
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<220>
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<220>
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<223> Xaa in position 5 is Ile, Leu or Val

<220>
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<222> (10)..(10)
<223> Xaa in position 10 is Ala or Ser

<220>
<221> Variant
<222> (15)..(15)
<223> Xaa in position 15 is Glu or Gln

<400> 1708
Tyr Xaa Ala Thr Xaa Glu Phe Tyr Trp Xaa Pro Phe Leu Val Xaa Ser
1          5          10          15
Asn Ser

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<220>
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<223> Xaa in position 2 is any or no amino acid

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<222> (4)..(4)
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<220>
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<222> (5)..(5)
<223> Xaa in position 5 is any amino acid

<220>
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<222> (6)..(6)
<223> Xaa in position 6 is Phe, Leu or Val

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<222> (7)..(7)
<223> Xaa in position 7 is Ile, Leu or Val

<220>
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<222> (8)..(8)
<223> Xaa in position 8 is Asp or Asn

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<223> Xaa in position 9 is Ile or Val

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<223> Xaa in position 23 is Phe, Leu or Val

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<223> Xaa in position 24 is His or Tyr

<220>
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<223> Xaa in position 25 is Gly, Ser or Thr

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Val Xaa Pro Xaa Xaa Xaa Xaa Xaa Thr Xaa Xaa Ser Xaa Xaa Arg
1      5      10      15
Lys Asp Xaa His Thr Ser Xaa Xaa Xaa
      20      25

<210> 1710
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<223> Xaa in position 4 to 5 is any amino acid

<220>
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<223> Xaa in position 7 is Glu, Gln or Arg

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<223> Xaa in position 9 is Thr or Val

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<223> Xaa in position 10 is any amino acid

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<222> (12)..(12)
<223> Xaa in position 12 is Ala, Glu or Asn

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<222> (13)..(15)
<223> Xaa in position 13 to 15 is any amino acid

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1      5      10      15

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PF59082SeqList_PF59082.txt

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<212> PRT
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<220>
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<222> (3)..(3)
<223> Xaa in position 3 is Ala, Gly or Asn

<220>
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<222> (4)..(4)
<223> Xaa in position 4 is Ile or Val

<220>
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<222> (5)..(5)
<223> Xaa in position 5 is Lys or Arg

<220>
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<222> (7)..(8)
<223> Xaa in position 7 to 8 is any amino acid

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<222> (10)..(10)
<223> Xaa in position 10 is any or no amino acid

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<223> Xaa in position 12 is any or no amino acid

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<222> (14)..(15)
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<222> (16)..(16)
<223> Xaa in position 16 is Asn or Ser

<220>
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<222> (17)..(20)
<223> Xaa in position 17 to 20 is any amino acid

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<222> (21)..(21)
<223> Xaa in position 21 is Phe, Ile, Leu or Val

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Pro Xaa Xaa Xaa Xaa Cys Xaa Xaa Glu Xaa Thr Xaa Pro Xaa Xaa Xaa
1          5          10          15
Xaa Xaa Xaa Xaa Xaa
                20

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PF59082SeqList_PF59082.txt

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<220>
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<220>
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 <222> (4)..(4)
 <223> Xaa in position 4 is Phe, Leu or Met

<220>
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 <222> (5)..(5)
 <223> Xaa in position 5 is Leu or Met

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 <222> (7)..(7)
 <223> Xaa in position 7 is any amino acid

<220>
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 <222> (8)..(8)
 <223> Xaa in position 8 is Leu or Met

<220>
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 <223> Xaa in position 10 is Gly or Asn

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 1 5 10

<210> 1713
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 <212> DNA
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<220>
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 Met Ser Leu Pro Glu Thr Lys Ser Asp Asp Ile Leu Leu Asp Ala Trp
 1 5 10 15
 gac ttc caa ggc cgt ccc gcc gat cgc tca aaa acc ggc ggc tgg gcc 96
 Asp Phe Gln Gly Arg Pro Ala Asp Arg Ser Lys Thr Gly Gly Trp Ala
 20 25 30
 agc gcc gcc atg att ctt tgt att gag gcc gtg gag agg ctg acg acg 144
 Ser Ala Ala Met Ile Leu Cys Ile Glu Ala Val Glu Arg Leu Thr Thr
 35 40 45
 tta ggt atc gga gtt aat ctg gtg acg tat ttg acg gga act atg cat 192
 Leu Gly Ile Gly Val Asn Leu Val Thr Tyr Leu Thr Gly Thr Met His
 50 55 60
 tta ggc aat gca act gcg gct aac acc gtt acc aat ttc ctc gga act 240
 Leu Gly Asn Ala Thr Ala Ala Asn Thr Val Thr Asn Phe Leu Gly Thr
 65 70 75 80

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Ser	Phe	Met	Leu	Cys	Leu	Leu	Gly	Gly	Phe	Ile	Ala	Asp	Thr	Phe	Leu	
				85					90					95		
ggc	agg	tac	cta	acg	att	gct	ata	ttc	gcc	gca	atc	caa	gcc	acg	ggt	336
Gly	Arg	Tyr	Leu	Thr	Ile	Ala	Ile	Phe	Ala	Ala	Ile	Gln	Ala	Thr	Gly	
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Lys	Gln	Ile	Val	Arg	Met	Leu	Pro	Ile	Trp	Ala	Thr	Cys	Ile	Leu	Phe	
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Ala Thr Ala Ala Asn Asn Val Thr Asn Trp Ser Gly Thr Cys Tyr Ile
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Thr Pro Leu Ile Gly Ala Phe Leu Ala Asp Ala Tyr Leu Gly Arg Tyr
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Trp Thr Ile Ala Thr Phe Val Phe Ile Tyr Val Ser Gly Met Thr Leu
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Leu Thr Leu Ser Ala Ser Val Pro Gly Leu Lys Pro Gly Asn Cys Asn
115 120 125
Gly Asp Thr Cys His Pro Asn Ser Gly Gln Thr Ala Val Phe Phe Val
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PF59082SeqList_PF59082.txt

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Phe	Tyr	Leu	Ser	Val	Tyr	Leu	Ile	Ala	Leu	Gly	Tyr	Gly	Gly	Tyr	Gln	
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Phe	385	Asp	Ile	Leu	Ser	Val	390	Ala	Phe	Phe	Val	Phe	395	Tyr	Arg
Leu	Asp	Pro	Leu	Phe	405	Ala	Arg	Leu	Asn	Lys	410	Thr	Glu	Pro	Asn
Leu	Thr	Glu	Leu	Gln	Arg	Met	Gly	425	Ile	Gly	Leu	Val	Ile	Ala	430
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Ala Ser Val Ile Ile Trp Val Pro Leu Tyr Asp Arg Phe Ile Val Pro	
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Leu Ala Arg Arg Phe Thr Gly Val Asp Lys Gly Phe Thr Glu Ile Gln	
415 420 425	
aga atg ggg gtc ggt ttg ttt gtc tct gtt ctc tgt atg gca gct gca	1345
Arg Met Gly Val Gly Leu Phe Val Ser Val Leu Cys Met Ala Ala Ala	
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Ala Val Val Glu Ile Ile Arg Leu His Leu Ala Asn Glu Leu Gly Leu	
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gtt gag tct gga gct cct gtt cct ata tct gtt tta tgg cag atc cca	1441
Val Glu Ser Gly Ala Pro Val Pro Ile Ser Val Leu Trp Gln Ile Pro	
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Gln Tyr Phe Ile Leu Gly Ala Ala Glu Val Phe Tyr Phe Ile Gly Gln	
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ctg gag ttt ttc tat gat cag tct cca gat gca atg agg agc ttg tgc	1537
Leu Glu Phe Phe Tyr Asp Gln Ser Pro Asp Ala Met Arg Ser Leu Cys	
495 500 505	
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Ser Ala Leu Ala Leu Leu Thr Asn Ala Leu Gly Asn Tyr Leu Ser Ser	
510 515 520	
ttg atc ctc acg ctg gtg act tac ttc acg acg agg aac ggt gga gaa	1633
Leu Ile Leu Thr Leu Val Thr Tyr Phe Thr Thr Arg Asn Gly Gly Glu	
525 530 535 540	
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Gly Trp Ile Ser Asp Asn Leu Asn Ser Gly His Leu Asp Tyr Tyr Phe	
545 550 555	
tgg ctt ttg gct ggt ctt agc ctt gtg aac atg gct gtt tac ttc ttc	1729
Trp Leu Leu Ala Gly Leu Ser Leu Val Asn Met Ala Val Tyr Phe Phe	
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Ser Ala Ala Arg Tyr Lys Gln Lys Lys Ala Ser Lys Leu	
575 580 585	
ctctctctct ctccttccat tacatacaat aagtatgttt ctcttcttgt gtaaattgtg	1841
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 35 40 45
 Phe Ile Leu Gly Asn Glu Cys Cys Glu Arg Leu Ala Tyr Tyr Gly Ile
 50 55 60
 Ala Gly Asn Leu Ile Thr Tyr Leu Thr Thr Lys Leu His Gln Gly Asn
 65 70 75 80

PF59082SeqList_PF59082.txt

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Trp	Thr	Ile	Ala	Cys	Phe	Ser	Gly	Ile	Tyr	Phe	Ile	Gly	Met	Ser	Ala
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Leu	Thr	Leu	Ser	Ala	Ser	Val	Pro	Ala	Leu	Lys	Pro	Ala	Glu	Cys	Ile
	130					135					140				
Gly	Gly	Phe	Cys	Pro	Ser	Ala	Thr	Pro	Ala	Gln	Tyr	Ala	Met	Phe	Phe
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Gly	Gly	Leu	Tyr	Leu	Ile	Ala	Leu	Gly	Thr	Gly	Gly	Ile	Lys	Pro	Cys
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Val	Ser	Ser	Phe	Gly	Ala	Asp	Gln	Phe	Asp	Asp	Thr	Asp	Ser	Arg	Glu
			180					185					190		
Arg	Val	Lys	Lys	Ala	Ser	Phe	Phe	Asn	Trp	Phe	Tyr	Phe	Ser	Ile	Asn
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Arg	Gly	Trp	Gly	Leu	Gly	Phe	Gly	Ile	Pro	Thr	Val	Phe	Met	Gly	Leu
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Ala	Ile	Ala	Ser	Phe	Phe	Phe	Gly	Thr	Pro	Leu	Tyr	Arg	Phe	Gln	Lys
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Phe	Arg	Lys	Ser	Thr	Leu	Lys	Val	Pro	Glu	Asp	Ala	Met	Leu	Leu	Tyr
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Glu	Thr	Gln	Asp	Lys	Asn	Ser	Ala	Ile	Ala	Gly	Ser	Arg	Lys	Ile	Glu
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Gln	Leu	Pro	Pro	Ala	Ala	Leu	Gly	Thr	Phe	Asp	Thr	Ala	Ser	Val	Ile
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Ile	Trp	Val	Pro	Leu	Tyr	Asp	Arg	Phe	Ile	Val	Pro	Leu	Ala	Arg	Arg
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Phe	Thr	Gly	Val	Asp	Lys	Gly	Phe	Thr	Glu	Ile	Gln	Arg	Met	Gly	Val
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Gly	Leu	Phe	Val	Ser	Val	Leu	Cys	Met	Ala	Ala	Ala	Ala	Val	Val	Glu
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Ile	Ile	Arg	Leu	His	Leu	Ala	Asn	Glu	Leu	Gly	Leu	Val	Glu	Ser	Gly
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Leu	Gly	Ala	Ala	Glu	Val	Phe	Tyr	Phe	Ile	Gly	Gln	Leu	Glu	Phe	Phe
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Tyr	Asp	Gln	Ser	Pro	Asp	Ala	Met	Arg	Ser	Leu	Cys	Ser	Ala	Leu	Ala
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Leu	Leu	Thr	Asn	Ala	Leu	Gly	Asn	Tyr	Leu	Ser	Ser	Leu	Ile	Leu	Thr
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Leu	Val	Thr	Tyr	Phe	Thr	Thr	Arg	Asn	Gly	Gly	Glu	Gly	Trp	Ile	Ser
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Asp	Asn	Leu	Asn	Ser	Gly	His	Leu	Asp	Tyr	Tyr	Phe	Trp	Leu	Leu	Ala
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Gly	Leu	Ser	Leu	Val	Asn	Met	Ala	Val	Tyr	Phe	Phe	Ser	Ala	Ala	Arg
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PF59082SeqList_PF59082.txt

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<222> (114)..(1886)

<400> 1721

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gaa gag gga agg gtt gtg agt gag tac aca aaa gat gga act gtg gat      164
Glu Glu Gly Arg Val Val Ser Glu Tyr Thr Lys Asp Gly Thr Val Asp
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ctt aaa ggg aaa ccc att ctc aaa tcc aaa agt ggt ggt tgg aaa gca      212
Leu Lys Gly Lys Pro Ile Leu Lys Ser Lys Ser Gly Gly Trp Lys Ala
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Cys Ser Phe Val Val Val Tyr Glu Ile Phe Glu Arg Met Ala Tyr Tyr
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Gly Ile Ser Ser Asn Leu Ile Leu Tyr Leu Thr Arg Lys Leu His Gln
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                                   55
gga act gtg acc tct tcc aac aac gtc acc aat tgg gtt ggc acc att      356
Gly Thr Val Thr Ser Ser Asn Asn Val Thr Asn Trp Val Gly Thr Ile
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                                   75
tgg ata act cct atc tta gga gcc tac gtt gcc gat gct cat ctt ggt      404
Trp Ile Thr Pro Ile Leu Gly Ala Tyr Val Ala Asp Ala His Leu Gly
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                                   90
cgc ttt tgg act ttt ctc att gcc tca gtc atc tat tta ttg ggt atg      452
Arg Phe Trp Thr Phe Leu Ile Ala Ser Val Ile Tyr Leu Leu Gly Met
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                                   105
tct cta ctt acg cta tcg gtg tcc ctt cca agc cta aag cca cca gag      500
Ser Leu Leu Thr Leu Ser Val Ser Leu Pro Ser Leu Lys Pro Pro Glu
                                   115
                                   120
tgc cat gaa ttg gat gtg aca aaa tgt gaa aaa gcc tcc aca cta cat      548
Cys His Glu Leu Asp Val Thr Lys Cys Glu Lys Ala Ser Thr Leu His
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cta gct gtg ttc tat ggt gca ctc tac act ctt gca cta gga acc ggt      596
Leu Ala Val Phe Tyr Gly Ala Leu Tyr Thr Leu Ala Leu Gly Thr Gly
                                   150
                                   155
gga acc aag cca aac att tcc aca att ggt gct gac caa ttt gat gac      644
Gly Thr Lys Pro Asn Ile Ser Thr Ile Gly Ala Asp Gln Phe Asp Asp
                                   165
                                   170
ttt gac tcc aaa gag aag aag ctc aag ctc tcc ttc ttc aat tgg tgg      692
Phe Asp Ser Lys Glu Lys Lys Leu Lys Leu Ser Phe Phe Asn Trp Trp
                                   180
                                   185
atg ttt agc atc ttc att ggg acc ctc ttt gca aat tct gtt ctg gtc      740
Met Phe Ser Ile Phe Ile Gly Thr Leu Phe Ala Asn Ser Val Leu Val
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Tyr Ile Gln Asp Asn Val Gly Trp Thr Leu Gly Tyr Ala Leu Pro Thr
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                                   215
ctt gga ctt gca ata tca atc atc ata ttc ttg gca ggc aca ccc ttt      836
Leu Gly Leu Ala Ile Ser Ile Ile Ile Phe Leu Ala Gly Thr Pro Phe
                                   230
                                   235
tat aga cac aaa ttg ccc acg ggg agt cca ttc act aag atg gcc aag      884
Tyr Arg His Lys Leu Pro Thr Gly Ser Pro Phe Thr Lys Met Ala Lys
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                                   250
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Val Ile Val Ala Ala Ile Arg Lys Trp Lys Val His Ile Pro Ser Asp
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                                   265
act aaa gaa ctt tat gag ctt gat ttg gaa gag tat gcc aag aga ggg      980
Thr Lys Glu Leu Tyr Glu Leu Asp Leu Glu Glu Tyr Ala Lys Arg Gly
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                                   280
                                   285
aga gtc aga att gat tcc act cca acc ttg agg ttc ctc aac aag gca      1028
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PF59082SeqList_PF59082.txt

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Ala	Ala	Thr	Leu	Ile	Pro	Ser	Ala	Met	Val	Ala	Gln	Ile	Gly	Thr	Leu	
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Phe	Val	Lys	Gln	Gly	Ile	Thr	Leu	Asp	Arg	Gly	Ile	Gly	Ser	Phe	Asn	
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Ile	Pro	Pro	Ala	Ser	Leu	Ala	Thr	Phe	Val	Thr	Leu	Ser	Met	Leu	Val	
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Cys	Val	Val	Leu	Tyr	Asp	Arg	Phe	Phe	Val	Lys	Ile	Met	Gln	Arg	Phe	
			390					395						400		
acc	aag	aac	cct	aga	ggg	ata	acc	ctt	ctc	caa	agg	att	gga	att	ggc	1364
Thr	Lys	Asn	Pro	Arg	Gly	Ile	Thr	Leu	Gln	Arg	Ile	Gly	Ile	Gly		
			405					410				415				
ctc	ata	atc	cac	ata	gtg	att	atg	gtg	att	gca	tct	cta	act	gaa	agg	1412
Leu	Ile	Ile	His	Ile	Val	Ile	Met	Val	Ile	Ala	Ser	Leu	Thr	Glu	Arg	
			420				425					430				
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Tyr	Arg	Leu	Arg	Val	Ala	Lys	Glu	His	Gly	Leu	Leu	Glu	Asn	Gly	Gly	
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Gln	Val	Pro	Leu	Ser	Ile	Phe	Ile	Leu	Leu	Pro	Gln	Tyr	Val	Leu	Met	
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Gly	Ala	Ala	Asp	Ala	Phe	Val	Glu	Val	Ala	Lys	Ile	Glu	Phe	Ser	Tyr	
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gac	caa	gcc	cca	gaa	agc	atg	aag	agc	ctt	ggc	act	tcc	tat	tca	atg	1604
Asp	Gln	Ala	Pro	Glu	Ser	Met	Lys	Ser	Leu	Gly	Thr	Ser	Tyr	Ser	Met	
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act	acc	tta	ggc	att	ggg	aat	ttc	cta	agc	act	ttt	ctt	ctc	aca	aca	1652
Thr	Thr	Leu	Gly	Ile	Gly	Asn	Phe	Leu	Ser	Thr	Phe	Leu	Leu	Thr	Thr	
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Asn	Leu	Asn	Ala	Ser	His	Leu	Asp	Tyr	Tyr	Tyr	Ala	Leu	Leu	Ala	Ile	
			530		535					540					545	
cta	aac	ttg	gtg	aac	ttc	gta	ttc	ttc	atg	gtt	gtg	aca	aag	ttc	tat	1796
Leu	Asn	Leu	Val	Asn	Phe	Val	Phe	Phe	Met	Val	Val	Thr	Lys	Phe	Tyr	
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gtg	tat	aga	gct	gaa	att	tca	gat	tcc	ata	aaa	gtg	ctt	gag	gaa	gag	1844
Val	Tyr	Arg	Ala	Glu	Ile	Ser	Asp	Ser	Ile	Lys	Val	Leu	Glu	Glu	Glu	
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ctc	aag	gaa	aag	aca	tca	aac	cag	gtg	att	cca	aga	gat	taa	ttagatattt		1896
Leu	Lys	Glu	Lys	Thr	Ser	Asn	Gln	Val	Ile	Pro	Arg	Asp				
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ataggggtctt	taatgtgtga	tataatttgg	acttcactct	tcaagaaacg	tcacgttcat											2076
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PF59082SeqList_PF59082.txt

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<213> Glycine max

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Tyr Gly Ile Ser Ser Asn Leu Ile Leu Tyr Leu Thr Arg Lys Leu His
      50      55      60
Gln Gly Thr Val Thr Ser Ser Asn Asn Val Thr Asn Trp Val Gly Thr
65      70      75      80
Ile Trp Ile Thr Pro Ile Leu Gly Ala Tyr Val Ala Asp Ala His Leu
      85      90      95
Gly Arg Phe Trp Thr Phe Leu Ile Ala Ser Val Ile Tyr Leu Leu Gly
      100      105      110
Met Ser Leu Leu Thr Leu Ser Val Ser Leu Pro Ser Leu Lys Pro Pro
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Glu Cys His Glu Leu Asp Val Thr Lys Cys Glu Lys Ala Ser Thr Leu
      130      135      140
His Leu Ala Val Phe Tyr Gly Ala Leu Tyr Thr Leu Ala Leu Gly Thr
145      150      155      160
Gly Gly Thr Lys Pro Asn Ile Ser Thr Ile Gly Ala Asp Gln Phe Asp
      165      170      175
Asp Phe Asp Ser Lys Glu Lys Lys Leu Lys Leu Ser Phe Phe Asn Trp
      180      185      190
Trp Met Phe Ser Ile Phe Ile Gly Thr Leu Phe Ala Asn Ser Val Leu
      195      200      205
Val Tyr Ile Gln Asp Asn Val Gly Trp Thr Leu Gly Tyr Ala Leu Pro
      210      215      220
Thr Leu Gly Leu Ala Ile Ser Ile Ile Ile Phe Leu Ala Gly Thr Pro
225      230      235      240
Phe Tyr Arg His Lys Leu Pro Thr Gly Ser Pro Phe Thr Lys Met Ala
      245      250      255
Lys Val Ile Val Ala Ala Ile Arg Lys Trp Lys Val His Ile Pro Ser
      260      265      270
Asp Thr Lys Glu Leu Tyr Glu Leu Asp Leu Glu Glu Tyr Ala Lys Arg
      275      280      285
Gly Arg Val Arg Ile Asp Ser Thr Pro Thr Leu Arg Phe Leu Asn Lys
      290      295      300
Ala Cys Val Asn Thr Asp Ser Ser Thr Ser Gly Trp Lys Leu Ser Pro
305      310      315      320
Val Thr His Val Glu Thr Lys Gln Met Leu Arg Met Ile Pro Ile
      325      330      335
Leu Ala Ala Thr Leu Ile Pro Ser Ala Met Val Ala Gln Ile Gly Thr
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Leu Phe Val Lys Gln Gly Ile Thr Leu Asp Arg Gly Ile Gly Ser Phe
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Asn Ile Pro Pro Ala Ser Leu Ala Thr Phe Val Thr Leu Ser Met Leu
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      450      455      460
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465      470      475      480
Tyr Asp Gln Ala Pro Glu Ser Met Lys Ser Leu Gly Thr Ser Tyr Ser
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PF59082SeqList_PF59082.txt

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116

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164

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 25 30 35

212

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 Glu Cys Cys Glu Arg Leu Ala Tyr Tyr Gly Met Ser Thr Asn Leu Val
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260

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 Leu Tyr Phe Lys Asn Arg Leu Asn Gln His Ser Ala Thr Ala Ser Lys
 55 60 65

308

aat gtc tct aat tgg agt gga act tgc tat atc aca cca ttg att ggg
 Asn Val Ser Asn Trp Ser Gly Thr Cys Tyr Ile Thr Pro Leu Ile Gly
 70 75 80 85

356

gca tat ttg gct gat tcc tac ctt gga aga tat tgg aca att gct gtt
 Ala Tyr Leu Ala Asp Ser Tyr Leu Gly Arg Tyr Trp Thr Ile Ala Val
 90 95 100

404

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 Phe Ser Ile Ile Tyr Ala Ile Gly Met Thr Leu Leu Thr Leu Ser Ala
 105 110 115

452

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 Ser Val Pro Gly Ile Lys Pro Thr Cys His Gly His Gly Asp Glu Asn
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500

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 Cys Arg Ala Thr Thr Leu Glu Ser Ala Val Cys Phe Leu Ala Leu Tyr
 135 140 145

548

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 150 155 160 165

596

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 170 175 180

644

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 Ser Ser Phe Phe Asn Trp Phe Tyr Phe Ser Ile Asn Ile Gly Ala Leu
 185 190 195

692

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 Ile Ala Ser Ser Leu Leu Val Trp Ile Gln Asp Asn Val Gly Trp Gly
 200 205 210

740

tgg ggc ttt ggt att cct gct gta gcc atg gca att gct gtg gtg agt
 Trp Gly Phe Gly Ile Pro Ala Val Ala Met Ala Ile Ala Val Val Ser
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788

ttc ttt tca ggc act agg ttg tat agg aat cag aag cct gga ggc agt

836

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Ala	Ile	Thr	Arg	Ile 250	Cys	Gln	Val	Val	Met 255	Ala	Ser	Ile	Arg	Lys 260	Tyr	
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Asn	Val	Glu	Val	Pro	Ala	Asp	Glu	Ser	Leu	Leu	Tyr	Glu	Thr	Ala	Glu	
act	gaa	tct	gct	ata	aaa	gga	agc	cga	aag	ctt	gac	cac	aca	aat	gag	980
Thr	Glu	Ser	Ala	Ile	Lys	Gly	Ser	Arg	Lys	Leu	Asp	His	Thr	Asn	Glu	
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Leu	Arg	Phe	Phe	Asp	Lys	Ala	Ala	Val	Leu	Ala	Gln	Ser	Asp	Lys	Val	
aag	gaa	tca	aca	aac	cct	tgg	aga	ctt	tgc	act	gta	act	caa	gtg	gaa	1076
Lys	Glu	Ser	Thr	Asn	Pro	Trp	Arg	Leu	Cys	Thr	Val	Thr	Gln	Val	Glu	
gag	ctg	aaa	tcc	att	tta	aga	ata	ctt	cct	gta	tgg	gcc	act	ggc	atc	1124
Glu	Leu	Lys	Ser	Ile 330	Leu	Arg	Ile	Leu	Pro	Val	Trp	Ala	Thr	Gly 340	Ile	
ata	ttt	tcc	act	gtc	tat	ggt	caa	atg	agc	acc	tta	ttt	gtg	ttg	caa	1172
Ile	Phe	Ser	Thr	Val	Tyr	Gly	Gln	Met	Ser	Thr	Leu	Phe	Val	Leu	Gln	
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Gly	Gln	Thr	Met	Asp	Thr	Arg	Val	Gly	Asn	Ser	Thr	Phe	Lys	Ile	Pro	
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Pro	Ala	Ser	Leu	Ser	Ile	Phe	Asp	Thr	Leu	Ser	Val	Ile	Phe	Trp	Val	
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Pro	Val	Tyr	Asp	Arg	Ile 395	Ile	Val	Pro	Ile	Ala	Thr	Lys	Phe	Thr	Gly 405	
aac	aaa	aat	ggc	cta	act	cag	ctc	cag	aga	atg	gga	att	ggc	ctc	ttc	1364
Asn	Lys	Asn	Gly	Leu	Thr	Gln	Leu	Gln	Arg	Met	Gly	Ile	Gly	Leu	Phe	
ata	tcc	ata	ttt	tcc	atg	gta	gct	gca	gca	ata	ttg	gag	ctc	ata	cgg	1412
Ile	Ser	Ile	Phe	Ser	Met	Val	Ala	Ala	Ala	Ile	Leu	Glu	Leu	Ile	Arg	
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Leu	Arg	Met	Val	Arg	Arg	His	Asn	Tyr	Tyr	Gln	Leu	Glu	Glu	Ile	Pro	
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Met	Thr	Ile	Phe	Trp	Gln	Val	Pro	Gln	Tyr	Phe	Ile	Ile	Gly	Cys	Ala	
gaa	gtc	ttc	tat	ttc	att	ggt	cag	ttg	gag	ttc	ttc	tat	gag	caa	gcc	1556
Glu	Val	Phe	Tyr	Phe	Ile 475	Gly	Gln	Leu	Glu	Phe	Phe	Tyr	Glu	Gln	Ala 485	
cct	gat	gct	atg	cga	agc	ttt	tgt	tct	gct	ctc	tca	ctt	acc	act	gtt	1604
Pro	Asp	Ala	Met	Arg	Ser	Phe	Cys	Ser	Ala	Leu	Ser	Leu	Thr	Thr	Val	
gcg	ctt	gga	cag	tac	ttg	agc	tct	ctg	ctt	gtg	aca	att	gtg	aca	aag	1652
Ala	Leu	Gly	Gln	Tyr	Leu	Ser	Ser	Leu	Leu	Val	Thr	Ile	Val	Thr	Lys	
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Ile	Ser	Thr	Arg	Asn	Gly	Ser	Pro	Gly	Trp	Ile	Pro	Asp	Asn	Leu	Asn	
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Phe	Gly	His	Ile	Asp	Tyr	Phe	Phe	Trp	Leu	Leu	Ala	Leu	Leu	Ser	Val	
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Val	Asn	Leu	Ile	Ala	Phe	Leu	Val	Val	Ser	Met	Leu	Tyr	Thr	Tyr	Lys 565	
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2029

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35 40 45
Ser Thr Asn Leu Val Leu Tyr Phe Lys Asn Arg Leu Asn Gln His Ser
50 55 60
Ala Thr Ala Ser Lys Asn Val Ser Asn Trp Ser Gly Thr Cys Tyr Ile
65 70 75 80
Thr Pro Leu Ile Gly Ala Tyr Leu Ala Asp Ser Tyr Leu Gly Arg Tyr
85 90 95
Trp Thr Ile Ala Val Phe Ser Ile Ile Tyr Ala Ile Gly Met Thr Leu
100 105 110
Leu Thr Leu Ser Ala Ser Val Pro Gly Ile Lys Pro Thr Cys His Gly
115 120 125
His Gly Asp Glu Asn Cys Arg Ala Thr Thr Leu Glu Ser Ala Val Cys
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Phe Leu Ala Leu Tyr Leu Ile Ala Leu Gly Thr Gly Gly Ile Lys Pro
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Cys Val Ser Ser Tyr Gly Ala Asp Gln Phe Asp Asp Thr Asp Ser Ala
165 170 175
Glu Lys Glu Arg Lys Ser Ser Phe Phe Asn Trp Phe Tyr Phe Ser Ile
180 185 190
Asn Ile Gly Ala Leu Ile Ala Ser Ser Leu Leu Val Trp Ile Gln Asp
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Asn Val Gly Trp Gly Trp Gly Phe Gly Ile Pro Ala Val Ala Met Ala
210 215 220
Ile Ala Val Val Ser Phe Phe Ser Gly Thr Arg Leu Tyr Arg Asn Gln
225 230 235 240
Lys Pro Gly Gly Ser Ala Ile Thr Arg Ile Cys Gln Val Val Met Ala
245 250 255
Ser Ile Arg Lys Tyr Asn Val Glu Val Pro Ala Asp Glu Ser Leu Leu
260 265 270
Tyr Glu Thr Ala Glu Thr Glu Ser Ala Ile Lys Gly Ser Arg Lys Leu
275 280 285
Asp His Thr Asn Glu Leu Arg Phe Phe Asp Lys Ala Ala Val Leu Ala
290 295 300
Gln Ser Asp Lys Val Lys Glu Ser Thr Asn Pro Trp Arg Leu Cys Thr
305 310 315 320
Val Thr Gln Val Glu Glu Leu Lys Ser Ile Leu Arg Ile Leu Pro Val
325 330 335
Trp Ala Thr Gly Ile Ile Phe Ser Thr Val Tyr Gly Gln Met Ser Thr
340 345 350
Leu Phe Val Leu Gln Gly Gln Thr Met Asp Thr Arg Val Gly Asn Ser
355 360 365
Thr Phe Lys Ile Pro Pro Ala Ser Leu Ser Ile Phe Asp Thr Leu Ser
370 375 380
Val Ile Phe Trp Val Pro Val Tyr Asp Arg Ile Ile Val Pro Ile Ala
385 390 395 400
Thr Lys Phe Thr Gly Asn Lys Asn Gly Leu Thr Gln Leu Gln Arg Met
405 410 415
Gly Ile Gly Leu Phe Ile Ser Ile Phe Ser Met Val Ala Ala Ile
420 425 430
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Leu Glu Glu Ile Pro Met Thr Ile Phe Trp Gln Val Pro Gln Tyr Phe

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	Ser	Leu	Thr	Thr	Val	Ala	Leu	Gly	Gln	Tyr	Leu	Ser	Ser	Leu	Leu	Val
	Thr	Ile	Val	Thr	Lys	Ile	Ser	Thr	Arg	Asn	Gly	Ser	Pro	Gly	Trp	Ile
	Pro	Asp	Asn	Leu	Asn	Phe	Gly	His	Ile	Asp	Tyr	Phe	Phe	Trp	Leu	Leu
	Ala	Leu	Leu	Ser	Val	Val	Asn	Leu	Ile	Ala	Phe	Leu	Val	Val	Ser	Met
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<400> 1725
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cggtctgctga ggagatccag cgaggaagtg agaa atg tct gcg aac gag gga gag 175
 Met Ser Ala Asn Glu Gly Glu

ctg aag atg agg gtg atc gcc atg ggc ggc gag gcc gcc gcc gag agg 223
 Leu Lys Met Arg Val Ile Ala Met Gly Gly Glu Ala Ala Ala Glu Arg

agg gct gcc gag gag aag ctc tgc gag tac acc ctg gac ggc tcc gtg 271
 Arg Ala Ala Glu Glu Lys Leu Cys Glu Tyr Thr Leu Asp Gly Ser Val

gac atc aag ggg cgg ccg gcg gtg aag ggc aag tcg gga gga tgg ctc 319
 Asp Ile Lys Gly Arg Pro Ala Val Lys Gly Lys Ser Gly Gly Trp Leu

gcc gga ggc ctt att ctc gtg aac cag ggc ctg gcg acg atg gcc ttc 367
 Ala Gly Gly Leu Ile Leu Val Asn Gln Gly Leu Ala Thr Met Ala Phe

ttc ggc gtg aac gtg aac ctg gtg ctg ttc ctg acg agg gtg gtg cag 415
 Phe Gly Val Asn Val Asn Leu Val Leu Phe Leu Thr Arg Val Val Gln

cag agc aac ggc gac gcg gcc aac aac gtg agc aag tgg acc ggc acc 463
 Gln Ser Asn Gly Asp Ala Ala Asn Asn Val Ser Lys Trp Thr Gly Thr

gtc tac atg ttc tcc ctc atc ggc gcc ttc ctc agc gac tcc tac tgg 511
 Val Tyr Met Phe Ser Leu Ile Gly Ala Phe Leu Ser Asp Ser Tyr Trp

ggc cgc tac aag acc tgc gcc atc ttc cag gcc atc ttc gtc ctc ggg 559
 Gly Arg Tyr Lys Thr Cys Ala Ile Phe Gln Ala Ile Phe Val Leu Gly

ctc ggg ctg ctg tcg ctc tcc tcg cgg cta tac ctc atc agg ccg gtg 607
 Leu Gly Leu Leu Ser Leu Ser Ser Arg Leu Tyr Leu Ile Arg Pro Val

ggg tgc ggc acg gag cac acg ccc tgc gcc tcg cac tcc ggc acg gag 655
 Gly Cys Gly Thr Glu His Thr Pro Cys Ala Ser His Ser Gly Thr Glu

atg ggg atc ttc tac atc gcg ctc tac atg atc gcc ttc ggc aac ggc 703
 Met Gly Ile Phe Tyr Ile Ala Leu Tyr Met Ile Ala Phe Gly Asn Gly

ggc tac cag ccc aac atc gcc acc ttc ggg gcc gac cag ttc gac gag 751

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Glu	Asp	Pro	Ala	Glu	Ala	His	Ser	Lys	Val	Ser	Phe	Phe	Ser	Tyr	Phe	
200					205					210					215	
tac	ctg	gcg	ctc	aac	ctc	ggc	tcg	ctc	ttc	tcc	aac	acc	ttc	ctc	agc	847
Tyr	Leu	Ala	Leu	Asn	Leu	Gly	Ser	Leu	Phe	Ser	Asn	Thr	Phe	Leu	Ser	
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tac	ctc	cag	gac	cac	ggc	aag	tgg	gtt	atc	ggg	ttc	tgg	gcc	tcc	acc	895
Tyr	Leu	Gln	Asp	His	Gly	Lys	Trp	Val	Ile	Gly	Phe	Trp	Ala	Ser	Thr	
			235					240					245			
gcc	gcc	gcc	gcc	acc	gcc	ctg	ctg	ctc	ttc	ctc	agc	ggc	acg	ccc	cag	943
Ala	Ala	Ala	Ala	Thr	Ala	Leu	Leu	Leu	Phe	Leu	Ser	Gly	Thr	Pro	Gln	
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Tyr	Arg	His	Ala	Gln	Pro	Cys	Gly	Asn	Pro	Met	Ala	Ser	Ile	Cys	Gln	
	265					270					275					
gtc	gcc	tcc	gcc	gcc	tgc	agg	aac	tgg	aag	tcc	ggc	ggc	gtg	tcg	cag	1039
Val	Ala	Ser	Ala	Ala	Cys	Arg	Asn	Trp	Lys	Ser	Gly	Gly	Val	Ser	Gln	
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Asp	Val	Glu	Ile	Leu	Tyr	Glu	Gly	Asp	Asp	Lys	Thr	Asp	Ala	Gly	Ser	
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Arg	Lys	Leu	Leu	His	Thr	Lys	Gly	Phe	Arg	Phe	Leu	Asp	Arg	Ala	Ala	
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Leu	Thr	Thr	Glu	Asp	Thr	Ser	Ser	Lys	Leu	Ala	Thr	Cys	Ser	Lys	Thr	
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Arg	Asp	Gln	Trp	Lys	Leu	Cys	Thr	Val	Thr	Gln	Val	Glu	Gln	Val	Lys	
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Ser	Ile	Leu	Arg	Ile	Leu	Pro	Ile	Trp	Val	Cys	Thr	Ile	Leu	Tyr	Ser	
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gtc	gtc	ttc	acc	cag	atg	gcg	tcg	ctc	ttc	gtc	gtg	cag	gga	gcc	gcg	1327
Val	Val	Phe	Thr	Gln	Met	Ala	Ser	Leu	Phe	Val	Val	Gln	Gly	Ala	Ala	
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Met	Arg	Arg	Ser	Thr	Pro	Leu	Gly	Ser	Phe	Ser	Ile	Pro	Ala	Ser	Ser	
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Met	Ser	Ala	Phe	Asp	Ile	Leu	Thr	Val	Ala	Thr	Thr	Ile	Phe	Leu	Tyr	
		410				415						420				
cgg	cgg	gcc	atc	tgc	ccg	ttc	ctg	gca	cgg	ttc	act	gga	cgc	tcg	acc	1471
Arg	Arg	Ala	Ile	Cys	Pro	Phe	Leu	Ala	Arg	Phe	Thr	Gly	Arg	Ser	Thr	
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Ala	Thr	Thr	Ala	Asn	Ser	Ser	Glu	Leu	His	Ile	Leu	Trp	Gln	Val	Pro	
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Gln	Tyr	Ala	Leu	Ile	Gly	Val	Ser	Glu	Val	Met	Met	Tyr	Val	Gly	Gln	
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Leu	Glu	Phe	Phe	Asn	Gly	Glu	Met	Pro	Asp	Gly	Phe	Lys	Ser	Phe	Gly	
		505				510					515					
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Ser	Ala	Leu	Cys	Met	Met	Ser	Met	Ser	Leu	Gly	Asn	Tyr	Phe	Ser	Asp	
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Ile	Ile	Val	Ser	Ala	Val	Thr	Lys	Ala	Thr	Ala	Val	Asp	Gly	Arg	Pro	
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<212> PRT

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Tyr	Thr	Leu	Asp	Gly	Ser	Val	Asp	Ile	Lys	Gly	Arg	Pro	Ala	Val	Lys		
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Gln	Ala	Ile	Phe	Val	Leu	Gly	Leu	Gly	Leu	Leu	Ser	Leu	Ser	Ser	Arg		
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			165						170					175			
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 Pro Met Ala Ser Ile Cys Gln Val Ala Ser Ala Ala Cys Arg Asn Trp
 275 280 285
 Lys Ser Gly Gly Val Ser Gln Asp Val Glu Ile Leu Tyr Glu Gly Asp
 290 295 300
 Asp Lys Thr Asp Ala Gly Ser Arg Lys Leu Leu His Thr Lys Gly Phe
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 Arg Phe Leu Asp Arg Ala Ala Leu Thr Thr Glu Asp Thr Ser Ser Lys
 325 330 335
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 340 345 350
 Thr Gln Val Glu Gln Val Lys Ser Ile Leu Arg Ile Leu Pro Ile Trp
 355 360 365
 Val Cys Thr Ile Leu Tyr Ser Val Val Phe Thr Gln Met Ala Ser Leu
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 Phe Val Val Gln Gly Ala Ala Met Arg Arg Ser Thr Pro Leu Gly Ser
 385 390 395 400
 Phe Ser Ile Pro Ala Ser Ser Met Ser Ala Phe Asp Ile Leu Thr Val
 405 410 415
 Ala Thr Thr Ile Phe Leu Tyr Arg Arg Ala Ile Cys Pro Phe Leu Ala
 420 425 430
 Arg Phe Thr Gly Arg Ser Thr Gly Pro Thr Glu Leu Gln Arg Met Gly
 435 440 445
 Leu Gly Leu Val Leu Gly Ala Met Ala Met Ala Thr Ala Gly Thr Val
 450 455 460
 Glu His Phe Arg Lys Ala Ser Ala Thr Thr Ala Asn Ser Ser Glu Leu
 465 470 475 480
 His Ile Leu Trp Gln Val Pro Gln Tyr Ala Leu Ile Gly Val Ser Glu
 485 490 495
 Val Met Met Tyr Val Gly Gln Leu Glu Phe Phe Asn Gly Glu Met Pro
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 Asp Gly Phe Lys Ser Phe Gly Ser Ala Leu Cys Met Met Ser Met Ser
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 Thr Ala Val Asp Gly Arg Pro Gly Trp Ile Pro Ala Asp Leu Asn Glu
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 Gly His Leu Asn Lys Phe Tyr Phe Leu Leu Ala Ile Leu Ser Val Ala
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<400> 1727

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Thr	Leu	Asp	His	Lys	Gly	Asn	Pro	Ala	Asp	Lys	Arg	Ile	Thr	
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tgg	aaa	gca	tgt	ccc	ttt	atc	ata	gga	aat	gaa	tgc	tgc	gag	
Trp	Lys	Ala	Cys	Pro	Phe	Ile	Ile	Gly	Asn	Glu	Cys	Cys	Glu	
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														cag

52

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148

196

PF59082SeqList_PF59082.txt

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Leu	Asn	Gln	Ser	Ser	Ala	Thr	Ala	Thr	Lys	Asn	Asn	Ser	Asp	Trp	Ser	
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gga	act	tgt	tac	ctc	aca	cct	cta	ttg	gga	gcc	ttt	ctt	gct	gat	gct	292
Gly	Thr	Cys	Tyr	Leu	Thr	Pro	Leu	Leu	Gly	Ala	Phe	Leu	Ala	Asp	Ala	
				80					85						90	
tat	ctt	ggt	aga	tac	tgg	act	att	gct	ggc	ttc	tca	atc	atc	tat	gtc	340
Tyr	Leu	Gly	Arg	Tyr	Trp	Thr	Ile	Ala	Gly	Phe	Ser	Ile	Ile	Tyr	Val	
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Phe	Gly	Met	Thr	Leu	Leu	Ala	Met	Ser	Ala	Ser	Val	Pro	Gly	Leu	Lys	
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cca	aca	tgc	ata	tca	aaa	gac	aac	tgc	cac	gcc	aca	gaa	gga	cag	agc	436
Pro	Thr	Cys	Ile	Ser	Lys	Asp	Asn	Cys	His	Ala	Thr	Glu	Gly	Gln	Ser	
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gcg	gtt	ttc	ttc	gta	gct	ctc	tac	atg	ata	gct	cta	ggg	aca	gga	ggg	484
Ala	Val	Phe	Phe	Val	Ala	Leu	Tyr	Met	Ile	Ala	Leu	Gly	Thr	Gly	Gly	
140				145						150					155	
atc	aag	cct	tgt	gtc	tca	tcc	tac	ggg	gcg	gac	cag	ttt	gat	gat	gct	532
Ile	Lys	Pro	Cys	Val	Ser	Ser	Tyr	Gly	Ala	Asp	Gln	Phe	Asp	Asp	Ala	
				160				165							170	
gac	gtg	gaa	gag	aag	gag	cac	aag	gcc	tct	ttc	ttc	aat	tgg	ttc	tac	580
Asp	Val	Glu	Glu	Lys	Glu	His	Lys	Ala	Ser	Phe	Phe	Asn	Trp	Phe	Tyr	
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ttc	tcc	atc	aac	gtt	ggt	gca	ttg	gtt	gct	agc	tcc	tta	ctg	gtt	tgg	628
Phe	Ser	Ile	Asn	Val	Gly	Ala	Leu	Val	Ala	Ser	Ser	Leu	Leu	Val	Trp	
		190				195						200				
gtc	cag	gag	aat	gtg	agc	tgg	gga	ttg	ggg	ttt	ggg	atc	ccg	gcc	ata	676
Val	Gln	Glu	Asn	Val	Ser	Trp	Gly	Leu	Gly	Phe	Gly	Ile	Pro	Ala	Ile	
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gcc	atg	gct	att	gct	gtt	gcg	agt	ttc	ttt	tca	ggg	acc	cgc	aag	tat	724
Ala	Met	Ala	Ile	Ala	Val	Ala	Ser	Phe	Phe	Ser	Gly	Thr	Arg	Lys	Tyr	
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agg	tat	cag	acg	cct	ggt	ggt	agc	cct	ctt	act	aga	atc	tgt	cag	gtc	772
Arg	Tyr	Gln	Thr	Pro	Gly	Gly	Ser	Pro	Leu	Thr	Arg	Ile	Cys	Gln	Val	
				240				245						250		
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Ile	Val	Ala	Ser	Cys	Arg	Lys	Tyr	Lys	Val	Ser	Pro	Pro	Asn	Asp	Lys	
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Ser	Leu	Leu	Tyr	Glu	Ser	Ala	Asp	Ser	Glu	Ser	Gly	Ile	Thr	Gly	Ser	
				270			275					280				
cgg	aaa	ctc	gat	cac	acc	aaa	gat	ttc	agt	ttc	ctg	gac	aag	gca	gca	916
Arg	Lys	Leu	Asp	His	Thr	Lys	Asp	Phe	Ser	Phe	Leu	Asp	Lys	Ala	Ala	
		285				290					295					
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Val	Glu	Thr	Glu	Lys	Asp	His	Ile	Lys	Asp	Thr	Ser	Val	Asn	Pro	Trp	
300				305						310					315	
agg	cta	tgc	aca	gta	acc	caa	atc	gag	gaa	ttc	aaa	gca	ata	atc	cgc	1012
Arg	Leu	Cys	Thr	Val	Thr	Gln	Ile	Glu	Glu	Phe	Lys	Ala	Ile	Ile	Arg	
				320				325						330		
ctg	ctc	ccg	atc	tgg	gca	acc	ggt	ata	gtc	ttc	gca	gca	gta	tac	agc	1060
Leu	Leu	Pro	Ile	Trp	Ala	Thr	Gly	Ile	Val	Phe	Ala	Ala	Val	Tyr	Ser	
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caa	atg	agc	aac	ctt	ttc	gtc	cta	cag	gga	gac	aca	atg	gac	aag	cga	1108
Gln	Met	Ser	Asn	Leu	Phe	Val	Leu	Gln	Gly	Asp	Thr	Met	Asp	Lys	Arg	
		350				355						360				
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Val	Gly	Asn	Ser	Lys	Phe	Lys	Ile	Ser	Ala	Ala	Asn	Val	Ser	Val	Phe	
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Asp	Thr	Ile	Ser	Val	Ile	Phe	Trp	Val	Pro	Ile	Tyr	Asp	Arg	Leu	Ile	
				385						390					395	
gtc	cca	gcc	gtc	aga	aaa	atc	aca	ggc	cac	aag	aac	ggg	ttc	acc	cag	1252
Val	Pro	Ala	Val	Arg	Lys	Ile	Thr	Gly	His	Lys	Asn	Gly	Phe	Thr	Gln	
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PF59082SeqList_PF59082.txt

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Tyr	Pro	Ala	Ile	Leu	Glu	Leu	Ile	Arg	Leu	Lys	Met	Val	Arg	Glu	His		
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Asn	Tyr	Tyr	Glu	Leu	Glu	Ser	Val	Pro	Ile	Ser	Ile	Phe	Trp	Gln	Val		
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ccg	cag	tat	ttc	ctg	atc	ggt	tgc	gct	gag	gtg	ttc	act	ttc	atc	ggt		1444
Pro	Gln	Tyr	Phe	Leu	Ile	Gly	Cys	Ala	Glu	Val	Phe	Thr	Phe	Ile	Gly		
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cag	ctc	gag	ttc	ttc	tac	gag	cag	gcg	ccc	gat	gcg	atg	agg	agc	ttg		1492
Gln	Leu	Glu	Phe	Phe	Tyr	Glu	Gln	Ala	Pro	Asp	Ala	Met	Arg	Ser	Leu		
			480					485						490			
tgt	tcg	gct	ctt	tcg	ttg	act	act	gtg	gcg	ttg	ggg	aat	tac	ttg	agc		1540
Cys	Ser	Ala	Leu	Ser	Leu	Thr	Thr	Val	Ala	Leu	Gly	Asn	Tyr	Leu	Ser		
			495					500					505				
tcg	ctg	ctg	gtg	acg	att	gtg	acg	ggt	ggt	acg	act	aag	gga	ggg	aag		1588
Ser	Leu	Leu	Val	Thr	Ile	Val	Thr	Gly	Val	Thr	Thr	Lys	Gly	Gly	Lys		
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ccc	ggg	tgg	att	cct	gat	aac	ttg	aac	tat	ggc	cat	ggt	gat	tac	ttc		1636
Pro	Gly	Trp	Ile	Pro	Asp	Asn	Leu	Asn	Tyr	Gly	His	Val	Asp	Tyr	Phe		
		525				530					535						
ttc	tgg	ctg	ctg	gct	gtg	ctt	agt	ggt	gtg	aat	ctg	atg	gcg	tat	atg		1684
Phe	Trp	Leu	Leu	Ala	Val	Leu	Ser	Val	Val	Asn	Leu	Met	Ala	Tyr	Met		
		540			545				550						555		
gtg	att	gct	agc	tgg	tat	act	tac	aag	aag	cct	gtg	ggg	act	ctg	cgt		1732
Val	Ile	Ala	Ser	Trp	Tyr	Thr	Tyr	Lys	Lys	Pro	Val	Gly	Thr	Leu	Arg		
			560					565						570			
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<213> Linum usitatissimum

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			20					25					30				
Phe	Ile	Ile	Gly	Asn	Glu	Cys	Cys	Glu	Arg	Leu	Ala	Tyr	Tyr	Gly	Met		
		35				40						45					
Ser	Ser	Asn	Leu	Val	Leu	Tyr	Phe	Lys	Asn	Gln	Leu	Asn	Gln	Ser	Ser		
		50				55					60						
Ala	Thr	Ala	Thr	Lys	Asn	Asn	Ser	Asp	Trp	Ser	Gly	Thr	Cys	Tyr	Leu		
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Thr	Pro	Leu	Leu	Gly	Ala	Phe	Leu	Ala	Asp	Ala	Tyr	Leu	Gly	Arg	Tyr		
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Trp	Thr	Ile	Ala	Gly	Phe	Ser	Ile	Ile	Tyr	Val	Phe	Gly	Met	Thr	Leu		
			100					105					110				
Leu	Ala	Met	Ser	Ala	Ser	Val	Pro	Gly	Leu	Lys	Pro	Thr	Cys	Ile	Ser		
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Lys	Asp	Asn	Cys	His	Ala	Thr	Glu	Gly	Gln	Ser	Ala	Val	Phe	Phe	Val		
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Ala	Leu	Tyr	Met	Ile	Ala	Leu	Gly	Thr	Gly	Gly	Ile	Lys	Pro	Cys	Val		
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PF59082SeqList_PF59082.txt

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 Ser Trp Gly Leu Gly Phe Gly Ile Pro Ala Ile Ala Met Ala Ile Ala
 210 215 220
 Val Ala Ser Phe Phe Ser Gly Thr Arg Lys Tyr Arg Tyr Gln Thr Pro
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 Gly Gly Ser Pro Leu Thr Arg Ile Cys Gln Val Ile Val Ala Ser Cys
 245 250 255
 Arg Lys Tyr Lys Val Ser Pro Pro Asn Asp Lys Ser Leu Leu Tyr Glu
 260 265 270
 Ser Ala Asp Ser Glu Ser Gly Ile Thr Gly Ser Arg Lys Leu Asp His
 275 280 285
 Thr Lys Asp Phe Ser Phe Leu Asp Lys Ala Ala Val Glu Thr Glu Lys
 290 295 300
 Asp His Ile Lys Asp Thr Ser Val Asn Pro Trp Arg Leu Cys Thr Val
 305 310 315 320
 Thr Gln Ile Glu Glu Phe Lys Ala Ile Ile Arg Leu Leu Pro Ile Trp
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 355 360 365
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 370 375 380
 Ile Phe Trp Val Pro Ile Tyr Asp Arg Leu Ile Val Pro Ala Val Arg
 385 390 395 400
 Lys Ile Thr Gly His Lys Asn Gly Phe Thr Gln Leu Gln Arg Met Gly
 405 410 415
 Ile Gly Leu Val Ile Ser Ile Phe Ala Met Val Tyr Pro Ala Ile Leu
 420 425 430
 Glu Leu Ile Arg Leu Lys Met Val Arg Glu His Asn Tyr Tyr Glu Leu
 435 440 445
 Glu Ser Val Pro Ile Ser Ile Phe Trp Gln Val Pro Gln Tyr Phe Leu
 450 455 460
 Ile Gly Cys Ala Glu Val Phe Thr Phe Ile Gly Gln Leu Glu Phe Phe
 465 470 475 480
 Tyr Glu Gln Ala Pro Asp Ala Met Arg Ser Leu Cys Ser Ala Leu Ser
 485 490 495
 Leu Thr Thr Val Ala Leu Gly Asn Tyr Leu Ser Ser Leu Leu Val Thr
 500 505 510
 Ile Val Thr Gly Val Thr Thr Lys Gly Gly Lys Pro Gly Trp Ile Pro
 515 520 525
 Asp Asn Leu Asn Tyr Gly His Val Asp Tyr Phe Phe Trp Leu Leu Ala
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 Tyr Thr Tyr Lys Lys Pro Val Gly Thr Leu Arg
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<211> 1110

<212> DNA

<213> Arabidopsis thaliana

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<221> CDS

<222> (1)..(1110)

<400> 1729

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caa ctc tgc tct tcc ttt cac ggc gag tac tta gct ccg tcg aga tgc 96
 Gln Leu Cys Ser Ser Phe His Gly Glu Tyr Leu Ala Pro Ser Arg Cys
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 Leu Arg

PF59082SeqList_PF59082.txt

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Lys	Asn	Ser	Tyr	Ser	Pro	Arg	Gln	Phe	His	Val	Ser	Ala	Lys	Lys	Val	
	50					55				60						
tct	ggg	tta	gag	gaa	gcc	att	aga	atc	aga	aaa	atg	aga	gag	ctt	gaa	240
Ser	Gly	Leu	Glu	Glu	Ala	Ile	Arg	Ile	Arg	Lys	Met	Arg	Glu	Leu	Glu	
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act	aaa	tca	aaa	gtt	agg	aga	aat	cca	cca	tta	aga	cgt	gga	aga	gta	288
Thr	Lys	Ser	Lys	Val	Arg	Arg	Asn	Pro	Pro	Leu	Arg	Arg	Gly	Arg	Val	
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tcg	cct	cgt	ctt	ctt	gta	cct	gat	cac	att	cca	agg	cct	cct	tat	gtt	336
Ser	Pro	Arg	Leu	Leu	Val	Pro	Asp	His	Ile	Pro	Arg	Pro	Pro	Tyr	Val	
			100					105					110			
gag	tct	ggt	gta	tta	ccg	gat	ata	tca	agt	gag	ttc	cag	att	cct	ggt	384
Glu	Ser	Gly	Val	Leu	Pro	Asp	Ile	Ser	Ser	Glu	Phe	Gln	Ile	Pro	Gly	
		115				120						125				
cct	gaa	ggc	att	gcg	aaa	atg	aga	gct	gct	tgc	gag	ctt	gct	gct	cgg	432
Pro	Glu	Gly	Ile	Ala	Lys	Met	Arg	Ala	Ala	Cys	Glu	Leu	Ala	Ala	Arg	
		130				135					140					
gtt	tta	aac	tat	gct	gga	act	ttg	gtt	aag	cca	tct	gtt	acg	act	aat	480
Val	Leu	Asn	Tyr	Ala	Gly	Thr	Leu	Val	Lys	Pro	Ser	Val	Thr	Thr	Asn	
145				150					155						160	
gaa	atc	gat	aaa	gct	gtg	cat	gat	atg	att	att	gaa	gct	ggg	gct	tat	528
Glu	Ile	Asp	Lys	Ala	Val	His	Asp	Met	Ile	Ile	Glu	Ala	Gly	Ala	Tyr	
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cct	tca	cct	ctt	gga	tat	ggt	gga	ttt	cct	aaa	agt	gtg	tgt	act	tca	576
Pro	Ser	Pro	Leu	Gly	Tyr	Gly	Gly	Phe	Pro	Lys	Ser	Val	Cys	Thr	Ser	
			180					185					190			
gtt	aat	gag	tgt	atg	tgt	cac	gga	ata	cca	gat	tct	cgc	cag	cta	cag	624
Val	Asn	Glu	Cys	Met	Cys	His	Gly	Ile	Pro	Asp	Ser	Arg	Gln	Leu	Gln	
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agc	ggg	gat	ata	atc	aac	atc	gat	gtc	acg	gtt	tac	ttg	gat	ggt	tac	672
Ser	Gly	Asp	Ile	Ile	Asn	Ile	Asp	Val	Thr	Val	Tyr	Leu	Asp	Gly	Tyr	
	210				215						220					
cat	gga	gat	acg	tcg	aga	act	ttc	ttc	tgt	gga	gaa	gtt	gac	gaa	ggt	720
His	Gly	Asp	Thr	Ser	Arg	Thr	Phe	Phe	Cys	Gly	Glu	Val	Asp	Glu	Gly	
225				230					235					240		
ttc	aaa	cga	ctt	gtg	aag	gtt	acg	gaa	gaa	tgt	ttg	gag	aga	ggg	att	768
Phe	Lys	Arg	Leu	Val	Lys	Val	Thr	Glu	Glu	Cys	Leu	Glu	Arg	Gly	Ile	
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gca	gtt	tgt	aaa	gac	gga	gca	agc	ttc	aag	aaa	atc	ggg	aaa	aga	atc	816
Ala	Val	Cys	Lys	Asp	Gly	Ala	Ser	Phe	Lys	Lys	Ile	Gly	Lys	Arg	Ile	
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agt	gag	cat	gcg	gaa	aag	ttc	ggc	tac	aac	gtt	gtg	gag	cgg	ttt	gtt	864
Ser	Glu	His	Ala	Glu	Lys	Phe	Gly	Tyr	Asn	Val	Val	Glu	Arg	Phe	Val	
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ggg	cat	ggt	gtt	gga	cca	gta	ttc	cac	tcc	gaa	cct	ctt	ata	tat	cat	912
Gly	His	Gly	Val	Gly	Pro	Val	Phe	His	Ser	Glu	Pro	Leu	Ile	Tyr	His	
	290				295						300					
tac	cga	aat	gat	gag	cct	gga	cta	atg	gtt	gag	gga	cag	aca	ttc	aca	960
Tyr	Arg	Asn	Asp	Glu	Pro	Gly	Leu	Met	Val	Glu	Gly	Gln	Thr	Phe	Thr	
305				310					315					320		
att	gaa	ccg	att	ctc	acg	att	gga	acc	aca	gaa	tgt	gta	aca	tgg	cca	1008
Ile	Glu	Pro	Ile	Leu	Thr	Ile	Gly	Thr	Thr	Glu	Cys	Val	Thr	Trp	Pro	
				325				330						335		
gac	aac	tgg	act	act	ctg	aca	gca	gat	ggg	ggc	gtc	gct	gct	cag	ttt	1056
Asp	Asn	Trp	Thr	Thr	Leu	Thr	Ala	Asp	Gly	Gly	Val	Ala	Ala	Gln	Phe	
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gag	cat	acc	att	ctg	att	act	aga	act	ggg	tca	gag	att	ctt	acc	aaa	1104
Glu	His	Thr	Ile	Leu	Ile	Thr	Arg	Thr	Gly	Ser	Glu	Ile	Leu	Thr	Lys	
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Cys																

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<212> PRT

<213> Arabidopsis thaliana

<400> 1730

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Phe Leu Gly Ala Pro Val Thr Ser Ser Ser Leu Ser Leu Ser Gly Lys
      35      40      45
Lys Asn Ser Tyr Ser Pro Arg Gln Phe His Val Ser Ala Lys Lys Val
      50      55      60
Ser Gly Leu Glu Glu Ala Ile Arg Ile Arg Lys Met Arg Glu Leu Glu
65      70      75      80
Thr Lys Ser Lys Val Arg Arg Asn Pro Pro Leu Arg Arg Gly Arg Val
      85      90      95
Ser Pro Arg Leu Leu Val Pro Asp His Ile Pro Arg Pro Pro Tyr Val
      100      105      110
Glu Ser Gly Val Leu Pro Asp Ile Ser Ser Glu Phe Gln Ile Pro Gly
      115      120      125
Pro Glu Gly Ile Ala Lys Met Arg Ala Ala Cys Glu Leu Ala Ala Arg
      130      135      140
Val Leu Asn Tyr Ala Gly Thr Leu Val Lys Pro Ser Val Thr Thr Asn
145      150      155      160
Glu Ile Asp Lys Ala Val His Asp Met Ile Ile Glu Ala Gly Ala Tyr
      165      170      175
Pro Ser Pro Leu Gly Tyr Gly Gly Phe Pro Lys Ser Val Cys Thr Ser
      180      185      190
Val Asn Glu Cys Met Cys His Gly Ile Pro Asp Ser Arg Gln Leu Gln
      195      200      205
Ser Gly Asp Ile Ile Asn Ile Asp Val Thr Val Tyr Leu Asp Gly Tyr
      210      215      220
His Gly Asp Thr Ser Arg Thr Phe Phe Cys Gly Glu Val Asp Glu Gly
225      230      235      240
Phe Lys Arg Leu Val Lys Val Thr Glu Glu Cys Leu Glu Arg Gly Ile
      245      250      255
Ala Val Cys Lys Asp Gly Ala Ser Phe Lys Lys Ile Gly Lys Arg Ile
      260      265      270
Ser Glu His Ala Glu Lys Phe Gly Tyr Asn Val Val Glu Arg Phe Val
      275      280      285
Gly His Gly Val Gly Pro Val Phe His Ser Glu Pro Leu Ile Tyr His
      290      295      300
Tyr Arg Asn Asp Glu Pro Gly Leu Met Val Glu Gly Gln Thr Phe Thr
305      310      315      320
Ile Glu Pro Ile Leu Thr Ile Gly Thr Thr Glu Cys Val Thr Trp Pro
      325      330      335
Asp Asn Trp Thr Thr Leu Thr Ala Asp Gly Gly Val Ala Ala Gln Phe
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<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (32)..(1138)

<400> 1731

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tcc act ttc tcg tct gct cac ctc tct tct tct ttc gcc ggc gac tac      100
Ser Thr Phe Ser Ser Ala His Leu Ser Ser Ser Phe Ala Gly Asp Tyr
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gta gcg tcg tcg agg tgc ttt atc gga gct ccc gtc gct tcc tcc tct      148
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PF59082SeqList_PF59082.txt

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Ser	Leu	Ser	Leu	Leu	Ser	Gly	Lys	Lys	Asn	Ser	Tyr	Pro	Leu	Arg	Lys	
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Phe	His	Val	Ser	Ala	Lys	Lys	Val	Ser	Gly	Leu	Glu	Glu	Ala	Ile	Arg	
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atc	aga	agg	atg	aga	gaa	gct	gaa	gct	agt	tca	aag	gtc	aag	aga	aac	292
Ile	Arg	Arg	Met	Arg	Glu	Ala	Glu	Ala	Ser	Ser	Lys	Val	Lys	Arg	Asn	
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cca	ccg	tta	aga	cga	ggg	aga	gtc	tca	cct	cgt	ctt	ctc	gtc	cct	gac	340
Pro	Pro	Leu	Arg	Arg	Gly	Arg	Val	Ser	Pro	Arg	Leu	Leu	Val	Pro	Asp	
	90					95					100					
cac	ata	cca	aag	cct	cct	tac	gct	gag	tcc	ggc	gtg	tta	cct	gat	atc	388
His	Ile	Pro	Lys	Pro	Pro	Tyr	Ala	Glu	Ser	Gly	Val	Leu	Pro	Asp	Ile	
	105					110					115					
tca	cct	gac	ttc	cag	att	cct	tcc	cct	gaa	ggc	ctt	gtc	aaa	atg	aga	436
Ser	Pro	Asp	Phe	Gln	Ile	Pro	Ser	Pro	Glu	Gly	Leu	Val	Lys	Met	Arg	
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gct	gct	tgc	gag	cta	gct	gct	cgg	gtt	cta	aac	ttt	gca	ggg	act	ttg	484
Ala	Ala	Cys	Glu	Leu	Ala	Ala	Arg	Val	Leu	Asn	Phe	Ala	Gly	Thr	Leu	
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Val	Lys	Pro	Ser	Val	Thr	Thr	Asn	Glu	Ile	Asp	Lys	Ala	Val	His	Asp	
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Met	Ile	Val	Glu	Ala	Gly	Ala	Tyr	Pro	Ser	Pro	Leu	Gly	Tyr	Gly	Gly	
	170					175						180				
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Phe	Pro	Lys	Ser	Val	Cys	Thr	Ser	Val	Asn	Glu	Cys	Met	Cys	His	Gly	
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ata	ccg	gat	tct	cgc	cag	ctt	cag	agt	ggg	gat	ata	att	aac	atc	gat	676
Ile	Pro	Asp	Ser	Arg	Gln	Leu	Gln	Ser	Gly	Asp	Ile	Ile	Asn	Ile	Asp	
	200				205				210					215		
gtc	acg	gtt	tac	ttg	gat	ggt	tac	cat	gga	gat	aca	tca	aga	act	ttc	724
Val	Thr	Val	Tyr	Leu	Asp	Gly	Tyr	His	Gly	Asp	Thr	Ser	Arg	Thr	Phe	
			220					225						230		
ttc	tgt	gga	gag	gtc	gat	gaa	ggt	ttt	aaa	cga	ctt	gtg	aag	gtt	acg	772
Phe	Cys	Gly	Glu	Val	Asp	Glu	Gly	Phe	Lys	Arg	Leu	Val	Lys	Val	Thr	
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gag	gaa	tgt	ttg	gag	aaa	ggt	ata	gcg	gtt	tgt	aaa	gat	gga	gca	aac	820
Glu	Glu	Cys	Leu	Glu	Lys	Gly	Ile	Ala	Val	Cys	Lys	Asp	Gly	Ala	Asn	
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Phe	Lys	Lys	Ile	Gly	Lys	Arg	Ile	Ser	Glu	His	Ala	Glu	Lys	Tyr	Gly	
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Tyr	Asn	Val	Val	Glu	Arg	Phe	Val	Gly	His	Gly	Val	Gly	Pro	Val	Phe	
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cac	tct	gaa	cct	ttg	att	tat	cat	tac	cga	aat	gat	gag	cca	ggg	cat	964
His	Ser	Glu	Pro	Leu	Ile	Tyr	His	Tyr	Arg	Asn	Asp	Glu	Pro	Gly	His	
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Met	Val	Glu	Gly	Gln	Thr	Phe	Thr	Ile	Glu	Pro	Ile	Leu	Thr	Ile	Gly	
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Thr	Thr	Glu	Cys	Val	Thr	Trp	Pro	Asp	Asn	Trp	Thr	Thr	Leu	Thr	Ala	
		330				335						340				
gat	ggt	ggt	gta	gcc	gca	cag	ttt	gag	cac	aca	att	ctg	att	act	aga	1108
Asp	Gly	Gly	Val	Ala	Ala	Gln	Phe	Glu	His	Thr	Ile	Leu	Ile	Thr	Arg	
	345					350					355					
act	ggt	tca	gag	att	ctt	acc	gta	tgc	tga	aacaattcac	ttttgattca					1158
Thr	Gly	Ser	Glu	Ile	Leu	Thr	Val	Cys								
	360				365											
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caatagaata	tacctttcat	atggttttta	tgattaatgc	gcgtgttgtc	gtagactttt											1278

PF59082SeqList_PF59082.txt

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caaataatta taattttctc aaaaaaaaaa aaaaa 1373

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<212> PRT
<213> Brassica napus

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35 40 45
Asn Ser Tyr Pro Leu Arg Lys Phe His Val Ser Ala Lys Lys Val Ser
50 55 60
Gly Leu Glu Glu Ala Ile Arg Ile Arg Arg Met Arg Glu Ala Glu Ala
65 70 75 80
Ser Ser Lys Val Lys Arg Asn Pro Pro Leu Arg Arg Gly Arg Val Ser
85 90 95
Pro Arg Leu Leu Val Pro Asp His Ile Pro Lys Pro Pro Tyr Ala Glu
100 105 110
Ser Gly Val Leu Pro Asp Ile Ser Pro Asp Phe Gln Ile Pro Ser Pro
115 120 125
Glu Gly Leu Val Lys Met Arg Ala Ala Cys Glu Leu Ala Ala Arg Val
130 135 140
Leu Asn Phe Ala Gly Thr Leu Val Lys Pro Ser Val Thr Thr Asn Glu
145 150 155 160
Ile Asp Lys Ala Val His Asp Met Ile Val Glu Ala Gly Ala Tyr Pro
165 170 175
Ser Pro Leu Gly Tyr Gly Gly Phe Pro Lys Ser Val Cys Thr Ser Val
180 185 190
Asn Glu Cys Met Cys His Gly Ile Pro Asp Ser Arg Gln Leu Gln Ser
195 200 205
Gly Asp Ile Ile Asn Ile Asp Val Thr Val Tyr Leu Asp Gly Tyr His
210 215 220
Gly Asp Thr Ser Arg Thr Phe Phe Cys Gly Glu Val Asp Glu Gly Phe
225 230 235 240
Lys Arg Leu Val Lys Val Thr Glu Glu Cys Leu Glu Lys Gly Ile Ala
245 250 255
Val Cys Lys Asp Gly Ala Asn Phe Lys Lys Ile Gly Lys Arg Ile Ser
260 265 270
Glu His Ala Glu Lys Tyr Gly Tyr Asn Val Val Glu Arg Phe Val Gly
275 280 285
His Gly Val Gly Pro Val Phe His Ser Glu Pro Leu Ile Tyr His Tyr
290 295 300
Arg Asn Asp Glu Pro Gly His Met Val Glu Gly Gln Thr Phe Thr Ile
305 310 315 320
Glu Pro Ile Leu Thr Ile Gly Thr Thr Glu Cys Val Thr Trp Pro Asp
325 330 335
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<213> Hordeum vulgare

<220>
<221> CDS

PF59082SeqList_PF59082.txt

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Gly	Ala	Leu	Ser	Ala	Arg	Pro	Leu	Leu	
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Gly	His	Arg	Arg	Val	Thr	Cys	Gln	Ala	
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Val	Asp	Ala	Leu	Phe	Asn	Arg	Arg	Ser	
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Asn	Pro	Arg	Arg	Leu	Arg	Gly	Lys	Val	
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ccc	agt	cat	ata	cag	cag	cct	cct	tat	343
Pro	Ser	His	Ile	Gln	Gln	Pro	Pro	Tyr	
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Gln	Met	Asn	Gly	Gly	Pro	Glu	Ile	His	
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Met	Arg	Ala	Ser	Gly	Lys	Leu	Ala	Ala	
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aca	ctt	gta	aat	cca	ggc	ata	aca	act	487
Thr	Leu	Val	Asn	Pro	Gly	Ile	Thr	Thr	
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cac	caa	atg	ata	atc	gat	aat	ggg	gca	535
His	Gln	Met	Ile	Ile	Asp	Asn	Gly	Ala	
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Cys	Gly	Phe	Pro	Lys	Ser	Val	Cys	Thr	
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cac	ggg	ata	cca	gat	tct	cg	cca	ctt	631
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Ile	Asp	Val	Thr	Val	Tyr	Leu	Asn	Gly	
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aca	ttt	ctc	tgt	ggg	gat	gtt	gat	gaa	727
Thr	Phe	Leu	Cys	Gly	Asp	Val	Asp	Asp	
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gta	aca	aaa	gaa	tct	ctt	gac	aag	gct	775
Val	Thr	Lys	Glu	Ser	Leu	Asp	Lys	Ala	
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gtg	gag	atc	aac	cg	att	ggg	aga	acc	823
Val	Glu	Ile	Asn	Arg	Ile	Gly	Arg	Thr	
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ttc	aag	tat	ggg	gta	gtt	caa	caa	ttt	871
Phe	Lys	Tyr	Gly	Val	Val	Gln	Gln	Phe	
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gtg	ttc	cat	tgc	gag	cct	gca	gtg	ctt	919
Val	Phe	His	Cys	Glu	Pro	Ala	Val	Leu	
					280				
ggc	cg	atg	att	ttg	aac	caa	aca	ttt	967
Gly	Arg	Met	Ile	Leu	Asn	Gln	Thr	Phe	
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Ile	Gly	Ser	Thr	Asn	Ser	Ser	Ile	Trp	
					310				
acg	gag	gat	ggg	agc	ctg	tca	gcg	cag	1063
Thr	Glu	Asp	Gly	Ser	Leu	Ser	Ala	Gln	
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PF59082SeqList_PF59082.txt

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 35 40 45
 Leu Ser Ser Leu Val Asp Ala Leu Phe Asn Arg Arg Ser Arg Asp Asp
 50 55 60
 Ser Leu Glu Asn Asn Pro Arg Arg Leu Arg Pro Gly Lys Val Ser Pro
 65 70 75 80
 Arg Leu Thr Val Pro Ser His Ile Gln Gln Pro Pro Tyr Val Asn Ser
 85 90 95
 Arg Gln Arg Pro Gln Met Asn Gly Gly Pro Glu Ile His Asp Glu Lys
 100 105 110
 Gly Ile Glu Cys Met Arg Ala Ser Gly Lys Leu Ala Ala Gln Val Leu
 115 120 125
 Lys Phe Ala Gly Thr Leu Val Asn Pro Gly Ile Thr Thr Asp Glu Ile
 130 135 140
 Asp Lys Ala Val His Gln Met Ile Ile Asp Asn Gly Ala Tyr Pro Ser
 145 150 155 160
 Pro Leu Gly Tyr Cys Gly Phe Pro Lys Ser Val Cys Thr Ser Val Asn
 165 170 175
 Glu Cys Ile Cys His Gly Ile Pro Asp Ser Arg Pro Leu Glu Asp Gly
 180 185 190
 Asp Ile Ile Asn Ile Asp Val Thr Val Tyr Leu Asn Gly Tyr His Gly
 195 200 205
 Asp Thr Ser Ala Thr Phe Leu Cys Gly Asp Val Asp Asp Glu Ala Lys
 210 215 220
 Lys Leu Val Gln Val Thr Lys Glu Ser Leu Asp Lys Ala Ile Ser Ile
 225 230 235 240
 Cys Ala Pro Gly Val Glu Ile Asn Arg Ile Gly Arg Thr Ile Gln Asp
 245 250 255
 Tyr Ala Asp Lys Phe Lys Tyr Gly Val Val Gln Gln Phe Val Gly His
 260 265 270
 Gly Val Gly Lys Val Phe His Cys Glu Pro Ala Val Leu His Phe Arg
 275 280 285
 Asn Ser Glu Lys Gly Arg Met Ile Leu Asn Gln Thr Phe Thr Ile Glu
 290 295 300

PF59082SeqList_PF59082.txt

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<220>
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 Thr Asn Phe Ala Pro Leu Leu Gly Ala Leu Ile Ser Asp Ala Tyr Ile
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 ggc cgt ttc aag acc atc gct tac gca tcc ctc ttc tca att cta gga 144
 Gly Arg Phe Lys Thr Ile Ala Tyr Ala Ser Leu Phe Ser Ile Leu Gly
 35 40 45
 cta atg acg gtg aca ctc acc gcc tgc ctg cct caa ctc cac cca cca 192
 Leu Met Thr Val Thr Leu Thr Ala Cys Leu Pro Gln Leu His Pro Pro
 50 55 60
 ccg tgc aac aac cct cat cca gac gaa tgc gac gat ccg aac aag ctc 240
 Pro Cys Asn Asn Pro His Pro Asp Glu Cys Asp Asp Pro Asn Lys Leu
 65 70 75 80
 cag ctc ggg att cta ttc ctc ggt ctc ggc ttt ctc tcc atc ggt agc 288
 Gln Leu Gly Ile Leu Phe Leu Gly Leu Gly Phe Leu Ser Ile Gly Ser
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 ggc gga atc cgg cct tgc agc att cca ttc gga gtt gat cag ttt gac 336
 Gly Gly Ile Arg Pro Cys Ser Ile Pro Phe Gly Val Asp Gln Phe Asp
 100 105 110
 caa cga aca gag caa ggc ctt aaa gga gtg gcc agt ttc ttt aat tgg 384
 Gln Arg Thr Glu Gln Gly Leu Lys Gly Val Ala Ser Phe Phe Asn Trp
 115 120 125
 tac tac ttg acc tta act atg gtt ctc atc ttt tcg cat acc gtt gtg 432
 Tyr Tyr Leu Thr Leu Thr Met Val Leu Ile Phe Ser His Thr Val Val
 130 135 140
 gtc tac tta cag act gtc agt tgg gtc atc ggg ttt agc atc ccg act 480
 Val Tyr Leu Gln Thr Val Ser Trp Val Ile Gly Phe Ser Ile Pro Thr
 145 150 155 160
 agt tta atg gct tgt gca gtg gtt ctg ttc ttt gtc ggt atg ccg ttt 528
 Ser Leu Met Ala Cys Ala Val Val Leu Phe Val Gly Met Arg Phe
 165 170 175
 tac gta tat gtc aaa ccg gaa ggt agt gta ttc tct ggt att gct ccg 576
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 180 185 190
 gtc atc gtg gca gct cgt aag aaa ccg gac ctc aaa att tcg ctt gtg 624
 Val Ile Val Ala Ala Arg Lys Lys Arg Asp Leu Lys Ile Ser Leu Val
 195 200 205
 gac gat ggg act gag gag tat tat gag ccg ccg gtg aaa cct ggc gtg 672
 Asp Asp Gly Thr Glu Glu Tyr Tyr Glu Pro Pro Val Lys Pro Gly Val
 210 215 220
 tta tcc aag tta cct ctt act gac caa ttc aag ttt ctg gac aaa gct 720
 Leu Ser Lys Leu Pro Leu Thr Asp Gln Phe Lys Phe Leu Asp Lys Ala
 225 230 235 240
 gcg gtg ata cta gac ggt gat ctt aca tct gaa gga gtt ccg gca aat 768
 Ala Val Ile Leu Asp Gly Asp Leu Thr Ser Glu Gly Val Pro Ala Asn
 245 250 255
 aag tgg cgg cta tgt agc atc caa gaa gtt gaa gag gtc aag tgc ctg 816
 Lys Trp Arg Leu Cys Ser Ile Gln Glu Val Glu Glu Val Lys Cys Leu
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 atc aga gtt gtt ccg gtt tgg tct gct gga ata att tca atc gtt gca 864

PF59082SeqList_PF59082.txt

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Met	Thr	Thr	Gln	Ala	Thr	Phe	Met	Val	Phe	Gln	Ala	Thr	Lys	Met	Asp	
	290					295					300					
cga	cac	atg	ggg	cca	cac	ttt	gag	atc	ccg	gcc	gcc	tcc	ata	acc	gtc	960
Arg	His	Met	Gly	Pro	His	Phe	Glu	Ile	Pro	Ala	Ala	Ser	Ile	Thr	Val	
305					310					315					320	
att	tct	tac	atc	act	ata	ggc	att	tgg	gtg	cct	atc	tac	gaa	cac	ctc	1008
Ile	Ser	Tyr	Ile	Thr	Ile	Gly	Ile	Trp	Val	Pro	Ile	Tyr	Glu	His	Leu	
				325					330					335		
tta	gtc	ccg	ttc	ctt	tgg	cga	atg	aga	aag	ttc	agg	gtc	act	ctc	ctt	1056
Leu	Val	Pro	Phe	Leu	Trp	Arg	Met	Arg	Lys	Phe	Arg	Val	Thr	Leu	Leu	
			340						345					350		
caa	cgg	atg	ggg	ata	ggg	atc	gtc	ttc	gcc	att	ctc	tcc	atg	ttc	act	1104
Gln	Arg	Met	Gly	Ile	Gly	Ile	Val	Phe	Ala	Ile	Leu	Ser	Met	Phe	Thr	
		355				360						365				
gca	ggg	ttt	gta	gag	gga	gtg	agg	cgg	aca	cgg	gct	act	gaa	atg	act	1152
Ala	Gly	Phe	Val	Glu	Gly	Val	Arg	Arg	Thr	Arg	Ala	Thr	Glu	Met	Thr	
	370					375					380					
caa	atg	tcg	gtg	ttt	tgg	ctg	gct	ttg	cca	ctg	att	ctg	atg	ggg	ctc	1200
Gln	Met	Ser	Val	Phe	Trp	Leu	Ala	Leu	Pro	Leu	Ile	Leu	Met	Gly	Leu	
385					390					395					400	
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Cys	Glu	Ser	Phe	Asn	Phe	Ile	Gly	Leu	Ile	Glu	Phe	Phe	Asn	Ser	Gln	
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Lys	Ile	Gly	Ile	Ile	Gly	Thr	Leu	Ser	Asn	Leu	Leu	Val	Tyr	Leu	Thr	
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Ile Tyr Val Ser Gly Met Thr Leu Leu Thr Leu Ser Ala Ser Val Pro
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acg gga ggt att aag ccg tgt gtt tcc tcc ttt gga gct gat cag ttc 653
Thr Gly Gly Ile Lys Pro Cys Val Ser Ser Phe Gly Ala Asp Gln Phe
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Asp Glu Asn Asp Glu Ala Glu Lys Leu Lys Lys Ser Ser Phe Phe Asn
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Trp Phe Tyr Phe Ser Ile Asn Val Gly Ala Leu Val Ala Ala Thr Val
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cgt tac tac agg ctt caa aga cct ggt ggg agt cca ctc acg agg atc 893
Arg Tyr Tyr Arg Leu Gln Arg Pro Gly Gly Ser Pro Leu Thr Arg Ile
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Phe Gln Val Ile Val Ala Ala Phe Arg Lys Val Ser Val Lys Val Pro
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Glu Asp Lys Ser Leu Leu Phe Glu Thr Ala Asp Asp Glu Ser Asn Ile
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Thr Gly Ser Arg Lys Leu Glu His Thr Asp Asn Leu Met Phe Phe Asp
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PF59082SeqList_PF59082.txt

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Val	Tyr	Ser	Gln	Met	Asn	Thr	Met	Phe	Val	Leu	Gln	Gly	Asn	Thr	Met		
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Phe	Ile	Val	Pro	Phe	Ala	Arg	Lys	Phe	Thr	Arg	Gln	Glu	Arg	Gly	Phe		
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Tyr	Phe	Phe	Tyr	Leu	Leu	Ala	Val	Leu	Ser	Phe	Leu	Asn	Phe	Leu	Val		
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Tyr	Leu	Trp	Ile	Ser	Lys	Arg	Tyr	Lys	Tyr	Lys	Lys	Ala	Ile	Gly	Arg		
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<213> Brassica napus

<400> 1740

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Gly Thr Asn Leu Val Asn Tyr Leu Glu Ser Arg Leu Asn Gln Gly Asn
      50      55      60
Ala Thr Ala Ala Asn Asn Val Thr Asn Trp Ser Gly Thr Cys Tyr Ile
65      70      75      80
Thr Pro Leu Ile Gly Ala Phe Leu Ala Asp Ala Tyr Leu Gly Arg Tyr
      85      90      95
Trp Thr Ile Ala Thr Phe Val Phe Ile Tyr Val Ser Gly Met Thr Leu
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Leu Thr Leu Ser Ala Ser Val Pro Gly Leu Lys Pro Gly Asn Cys Asn
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130      135      140
Ala Leu Tyr Met Ile Ala Leu Gly Thr Gly Gly Ile Lys Pro Cys Val
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Ser Ser Phe Gly Ala Asp Gln Phe Asp Glu Asn Asp Glu Ala Glu Lys
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Leu Lys Lys Ser Phe Phe Asn Trp Phe Tyr Phe Ser Ile Asn Val
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Gly Ala Leu Val Ala Ala Thr Val Leu Val Trp Ile Gln Met Asn Val
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Asp Ser Ile Lys Asp Gly Glu Val Asn Pro Trp Arg Leu Cys Ser Val
305      310      315      320
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Ala Ser Gly Ile Val Phe Ala Thr Val Tyr Ser Gln Met Asn Thr Met
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Glu Ile Pro Ser Ala Ser Leu Ser Leu Phe Asp Thr Val Ser Val Leu
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Gly Leu Val Ile Ser Ile Phe Ala Met Val Thr Ala Gly Val Leu Glu
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Val Val Arg Leu Asp Tyr Val Lys Ser His Asn Ala Tyr Asp Asp Lys
435      440      445
Lys Ile Pro Met Ser Ile Phe Thr Phe Ile Gly Gln Leu Glu Phe Phe Tyr
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Gly Cys Ala Glu Val Phe Thr Phe Ile Gly Gln Leu Glu Phe Phe Tyr
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Val Met Lys Leu Thr Lys Lys Asn Gly Lys Pro Gly Trp Ile Pro Asp
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PF59082SeqList_PF59082.txt

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 Gly Asn Pro Ala Ile Arg Ala Lys Thr Gly Lys Trp Leu Ser Ala Ile
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 ctc att ctt gtg aac caa ggg ctt gca acg ctt gcc ttc ttc ggt gta 201
 Leu Ile Leu Val Asn Gln Gly Leu Ala Thr Leu Ala Phe Phe Gly Val
 40 45 50
 gga gtg aac tta gtt ctg ttt ctg acg aga gtg atg gga caa gac aat 249
 Gly Val Asn Leu Val Leu Phe Leu Thr Arg Val Met Gly Gln Asp Asn
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 gca gaa gct gcc aat agt gtc agt aaa tgg aca gga act gtt tac atc 297
 Ala Glu Ala Ala Asn Ser Val Ser Lys Trp Thr Gly Thr Val Tyr Ile
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 aag act tgt gca atc ttc caa gga agt ttc gtt gtg gga ctg gtg atg 393
 Lys Thr Cys Ala Ile Phe Gln Gly Ser Phe Val Val Gly Leu Val Met
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 Leu Ser Leu Ser Thr Ala Ala Leu Leu Leu Glu Pro Ser Gly Cys Gly
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 Val Glu Glu Ser Pro Cys Lys Pro His Ser Thr Phe Lys Thr Val Ile
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 Phe Tyr Leu Ser Val Tyr Leu Ile Ala Leu Gly Tyr Gly Gly Tyr Gln
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 Pro Asn Ile Ala Thr Phe Gly Ala Asp Gln Phe Asp Ala Asp Asp Ser
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 Phe Ala Gly Leu Val Leu Phe Leu Thr Gly Thr Pro Lys Tyr Arg His
 230 235 240
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PF59082SeqList_PF59082.txt

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Leu	Tyr	Asp	Ser	Glu	Thr	Gln	Arg	Thr	Gly	Asp	Lys	Lys	Ile	Leu	His	
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Thr	Ser	Gly	Phe	Arg	Phe	Leu	Asp	Arg	Ala	Ala	Ile	Val	Thr	Pro	Asp	
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Leu	Cys	Ser	Val	Thr	Gln	Val	Glu	Glu	Val	Lys	Cys	Val	Phe	Arg	Leu	
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Gln	Arg	Met	Gly	Ile	Gly	Leu	Val	Ile	Ala	Ile	Met	Ala	Met	Ile	Ser	
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Gly	Leu	Thr	Ala	Ala	Asp	Phe	Val	Val	Tyr	Leu	Val	Cys	Ala	Lys	Trp	
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Tyr	Lys	Tyr	Ile	Lys	Ser	Glu	Ala	Ser	Phe	Ser	Glu	Ser	Thr	Ser	Glu	
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PF59082SeqList_PF59082.txt

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 85 90 95
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 260 265 270
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 275 280 285
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 305 310 315 320
 Asn Pro Trp Arg Leu Cys Ser Val Thr Gln Val Glu Glu Val Lys Cys
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 385 390 395 400
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 405 410 415
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 420 425 430
 Ala Met Ile Ser Ala Gly Ile Val Glu Ile Tyr Arg Leu Lys His Lys
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PF59082SeqList_PF59082.txt

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 Glu Gly Leu Ile Ser Gln Glu Pro Lys Leu Tyr Ala Gln Asp Gly Ser 15 20 25
 gtg gac ctt cat gga aac cca ccg ttg aag gag aag aca ggc aac tgg 145
 Val Asp Leu His Gly Asn Pro Pro Leu Lys Glu Lys Thr Gly Asn Trp 30 35 40
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 Lys Ala Cys Pro Phe Ile Leu Gly Asn Glu Cys Cys Glu Arg Leu Ala 45 50 55 60
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 Tyr Tyr Gly Ile Ala Gly Asn Leu Ile Thr Tyr Leu Thr Thr Lys Leu 65 70 75
 cac caa gga aac gtt tca gct gct aga aac gtc acc aca tgg cag ggg 289
 His Gln Gly Asn Val Ser Ala Ala Arg Asn Val Thr Thr Trp Gln Gly 80 85 90
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 Thr Cys Tyr Leu Thr Pro Leu Ile Gly Ala Val Leu Ala Asp Ala Tyr 95 100 105
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 Trp Gly Arg Tyr Trp Thr Ile Ala Cys Phe Ser Gly Ile Tyr Phe Ile 110 115 120
 ggc atg tct gcg cta act ctc tca gcg tca gtt cca gca ttg aaa cca 433
 Gly Met Ser Ala Leu Thr Leu Ser Ala Ser Val Pro Ala Leu Lys Pro 125 130 135 140
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 Ala Glu Cys Ile Gly Gly Phe Cys Pro Ser Ala Thr Pro Ala Gln Tyr 145 150 155
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 Ile Lys Pro Cys Val Ser Ser Phe Gly Ala Asp Gln Phe Asp Asp Thr 175 180 185
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 Asp Ser Arg Glu Arg Val Lys Lys Ala Ser Phe Phe Asn Trp Phe Tyr 190 195 200
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 Phe Ser Ile Asn Ile Gly Ala Leu Val Ser Ser Ser Leu Leu Val Trp 205 210 215 220
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Met	Leu	Leu	Tyr	Glu	Thr	Gln	Asp	Lys	Asn	Ser	Ala	Ile	Ala	Gly	Ser	
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Val	Glu	Ser	Gly	Ala	Pro	Val	Pro	Ile	Ser	Val	Leu	Trp	Gln	Ile	Pro	
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ggg	tgg	ata	tca	gat	aat	ctg	aac	tcg	ggg	cat	ctt	gat	tac	tac	ttc	1681
Gly	Trp	Ile	Ser	Asp	Asn	Leu	Asn	Ser	Gly	His	Leu	Asp	Tyr	Tyr	Phe	
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Trp	Leu	Leu	Ala	Gly	Leu	Ser	Leu	Val	Asn	Met	Ala	Val	Tyr	Phe	Phe	
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Ser	Ala	Ala	Arg	Tyr	Lys	Gln	Lys	Lys	Ala	Ser	Lys	Leu				
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Phe Ile Leu Gly Asn Glu Cys Cys Glu Arg Leu Ala Tyr Tyr Gly Ile
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Ala Gly Asn Leu Ile Thr Tyr Leu Thr Thr Lys Leu His Gln Gly Asn
65 70 75 80
Val Ser Ala Ala Arg Asn Val Thr Thr Trp Gln Gly Thr Cys Tyr Leu
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Thr Pro Leu Ile Gly Ala Val Leu Ala Asp Ala Tyr Trp Gly Arg Tyr
100 105 110
Trp Thr Ile Ala Cys Phe Ser Gly Ile Tyr Phe Ile Gly Met Ser Ala
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130 135 140
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145 150 155 160
Gly Gly Leu Tyr Leu Ile Ala Leu Gly Thr Gly Gly Ile Lys Pro Cys
165 170 175
Val Ser Ser Phe Gly Ala Asp Gln Phe Asp Asp Thr Asp Ser Arg Glu
180 185 190
Arg Val Lys Lys Ala Ser Phe Phe Asn Trp Phe Tyr Phe Ser Ile Asn
195 200 205
Ile Gly Ala Leu Val Ser Ser Ser Leu Leu Val Trp Ile Gln Glu Asn
210 215 220
Arg Gly Trp Gly Leu Gly Phe Gly Ile Pro Thr Val Phe Met Gly Leu
225 230 235 240
Ala Ile Ala Ser Phe Phe Phe Gly Thr Pro Leu Tyr Arg Phe Gln Lys
245 250 255
Pro Gly Gly Ser Pro Ile Thr Arg Ile Ser Gln Val Val Val Ala Ser
260 265 270
Phe Arg Lys Ser Thr Leu Lys Val Pro Glu Asp Ala Met Leu Leu Tyr
275 280 285
Glu Thr Gln Asp Lys Asn Ser Ala Ile Ala Gly Ser Arg Lys Ile Glu
290 295 300
His Thr Asp Asp Cys Gln Tyr Leu Asp Lys Ala Ala Val Ile Ser Glu
305 310 315 320
Glu Glu Ser Lys Ala Gly Asp Val Ser Asn Ser Trp Arg Leu Cys Thr
325 330 335
Val Thr Gln Val Glu Glu Leu Lys Ile Leu Ile Arg Met Phe Pro Ile
340 345 350
Trp Ala Ser Gly Ile Ile Phe Ser Ala Val Tyr Ala Gln Met Ser Thr
355 360 365
Met Phe Val Gln Gln Gly Arg Ala Met Asp Cys Lys Ile Gly Ser Phe
370 375 380
Gln Leu Pro Pro Ala Ala Leu Gly Thr Phe Asp Thr Ala Ser Val Ile
385 390 395 400
Ile Trp Val Pro Leu Tyr Asp Arg Phe Ile Val Pro Leu Ala Arg Arg
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PF59082SeqList_PF59082.txt

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465      470      475
Leu Gly Ala Ala Glu Val Phe Tyr Phe Ile Gly Gln Leu Glu Phe Phe
      485      490      495
Tyr Asp Gln Ser Pro Asp Ala Met Arg Ser Leu Cys Ser Ala Leu Ala
      500      505      510
Leu Leu Thr Asn Ala Leu Gly Asn Tyr Leu Ser Ser Leu Ile Leu Thr
      515      520      525
Leu Val Thr Tyr Phe Thr Thr Arg Asn Gly Gly Glu Gly Trp Ile Ser
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Asp Asn Leu Asn Ser Gly His Leu Asp Tyr Tyr Phe Trp Leu Leu Ala
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Tyr Lys Gln Lys Lys Ala Ser Lys Leu
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120

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 Met Ala Asp His Asp Ala Lys Glu Glu Gln Arg
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171

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 Pro Leu Asn Gln Trp Arg Arg Ser Lys Gly Gly Phe Met Ala Ser Met
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219

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 Phe Ile Phe Val Leu Ser Ala Leu Asp Asn Met Gly Phe Val Ala Asn
 30 35 40

267

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 Met Val Ser Ile Val Leu Tyr Phe Tyr Gly Val Met His Phe Asp Leu
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315

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 Ala Ser Ser Ala Asn Thr Leu Thr Asn Phe Met Gly Ser Thr Tyr Leu
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363

ctt tcc ctt gtt ggt ggc ttc atc tca gat act tac ttg aac aga ttc
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411

acc aca tgc ttg ctt ttc gga tca ctc gag gtt ctg gct ttg gca atg
 Thr Thr Cys Leu Leu Phe Gly Ser Leu Glu Val Leu Ala Leu Ala Met
 95 100 105

459

ctc aca gtc caa gct gct tca aaa cat tta cac cct gaa gca tgt ggc
 Leu Thr Val Gln Ala Ala Ser Lys His Leu His Pro Glu Ala Cys Gly
 110 115 120

507

aag tca agc tgt gtg aaa ggt ggc ata gca gtg atg ttc tac aca tca
 Lys Ser Ser Cys Val Lys Gly Gly Ile Ala Val Met Phe Tyr Thr Ser
 125 130 135

555

ctg tgc ttg ttg gca ttg gga atg gga ggg gtg aga gga tcc atg act
 Leu Cys Leu Leu Ala Leu Gly Met Gly Gly Val Arg Gly Ser Met Thr
 140 145 150 155

603

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 Ala Phe Gly Ala Asp Gln Phe Asp Glu Lys Asp Pro Thr Glu Ala Lys
 160 165 170

651

PF59082SeqList_PF59082.txt

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Trp	His	Trp	Gly	Phe	Phe	Ile	Ile	Thr	Ile	Ala	Ser	Ser	Val	Gly	Phe	
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Val	Thr	Leu	Ala	Leu	Gly	Lys	Gln	Phe	Tyr	Arg	Ile	Lys	Thr	Pro	Gly	
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Asp	Ser	Pro	Thr	Leu	Arg	Ile	Ala	Gln	Val	Ile	Val	Val	Ser	Phe	Lys	
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aac	cga	aag	ttg	tca	ttg	ccg	gag	tca	cat	gga	gaa	cta	tat	gaa	atc	939
Asn	Arg	Lys	Leu	Ser	Leu	Pro	Glu	Ser	His	Gly	Glu	Leu	Tyr	Glu	Ile	
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Ser	Asp	Lys	Asp	Ala	Thr	Ala	Glu	Lys	Ile	Ala	His	Thr	Asn	Arg	Met	
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Arg	Phe	Leu	Asp	Lys	Ala	Ala	Ile	Ile	Gln	Glu	Ser	Ser	Lys	Pro	Gln	
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Pro	Leu	Val	Phe	Ile	Ser	Val	Leu	Val	Pro	Leu	Tyr	Glu	Leu	Phe	Phe	
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Leu	His	Gly	Phe	Asp	Leu	Asn	Gln	Asn	Asn	Leu	Asn	Leu	Phe	Tyr	Trp	
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Glu Val Ser Arg Glu
          575
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Leu Tyr Phe Tyr Gly Val Met His Phe Asp Leu Ala Ser Ser Ala Asn
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Thr Leu Thr Asn Phe Met Gly Ser Thr Tyr Leu Leu Ser Leu Val Gly
65          70          75          80
Gly Phe Ile Ser Asp Thr Tyr Leu Asn Arg Phe Thr Thr Cys Leu Leu
          85          90          95
Phe Gly Ser Leu Glu Val Leu Ala Leu Ala Met Leu Thr Val Gln Ala
          100          105          110
Ala Ser Lys His Leu His Pro Glu Ala Cys Gly Lys Ser Ser Cys Val
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Lys Gly Gly Ile Ala Val Met Phe Tyr Thr Ser Leu Cys Leu Leu Ala
130          135          140
Leu Gly Met Gly Gly Val Arg Gly Ser Met Thr Ala Phe Gly Ala Asp
145          150          155          160
Gln Phe Asp Glu Lys Asp Pro Thr Glu Ala Lys Ala Leu Ala Ser Phe
          165          170          175
Phe Asn Trp Leu Leu Ser Ser Thr Val Gly Ala Ile Thr Gly Val
          180          185          190
Thr Gly Val Val Trp Val Ser Thr Gln Lys Ala Trp His Trp Gly Phe
          195          200          205
Phe Ile Ile Thr Ile Ala Ser Ser Val Gly Phe Val Thr Leu Ala Leu
210          215          220
Gly Lys Gln Phe Tyr Arg Ile Lys Thr Pro Gly Asp Ser Pro Thr Leu
225          230          235          240
Arg Ile Ala Gln Val Ile Val Val Ser Phe Lys Asn Arg Lys Leu Ser
          245          250          255
Leu Pro Glu Ser His Gly Glu Leu Tyr Glu Ile Ser Asp Lys Asp Ala
          260          265          270
Thr Ala Glu Lys Ile Ala His Thr Asn Arg Met Arg Phe Leu Asp Lys
          275          280          285
Ala Ala Ile Ile Gln Glu Ser Ser Lys Pro Gln Ala Trp Lys Ile Cys
290          295          300

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PF59082SeqList_PF59082.txt

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 305 310 315 320
 Ile Val Ala Ser Thr Ile Ile Leu Asn Thr Cys Met Ala Gln Leu Gln
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 Thr Phe Ser Val Gln Gln Gly Asn Val Met Asp Leu Lys Leu Gly Ser
 340 345 350
 Leu Thr Val Pro Ala Pro Ser Ile Pro Val Ile Pro Leu Val Phe Ile
 355 360 365
 Ser Val Leu Val Pro Leu Tyr Glu Leu Phe Phe Val Pro Phe Ala Arg
 370 375 380
 Lys Ile Thr Asn His Pro Ser Gly Ile Thr Gln Leu Gln Arg Val Gly
 385 390 395 400
 Val Gly Leu Val Leu Ser Ala Ile Ser Met Ala Val Ala Gly Ile Val
 405 410 415
 Glu Val Lys Arg Arg Asp Gln Gly Arg Lys Asp Pro Ser Lys Pro Ile
 420 425 430
 Ser Leu Phe Trp Leu Ser Phe Gln Tyr Gly Ile Phe Gly Ile Ala Asp
 435 440 445
 Met Phe Thr Leu Val Gly Leu Leu Glu Phe Phe Tyr Arg Glu Ser Pro
 450 455 460
 Ala Ser Met Lys Ser Leu Ser Thr Ser Leu Thr Trp Leu Ser Thr Ser
 465 470 475 480
 Leu Gly Tyr Phe Leu Ser Thr Val Phe Val Asn Val Ile Asn Ala Val
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 Thr Lys Arg Ile Thr Arg Ser Lys Gln Gly Trp Leu His Gly Phe Asp
 500 505 510
 Leu Asn Gln Asn Asn Leu Asn Leu Phe Tyr Trp Phe Leu Ala Thr Leu
 515 520 525
 Ser Cys Leu Asn Phe Phe Asn Tyr Leu Tyr Trp Ala Ser Arg Tyr Gln
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 Tyr Lys Arg Glu Asp Ser Gly Pro Gly Phe Lys Pro Leu Gly Glu Met
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 Met
 1

gaa gag gga agg gtt gtg agt gag tac aca aaa gat gga act gtg gat 164
 Glu Glu Gly Arg Val Val Ser Glu Tyr Thr Lys Asp Gly Thr Val Asp
 5 10 15

ctt aaa ggg aaa ccc att ctc aaa tcc aaa agt ggt ggt tgg aaa gca 212
 Leu Lys Gly Lys Pro Ile Leu Lys Ser Lys Ser Gly Gly Trp Lys Ala
 20 25 30

tgc tcc ttt gtt gtt gtg tac gag ata ttt gaa aga atg gct tat tat 260
 Cys Ser Phe Val Val Val Tyr Glu Ile Phe Glu Arg Met Ala Tyr Tyr
 35 40 45

gga ata tca tca aat ttg ata ctg tat ctg act agg aag ctt cac caa 308
 Gly Ile Ser Ser Asn Leu Ile Leu Tyr Leu Thr Arg Lys Leu His Gln
 50 55 60 65

ggc act gtg acc tct tcc aac aac gtc acc aat tgg gtt ggc acc att 356
 Gly Thr Val Thr Ser Ser Asn Asn Val Thr Asn Trp Val Gly Thr Ile
 70 75 80

tgg ata act cct atc tta gga gcc tac gtt gcc gat gct cat ctt ggt 404
 Trp Ile Thr Pro Ile Leu Gly Ala Tyr Val Ala Asp Ala His Leu Gly
 85 90 95

PF59082SeqList_PF59082.txt

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Arg	Phe	Trp	Thr	Phe	Leu	Ile	Ala	Ser	Val	Ile	Tyr	Leu	Leu	Gly	Met	
		100					105					110				
tct	cta	ctt	acg	cta	tcg	gtg	tcc	ctt	cca	agc	cta	aag	cca	cca	gag	500
Ser	Leu	Leu	Thr	Leu	Ser	Val	Ser	Leu	Pro	Ser	Leu	Lys	Pro	Pro	Glu	
	115					120					125					
tgc	cat	gaa	ttg	gat	gtg	aca	aaa	tgt	gaa	aaa	gcc	tcc	aca	cta	cat	548
Cys	His	Glu	Leu	Asp	Val	Thr	Lys	Cys	Glu	Lys	Ala	Ser	Thr	Leu	His	
130					135					140					145	
cta	gct	gtg	ttc	tat	ggt	gca	ctc	tac	act	ctt	gca	cta	gga	acc	ggt	596
Leu	Ala	Val	Phe	Tyr	Gly	Ala	Leu	Tyr	Thr	Leu	Ala	Leu	Gly	Thr	Gly	
				150					155					160		
gga	acc	aag	cca	aac	att	tcc	aca	att	ggt	gct	gac	caa	ttt	gat	gac	644
Gly	Thr	Lys	Pro	Asn	Ile	Ser	Thr	Ile	Gly	Ala	Asp	Gln	Phe	Asp	Asp	
		165					170						175			
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Phe	Asp	Ser	Lys	Glu	Lys	Lys	Leu	Lys	Leu	Ser	Phe	Phe	Asn	Trp	Trp	
	180					185					190					
atg	ttt	agc	atc	ttc	att	ggg	acc	ctc	ttt	gca	aat	tct	ggt	ctg	gtc	740
Met	Phe	Ser	Ile	Phe	Ile	Gly	Thr	Leu	Phe	Ala	Asn	Ser	Val	Leu	Val	
	195					200				205						
tat	ata	caa	gac	aat	gtg	ggg	tgg	act	ctt	ggg	tat	gct	ctt	ccc	act	788
Tyr	Ile	Gln	Asp	Asn	Val	Gly	Trp	Thr	Leu	Gly	Tyr	Ala	Leu	Pro	Thr	
210					215					220					225	
ctt	gga	ctt	gca	ata	tca	atc	atc	ata	ttc	ttg	gca	ggc	aca	ccc	ttt	836
Leu	Gly	Leu	Ala	Ile	Ser	Ile	Ile	Ile	Phe	Leu	Ala	Gly	Thr	Pro	Phe	
				230					235					240		
tat	aga	cac	aaa	ttg	ccc	acg	ggg	agt	cca	ttc	act	aag	atg	gcc	aag	884
Tyr	Arg	His	Lys	Leu	Pro	Thr	Gly	Ser	Pro	Phe	Thr	Lys	Met	Ala	Lys	
		245					250					255				
gtc	ata	gtg	gct	gct	ata	agg	aaa	tgg	aaa	gtg	cat	att	cct	agt	gac	932
Val	Ile	Val	Ala	Ala	Ile	Arg	Lys	Trp	Lys	Val	His	Ile	Pro	Ser	Asp	
	260					265				270						
act	aaa	gaa	ctt	tat	gag	ctt	gat	ttg	gaa	gag	tat	gcc	aag	aga	ggg	980
Thr	Lys	Glu	Leu	Tyr	Glu	Leu	Asp	Leu	Glu	Glu	Tyr	Ala	Lys	Arg	Gly	
	275				280					285						
aga	gtc	aga	att	gat	tcc	act	cca	acc	ttg	agg	ttc	ctc	aac	aag	gca	1028
Arg	Val	Arg	Ile	Asp	Ser	Thr	Pro	Thr	Leu	Arg	Phe	Leu	Asn	Lys	Ala	
290					295				300						305	
tgt	gtc	aac	acc	gat	tca	agt	act	agt	gga	agg	aag	cta	agc	cct	gtt	1076
Cys	Val	Asn	Thr	Asp	Ser	Ser	Thr	Ser	Gly	Trp	Lys	Leu	Ser	Pro	Val	
				310					315					320		
acc	cat	gtg	gag	gag	acc	aaa	caa	atg	cta	aga	atg	atc	cca	atc	ttg	1124
Thr	His	Val	Glu	Glu	Thr	Lys	Gln	Met	Leu	Arg	Met	Ile	Pro	Ile	Leu	
		325						330				335				
gct	gct	aca	ttg	atc	cct	agt	gca	atg	gtt	gca	caa	ata	ggt	acc	ctt	1172
Ala	Ala	Thr	Leu	Ile	Pro	Ser	Ala	Met	Val	Ala	Gln	Ile	Gly	Thr	Leu	
	340						345			350						
ttt	gtg	aag	caa	ggg	att	aca	ctt	gac	aga	ggc	att	ggc	agc	ttc	aat	1220
Phe	Val	Lys	Gln	Gly	Ile	Thr	Leu	Asp	Arg	Gly	Ile	Gly	Ser	Phe	Asn	
	355				360					365						
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Ile	Pro	Pro	Ala	Ser	Leu	Ala	Thr	Phe	Val	Thr	Leu	Ser	Met	Leu	Val	
370					375				380						385	
tgt	gtg	gtg	ctc	tat	gac	cgt	ttc	ttt	gtc	aag	atc	atg	caa	agg	ttt	1316
Cys	Val	Val	Leu	Tyr	Asp	Arg	Phe	Phe	Val	Lys	Ile	Met	Gln	Arg	Phe	
				390				395					400			
acc	aag	aac	cct	aga	ggg	ata	acc	ctt	ctc	caa	agg	att	gga	att	ggc	1364
Thr	Lys	Asn	Pro	Arg	Gly	Ile	Thr	Leu	Leu	Gln	Arg	Ile	Gly	Ile	Gly	
		405					410					415				
ctc	ata	atc	cac	ata	gtg	att	atg	gtg	att	gca	tct	cta	act	gaa	agg	1412
Leu	Ile	Ile	His	Ile	Val	Ile	Met	Val	Ile	Ala	Ser	Leu	Thr	Glu	Arg	
	420					425				430						
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Tyr	Arg	Leu	Arg	Val	Ala	Lys	Glu	His	Gly	Leu	Leu	Glu	Asn	Gly	Gly	
	435				440					445						
caa	gtt	cct	ttg	agc	att	ttc	atc	ttg	ctt	cct	caa	tat	gtt	ctt	atg	1508
Gln	Val	Pro	Leu	Ser	Ile	Phe	Ile	Leu	Leu	Pro	Gln	Tyr	Val	Leu	Met	
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Gly Ala Ala Asp Ala Phe Val Glu Val Ala Lys Ile Glu Phe Ser Tyr	
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gac caa gcc cca gaa agc atg aag agc ctt ggc act tcc tat tca atg	1604
Asp Gln Ala Pro Glu Ser Met Lys Ser Leu Gly Thr Ser Tyr Ser Met	
	485 490 495
act acc tta ggc att ggg aat ttc cta agc act ttt ctt ctc aca aca	1652
Thr Thr Leu Gly Ile Gly Asn Phe Leu Ser Thr Phe Leu Leu Thr Thr	
	500 505 510
att tca cat gtc acc aag aaa cat ggc cac cga gga tgg gtt ttg aac	1700
Ile Ser His Val Thr Lys His Gly His Arg Gly Trp Val Leu Asn	
	515 520 525
aac ttg aat gct tct cat ctt gac tac tac tat gca ctt ttg gcc ata	1748
Asn Leu Asn Ala Ser His Leu Asp Tyr Tyr Tyr Ala Leu Leu Ala Ile	
	530 535 540 545
cta aac ttg gtg aac ttc gta ttc ttc atg gtt gtg aca aag ttc tat	1796
Leu Asn Leu Val Asn Phe Val Phe Phe Met Val Val Thr Lys Phe Tyr	
	550 555 560
gtg tat aga gct gaa att tca gat tcc ata aaa gtg ctt gag gaa gag	1844
Val Tyr Arg Ala Glu Ile Ser Asp Ser Ile Lys Val Leu Glu Glu Glu	
	565 570 575
ctc aag gaa aag aca tca aac cag gtg att cca aga gat taa ttagatatatt	1896
Leu Lys Glu Lys Thr Ser Asn Gln Val Ile Pro Arg Asp	
	580 585 590
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tggttttagat aatttgaagc catttttttag aagaaatgga gaatatatat gtcattgggcg	2016
atagggtctt taatgtgtga tataatttgg acttcactct tcaagaaacg tcacgttcat	2076
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Tyr Gly Ile Ser Ser Asn Leu Ile Leu Tyr Leu Thr Arg Lys Leu His	50 55 60
Gln Gly Thr Val Thr Ser Ser Asn Asn Val Thr Asn Trp Val Gly Thr	65 70 75 80
Ile Trp Ile Thr Pro Ile Leu Gly Ala Tyr Val Ala Asp Ala His Leu	85 90 95
Gly Arg Phe Trp Thr Phe Leu Ile Ala Ser Val Ile Tyr Leu Leu Gly	100 105 110
Met Ser Leu Leu Thr Leu Ser Val Ser Leu Pro Ser Leu Lys Pro Pro	115 120 125
Glu Cys His Glu Leu Asp Val Thr Lys Cys Glu Lys Ala Ser Thr Leu	130 135 140
His Leu Ala Val Phe Tyr Gly Ala Leu Tyr Thr Leu Ala Leu Gly Thr	145 150 155 160
Gly Gly Thr Lys Pro Asn Ile Ser Thr Ile Gly Ala Asp Gln Phe Asp	165 170 175
Asp Phe Asp Ser Lys Glu Lys Lys Leu Lys Leu Ser Phe Phe Asn Trp	180 185 190
Trp Met Phe Ser Ile Phe Ile Gly Thr Leu Phe Ala Asn Ser Val Leu	195 200 205

PF59082SeqList_PF59082.txt

Val Tyr Ile Gln Asp Asn Val Gly Trp Thr Leu Gly Tyr Ala Leu Pro
 210 215 220
 Thr Leu Gly Leu Ala Ile Ser Ile Ile Ile Phe Leu Ala Gly Thr Pro
 225 230 235 240
 Phe Tyr Arg His Lys Leu Pro Thr Gly Ser Pro Phe Thr Lys Met Ala
 245 250 255
 Lys Val Ile Val Ala Ala Ile Arg Lys Trp Lys Val His Ile Pro Ser
 260 265 270
 Asp Thr Lys Glu Leu Tyr Glu Leu Asp Leu Glu Glu Tyr Ala Lys Arg
 275 280 285
 Gly Arg Val Arg Ile Asp Ser Thr Pro Thr Leu Arg Phe Leu Asn Lys
 290 295 300
 Ala Cys Val Asn Thr Asp Ser Ser Thr Ser Gly Trp Lys Leu Ser Pro
 305 310 315 320
 Val Thr His Val Glu Thr Lys Gln Met Leu Arg Met Ile Pro Ile
 325 330 335
 Leu Ala Ala Thr Leu Ile Pro Ser Ala Met Val Ala Gln Ile Gly Thr
 340 345 350
 Leu Phe Val Lys Gln Gly Ile Thr Leu Asp Arg Gly Ile Gly Ser Phe
 355 360 365
 Asn Ile Pro Pro Ala Ser Leu Ala Thr Phe Val Thr Leu Ser Met Leu
 370 375 380
 Val Cys Val Val Leu Tyr Asp Arg Phe Phe Val Lys Ile Met Gln Arg
 385 390 395 400
 Phe Thr Lys Asn Pro Arg Gly Ile Thr Leu Gln Arg Ile Gly Ile
 405 410 415
 Gly Leu Ile Ile His Ile Val Ile Met Val Ile Ala Ser Leu Thr Glu
 420 425 430
 Arg Tyr Arg Leu Arg Val Ala Lys Glu His Gly Leu Leu Glu Asn Gly
 435 440 445
 Gly Gln Val Pro Leu Ser Ile Phe Ile Leu Leu Pro Gln Tyr Val Leu
 450 455 460
 Met Gly Ala Ala Asp Ala Phe Val Glu Val Ala Lys Ile Glu Phe Ser
 465 470 475 480
 Tyr Asp Gln Ala Pro Glu Ser Met Lys Ser Leu Gly Thr Ser Tyr Ser
 485 490 495
 Met Thr Thr Leu Gly Ile Gly Asn Phe Leu Ser Thr Phe Leu Leu Thr
 500 505 510
 Thr Ile Ser His Val Thr Lys Lys His Gly His Arg Gly Trp Val Leu
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 Asn Asn Leu Asn Ala Ser His Leu Asp Tyr Tyr Tyr Ala Leu Leu Ala
 530 535 540
 Ile Leu Asn Leu Val Asn Phe Val Phe Phe Met Val Val Thr Lys Phe
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 Met Ala Glu Asp Asp
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116

ggt tac acg aaa gat gga aca gtc gat tac tgt gga aat cca gct aat
 Gly Tyr Thr Lys Asp Gly Thr Val Asp Tyr Cys Gly Asn Pro Ala Asn
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164

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 212

PF59082SeqList_PF59082.txt

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Glu	Cys	Cys	Glu	Arg	Leu	Ala	Tyr	Tyr	Gly	Met	Ser	Thr	Asn	Leu	Val	
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ctt	tat	ttc	aag	aac	cgg	cta	aat	cag	cat	agt	gct	act	gct	tcc	aag	308
Leu	Tyr	Phe	Lys	Asn	Arg	Leu	Asn	Gln	His	Ser	Ala	Thr	Ala	Ser	Lys	
	55					60					65					
aat	gtc	tct	aat	tgg	agt	gga	act	tgc	tat	atc	aca	cca	ttg	att	ggg	356
Asn	Val	Ser	Asn	Trp	Ser	Gly	Thr	Cys	Tyr	Ile	Thr	Pro	Leu	Ile	Gly	
	70				75					80					85	
gca	tat	ttg	gct	gat	tcc	tac	ctt	gga	aga	tat	tgg	aca	att	gct	gtt	404
Ala	Tyr	Leu	Ala	Asp	Ser	Tyr	Leu	Gly	Arg	Tyr	Trp	Thr	Ile	Ala	Val	
			90						95					100		
ttt	tca	ata	att	tat	gct	att	gga	atg	aca	ctc	ttg	aca	ttg	tct	gca	452
Phe	Ser	Ile	Ile	Tyr	Ala	Ile	Gly	Met	Thr	Leu	Leu	Thr	Leu	Ser	Ala	
			105					110								
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Ser	Val	Pro	Gly	Ile	Lys	Pro	Thr	Cys	His	Gly	His	Gly	Asp	Glu	Asn	
		120					125					130				
tgt	cgt	gct	act	act	cta	gag	agt	gca	gtg	tgc	ttc	cta	gct	ctt	tac	548
Cys	Arg	Ala	Thr	Thr	Leu	Glu	Ser	Ala	Val	Cys	Phe	Leu	Ala	Leu	Tyr	
	135					140					145					
ctt	att	gct	ctt	ggc	acc	ggt	ggc	att	aag	cct	tgt	gtc	tca	tcc	tat	596
Leu	Ile	Ala	Leu	Gly	Thr	Gly	Gly	Ile	Lys	Pro	Cys	Val	Ser	Ser	Tyr	
	150				155					160					165	
gga	gca	gat	cag	ttt	gat	gac	act	gac	tcg	gct	gag	aag	gaa	cgc	aag	644
Gly	Ala	Asp	Gln	Phe	Asp	Asp	Thr	Asp	Ser	Ala	Glu	Lys	Glu	Arg	Lys	
			170					175						180		
agt	tct	ttc	ttc	aat	tgg	ttc	tat	ttt	tca	atc	aac	att	ggc	gct	ctt	692
Ser	Ser	Phe	Phe	Asn	Trp	Phe	Tyr	Phe	Ser	Ile	Asn	Ile	Gly	Ala	Leu	
			185					190								
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Ile	Ala	Ser	Ser	Leu	Leu	Val	Trp	Ile	Gln	Asp	Asn	Val	Gly	Trp	Gly	
		200					205					210				
tgg	ggc	ttt	ggt	att	cct	gct	gta	gcc	atg	gca	att	gct	gtg	gtg	agt	788
Trp	Gly	Phe	Gly	Ile	Pro	Ala	Val	Ala	Met	Ala	Ile	Ala	Val	Val	Ser	
	215					220					225					
ttc	ttt	tca	ggc	act	agg	ttg	tat	agg	aat	cag	aag	cct	gga	ggc	agt	836
Phe	Phe	Ser	Gly	Thr	Arg	Leu	Tyr	Arg	Asn	Gln	Lys	Pro	Gly	Gly	Ser	
	230				235					240					245	
gcc	atc	act	aga	atc	tgt	cag	gtg	gta	atg	gca	tcc	ata	aga	aaa	tac	884
Ala	Ile	Thr	Arg	Ile	Cys	Gln	Val	Val	Met	Ala	Ser	Ile	Arg	Lys	Tyr	
			250					255						260		
aat	gtt	gaa	gta	cct	gct	gac	gag	tca	ctt	tta	tat	gag	act	gct	gaa	932
Asn	Val	Glu	Val	Pro	Ala	Asp	Glu	Ser	Leu	Leu	Tyr	Glu	Thr	Ala	Glu	
			265					270					275			
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Thr	Glu	Ser	Ala	Ile	Lys	Gly	Ser	Arg	Lys	Leu	Asp	His	Thr	Asn	Glu	
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Leu	Arg	Phe	Phe	Asp	Lys	Ala	Ala	Val	Leu	Ala	Gln	Ser	Asp	Lys	Val	
		295				300					305					
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Lys	Glu	Ser	Thr	Asn	Pro	Trp	Arg	Leu	Cys	Thr	Val	Thr	Gln	Val	Glu	
	310				315					320					325	
gag	ctg	aaa	tcc	att	tta	aga	ata	ctt	cct	gta	tgg	gcc	act	ggc	atc	1124
Glu	Leu	Lys	Ser	Ile	Leu	Arg	Ile	Leu	Pro	Val	Trp	Ala	Thr	Gly	Ile	
			330						335					340		
ata	ttt	tcc	act	gtc	tat	ggt	caa	atg	agc	acc	tta	ttt	gtg	ttg	caa	1172
Ile	Phe	Ser	Thr	Val	Tyr	Gly	Gln	Met	Ser	Thr	Leu	Phe	Val	Leu	Gln	
			345					350					355			
gga	caa	acc	atg	gac	act	cgt	gtt	ggc	aac	tcc	act	ttc	aaa	atc	cca	1220
Gly	Gln	Thr	Met	Asp	Thr	Arg	Val	Gly	Asn	Ser	Thr	Phe	Lys	Ile	Pro	
		360				365						370				
cca	gct	tca	ctg	tcc	atc	ttt	gac	acc	ctc	agt	gtc	ata	ttt	tgg	gtc	1268
Pro	Ala	Ser	Leu	Ser	Ile	Phe	Asp	Thr	Leu	Ser	Val	Ile	Phe	Trp	Val	
			375			380					385					
cca	gtg	tat	gac	agg	atc	att	gtg	cca	att	gct	aca	aag	ttc	act	ggg	1316

PF59082SeqList_PF59082.txt

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Asn	Lys	Asn	Gly	Leu	Thr	Gln	Leu	Gln	Arg	Met	Gly	Ile	Gly	Leu	Phe		
				410					415					420			
ata	tcc	ata	ttt	tcc	atg	gta	gct	gca	gca	ata	ttg	gag	ctc	ata	cgg	1412	
Ile	Ser	Ile	Phe	Ser	Met	Val	Ala	Ala	Ala	Ile	Leu	Glu	Leu	Ile	Arg		
			425					430					435				
ctt	aga	atg	gtg	agg	agg	cac	aac	tac	tat	caa	ctt	gag	gag	ata	cca	1460	
Leu	Arg	Met	Val	Arg	Arg	His	Asn	Tyr	Tyr	Gln	Leu	Glu	Glu	Ile	Pro		
			440				445					450					
atg	aca	ata	ttt	tgg	cag	gtt	cct	caa	tat	ttc	atc	ata	ggc	tgt	gca	1508	
Met	Thr	Ile	Phe	Trp	Gln	Val	Pro	Gln	Tyr	Phe	Ile	Ile	Gly	Cys	Ala		
	455				460					465							
gaa	gtc	ttc	tat	ttc	att	ggt	cag	ttg	gag	ttc	ttc	tat	gag	caa	gcc	1556	
Glu	Val	Phe	Tyr	Phe	Ile	Gly	Gln	Leu	Glu	Phe	Phe	Tyr	Glu	Gln	Ala		
470					475					480					485		
cct	gat	gct	atg	cga	agc	ttt	tgt	tct	gct	ctc	tca	ctt	acc	act	gtt	1604	
Pro	Asp	Ala	Met	Arg	Ser	Phe	Cys	Ser	Ala	Leu	Ser	Leu	Thr	Thr	Val		
				490				495						500			
gcg	ctt	gga	cag	tac	ttg	agc	tct	ctg	ctt	gtg	aca	att	gtg	aca	aag	1652	
Ala	Leu	Gly	Gln	Tyr	Leu	Ser	Ser	Leu	Leu	Val	Thr	Ile	Val	Thr	Lys		
			505				510						515				
atc	agc	act	agg	aat	gga	agt	cca	ggg	tgg	ata	cct	gat	aat	cta	aac	1700	
Ile	Ser	Thr	Arg	Asn	Gly	Ser	Pro	Gly	Trp	Ile	Pro	Asp	Asn	Leu	Asn		
			520				525					530					
ttt	ggt	cac	ata	gat	tat	ttc	ttc	tgg	cta	ttg	gca	ttg	cta	agt	gta	1748	
Phe	Gly	His	Ile	Asp	Tyr	Phe	Phe	Trp	Leu	Leu	Ala	Leu	Leu	Ser	Val		
	535				540					545							
gtg	aac	ttg	ata	gca	ttc	ctt	gtg	gtg	tct	atg	ttg	tat	aca	tat	aag	1796	
Val	Asn	Leu	Ile	Ala	Phe	Leu	Val	Val	Ser	Met	Leu	Tyr	Thr	Tyr	Lys		
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aga	cct	gtg	gga	act	ctg	cgc	tga	aaagtgggtt	aagttgtaca	ttggaagtag						1850	
Arg	Pro	Val	Gly	Thr	Leu	Arg											
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 <212> PRT
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<400> 1750
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 35 40 45
 Ser Thr Asn Leu Val Leu Tyr Phe Lys Asn Arg Leu Asn Gln His Ser
 50 55 60
 Ala Thr Ala Ser Lys Asn Val Ser Asn Trp Ser Gly Thr Cys Tyr Ile
 65 70 75 80
 Thr Pro Leu Ile Gly Ala Tyr Leu Ala Asp Ser Tyr Leu Gly Arg Tyr
 85 90 95
 Trp Thr Ile Ala Val Phe Ser Ile Ile Tyr Ala Ile Gly Met Thr Leu
 100 105 110
 Leu Thr Leu Ser Ala Ser Val Pro Gly Ile Lys Pro Thr Cys His Gly
 115 120 125
 His Gly Asp Glu Asn Cys Arg Ala Thr Thr Leu Glu Ser Ala Val Cys
 130 135 140

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Phe 145 Leu Ala Leu Tyr 150 Leu Ile Ala Leu Gly 155 Thr Gly Gly Ile Lys Pro 160
 Cys Val Ser Ser Tyr 165 Gly Ala Asp Gln Phe 170 Asp Asp Thr Asp Ser Ala 175
 Glu Lys Glu Arg 180 Lys Ser Ser Phe 185 Asn Trp Phe Tyr Phe Ser Ile 190
 Asn Ile Gly Ala Leu Ile Ala Ser Ser Leu Leu Val Trp Ile Gln Asp 205
 Asn Val Gly Trp Gly Trp Gly Phe Gly Ile Pro Ala Val Ala Met Ala 220
 Ile 225 Ala Val Val Ser Phe 230 Phe Ser Gly Thr Arg 235 Leu Tyr Arg Asn Gln 240
 Lys Pro Gly Gly Ser 245 Ala Ile Thr Arg Ile Cys Gln Val Val Met Ala 255
 Ser Ile Arg Lys Tyr Asn Val Glu Val 265 Pro Ala Asp Glu Ser Leu Leu 270
 Tyr Glu Thr Ala Glu Thr Glu Ser Ala Ile Lys Gly Ser Arg Lys Leu 285
 Asp His 290 Thr Asn Glu Leu Arg 295 Phe Phe Asp Lys Ala Ala Val Leu Ala 300
 Gln 305 Ser Asp Lys Val Lys 310 Glu Ser Thr Asn Pro 315 Trp Arg Leu Cys Thr 320
 Val Thr Gln Val Glu 325 Glu Leu Lys Ser Ile Leu Arg Ile Leu Pro Val 335
 Trp Ala Thr Gly Ile Ile Phe Ser Thr Val Tyr Gly Gln Met Ser Thr 350
 Leu Phe Val Leu Gln Gly Gln Thr Met Asp Thr Arg Val Gly Asn Ser 365
 Thr Phe Lys Ile Pro Pro Ala Ser Leu Ser Ile Phe Asp Thr Leu Ser 380
 Val 385 Ile Phe Trp Val Pro Val Tyr Asp Arg Ile Ile Val Pro Ile Ala 400
 Thr Lys Phe Thr Gly 405 Asn Lys Asn Gly Leu Thr Gln Leu Gln Arg Met 415
 Gly Ile Gly Leu Phe Ile Ser Ile Phe 425 Ser Met Val Ala Ala Ala Ile 430
 Leu Glu Leu Ile Arg Leu Arg Met Val Arg Arg His Asn Tyr Tyr Gln 445
 Leu Glu Glu Ile Pro Met Thr 455 Ile Phe Trp Gln Val Pro Gln Tyr Phe 460
 Ile 465 Ile Gly Cys Ala Glu Val Phe Tyr Phe Ile Gly Gln Leu Glu Phe 480
 Phe Tyr Glu Gln Ala 485 Pro Asp Ala Met Arg Ser Phe Cys Ser Ala Leu 495
 Ser Leu Thr Thr Val Ala Leu Gly Gln Tyr Leu Ser Ser Leu Val 510
 Thr Ile Val Thr Lys Ile Ser Thr Arg Asn Gly Ser Pro Gly Trp Ile 525
 Pro Asp Asn Leu Asn Phe Gly 535 His Ile Asp Tyr Phe Phe Trp Leu Leu 540
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120

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ctg	aag	atg	agg	gtg	atc	gcc	atg	ggc	ggc	gag		223
Leu	Lys	Met	Arg	Val	Ile	Ala	Met	Gly	Gly	Glu		
		10					15			20		
agg	gct	gcc	gag	gag	aag	ctc	tgc	gag	tac	acc	ctg	271
Arg	Ala	Ala	Glu	Glu	Lys	Leu	Cys	Glu	Tyr	Thr	Leu	
	25					30				35		
gac	atc	aag	ggg	cgg	ccg	gcg	gtg	aag	ggc	aag	tcg	319
Asp	Ile	Lys	Gly	Arg	Pro	Ala	Val	Lys	Gly	Lys	Ser	
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gcc	gga	ggc	ctt	att	ctc	gtg	aac	cag	ggc	ctg	gcg	367
Ala	Gly	Gly	Leu	Ile	Leu	Val	Asn	Gln	Gly	Leu	Ala	
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ttc	ggc	gtg	aac	gtg	aac	ctg	gtg	ctg	ttc	ctg	acg	415
Phe	Gly	Val	Asn	Val	Asn	Leu	Val	Leu	Phe	Leu	Thr	
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cag	agc	aac	ggc	gac	gcg	gcc	aac	aac	gtg	agc	aag	463
Gln	Ser	Asn	Gly	Asp	Ala	Ala	Asn	Asn	Val	Ser	Lys	
	90						95					
gtc	tac	atg	ttc	tcc	ctc	atc	ggc	gcc	ttc	ctc	agc	511
Val	Tyr	Met	Phe	Ser	Leu	Ile	Gly	Ala	Phe	Leu	Ser	
	105					110				115		
ggc	cgc	tac	aag	acc	tgc	gcc	atc	ttc	cag	gcc	atc	559
Gly	Arg	Tyr	Lys	Thr	Cys	Ala	Ile	Phe	Gln	Ala	Ile	
	120				125				130			
ctc	ggg	ctg	ctg	tcg	ctc	tcc	tcg	cgg	cta	ctc	atc	607
Leu	Gly	Leu	Leu	Ser	Leu	Ser	Ser	Arg	Leu	Tyr	Leu	
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ggg	tgc	ggc	acg	gag	cac	acg	ccc	tgc	gcc	tcg	cac	655
Gly	Cys	Gly	Thr	Glu	His	Thr	Pro	Cys	Ala	Ser	His	
		155						160				
atg	ggg	atc	ttc	tac	atc	gcg	ctc	tac	atg	atc	gcc	703
Met	Gly	Ile	Phe	Tyr	Ile	Ala	Leu	Tyr	Met	Ile	Ala	
	170						175				180	
ggc	tac	cag	ccc	aac	atc	gcc	acc	ttc	ggg	gcc	gac	751
Gly	Tyr	Gln	Pro	Asn	Ile	Ala	Thr	Phe	Gly	Ala	Asp	
	185					190				195		
gag	gac	ccc	gcc	gag	gcg	cac	tcc	aag	gtc	tcc	ttc	799
Glu	Asp	Pro	Ala	Glu	Ala	His	Ser	Lys	Val	Ser	Phe	
	200				205				210			
tac	ctg	gcg	ctc	aac	ctc	ggc	tcg	ctc	ttc	tcc	aac	847
Tyr	Leu	Ala	Leu	Asn	Leu	Gly	Ser	Leu	Phe	Ser	Asn	
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tac	ctc	cag	gac	cac	ggc	aag	tgg	gtt	atc	ggg	ttc	895
Tyr	Leu	Gln	Asp	His	Gly	Lys	Trp	Val	Ile	Gly	Phe	
		235						240				
gcc	gcc	gcc	gcc	acc	gcc	ctg	ctg	ctc	ttc	ctc	agc	943
Ala	Ala	Ala	Ala	Thr	Ala	Leu	Leu	Leu	Phe	Leu	Ser	
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tac	cgc	cac	gcg	cag	ccc	tgc	ggc	aac	ccc	atg	gcc	991
Tyr	Arg	His	Ala	Gln	Pro	Cys	Gly	Asn	Pro	Met	Ala	
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gtc	gcc	tcc	gcc	gcc	tgc	agg	aac	tgg	aag	tcc	ggc	1039
Val	Ala	Ser	Ala	Ala	Cys	Arg	Asn	Trp	Lys	Ser	Gly	
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gac	gtc	gag	atc	ctg	tac	gag	ggc	gac	gac	aag	acg	1087
Asp	Val	Glu	Ile	Leu	Tyr	Glu	Gly	Asp	Asp	Lys	Thr	
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agg	aag	ctc	ctg	cac	acc	aaa	ggc	ttc	agg	ttc	ttg	1135
Arg	Lys	Leu	Leu	His	Thr	Lys	Gly	Phe	Arg	Phe	Leu	
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ctc	acc	acc	gaa	gac	acc	agc	tcg	aag	ctc	gcc	acc	1183
Leu	Thr	Thr	Glu	Asp	Thr	Ser	Ser	Lys	Leu	Ala	Thr	
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cgc	gac	cag	tgg	aag	ctg	tgc	acg	gtg	acg	cag	gtg	1231

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Ser	Ile	Leu	Arg	Ile	Leu	Pro	Ile	Trp	Val	Cys	Thr	Ile	Leu	Tyr	Ser	
360					365					370					375	
gtc	gtc	ttc	acc	cag	atg	gcg	tcg	ctc	ttc	gtc	gtg	cag	gga	gcc	gcg	1327
Val	Val	Phe	Thr	Gln	Met	Ala	Ser	Leu	Phe	Val	Val	Gln	Gly	Ala	Ala	
				380					385					390		
atg	cgc	cga	tca	aca	cct	ttg	ggc	agc	ttc	tcg	atc	ccg	gcc	tcc	agc	1375
Met	Arg	Arg		Thr	Pro	Leu	Gly	Ser	Phe	Ser	Ile	Pro	Ala	Ser	Ser	
				395				400					405			
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Met	Ser	Ala	Phe	Asp	Ile	Leu	Thr	Val	Ala	Thr	Thr	Ile	Phe	Leu	Tyr	
		410				415					420					
cgg	cgg	gcc	atc	tgc	ccg	ttc	ctg	gca	cgg	ttc	act	gga	cgc	tcg	acc	1471
Arg	Arg	Ala	Ile	Cys	Pro	Phe	Leu	Ala	Arg	Phe	Thr	Gly	Arg	Ser	Thr	
		425				430					435					
gga	ccc	acg	gag	ctg	cag	agg	atg	ggc	ctc	ggc	ctg	gtc	ctc	ggc	gca	1519
Gly	Pro	Thr	Glu	Leu	Gln	Arg	Met	Gly	Leu	Gly	Leu	Val	Leu	Gly	Ala	
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Met	Ala	Met	Ala	Thr	Ala	Gly	Thr	Val	Glu	His	Phe	Arg	Lys	Ala	Ser	
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gcg	acc	acg	gcg	aac	agc	agc	gag	ctg	cac	atc	cta	tgg	cag	gtg	ccg	1615
Ala	Thr	Thr		Asn	Ser	Ser	Glu	Leu	His	Ile	Leu	Trp	Gln	Val	Pro	
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Gln	Tyr	Ala	Leu	Ile	Gly	Val	Ser	Glu	Val	Met	Met	Tyr	Val	Gly	Gln	
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ctc	gag	ttc	ttc	aac	ggc	gag	atg	ccc	gac	ggg	ttc	aag	agc	ttc	ggc	1711
Leu	Glu	Phe	Phe	Asn	Gly	Glu	Met	Pro	Asp	Gly	Phe	Lys	Ser	Phe	Gly	
		505				510					515					
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Ser	Ala	Leu	Cys	Met	Met	Ser	Met	Ser	Leu	Gly	Asn	Tyr	Phe	Ser	Asp	
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Ile	Ile	Val	Ser	Ala	Val	Thr	Lys	Ala	Thr	Ala	Val	Asp	Gly	Arg	Pro	
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Gly	Trp	Ile	Pro	Ala	Asp	Leu	Asn	Glu	Gly	His	Leu	Asn	Lys	Phe	Tyr	
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Phe	Leu	Leu	Ala	Ile	Leu	Ser	Val	Ala	Asp	Phe	Ala	Val	Tyr	Leu	Val	
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Phe	Ala	Gly	Arg	Tyr	Arg	Lys	Ser	Cys	Lys	Val	Asp	Gly	Arg	Ser	Asp	
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PF59082SeqList_PF59082.txt

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 <213> Triticum aestivum

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 Gly Lys Ser Gly Gly Trp Leu Ala Gly Gly Leu Ile Leu Val Asn Gln
 50 55 60
 Gly Leu Ala Thr Met Ala Phe Phe Gly Val Asn Val Asn Leu Val Leu
 65 70 75 80
 Phe Leu Thr Arg Val Val Gln Gln Ser Asn Gly Asp Ala Ala Asn Asn
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 Val Ser Lys Trp Thr Gly Thr Val Tyr Met Phe Ser Leu Ile Gly Ala
 100 105 110
 Phe Leu Ser Asp Ser Tyr Trp Gly Arg Tyr Lys Thr Cys Ala Ile Phe
 115 120 125
 Gln Ala Ile Phe Val Leu Gly Leu Gly Leu Leu Ser Leu Ser Ser Arg
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 Leu Tyr Leu Ile Arg Pro Val Gly Cys Gly Thr Glu His Thr Pro Cys
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 Gly Ala Asp Gln Phe Asp Glu Glu Asp Pro Ala Glu Ala His Ser Lys
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 Val Ser Phe Phe Ser Tyr Phe Tyr Leu Ala Leu Asn Leu Gly Ser Leu
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 Ile Gly Phe Trp Ala Ser Thr Ala Ala Ala Thr Ala Leu Leu Leu
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 260 265 270
 Pro Met Ala Ser Ile Cys Gln Val Ala Ser Ala Ala Cys Arg Asn Trp
 275 280 285
 Lys Ser Gly Gly Val Ser Gln Asp Val Glu Ile Leu Tyr Glu Gly Asp
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 Asp Lys Thr Asp Ala Gly Ser Arg Lys Leu Leu His Thr Lys Gly Phe
 305 310 315 320
 Arg Phe Leu Asp Arg Ala Ala Leu Thr Thr Glu Asp Thr Ser Ser Lys
 325 330 335
 Leu Ala Thr Cys Ser Lys Thr Arg Asp Gln Trp Lys Leu Cys Thr Val
 340 345 350
 Thr Gln Val Glu Gln Val Lys Ser Ile Leu Arg Ile Leu Pro Ile Trp
 355 360 365
 Val Cys Thr Ile Leu Tyr Ser Val Val Phe Thr Gln Met Ala Ser Leu
 370 375 380
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 385 390 395 400
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PF59082SeqList_PF59082.txt

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 515 520 525
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 545 550 555 560
 Gly His Leu Asn Lys Phe Tyr Phe Leu Leu Ala Ile Leu Ser Val Ala
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Thr Leu Asp His Lys Gly Asn Pro Ala Asp Lys Arg Ile Thr Gly Thr	
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Trp Lys Ala Cys Pro Phe Ile Ile Gly Asn Glu Cys Cys Glu Arg Leu	
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gct tac tat ggc atg agc tcc aat cta gtg ctc tac ttc aag aat cag	196
Ala Tyr Tyr Gly Met Ser Ser Asn Leu Val Leu Tyr Phe Lys Asn Gln	
45 50 55	
ctg aac caa agc agt gca act gct acc aag aac aac tct gac tgg agt	244
Leu Asn Gln Ser Ser Ala Thr Ala Thr Lys Asn Asn Ser Asp Trp Ser	
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gga act tgt tac ctc aca cct cta ttg gga gcc ttt ctt gct gat gct	292
Gly Thr Cys Tyr Leu Thr Pro Leu Leu Gly Ala Phe Leu Ala Asp Ala	
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tat ctt ggt aga tac tgg act att gct ggc ttc tca atc atc tat gtc	340
Tyr Leu Gly Arg Tyr Trp Thr Ile Ala Gly Phe Ser Ile Ile Tyr Val	
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ttt gga atg aca ctt tta gca atg tca gca tca gtc ccg ggc ctg aaa	388
Phe Gly Met Thr Leu Leu Ala Met Ser Ala Ser Val Pro Gly Leu Lys	
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Pro Thr Cys Ile Ser Lys Asp Asn Cys His Ala Thr Glu Gly Gln Ser	
125 130 135	
gcg gtt ttc ttc gta gct ctc tac atg ata gct cta ggg aca gga ggg	484
Ala Val Phe Phe Val Ala Leu Tyr Met Ile Ala Leu Gly Thr Gly Gly	
140 145 150 155	
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Ile Lys Pro Cys Val Ser Ser Tyr Gly Ala Asp Gln Phe Asp Asp Ala	
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Asp Val Glu Lys Glu His Lys Ala Ser Phe Phe Asn Trp Phe Tyr	
175 180 185	
ttc tcc atc aac gtt ggt gca ttg gtt gct agc tcc tta ctg gtt tgg	628
Phe Ser Ile Asn Val Gly Ala Leu Val Ala Ser Ser Leu Leu Val Trp	
190 195 200	
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PF59082SeqList_PF59082.txt

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gcc	atg	gct	att	gct	gtt	gcg	agt	ttc	ttt	tca	ggg	acc	cgc	aag	tat	724
Ala	Met	Ala	Ile	Ala	Val	Ala	Ser	Phe	Phe	Ser	Gly	Thr	Arg	Lys	Tyr	
220					225					230					235	
agg	tat	cag	acg	cct	ggt	ggt	agc	cct	ctt	act	aga	atc	tgt	cag	gtc	772
Arg	Tyr	Gln	Thr	Pro	Gly	Gly	Ser	Pro	Leu	Thr	Arg	Ile	Cys	Gln	Val	
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Ile	Val	Ala	Ser	Cys	Arg	Lys	Tyr	Lys	Val	Ser	Pro	Pro	Asn	Asp	Lys	
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tcg	ctt	ctt	tat	gag	agt	gct	gat	tct	gaa	tcc	ggc	atc	aca	ggc	agc	868
Ser	Leu	Leu	Tyr	Glu	Ser	Ala	Asp	Ser	Glu	Ser	Gly	Ile	Thr	Gly	Ser	
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cgg	aaa	ctc	gat	cac	acc	aaa	gat	ttc	agt	ttc	ctg	gac	aag	gca	gca	916
Arg	Lys	Leu	Asp	His	Thr	Lys	Asp	Phe	Ser	Phe	Leu	Asp	Lys	Ala	Ala	
	285					290					295					
gtg	gag	aca	gag	aaa	gac	cac	ata	aag	gac	aca	tca	gta	aac	cca	tgg	964
Val	Glu	Thr	Glu	Lys	Asp	His	Ile	Lys	Asp	Thr	Ser	Val	Asn	Pro	Trp	
300					305					310					315	
agg	cta	tgc	aca	gta	acc	caa	atc	gag	gaa	ttc	aaa	gca	ata	atc	cgc	1012
Arg	Leu	Cys	Thr	Val	Thr	Gln	Ile	Glu	Glu	Phe	Lys	Ala	Ile	Ile	Arg	
				320				325						330		
ctg	ctc	ccg	atc	tgg	gca	acc	ggt	ata	gtc	ttc	gca	gca	gta	tac	agc	1060
Leu	Leu	Pro	Ile	Trp	Ala	Thr	Gly	Ile	Val	Phe	Ala	Ala	Val	Tyr	Ser	
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caa	atg	agc	aac	ctt	ttc	gtc	cta	cag	gga	gac	aca	atg	gac	aag	cga	1108
Gln	Met	Ser	Asn	Leu	Phe	Val	Leu	Gln	Gly	Asp	Thr	Met	Asp	Lys	Arg	
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gta	gga	aac	tcc	aag	ttc	aaa	atc	tcc	gca	gcc	aac	gta	tca	gta	ttc	1156
Val	Gly	Asn	Ser	Lys	Phe	Lys	Ile	Ser	Ala	Ala	Asn	Val	Ser	Val	Phe	
	365					370					375					
gac	aca	atc	agt	gtc	ata	ttc	tgg	gta	cca	atc	tac	gac	agg	ctt	ata	1204
Asp	Thr	Ile	Ser	Val	Ile	Phe	Trp	Val	Pro	Ile	Tyr	Asp	Arg	Leu	Ile	
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gtc	cca	gcc	gtc	aga	aaa	atc	aca	ggc	cac	aag	aac	ggg	ttc	acc	cag	1252
Val	Pro	Ala	Val	Arg	Lys	Ile	Thr	Gly	His	Lys	Asn	Gly	Phe	Thr	Gln	
				400				405						410		
ctc	caa	cg	atg	ggg	atc	ggc	cta	gtc	atc	tcg	att	ttc	gcc	atg	gtg	1300
Leu	Gln	Arg	Met	Gly	Ile	Gly	Leu	Val	Ile	Ser	Ile	Phe	Ala	Met	Val	
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tac	ccc	gcg	atc	ctg	gag	ctg	atc	agg	ctt	aaa	atg	gtg	agg	gag	cac	1348
Tyr	Pro	Ala	Ile	Leu	Glu	Leu	Ile	Arg	Leu	Lys	Met	Val	Arg	Glu	His	
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Asn	Tyr	Tyr	Glu	Leu	Glu	Ser	Val	Pro	Ile	Ser	Ile	Phe	Trp	Gln	Val	
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ccg	cag	tat	ttc	ctg	atc	ggt	tgc	gct	gag	gtg	ttc	act	ttc	atc	ggt	1444
Pro	Gln	Tyr	Phe	Leu	Ile	Gly	Cys	Ala	Glu	Val	Phe	Thr	Phe	Ile	Gly	
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cag	ctc	gag	ttc	ttc	tac	gag	cag	gcg	ccc	gat	gcg	atg	agg	agc	ttg	1492
Gln	Leu	Glu	Phe	Phe	Tyr	Glu	Gln	Ala	Pro	Asp	Ala	Met	Arg	Ser	Leu	
				480				485						490		
tgt	tcg	gct	ctt	tcg	ttg	act	act	gtg	gcg	ttg	ggg	aat	tac	ttg	agc	1540
Cys	Ser	Ala	Leu	Ser	Leu	Thr	Thr	Val	Ala	Leu	Gly	Asn	Tyr	Leu	Ser	
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tcg	ctg	ctg	gtg	acg	att	gtg	acg	ggt	gtt	acg	act	aag	gga	ggg	aag	1588
Ser	Leu	Leu	Val	Thr	Ile	Val	Thr	Gly	Val	Thr	Thr	Lys	Gly	Gly	Lys	
				510			515					520				
ccc	ggg	tgg	att	cct	gat	aac	ttg	aac	tat	ggc	cat	ggt	gat	tac	ttc	1636
Pro	Gly	Trp	Ile	Pro	Asp	Asn	Leu	Asn	Tyr	Gly	His	Val	Asp	Tyr	Phe	
				525		530					535					
ttc	tgg	ctg	ctg	gct	gtg	ctt	agt	gtt	gtg	aat	ctg	atg	gcg	tat	atg	1684
Phe	Trp	Leu	Leu	Ala	Val	Leu	Ser	Val	Val	Asn	Leu	Met	Ala	Tyr	Met	
				545						550					555	
gtg	att	gct	agc	tgg	tat	act	tac	aag	aag	cct	gtg	ggg	act	ctg	cgt	1732
Val	Ile	Ala	Ser	Trp	Tyr	Thr	Tyr	Lys	Lys	Pro	Val	Gly	Thr	Leu	Arg	
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tga	atg	ctg	ggt	gat	gtatt	gtt	tcttc	ctg	ggt	gtgt	gtag	tt	tg	gaa	agga	1785

PF59082SeqList_PF59082.txt

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 <213> Linum usitatissimum

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 35 40 45
 Ser Ser Asn Leu Val Leu Tyr Phe Lys Asn Gln Leu Asn Gln Ser Ser
 50 55 60
 Ala Thr Ala Thr Lys Asn Asn Ser Asp Trp Ser Gly Thr Cys Tyr Leu
 65 70 75 80
 Thr Pro Leu Leu Gly Ala Phe Leu Ala Asp Ala Tyr Leu Gly Arg Tyr
 85 90 95
 Trp Thr Ile Ala Gly Phe Ser Ile Ile Tyr Val Phe Gly Met Thr Leu
 100 105 110
 Leu Ala Met Ser Ala Ser Val Pro Gly Leu Lys Pro Thr Cys Ile Ser
 115 120 125
 Lys Asp Asn Cys His Ala Thr Glu Gly Gln Ser Ala Val Phe Phe Val
 130 135 140
 Ala Leu Tyr Met Ile Ala Leu Gly Thr Gly Gly Ile Lys Pro Cys Val
 145 150 155 160
 Ser Ser Tyr Gly Ala Asp Gln Phe Asp Asp Ala Asp Val Glu Glu Lys
 165 170 175
 Glu His Lys Ala Ser Phe Phe Asn Trp Phe Tyr Phe Ser Ile Asn Val
 180 185 190
 Gly Ala Leu Val Ala Ser Ser Leu Leu Val Trp Val Gln Glu Asn Val
 195 200 205
 Ser Trp Gly Leu Gly Phe Gly Ile Pro Ala Ile Ala Met Ala Ile Ala
 210 215 220
 Val Ala Ser Phe Phe Ser Gly Thr Arg Lys Tyr Arg Tyr Gln Thr Pro
 225 230 235 240
 Gly Gly Ser Pro Leu Thr Arg Ile Cys Gln Val Ile Val Ala Ser Cys
 245 250 255
 Arg Lys Tyr Lys Val Ser Pro Pro Asn Asp Lys Ser Leu Leu Tyr Glu
 260 265 270
 Ser Ala Asp Ser Glu Ser Gly Ile Thr Gly Ser Arg Lys Leu Asp His
 275 280 285
 Thr Lys Asp Phe Ser Phe Leu Asp Lys Ala Ala Val Glu Thr Glu Lys
 290 295 300
 Asp His Ile Lys Asp Thr Ser Val Asn Pro Trp Arg Leu Cys Thr Val
 305 310 315 320
 Thr Gln Ile Glu Glu Phe Lys Ala Ile Ile Arg Leu Leu Pro Ile Trp
 325 330 335
 Ala Thr Gly Ile Val Phe Ala Ala Val Tyr Ser Gln Met Ser Asn Leu
 340 345 350
 Phe Val Leu Gln Gly Asp Thr Met Asp Lys Arg Val Gly Asn Ser Lys
 355 360 365
 Phe Lys Ile Ser Ala Ala Asn Val Ser Val Phe Asp Thr Ile Ser Val
 370 375 380
 Ile Phe Trp Val Pro Ile Tyr Asp Arg Leu Ile Val Pro Ala Val Arg
 385 390 395 400
 Lys Ile Thr Gly His Lys Asn Gly Phe Thr Gln Leu Gln Arg Met Gly

PF59082SeqList_PF59082.txt

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      405      410      415
Ile Gly Leu Val Ile Ser Ile Phe Ala Met Val Tyr Pro Ala Ile Leu
      420      425      430
Glu Leu Ile Arg Leu Lys Met Val Arg Glu His Asn Tyr Tyr Glu Leu
      435      440      445
Glu Ser Val Pro Ile Ser Ile Phe Trp Gln Val Pro Gln Tyr Phe Leu
      450      455      460
Ile Gly Cys Ala Glu Val Phe Thr Phe Ile Gly Gln Leu Glu Phe Phe
      465      470      475
Tyr Glu Gln Ala Pro Asp Ala Met Arg Ser Leu Cys Ser Ala Leu Ser
      485      490      495
Leu Thr Thr Val Ala Leu Gly Asn Tyr Leu Ser Ser Leu Leu Val Thr
      500      505      510
Ile Val Thr Gly Val Thr Thr Lys Gly Gly Lys Pro Gly Trp Ile Pro
      515      520      525
Asp Asn Leu Asn Tyr Gly His Val Asp Tyr Phe Phe Trp Leu Leu Ala
      530      535      540
Val Leu Ser Val Val Asn Leu Met Ala Tyr Met Val Ile Ala Ser Trp
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<222> (9)..(1763)

<400> 1755

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atc cgt aag gag gga acg ccc aga aag cca aag ggt ggc ttc aga acc      98
Ile Arg Lys Glu Gly Thr Pro Arg Lys Pro Lys Gly Gly Phe Arg Thr
      15      20      25      30
atc ccc ttc atc ata ttg aat gaa ggg ttt cag tcg ttg gca agc aca      146
Ile Pro Phe Ile Ile Leu Asn Glu Gly Phe Gln Ser Leu Ala Ser Thr
      35      40      45
ggg cta cac gca aac atg gta ata tac ttg acg aac gag ttc cag atg      194
Gly Leu His Ala Asn Met Val Ile Tyr Leu Thr Asn Glu Phe Gln Met
      50      55      60
ggg gca gtg aca tcg agc agc atc atc tca ctc tgg tca gct gct tct      242
Gly Ala Val Thr Ser Ser Ser Ile Ile Ser Leu Trp Ser Ala Ala Ser
      65      70      75
tca ttc atg gca gtg ttt ggc gct gtg ctt tcc gac tct ttc tta ggc      290
Ser Phe Met Ala Val Phe Gly Ala Val Leu Ser Asp Ser Phe Leu Gly
      80      85      90
cgg ttc aca gtc att ctc att ggt tcc tct ttc tcc ctt ctc gga acc      338
Arg Phe Thr Val Ile Leu Ile Gly Ser Ser Phe Ser Leu Leu Gly Thr
      95      100      105      110
att ggg ttg tgg tca aca gca gtg gtt ccg gag tta agg cca cca cca      386
Ile Gly Leu Trp Ser Thr Ala Val Val Pro Glu Leu Arg Pro Pro Pro
      115      120      125
tgc gag tcg atc aat tgc gag act aca gct gcg acg cca act cag tta      434
Cys Glu Ser Ile Asn Cys Glu Thr Thr Ala Ala Thr Pro Thr Gln Leu
      130      135      140
gca atc ctg tac gca tct ctg gga ctc ata tcc ctt gga tca ggc tgc      482
Ala Ile Leu Tyr Ala Ser Leu Gly Leu Ile Ser Leu Gly Ser Gly Cys
      145      150      155
ctt ctg cct tgc tca atg gca ttc ggt gct gac caa ttg gac aag aaa      530
Leu Leu Pro Cys Ser Met Ala Phe Gly Ala Asp Gln Leu Asp Lys Lys
      160      165      170
gac aac cca aat aac gaa aga gtg ttg cag ggc ttc ttc aac tgg tac      578
Asp Asn Pro Asn Asn Glu Arg Val Leu Gln Gly Phe Phe Asn Trp Tyr
      175      180      185      190
tac gcc att ggc gga gtt gcc act ttg ctt ggg ctc acc gtc gtg gtg      626

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PF59082SeqList_PF59082.txt

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Tyr	Ile	Gln	Asp	Thr	Tyr	Gly	Trp	Pro	Val	Gly	Leu	Ser	Val	Pro
		210					215					220		
ttc	cta	gtc	ttg	tct	act	ctc	ttg	ttt	ttg	ttg	cct	tcc	tcc	att
Phe	Leu	Val	Leu	Phe	Ser	Thr	Leu	Leu	Phe	Leu	Leu	Pro	Ser	Ser
		225					230					235		
tac	gtt	aag	cac	aag	gct	aga	ggc	agc	ttg	ttt	gtg	ggg	tgc	ctc
Tyr	Val	Lys	His	Lys	Ala	Arg	Gly	Ser	Leu	Phe	Val	Gly	Cys	Leu
	240					245					250			Arg
gtt	ttg	gtg	gct	gct	atc	tgc	aag	gct	agt	tct	aat	agt	ggt	aaa
Val	Leu	Val	Ala	Ala	Ile	Cys	Lys	Ala	Ser	Ser	Asn	Ser	Val	Lys
255					260					265				270
aat	gga	gaa	caa	gaa	gga	gtc	aac	agt	agt	ggt	ggg	ctt	ctt	gag
Asn	Gly	Glu	Gln	Glu	Gly	Val	Asn	Ser	Ser	Val	Gly	Leu	Leu	Glu
				275				280						285
ttg	gat	gac	agt	agg	cat	gac	tat	ttt	cac	ggc	ctt	gat	cac	aat
Leu	Asp	Asp	Ser	Arg	His	Asp	Tyr	Phe	His	Gly	Leu	Asp	His	Asn
			290				295						300	
ttc	atc	acc	cct	act	cct	cat	ttg	agg	tgc	ctg	aac	aaa	gct	tgc
Phe	Ile	Thr	Pro	Thr	Pro	His	Leu	Arg	Cys	Leu	Asn	Lys	Ala	Cys
		305					310					315		
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Ile	Val	Asn	Ser	Glu	Thr	Asp	Ile	Asn	Pro	Asp	Asp	Gly	Ser	Ala
	320					325					330			Lys
aac	cca	tgg	acc	tta	tgc	aca	gta	gaa	gag	gta	gaa	gcc	atg	aaa
Asn	Pro	Trp	Thr	Leu	Cys	Thr	Val	Glu	Glu	Val	Glu	Ala	Met	Lys
335					340					345				350
ata	gtc	aaa	gtg	tta	ccc	att	tgg	tca	aca	ggc	ttc	cta	ttt	tac
Ile	Val	Lys	Val	Leu	Pro	Ile	Trp	Ser	Thr	Gly	Phe	Leu	Phe	Tyr
				355				360						365
agc	tta	gct	cag	tca	cca	ttc	atg	atc	ctc	caa	gca	gaa	acc	atg
Ser	Leu	Ala	Gln	Ser	Pro	Phe	Met	Ile	Leu	Gln	Ala	Glu	Thr	Met
			370				375						380	
aga	cac	atc	ttc	tcc	aac	tct	ttc	gaa	ttc	ccg	ccg	gga	tca	ctt
Arg	His	Ile	Phe	Ser	Asn	Ser	Phe	Glu	Phe	Pro	Pro	Gly	Ser	Leu
		385					390					395		ggt
tcg	ttc	aac	ttg	ata	agt	ttc	acc	ctc	tcc	atc	atc	atc	tac	gac
Ser	Phe	Asn	Leu	Ile	Ser	Phe	Thr	Leu	Ser	Ile	Ile	Ile	Tyr	Asp
	400					405					410			tcc
ata	cta	atc	ccc	atc	ctt	tcc	aag	ttc	act	ggg	aac	ccg	cgt	ggc
Ile	Leu	Ile	Pro	Ile	Leu	Ser	Lys	Phe	Thr	Gly	Asn	Pro	Arg	Gly
415					420					425				430
agc	acc	aac	gtc	cgc	ctc	gga	gca	ggg	atg	gtc	ctg	gcc	atc	ttg
Ser	Thr	Asn	Val	Arg	Leu	Gly	Ala	Gly	Met	Val	Leu	Ala	Ile	Leu
				435				440					445	gca
atg	gcc	atc	ttg	gcc	atg	gcc	atc	tct	gga	gct	gtg	gag	tct	atg
Met	Ala	Ile	Leu	Ala	Met	Ala	Ile	Ser	Gly	Ala	Val	Glu	Ser	Met
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aga	tgg	aac	gct	acc	gca	gag	caa	gac	gcg	gtg	gag	att	tct	ggt
Arg	Trp	Asn	Ala	Thr	Ala	Glu	Gln	Asp	Ala	Val	Glu	Ile	Ser	Val
		465				470					475			ttt
tgg	ttg	atg	cct	tct	ctt	gtt	ttg	ctc	ggg	acg	gct	cag	gct	ctg
Trp	Leu	Met	Pro	Ser	Leu	Val	Leu	Leu	Gly	Thr	Ala	Gln	Ala	Leu
		480				485					490			aat
tac	att	gag	cag	att	tcg	ttt	tac	tac	acc	cac	ttg	cct	aag	gca
Tyr	Ile	Glu	Gln	Ile	Ser	Phe	Tyr	Tyr	Thr	His	Leu	Pro	Lys	Ala
495					500					505				Met
tca	agt	att	gct	gtg	gcc	atg	ctc	act	ttg	atg	acg	gcc	att	ggg
Ser	Ser	Ile	Ala	Val	Ala	Met	Leu	Thr	Leu	Met	Thr	Ala	Ile	Gly
				515					520					525
ttg	ttg	gcg	agt	gcg	ttg	att	gat	gtt	gtg	gat	ggt	ttc	agt	tcc
Leu	Leu	Ala	Ser	Ala	Leu	Ile	Asp	Val	Val	Asp	Gly	Phe	Ser	Ser
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gga	ggg	aag	gag	agc	tgg	ttg	tct	act	aat	ctt	aac	gag	ggg	cac
Gly	Gly	Lys	Glu	Ser	Trp	Leu	Ser	Thr	Asn	Leu	Asn	Glu	Gly	His
		545					550					555		Leu
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Phe	Ile	Ile	Leu	Asn	Glu	Gly	Phe	Gln	Ser	Leu	Ala	Ser	Thr	Gly	Leu
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His	Ala	Asn	Met	Val	Ile	Tyr	Leu	Thr	Asn	Glu	Phe	Gln	Met	Gly	Ala
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Val	Thr	Ser	Ser	Ser	Ile	Ile	Ser	Leu	Trp	Ser	Ala	Ala	Ser	Ser	Phe
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Met	Ala	Val	Phe	Gly	Ala	Val	Leu	Ser	Asp	Ser	Phe	Leu	Gly	Arg	Phe
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Ser	Ile	Asn	Cys	Glu	Thr	Thr	Ala	Ala	Thr	Pro	Thr	Gln	Leu	Ala	Ile
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Leu	Tyr	Ala	Ser	Leu	Gly	Leu	Ile	Ser	Leu	Gly	Ser	Gly	Cys	Leu	Leu
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Pro	Cys	Ser	Met	Ala	Phe	Gly	Ala	Asp	Gln	Leu	Asp	Lys	Lys	Asp	Asn
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Pro	Asn	Asn	Glu	Arg	Val	Leu	Gln	Gly	Phe	Phe	Asn	Trp	Tyr	Tyr	Ala
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Ile	Gly	Gly	Val	Ala	Thr	Leu	Leu	Gly	Leu	Thr	Val	Val	Val	Tyr	Ile
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Gln	Asp	Thr	Tyr	Gly	Trp	Pro	Val	Gly	Leu	Ser	Val	Pro	Ala	Phe	Leu
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Val	Leu	Phe	Ser	Thr	Leu	Phe	Leu	Leu	Leu	Pro	Ser	Ser	Ile	Tyr	Val
225					230					235					240
Lys	His	Lys	Ala	Arg	Gly	Ser	Leu	Phe	Val	Gly	Cys	Leu	Arg	Val	Leu
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Val	Ala	Ala	Ile	Cys	Lys	Ala	Ser	Ser	Asn	Ser	Val	Lys	Asp	Asn	Gly
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Glu	Gln	Glu	Gly	Val	Asn	Ser	Ser	Val	Gly	Leu	Leu	Glu	Asp	Leu	Asp
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Asp	Ser	Arg	His	Asp	Tyr	Phe	His	Gly	Leu	Asp	His	Asn	Gly	Phe	Ile
	290					295					300				
Thr	Pro	Thr	Pro	His	Leu	Arg	Cys	Leu	Asn	Lys	Ala	Cys	Leu	Ile	Val
305					310					315					320
Asn	Ser	Glu	Thr	Asp	Ile	Asn	Pro	Asp	Asp	Gly	Ser	Ala	Lys	Asn	Pro
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Trp	Thr	Leu	Cys	Thr	Val	Glu	Glu	Val	Glu	Ala	Met	Lys	Ser	Ile	Val
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PF59082SeqList_PF59082.txt

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 Ile Leu Ala Met Ala Ile Ser Gly Ala Val Glu Ser Met Arg Arg Trp
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 465 470 475 480
 Met Pro Ser Leu Val Leu Leu Gly Thr Ala Gln Ala Leu Asn Tyr Ile
 485 490 495
 Glu Gln Ile Ser Phe Tyr Tyr Thr His Leu Pro Lys Ala Met Ser Ser
 500 505 510
 Ile Ala Val Ala Met Leu Thr Leu Met Thr Ala Ile Gly Ser Leu Leu
 515 520 525
 Ala Ser Ala Leu Ile Asp Val Val Asp Gly Phe Ser Ser Ser Gly Gly
 530 535 540
 Lys Glu Ser Trp Leu Ser Thr Asn Leu Asn Glu Gly His Leu Asp Tyr
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<222> (92)..(1807)

<400> 1757

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ctttcttccc catccttcaa aggtgctatc g atg gct cag aac atc gag caa 112
 Met Ala Gln Asn Ile Glu Gln

gat gat aac tat acg aac gat gga acg gtt gat att cat gga aac cca 160
 Asp Asp Asn Tyr Thr Asn Asp Gly Thr Val Asp Ile His Gly Asn Pro
 10 15 20

gct gat aag cgg aag aca gga aac tgg aga gct tgc cgc ttc att ctg 208
 Ala Asp Lys Arg Lys Thr Gly Asn Trp Arg Ala Cys Arg Phe Ile Leu
 25 30 35

ggg aac gaa tgt tgc gag aga ttg gca tac tac ggg atg agt acc aac 256
 Gly Asn Glu Cys Cys Arg Leu Ala Tyr Tyr Gly Met Ser Thr Asn
 40 45 50 55

ctg gtg aac ttc ctt cag gaa cgt ctc aac atg ggg aat gct aaa gca 304
 Leu Val Asn Phe Leu Gln Glu Arg Leu Asn Met Gly Asn Ala Lys Ala
 60 65 70

tca act act gtc acc aac tgg tca gga act tgc tac gcc aca cca tta 352
 Ser Thr Thr Val Thr Asn Trp Ser Gly Thr Cys Tyr Ala Thr Pro Leu
 75 80 85

atc gga gcc ttc ctg gct gat gcc tac tta gga aga ttc aag acc atc 400
 Ile Gly Ala Phe Leu Ala Asp Ala Tyr Leu Gly Arg Phe Lys Thr Ile
 90 95 100

aca att ttt gtg atg gtc tac atc tgc ggg atg aca ctc ctg aca atg 448
 Thr Ile Phe Val Met Val Tyr Ile Cys Gly Met Thr Leu Leu Thr Met
 105 110 115

tcc gca gct att cca gga ctc cgt cca tct tgc aac gga gat tcc tgc 496
 Ser Ala Ala Ile Pro Gly Leu Arg Pro Ser Cys Asn Gly Asp Ser Cys
 120 125 130 135

cag gcc aca tca agc cag acc gct gta tgc ttc gta gcg ctc tac ttg 544
 Gln Ala Thr Ser Ser Gln Thr Ala Val Cys Phe Val Ala Leu Tyr Leu
 140 145 150

att gct ctc gga acc ggc gga atc aag ccg tgc gtt tcg tcc ttt ggt 592
 Ile Ala Leu Gly Thr Gly Gly Ile Lys Pro Cys Val Ser Ser Phe Gly
 155 160 165

gcg gat cag ttt gac gac aat gac gag tct gag aag aag caa aag agc 640
 Ala Asp Gln Phe Asp Asp Asn Asp Glu Ser Glu Lys Lys Gln Lys Ser

PF59082SeqList_PF59082.txt

tcc	ttc	ttc	aac	tgg	ttc	tac	ttc	tcg	atc	aac	ggt	ggt	gct	atg	gtc	688
Ser	Phe	Phe	Asn	Trp	Phe	Tyr	Phe	Ser	Ile	Asn	Val	Gly	Ala	Met	Val	
gct	tcc	tcg	gtg	ctg	gtg	tgg	ata	cag	atg	aat	ggt	ggt	tgg	gac	tgg	736
Ala	Ser	Ser	Val	Leu	Val	Trp	Ile	Gln	Met	Asn	Val	Gly	Trp	Asp	Trp	
200					205					210					215	
ggg	ttc	ggg	att	ccg	gca	ggt	gcc	atg	gcc	ggt	gct	att	gtg	ttc	ttc	784
Gly	Phe	Gly	Ile	Pro	Ala	Val	Ala	Met	Ala	Val	Ala	Ile	Val	Phe	Phe	
				220					225					230		
ttt	gca	gga	agc	aag	ctg	tac	agg	ggt	cag	aaa	cct	ggt	gga	agt	ccc	832
Phe	Ala	Gly	Ser	Lys	Leu	Tyr	Arg	Val	Gln	Lys	Pro	Gly	Gly	Ser	Pro	
			235				240						245			
ctg	acc	agg	att	ttc	cag	gtc	att	ggt	gct	tct	ttc	aga	aaa	gtg	aat	880
Leu	Thr	Arg	Ile	Phe	Gln	Val	Ile	Val	Ala	Ser	Phe	Arg	Lys	Val	Asn	
			250				255					260				
ggt	gaa	gtc	cca	gat	gat	aag	tcg	ctc	ctc	tat	gag	att	gct	gat	tcc	928
Val	Glu	Val	Pro	Asp	Asp	Lys	Ser	Leu	Leu	Tyr	Glu	Ile	Ala	Asp	Ser	
	265					270					275					
gaa	agc	tcc	atc	caa	ggc	agc	cgc	agg	ctt	gag	cac	acc	gat	gag	ttc	976
Glu	Ser	Ser	Ile	Gln	Gly	Ser	Arg	Arg	Leu	Glu	His	Thr	Asp	Glu	Phe	
280					285					290					295	
aag	ttc	ttt	gac	aag	gca	gcc	gta	gaa	acg	aga	acc	gag	gat	acc	aag	1024
Lys	Phe	Phe	Asp	Lys	Ala	Ala	Val	Glu	Thr	Arg	Thr	Glu	Asp	Thr	Lys	
				300					305					310		
ggc	gta	cca	aac	cca	tgg	aaa	ctc	tgc	aca	gtg	acc	caa	gtc	gaa	gag	1072
Gly	Val	Pro	Asn	Pro	Trp	Lys	Leu	Cys	Thr	Val	Thr	Gln	Val	Glu	Glu	
			315					320					325			
ctg	aaa	tcc	atc	atc	aga	ctg	ctt	cca	gta	tgg	gca	agc	ggc	atc	ata	1120
Leu	Lys	Ser	Ile	Ile	Arg	Leu	Leu	Pro	Val	Trp	Ala	Ser	Gly	Ile	Ile	
			330				335						340			
ttc	tca	gca	gtc	tat	agc	caa	atg	tcc	aca	gtg	ttc	gtc	ctc	caa	ggc	1168
Phe	Ser	Ala	Val	Tyr	Ser	Gln	Met	Ser	Thr	Val	Phe	Val	Leu	Gln	Gly	
	345					350					355					
aac	acg	atg	gac	caa	cac	ggc	ccg	aaa	ttc	aag	atc	cca	tcg	gca		1216
Asn	Thr	Met	Asp	Gln	His	Ile	Gly	Pro	Lys	Phe	Lys	Ile	Pro	Ser	Ala	
360					365					370					375	
tca	ctc	tcc	ctc	ttc	gac	acc	tta	agc	gtc	ctg	ttc	tgg	gct	ccc	gta	1264
Ser	Leu	Ser	Leu	Phe	Asp	Thr	Leu	Ser	Val	Leu	Phe	Trp	Ala	Pro	Val	
				380					385					390		
tac	gac	cgc	cta	atc	gtc	ccg	gca	gcg	aga	aac	ttc	act	ggc	cac	gaa	1312
Tyr	Asp	Arg	Leu	Ile	Val	Pro	Ala	Ala	Arg	Asn	Phe	Thr	Gly	His	Glu	
			395				400						405			
cac	ggg	ttc	acc	caa	cta	caa	agg	atg	ggg	atc	gga	ctc	gtg	atc	tcg	1360
His	Gly	Phe	Thr	Gln	Leu	Gln	Met	Gly	Ile	Gly	Gly	Leu	Val	Ile	Ser	
			410				415						420			
acc	ttc	gcc	atg	gta	gtc	gca	gga	gta	ctg	gaa	gtg	gct	cgt	ctc	cag	1408
Thr	Phe	Ala	Met	Val	Val	Ala	Gly	Val	Leu	Glu	Val	Ala	Arg	Leu	Gln	
	425					430					435					
atg	gtg	agg	cac	cac	ggc	tac	tac	gac	gtg	gag	acg	ggt	ccg	atg	tcg	1456
Met	Val	Arg	His	His	Gly	Tyr	Tyr	Asp	Val	Glu	Thr	Val	Pro	Met	Ser	
440					445					450					455	
att	ttc	tgg	cag	gtt	ccg	cag	tat	ttc	ctg	gtg	ggt	tgt	gcc	gaa	gtg	1504
Ile	Phe	Trp	Gln	Val	Pro	Gln	Tyr	Phe	Leu	Val	Gly	Cys	Ala	Glu	Val	
				460					465					470		
ttt	acc	ttc	atc	ggg	cag	ctc	gag	ttc	ttc	tac	gat	cag	gct	cct	gac	1552
Phe	Thr	Phe	Ile	Gly	Gln	Leu	Glu	Phe	Phe	Tyr	Asp	Gln	Ala	Pro	Asp	
			475				480						485			
gct	atg	agg	agc	ctc	tgc	tcg	gcg	ctg	tct	ctg	gcg	acg	gtg	gct	ctg	1600
Ala	Met	Arg	Ser	Leu	Cys	Ser	Ala	Leu	Ser	Leu	Ala	Thr	Val	Ala	Leu	
			490				495						500			
ggg	aac	tac	ctg	agc	act	ctg	ctc	gtc	acg	gtg	gtg	act	gaa	gtg	acg	1648
Gly	Asn	Tyr	Leu	Ser	Thr	Leu	Leu	Val	Thr	Val	Val	Thr	Glu	Val	Thr	
	505					510					515					
acg	aaa	ggg	gga	aag	ctt	ggg	tgg	att	cct	gac	aac	ttg	aat	aga	ggg	1696
Thr	Lys	Gly	Gly	Lys	Leu	Gly	Trp	Ile	Pro	Asp	Asn	Leu	Asn	Arg	Gly	
520					525					530					535	
cat	ctg	gat	tac	ttc	tac	tgg	ctt	ctg	gcc	att	ctg	agc	ttg	gtg	aat	1744
His	Leu	Asp	Tyr	Phe	Tyr	Trp	Leu	Leu	Ala	Ile	Leu	Ser	Leu	Val	Asn	

PF59082SeqList_PF59082.txt

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          540          545          550
ttc ttc atc tac ctg tgg att gct aag tgg tat tct tat aag aag acc 1792
Phe Phe Ile Tyr Leu Trp Ile Ala Lys Trp Tyr Ser Tyr Lys Lys Thr
          555          560          565
agt ggg aag gtc tga gtagaaaaag gatgatgtgg aggatgaaca ggctgaaccg 1847
Ser Gly Lys Val
          570
tgggtttgat ttgtttatgg ttatgaaccg aaatccttagt gtgttgagtt tagtaaagct 1907

tgtgattttg tcgtcttttt taggaaggga ttaagttgct tgtgaatatc attgctgaac 1967

ttcgtaatTTT aggatagttc acaacataaa tgaataaatg atagttatTTT gatttcgata 2027

tcaaaaaaaaa aaaaaaa 2044

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<210> 1758
 <211> 571
 <212> PRT
 <213> Linum usitatissimum

<400> 1758

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Met Ala Gln Asn Ile Glu Gln Asp Asp Asn Tyr Thr Asn Asp Gly Thr
1          5          10          15
Val Asp Ile His Gly Asn Pro Ala Asp Lys Arg Lys Thr Gly Asn Trp
          20          25          30
Arg Ala Cys Arg Phe Ile Leu Gly Asn Glu Cys Cys Glu Arg Leu Ala
          35          40          45
Tyr Tyr Gly Met Ser Thr Asn Leu Val Asn Phe Leu Gln Glu Arg Leu
          50          55          60
Asn Met Gly Asn Ala Lys Ala Ser Thr Thr Val Thr Asn Trp Ser Gly
65          70          75          80
Thr Cys Tyr Ala Thr Pro Leu Ile Gly Ala Phe Leu Ala Asp Ala Tyr
          85          90          95
Leu Gly Arg Phe Lys Thr Ile Thr Ile Phe Val Met Val Tyr Ile Cys
          100          105          110
Gly Met Thr Leu Leu Thr Met Ser Ala Ala Ile Pro Gly Leu Arg Pro
          115          120          125
Ser Cys Asn Gly Asp Ser Cys Gln Ala Thr Ser Ser Gln Thr Ala Val
130          135          140
Cys Phe Val Ala Leu Tyr Leu Ile Ala Leu Gly Thr Gly Gly Ile Lys
145          150          155          160
Pro Cys Val Ser Ser Phe Gly Ala Asp Gln Phe Asp Asp Asn Asp Glu
          165          170          175
Ser Glu Lys Lys Gln Lys Ser Ser Phe Asn Trp Phe Tyr Phe Ser
          180          185          190
Ile Asn Val Gly Ala Met Val Ala Ser Ser Val Leu Val Trp Ile Gln
          195          200          205
Met Asn Val Gly Trp Asp Trp Gly Phe Gly Ile Pro Ala Val Ala Met
210          215          220
Ala Val Ala Ile Val Phe Phe Phe Ala Gly Ser Lys Leu Tyr Arg Val
225          230          235          240
Gln Lys Pro Gly Gly Ser Pro Leu Thr Arg Ile Phe Gln Val Ile Val
          245          250          255
Ala Ser Phe Arg Lys Val Asn Val Glu Val Pro Asp Asp Lys Ser Leu
          260          265          270
Leu Tyr Glu Ile Ala Asp Ser Glu Ser Ser Ile Gln Gly Ser Arg Arg
          275          280          285
Leu Glu His Thr Asp Glu Phe Lys Phe Phe Asp Lys Ala Ala Val Glu
290          295          300
Thr Arg Thr Glu Asp Thr Lys Gly Val Pro Asn Pro Trp Lys Leu Cys
305          310          315          320
Thr Val Thr Gln Val Glu Glu Leu Lys Ser Ile Ile Arg Leu Leu Pro
          325          330          335
Val Trp Ala Ser Gly Ile Ile Phe Ser Ala Val Tyr Ser Gln Met Ser

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PF59082SeqList_PF59082.txt

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      340      345      350
Thr Val Phe Val Leu Gln Gly Asn Thr Met Asp Gln His Ile Gly Pro
      355      360      365
Lys Phe Lys Ile Pro Ser Ala Ser Leu Ser Leu Phe Asp Thr Leu Ser
      370      375      380
Val Leu Phe Trp Ala Pro Val Tyr Asp Arg Leu Ile Val Pro Ala Ala
385      390      395
Arg Asn Phe Thr Gly His Glu His Gly Phe Thr Gln Leu Gln Arg Met
      400      405      410
Gly Ile Gly Leu Val Ile Ser Thr Phe Ala Met Val Val Ala Gly Val
      415      420      425
Leu Glu Val Ala Arg Leu Gln Met Val Arg His His Gly Tyr Tyr Asp
      430      435      440
Val Glu Thr Val Pro Met Ser Ile Phe Trp Gln Val Pro Gln Tyr Phe
      445      450      455
Leu Val Gly Cys Ala Glu Val Phe Thr Phe Ile Gly Gln Leu Glu Phe
465      470      475
Phe Tyr Asp Gln Ala Pro Asp Ala Met Arg Ser Leu Cys Ser Ala Leu
      480      485      490
Ser Leu Ala Thr Val Ala Leu Gly Asn Tyr Leu Ser Thr Leu Leu Val
      495      500      505
Thr Val Val Thr Glu Val Thr Thr Lys Gly Gly Lys Leu Gly Trp Ile
      510      515      520
Pro Asp Asn Leu Asn Arg Gly His Leu Asp Tyr Phe Tyr Trp Leu Leu
      525      530      535
Ala Ile Leu Ser Leu Val Asn Phe Phe Ile Tyr Leu Trp Ile Ala Lys
545      550      555
Trp Tyr Ser Tyr Lys Lys Thr Ser Gly Lys Val
      560      565      570

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<210> 1759

<211> 1959

<212> DNA

<213> Helianthus annuus

<220>

<221> CDS

<222> (4)..(1803)

<400> 1759

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  Met Glu Pro Leu Asn Glu Asn Asn Lys Asp Asp Glu Ser Ile Glu
      1      5      10
atg tca aac caa aag aag ctt ggt ggg gtc aag acc tta ccc ttt atc      96
Met Ser Asn Gln Lys Lys Leu Gly Gly Val Lys Thr Leu Pro Phe Ile
      20      25      30
ctt gcg aat gag ata tgt gac aga ttc gct gcg acc gga ttc cac gcc      144
Leu Ala Asn Glu Ile Cys Asp Arg Phe Ala Ala Thr Gly Phe His Ala
      35      40      45
aat ctg ata aca tac tta act gta caa ctt aac ata cca cta gtg aag      192
Asn Leu Ile Thr Tyr Leu Thr Val Gln Leu Asn Ile Pro Leu Val Lys
      50      55      60
gca tcc aat acc ctg acc aac ttc act gga ctt tct agt ttt acg cct      240
Ala Ser Asn Thr Leu Thr Asn Phe Thr Gly Leu Ser Ser Phe Thr Pro
      65      70      75
att atc ggt gca cta gtt gct gac tct ttt gct ggt cgc tac tgg acc      288
Ile Ile Gly Ala Leu Val Ala Asp Ser Phe Ala Gly Arg Tyr Trp Thr
      80      85      90
atc gtc gtc gcc ttg ctc att tac gaa ctg ggc atg atc atc att acc      336
Ile Val Val Ala Leu Leu Ile Tyr Glu Leu Gly Met Ile Ile Ile Thr
      100      105      110
ata tca gca ttc ttg cca caa ttc cat cca cca caa tgt ccc act caa      384
Ile Ser Ala Phe Leu Pro Gln Phe His Pro Pro Gln Cys Pro Thr Gln
      115      120      125
gtc aac tgc aaa gaa gca tca caa tct caa tta tca gtg ctt tat gtc      432
Val Asn Cys Lys Glu Ala Ser Gln Ser Gln Leu Ser Val Leu Tyr Val
      130      135      140
tct ctt ttt ttg act gca atc ggg tta gga ggc aca cgg cct tct gtt      480
Ser Leu Phe Leu Thr Ala Ile Gly Leu Gly Gly Thr Arg Pro Ser Val

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PF59082SeqList_PF59082.txt

145	gtt gcg ttt gcc gca gat	150	caa ctt gat att tca aag ccg aaa aaa cag	528
Val Ala Phe Ala Ala Asp	155	Gln Leu Asp Ile Ser Lys Pro Lys Lys Gln		
160	gca aca agc tgg aat ttc ttc aac tgg tac ttc tta tta tca cta	170	175	576
Ala Thr Ser Trp Asn Phe	180	Leu Leu Leu Leu Ser Leu		
185	gca agt tta tct gca ctg acg cta gtc gtc tac atc caa gat cgg gtg	190	200	624
Ala Ser Leu Ser Ala Leu Thr	205	Val Val Tyr Ile Gln Asp Arg Val		
210	agt tgg ggt tgg ggt ctc ggg att cct acc atc gca atg gtg gtt gcg	215	220	672
Ser Trp Gly Trp Gly Leu Gly	225	Ile Pro Thr Ile Ala Met Val Val Ala		
230	ttt gta gcg ttt tta gtt gga tct ccg ctt tat cag aaa gca aaa ccc	235	240	720
Phe Val Ala Phe Leu Val Gly Ser Pro Leu Tyr Gln Lys Ala Lys Pro	245			
250	gaa gga agt ccg ttt gtt aga gtt gct caa gtg att gtt gct gcg atc	255	260	768
Glu Gly Ser Pro Phe Val Arg Val Ala Gln Val Ile Val Ala Ala Ile	265	270		
275	aag aag cgt ggt gtt gag gta ccg gta gat gat aaa ctt ctt tat gag	280	285	816
Lys Lys Arg Gly Val Glu Val Pro Val Asp Asp Lys Leu Leu Tyr Glu	290	295	300	864
305	aac aaa gat ctt gat gcg ggt att tct aag gac ggg cag ctt gtt cat	310	315	912
Asn Lys Asp Leu Asp Ala Gly Ile Ser Lys Asp Gly Gln Leu Val His	320	325	330	960
335	act aat caa ttg agg tgg ttt gat agg gct gcc att atg acc caa gat	340	345	1008
Thr Asn Gln Leu Arg Trp Phe Asp Arg Ala Ala Ile Met Thr Gln Asp	350	355	360	1056
365	gat act gtc cat ctc ctt aca aac tcg ccg aaa cta tgg cga att gct	370	375	1104
Asp Thr Val His Leu Leu 310	380	385	390	1152
395	acc gtg cat aga gtt gaa gaa cta aaa tcc atg att aga ctg tta cca	400	405	1200
Thr Val His Arg Val Glu Glu Leu Lys Ser Met Ile Arg Leu Leu Pro	410	415	420	1248
425	ttt gtg tca acg ggt ata tta ttc gta atg gca tat tca cac cag ggt	430	435	1296
Phe Val Ser Thr Gly Ile Leu Phe Val Met Ala Tyr Ser His Gln Gly	440	445	450	1344
455	agc ttc acc atc atg caa gct cga acc atg gac cgt cac ata acc aaa	460	465	1392
Ser Phe Thr Ile Met Gln Ala Arg Thr Met Asp Arg His Ile Thr Lys	470	475	480	1440
485	act agc tcg ttt gaa ata cct cca gct agc atg gcg gtc ttt gat gtc	490	495	1488
Thr Ser Ser Phe Glu Ile Pro Pro Ala Ser Met Ala Val Phe Asp Val	500	505	510	1536
515	cta gcc cta att att acc ctc gca tta tac gac cgt tta ttt gtc cct	520	525	1584
Leu Ala Leu Ile Ile Thr 390	530	535	540	
545	ttt gca tct cgc ttc aca aag aac cct gca ggc atc aca tgt tta caa	550	555	
Phe Ala Ser Arg Phe Thr 405	560	565	570	
575	cgg atg ggt gtt ggg ttc gct gta aac ata tgt gca aca ttg gtg ggg	580	585	
Arg Met Gly Val Gly Phe Ala Val Asn Ile Cys Ala Thr Leu Val Gly	590	595	600	
605	tcg ttt gtg gag atc aaa cga aaa cac gta gca aga gat cat aaa ctg	610	615	
Ser Phe Val Glu Ile Lys Arg Lys His Val Ala Arg Asp His Lys Leu	620	625	630	
635	atc gac cag cca acg caa ata ata ccc ata agc gtt tat tgg ttg gtt	640	645	
Ile Asp Gln Pro Thr Gln Ile Ile Pro Ile Ser Val Tyr Trp Leu Val	650	655	660	
665	cct cag tat acg ctt cat ggt gta gct caa gca ttt tat caa gtt ggg	670	675	
Pro Gln Tyr Thr Leu His 470	680	685	690	
695	aaa ttg gag ttt ctt tat gat cag tca ccc gaa agt atg aaa agc acc	700	705	
Lys Leu Glu Phe Leu Tyr 485	710	715	720	
725	gca atg gct tta tat tgg att gca att gga tta gga cag tat gca ggg	730	735	
Ala Met Ala Leu Tyr Trp Ile Ala Ile Gly Leu Gly Gln Tyr Ala Gly	740	745	750	
755	aca tta atg gtg aca ttg gtc cat aag tat agc gcg gat aaa aac ggg	760	765	
Thr Leu Met Val Thr Leu Val His Lys Tyr Ser Ala Asp Lys Asn Gly	770	775	780	

PF59082SeqList_PF59082.txt

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          515          520          525
aga aat tgg ctt ccg gat agg aat ata aat aaa ggt aga ttg gaa tac      1632
Arg Asn Trp Leu Pro Asp Arg Asn Ile Asn Lys Gly Arg Leu Glu Tyr
          530          535          540
tac tac atg ctt gta act ggg ata caa gta gta aac ctt gtg tat tat      1680
Tyr Tyr Met Leu Val Thr Gly Ile Gln Val Val Asn Leu Val Tyr Tyr
          545          550          555
tac ata tgt gcc tgg ttc tat act tat aag ccg tta gaa gag gtc gct      1728
Tyr Ile Cys Ala Trp Phe Tyr Thr Tyr Lys Pro Leu Glu Glu Val Ala
          560          565          570
aaa agc ggt gaa gag gga gat cta gag ttg gtt gta gat aac aac atg      1776
Lys Ser Gly Glu Glu Gly Asp Leu Glu Leu Val Val Asp Asn Asn Met
          580          585          590
gta gtt gat gta ata aac aag tca tga tggaaaagaa gccaaaggata      1823
Val Val Asp Val Ile Asn Lys Ser
          595
catagcatta gcgagaatcg tcaatgaacg cgtgtatttta atccgatttc tagatgtcaa      1883

gtattttcat tagctttcaa aagtaaaatc aagtaatctg atgtctaata gtttaaactc      1943

gaaaaaaaa aaaaaa      1959

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<210> 1760
 <211> 599
 <212> PRT
 <213> Helianthus annuus

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<400> 1760
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Ser Asn Gln Lys Leu Gly Gly Val Lys Thr Leu Pro Phe Ile Leu
          20          25          30
Ala Asn Glu Ile Cys Asp Arg Phe Ala Ala Thr Gly Phe His Ala Asn
          35          40          45
Leu Ile Thr Tyr Leu Thr Val Gln Leu Asn Ile Pro Leu Val Lys Ala
          50          55          60
Ser Asn Thr Leu Thr Asn Phe Thr Gly Leu Ser Ser Phe Thr Pro Ile
65          70          75          80
Ile Gly Ala Leu Val Ala Asp Ser Phe Ala Gly Arg Tyr Trp Thr Ile
          85          90          95
Val Val Ala Leu Ile Tyr Glu Leu Gly Met Ile Ile Ile Thr Ile
          100          105          110
Ser Ala Phe Leu Pro Gln Phe His Pro Pro Gln Cys Pro Thr Gln Val
          115          120          125
Asn Cys Lys Glu Ala Ser Gln Ser Gln Leu Ser Val Leu Tyr Val Ser
          130          135          140
Leu Phe Leu Thr Ala Ile Gly Leu Gly Gly Thr Arg Pro Ser Val Val
145          150          155          160
Ala Phe Ala Ala Asp Gln Leu Asp Ile Ser Lys Pro Lys Lys Gln Ala
          165          170          175
Thr Ser Trp Asn Phe Phe Asn Trp Tyr Tyr Leu Leu Leu Ser Leu Ala
          180          185          190
Ser Leu Ser Ala Leu Thr Leu Val Val Tyr Ile Gln Asp Arg Val Ser
          195          200          205
Trp Gly Trp Gly Leu Gly Ile Pro Thr Ile Ala Met Val Val Ala Phe
210          215          220          225
Val Ala Phe Leu Val Gly Ser Pro Leu Tyr Gln Lys Ala Lys Pro Glu
          230          235          240
Gly Ser Pro Phe Val Arg Val Ala Gln Val Ile Val Ala Ala Ile Lys
          245          250          255
Lys Arg Gly Val Glu Val Pro Val Asp Asp Lys Leu Leu Tyr Glu Asn
          260          265          270
Lys Asp Leu Asp Ala Gly Ile Ser Lys Asp Gly Gln Leu Val His Thr
          275          280          285
Asn Gln Leu Arg Trp Phe Asp Arg Ala Ala Ile Met Thr Gln Asp Asp
          290          295          300

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PF59082SeqList_PF59082.txt

290 295 300
 Thr Val His Leu Leu Thr Asn Ser Pro Lys Leu Trp Arg Ile Ala Thr
 305 Val His Arg Val Glu Glu Leu Lys Ser Met Ile Arg Leu Leu Pro Phe
 Val Ser Thr Gly Ile Leu Phe Val Met Ala Tyr Ser His Gln Gly Ser
 325 330 335
 Phe Thr Ile Met Gln Ala Arg Thr Met Asp Arg His Ile Thr Lys Thr
 340 345 350
 Ser Ser Phe Glu Ile Pro Pro Ala Ser Met Ala Val Phe Asp Val Leu
 355 360 365
 Ala Leu Ile Ile Thr Leu Ala Leu Tyr Asp Arg Leu Phe Val Pro Phe
 370 375 380
 Ala Ser Arg Phe Thr Lys Asn Pro Ala Gly Ile Thr Cys Leu Gln Arg
 385 390 400
 Met Gly Val Gly Phe Ala Val Asn Ile Cys Ala Thr Leu Val Gly Ser
 405 410 415
 Phe Val Glu Ile Lys Arg Lys His Val Ala Arg Asp His Lys Leu Ile
 420 425 430
 Asp Gln Pro Thr Gln Ile Ile Pro Ile Ser Val Tyr Trp Leu Val Pro
 435 440 445
 Gln Tyr Thr Leu His Gly Val Ala Gln Ala Phe Tyr Gln Val Gly Lys
 450 455 460
 Leu Glu Phe Leu Tyr Asp Gln Ser Pro Glu Ser Met Lys Ser Thr Ala
 465 470 475
 Met Ala Leu Tyr Trp Ile Ala Ile Gly Leu Gly Gln Tyr Ala Gly Thr
 485 490 495
 Leu Met Val Thr Leu Val His Lys Tyr Ser Ala Asp Lys Asn Gly Arg
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 Asn Trp Leu Pro Asp Arg Asn Ile Asn Lys Gly Arg Leu Glu Tyr Tyr
 515 520 525
 Tyr Met Leu Val Thr Gly Ile Gln Val Val Asn Leu Val Tyr Tyr Tyr
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 Ile Cys Ala Trp Phe Tyr Thr Tyr Lys Pro Leu Glu Glu Val Ala Lys
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 Val Asp Val Ile Asn Lys Ser
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 <211> 1957
 <212> DNA
 <213> Helianthus annuus

<220>
 <221> CDS
 <222> (34)..(1746)

<400> 1761
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 Thr Asp Tyr Ser Arg Val Asn Ser Pro Leu Leu Asn Asn Phe Val Asp
 10 15 20
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 Gly Ala Val Asp Tyr Lys Gly Arg Pro Val Leu Arg Ser Lys Ser Gly
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 tgc tgg cga tcc gca tct ttc atc att ggt gtg gaa gtg gca gag aga 198
 Cys Trp Arg Ser Ala Ser Phe Ile Ile Gly Val Glu Val Ala Glu Arg
 40 45 50 55
 ttt gca tac tat gga gtc agt tca aat ctg atc acc tac ttg acg gga 246
 Phe Ala Tyr Tyr Gly Val Ser Ser Asn Leu Ile Thr Tyr Leu Thr Gly
 60 65 70
 cca ttg ggc caa tct aca gct act gca gct gag aat gtc aac atc tgg 294
 Pro Leu Gly Gln Ser Thr Ala Thr Ala Ala Glu Asn Val Asn Ile Trp
 75 80 85
 tct gga acg tcg tcg ctt ctt ccc cta gtt gga gct ttc atc gcg gat 342
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PF59082SeqList_PF59082.txt

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Ala	Tyr	Leu	Gly	Arg	Tyr	Leu	Thr	Ala	Ile	Leu	Ala	Ser	Leu	Leu	Tyr	
atc	ctg	gca	ctt	gca	tgt	ctg	gct	ttt	tca	aca	tcg	att	aca	tct	gac	438
Ile	Leu	Ala	Leu	Ala	Leu	Leu	Ala	Phe	Ser	Thr	Ser	Ile	Thr	Ser	Asp	
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tgt	aca	aac	tcc	att	gat	ggc	tca	tca	tgt	tca	cct	cag	ctc	caa	ggt	486
Cys	Thr	Asn	Ser	Ile	Asp	Gly	Ser	Ser	Cys	Ser	Pro	Gln	Leu	Gln	Val	
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Val	Ile	Phe	Phe	Ile	Ala	Leu	Tyr	Leu	Val	Ala	Phe	Ala	Gln	Cys	Gly	
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His	Lys	Pro	Cys	Val	Glu	Ala	Phe	Gly	Ala	Asp	Gln	Phe	Asp	Ala	Asp	
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Phe	Gly	Leu	Cys	Ala	Gly	Ala	Thr	Val	Gly	Ile	Phe	Val	Leu	Ser	Tyr	
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Ile	Gln	Asp	Asn	Leu	Ser	Trp	Gly	Leu	Gly	Phe	Gly	Ile	Pro	Cys	Val	
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Met	Met	Gly	Phe	Ala	Leu	Ile	Met	Phe	Leu	Phe	Gly	Thr	Val	Thr	Tyr	
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Arg	Phe	Gly	Glu	Lys	Thr	Gln	Glu	Lys	Asn	Ala	Phe	Ala	Arg	Ile	Ser	
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His	Val	Phe	Leu	Thr	Ala	Ala	Arg	Asn	Arg	Arg	Val	Thr	Ser	Leu	Glu	
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Ile	Cys	Ala	Glu	Glu	Glu	Ala	Ser	Gly	Ile	Met	His	His	Gln	Asp	Ser	
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caa	cag	ttc	aga	ttt	ctc	aac	aaa	gct	ttg	ggt	tcc	cat	gac	ggg	tca	966
Gln	Gln	Phe	Arg	Phe	Leu	Asn	Lys	Ala	Leu	Val	Ser	His	Asp	Gly	Ser	
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Asn	Glu	His	Gly	Thr	Val	Cys	Ser	Val	Asp	Asp	Val	Glu	Glu	Ala	Lys	
			315					320					325			
gcg	att	ctt	aga	ctt	att	cca	ata	tgg	gtc	agc	tgt	tta	ggt	tat	gga	1062
Ala	Ile	Leu	Arg	Leu	Ile	Pro	Ile	Trp	Val	Ser	Cys	Leu	Gly	Tyr	Gly	
		330					335					340				
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Ile	Val	Phe	Ala	Gln	Thr	Ser	Thr	Phe	Phe	Thr	Lys	Gln	Gly	Ser	Thr	
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Met	Asp	Arg	Leu	Ile	Gly	Ser	Ser	Phe	Glu	Ile	Pro	Pro	Ala	Thr	Leu	
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Gln	Ser	Phe	Thr	Gly	Leu	Ser	Ile	Met	Ile	Leu	Ile	Pro	Ile	Tyr	Asp	
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Thr	Ile	Leu	Val	Pro	Phe	Thr	Arg	Ala	Ile	Thr	Lys	Lys	Pro	Ser	Gly	
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Ser	Met	Gly	Val	Ala	Ala	Ile	Val	Glu	Thr	Lys	Arg	Leu	Lys	Val	Ala	
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Arg	Glu	Tyr	Gly	Leu	Leu	Asp	Asp	Pro	Asp	Ala	Met	Ile	Pro	Met	Lys	
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475				480									485			
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Asp	Leu	Lys	Ser	Ile	Gly	Leu	Ala	Leu	Tyr	Leu	Ser	Val	Leu	Gly	Ile	
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Gly	Ser	Phe	Leu	Ser	Gly	Phe	Ile	Ile	Trp	Ile	Val	Glu	Lys	Thr	Thr	
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Gly	Gly	Asn	Gly	Gln	Asp	Gly	Trp	Ile	Ser	Asp	Asn	Leu	Asn	His	Gly	
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His	Ile	Asp	Tyr	Leu	Tyr	Tyr	Leu	Leu	Ala	Gly	Ile	Ser	Ala	Val	Ala	
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Phe	Val	Met	Phe	Val	Tyr	Ser	Ala	Lys	Ser	Tyr	Val	Tyr	Asn	Gly	Glu	
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Arg	Gly	Lys														
570																
aattaatggt	catagatgca	gctggatgta	atgggttgcct	gaattactga	atgtacttgg											1846
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<212> PRT

<213> Helianthus annuus

<400> 1762

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Gly	Val	Glu	Val	Ala	Glu	Arg	Phe	Ala	Tyr	Tyr	Gly	Val	Ser	Ser	Asn	
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Leu	Ile	Thr	Tyr	Leu	Thr	Gly	Pro	Leu	Gly	Gln	Ser	Thr	Ala	Thr	Ala	
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Ala	Glu	Asn	Val	Asn	Ile	Trp	Ser	Gly	Thr	Ser	Ser	Leu	Leu	Pro	Leu	
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Val	Gly	Ala	Phe	Ile	Ala	Asp	Ala	Tyr	Leu	Gly	Arg	Tyr	Leu	Thr	Ala	
		100						105					110			
Ile	Leu	Ala	Ser	Leu	Leu	Tyr	Ile	Leu	Ala	Leu	Ala	Leu	Ala	Phe		
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Ser	Thr	Ser	Ile	Thr	Ser	Asp	Cys	Thr	Asn	Ser	Ile	Asp	Gly	Ser	Ser	
	130					135					140					
Cys	Ser	Pro	Gln	Leu	Gln	Val	Val	Ile	Phe	Phe	Ile	Ala	Leu	Tyr	Leu	
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Val	Ala	Phe	Ala	Gln	Cys	Gly	His	Lys	Pro	Cys	Val	Glu	Ala	Phe	Gly	
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Gly	Ile	Phe	Val	Leu	Ser	Tyr	Ile	Gln	Asp	Asn	Leu	Ser	Trp	Gly	Leu	
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PF59082SeqList_PF59082.txt

Leu Phe Gly Thr Val Thr Tyr Arg Phe Gly Glu Lys Thr Gln Glu Lys
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 260 265 270
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 275 280 285
 Ile Met His His Gln Asp Ser Gln Gln Phe Arg Phe Leu Asn Lys Ala
 290 295 300
 Leu Val Ser His Asp Gly Ser Asn Glu His Gly Thr Val Cys Ser Val
 305 310 315 320
 Asp Asp Val Glu Glu Ala Lys Ala Ile Leu Arg Leu Ile Pro Ile Trp
 325 330 335
 Val Ser Cys Leu Gly Tyr Gly Ile Val Phe Ala Gln Thr Ser Thr Phe
 340 345 350
 Phe Thr Lys Gln Gly Ser Thr Met Asp Arg Leu Ile Gly Ser Ser Phe
 355 360 365
 Glu Ile Pro Pro Ala Thr Leu Gln Ser Phe Thr Gly Leu Ser Ile Met
 370 375 380
 Ile Leu Ile Pro Ile Tyr Asp Thr Ile Leu Val Pro Phe Thr Arg Ala
 385 390 395 400
 Ile Thr Lys Lys Pro Ser Gly Ile Thr Met Leu Gln Arg Ile Gly Ile
 405 410 415
 Gly Ile Leu Ile Ser Ile Val Ser Met Gly Val Ala Ala Ile Val Glu
 420 425 430
 Thr Lys Arg Leu Lys Val Ala Arg Glu Tyr Gly Leu Leu Asp Asp Pro
 435 440 445
 Asp Ala Met Ile Pro Met Lys Ile Trp Trp Leu Leu Pro Gln Tyr Leu
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 Leu Val Gly Ala Gly Glu Val Phe Thr Ile Val Gly Met Gln Glu Phe
 465 470 475 480
 Phe Tyr Asp Gln Met Pro Ser Asp Leu Lys Ser Ile Gly Leu Ala Leu
 485 490 495
 Tyr Leu Ser Val Leu Gly Ile Gly Ser Phe Leu Ser Gly Phe Ile Ile
 500 505 510
 Trp Ile Val Glu Lys Thr Thr Gly Asn Gly Gln Asp Gly Trp Ile
 515 520 525
 Ser Asp Asn Leu Asn His Gly His Ile Asp Tyr Leu Tyr Tyr Leu Leu
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 Ser Tyr Val Tyr Asn Gly Glu Arg Gly Lys 570
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<211> 555

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(555)

<400> 1763

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cag ttg tcc tac aga ggc att cgt cgg agg aaa tgg ggc aaa tgg gta	96
Gln Leu Ser Tyr Arg Gly Ile Arg Arg Lys Trp Gly Lys Trp Val	
20 25 30	
tcg gag atc cga gaa ccc ggt aag aaa aca agg att tgg ctt gga agc	144
Ser Glu Ile Arg Glu Pro Gly Lys Lys Thr Arg Ile Trp Leu Gly Ser	
35 40 45	
tac gag acg gcc gag atg gct gca gcg gcc tac gat gct gcg gct ctt	192
Tyr Glu Thr Ala Glu Met Ala Ala Ala Tyr Asp Ala Ala Ala Leu	
50 55 60	
cac ctc cga gga cgt ggg acc aat ctc aac ttt ccg gaa ctc gtc gac	240
His Leu Arg Gly Arg Gly Thr Asn Leu Asn Phe Pro Glu Leu Val Asp	
65 70 75 80	
agt ttt cct cgg ccg gaa agc tct agt tcg gag cac att caa gcg gct	288

PF59082SeqList_PF59082.txt

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			115				120					125					
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Gln	Ile	Gln	Ala	Ile	Asn	Glu	Ser	Pro	Leu	Asp	Ser	Pro	Arg	Met	Gly		
			130			135					140						
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Trp	Met	Gln	Asp	Leu	Glu	Val	Ala	Asp	Tyr	Glu	Glu	Leu	Tyr	Gly	Gln		
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Phe	Phe	Gly	Gln	His	Asp	Arg	Asp	Glu	Phe	Phe	Glu	Met	Gln	Gln	Phe		
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Ser	Glu	Ile	Arg	Glu	Pro	Gly	Lys	Lys	Thr	Arg	Ile	Trp	Leu	Gly	Ser		
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Tyr	Glu	Thr	Ala	Glu	Met	Ala	Ala	Ala	Ala	Tyr	Asp	Ala	Ala	Ala	Leu		
	50					55				60							
His	Leu	Arg	Gly	Arg	Gly	Thr	Asn	Leu	Asn	Phe	Pro	Glu	Leu	Val	Asp		
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Ser	Phe	Pro	Arg	Pro	Glu	Ser	Ser	Ser	Ser	Glu	His	Ile	Gln	Ala	Ala		
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Ala	Gln	Asp	Ala	Ala	Leu	Met	Phe	Lys	Pro	Gly	Arg	Leu	Ser	Glu	Pro		
			100					105					110				
Ala	Leu	Glu	Ser	Gly	Gln	Gly	Leu	Ser	Arg	Val	Gly	Leu	Ser	Pro	Asp		
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Gln	Ile	Gln	Ala	Ile	Asn	Glu	Ser	Pro	Leu	Asp	Ser	Pro	Arg	Met	Gly		
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Phe	Phe	Gly	Gln	His	Asp	Arg	Asp	Glu	Phe	Phe	Glu	Met	Gln	Gln	Phe		
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 <222> (36)..(587)

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Ser	Ile	Asn	Asn	Gly	Arg	Tyr	Asp	Gly	Gln	Ala	Gly	Met	Pro	Ser	Val		
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PF59082SeqList_PF59082.txt

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Arg	Gln	Pro	Gly	Thr	Lys	Asn	Arg	Ile	Trp	Leu	Gly	Ser	Phe	Glu	Thr		
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cct	gaa	atg	gct	gca	acc	gcc	tat	gac	gtt	gca	gca	ttc	cat	ttc	agg	245	
Pro	Glu	Met	Ala	Ala	Thr	Ala	Tyr	Asp	Val	Ala	Ala	Phe	His	Phe	Arg		
	55				60					65					70		
gga	cga	gag	gct	cgt	ctc	aac	ttc	cct	gag	ctc	gtc	ggc	agc	ctg	cca	293	
Gly	Arg	Glu	Ala	Arg	Leu	Asn	Phe	Pro	Glu	Leu	Val	Gly	Ser	Leu	Pro		
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cgt	cct	gca	gac	tcg	agc	tcc	gac	agc	att	cgc	atg	gcg	gct	cat	gag	341	
Arg	Pro	Ala	Asp	Ser	Ser	Ser	Asp	Ser	Ile	Arg	Met	Ala	Ala	His	Glu		
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Ala	Ala	Leu	Cys	Leu	Arg	Thr	Glu	Pro	Leu	Glu	Ser	Asp	Met	His	Val		
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Asp	Thr	Ser	Ser	Ser	Ser	Asn	Gly	Gly	Pro	Thr	Met	Val	Arg	Leu	Ser		
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ccc	aga	gaa	att	caa	gcg	atc	aac	gag	tca	act	ttg	ggg	tct	cct	acc	485	
Pro	Arg	Glu	Ile	Gln	Ala	Ile	Asn	Glu	Ser	Thr	Leu	Gly	Ser	Pro	Thr		
	135				140					145				150			
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Met	Leu	Met	His	Ser	Thr	Asp	Asp	Tyr	Ser	Met	Gly	Phe	Ala	Asn	Tyr		
				155				160					165				
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Asn Lys Lys Arg Val Arg Pro Asp Pro Gly Tyr Arg Gly Val Arg Met
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180      185      190
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Ser Phe Leu Ser Ile Met Ala Ala Val Met Ser Phe Thr Tyr Ala Thr
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att gga atc ggt cta gcc atc gca acc gtc gca ggt ggg aaa gtg ggt      672
Ile Gly Ile Gly Leu Ala Ile Ala Thr Val Ala Gly Lys Val Gly
210      215      220
aag acg agt atg acg ggc aca gcg gtt gga gta gat gta acc gca gct      720
Lys Thr Ser Met Thr Gly Thr Ala Val Gly Val Asp Val Thr Ala Ala
225      230      235      240
caa aag ata tgg aga tcg ttt caa gcg gtt ggg gac ata gcg ttc gcc      768
Gln Lys Ile Trp Arg Ser Phe Gln Ala Val Gly Asp Ile Ala Phe Ala
245      250      255
tat gct tat gcc acg gtt ctc atc gag att cag gat aca cta aga tct      816
Tyr Ala Tyr Ala Thr Val Leu Ile Glu Ile Gln Asp Thr Leu Arg Ser
260      265      270
agc cca gct gag aac aaa gcc atg aaa aga gca agt ctt gtg gga gta      864
Ser Pro Ala Glu Asn Lys Ala Met Lys Arg Ala Ser Leu Val Gly Val
275      280      285
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Ser Thr Thr Phe Phe Tyr Ile Leu Cys Gly Cys Ile Gly Tyr Ala
290      295      300      305
gca ttt gga aac aat gcc cct gga gat ttc ctc aca gat ttc ggg ttt      960
Ala Phe Gly Asn Asn Ala Pro Gly Asp Phe Leu Thr Asp Phe Gly Phe
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PF59082SeqList_PF59082.txt

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cac ctt att ggt gcc tat cag gtg ttc gcg cag ccg ata ttc cag ttt	1056
His Leu Ile Gly Ala Tyr Gln Val Phe Ala Gln Pro Ile Phe Gln Phe	
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gtt gag aaa aaa tgc aac aga aac tat cca gac aac aag ttc atc act	1104
Val Glu Lys Lys Cys Asn Arg Asn Tyr Pro Asp Asn Lys Phe Ile Thr	
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tct gaa tat tca gta aac gta cct ttc ctt gga aaa ttc aac att agc	1152
Ser Glu Tyr Ser Val Asn Val Pro Phe Leu Gly Lys Phe Asn Ile Ser	
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Leu Phe Arg Leu Val Trp Arg Thr Ala Tyr Val Val Ile Thr Thr Val	
	385
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Val Ala Met Ile Phe Pro Phe Phe Asn Ala Ile Leu Gly Leu Ile Gly	
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gca gct tcc ttc tgg cct tta acg gtt tat ttc cct gtg gag atg cac	1296
Ala Ala Ser Phe Trp Pro Leu Thr Val Tyr Phe Pro Val Glu Met His	
	420
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Ile Ala Gln Thr Lys Ile Lys Lys Tyr Ser Ala Arg Trp Ile Ala Leu	
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aaa acg atg tgc tat gtt tgc ttg atc gtc tcg ctc tta gct gca gcc	1392
Lys Thr Met Cys Tyr Val Cys Leu Ile Val Ser Leu Leu Ala Ala Ala	
	450
gga tcc atc gca gga ctt ata agt agt gtc aaa acc tac aag ccc ttc	1440
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Arg Thr Met His Glu	
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<212> PRT

<213> Arabidopsis thaliana

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	35 40 45
Ile Thr Ala Val Ile Gly Ser Gly Val Leu Ser Leu Ala Trp Ala Ile	
	50 55 60
Ala Gln Leu Gly Trp Ile Ala Gly Thr Ser Ile Leu Leu Ile Phe Ser	
65 70 75 80	
Phe Ile Thr Tyr Phe Thr Ser Thr Met Leu Ala Asp Cys Tyr Arg Ala	
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Pro Asp Pro Val Thr Gly Lys Arg Asn Tyr Thr Tyr Met Asp Val Val	
	100 105 110
Arg Ser Tyr Leu Gly Gly Arg Lys Val Gln Leu Cys Gly Val Ala Gln	
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Tyr Gly Asn Leu Ile Gly Val Thr Val Gly Tyr Thr Ile Thr Ala Ser	
	130 135 140
Ile Ser Leu Val Ala Val Gly Lys Ser Asn Cys Phe His Asp Lys Gly	
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His Thr Ala Asp Cys Thr Ile Ser Asn Tyr Pro Tyr Met Ala Val Phe	
	165 170 175
Gly Ile Ile Gln Val Ile Leu Ser Gln Ile Pro Asn Phe His Lys Leu	
	180 185 190
Ser Phe Leu Ser Ile Met Ala Ala Val Met Ser Phe Thr Tyr Ala Thr	
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Ile Gly Ile Gly Leu Ala Ile Ala Thr Val Ala Gly Gly Lys Val Gly	
	210 215 220
Lys Thr Ser Met Thr Gly Thr Ala Val Gly Val Asp Val Thr Ala Ala	

PF59082SeqList_PF59082.txt

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 Gln Lys Ile Trp Arg Ser Phe Gln Ala Val Gly Asp Ile Ala Phe Ala
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 Ser Pro Ala Glu Asn Lys Ala Met Lys Arg Ala Ser Leu Val Gly Val
 Ser Thr Thr Thr Phe Phe Tyr Ile Leu Cys Gly Cys Ile Gly Tyr Ala
 Ala Phe Gly Asn Asn Ala Pro Gly Asp Phe Leu Thr Asp Phe Gly Phe
 Phe Glu Pro Phe Trp Leu Ile Asp Phe Ala Asn Ala Cys Ile Ala Val
 His Leu Ile Gly Ala Tyr Gln Val Phe Ala Gln Pro Ile Phe Gln Phe
 Val Glu Lys Lys Cys Asn Arg Asn Tyr Pro Asp Asn Lys Phe Ile Thr
 Ser Glu Tyr Ser Val Asn Val Pro Phe Leu Gly Lys Phe Asn Ile Ser
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 Val Ala Met Ile Phe Pro Phe Phe Asn Ala Ile Leu Gly Leu Ile Gly
 Ala Ala Ser Phe Trp Pro Leu Thr Val Tyr Phe Pro Val Glu Met His
 Ile Ala Gln Thr Lys Ile Lys Lys Tyr Ser Ala Arg Trp Ile Ala Leu
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 Gly Ser Ile Ala Gly Leu Ile Ser Ser Val Lys Thr Tyr Lys Pro Phe
 Arg Thr Met His Glu
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 Pro Ser Ala Val Glu Ala Ala Gly Asn Asn Phe Asp Asp Asp Gly Arg
 10 15 20 25
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 Glu Lys Arg Thr Gly Thr Val Met Thr Ala Ser Ala His Ile Ile Thr
 30 35 40
 gct gtg ata ggt tcc gga gtc ttg tcc ttg gct tgg gct ata gca caa 197
 Ala Val Ile Gly Ser Gly Val Leu Ser Leu Ala Trp Ala Ile Ala Gln
 45 50 55
 ctt ggt tgg gtg gca gga aca gtg att ttg gta act ttt gcc gtt ata 245
 Leu Gly Trp Val Ala Gly Thr Val Ile Leu Val Thr Phe Ala Val Ile
 60 65 70
 aat tac ttc aca tct aca atg ctt gcc gac tgt tat cga tct ccg gac 293
 Asn Tyr Phe Thr Ser Thr Met Leu Ala Asp Cys Tyr Arg Ser Pro Asp
 75 80 85
 aca gga ata cgt aat tat aat tac atg gac gtt gtc aga gct tac ctt 341
 Thr Gly Ile Arg Asn Tyr Asn Tyr Met Asp Val Val Arg Ala Tyr Leu
 90 95 100 105
 ggt ggt tgg aaa gtg aag cta tgt ggt ctg gca cag tac ggg agt cta 389
 Gly Gly Trp Lys Val Lys Leu Cys Gly Leu Ala Gln Tyr Gly Ser Leu
 110 115 120
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 2327
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PF59082SeqList_PF59082.txt

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Ala	Ile	Gly	Lys	Ala	Asn	Cys	Phe	His	Glu	Lys	Gly	His	Gly	Ala	Lys		
		140					145					150					
tgt	tcc	gta	tcg	aat	tat	cca	ctc	atg	gcg	gcg	ttt	ggt	atc	atc	cag	533	
Cys	Ser	Val	Ser	Asn	Tyr	Pro	Leu	Met	Ala	Ala	Phe	Gly	Ile	Ile	Gln		
		155				160					165						
att	gtt	ctt	agt	cag	att	cat	aat	ttt	cac	aag	ctc	tct	ttt	ctc	tcc	581	
Ile	Val	Leu	Ser	Gln	Ile	His	Asn	Phe	His	Lys	Leu	Ser	Phe	Leu	Ser		
		170			175					180					185		
att	atc	gcc	acc	gtt	atg	tcc	ttc	tct	tat	gca	tcc	atc	gga	att	ggc	629	
Ile	Ile	Ala	Thr	Val	Met	Ser	Phe	Ser	Tyr	Ala	Ser	Ile	Gly	Ile	Gly		
			190					195						200			
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Leu	Ala	Leu	Ala	Ala	Leu	Ala	Ser	Gly	Lys	Val	Gly	Lys	Thr	Asp	Leu		
			205					210									
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Thr	Gly	Thr	Val	Val	Gly	Val	Asp	Val	Thr	Ala	Ser	Asp	Lys	Ile	Trp		
		220					225					230					
agg	tcg	ttt	caa	gca	gct	gga	gac	att	gcc	ttt	tcg	tac	gca	ttt	tcc	773	
Arg	Ser	Phe	Gln	Ala	Ala	Gly	Asp	Ile	Ala	Phe	Ser	Tyr	Ala	Phe	Ser		
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gtt	gtt	ctc	gtt	gag	att	cag	gat	aca	ctg	aga	tca	agc	cca	cca	gag	821	
Val	Val	Leu	Val	Glu	Ile	Gln	Asp	Thr	Leu	Arg	Ser	Ser	Pro	Pro	Glu		
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Asn	Lys	Val	Met	Lys	Lys	Ala	Ser	Leu	Ala	Gly	Val	Ser	Thr	Thr	Thr		
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Gly	Phe	Tyr	Ile	Leu	Cys	Gly	Cys	Ile	Gly	Tyr	Ala	Ala	Phe	Gly	Asn		
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caa	gcc	cct	gga	gac	ttc	cta	act	gac	ttt	ggt	ttt	tat	gag	cct	tac	965	
Gln	Ala	Pro	Gly	Asp	Phe	Leu	Thr	Asp	Phe	Gly	Phe	Tyr	Glu	Pro	Tyr		
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Trp	Leu	Ile	Asp	Phe	Ala	Asn	Ala	Cys	Ile	Ala	Val	His	Leu	Ile	Ala		
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Ala	Tyr	Gln	Val	Phe	Ala	Gln	Pro	Ile	Phe	Gln	Phe	Ile	Glu	Lys	Lys		
		330			335					340					345		
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Cys	Asn	Lys	Ala	Trp	Pro	Glu	Ser	Asn	Phe	Ile	Thr	Lys	Asp	Tyr	Ser		
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Ile	Asn	Ile	Pro	Leu	Leu	Gly	Lys	Cys	Arg	Ile	Asn	Phe	Phe	Arg	Leu		
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Val	Trp	Arg	Ser	Thr	Tyr	Val	Ile	Leu	Thr	Thr	Val	Ala	Ala	Met	Ile		
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Phe	Pro	Phe	Phe	Asn	Ala	Ile	Leu	Gly	Leu	Ile	Gly	Ala	Leu	Thr	Phe		
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Trp	Pro	Leu	Thr	Val	Tyr	Phe	Pro	Val	Glu	Met	His	Ile	Ser	Gln	Lys		
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Lys	Val	Lys	Lys	Tyr	Thr	Met	Arg	Trp	Ile	Gly	Leu	Lys	Leu	Leu	Val		
				430				435						440			
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Leu	Val	Cys	Leu	Val	Val	Ser	Leu	Leu	Ala	Ala	Val	Gly	Ser	Ile	Val		
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Gly	Leu	Ile	Ser	Ser	Val	Lys	Ala	Tyr	Lys	Pro	Phe	His	Asn	Leu	Asp		
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1568

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 <211> 473
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 35 40 45
 Leu Ser Leu Ala Trp Ala Ile Ala Gln Leu Gly Trp Val Ala Gly Thr
 50 55 60
 Val Ile Leu Val Thr Phe Ala Val Ile Asn Tyr Phe Thr Ser Thr Met
 65 70 75 80
 Leu Ala Asp Cys Tyr Arg Ser Pro Asp Thr Gly Ile Arg Asn Tyr Asn
 85 90 95
 Tyr Met Asp Val Arg Ala Tyr Leu Gly Gly Trp Lys Val Lys Leu
 100 105 110
 Cys Gly Leu Ala Gln Tyr Gly Ser Leu Val Gly Ile Thr Ile Gly Tyr
 115 120 125
 Thr Ile Thr Ala Ser Ile Ser Leu Val Ala Ile Gly Lys Ala Asn Cys
 130 135 140
 Phe His Glu Lys Gly His Gly Ala Lys Cys Ser Val Ser Asn Tyr Pro
 145 150 155 160
 Leu Met Ala Ala Phe Gly Ile Ile Gln Ile Val Leu Ser Gln Ile His
 165 170 175
 Asn Phe His Lys Leu Ser Phe Leu Ser Ile Ile Ala Thr Val Met Ser
 180 185 190
 Phe Ser Tyr Ala Ser Ile Gly Ile Gly Leu Ala Leu Ala Ala Leu Ala
 195 200 205
 Ser Gly Lys Val Gly Lys Thr Asp Leu Thr Gly Thr Val Val Gly Val
 210 215 220
 Asp Val Thr Ala Ser Asp Lys Ile Trp Arg Ser Phe Gln Ala Ala Gly
 225 230 235 240
 Asp Ile Ala Phe Ser Tyr Ala Phe Ser Val Val Leu Val Glu Ile Gln
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 Asp Thr Leu Arg Ser Ser Pro Pro Glu Asn Lys Val Met Lys Lys Ala
 260 265 270
 Ser Leu Ala Gly Val Ser Thr Thr Thr Gly Phe Tyr Ile Leu Cys Gly
 275 280 285
 Cys Ile Gly Tyr Ala Ala Phe Gly Asn Gln Ala Pro Gly Asp Phe Leu
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 Thr Asp Phe Gly Phe Tyr Glu Pro Tyr Trp Leu Ile Asp Phe Ala Asn
 305 310 315 320
 Ala Cys Ile Ala Val His Leu Ile Ala Ala Tyr Gln Val Phe Ala Gln
 325 330 335
 Pro Ile Phe Gln Phe Ile Glu Lys Lys Cys Asn Lys Ala Trp Pro Glu
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 Ser Asn Phe Ile Thr Lys Asp Tyr Ser Ile Asn Ile Pro Leu Leu Gly
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 Lys Cys Arg Ile Asn Phe Phe Arg Leu Val Trp Arg Ser Thr Tyr Val
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 Leu Gly Leu Ile Gly Ala Leu Thr Phe Trp Pro Leu Thr Val Tyr Phe
 405 410 415
 Pro Val Glu Met His Ile Ser Gln Lys Lys Val Lys Lys Tyr Thr Met
 420 425 430
 Arg Trp Ile Gly Leu Lys Leu Leu Val Leu Val Cys Leu Val Val Ser
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PF59082SeqList_PF59082.txt

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455 460
Asn Leu Asp

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Met Ser Pro Ser Pro Leu Thr Met Lys Ser Leu Asp
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Thr Leu His Asn Pro Ser Ala Val Glu Ser Gly Asn Ala Ala Val Lys
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Asn Val Asp Gly Asp Gly Arg Glu Lys Arg Thr Gly Thr Phe Leu Thr
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gcg agt gcg cac att atc acg gcg gtg ata ggc tca gga gtg ttg tct 255
Ala Ser Ala His Ile Ile Thr Ala Val Ile Gly Ser Gly Val Leu Ser
50 55 60
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Leu Ala Trp Ala Leu Ala Gln Leu Gly Trp Val Ala Gly Thr Met Ile
65 70 75
ttg gtg att ttc gcc atc atc act tac tac acg tct act ttg ctc gcc 351
Leu Val Ile Phe Ala Ile Ile Thr Tyr Tyr Thr Ser Thr Leu Leu Ala
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gat tgc tac aga gcg ccg gac ccc atc acc gga aca cgc aac tac acg 399
Asp Cys Tyr Arg Ala Pro Asp Pro Ile Thr Gly Thr Arg Asn Tyr Thr
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110 115 120 125
tgt gga cta gca cag tac gga aac ctc gtt ggg gtc tct att ggt tac 495
Cys Gly Leu Ala Gln Tyr Gly Asn Leu Val Gly Val Ser Ile Gly Tyr
130 135 140
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Thr Ile Thr Ala Ser Ile Ser Leu Val Ala Ile Gly Arg Ala Asn Cys
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Tyr Met Val Ala Phe Gly Gly Leu Gln Ile Leu Leu Ser Gln Ile Pro
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Asn Phe His Lys Leu Ser Phe Leu Ser Ile Ile Ala Ala Val Met Ser
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210 215 220
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Asp Val Ser Ala Ser Glu Lys Val Trp Lys Ala Phe Gln Ala Val Gly
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Asp Ile Ala Phe Ser Tyr Ala Tyr Thr Thr Ile Leu Ile Glu Ile Gln
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PF59082SeqList_PF59082.txt

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Ser	Leu	Ile	Gly	Val 290	Ser	Thr	Thr	Thr	Val 295	Phe	Tyr	Leu	Leu	Cys 300	Gly	
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Cys	Ile	Gly	Tyr	Ala 305	Ala	Phe	Gly	Asn	Ile	Ala	Pro	Gly	Asp	Phe	Leu	
acc	gac	ttt	ggg	ttt	tac	gaa	cca	ttc	tgg	ctc	gtc	att	ttc	gcc	aat	1071
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Val	Cys 335	Ile	Ala	Val	His	Leu	Val	Gly	Ala	Tyr	Gln	Val	Tyr	Val	Gln	
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Pro	Phe	Phe	Gln	Phe	Val 355	Glu	Ser	Lys	Cys	Asn 360	Lys	Lys	Trp	Pro	Glu	
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Ser	Asn	Phe	Ile	Asn 370	Lys	Glu	Tyr	Ser	Leu	Lys 375	Ile	Pro	Leu	Leu	Gly	
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Lys	Val	Arg	Val 385	Asn	Phe	Phe	Arg	Leu	Val	Trp	Arg	Thr	Asn	Tyr	Val	
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Ile	Leu	Thr 400	Thr	Phe	Ile	Ala	Met	Ile	Phe	Pro	Phe	Phe	Asn	Ser	Ile	
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Leu	Gly 415	Leu	Leu	Gly	Ala	Leu	Ala	Phe	Trp	Pro	Leu	Thr	Val	Tyr	Phe	
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Arg	Trp	Leu	Ala	Leu	Asn	Leu	Leu	Val	Leu	Val 455	Cys	Leu	Ile	Val	Ser	
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Ala	Leu	Ala	Ala	Val	Gly	Ser	Ile	Val	Gly	Leu	Ile	Asn	Asn	Val	Lys	
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 <213> Brassica napus

<400> 1776
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 Ala Leu Ala Gln Leu Gly Trp Val Ala Gly Thr Met Ile Leu Val Ile
 65 70 75 80
 Phe Ala Ile Ile Thr Tyr Tyr Thr Ser Thr Leu Leu Ala Asp Cys Tyr
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 Arg Ala Pro Asp Pro Ile Thr Gly Thr Arg Asn Tyr Thr Tyr Met Asp
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 Val Val Arg Ala Tyr Leu Gly Gly Lys Val Gln Leu Cys Gly Leu

PF59082SeqList_PF59082.txt

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Ala	Phe	Gly	Gly	Leu	Gln	Ile	Leu	Leu	Ser	Gln	Ile	Pro	Asn	Phe	His
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Lys	Leu	Ser	Phe	Leu	Ser	Ile	Ile	Ala	Ala	Val	Met	Ser	Phe	Ser	Tyr
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Ala	Ser	Glu	Lys	Val	Trp	Lys	Ala	Phe	Gln	Ala	Val	Gly	Asp	Ile	Ala
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Phe	Ser	Tyr	Ala	Tyr	Thr	Thr	Ile	Leu	Ile	Glu	Ile	Gln	Asp	Thr	Leu
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Tyr	Ala	Ala	Phe	Gly	Asn	Ile	Ala	Pro	Gly	Asp	Phe	Leu	Thr	Asp	Phe
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Gly	Phe	Tyr	Glu	Pro	Phe	Trp	Leu	Val	Ile	Phe	Ala	Asn	Val	Cys	Ile
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Thr	Phe	Ile	Ala	Met	Ile	Phe	Pro	Phe	Phe	Asn	Ser	Ile	Leu	Gly	Leu
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Leu	Gly	Ala	Leu	Ala	Phe	Trp	Pro	Leu	Thr	Val	Tyr	Phe	Pro	Val	Ala
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Ala	Leu	Asn	Leu	Leu	Val	Leu	Val	Cys	Leu	Ile	Val	Ser	Ala	Leu	Ala
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<210> 1777

<211> 1882

<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (220)..(1683)

<400> 1777

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gaaaaatattc attcaacctc cctttgattc ctttccattc aatttcaaga tctaaccgag 180

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Met Val Glu Asn Leu

PF59082SeqList_PF59082.txt

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Ser	Ser	Asp	Leu	Phe	Asp	Glu	Asp	Gly	Arg	Pro	Lys	Arg	Thr	Gly	Thr	
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Val	Trp	Thr	Ala	Ser	Ala	His	Ile	Ile	Thr	Ala	Val	Ile	Gly	Ser	Gly	
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Val	Leu	Ser	Leu	Ala	Trp	Ala	Val	Ala	Gln	Ile	Gly	Trp	Val	Gly	Gly	
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Pro	Ala	Val	Met	Ile	Leu	Phe	Ser	Leu	Val	Thr	Tyr	Tyr	Thr	Ser	Ile	
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Leu	Leu	Cys	Thr	Cys	Tyr	Arg	Ser	Gly	Asp	Ser	Val	Thr	Gly	Lys	Arg	
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Gln	Ile	Pro	Asp	Phe	Asp	Gln	Leu	Trp	Trp	Leu	Ser	Ile	Val	Ala	Ala	
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Asp	Ser	Ser	Pro	Gly	Asn	Leu	Leu	Ala	Ala	Gly	Gly	Phe	Arg	Asn	Pro	
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Tyr	Trp	Leu	Leu	Asp	Ile	Ala	Asn	Leu	Ala	Ile	Val	Ile	His	Leu	Val	
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Gly	Ala	Tyr	Gln	Val	Tyr	Cys	Gln	Pro	Leu	Phe	Ala	Phe	Val	Glu	Lys	
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PF59082SeqList_PF59082.txt

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Met Leu Met Pro Phe Phe Asn Asp Val Leu Gly Leu Leu Gly Ala Ile
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Asp Phe

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<212> PRT

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<400> 1778

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Tyr Tyr Thr Ser Ile Leu Leu Cys Thr Cys Tyr Arg Ser Gly Asp Ser
85 90 95
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Leu Gly Gly Ile Lys Val Lys Ile Cys Gly Val Val Gln Tyr Val Asn
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145 150 155 160
Pro Cys His Val Asn Gly Asn Pro Tyr Met Ile Ala Phe Gly Val Ile
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Gln Ile Val Phe Ser Gln Ile Pro Asp Phe Asp Gln Leu Trp Trp Leu
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Gly Leu Gly Ile Ser Lys Val Val Glu Asn Lys Glu Ile Lys Gly Thr
210 215 220

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PF59082SeqList_PF59082.txt

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 260 265 270
 Lys Ser Pro Pro Ala Glu Glu Asn Thr Met Arg Lys Ala Thr Leu Ile
 275 280 285
 Ser Val Val Val Thr Thr Leu Phe Tyr Met Leu Cys Gly Cys Val Gly
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 Tyr Ala Ala Phe Gly Asp Ser Ser Pro Gly Asn Leu Leu Ala Ala Gly
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 Gly Phe Arg Asn Pro Tyr Trp Leu Leu Asp Ile Ala Asn Leu Ala Ile
 325 330 335
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 Lys Leu Asn Leu Phe Arg Leu Val Trp Arg Thr Ile Phe Val Ile Thr
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<400> 1779
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 Pro Gln Gln Pro Ala Phe Lys Cys Phe Asp Asp Asp Gly Arg Leu Lys
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 Arg Thr Gly Thr Val Trp Thr Ala Ser Ala His Ile Ile Thr Ala Val
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Lys	Ile	Pro	Gly	Phe	Arg	Ser	Pro	Tyr	Lys	Thr	Asn	Val	Phe	Arg	Val	
				380					385					390		
gtt	ttc	cgg	tgc	tgt	ttc	gtc	gtt	cta	acc	gtg	ata	tca	atg	cta		1315
Val	Phe	Arg	Cys	Cys	Phe	Val	Val	Leu	Thr	Thr	Val	Ile	Ser	Met	Leu	
			395					400				405				
atg	ccg	ttc	ttc	aac	gac	gtg	gtt	ggg	atc	tta	gga	gcc	tta	ggg	ttc	1363
Met	Pro	Phe	Phe	Asn	Asp	Val	Val	Gly	Ile	Leu	Gly	Ala	Leu	Gly	Phe	
		410				415						420				
tgg	ccc	ttg	acg	gtt	tat	ttc	ccg	gtg	gag	atg	tat	ata	aag	cag	agg	1411
Trp	Pro	Leu	Thr	Val	Tyr	Phe	Pro	Val	Glu	Met	Tyr	Ile	Lys	Gln	Arg	
	425				430						435					
aag	gtg	gag	aag	tgg	agc	acg	agg	tgg	gtt	tgt	tta	cag	atg	ctt	agt	1459
Lys	Val	Glu	Lys	Trp	Ser	Thr	Arg	Trp	Val	Cys	Leu	Gln	Met	Leu	Ser	
440					445					450					455	
gtt	gct	tat	cta	gtg	atc	tcg	gtg	gtc	gcc	gga	gtt	gga	tca	atc	gct	1507
Val	Ala	Tyr	Leu	Val	Ile	Ser	Val	Val	Ala	Gly	Val	Gly	Ser	Ile	Ala	
				460					465					470		

PF59082SeqList_PF59082.txt

gga gta atg ctt gat ctt aag gtc tac aag ccc ttc cag tct acg tat 1555
 Gly Val Met Leu Asp Leu Lys Val Tyr Lys Pro Phe Gln Ser Thr Tyr
 475 480 485
 tga tgattgatga tggaccaaga acaaaaagaaa actggtgtat aaagattatt 1608

 gtttatgtta tgcctttgaa agaaaaaac tgaacatgtg tataatgtaa gtttccattt 1668

 cgtatgatat ctctgtaata aatttataaa atatgttata aaaaccatat gattcgtgcg 1728

 aaaaaaaaaa aaaaaa 1743

<210> 1780
 <211> 487
 <212> PRT
 <213> Brassica napus

<400> 1780
 Met Gly Glu Thr Ala Ala Ala Asn Asn His His His His His Gly His
 1 5 10 15
 Gln Val Phe Asp Ala Ser Val Pro Gln Gln Pro Ala Phe Lys Cys Phe
 20 25 30
 Asp Asp Asp Gly Arg Leu Lys Arg Thr Gly Thr Val Trp Thr Ala Ser
 35 40 45
 Ala His Ile Ile Thr Ala Val Ile Gly Ser Gly Val Leu Ser Leu Ala
 50 55 60
 Trp Ala Ile Ala Gln Leu Gly Trp Ile Ala Gly Pro Ala Val Met Leu
 65 70 75 80
 Leu Phe Ser Phe Val Thr Leu Tyr Ser Ser Thr Leu Leu Ser Asp Cys
 85 90 95
 Tyr Arg Thr Gly Asp Ala Val Phe Gly Lys Arg Asn Tyr Thr Tyr Met
 100 105 110
 Asp Ala Val Arg Ser Ile Leu Gly Gly Phe Lys Phe Lys Ile Cys Gly
 115 120 125
 Leu Ile Gln Tyr Leu Asn Leu Phe Gly Ile Ala Val Gly Tyr Thr Ile
 130 135 140
 Ala Ala Ser Ile Ser Met Met Ala Ile Lys Arg Ser Asn Cys Phe His
 145 150 155 160
 Lys Ser Gly Gly Lys Asp Pro Cys His Met Ser Ser Asn Pro Tyr Met
 165 170 175
 Ile Ile Phe Gly Val Thr Glu Ile Leu Ser Gln Val Pro Asp Phe
 180 185 190
 Asp Gln Ile Trp Trp Ile Ser Ile Val Ala Ala Val Met Ser Phe Thr
 195 200 205
 Tyr Ser Ala Ile Gly Leu Ala Leu Gly Ile Val Gln Val Ala Ala Asn
 210 215 220
 Gly Val Phe Lys Gly Ser Leu Thr Gly Ile Ser Ile Gly Thr Val Thr
 225 230 235 240
 Gln Thr Gln Lys Ile Trp Arg Thr Phe Gln Ala Leu Gly Asp Thr Ala
 245 250 255
 Phe Ala Tyr Ser Tyr Ser Val Val Leu Ile Glu Ile Gln Asp Thr Val
 260 265 270
 Arg Ser Pro Pro Ser Glu Ser Thr Thr Met Lys Lys Ala Thr Lys Ile
 275 280 285
 Ser Ile Ala Val Thr Thr Ile Phe Tyr Met Leu Cys Gly Ser Met Gly
 290 295 300
 Tyr Ala Ala Phe Gly Asp Ala Ala Pro Gly Asn Leu Leu Thr Gly Phe
 305 310 315 320
 Gly Phe Tyr Asn Pro Phe Trp Leu Leu Asp Ile Ala Asn Ala Ala Ile
 325 330 335
 Val Val His Leu Ile Gly Ala Tyr Gln Val Phe Ser Gln Pro Ile Phe
 340 345 350
 Ala Phe Val Glu Lys Ser Val Ser Glu Arg Phe Pro Asp Ser Asp Leu
 355 360 365
 Leu Thr Lys Glu Leu Gln Ile Lys Ile Pro Gly Phe Arg Ser Pro Tyr

PF59082SeqList_PF59082.txt

Lys 370	Thr	Asn	Val	Phe	Arg	Val 375	Val	Phe	Arg	Cys 380	Cys	Phe	Val	Val	Leu
385	Thr	Thr	Val	Ile	Ser 390	Met	Leu	Met	Pro	Phe 395	Phe	Asn	Asp	Val	Val 400
					405					410					415
Ile	Leu	Gly	Ala	Leu	Gly	Phe	Trp	Pro	Leu	Thr	Val	Tyr	Phe	Pro	Val
			420					425					430		
Glu	Met	Tyr	Ile	Lys	Gln	Arg	Lys	Val	Glu	Lys	Trp	Ser	Thr	Arg	Trp
		435					440					445			
Val	Cys	Leu	Gln	Met	Leu	Ser	Val	Ala	Tyr	Leu	Val	Ile	Ser	Val	Val
	450					455					460				
Ala	Gly	Val	Gly	Ser	Ile	Ala	Gly	Val	Met	Leu	Asp	Leu	Lys	Val	Tyr
465					470					475					480
Lys	Pro	Phe	Gln	Ser	Thr	Tyr									
				485											

<210> 1781

<211> 1726

<212> DNA

<213> Triticum aestivum

<220>

<221> CDS

<222> (73)..(1536)

<400> 1781

agctcccgcg agccgctagc tagctaataca accccaccgg cgagacacgc gccagttgcc 60

atcgcttccc tg atg gag aag aag cag gcg agc tac ggg aag ggc gcg gcc 111

Met Glu Lys Lys Gln Ala Ser Tyr Gly Lys Gly Ala Ala
1 5 10

agg atg gcg ccg atg gag gtg tcg gtg gag gcc ggg aac ggc gcc gag 159
Arg Met Ala Pro Met Glu Val Ser Val Glu Ala Gly Asn Gly Ala Glu

15 20 25

tcc gac tgg ctt gac gac gac ggg cgc ccg cgt cgg acg ggc acg gtg 207
Ser Asp Trp Leu Asp Asp Asp Gly Arg Pro Arg Arg Thr Gly Thr Val

30 35 40 45

tgg acg gcg agc gcc cac atc atc acc gcc gtc atc ggc tcg ggc gtc 255
Trp Thr Ala Ser Ala His Ile Ile Thr Ala Val Ile Gly Ser Gly Val

50 55 60

ctc tcg ctg gcg tgg gcc atc gcc cag ctc ggc tgg gcg gcg ggc ccc 303
Leu Ser Leu Ala Trp Ala Ile Ala Gln Leu Gly Trp Ala Ala Gly Pro

65 70 75

gcc atc atg ctc ctg ttc gcg ctc gtc atc tac tac acc tcc acg ctc 351
Ala Ile Met Leu Leu Phe Ala Leu Val Ile Tyr Tyr Thr Ser Thr Leu

80 85 90

ctc gcc gag tgc tac cgc tcc ggc gac ccg gag acc ggc aag cgc aac 399
Leu Ala Glu Cys Tyr Arg Ser Gly Asp Pro Glu Thr Gly Lys Arg Asn

95 100 105

tac acc tac atg gac gcc gtc cgc tcc tac ctc ccg ggc acc aag gtg 447
Tyr Thr Tyr Met Asp Ala Val Arg Ser Tyr Leu Pro Gly Thr Lys Val

110 115 120 125

aag ctc tgc ggc gtc atc cag tac gcc aac ctc gtg ggc gtc gcc atc 495
Lys Leu Cys Gly Val Ile Gln Tyr Ala Asn Leu Val Gly Val Ala Ile

130 135 140

ggc tac acc atc gcc gcc tcc atc agc atg cgg gcg atc ggg agg gcg 543
Gly Tyr Thr Ile Ala Ala Ser Ile Ser Met Arg Ala Ile Gly Arg Ala

145 150 155

gac tgc ttc cac tac cac gac gtc agg ggc cgc agc ggg aag gac gag 591
Asp Cys Phe His Tyr His Asp Val Arg Gly Arg Ser Gly Lys Asp Glu

160 165 170

tgc aag agc tcc agc aac ccc tac atg atc gtc ttc ggg gtg gtg cag 639
Cys Lys Ser Ser Ser Asn Pro Tyr Met Ile Val Phe Gly Val Val Gln

175 180 185

atc ctc ttc tcg cag ata ccg gac ttc gac cag ata tgg tgg ctc tcc 687
Ile Leu Phe Ser Gln Ile Pro Asp Phe Asp Gln Ile Trp Trp Leu Ser

190 195 200 205

atc gtc gcc gcc gtc atg tcc ttc acc tac tcc acc atc ggg ctc ggg 735

PF59082SeqList_PF59082.txt

Ile Val Ala Ala Val Met Ser Phe Thr Tyr Ser Thr Ile Gly Leu Gly	
210 215 220	
ctc ggc atc gcg cag acc gtc gcc aac ggt ggc atc cag gga agc ctc	783
Leu Gly Ile Ala Gln Thr Val Ala Asn Gly Gly Ile Gln Gly Ser Leu	
225 230 235	
acc ggc ctc agc gtc ggc ccg ggc gtg acc tcc atg cag aag gtg tgg	831
Thr Gly Leu Ser Val Gly Pro Gly Val Thr Ser Met Gln Lys Val Trp	
240 245 250	
cgc agc ctc cag gcc ttc ggc aac atc gcc ttc gcc tac tcc tac tcc	879
Arg Ser 255 Leu Gln Ala Phe Gly Asn Ile Ala Phe 265 Tyr Ser Tyr Ser	
270 275 280	
atc atc ctc atc gaa atc cag gac acg gtg aag gcg ccg ccg ccg tcg	927
Ile Ile Leu Ile Glu Ile Gln Asp Thr Val Lys Ala Pro Pro Pro Ser	
285 290 295	
gag gcg aag gtg atg aag aag gcg acg ggg ata agc gtg gcg acg acg	975
Glu Ala Lys Val Met Lys Lys Ala Thr Gly Ile Ser Val Ala Thr Thr	
300 305 310	
acg gta ttc tac atg ctg tgc ggg tgc atg ggg tac gcg gcg ttc ggc	1023
Thr Val Phe Tyr Met Leu Cys Gly Cys Met Gly Tyr Ala Ala Phe Gly	
315 320 325	
gac gcg gcg ccc gac aac ctg ctc acg ggg ttc ggc ttc tac gag ccc	1071
Asp Ala Ala Pro Asp Asn Leu Leu Thr Gly Phe Gly Phe Tyr Glu Pro	
330 335 340	
ttc tgg ctg ctg gac gtc gcc aac gcc gcc atc gtg ctg cac ctc gtc	1119
Phe Trp Leu Leu Asp Val Ala Asn Ala Ala Ile Val Leu His Leu Val	
345 350 355	
ggc gcc tac cag gtc ttc tgc cag ccc ctc ttc gcc ttc gtc gag aag	1167
Gly Ala Tyr Gln Val Phe Cys Gln Pro Leu Phe Ala Phe Val Glu Lys	
360 365 370	
tgg gcg gcg gcg agg tgg ccc gac agc gcc ttc atc gcc cgg gag ctc	1215
Trp Ala Ala Arg Trp Pro Asp Ser Ala Phe Ile Ala Arg Glu Leu	
375 380 385	
cgc gtg ggg cca ttc gcc atc agc gtc ttc cgg ctc acc tgg cgc acg	1263
Arg Val Gly Pro Phe Ala Ile Ser Val Phe Arg Leu Thr Trp Arg Thr	
390 400 405	
gcc ttc gtc tgc ctc acc acc gtc gtc tcc atg ctg ctc ccc ttc ttc	1311
Ala Phe Val Cys Leu Thr Thr Val Val Ser Met Leu Leu Pro Phe Phe	
410 415 420	
ggc gac gtc gtg ggc ctc ctc ggc gcc gtc gcc ttc tgg ccg ctc acc	1359
Gly Asp Val Val Gly Leu Leu Gly Ala Val Ala Phe Trp Pro Leu Thr	
425 430 435	
gtc tac ttc ccc gtc gag atg tac atc gtg cag cgc ggc gtg cgg cgg	1407
Val Tyr Phe Pro Val Glu Met Tyr Ile Val Gln Arg Gly Val Arg Arg	
440 445 450	
ggg agc acg cgg tgg gtt tgc ctc aag atg ctc agc gcc gcc tgc ctc	1455
Gly Ser Thr Arg Trp Val Cys Leu Lys Met Leu Ser Ala Ala Cys Leu	
455 460 465	
gtc gtg tcc gtc gcc gcc gcc gcc ggc tcc ata gcc gac gtc atc ggc	1503
Val Val Ser Val Ala Ala Ala Ala Gly Ser Ile Ala Asp Val Ile Gly	
470 475 480	
gag ctc aag gag tac cgg ccg ttc agc ggc tga gcgatatattg tgtaggatgg	1556
Glu Leu Lys Glu Tyr Arg Pro Phe Ser Gly	
485 490	
tggtgtacac agcggcacat gggagcacat gtgtacgtac ggattgtgtg ctgcatggag	1616
acggaacaa attaccatta ccaaccttgt gaacttttat caagtagcac ctcgtagata	1676
cttgtatttt cctcgtaaaa gtactctttc cctacaaaaa aaaaaaaaaa	1726

<210> 1782

<211> 487

<212> PRT

<213> Triticum aestivum

<400> 1782

PF59082SeqList_PF59082.txt

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Met Glu Lys Lys Gln Ala Ser Tyr Gly Lys Gly Ala Ala Arg Met Ala
1      5      10      15
Pro Met Glu Val Ser Val Glu Ala Gly Asn Gly Ala Glu Ser Asp Trp
      20      25      30
Leu Asp Asp Gly Arg Pro Arg Thr Gly Thr Val Trp Thr Ala
      35      40      45
Ser Ala His Ile Ile Thr Ala Val Ile Gly Ser Gly Val Leu Ser Leu
      50      55      60
Ala Trp Ala Ile Ala Gln Leu Gly Trp Ala Ala Gly Pro Ala Ile Met
65      70      75      80
Leu Leu Phe Ala Leu Val Ile Tyr Tyr Thr Ser Thr Leu Leu Ala Glu
      85      90      95
Cys Tyr Arg Ser Gly Asp Pro Glu Thr Gly Lys Arg Asn Tyr Thr Tyr
      100      105      110
Met Asp Ala Val Arg Ser Tyr Leu Pro Gly Thr Lys Val Lys Leu Cys
      115      120      125
Gly Val Ile Gln Tyr Ala Asn Leu Val Gly Val Ala Ile Gly Tyr Thr
      130      135      140
Ile Ala Ala Ser Ile Ser Met Arg Ala Ile Gly Arg Ala Asp Cys Phe
145      150      155      160
His Tyr His Asp Val Arg Gly Arg Ser Gly Lys Asp Glu Cys Lys Ser
      165      170      175
Ser Ser Asn Pro Tyr Met Ile Val Phe Gly Val Val Gln Ile Leu Phe
      180      185      190
Ser Gln Ile Pro Asp Phe Asp Gln Ile Trp Trp Leu Ser Ile Val Ala
      195      200      205
Ala Val Met Ser Phe Thr Tyr Ser Thr Ile Gly Leu Gly Leu Gly Ile
      210      215      220
Ala Gln Thr Val Ala Asn Gly Gly Ile Gln Gly Ser Leu Thr Gly Leu
225      230      235      240
Ser Val Gly Pro Gly Val Thr Ser Met Gln Lys Val Trp Arg Ser Leu
      245      250      255
Gln Ala Phe Gly Asn Ile Ala Phe Ala Tyr Ser Tyr Ser Ile Ile Leu
      260      265      270
Ile Glu Ile Gln Asp Thr Val Lys Ala Pro Pro Pro Ser Glu Ala Lys
      275      280      285
Val Met Lys Lys Ala Thr Gly Ile Ser Val Ala Thr Thr Thr Val Phe
      290      295      300
Tyr Met Leu Cys Gly Cys Met Gly Tyr Ala Ala Phe Gly Asp Ala Ala
305      310      315      320
Pro Asp Asn Leu Leu Thr Gly Phe Gly Phe Tyr Glu Pro Phe Trp Leu
      325      330      335
Leu Asp Val Ala Asn Ala Ala Ile Val Leu His Leu Val Gly Ala Tyr
      340      345      350
Gln Val Phe Cys Gln Pro Leu Phe Ala Phe Val Glu Lys Trp Ala Ala
      355      360      365
Ala Arg Trp Pro Asp Ser Ala Phe Ile Ala Arg Glu Leu Arg Val Gly
      370      375      380
Pro Phe Ala Ile Ser Val Phe Arg Leu Thr Trp Arg Thr Ala Phe Val
385      390      395      400
Cys Leu Thr Thr Val Val Ser Met Leu Leu Pro Phe Phe Gly Asp Val
      405      410      415
Val Gly Leu Leu Gly Ala Val Ala Phe Trp Pro Leu Thr Val Tyr Phe
      420      425      430
Pro Val Glu Met Tyr Ile Val Gln Arg Gly Val Arg Arg Gly Ser Thr
      435      440      445
Arg Trp Val Cys Leu Lys Met Leu Ser Ala Ala Cys Leu Val Val Ser
      450      455      460
Val Ala Ala Ala Ala Gly Ser Ile Ala Asp Val Ile Gly Glu Leu Lys
465      470      475      480
Glu Tyr Arg Pro Phe Ser Gly
      485

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<210> 1783

<211> 1781

<212> DNA

<213> Glycine max

<220>

PF59082SeqList_PF59082.txt

<221> CDS

<222> (194)..(1570)

<400> 1783

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caaaagctaa caccaactat aggccaaatc accaataaat attattttccc gttcctttgg      120

cgtgttgggc acccactgaa cacatttgca ctcacacata gaagcagaga gaggccattg      180

gttgggtttca gag atg gga agc atg cac ata gaa acc cca gaa act ttt      229
                Met Gly Ser Met His Ile Glu Thr Pro Glu Thr Phe
                1          5          10
gct gat ggt agc aaa aac ttc gat gat gat gga cga gct aaa aga act      277
Ala Asp Gly Ser Lys Asn Phe Asp Asp Asp Gly Arg Ala Lys Arg Thr
                15          20          25
ggg act tgg att act gca agt gct cat atc ata acg gct gtg att ggt      325
Gly Thr Trp Ile Thr Ala Ser Ala His Ile Ile Thr Ala Val Ile Gly
                30          35          40
tct gga gtg cta tct ctt gca tgg gca att gca cag atg ggt tgg gta      373
Ser Gly Val Leu Ser Leu Ala Trp Ala Ile Ala Gln Met Gly Trp Val
                45          50          55
gct ggt cct gca gtg ctc ttt gtc ttc tct ttg ata aca tac ttc acc      421
Ala Gly Pro Ala Val Leu Phe Val Phe Ser Leu Ile Thr Tyr Phe Thr
                60          65          70          75
tcc act ctt ctc gct gac tgt tac cgt tca cct gac cct gta cat ggc      469
Ser Thr Leu Leu Ala Asp Cys Tyr Arg Ser Pro Asp Pro Val His Gly
                80          85          90
aag cga aac tac aca tat tct gag gtt gtc aaa gcc aac cta gga gga      517
Lys Arg Asn Tyr Thr Tyr Ser Glu Val Val Lys Ala Asn Leu Gly Gly
                95          100          105
aga aaa ttt cag ctg tgt gga ttg gct cag tat ata aat ctt gtt ggt      565
Arg Lys Phe Gln Leu Cys Gly Leu Ala Gln Tyr Ile Asn Leu Val Gly
                110          115          120
gta aca atc ggc tac act ata act gca tca ctt agt atg ggg gcg gtg      613
Val Thr Ile Gly Tyr Thr Ile Thr Ala Ser Leu Ser Met Gly Ala Val
                125          130          135          140
aag aag tcg aac tgt tta cac aaa cat ggc cat caa gac gag tgc aaa      661
Lys Lys Ser Asn Cys Leu His Lys His Gly His Gln Asp Glu Cys Lys
                145          150          155
gtt aag gac aac gct ttt atg att gct ttt gcc tgc atc caa att ctt      709
Val Lys Asp Asn Ala Phe Met Ile Ala Phe Ala Cys Ile Gln Ile Leu
                160          165          170
cta agc caa ata cca aac ttc cat aag ctc tct tgg ctc tct atc gta      757
Leu Ser Gln Ile Pro Asn Phe His Lys Leu Ser Trp Leu Ser Ile Val
                175          180          185
gca gct gtt atg tct ttt gct tat tct tcc att ggg ctt ggc ctt tcc      805
Ala Ala Val Met Ser Phe Ala Tyr Ser Ser Ile Gly Leu Gly Leu Ser
                190          195          200
ata gcc aaa atc ata ggt ggg gga cac gtg cga aca acc tta aca ggg      853
Ile Ala Lys Ile Ile Gly Gly His Val Arg Thr Thr Leu Thr Gly
                205          210          215          220
gtg gaa gtt tcg gga acg gaa aag gtt tgg aaa atg ttt caa gct atc      901
Val Glu Val Ser Gly Thr Glu Lys Val Trp Lys Met Phe Gln Ala Ile
                225          230          235
ggg gac att gcc ttt gct tat gct ttt tct aat gtc cta att gag atc      949
Gly Asp Ile Ala Phe Ala Tyr Ala Phe Ser Asn Val Leu Ile Glu Ile
                240          245          250
cag gac aca ctg aaa tca agc cca cct gag aac aaa gtc atg aag aga      997
Gln Asp Thr Leu Lys Ser Ser Pro Pro Glu Asn Lys Val Met Lys Arg
                255          260          265
gca agt ttg att ggc att atg act aca aca ttg ttt tat gta cta tgt      1045
Ala Ser Leu Ile Gly Ile Met Thr Thr Thr Leu Phe Tyr Val Leu Cys
                270          275          280
ggg tgc tta ggc tat gct gca ttt gga aat gat gca cca tct aat ttc      1093
Gly Cys Leu Gly Tyr Ala Ala Phe Gly Asn Asp Ala Pro Ser Asn Phe

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PF59082SeqList_PF59082.txt

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285          290          295          300
ctc aca gga ttc ggc ttc tat gag ccc ttt tgg cta ata gac ttt gcc      1141
Leu Thr Gly Phe Gly Phe Tyr Glu Pro Phe Trp Leu Ile Asp Phe Ala
          305          310          315
aat gtc tgc ata gca gtg cac tta gtt ggg gca tac cag gtc ttt gtc      1189
Asn Val Cys Ile Ala Val His Leu Val Gly Ala Tyr Gln Val Phe Val
          320          325          330
caa cct ata ttt ggg ttt gtg gaa aag tgg agc aaa gaa aat tgg aca      1237
Gln Pro Ile Phe Gly Phe Val Glu Lys Trp Ser Lys Glu Asn Trp Thr
          335          340          345
gaa agc caa ttt ata aat ggc gag cat act ttg aac att cct cta tgt      1285
Glu Ser Gln Phe Ile Asn Gly Glu His Thr Leu Asn Ile Pro Leu Cys
          350          355          360
gga agc tac aat gtg aac ttc ttt agg gta gtg tgg agg act gca tat      1333
Gly Ser Tyr Asn Val Asn Phe Phe Arg Val Val Trp Arg Thr Ala Tyr
          365          370          375
gtg att atc act gcc gtt gta gct atg tta ctc cca ttc ttc aat gac      1381
Val Ile Ile Thr Ala Val Val Ala Met Leu Leu Pro Phe Phe Asn Asp
          385          390          395
ttt ttg gcc ctt atc ggt gca ctc tct ttc tgg cca ttg acg gtt tac      1429
Phe Leu Ala Leu Ile Gly Ala Leu Ser Phe Trp Pro Leu Thr Val Tyr
          400          405          410
ttc cct ata gag atg tac att aag aag tca aat atg caa aga ttt tcc      1477
Phe Pro Ile Glu Met Tyr Ile Lys Lys Ser Asn Met Gln Arg Phe Ser
          415          420          425
ttc acc tgg act tgg ctc aag ata ttg agt tgg gtt tgc ttg atc att      1525
Phe Thr Trp Thr Trp Leu Lys Ile Leu Ser Trp Val Cys Leu Ile Ile
          430          435          440
tct att atc tca ctt gtg ggt tcc atc caa ggc ctt ttc ggt tag      1570
Ser Ile Ile Ser Leu Val Gly Ser Ile Gln Gly Leu Phe Gly
          445          450          455
tatcaagaaa tacaagccct tccaagcaga acaatagaac tttcatactt agtattccaa      1630

cttgagccaa gagtttctat tgagggcgac aaaatttgta ttactatggt ttgaaatagt      1690

tgttatatatt tcaattctcg aaatcgagac aacttggtat actaaagtaa tataataaaa      1750

tgtttagttt gctatgttaa aaaaaaaaaa a      1781

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<210> 1784
 <211> 458
 <212> PRT
 <213> Glycine max

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<400> 1784
Met Gly Ser Met His Ile Glu Thr Pro Glu Thr Phe Ala Asp Gly Ser
1          5          10          15
Lys Asn Phe Asp Asp Asp Gly Arg Ala Lys Arg Thr Gly Thr Trp Ile
          20          25          30
Thr Ala Ser Ala His Ile Ile Thr Ala Val Ile Gly Ser Gly Val Leu
          35          40          45
Ser Leu Ala Trp Ala Ile Ala Gln Met Gly Trp Val Ala Gly Pro Ala
          50          55          60
Val Leu Phe Val Phe Ser Leu Ile Thr Tyr Phe Thr Ser Thr Leu Leu
65          70          75          80
Ala Asp Cys Tyr Arg Ser Pro Asp Pro Val His Gly Lys Arg Asn Tyr
          85          90          95
Thr Tyr Ser Glu Val Val Lys Ala Asn Leu Gly Gly Arg Lys Phe Gln
          100          105          110
Leu Cys Gly Leu Ala Gln Tyr Ile Asn Leu Val Gly Val Thr Ile Gly
          115          120          125
Tyr Thr Ile Thr Ala Ser Leu Ser Met Gly Ala Val Lys Lys Ser Asn
          130          135          140
Cys Leu His Lys His Gly His Gln Asp Glu Cys Lys Val Lys Asp Asn

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PF59082SeqList_PF59082.txt

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145          150          155          160
Ala Phe Met Ile Ala Phe Ala Cys Ile Gln Ile Leu Leu Ser Gln Ile
165          170          175
Pro Asn Phe His Lys Leu Ser Trp Leu Ser Ile Val Ala Ala Val Met
180          185          190
Ser Phe Ala Tyr Ser Ser Ile Gly Leu Gly Leu Ser Ile Ala Lys Ile
195          200          205
Ile Gly Gly Gly His Val Arg Thr Thr Leu Thr Gly Val Glu Val Ser
210          215          220
Gly Thr Glu Lys Val Trp Lys Met Phe Gln Ala Ile Gly Asp Ile Ala
225          230          235          240
Phe Ala Tyr Ala Phe Ser Asn Val Leu Ile Glu Ile Gln Asp Thr Leu
245          250          255
Lys Ser Ser Pro Pro Glu Asn Lys Val Met Lys Arg Ala Ser Leu Ile
260          265          270
Gly Ile Met Thr Thr Leu Phe Tyr Val Leu Cys Gly Cys Leu Gly
275          280          285          290
Tyr Ala Ala Phe Gly Asn Asp Ala Pro Ser Asn Phe Leu Thr Gly Phe
295          300          305
Gly Phe Tyr Glu Pro Phe Trp Leu Ile Asp Phe Ala Asn Val Cys Ile
310          315          320
Ala Val His Leu Val Gly Ala Tyr Gln Val Phe Val Gln Pro Ile Phe
325          330          335
Gly Phe Val Glu Lys Trp Ser Lys Glu Asn Trp Thr Glu Ser Gln Phe
340          345          350
Ile Asn Gly Glu His Thr Leu Asn Ile Pro Leu Cys Gly Ser Tyr Asn
355          360          365
Val Asn Phe Phe Arg Val Val Trp Arg Thr Ala Tyr Val Ile Ile Thr
370          375          380
Ala Val Val Ala Met Leu Leu Pro Phe Phe Asn Asp Phe Leu Ala Leu
385          390          395          400
Ile Gly Ala Leu Ser Phe Trp Pro Leu Thr Val Tyr Phe Pro Ile Glu
405          410          415
Met Tyr Ile Lys Lys Ser Asn Met Gln Arg Phe Ser Phe Thr Trp Thr
420          425          430
Trp Leu Lys Ile Leu Ser Trp Val Cys Leu Ile Ile Ser Ile Ile Ser
435          440          445
Leu Val Gly Ser Ile Gln Gly Leu Phe Gly
450          455

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<210> 1785
 <211> 1764
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (183)..(1592)

<400> 1785
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60

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120

acttttcctc acacgactct gctcactcat atttatattg aacaaacaga gatcccaa

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 Met Asp Ile Glu Ala Gly Lys Asp Ile Pro Val Arg Asp Pro Ala

227

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 Leu Leu Asp Asp Asp Gly Arg Ile Lys Arg Thr Gly Asn Val Phe Thr

275

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323

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371

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Met	Ile	Leu	Phe	Ala	Cys	Ile	Ser	Val	Tyr	Thr	Tyr	Asn	Leu	Val	Ala		
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Asp	Cys	Tyr	Arg	Phe	Pro	Asp	Pro	Val	Ser	Gly	Lys	Arg	Asn	Tyr	Thr		
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Tyr	Met	Gln	Ala	Val	Asp	Ala	Tyr	Leu	Gly	Gly	Lys	Met	His	Val	Phe		
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Cys	Gly	Ser	Val	Leu	Tyr	Gly	Lys	Leu	Ala	Gly	Val	Thr	Val	Gly	Tyr		
act	ata	act	agt	tct	gtg	agc	ttg	gtg	gct	ata	aag	aaa	gct	att	tgc	611	
Thr	Ile	Thr	Ser	Ser	Val	Ser	Leu	Val	Ala	Ile	Lys	Lys	Ala	Ile	Cys		
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Phe	His	Lys	Lys	Gly	His	Asp	Ala	Tyr	Cys	Lys	Phe	Ser	Asn	Asn	Pro		
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Tyr	Met	Ile	Gly	Phe	Gly	Ile	Cys	Gln	Ile	Leu	Leu	Ser	Gln	Ile	Pro		
aat	ttc	cac	aag	tta	acg	tgg	ctt	tca	acc	att	gct	gct	gct	acc	tct	755	
Asn	Phe	His	Lys	Leu	Thr	Trp	Leu	Ser	Thr	Ile	Ala	Ala	Ala	Thr	Ser		
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Gly	Leu	Gly	Tyr	Ala	Ala	Phe	Gly	Asp	Asp	Thr	Pro	Gly	Asn	Ile	Leu		
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Thr	Gly	Phe	Gly	Phe	Tyr	Glu	Pro	Phe	Trp	Leu	Val	Ala	Leu	Gly	Asn		
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Val	Phe	Ile	Val	Val	His	Met	Val	Gly	Ala	Tyr	Gln	Val	Met	Ala	Gln		
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Pro	Leu	Phe	Arg	Val	Ile	Glu	Met	Gly	Ala	Asn	Met	Ala	Trp	Pro	Arg		
tca	gat	ttc	att	aac	aag	agc	tat	ccc	atc	aaa	atg	ggc	tcc	tta	aca	1283	
Ser	Asp	Phe	Ile	Asn	Lys	Ser	Tyr	Pro	Ile	Lys	Met	Gly	Ser	Leu	Thr		
tgt	aac	atc	aac	ttg	ttt	agg	ata	att	tgg	agg	tca	atg	tat	gtg	gca	1331	
Cys	Asn	Ile	Asn	Leu	Phe	Arg	Ile	Ile	Trp	Arg	Ser	Met	Tyr	Val	Ala		
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Val	Ala	Thr	Val	Ile	Ala	Met	Ala	Met	Pro	Phe	Asn	Glu	Phe	Leu			
gcc	ttg	ctt	gga	gca	ata	ggg	ttt	tgg	cct	ctc	att	gtc	ttc	ttc	cct	1427	
Ala	Leu	Leu	Gly	Ala	Ile	Gly	Phe	Trp	Pro	Leu	Ile	Val	Phe	Phe	Pro		
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PF59082SeqList_PF59082.txt

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 Trp Cys Cys Leu Gln Ile Leu Ser Phe Ala Cys Phe Leu Val Thr Val
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 Ser Ala Ala Val Gly Ser Val Arg Gly Ile Ser Lys Asn Ile Lys Lys
 450 455 460
 ata caa act ttt cca gta taa acaatagggc atttggttgc acattccagt 1622
 Ile Gln Thr Phe Pro Val
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 gtctcacatt tgagaaatgt gaaaatagct atagctaggc agaaaaagaa gggagacaag 1682

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 50 55 60
 Ile Leu Phe Ala Cys Ile Ser Val Tyr Thr Tyr Asn Leu Val Ala Asp
 65 70 75 80
 Cys Tyr Arg Phe Pro Asp Pro Val Ser Gly Lys Arg Asn Tyr Thr Tyr
 85 90 95
 Met Gln Ala Val Asp Ala Tyr Leu Gly Gly Lys Met His Val Phe Cys
 100 105 110
 Gly Ser Val Leu Tyr Gly Lys Leu Ala Gly Val Thr Val Gly Tyr Thr
 115 120 125
 Ile Thr Ser Ser Val Ser Leu Val Ala Ile Lys Lys Ala Ile Cys Phe
 130 135 140
 His Lys Lys Gly His Asp Ala Tyr Cys Lys Phe Ser Asn Asn Pro Tyr
 145 150 155 160
 Met Ile Gly Phe Gly Ile Cys Gln Ile Leu Leu Ser Gln Ile Pro Asn
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 Phe His Lys Leu Thr Trp Leu Ser Thr Ile Ala Ala Ala Thr Ser Phe
 180 185 190
 Gly Tyr Ala Phe Ile Gly Ser Gly Leu Ser Leu Ser Val Val Val Ser
 195 200 205
 Gly Lys Gly Glu Ala Thr Ser Ile Phe Gly Ser Lys Val Gly Pro Asp
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 Leu Ser Glu Ala Asp Lys Val Trp Lys Val Phe Ser Ala Leu Gly Asn
 225 230 235 240
 Ile Ala Leu Ala Cys Ser Phe Ala Thr Val Ile Tyr Asp Ile Met Asp
 245 250 255
 Thr Leu Lys Ser Tyr Pro Pro Glu Asn Lys Gln Met Lys Lys Ala Asn
 260 265 270
 Met Leu Gly Ile Thr Thr Met Thr Ile Leu Phe Leu Leu Cys Gly Gly
 275 280 285
 Leu Gly Tyr Ala Ala Phe Gly Asp Asp Thr Pro Gly Asn Ile Leu Thr
 290 295 300
 Gly Phe Gly Phe Tyr Glu Pro Phe Trp Leu Val Ala Leu Gly Asn Val
 305 310 315 320
 Phe Ile Val Val His Met Val Gly Ala Tyr Gln Val Met Ala Gln Pro
 325 330 335

PF59082SeqList_PF59082.txt

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 370 375 380
 Ala Thr Val Ile Ala Met Ala Met Pro Phe Phe Asn Glu Phe Leu Ala
 385 390 395 400
 Leu Leu Gly Ala Ile Gly Phe Trp Pro Leu Ile Val Phe Phe Pro Val
 405 410 415
 Gln Met His Ile Ala Gln Lys Arg Val Lys Arg Leu Ser Leu Lys Trp
 420 425 430
 Cys Cys Leu Gln Ile Leu Ser Phe Ala Cys Phe Leu Val Thr Val Ser
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<211> 1970

<212> DNA

<213> Triticum aestivum

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<400> 1787

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 Ala Val Gly Asn Gly Gly Ala Lys Val Val Ala Pro Met Glu Val 15

tcc gtg gag gcc ggg aac gcc ggg gac gcg gcg tgg atg gac gac gac 273
 Ser Val Glu Ala Gly Asn Ala Gly Asp Ala Ala Trp Met Asp Asp Asp 20 25 30

ggc cgg ccc cgc cgc tcc ggc acg ttc tgg acg gcg agt gcg cac atc 321
 Gly Arg Pro Arg Arg Ser Gly Thr Phe Trp Thr Ala Ser Ala His Ile 35 40 45

atc acc gcc gtc atc ggc tcc ggc gtg ctc tcg ctg gcc tgg gcc atc 369
 Ile Thr Ala Val Ile Gly Ser Gly Val Leu Ser Leu Ala Trp Ala Ile 50 55 60 65

gcg cag ctc ggt tgg gtg gct ggc cca gct gtc atg ctc ctc ttc gcc 417
 Ala Gln Leu Gly Trp Val Ala Gly Pro Ala Val Met Leu Leu Phe Ala 70 75 80

gcc gtc atc tac tac acc tcc acc ctg ctc gcc gag tgc tac cgc acg 465
 Ala Val Ile Tyr Tyr Thr Ser Thr Leu Leu Ala Glu Cys Tyr Arg Thr 85 90 95

ggg gat ccg gcc acc ggg aag cgc aac tac acc tac atg gac gcc gtc 513
 Gly Asp Pro Ala Thr Gly Lys Arg Asn Tyr Thr Tyr Met Asp Ala Val 100 105 110

cgc tcc aac ctc ggc ggt ccc aag gtc atc ttc tgc ggt gtc atc cag 561
 Arg Ser Asn Leu Gly Gly Pro Lys Val Ile Phe Cys Gly Val Ile Gln 115 120 125

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 Tyr Ala Asn Leu Val Gly Val Ala Ile Gly Tyr Thr Ile Ala Ser 130 135 140 145

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 Ile Ser Met Arg Ala Ile Arg Arg Ala Asp Cys Phe His Ala Asn Gly 150 155 160

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PF59082SeqList_PF59082.txt

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Gly	Leu	Val	Gln	Ile	Val	Phe	Ser	Gln	Ile	Pro	Asp	Phe	Asp	Gln	Ile
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Trp	Trp	Leu	Ser	Ile	Val	Ala	Ala	Val	Met	Ser	Phe	Thr	Tyr	Ser	Gly
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Ile	Gly	Leu	Ser	Leu	Gly	Ile	Thr	Gln	Thr	Ile	Ser	Asn	Gly	Gly	Ile
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Lys	Gly	Ser	Leu	Thr	Gly	Ile	Ser	Ile	Gly	Val	Gly	Ile	Thr	Ala	Thr
			230						235					240	
cag	aag	gtg	tgg	cgc	agc	ctg	cag	gca	ttt	ggc	gac	atc	gcc	ttc	gcc
Gln	Lys	Val	Trp	Arg	Ser	Leu	Gln	Ala	Phe	Gly	Asp	Ile	Ala	Phe	Ala
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Tyr	Ser	Phe	Ser	Asn	Ile	Leu	Ile	Glu	Ile	Gln	Asp	Thr	Ile	Arg	Ala
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Pro	Pro	Pro	Ser	Glu	Ala	Lys	Val	Met	Lys	Gln	Ala	Thr	Arg	Leu	Ser
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Val	Ala	Thr	Thr	Thr	Val	Phe	Tyr	Met	Leu	Cys	Gly	Cys	Met	Gly	Tyr
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Phe	Val	Glu	Arg	Trp	Ala	Ala	Ser	Thr	Trp	Pro	Asp	Ser	Val	Phe	Ile
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			405					410					415		
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Trp	Pro	Leu	Thr	Val	Tyr	Phe	Pro	Val	Glu	Met	Tyr	Ile	Arg	Gln	Arg
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<211> 479

<212> PRT

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<400> 1788

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Asp	Gly	Arg	Pro	Arg	Arg	Ser	Gly	Thr	Phe	Trp	Thr	Ala	Ser	Ala	His
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Ala	Ala	Val	Ile	Tyr	Tyr	Thr	Ser	Thr	Leu	Leu	Ala	Glu	Cys	Tyr	Arg
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Gly	Phe	Tyr	Glu	Pro	Phe	Trp	Leu	Leu	Asp	Ile	Ala	Asn	Val	Ala	Ile
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PF59082SeqList_PF59082.txt

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 Ala Ala Asn 5 Glu Glu Phe Gly Tyr 10 Pro Asp Val His Ser Leu Asp Leu
 gcc aag gaa tcg ctc gac gac gat ggt cgt ccc agg cgg act ggg agt 213
 Ala Lys Glu Ser Leu Asp Asp Asp Gly Arg Pro Arg Arg Thr Gly Ser
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 gtg tgg acg gcg agc gca cac ata ata acg gcg gtg atc ggg tcg gga 261
 Val Trp Thr Ala Ser Ala His Ile Ile Thr Ala Val Ile Gly Ser Gly
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 Val Leu Ser Leu Ala Trp Ala Met Ala Gln Leu Gly Trp Ile Ala Gly
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 ccg gtg gtt atg att ctg ttt tcg ttt gtg act tat tat act tcg act 357
 Pro Val Val Met Ile Leu Phe Ser Phe Val Thr Tyr Tyr Thr Ser Thr
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 ctg ttg gct acc tgt tac cgt act gga gat cct gtc act gga aag agg 405
 Leu Leu Ala Thr Cys Tyr Arg Thr Gly Asp Pro Val Thr Gly Lys Arg
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 aat tat act tac atg gat gct gtc aaa tca aac ctt ggt ggg tct acg 453
 Asn Tyr Thr Tyr Met Asp Ala Val Lys Ser Asn Leu Gly Gly Ser Thr
 100 105 110
 gtg aaa att tgt gga tat gtt cag tat gtc aat ctg ttt gga att gcg 501
 Val Lys Ile Cys Gly Tyr Val Gln Tyr Val Asn Leu Phe Gly Ile Ala
 115 120 125 130
 att ggg tac act ata gca tca acc att agc atg atg gca gtg aag agg 549
 Ile Gly Tyr Thr Ile Ala Ser Thr Ile Ser Met Met Ala Val Lys Arg
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 Ser Asn Cys His His Asn Asn Gly Asp Thr Gly Ser Arg Cys Glu Val
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 aat gcc aat cca ttc atg gtc gga ttc gga atc gtg gag ata ttt ctg 645
 Asn Ala Asn Pro Phe Met Val Gly Phe Gly Ile Val Glu Ile Phe Leu
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 gca gtc atg tcc ttc act tac tcc ggc atc gga cta ggc ctt ggc att 741
 Ala Val Met Ser Phe Thr Tyr Ser Gly Ile Gly Leu Gly Leu Gly Ile
 195 200 205 210
 gcc aaa gtc ggc gaa aac gga gaa atc aaa gga act tcg acg gga gtc 789
 Ala Lys Val Gly Glu Asn Gly Glu Ile Lys Gly Thr Ser Thr Gly Val
 215 220 225
 acc gtc gga gcc ata acg gag atg cag aaa cta tgg agg tcg ttc cag 837
 Thr Val Gly Ala Ile Thr Glu Met Gln Lys Leu Trp Arg Ser Phe Gln
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PF59082SeqList_PF59082.txt

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Glu	Ile	Gln	Asp	Thr	Val	Lys	Ser	Pro	Pro	Ser	Glu	Val	Lys	Thr	Met	
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aag	aaa	gca	aca	gcc	ata	agc	gta	gca	atc	aca	agc	att	ttc	tac	att	981
Lys	Lys	Ala	Thr	Ala	Ile	Ser	Val	Ala	Ile	Thr	Ser	Ile	Phe	Tyr	Ile	
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Leu	Cys	Gly	Ser	Phe	Gly	Tyr	Ala	Ala	Phe	Gly	Asp	Leu	Ala	Pro	Gly	
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Asn	Leu	Leu	Thr	Gly	Lys	Gly	Phe	Tyr	Glu	Pro	Tyr	Trp	Leu	Val	Asp	
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atc	gcc	aac	gta	gca	gtc	cta	gtc	cat	ctg	gta	ggt	gca	tac	cag	gta	1125
Ile	Ala	Asn	Val	Ala	Val	Leu	Val	His	Leu	Val	Gly	Ala	Tyr	Gln	Val	
		325				330						335				
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Phe	Ala	Gln	Pro	Ile	Phe	Ala	Phe	Val	Glu	Lys	His	Ala	Ser	Ala	Arg	
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Tyr	Pro	His	Ser	Gln	Phe	Ile	Thr	Lys	Glu	Ile	Arg	Val	Ser	Ser	Lys	
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Tyr	Ser	Leu	Asn	Leu	Phe	Arg	Leu	Thr	Trp	Arg	Thr	Ser	Phe	Val	Ile	
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Leu	Thr	Thr	Leu	Ile	Ser	Met	Ile	Leu	Pro	Phe	Phe	Asn	Asp	Ile	Val	
			390					395					400			
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Gly	Leu	Leu	Gly	Ala	Val	Gly	Tyr	Trp	Pro	Leu	Thr	Val	Tyr	Phe	Pro	
		405				410						415				
atc	gag	atg	tac	att	gcg	gcg	aac	agg	att	ccg	aag	tgg	agc	acg	agg	1413
Ile	Glu	Met	Tyr	Ile	Ala	Ala	Asn	Arg	Ile	Pro	Lys	Trp	Ser	Thr	Arg	
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Trp	Val	Gly	Leu	Glu	Ile	Leu	Ser	Met	Val	Cys	Leu	Ile	Val	Ala	Ile	
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Ala	Ala	Ala	Val	Gly	Ser	Ile	Val	Gly	Val	Ile	Gly	Asp	Leu	Lys	Ser	
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gtg	aaa	ccg	ttc	cat	gcc	gat	ttc	tga	gctgggggta	aaatggggaa						1556
Val	Lys	Pro	Phe	His	Ala	Asp	Phe									
			470													
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 Ala Gly Pro Val Val Met Ile Leu Phe Ser Phe Val Thr Tyr Tyr Thr
 Seite 2350

PF59082SeqList_PF59082.txt

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 Ile Ala Ile Gly Tyr Thr Ile Ala Ser Thr Ile Ser Met Met Ala Val
 130 135 140
 Lys Arg Ser Asn Cys His His Asn Asn Gly Asp Thr Gly Ser Arg Cys
 145 150 155 160
 Glu Val Asn Ala Asn Pro Phe Met Val Gly Phe Gly Ile Val Glu Ile
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 Phe Leu Ser Gln Ile Pro Asp Phe Asp Gln Leu Trp Trp Leu Ser Ile
 180 185 190
 Val Ala Ala Val Met Ser Phe Thr Tyr Ser Gly Ile Gly Leu Gly Leu
 195 200 205
 Gly Ile Ala Lys Val Gly Glu Asn Gly Glu Ile Lys Gly Thr Ser Thr
 210 215 220
 Gly Val Thr Val Gly Ala Ile Thr Glu Met Gln Lys Leu Trp Arg Ser
 225 230 235 240
 Phe Gln Ala Leu Gly Asn Ile Ala Phe Ala Tyr Ala Tyr Ser Ile Ile
 245 250 255
 Leu Ile Glu Ile Gln Asp Thr Val Lys Ser Pro Pro Ser Glu Val Lys
 260 265 270
 Thr Met Lys Lys Ala Thr Ala Ile Ser Val Ala Ile Thr Ser Ile Phe
 275 280 285
 Tyr Ile Leu Cys Gly Ser Phe Gly Tyr Ala Ala Phe Gly Asp Leu Ala
 290 295 300
 Pro Gly Asn Leu Leu Thr Gly Lys Gly Phe Tyr Glu Pro Tyr Trp Leu
 305 310 315 320
 Val Asp Ile Ala Asn Val Ala Val Leu Val His Leu Val Gly Ala Tyr
 325 330 335
 Gln Val Phe Ala Gln Pro Ile Phe Ala Phe Val Glu Lys His Ala Ser
 340 345 350
 Ala Arg Tyr Pro His Ser Gln Phe Ile Thr Lys Glu Ile Arg Val Ser
 355 360 365
 Ser Lys Tyr Ser Leu Asn Leu Phe Arg Leu Thr Trp Arg Thr Ser Phe
 370 375 380
 Val Ile Leu Thr Thr Leu Ile Ser Met Ile Leu Pro Phe Phe Asn Asp
 385 390 395 400
 Ile Val Gly Leu Leu Gly Ala Val Gly Tyr Trp Pro Leu Thr Val Tyr
 405 410 415
 Phe Pro Ile Glu Met Tyr Ile Ala Ala Asn Arg Ile Pro Lys Trp Ser
 420 425 430
 Thr Arg Trp Val Gly Leu Glu Ile Leu Ser Met Val Cys Leu Ile Val
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aaa tgg cga gcg gaa gct gaa att ggt ggc aac gag aga gct ctg caa 96

Lys Trp Arg Ala Glu Ala Glu Ile Gly Gly Asn Glu Arg Ala Leu Gln
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PF59082SeqList_PF59082.txt

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Arg	Thr	Leu	Gly	Leu	Lys	Trp	Pro	Arg	Gly	Leu	Leu	Leu	Tyr	Gly	Pro		
	50					55					60						
cct	gga	acc	ggc	aag	aca	agc	ttg	gtc	cgt	gct	ggt	gtc	cag	gaa	tgt	240	
Pro	Gly	Thr	Gly	Lys	Thr	Ser	Leu	Val	Arg	Ala	Val	Val	Gln	Glu	Cys		
	65				70					75					80		
gat	gca	cat	ttg	att	ggt	tta	agc	cct	cat	tct	gta	cat	cga	gca	cat	288	
Asp	Ala	His	Leu	Ile	Val	Leu	Ser	Pro	His	Ser	Val	His	Arg	Ala	His		
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gct	gga	gaa	agc	gag	aaa	gtc	tta	agg	gaa	gct	ttc	gct	gag	gct	tct	336	
Ala	Gly	Glu	Ser	Glu	Lys	Val	Leu	Arg	Glu	Ala	Phe	Ala	Glu	Ala	Ser		
			100					105					110				
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Ser	His	Ala	Val	Ser	Asp	Lys	Pro	Ser	Val	Ile	Phe	Ile	Asp	Glu	Ile		
		115					120					125					
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Asp	Val	Leu	Cys	Pro	Arg	Arg	Asp	Ala	Arg	Arg	Glu	Gln	Asp	Val	Arg		
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Ile	Ala	Ser	Gln	Leu	Phe	Thr	Leu	Met	Asp	Ser	Asn	Lys	Pro	Ser	Ser		
	145				150				155						160		
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Ser	Ala	Pro	Arg	Val	Val	Val	Ala	Ser	Thr	Asn	Arg	Val	Asp	Ala			
				165				170					175				
att	gac	cca	gcg	cta	aga	aga	gcg	gga	cga	ttt	gat	gct	tta	ggt	gaa	576	
Ile	Asp	Pro	Ala	Leu	Arg	Arg	Ala	Gly	Arg	Phe	Asp	Ala	Leu	Val	Glu		
			180					185					190				
gtg	agc	aca	cca	aat	gag	gag	gat	cgt	tta	aaa	atc	ctg	cag	ctg	tac	624	
Val	Ser	Thr	Pro	Asn	Glu	Glu	Asp	Arg	Leu	Lys	Ile	Leu	Gln	Leu	Tyr		
		195					200					205					
aca	aag	aaa	gtc	aat	tta	gat	cct	agt	gtc	gat	ctt	caa	gcc	att	gca	672	
Thr	Lys	Lys	Val	Asn	Leu	Asp	Pro	Ser	Val	Asp	Leu	Gln	Ala	Ile	Ala		
	210					215					220						
ata	tct	tgc	aac	ggt	tat	ggt	gga	gca	gat	ttg	gaa	gct	tta	tgt	cgt	720	
Ile	Ser	Cys	Asn	Gly	Tyr	Val	Gly	Ala	Asp	Leu	Glu	Ala	Leu	Cys	Arg		
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Glu	Ala	Thr	Ile	Ser	Ala	Ser	Lys	Arg	Ser	250	Asp	Ser	Leu	Ile	Leu		
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aca	tct	caa	gac	ttc	aag	att	gca	aaa	tct	gtg	ggt	cca	agt	ata		816	
Thr	Ser	Gln	Asp	Phe	Lys	Ile	Ala	Lys	Ser	Val	Val	Gly	Pro	Ser	Ile		
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Asn	Arg	Gly	Ile	Thr	Val	Glu	Ile	Pro	Lys	Val	Thr	Trp	Asp	Asp	Val		
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Pro	Ile	Lys	His	Ser	Ala	Ala	Phe	Val	Lys	Met	Gly	Ile	Ser	Pro	Met		
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cgt	ggg	ata	ctt	cta	cat	ggt	cct	cca	ggt	tgc	tca	aag	aca	act	ctt	1008	
Arg	Gly	Ile	Leu	His	Gly	Pro	Pro	Pro	Gly	Cys	Ser	Lys	Thr	Thr	Leu		
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gct	aaa	gcc	gct	gca	aat	gct	gct	caa	gcc	tcc	ttc	ttt	tcc	tta	agc	1056	
Ala	Lys	Ala	Ala	Ala	Asn	Ala	Ala	Gln	Ala	Ser	Phe	Phe	Ser	Leu	Ser		
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Cys	Ala	Glu	Leu	Phe	Ser	Met	Tyr	Val	Gly	Glu	Gly	Glu	Ala	Leu	Leu		
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Arg	Asn	Thr	Phe	Gln	Arg	Ala	Arg	Leu	Ala	Ser	Pro	Ser	Ile	Ile	Phe		
	370					375					380						
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Phe	Asp	Glu	Ala	Asp	Val	Val	Ala	Cys	Lys	Arg	Gly	Asp	Glu	Ser	Ser		
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Glu	Met	Asp	Gly	Leu	Glu	Glu	Ala	Lys	Gly	Ile	Leu	Val	Leu	Ala	Ala	
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Thr	Asn	Arg	Pro	Tyr	Ala	Ile	Asp	Ala	Ala	Leu	Met	Arg	Pro	Gly	Arg	
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Phe	Asp	Leu	Val	Leu	Tyr	Val	Pro	Pro	Pro	Asp	Leu	Glu	Ala	Arg	Phe	
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Asp	Leu	Arg	Lys	Ile	Ala	Glu	Glu	Thr	Asp	Leu	Phe	Thr	Gly	Ala	Glu	
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ctc	gag	ggt	cta	tgc	aga	gaa	agc	gga	act	gtc	tca	ctt	aga	gaa	aac	1536
Leu	Glu	Gly	Leu	Cys	Arg	Glu	Ser	Gly	Thr	Val	Ser	Leu	Arg	Glu	Asn	
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Ile	Ala	Ala	Thr	Ala	Val	Phe	Asn	Arg	His	Phe	Gln	Thr	Ala	Lys	Ser	
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Ser	Leu	Lys	Pro	Ala	Leu	Thr	Ile	Glu	Glu	Val	Glu	Thr	Tyr	Ser	Ser	
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Phe	Arg	Lys	Ala	Ala	Lys	Arg	Ser	Asp	Ser	Lys	Pro	Ile	Pro	Ile	Asn	
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Lys	Lys	Lys	Ala	Thr	Ser	Thr	Val	Phe	Gly	Phe	Ser	Trp	Gln	Leu	Gly	
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Val	Leu	Ser	Leu	Leu	Leu	Leu	Ala	Thr	Gly	Asn	Tyr	Tyr	Phe	Asn	His	
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<212> PRT

<213> Arabidopsis thaliana

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Asp	Ala	His	Leu	Ile	Val	Leu	Ser	Pro	His	Ser	Val	His	Arg	Ala	His	
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PF59082SeqList_PF59082.txt

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 Glu Ala Thr Ile Ser Ala Ser Lys Arg Ser Ser Asp Ser Leu Ile Leu
 245 250 255
 Thr Ser Gln Asp Phe Lys Ile Ala Lys Ser Val Val Gly Pro Ser Ile
 260 265 270
 Asn Arg Gly Ile Thr Val Glu Ile Pro Lys Val Thr Trp Asp Asp Val
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 Gly Gly Leu Lys Asp Leu Lys Lys Lys Leu Gln Gln Ala Val Glu Trp
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 Pro Ile Lys His Ser Ala Ala Phe Val Lys Met Gly Ile Ser Pro Met
 305 310 315 320
 Arg Gly Ile Leu Leu His Gly Pro Pro Gly Cys Ser Lys Thr Thr Leu
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 Ala Lys Ala Ala Asn Ala Ala Gln Ala Ser Phe Phe Ser Leu Ser
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 Lys Lys Lys Ala Thr Ser Thr Val Phe Gly Phe Ser Trp Gln Leu Gly
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 Met Ser Asn Pro

114

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Val	Ala	Asn	Glu	Thr	Gly	Ala	Phe	Phe	Phe	Cys	Ile	Asn	Gly	Pro	Glu	
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Ile	Met	Ser	Lys	Leu	Ala	Gly	Glu	Ser	Glu	Ser	Asn	Leu	Arg	Lys	Ala	
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gac Asp 405	act Thr	cac His	ggt Gly	tat Tyr	gtc Val 410	ggt Gly	gct Ala	gat Asp	ctt Leu	gca Ala 415	gct Ala	ctg Leu	tgc Cys	act Thr	gaa Glu 420	1362
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cag Gln 645	ctc Leu	att Ile	tac Tyr	att Ile	cca Pro 650	ctg Leu	cca Pro	gac Asp	gag Glu	gac Asp 655	tca Ser	cgt Arg	ctc Leu	aac Asn	atc Ile 660	2082
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aag Lys	gac Asp 710	att Ile	gaa Glu	aag Lys	gag Glu	aag Lys 715	agg Arg	agg Arg	agc Ser	gag Glu	aac Asn 720	cca Pro	gaa Glu	gcc Ala	atg Met	2274
gag Glu 725	gaa Glu	gat Asp	atg Met	gat Asp	gaa Glu 730	gta Val	tca Ser	gag Glu	atc Ile	aaa Lys 735	gct Ala	gca Ala	cac His	ttc Phe	gag Glu 740	2322

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 Pro Asn Ser Ile Asp Pro Ala Leu Arg Arg Phe Gly Arg Phe Asp Arg
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 Val Lys Gly Pro Glu Leu Thr Met Trp Phe Gly Glu Ser Glu Ala
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 Ser Gly Gly Asp Gly Gly Gly Ala Ala Asp Arg Val Leu Asn Gln Leu
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 690 695 700
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ttccatc atg tcg aac cca gct gaa tct tca gac tcg aaa tcg aag aaa 169
Met Ser Asn Pro Ala Glu Ser Ser Asp Ser Lys Ser Lys Lys

gac ttc agt act gct att ctg gag agg aag aag tct cct aac aga ctc 217
Asp Phe Ser Thr Ala Ile Leu Glu Arg Lys Lys Ser Pro Asn Arg Leu

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Val Val Asp Glu Ala Ile Asn Asp Asp Asn Ser Val Val Ser Leu His

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Ile Lys Gly Lys Lys Arg Lys Asp Thr Ile Cys Ile Ala Leu Ala Asp

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Glu Ser Cys Glu Glu Pro Lys Ile Arg Met Asn Lys Val Val Arg Ser

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Ala Glu Tyr Cys Val Val Ala Pro Asp Thr Glu Ile Phe Cys Glu Gly

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Glu Pro Val Lys Arg Glu Asp Glu Glu Arg Leu Asp Glu Val Gly Tyr

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Val Glu Leu Pro Leu Arg His Pro Gln Leu Phe Lys Ser Ile Gly Val

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Lys Pro Pro Lys Gly Ile Leu Leu Tyr Gly Pro Gly Ser Gly Lys

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Cys Ile Asn Gly Pro Glu Ile Met Ser Lys Leu Ala Gly Glu Ser Glu

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Ser Asn Leu Arg Lys Ala Phe Glu Glu Ala Glu Lys Asn Ala Pro Ser

PF59082SeqList_PF59082.txt

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Trp	Asp	Asp	Ile	Gly	Gly	Leu	Glu	Asn	Val	Lys	Arg	Glu	Leu	Gln	Glu	
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Lys	Thr	Leu	Leu	Ala	Lys	Ala	Ile	Ala	Asn	Glu	Cys	Gln	Ala	Asn	Phe	
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Gln	Leu	Leu	Thr	Glu	Met	Asp	Gly	Met	Asn	Ala	Lys	Lys	Thr	Val	Phe	
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Glu	Asn	Pro	Glu	Ala	Met	Glu	Glu	Asp	Gly	Val	Asp	Glu	Val	Ser	Glu	
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Val	Ser	Asp	Ala	Asp	Ile	Arg	Lys	Tyr	Gln	Ala	Phe	Ala	Gln	Thr	Leu	
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Gln	Gln	Ser	Arg	Gly	Phe	Gly	Ser	Glu	Phe	Arg	Phe	Glu	Thr	Asn	Ala	
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Ala	Gly	Ser	Gly	Ala	Thr	Thr	Gly	Val	Ala	Asp	Pro	Phe	Ala	Thr	Ser	
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Lys	Tyr	Gly	Gln	Arg	Val	His	Ile	Leu	Pro	Val	Asp	Asp	Thr	Val	Glu
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Gly	Val	Thr	Glu	Asn	Leu	Phe	Asp	Ala	Tyr	Leu	Lys	Pro	Tyr	Phe	Leu
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Glu	Ala	Tyr	Arg	Pro	Val	Arg	Lys	Gly	Asp	Leu	Phe	Leu	Val	Arg	Gly
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PF59082SeqList_PF59082.txt

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Arg	Ile	Ser	Lys	Asp	Thr	His	Gly	Tyr	Val	Gly	Ala	Asp	Leu	Ala
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Gln	Tyr	Pro	Val	Glu	His	Pro	Glu	Lys	Phe	Glu	Lys	Phe	Gly	Met
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		675					680					685		Gly
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PF59082SeqList_PF59082.txt

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Lys Ala Ser Lys Lys Arg Ser Asn Lys Arg Ser Asp Phe Phe Asp Leu
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gac gat gat ttc gaa gct gat ttc caa ggg ttt aag gat gac tcg gct 192
Asp Asp Asp Phe Glu Ala Asp Phe Gln Gly Phe Lys Asp Asp Ser Ala
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<213> Arabidopsis thaliana

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Ala	Glu	Gln	Ala	Glu	Lys	Ser	Ser	Lys	Arg	Lys	Arg	Lys	Asn	Gln	Tyr
		115					120					125			
Arg	Gly	Ile	Arg	Gln	Arg	Pro	Trp	Gly	Lys	Trp	Ala	Ala	Glu	Ile	Arg
	130					135					140				
Asp	Pro	Arg	Lys	Gly	Ser	Arg	Glu	Trp	Leu	Gly	Thr	Phe	Asp	Thr	Ala
145				150					155						160
Glu	Glu	Ala	Ala	Arg	Ala	Tyr	Asp	Ala	Ala	Ala	Arg	Arg	Ile	Arg	Gly
			165					170						175	
Thr	Lys	Ala	Lys	Val	Asn	Phe	Pro	Glu	Glu	Lys	Asn	Pro	Ser	Val	Val
			180					185					190		
Ser	Gln	Lys	Arg	Pro	Ser	Ala	Lys	Thr	Asn	Asn	Leu	Gln	Lys	Ser	Val
		195					200					205			
Ala	Lys	Pro	Asn	Lys	Ser	Val	Thr	Leu	Val	Gln	Gln	Pro	Thr	His	Leu
	210					215					220				
Ser	Gln	Gln	Tyr	Cys	Asn	Asn	Ser	Phe	Asp	Asn	Ser	Phe	Gly	Asp	Met
225				230					235						240
Ser	Phe	Met	Glu	Glu	Lys	Pro	Gln	Met	Tyr	Asn	Asn	Gln	Phe	Gly	Leu
			245					250						255	
Thr	Asn	Ser	Phe	Asp	Ala	Gly	Gly	Asn	Asn	Gly	Tyr	Gln	Tyr	Phe	Ser
			260					265					270		
Ser	Asp	Gln	Gly	Ser	Asn	Ser	Phe	Asp	Cys	Ser	Glu	Phe	Gly	Trp	Ser
		275					280					285			
Asp	His	Gly	Pro	Lys	Thr	Pro	Glu	Ile	Ser	Ser	Met	Leu	Val	Asn	Asn
	290					295					300				
Asn	Glu	Ala	Ser	Phe	Val	Glu	Glu	Thr	Asn	Ala	Ala	Lys	Lys	Leu	Lys
	305				310					315					320
Pro	Asn	Ser	Asp	Glu	Ser	Asp	Asp	Leu	Met	Ala	Tyr	Leu	Asp	Asn	Ala
				325				330						335	
Leu	Trp	Asp	Thr	Pro	Leu	Glu	Val	Glu	Ala	Met	Leu	Gly	Ala	Asp	Ala
			340					345					350		

PF59082SeqList_PF59082.txt

Gly Ala Val Thr Gln Glu Glu Glu Asn Pro Val Glu Leu Trp Ser Leu
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 Asp Glu Ile Asn Phe Met Leu Glu Gly Asp Phe
 370 375

<210> 1799
 <211> 1364
 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (101)..(1159)

<400> 1799
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tttcaacatt taacaccctt taaaagactt taacgccgcc atg tgt gga gga gct 115
 Met Cys Gly Gly Ala
 1 5
 ata atc tcc gaa ttc atc cct ccg ccg aag tcc cgc cgc gtc acc agc 163
 Ile Ile Ser Glu Phe Ile Pro Pro Pro Lys Ser Arg Arg Val Thr Ser
 10 15 20
 gag ttc atc tgg ccg gat ctg aaa aat ctg aag aag aag tcg agg aag 211
 Glu Phe Ile Trp Pro Asp Leu Lys Asn Leu Lys Lys Lys Ser Arg Lys
 25 30 35
 cga tcc cat ttc ttc gat ctg gac aac gag ttc gag gct gat ttc aaa 259
 Arg Ser His Phe Phe Asp Leu Asp Asn Glu Phe Glu Ala Asp Phe Lys
 40 45 50
 ggg ttt aag gat gat gat tcg tct ttt gag tgt gaa gat gga ttc gat 307
 Gly Phe Lys Asp Asp Asp Ser Ser Phe Glu Cys Glu Asp Gly Phe Asp
 55 60 65
 gtg aag ccc ttt gcc ttc acc gca gct acc aaa ccc gta gct tcc ctt 355
 Val Lys Pro Phe Ala Phe Thr Ala Ala Thr Lys Pro Val Ala Ser Leu
 70 75 80 85
 ccc acc aac gtc gcc acg act ggt tca gtt tct gac aag aaa gct gtg 403
 Pro Thr Asn Val Ala Thr Thr Gly Ser Val Ser Asp Lys Lys Ala Val
 90 95 100
 gag tcc gat gag aag tct ggc aag agg aag aga aag aat cag tac aga 451
 Glu Ser Asp Glu Lys Ser Gly Lys Arg Lys Arg Lys Asn Gln Tyr Arg
 105 110 115
 ggg att agg ctg cgc ccc tgg gga aaa tgg gct gct gag atc cgt gat 499
 Gly Ile Arg Leu Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp
 120 125 130
 cct aaa aaa ggc tca cga gaa tgg ctt gga acg ttc gaa acc gct gag 547
 Pro Lys Lys Gly Ser Arg Glu Trp Leu Gly Thr Phe Glu Thr Ala Glu
 135 140 145
 gaa gca gca aga gct tat gac gca gct gcg cgc agg atc cgt ggc gat 595
 Glu Ala Ala Arg Ala Tyr Asp Ala Ala Ala Arg Ile Arg Gly Asp
 150 155 160 165
 aaa gct aag gtg aac ttc cct gag gag gtg atc agt agt cct aag aag 643
 Lys Ala Lys Val Asn Phe Pro Glu Glu Val Ile Ser Ser Pro Lys Lys
 170 175 180
 cca gtg gct aaa cca aac cag acc cca gct ttg gtt cag cag cca acg 691
 Pro Val Ala Lys Pro Asn Gln Thr Pro Ala Leu Val Gln Gln Pro Thr
 185 190 195
 cat gtg agt cag tac tgc aac aac tcc ttt gac aac atg gga cat gac 739
 His Val Ser Gln Tyr Cys Asn Asn Ser Phe Asp Asn Met Gly His Asp
 200 205 210
 tcc ttg agt ttc atg gaa gag aag cct cgg gtt tac aac aat cag ttc 787
 Ser Leu Ser Phe Met Glu Glu Lys Pro Arg Val Tyr Asn Asn Gln Phe
 215 220 225
 ttc gat gtt gga cag tat ttc ggt tcc gac cag ggg agt aac tca ttt 835
 Phe Asp Val Gly Gln Tyr Phe Gly Ser Asp Gln Gly Ser Asn Ser Phe
 230 235 240 245
 gac tgc tct gag ttt ggg tgg agt gat cac gcc ccc aag aca cca cca 883
 Asp Cys Ser Glu Phe Gly Trp Ser Asp His Ala Pro Lys Thr Pro Pro
 250 255 260

PF59082SeqList_PF59082.txt

gag aat tct tca atg gta gtt aac aac aac caa gct acc ttt gct gaa	931
Glu Asn Ser Ser Met Val Val Asn Asn Asn Gln Ala Thr Phe Ala Glu	
265 270 275	
gaa acc att gca gcc aag aag gtc aaa ctc agc tct gag gac gag aca	979
Glu Thr Ile Ala Ala Lys Lys Val Lys Leu Ser Ser Glu Asp Glu Thr	
280 285 290	
agc gac aat gat gat ctg atg gcg tat ctt gac aac gcc ctg tgg gag	1027
Ser Asp Asn Asp Asp Leu Met Ala Tyr Leu Asp Asn Ala Leu Trp Glu	
295 300 305	
tct ccg tta gaa gtg gaa gct atg ctc ggc gta gat gct gct gct gct	1075
Ser Pro Leu Glu Val Glu Ala Met Leu Gly Val Asp Ala Ala Ala Ala	
310 315 320 325	
gct ggt gtg gct cag gaa gag gca aac cca atg gag ctg tgg agc tta	1123
Ala Gly Val Ala Gln Glu Glu Ala Asn Pro Met Glu Leu Trp Ser Leu	
330 335 340	
gat gat atc aac ttt atg ctg gat gga gac ttc tga agtgagtgat	1169
Asp Asp Ile Asn Phe Met Leu Asp Gly Asp Phe	
345 350	
gggttcgcta gtttgtaaataaagctgtgt ttgtgtgtgt gtgttggtga gtttcaagcc	1229
cattgtgaag acaaacagcc gtaacttttta cttaatcttc agtttggttt ttgtgtttgt	1289
tgtcttgttt tgtatcccta agacttggttt aacaagtata ataaaaacgg tgttggaacc	1349
aaaaaaaaa aaaaa	1364

<210> 1800
 <211> 352
 <212> PRT
 <213> Brassica napus

<400> 1800

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20 25 30	
Lys Lys Ser Arg Lys Arg Ser His Phe Phe Asp Leu Asp Asn Glu Phe	
35 40 45	
Glu Ala Asp Phe Lys Gly Phe Lys Asp Asp Asp Ser Ser Phe Glu Cys	
50 55 60	
Glu Asp Gly Phe Asp Val Lys Pro Phe Ala Phe Thr Ala Ala Thr Lys	
65 70 75 80	
Pro Val Ala Ser Leu Pro Thr Asn Val Ala Thr Thr Gly Ser Val Ser	
85 90 95	
Asp Lys Lys Ala Val Glu Ser Asp Glu Lys Ser Gly Lys Arg Lys Arg	
100 105 110	
Lys Asn Gln Tyr Arg Gly Ile Arg Leu Arg Pro Trp Gly Lys Trp Ala	
115 120 125	
Ala Glu Ile Arg Asp Pro Lys Lys Gly Ser Arg Glu Trp Leu Gly Thr	
130 135 140	
Phe Glu Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Ala Ala Ala Arg	
145 150 155 160	
Arg Ile Arg Gly Asp Lys Ala Lys Val Asn Phe Pro Glu Glu Val Ile	
165 170 175	
Ser Ser Pro Lys Lys Pro Val Ala Lys Pro Asn Gln Thr Pro Ala Leu	
180 185 190	
Val Gln Gln Pro Thr His Val Ser Gln Tyr Cys Asn Asn Ser Phe Asp	
195 200 205	
Asn Met Gly His Asp Ser Leu Ser Phe Met Glu Glu Lys Pro Arg Val	
210 215 220	
Tyr Asn Asn Gln Phe Phe Asp Val Gly Gln Tyr Phe Gly Ser Asp Gln	
225 230 235 240	
Gly Ser Asn Ser Phe Asp Cys Ser Glu Phe Gly Trp Ser Asp His Ala	
245 250 255	

PF59082SeqList_PF59082.txt

Pro Lys Thr Pro Pro Glu Asn Ser Ser Met Val Val Asn Asn Asn Gln
 260 265 270
 Ala Thr Phe Ala Glu Glu Thr Ile Ala Ala Lys Lys Val Lys Leu Ser
 275 280 285
 Ser Glu Asp Glu Thr Ser Asp Asn Asp Asp Leu Met Ala Tyr Leu Asp
 290 295 300
 Asn Ala Leu Trp Glu Ser Pro Leu Glu Val Glu Ala Met Leu Gly Val
 305 310 315 320
 Asp Ala Ala Ala Ala Glu Gly Val Ala Gln Glu Glu Ala Asn Pro Met
 325 330 335
 Glu Leu Trp Ser Leu Asp Asp Ile Asn Phe Met Leu Asp Gly Asp Phe
 340 345 350

<210> 1801
 <211> 1406
 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (73)..(1212)

<400> 1801
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60

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 Met Cys Gly Gly Ala Ile Ile Ser Glu Phe Ile Pro Pro

111

tcg agg tcc cgc cgc gtc acg agc gag cat ctc tgg ccg gat ctg aag
 Ser Arg Ser Arg Arg Val Thr Ser Glu His Leu Trp Pro Asp Leu Lys
 15 20 25

159

aac aaa ggg aaa gct tcg aag aag aag cga tcc ggt ttc atc gat ctg
 Asn Lys Gly Lys Ala Ser Lys Lys Lys Arg Ser Gly Phe Ile Asp Leu
 30 35 40 45

207

gac gat gag ttc gag gct gac ttt caa ggg ttt aag gac gat gca tcg
 Asp Asp Glu Phe Glu Ala Asp Phe Gln Gly Phe Lys Asp Asp Ala Ser
 50 55 60

255

ttc gat tgc gaa gat gaa ttc gat gtg gat gat gac gtc ttc gcc gat
 Phe Asp Cys Glu Asp Glu Phe Asp Val Asp Asp Asp Val Phe Ala Asp
 65 70 75

303

gtc aaa ccc ttt gtc ttc gcc gca ggt gcc aag ccc gta gct tcc cct
 Val Lys Pro Phe Val Phe Ala Ala Gly Ala Lys Pro Val Ala Ser Pro
 80 85 90

351

ccc gcc gcc ttg gct tcc act ggt tca gtc tct ggg aag aaa acc ata
 Pro Ala Ala Leu Ala Ser Thr Gly Ser Val Ser Gly Lys Lys Thr Ile
 95 100 105

399

gag tct ggt gga caa gct gag aag tct gct aag aga aag agg aag aat
 Glu Ser Gly Gly Gln Ala Glu Lys Ser Ala Lys Arg Lys Arg Lys Asn
 110 115 120 125

447

cag tac agg ggg att agg cag cgc cct tgg ggc aaa tgg gct gct gag
 Gln Tyr Arg Gly Ile Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu
 130 135 140

495

atc cgt gat ccc aga aaa ggc tcc cgg gag tgg ctt gga aca ttc gac
 Ile Arg Asp Pro Arg Lys Gly Ser Arg Glu Trp Leu Gly Thr Phe Asp
 145 150 155

543

acc gct gag gaa gca gca aga gct tat gat gca gct gca cgc agg atc
 Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Ala Ala Arg Arg Ile
 160 165 170

591

cgc ggc aat aaa gct aag gtg aac ttc cca gag gag atg gtc cct agc
 Arg Gly Asn Lys Ala Lys Val Asn Phe Pro Glu Glu Met Val Pro Ser
 175 180 185

639

gtc tcc cag aaa cgc cct gct gct aag aag gca gtg gct aaa cca aac
 Val Ser Gln Lys Arg Pro Ala Ala Lys Lys Ala Val Ala Lys Pro Asn
 190 195 200 205

687

caa agc cca gca tcc gtt cag cag cca aca cat gtg agt cag tac tgc
 Gln Ser Pro Ala Ser Val Gln Gln Pro Thr His Val Ser Gln Tyr Cys
 210 215 220

735

aac aac tcc ttt gac aac atg gga cat gac tcc tcc ttt ggt gat gtg

783

PF59082SeqList_PF59082.txt

Asn	Asn	Ser	Phe	Asp	Asn	Met	Gly	His	Asp	Ser	Ser	Phe	Gly	Asp	Val		
			225					230					235				
agt	ttc	atg	gaa	gag	aag	cct	cag	atg	tgt	aac	aat	cag	ttc	ttt	gat		831
Ser	Phe	Met	Glu	Glu	Lys	Pro	Gln	Met	Cys	Asn	Asn	Gln	Phe	Phe	Asp		
		240					245					250					
gtc	gga	ggc	aac	aat	gga	tac	cag	tat	ttc	agt	tct	gac	cag	ggc	agt		879
Val	Gly	Gly	Asn	Asn	Gly	Tyr	Gln	Tyr	Phe	Ser	Ser	Asp	Gln	Gly	Ser		
	255					260					265						
aac	tca	ctg	gac	tgc	tct	gag	ttt	ggg	tgg	agt	gat	caa	acc	ccc	aag		927
Asn	Ser	Leu	Asp	Cys	Ser	Glu	Phe	Gly	Trp	Ser	Asp	Gln	Thr	Pro	Lys		
					275					280					285		
aca	cct	gag	atc	tct	tca	atg	cta	gtc	aac	aat	aac	caa	gct	cct	ttc		975
Thr	Pro	Glu	Ile	Ser	Ser	Met	Leu	Val	Asn	Asn	Asn	Gln	Ala	Pro	Phe		
				290					295					300			
att	gaa	gaa	acc	aat	cca	gcc	aag	aag	ctc	aaa	acc	agc	tct	gag	gac		1023
Ile	Glu	Glu		Asn	Pro	Ala	Lys	Lys	Leu	Lys	Thr	Ser	Ser	Glu	Asp		
			305				310						315				
ggg	aca	agc	aac	aat	gat	agt	tct	gat	gat	ctg	atg	gca	tac	ctg	aac		1071
Gly	Thr	Ser	Asn	Asn	Asp	Ser	Ser	Asp	Asp	Leu	Met	Ala	Tyr	Leu	Asn		
		320				325						330					
aac	gcc	ttg	tgg	gag	tct	cca	ttg	gaa	gtg	gaa	gct	atg	ttc	ggg	ggg		1119
Asn	Ala	Leu	Trp	Glu	Ser	Pro	Leu	Glu	Val	Glu	Ala	Met	Phe	Gly	Gly		
						340					345						
gat	gct	gct	act	atg	act	cag	gaa	gag	gga	aac	cca	atg	gac	cta	tgg		1167
Asp	Ala	Ala	Thr	Met	Thr	Gln	Glu	Glu	Gly	Asn	Pro	Met	Asp	Leu	Trp		
					355					360					365		
agc	tta	gat	gat	atc	aac	tcc	atg	ctg	gat	ggg	gga	gtc	ttc	tga			1212
Ser	Leu	Asp	Asp	Ile	Asn	Ser	Met	Leu	Asp	Gly	Gly	Val	Phe				
				370			375										
aagtgattga	tgggttgccct	agtttgtaaa	taaagctctt	tgtgtgttgg	tgtgtttcaa												1272
gttcattggt	gaagacaaac	agccttagct	ttggttttac	ttaaacttcg	gtttggtttt												1332
tgtgtgttgt	tgtctcacag	ggttttgctg	ttggcggggg	aatggtacaa	gttcatacca												1392
aaaaaaaaaa	aaaa																1406

<210> 1802
 <211> 379
 <212> PRT
 <213> Brassica napus

<400> 1802
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 20 25 30
 Lys Ala Ser Lys Lys Lys Arg Ser Gly Phe Ile Asp Leu Asp Asp Glu
 35 40 45
 Phe Glu Ala Asp Phe Gln Gly Phe Lys Asp Asp Ala Ser Phe Asp Cys
 50 55 60
 Glu Asp Glu Phe Asp Val Asp Asp Asp Val Phe Ala Asp Val Lys Pro
 65 70 75 80
 Phe Val Phe Ala Ala Gly Ala Lys Pro Val Ala Ser Pro Pro Ala Ala
 85 90 95
 Leu Ala Ser Thr Gly Ser Val Ser Gly Lys Lys Thr Ile Glu Ser Gly
 100 105 110
 Gly Gln Ala Glu Lys Ser Ala Lys Arg Lys Arg Lys Asn Gln Tyr Arg
 115 120 125
 Gly Ile Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp
 130 135 140
 Pro Arg Lys Gly Ser Arg Glu Trp Leu Gly Thr Phe Asp Thr Ala Glu
 145 150 155 160
 Glu Ala Ala Arg Ala Tyr Asp Ala Ala Ala Arg Ile Arg Gly Asn

PF59082SeqList_PF59082.txt

165 170 175
 Lys Ala Lys Val Asn Phe Pro Glu Glu Met Val Pro Ser Val Ser Gln
 180 185 190
 Lys Arg Pro Ala Ala Lys Lys Ala Val Ala Lys Pro Asn Gln Ser Pro
 195 200 205
 Ala Ser Val Gln Gln Pro Thr His Val Ser Gln Tyr Cys Asn Asn Ser
 210 215 220
 Phe Asp Asn Met Gly His Asp Ser Ser Phe Gly Asp Val Ser Phe Met
 225 230 235 240
 Glu Glu Lys Pro Gln Met Cys Asn Asn Gln Phe Phe Asp Val Gly Gly
 245 250 255
 Asn Asn Gly Tyr Gln Tyr Phe Ser Ser Asp Gln Gly Ser Asn Ser Leu
 260 265 270
 Asp Cys Ser Glu Phe Gly Trp Ser Asp Gln Thr Pro Lys Thr Pro Glu
 275 280 285
 Ile Ser Ser Met Leu Val Asn Asn Gln Ala Pro Phe Ile Glu Glu
 290 295 300
 Thr Asn Pro Ala Lys Lys Leu Lys Thr Ser Ser Glu Asp Gly Thr Ser
 305 310 315 320
 Asn Asn Asp Ser Ser Asp Asp Leu Met Ala Tyr Leu Asn Asn Ala Leu
 325 330 335
 Trp Glu Ser Pro Leu Glu Val Glu Ala Met Phe Gly Gly Asp Ala Ala
 340 345 350
 Thr Met Thr Gln Glu Glu Gly Asn Pro Met Asp Leu Trp Ser Leu Asp
 355 360 365
 Asp Ile Asn Ser Met Leu Asp Gly Gly Val Phe
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 <211> 1256
 <212> DNA
 <213> Brassica napus

<220>
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 <222> (95)..(1048)

<400> 1803
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60

agattctgtt tctgaacatt tacaccctca cgcc atg tgt gga gga gca ata atc
 Met Cys Gly Gly Ala Ile Ile

115

1 5
 tcc gat ttc atc ccg ccg ccg agg tct cgc cgc gtc acc agc gag ttt
 Ser Asp Phe Ile Pro Pro Pro Arg Ser Arg Arg Val Thr Ser Glu Phe
 10 15 20

163

ctc tgg ccg gat ctg aag aag agc tcg aag aaa cgc tcg agt ttc ttc
 Leu Trp Pro Asp Leu Lys Lys Ser Ser Lys Lys Arg Ser Ser Phe Phe
 25 30 35

211

gat ctt gac gat gag ttc gag gct gac ttc cag ggc ttc aag gat gat
 Asp Leu Asp Asp Glu Phe Glu Ala Asp Phe Gln Gly Phe Lys Asp Asp
 40 45 50 55

259

tcc tct atc gat tgc gat gat gcg aag ccg ttc gtt ttc gcc ggg gct
 Ser Ser Ile Asp Cys Asp Asp Ala Lys Pro Phe Val Phe Ala Gly Ala
 60 65 70

307

cgt aag ccc gcc gta tcc gcc gcc act gcc gat tca gtg ttt ggc aag
 Arg Lys Pro Ala Val Ser Ala Ala Thr Ala Asp Ser Val Phe Gly Lys
 75 80 85

355

aaa gtt gtt gat gga gaa ggt gag agg tct gca aag agg aag aag
 Lys Val Val Asp Gly Glu Gly Glu Arg Ser Ala Lys Arg Lys Arg Lys
 90 95 100

403

agc cag tac cga ggg ata agg caa cgt cct tgg ggc aaa tgg gct gct
 Ser Gln Tyr Arg Gly Ile Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala
 105 110 115

451

gag att cgt gat cca agg gaa ggt tca aga gtt tgg ctt gga act ttc
 Glu Ile Arg Asp Pro Arg Glu Gly Ser Arg Val Trp Leu Gly Thr Phe
 120 125 130 135

499

aaa acc gcc gag gaa gct gca aga gct tac gac gct gca gct cgt aga

547

PF59082SeqList_PF59082.txt

Lys	Thr	Ala	Glu	Glu	Ala	Ala	Arg	Ala	Tyr	Asp	Ala	Ala	Ala	Arg	Arg	
				140					145					150		
atc	cgt	ggt	tcc	aaa	gct	aag	gtg	aat	ttc	cct	gag	gag	aag	gag	aac	595
Ile	Arg	Gly	Ser	Lys	Ala	Lys	Val	Asn	Phe	Pro	Glu	Glu	Lys	Glu	Asn	
			155					160					165			
cca	cct	gcc	aag	aag	gtg	gct	cca	aac	cca	agt	cca	gtt	ttg	gct	cag	643
Pro	Pro	Ala	Lys	Lys	Val	Ala	Pro	Asn	Pro	Ser	Pro	Val	Leu	Ala	Gln	
		170					175					180				
aac	ttg	gac	aac	tcc	ttt	gac	aac	atg	tgt	ttc	atg	gag	gag	aag	cac	691
Asn	Leu	Asp	Asn	Ser	Phe	Asp	Asn	Met	Cys	Phe	Met	Glu	Glu	Lys	His	
	185					190					195					
caa	gtt	aac	aac	aac	aac	aac	aac	atg	tgt	ttc	atg	gag	gag	aag	cac	739
Gln	Val	Asn	Asn	Asn	Asn	Asn	Gln	Phe	Gly	Gly	Asn	Gly	Tyr	His	Gln	
200				205					210						215	
tat	ttc	agc	tca	gac	cag	ggt	agt	aac	tca	ttc	ggt	tgt	tct	gag	ttt	787
Tyr	Phe	Ser	Ser	Asp	Gln	Gly	Ser	Asn	Ser	Phe	Gly	Cys	Ser	Glu	Phe	
				220				225						230		
ggt	tgg	aac	gat	caa	gct	cct	ata	act	cct	gag	atc	tcc	tct	gct	ttt	835
Gly	Trp	Asn	Asp	Gln	Ala	Pro	Ile	Thr	Pro	Glu	Ile	Ser	Ser	Ala	Phe	
			235				240					245				
atc	aac	aac	aac	tct	gtc	aca	ttc	gcc	gag	gaa	gct	gat	cca	gct	aag	883
Ile	Asn	Asn	Asn	Ser	Val	Thr	Phe	Ala	Glu	Glu	Ala	Asp	Pro	Ala	Lys	
		250					255				260					
cag	ctc	aag	gtc	atg	gat	ttt	gag	aca	act	tac	aac	agc	act	gaa	tgg	931
Gln	Leu	Lys	Val	Met	Asp	Phe	Glu	Thr	Thr	Tyr	Asn	Ser	Thr	Glu	Trp	
	265					270				275						
gat	tct	tca	ctt	gat	ttc	ttc	agt	gga	gac	gct	gtg	gcg	act	cag	gac	979
Asp	Ser	Ser	Leu	Asp	Phe	Phe	Ser	Gly	Asp	Ala	Val	Ala	Thr	Gln	Asp	
280				285				290						295		
aat	ggt	gca	aat	cct	atg	gag	cta	tgg	agc	att	gat	gag	atc	aat	tcc	1027
Asn	Gly	Ala	Asn	Pro	Met	Glu	Leu	Trp	Ser	Ile	Asp	Glu	Ile	Asn	Ser	
			300					305						310		
atg	att	gga	gga	gtc	ttc	taa	agagatccat	tgatcatttaa	agagttttaa							1078
Met	Ile	Gly	Gly	Val	Phe											
		315														
aaacatttttg	aactcttttct	tgttgtcttt	tgtgttttg	ttttgttact	ttgtgccct											1138
aaacatcttc	tttaacattg	tcataagtta	atatgttgaa	ccattgttct	cttttgtgat											1198
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 <211> 317
 <212> PRT
 <213> Brassica napus

<400> 1804
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 20 25 30
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 35 40 45
 Phe Gln Gly Phe Lys Asp Asp Ser Ser Ile Asp Cys Asp Asp Ala Lys
 50 55 60
 Pro Phe Val Phe Ala Gly Ala Arg Lys Pro Ala Val Ser Ala Ala Thr
 65 70 75 80
 Ala Asp Ser Val Phe Gly Lys Lys Val Val Asp Gly Glu Gly Glu Arg
 85 90 95
 Ser Ala Lys Arg Lys Arg Lys Ser Gln Tyr Arg Gly Ile Arg Gln Arg
 100 105 110
 Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp Pro Arg Glu Gly Ser
 115 120 125
 Arg Val Trp Leu Gly Thr Phe Lys Thr Ala Glu Glu Ala Ala Arg Ala
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PF59082SeqList_PF59082.txt

Tyr Asp Ala Ala Ala Arg Arg Ile Arg Gly Ser Lys Ala Lys Val Asn
 145 150 155 160
 Phe Pro Glu Glu Lys Glu Asn Pro Pro Ala Lys Lys Val Ala Pro Asn
 165 170 175
 Pro Ser Pro Val Leu Ala Gln Asn Leu Asp Asn Ser Phe Asp Asn Met
 180 185 190
 Cys Phe Met Glu Glu Lys His Gln Val Asn Asn Asn Asn Asn Gln Phe
 195 200 205
 Gly Gly Asn Gly Tyr His Gln Tyr Phe Ser Ser Asp Gln Gly Ser Asn
 210 215 220
 Ser Phe Gly Cys Ser Glu Phe Gly Trp Asn Asp Gln Ala Pro Ile Thr
 225 230 235 240
 Pro Glu Ile Ser Ser Ala Phe Ile Asn Asn Asn Ser Val Thr Phe Ala
 245 250 255
 Glu Glu Ala Asp Pro Ala Lys Gln Leu Lys Val Met Asp Phe Glu Thr
 260 265 270
 Thr Tyr Asn Ser Thr Glu Trp Asp Ser Ser Leu Asp Phe Phe Ser Gly
 275 280 285
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<210> 1805

<211> 1506

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1506)

<400> 1805

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ttc aca ctc ctc tcc gcc act aaa ccc cta aat ctc act ctc cct cac	96
Phe Thr Leu Leu Ser Ala Thr Lys Pro Leu Asn Leu Thr Leu Pro His	
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caa cac cct tcc cct gat tcc gtc gct ctc cat gtc atc agg agt gta	144
Gln His Pro Ser Pro Asp Ser Val Ala Leu His Val Ile Arg Ser Val	
35 40 45	
aat gaa tct ctt gca aga aga caa cta agc tca cca tca tca tcc tca	192
Asn Glu Ser Leu Ala Arg Arg Gln Leu Ser Ser Pro Ser Ser Ser Ser	
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Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Cys Arg Thr Gly Asn Pro	
65 70 75 80	
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Ile Asp Asp Cys Trp Arg Cys Ser Asp Ala Asp Trp Ser Thr Asn Arg	
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Gln Arg Leu Ala Asp Cys Ser Ile Gly Phe Gly His Gly Thr Leu Gly	
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ggc aaa aac ggc aag atc tac gtc gta act gac tca tcc gac aac aac	384
Gly Lys Asn Gly Lys Ile Tyr Val Val Thr Asp Ser Ser Asp Asn Asn	
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cca aca aac cca aca cca gga aca ctc cgt tac ggc gta atc caa gaa	432
Pro Thr Asn Pro Thr Pro Gly Thr Leu Arg Tyr Gly Val Ile Gln Glu	
130 135 140	
gag cca ctc tgg atc gtc ttc tct tca aac atg ctc atc aga cta aaa	480
Glu Pro Leu Trp Ile Val Phe Ser Ser Asn Met Leu Ile Arg Leu Lys	
145 150 155 160	
caa gaa ctc atc atc aac agc tac aaa acc tta gat ggt cgt ggc tca	528
Gln Glu Leu Ile Ile Asn Ser Tyr Lys Thr Leu Asp Gly Arg Gly Ser	
165 170 175	
gcc gtt cac att acc gga aac ggt tgc tta act ctc caa tac gtt caa	576
Ala Val His Ile Thr Gly Asn Gly Cys Leu Thr Leu Gln Tyr Val Gln	
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Gly	Phe	Glu	Lys	Arg	Gly	Arg	Ser	Asp	Gly	Asp	Gly	Ile	Ser	Ile	Phe	
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Gly	Ser	Gln	Lys	Ile	Trp	Val	Asp	His	Cys	Ser	Met	Ser	His	Cys	Thr	
225					230					235					240	
gac	ggg	cta	att	gat	gct	gtg	atg	ggt	tct	aca	gct	ata	act	ata	tct	768
Asp	Gly	Leu	Ile	Asp	Ala	Val	Met	Gly	Ser	Thr	Ala	Ile	Thr	Ile	Ser	
				245				250						255		
aac	aat	tac	ttc	acc	cac	cac	gac	gag	gtt	atg	ttg	ttg	ggt	cat	gat	816
Asn	Asn	Tyr	Phe	Thr	His	His	Asp	Glu	Val	Met	Leu	Leu	Gly	His	Asp	
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gat	aac	tat	gct	cct	gat	acg	ggg	atg	caa	gtg	acg	ata	gcg	ttt	aat	864
Asp	Asn	Tyr	Ala	Pro	Asp	Thr	Gly	Met	Gln	Val	Thr	Ile	Ala	Phe	Asn	
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Tyr	Ile	His	Val	Val	Asn	Asn	Asp	Phe	Thr	Glu	Trp	Lys	Met	Tyr	Ala	
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Ile	Gly	Gly	Ser	Gly	Asn	Pro	Thr	Ile	Asn	Ser	Gln	Gly	Asn	Arg	Tyr	
				325				330						335		
tct	gct	cct	tct	gat	cct	agc	gcc	aaa	gag	gtg	acg	aag	cga	gtg	gac	1056
Ser	Ala	Pro	Ser	Asp	Pro	Ser	Ala	Lys	Glu	Val	Thr	Lys	Arg	Val	Asp	
			340				345						350			
tcg	aag	gac	gat	ggt	gaa	tgg	tcg	aat	tgg	aat	tgg	aga	aca	gaa	ggg	1104
Ser	Lys	Asp	Asp	Gly	Glu	Trp	Ser	Asn	Trp	Asn	Trp	Arg	Thr	Glu	Gly	
		355				360					365					
gat	ttg	atg	gag	aat	gga	gct	ttc	ttt	gtg	gcc	tct	ggt	gaa	gga	atg	1152
Asp	Leu	Met	Glu	Asn	Gly	Ala	Phe	Phe	Val	Ala	Ser	Gly	Glu	Gly	Met	
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agc	tca	atg	tac	tct	aaa	gct	tct	agt	gtt	gac	cct	aaa	gct	gct	tct	1200
Ser	Ser	Met	Tyr	Ser	Lys	Ala	Ser	Ser	Val	Asp	Pro	Lys	Ala	Ala	Ser	
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Leu	Val	Asp	Gln	Leu	Thr	Arg	Asn	Ala	Gly	Val	Phe	Gly	Gly	Pro	Arg	
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Asp	Asp	Gln	Gly	Gln	Ser	Gly	Asn	Ser	Tyr	Ser	Pro	Tyr	Gly	Gly	Asp	
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ggc	ggt	ggc	ggt	ggg	agc	agc	ggt	ggg	agc	agc	ggt	gga	ggg	atg	gac	1344
Gly	Gly	Gly	Gly	Gly	Ser	Ser	Gly	Gly	Ser	Ser	Gly	Gly	Gly	Met	Asp	
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Val	Met	Gly	Gly	Thr	Thr	Arg	Gly	Ser	Ser	Ser	Ser	Ser	Gly	Asp	Asp	
	450					455					460					
agc	aat	gtc	ttc	cag	atg	ata	ttt	gga	agc	gat	gca	ccg	tct	cgg	ccg	1440
Ser	Asn	Val	Phe	Gln	Met	Ile	Phe	Gly	Ser	Asp	Ala	Pro	Ser	Arg	Pro	
465					470			475						480		
cgt	tta	acg	tta	ttg	ttt	tct	ttg	tta	atg	att	tcg	gtt	ttg	tcg	tta	1488
Arg	Leu	Thr	Leu	Leu	Phe	Ser	Leu	Leu	Met	Ile	Ser	Val	Leu	Ser	Leu	
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Ser	Thr	Leu	Leu	Leu												
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<211> 501

<212> PRT

<213> Arabidopsis thaliana

<400> 1806

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 65 70 75 80
 Ile Asp Asp Cys Trp Arg Cys Ser Asp Ala Asp Trp Ser Thr Asn Arg
 85 90 95
 Gln Arg Leu Ala Asp Cys Ser Ile Gly Phe Gly His Gly Thr Leu Gly
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 Gly Lys Asn Gly Lys Ile Tyr Val Val Thr Asp Ser Ser Asp Asn Asn
 115 120 125
 Pro Thr Asn Pro Thr Pro Gly Thr Leu Arg Tyr Gly Val Ile Gln Glu
 130 135 140
 Glu Pro Leu Trp Ile Val Phe Ser Ser Asn Met Leu Ile Arg Leu Lys
 145 150 155 160
 Gln Glu Leu Ile Ile Asn Ser Tyr Lys Thr Leu Asp Gly Arg Gly Ser
 165 170 175
 Ala Val His Ile Thr Gly Asn Gly Cys Leu Thr Leu Gln Tyr Val Gln
 180 185 190
 His Ile Ile Ile His Asn Leu His Ile Tyr Asp Cys Lys Pro Ser Ala
 195 200 205
 Gly Phe Glu Lys Arg Gly Arg Ser Asp Gly Asp Gly Ile Ser Ile Phe
 210 215 220
 Gly Ser Gln Lys Ile Trp Val Asp His Cys Ser Met Ser His Cys Thr
 225 230 235 240
 Asp Gly Leu Ile Asp Ala Val Met Gly Ser Thr Ala Ile Thr Ile Ser
 245 250 255
 Asn Asn Tyr Phe Thr His His Asp Glu Val Met Leu Leu Gly His Asp
 260 265 270
 Asp Asn Tyr Ala Pro Asp Thr Gly Met Gln Val Thr Ile Ala Phe Asn
 275 280 285
 His Phe Gly Gln Gly Leu Val Gln Arg Met Pro Arg Cys Arg Arg Gly
 290 295 300
 Tyr Ile His Val Val Asn Asn Asp Phe Thr Glu Trp Lys Met Tyr Ala
 305 310 315 320
 Ile Gly Gly Ser Gly Asn Pro Thr Ile Asn Ser Gln Gly Asn Arg Tyr
 325 330 335
 Ser Ala Pro Ser Asp Pro Ser Ala Lys Glu Val Thr Lys Arg Val Asp
 340 345 350
 Ser Lys Asp Asp Gly Glu Trp Ser Asn Trp Asn Trp Arg Thr Glu Gly
 355 360 365
 Asp Leu Met Glu Asn Gly Ala Phe Phe Val Ala Ser Gly Glu Gly Met
 370 375 380
 Ser Ser Met Tyr Ser Lys Ala Ser Ser Val Asp Pro Lys Ala Ala Ser
 385 390 395 400
 Leu Val Asp Gln Leu Thr Arg Asn Ala Gly Val Phe Gly Gly Pro Arg
 405 410 415
 Asp Asp Gln Gly Gln Ser Gly Asn Ser Tyr Ser Pro Tyr Gly Gly Asp
 420 425 430
 Gly Gly Gly Gly Gly Ser Ser Gly Gly Ser Ser Gly Gly Met Asp
 435 440 445
 Val Met Gly Gly Thr Thr Arg Gly Ser Ser Ser Ser Gly Asp Asp
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 Ser Asn Val Phe Gln Met Ile Phe Gly Ser Asp Ala Pro Ser Arg Pro
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<222> (42)..(1427)

<400> 1807

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Thr Leu Ser Ser Val Ser Ala Thr Val Ile Ile Ile Leu Thr Leu Phe
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gtc cat gta aat gga gtt caa gat aca aag gag ttg aga cct gat cag 152
Val His Val Asn Gly Val Gln Asp Thr Lys Glu Leu Arg Pro Asp Gln
                                   25                                   30                                   35
agc tca aga aat aca tca atg act gat tat gaa tgg cat gaa cac gcc 200
Ser Ser Arg Asn Thr Ser Met Thr Asp Tyr Glu Trp His Glu His Ala
                                   40                                   45                                   50
gta aaa gac cca gaa gaa ata gca gcc atg gtc gat atg aag ata cga 248
Val Lys Asp Pro Glu Glu Ile Ala Ala Met Val Asp Met Lys Ile Arg
                                   55                                   60                                   65
aac agt aca gaa cgt agg agg tta ggc tac ttc tcc tgc tca acc gga 296
Asn Ser Thr Glu Arg Arg Arg Leu Gly Tyr Phe Ser Cys Ser Thr Gly
                                   70                                   75                                   80                                   85
aac cca atc gac gat tgt tgg cgt tgc gat aaa aaa tgg cat cgc cag 344
Asn Pro Ile Asp Asp Cys Trp Arg Cys Asp Lys Lys Trp His Arg Gln
                                   90                                   95                                   100
aga aag cgt cta gcg agt tgc gcc atc gga ttc gga cgt aac gcc gtc 392
Arg Lys Arg Leu Ala Ser Cys Ala Ile Gly Phe Gly Arg Asn Ala Val
                                   105                                   110                                   115
gga ggc cga gac gga cgt ttc tac gtc gtc aca gac cca tcg gat cat 440
Gly Gly Arg Asp Gly Arg Phe Tyr Val Val Thr Asp Pro Ser Asp His
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gat ccg gtt aaa cct aaa ctc ggt acg ctc cgg tac gca gtg ata caa 488
Asp Pro Val Lys Pro Lys Leu Gly Thr Leu Arg Tyr Ala Val Ile Gln
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gac cga ccg cta tgg atc gtc ttc aaa cgc gac atg gtc atc acc cta 536
Asp Arg Pro Leu Trp Ile Val Phe Lys Arg Asp Met Val Ile Thr Leu
                                   150                                   155                                   160                                   165
agt caa gag ctc atc atg aat agc ttc aaa acg atc gat ggt cgc ggc 584
Ser Gln Glu Leu Ile Met Asn Ser Phe Lys Thr Ile Asp Gly Arg Gly
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gtg aac gtg cac atc gct ggt gga gca tgt att acg att cag tac gtg 632
Val Asn Val His Ile Ala Gly Gly Ala Cys Ile Thr Ile Gln Tyr Val
                                   185                                   190                                   195
acg aac atc atc att cac ggg att aac att cac gac tgt aag cgt act 680
Thr Asn Ile Ile His Gly Ile Asn Ile His Asp Cys Lys Arg Thr
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ggt aac gcc atg gtt aga agc tcg gag acg cat tat ggt tgg aga acg 728
Gly Asn Ala Met Val Arg Ser Ser Glu Thr His Tyr Gly Trp Arg Thr
                                   215                                   220                                   225
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Met Ala Asp Gly Asp Gly Ile Ser Ile Phe Gly Ser Ser His Ile Trp
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                                   265                                   270                                   275
cac aac gag gct att ttg ttg ggg cat acc gat tcc tac acc aga gac 920
His Asn Glu Ala Ile Leu Leu Gly His Thr Asp Ser Tyr Thr Arg Asp
                                   280                                   285                                   290
aaa atg atg caa gtg acc att gca tat aat cat ttt ggg gag ggt ctt 968
Lys Met Met Gln Val Thr Ile Ala Tyr Asn His Phe Gly Glu Gly Leu
                                   295                                   300                                   305
ata cag aga atg cca agg ttt ttc atc ttt gat ttc cta ttg gtt 1016
Ile Gln Arg Met Pro Arg Phe Phe Ile Phe Asp Phe Leu Leu Leu Val
                                   310                                   315                                   320                                   325
aat tgg tat cag aat ttt gta gag ttc ttg aaa ctt tgg tgc tat ttc 1064
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PF59082SeqList_PF59082.txt

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tgg gaa atg tat gca atc ggt gga agt gca aac cct aca atc aac agt      1160
Trp Glu Met Tyr Ala Ile Gly Gly Ser Ala Asn Pro Thr Ile Asn Ser
          360          365          370
caa gga aat cga ttc ctt gcc ccg gga aac cgt ttt gct aaa gag gtg      1208
Gln Gly Asn Arg Phe Leu Ala Pro Gly Asn Arg Phe Ala Lys Glu Val
          375          380          385
aca aag agg gta ggt gca ggg aaa gga gaa tgg aac cag tgg aac tgg      1256
Thr Lys Arg Val Gly Ala Gly Lys Gly Glu Trp Asn Gln Trp Asn Trp
          390          395          400
aga tca caa gga gac tta ttg ctc aat ggt gct tac ttc act tca tct      1304
Arg Ser Gln Gly Asp Leu Leu Leu Asn Gly Ala Tyr Phe Thr Ser Ser
          410          415          420
gga gct gga gct tct tca agc tac gct aga gcc tct agt ttg gct gct      1352
Gly Ala Gly Ala Ser Ser Ser Tyr Ala Arg Ala Ser Ser Leu Ala Ala
          425          430          435
aaa tca tct tcc ctt gta ggt atg ctt acc tat agc tct ggt gcc ctg      1400
Lys Ser Ser Ser Leu Val Gly Met Leu Thr Tyr Ser Ser Gly Ala Leu
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Lys Cys Arg Ile Gly Thr Pro Cys
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caaaagctga acacatagaa acgatatgaa atgggaaaga acaaagaaaa agaactcggt      1507

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<210> 1808
 <211> 461
 <212> PRT
 <213> Brassica napus

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Leu Arg Pro Asp Gln Ser Ser Arg Asn Thr Ser Met Thr Asp Tyr Glu
          35          40          45
Trp His Glu His Ala Val Lys Asp Pro Glu Glu Ile Ala Ala Met Val
          50          55          60
Asp Met Lys Ile Arg Asn Ser Thr Glu Arg Arg Arg Leu Gly Tyr Phe
65          70          75          80
Ser Cys Ser Thr Gly Asn Pro Ile Asp Asp Cys Trp Arg Cys Asp Lys
          85          90          95
Lys Trp His Arg Gln Arg Lys Arg Leu Ala Ser Cys Ala Ile Gly Phe
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Gly Arg Asn Ala Val Gly Gly Arg Asp Gly Arg Phe Tyr Val Val Thr
          115          120          125
Asp Pro Ser Asp His Asp Pro Val Lys Pro Lys Leu Gly Thr Leu Arg
130          135          140
Tyr Ala Val Ile Gln Asp Arg Pro Leu Trp Ile Val Phe Lys Arg Asp
145          150          155          160
Met Val Ile Thr Leu Ser Gln Glu Leu Ile Met Asn Ser Phe Lys Thr
          165          170          175
Ile Asp Gly Arg Gly Val Asn Val His Ile Ala Gly Gly Ala Cys Ile
          180          185          190
Thr Ile Gln Tyr Val Thr Asn Ile Ile Ile His Gly Ile Asn Ile His
          195          200          205
Asp Cys Lys Arg Thr Gly Asn Ala Met Val Arg Ser Ser Glu Thr His
210          215          220

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PF59082SeqList_PF59082.txt

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 Gly Leu Ile Asp Ala Ile Met Gly Ser Thr Ala Ile Thr Ile Ser Asn
 260 265 270
 Asn Tyr Phe Thr His His Asn Glu Ala Ile Leu Leu Gly His Thr Asp
 275 280 285
 Ser Tyr Thr Arg Asp Lys Met Met Gln Val Thr Ile Ala Tyr Asn His
 290 295 300
 Phe Gly Glu Gly Leu Ile Gln Arg Met Pro Arg Phe Phe Ile Phe Asp
 305 310 315 320
 Phe Leu Leu Leu Val Asn Trp Tyr Gln Asn Phe Val Glu Phe Leu Lys
 325 330 335
 Leu Trp Cys Tyr Phe Arg Cys Arg His Gly Tyr Phe His Val Val Asn
 340 345 350
 Asn Asp Tyr Thr His Trp Glu Met Tyr Ala Ile Gly Gly Ser Ala Asn
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 Pro Thr Ile Asn Ser Gln Gly Asn Arg Phe Leu Ala Pro Gly Asn Arg
 370 375 380
 Phe Ala Lys Glu Val Thr Lys Arg Val Gly Ala Gly Lys Gly Glu Trp
 385 390 395 400
 Asn Gln Trp Asn Trp Arg Ser Gln Gly Asp Leu Leu Leu Asn Gly Ala
 405 410 415
 Tyr Phe Thr Ser Gly Ala Gly Ala Ser Ser Ser Tyr Ala Arg Ala
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 <211> 1702
 <212> DNA
 <213> Brassica napus

<220>
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 <222> (88)..(1467)

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 Met Ala Ala Ala Phe Leu Asn Ile Gly
 1 5
 agc tac gtt ttc gtc ttg ttc tta tcg tca tta gcc aca tta gca cca 162
 Ser Tyr Val Phe Val Leu Phe Leu Ser Ser Leu Ala Thr Leu Ala Pro 25
 10 15 20
 cag gtt caa gcc aat att gcc gtc ttc gac gac tac tgg acg cag cgt 210
 Gln Val Gln Ala Asn Ile Ala Val Phe Asp Asp Tyr Trp Thr Gln Arg 40
 30 35 40
 caa ggc gat gcg ttg aaa caa act ttg gcc tct ttc gat cct tat cct 258
 Gln Gly Asp Ala Leu Lys Gln Thr Leu Ala Ser Phe Asp Pro Tyr Pro 55
 45 50 55
 ctt aac gtc acc aac cac ttg aat tac cat gtc gct tta gca ctt gac 306
 Leu Asn Val Thr Asn His Leu Asn Tyr His Val Ala Leu Ala Leu Asp 70
 60 65 70
 acc acg gaa tca atc aac agc aca aga aga gag ctt tca cag gcg aga 354
 Thr Thr Glu Ser Ile Asn Ser Thr Arg Arg Glu Leu Ser Gln Ala Arg 85
 75 80 85
 cgt ggt cgt aaa atg caa aac aga aga gga aaa tgc gta gct cat aac 402
 Arg Gly Arg Lys Met Gln Asn Arg Arg Gly Lys Cys Val Ala His Asn 105
 90 95 100
 ccg ata gac aaa tgc tgg aga tgc gac cgt gat tgg gaa aag aac cgt 450
 Pro Ile Asp Lys Cys Trp Arg Cys Asp Arg Asp Trp Glu Lys Asn Arg 120
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 aag aaa cta gcg gtc tgt gcc ctc gga ttc ggc agg aga acc agc gga 498
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Gly	Lys	Asp	Gly	Pro	Ile	Tyr	Val	Val	Thr	Asp	Ala	Ser	Asp	Asp	Glu		
		140					145					150					
ctt	atc	agc	cct	agg	cca	gga	aca	tta	aga	cac	gcg	gtg	aca	cga	gaa	594	
Leu	Ile	Ser	Pro	Arg	Pro	Gly	Thr	Leu	Arg	His	Ala	Val	Thr	Arg	Glu		
	155					160					165						
gga	ccg	ctt	tgg	atc	atc	ttc	gca	aga	agc	atg	gtc	ata	aaa	ctg	caa	642	
Gly	Pro	Leu	Trp	Ile	Ile	Phe	Ala	Arg	Ser	Met	Val	Ile	Lys	Leu	Gln		
170					175					180					185		
cag	gaa	ctg	atg	atg	acg	agc	gat	aaa	acg	atc	gat	gga	cgt	gga	gct	690	
Gln	Glu	Leu	Met	Met	Thr	Ser	Asp	Lys	Thr	Ile	Asp	Gly	Arg	Gly	Ala		
			190						195				200				
agg	gtg	tac	atc	atg	gga	ggt	tct	gga	tta	acg	ctg	cag	ttt	gtg	aat	738	
Arg	Val	Tyr	Ile	Met	Gly	Gly	Ser	Gly	Leu	Thr	Leu	Gln	Phe	Val	Asn		
			205					210					215				
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Asn	Val	Ile	Val	His	Asn	Ile	Tyr	Ile	Lys	Gln	Ile	Val	Pro	Ala	Asn		
		220					225					230					
ggc	ggt	ttg	atc	aga	gac	tcc	gag	caa	cat	ata	ggg	ctc	agg	aca	aga	834	
Gly	Gly	Leu	Ile	Arg	Asp	Ser	Glu	Gln	His	Ile	Gly	Leu	Arg	Thr	Arg		
	235					240					245						
agt	gat	ggt	gat	gga	atc	aat	ttg	ttt	gga	gca	act	aat	gtt	tgg	atc	882	
Ser	Asp	Gly	Asp	Gly	Ile	Asn	Leu	Phe	Gly	Ala	Thr	Asn	Val	Trp	Ile		
250					255					260					265		
gat	cat	gtc	tcg	atg	acg	aga	tgt	tct	gat	ggt	atg	att	gat	gcg	att	930	
Asp	His	Val	Ser	Met	Thr	Arg	Cys	Ser	Asp	Gly	Met	Ile	Asp	Ala	Ile		
			270						275					280			
cta	gga	tcc	act	gca	gtg	act	gtc	tcc	aac	agc	cac	ttc	aca	gac	cac	978	
Leu	Gly	Ser	Thr	Ala	Val	Thr	Val	Ser	Asn	Ser	His	Phe	Thr	Asp	His		
			285					290					295				
caa	gag	gtg	atg	ctt	ttt	ggg	gcc	aat	gac	aaa	cac	gag	atc	gac	aag	1026	
Gln	Glu	Val	Met	Leu	Phe	Gly	Ala	Asn	Asp	Lys	His	Glu	Ile	Asp	Lys		
		300					305					310					
aag	atg	cag	ata	aca	gtt	gca	ttc	aac	cac	ttt	ggt	aag	aga	ctg	gaa	1074	
Lys	Met	Gln	Ile	Thr	Val	Ala	Phe	Asn	His	Phe	Gly	Lys	Arg	Leu	Glu		
	315					320					325						
cag	aga	atg	ccc	cgg	gtc	aga	ttc	gga	acg	ata	cat	gtg	gtg	aac	aat	1122	
Gln	Arg	Met	Pro	Arg	Val	Arg	Phe	Gly	Thr	Ile	His	Val	Val	Asn	Asn		
330					335					340					345		
gac	tac	aca	cat	tgg	gaa	atg	tat	gca	att	ggt	gga	aac	atg	aac	cct	1170	
Asp	Tyr	Thr	His	Trp	Glu	Met	Tyr	Ala	Ile	Gly	Gly	Asn	Met	Asn	Pro		
			350						355					360			
aca	atc	att	agt	cat	ggc	aac	cgt	ttc	att	gct	cct	cct	aac	gaa	caa	1218	
Thr	Ile	Ile	Ser	His	Gly	Asn	Arg	Phe	Ile	Ala	Pro	Pro	Asn	Glu	Gln		
			365					370					375				
gcc	aaa	cag	atc	aca	aag	aga	gag	tac	act	tct	tac	gtt	gat	tgg	aaa	1266	
Ala	Lys	Gln	Ile	Thr	Lys	Arg	Glu	Tyr	Thr	Ser	Tyr	Val	Asp	Trp	Lys		
		380					385					390					
ctt	tgg	aac	tgg	caa	tca	gaa	gga	gat	tac	ttc	ctg	aat	gga	gct	tac	1314	
Leu	Trp	Asn	Trp	Gln	Ser	Glu	Gly	Asp	Tyr	Phe	Leu	Asn	Gly	Ala	Tyr		
	395					400					405						
ttt	gtg	caa	tcc	ggt	aaa	cct	aat	gcg	tgg	agc	cct	aaa	ccg	aag	aac	1362	
Phe	Val	Gln	Ser	Gly	Lys	Pro	Asn	Ala	Trp	Ser	Pro	Lys	Pro	Lys	Asn		
410					415					420					425		
cct	atc	ccg	aac	aag	ttt	gcg	atc	cga	cct	aag	ccg	gga	acg	atg	gtc	1410	
Pro	Ile	Pro	Asn	Lys	Phe	Ala	Ile	Arg	Pro	Lys	Pro	Gly	Thr	Met	Val		
			430						435					440			
cgt	ata	ctc	acc	atg	gac	gca	gga	gta	ctg	ggc	tgc	aaa	caa	ggt	caa	1458	
Arg	Ile	Leu	Thr	Met	Asp	Ala	Gly	Val	Leu	Gly	Cys	Lys	Gln	Gly	Gln		
			445					450					455				
gcc	tgc	tga	tgattaaaat	taccattttg	ttgccttcca	acaaacaaag	cttgtgctcc									1517	
Ala	Cys																
ctgtattttgc	ttgttgtcca	agaaaagaga	gagagagaga	gagaggggaa	aaaaggaaat											1577	
gaaagtgggc	ttttctatga	ttgggggtttt	gtaatatattat	tcttattagg	attcagtttc											1637	

PF59082SeqList_PF59082.txt

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<212> PRT
<213> Brassica napus

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Val Phe Asp Asp Tyr Trp Thr Gln Arg Gln Gly Asp Ala Leu Lys Gln
35 40 45
Thr Leu Ala Ser Phe Asp Pro Tyr Pro Leu Asn Val Thr Asn His Leu
50 55 60
Asn Tyr His Val Ala Leu Ala Leu Asp Thr Thr Glu Ser Ile Asn Ser
65 70 75 80
Thr Arg Arg Glu Leu Ser Gln Ala Arg Arg Gly Arg Lys Met Gln Asn
85 90 95
Arg Arg Gly Lys Cys Val Ala His Asn Pro Ile Asp Lys Cys Trp Arg
100 105 110
Cys Asp Arg Asp Trp Glu Lys Asn Arg Lys Lys Leu Ala Val Cys Ala
115 120 125
Leu Gly Phe Gly Arg Arg Thr Ser Gly Gly Lys Asp Gly Pro Ile Tyr
130 135 140
Val Val Thr Asp Ala Ser Asp Asp Glu Leu Ile Ser Pro Arg Pro Gly
145 150 155 160
Thr Leu Arg His Ala Val Thr Arg Glu Gly Pro Leu Trp Ile Ile Phe
165 170 175
Ala Arg Ser Met Val Ile Lys Leu Gln Gln Glu Leu Met Met Thr Ser
180 185 190
Asp Lys Thr Ile Asp Gly Arg Gly Ala Arg Val Tyr Ile Met Gly Gly
195 200 205
Ser Gly Leu Thr Leu Gln Phe Val Asn Asn Val Ile Val His Asn Ile
210 215 220
Tyr Ile Lys Gln Ile Val Pro Ala Asn Gly Gly Leu Ile Arg Asp Ser
225 230 235 240
Glu Gln His Ile Gly Leu Arg Thr Arg Ser Asp Gly Asp Gly Ile Asn
245 250 255
Leu Phe Gly Ala Thr Asn Val Trp Ile Asp His Val Ser Met Thr Arg
260 265 270
Cys Ser Asp Gly Met Ile Asp Ala Ile Leu Gly Ser Thr Ala Val Thr
275 280 285
Val Ser Asn Ser His Phe Thr Asp His Gln Glu Val Met Leu Phe Gly
290 295 300
Ala Asn Asp Lys His Glu Ile Asp Lys Lys Met Gln Ile Thr Val Ala
305 310 315 320
Phe Asn His Phe Gly Lys Arg Leu Glu Gln Arg Met Pro Arg Val Arg
325 330 335
Phe Gly Thr Ile His Val Val Asn Asn Asp Tyr Thr His Trp Glu Met
340 345 350
Tyr Ala Ile Gly Gly Asn Met Asn Pro Thr Ile Ile Ser His Gly Asn
355 360 365
Arg Phe Ile Ala Pro Pro Asn Glu Gln Ala Lys Gln Ile Thr Lys Arg
370 375 380
Glu Tyr Thr Ser Tyr Val Asp Trp Lys Leu Trp Asn Trp Gln Ser Glu
385 390 395 400
Gly Asp Tyr Phe Leu Asn Gly Ala Tyr Phe Val Gln Ser Gly Lys Pro
405 410 415
Asn Ala Trp Ser Pro Lys Pro Lys Asn Pro Ile Pro Asn Lys Phe Ala
420 425 430

PF59082SeqList_PF59082.txt

Ile Arg Pro Lys Pro Gly Thr Met Val Arg Ile Leu Thr Met Asp Ala
 435 440 445
 Gly Val Leu Gly Cys Lys Gln Gly Gln Ala Cys
 450 455

<210> 1811
 <211> 1400
 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (35)..(1198)

<400> 1811
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 ttc ttg ttt ctc tta acc act tct tcc gcg ttt gcg tct gcg ttt cct 103
 Phe Leu Phe Leu Leu Thr Thr Ser Ser Ala Phe Ala Ser Ala Phe Pro
 10 20
 aaa ccg gca ccc gta ccg caa tgg tca aca tca gag aca tca aac tca 151
 Lys Pro Ala Pro Val Pro Gln Trp Ser Thr Ser Glu Thr Ser Asn Ser
 25 30 35
 aca gct tct tgc tca gca act gga aat cca atc gat gac tgc tgg aga 199
 Thr Ala Ser Cys Ser Ala Thr Gly Asn Pro Ile Asp Asp Cys Trp Arg
 40 45 50 55
 tgc gac aag aag tgg aaa tcc aac cgc aag agc ctc gcg gac tgc gcg 247
 Cys Asp Lys Lys Trp Lys Ser Asn Arg Lys Ser Leu Ala Asp Cys Ala
 60 65 70
 gtt gga ttc gga cgc gac tcg gta ggc ggt aga gca ggg gag ttc tac 295
 Val Gly Phe Gly Arg Asp Ser Val Gly Gly Arg Ala Gly Glu Phe Tyr
 75 80 85
 acc gtg acc gat tca gga gac gag gat cct cta aac cca tct cca ggt 343
 Thr Val Thr Asp Ser Gly Asp Glu Asp Pro Leu Asn Pro Ser Pro Gly
 90 95 100
 aca tta cgt tac gcc gca aca caa gac caa cct cta tgg atc ata ttc 391
 Thr Leu Arg Tyr Ala Ala Thr Gln Asp Gln Pro Leu Trp Ile Ile Phe
 105 110 115
 gat aga gac atg gta ata aca cta aaa gaa gat att caa gtg act tca 439
 Asp Arg Asp Met Val Ile Thr Leu Lys Glu Asp Ile Gln Val Thr Ser
 120 125 130 135
 tac aaa acc ata gac ggt aga gga aat aac gtg cag ata gct tat gga 487
 Tyr Lys Thr Ile Asp Gly Arg Gly Asn Asn Val Gln Ile Ala Tyr Gly
 140 145 150
 ccg tgt tta gct ttg tat caa gta agt aac gtt atc ata cac aat att 535
 Pro Cys Leu Ala Leu Tyr Gln Val Ser Asn Val Ile Ile His Asn Ile
 155 160 165
 tac att cac cat tgt gtt ccg gcg aaa cgg tcg ttg gga ggc tat tct 583
 Tyr Ile His His Cys Val Pro Ala Lys Arg Ser Leu Gly Gly Tyr Ser
 170 175 180
 gat gga gat ggg atc tcg ata ttc gag tca cga gat gtt tgg att gat 631
 Asp Gly Asp Gly Ile Ser Ile Phe Glu Ser Arg Asp Val Trp Ile Asp
 185 190 195
 cat tgt acg tta gag aag tgt cac gat ggg ctt att gat gcg gtg ggt 679
 His Cys Thr Leu Glu Lys Cys His Asp Gly Leu Ile Asp Ala Val Gly
 200 205 210 215
 ggg tca acg gat ata acg ata tcg aat aac tac atg ttg aat cat aac 727
 Gly Ser Thr Asp Ile Thr Ile Ser Asn Asn Tyr Met Leu Asn His Asn
 220 225 230
 gaa gtc atg ctt tta ggt cat agt gat gag ttt gtc ggt gat cgt gat 775
 Glu Val Met Leu Leu Gly His Ser Asp Glu Phe Val Gly Asp Arg Asp
 235 240 245
 atg agg gtt tcg atc gcc ttt aat tat ttt ggt gaa gga ctt gtc cag 823
 Met Arg Val Ser Ile Ala Phe Asn Tyr Phe Gly Glu Gly Leu Val Gln
 250 255 260
 cga atg cct agg tgt agg cat gga ttt ttt cac att gtg aat aat att 871
 Arg Met Pro Arg Cys Arg His Gly Phe Phe His Ile Val Asn Asn Ile
 265 270

PF59082SeqList_PF59082.txt

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Tyr	Arg	Glu	Trp	Glu	Met	Tyr	Ala	Ile	Gly	Gly	Ser	Ala	Asn	Pro	Thr	
280					285				290						295	
att	ttt	agt	caa	gga	aat	gtt	ttc	ata	gct	tcg	gat	aat	caa	ttc	aca	967
Ile	Phe	Ser	Gln	Gly	Asn	Val	Phe	Ile	Ala	Ser	Asp	Asn	Gln	Phe	Thr	
			300					305						310		
aag	gag	gtt	aca	aag	cga	gag	agt	gta	gat	gga	gac	gat	gaa	tgg	aag	1015
Lys	Glu	Val	Thr	Lys	Arg	Glu	Ser	Val	Asp	Gly	Asp	Asp	Glu	Trp	Lys	
			315					320					325			
gaa	tgg	aat	tgg	aaa	tca	gaa	gga	gat	gaa	atg	cta	aac	ggg	gct	ttc	1063
Glu	Trp	Asn	Trp	Lys	Ser	Glu	Gly	Asp	Glu	Met	Leu	Asn	Gly	Ala	Phe	
			330				335						340			
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Phe	Thr	Pro	Ser	Gly	Asn	Glu	Asp	Ser	Pro	Ser	Tyr	Thr	Lys	Met	Ser	
			345			350					355					
agt	atg	gta	gct	cgg	cca	gct	tca	ctt	ctt	aag	act	aca	cat	cca	tca	1159
Ser	Met	Val	Ala	Arg	Pro	Ala	Ser	Leu	Leu	Lys	Thr	Thr	His	Pro	Ser	
					365					370					375	
gta	ggg	gtt	ctt	agt	tgc	caa	att	gac	caa	cct	tgt	tag	aacacattca			1208
Val	Gly	Val	Leu	Ser	Cys	Gln	Ile	Asp	Gln	Pro	Cys					
			380					385								
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ttataggatt	tgtattgaat	atgtgatgat	catagaggca	gagccaaaca	aaacaattgc											1328
atagctcatt	gtcaagttca	ccagaatggt	tcaattaa	gtcactgaga	tttcaccaa											1388
aaaaaaaaa	aa															1400

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 <212> PRT
 <213> Brassica napus

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 Thr Ser Glu Thr Ser Asn Ser Thr Ala Ser Cys Ser Ala Thr Gly Asn
 35 40 45
 Pro Ile Asp Asp Cys Trp Arg Cys Asp Lys Lys Trp Lys Ser Asn Arg
 50 55 60
 Lys Ser Leu Ala Asp Cys Ala Val Gly Phe Gly Arg Asp Ser Val Gly
 65 70 75 80
 Gly Arg Ala Gly Glu Phe Tyr Thr Val Thr Asp Ser Gly Asp Glu Asp
 85 90 95
 Pro Leu Asn Pro Ser Pro Gly Thr Leu Arg Tyr Ala Ala Thr Gln Asp
 100 105 110
 Gln Pro Leu Trp Ile Ile Phe Asp Arg Asp Met Val Ile Thr Leu Lys
 115 120 125
 Glu Asp Ile Gln Val Thr Ser Tyr Lys Thr Ile Asp Gly Arg Gly Asn
 130 135 140
 Asn Val Gln Ile Ala Tyr Gly Pro Cys Leu Ala Leu Tyr Gln Val Ser
 145 150 155 160
 Asn Val Ile Ile His Asn Ile Tyr Ile His His Cys Val Pro Ala Lys
 165 170 175
 Arg Ser Leu Gly Gly Tyr Ser Asp Gly Asp Gly Ile Ser Ile Phe Glu
 180 185 190
 Ser Arg Asp Val Trp Ile Asp His Cys Thr Leu Glu Lys Cys His Asp
 195 200 205
 Gly Leu Ile Asp Ala Val Gly Gly Ser Thr Asp Ile Thr Ile Ser Asn
 210 215 220
 Asn Tyr Met Leu Asn His Asn Glu Val Met Leu Leu Gly His Ser Asp
 225 230 235 240 245 250 255 260 265 270 275 280
 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400

PF59082SeqList_PF59082.txt

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Phe Gly Glu Gly Leu Val Gln Arg Met Pro Arg Cys Arg His Gly Phe
      260      265      270
Phe His Ile Val Asn Asn Ile Tyr Arg Glu Trp Glu Met Tyr Ala Ile
      275      280      285
Gly Gly Ser Ala Asn Pro Thr Ile Phe Ser Gln Gly Asn Val Phe Ile
      290      295      300
Ala Ser Asp Asn Gln Phe Thr Lys Glu Val Thr Lys Arg Glu Ser Val
      305      310      315
Asp Gly Asp Asp Glu Trp Lys Glu Trp Asn Trp Lys Ser Glu Gly Asp
      320      325      330
Glu Met Leu Asn Gly Ala Phe Phe Thr Pro Ser Gly Asn Glu Asp Ser
      335      340      345
Pro Ser Tyr Thr Lys Met Ser Ser Met Val Ala Arg Pro Ala Ser Leu
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Leu Lys Thr Thr His Pro Ser Val Gly Val Leu Ser Cys Gln Ile Asp
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Gln Pro Cys
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 <213> Brassica napus

<220>
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 <222> (75)..(1295)

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      Met Gln Thr Lys Lys Leu Phe Ile Ser Ile Val Ser
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ttt ctt ctc tat gct cca ttg atc ttc tct tca cca gtt cca gac cca      158
Phe Leu Leu Tyr Ala Pro Leu Ile Phe Ser Ser Pro Val Pro Asp Pro
      15      20      25
gaa gcc atc gtc gaa gaa gtt cac aag agc att aac gca tcg gtc gca      206
Glu Ala Ile Val Glu Glu Val His Lys Ser Ile Asn Ala Ser Val Ala
      30      35      40
gca cgg agg aag cta ggc tac ctc tcc tgc aca acc ggc aac cca atc      254
Ala Arg Arg Lys Leu Gly Tyr Leu Ser Cys Thr Thr Gly Asn Pro Ile
      45      50      55
gac gac tgc tgg cgc tgc gac ccg cat tgg gag acc cac cgc caa cgc      302
Asp Asp Cys Trp Arg Cys Asp Pro His Trp Glu Thr His Arg Gln Arg
      60      65      70      75
ctc gcc gac tgc gcc atc ggg ttc ggc aaa aac gcc atc gga ggc cgc      350
Leu Ala Asp Cys Ala Ile Gly Phe Gly Lys Asn Ala Ile Gly Gly Arg
      80      85      90
gac ggt cgc atc tac gtc gtc acc gac tca ggc aac gac gac ccg gtg      398
Asp Gly Arg Ile Tyr Val Val Thr Asp Ser Gly Asn Asp Asp Pro Val
      95      100      105
acc ccc aag ccc gga act tta cgc cac gcc gtg gtc cag gac gag cct      446
Thr Pro Lys Pro Gly Thr Leu Arg His Ala Val Val Gln Asp Glu Pro
      110      115      120
ctc tgg atc atc ttc cag cga gac atg acc atc cgc ctc aaa gag gag      494
Leu Trp Ile Ile Phe Gln Arg Asp Met Thr Ile Arg Leu Lys Glu Glu
      125      130      135
ctc atc atg aac tct ttc aag acc atc gac ggc cgc ggc gcc tcc gtg      542
Leu Ile Met Asn Ser Phe Lys Thr Ile Asp Gly Arg Gly Ala Ser Val
      140      145      150      155
cac atc gcc ggc gga cct tgc gtg acg atc cag tac gtg acg aac atc      590
His Ile Ala Gly Gly Pro Cys Val Thr Ile Gln Tyr Val Thr Asn Ile
      160      165      170
atc atc cac ggg gtt cat atc cac gac tgc aag cga ggc ggc aac gct      638

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PF59082SeqList_PF59082.txt

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Met	Val	Arg	Ser	Ser	Pro	Arg	His	Tyr	Gly	Trp	Arg	Thr	Val	Ser	Asp	
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ggc	gac	ggg	gtg	tct	atc	ttc	gga	ggg	agt	cat	gtc	tgg	gtt	gat	cac	734
Gly	Asp	Gly	Val	Ser	Ile	Phe	Gly	Gly	Ser	His	Val	Trp	Val	Asp	His	
205					210					215					220	
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Cys	Ser	Leu	Ser	Asn	Cys	Glu	Asp	Gly	Leu	Ile	Asp	Ala	Ile	Met	Gly	
				225					230					235		
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Ser	Thr	Ala	Ile	Thr	Leu	Ser	Asn	Asn	Tyr	Met	Thr	His	His	Asp	Lys	
			240				245						250			
gtc	att	ttg	ctt	ggg	cat	agt	gat	act	tac	gct	cgt	gac	aag	aac	atg	878
Val	Ile	Leu	Gly	His	Ser	Asp	Thr	Tyr	Ala	Arg	Asp	Lys	Asn	Met		
		255				260					265					
cag	att	act	att	gct	ttt	aat	cat	ttt	ggg	gaa	ggg	ctt	gtt	caa	aga	926
Gln	Ile	Thr	Ile	Ala	Phe	Asn	His	Phe	Gly	Glu	Gly	Leu	Val	Gln	Arg	
	270					275				280						
atg	ccg	agg	tgt	aga	cat	ggg	tac	ttc	cat	gtg	aac	aat	gac	tat		974
Met	Pro	Arg	Cys	Arg	His	Gly	Tyr	Phe	His	Val	Val	Asn	Asn	Asp	Tyr	
285					290				295					300		
aca	cat	tgg	gag	atg	tat	gcg	att	ggg	gga	agt	gct	aat	cct	act	atc	1022
Thr	His	Trp	Glu	Met	Tyr	Ala	Ile	Gly	Ser	Ala	Asn	Pro	Thr	Ile		
			305					310					315			
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Asn	Ser	Gln	Gly	Asn	Arg	Phe	Val	Ala	Pro	Asn	Ile	Arg	Phe	Ser	Lys	
			320			325						330				
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Glu	Val	Thr	Lys	His	Glu	Asp	Ala	Pro	Glu	Ser	Glu	Trp	Lys	Arg	Trp	
		335				340					345					
aac	tgg	aga	tca	tct	ggt	gat	ttg	ttg	tta	aac	ggt	gcg	ttt	ttt	act	1166
Asn	Trp	Arg	Ser	Ser	Gly	Asp	Leu	Leu	Leu	Asn	Gly	Ala	Phe	Phe	Thr	
	350				355					360						
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Pro	Ser	Gly	Gly	Ala	Gln	Ser	Ser	Ser	Tyr	Ala	Lys	Ala	Ser	Ser	Leu	
365					370				375					380		
ggg	gcg	aaa	ccg	tct	tct	ctt	gtt	gga	ccg	ttg	acg	gtg	ggg	tct	ggg	1262
Gly	Ala	Lys	Pro	Ser	Ser	Leu	Val	Gly	Pro	Leu	Thr	Val	Gly	Ser	Gly	
			385					390					395			
gca	ctg	aat	tgc	cgc	aag	ggt	tct	cgt	tgc	tga	ttgtggtggt	cacttaaggt				1315
Ala	Leu	Asn	Cys	Arg	Lys	Gly	Ser	Arg	Cys							
		400				405										
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ttaaggagaa	tacaacctct	ggctttactg	ctcttttagga	cccttgtaag	gattctctgt											1495
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<212> PRT

<213> Brassica napus

<400> 1814

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15

Ala Pro Leu Ile Phe Ser Ser Pro Val Pro Asp Pro Glu Ala Ile Val

PF59082SeqList_PF59082.txt

20 25 30
 Glu Glu Val His Lys Ser Ile Asn Ala Ser Val Ala Ala Arg Arg Lys
 35 40 45
 Leu Gly Tyr Leu Ser Cys Thr Thr Gly Asn Pro Ile Asp Asp Cys Trp
 50 55 60
 Arg Cys Asp Pro His Trp Glu Thr His Arg Gln Arg Leu Ala Asp Cys
 65 70 75 80
 Ala Ile Gly Phe Gly Lys Asn Ala Ile Gly Gly Arg Asp Gly Arg Ile
 85 90 95
 Tyr Val Val Thr Asp Ser Gly Asn Asp Asp Pro Val Thr Pro Lys Pro
 100 105 110
 Gly Thr Leu Arg His Ala Val Val Gln Asp Glu Pro Leu Trp Ile Ile
 115 120 125
 Phe Gln Arg Asp Met Thr Ile Arg Leu Lys Glu Glu Leu Ile Met Asn
 130 135 140
 Ser Phe Lys Thr Ile Asp Gly Arg Gly Ala Ser Val His Ile Ala Gly
 145 150 155 160
 Gly Pro Cys Val Thr Ile Gln Tyr Val Thr Asn Ile Ile Ile His Gly
 165 170 175
 Val His Ile His Asp Cys Lys Arg Gly Gly Asn Ala Met Val Arg Ser
 180 185 190
 Ser Pro Arg His Tyr Gly Trp Arg Thr Val Ser Asp Gly Asp Gly Val
 195 200 205
 Ser Ile Phe Gly Gly Ser His Val Trp Val Asp His Cys Ser Leu Ser
 210 215 220
 Asn Cys Glu Asp Gly Leu Ile Asp Ala Ile Met Gly Ser Thr Ala Ile
 225 230 235 240
 Thr Leu Ser Asn Asn Tyr Met Thr His His Asp Lys Val Ile Leu Leu
 245 250 255
 Gly His Ser Asp Thr Tyr Ala Arg Asp Lys Asn Met Gln Ile Thr Ile
 260 265 270
 Ala Phe Asn His Phe Gly Glu Gly Leu Val Gln Arg Met Pro Arg Cys
 275 280 285
 Arg His Gly Tyr Phe His Val Val Asn Asn Asp Tyr Thr His Trp Glu
 290 295 300
 Met Tyr Ala Ile Gly Gly Ser Ala Asn Pro Thr Ile Asn Ser Gln Gly
 305 310 315 320
 Asn Arg Phe Val Ala Pro Asn Ile Arg Phe Ser Lys Glu Val Thr Lys
 325 330 335
 His Glu Asp Ala Pro Glu Ser Glu Trp Lys Arg Trp Asn Trp Arg Ser
 340 345 350
 Ser Gly Asp Leu Leu Leu Asn Gly Ala Phe Phe Thr Pro Ser Gly Gly
 355 360 365
 Ala Gln Ser Ser Ser Tyr Ala Lys Ala Ser Ser Leu Gly Ala Lys Pro
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 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (14)..(1369)

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 Met Ala Ser Ser Ser Gln Lys Val Thr Ser Val Cys
 1 5 10
 ttg acc gtc ctc gtc ctc tta gct ctc agt gca acg att ctc cgg aaa 97
 Leu Thr Val Leu Val Leu Leu Ala Leu Ser Ala Thr Ile Leu Arg Lys
 15 20 25
 att gaa atc cct agc tcc agg aag gtg aaa aca gag gag ttg cag agc 145
 Ile Glu Ile Pro Ser Ser Arg Lys Val Lys Thr Glu Glu Leu Gln Ser
 30 35 40

PF59082SeqList_PF59082.txt

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Ser	Lys	Asn	Thr	Ser	Thr	Met	Ala	Ala	Asn	Arg	Leu	Glu	Gly	Val	Glu	
45					50				55						60	
ttg	aat	gaa	cag	cac	gcg	ggt	gat	gat	cca	gat	aaa	ggt	gct	gat	gaa	241
Leu	Asn	Glu	Gln	His	Ala	Val	Asp	Asp	Pro	Asp	Lys	Val	Ala	Asp	Glu	
				65					70					75		
gtc	tct	acc	ctt	ggt	cag	atg	agc	gaa	cat	aac	atc	aca	gca	agg	agg	289
Val	Ser	Thr	Leu	Val	Gln	Met	Ser	Glu	His	Asn	Ile	Thr	Ala	Arg	Arg	
			80					85					90			
aag	ctt	gga	ttt	ttc	tca	tgt	gga	acc	ggt	aac	ccg	atc	gat	gac	tgt	337
Lys	Leu	Gly	Phe	Phe	Ser	Cys	Gly	Thr	Gly	Asn	Pro	Ile	Asp	Asp	Cys	
		95					100					105				
tgg	cgt	tgt	gac	cgt	aac	tgg	cat	aag	aac	cg	aaa	cg	ctg	gcc	gat	385
Trp	Arg	Cys	Asp	Arg	Asn	Trp	His	Lys	Asn	Arg	Lys	Arg	Leu	Ala	Asp	
	110					115					120					
tgt	ggg	atc	ggt	ttt	gga	cg	aac	gct	ggt	ggt	cg	gat	gga	cg		433
Cys	Gly	Ile	Gly	Phe	Gly	Arg	Asn	Ala	Val	Gly	Gly	Arg	Asp	Gly	Arg	
125					130					135					140	
ttc	tac	ggt	gtc	act	gac	ccc	act	gat	gaa	gac	ggt	att	aac	ccc	aaa	481
Phe	Tyr	Val	Val	Thr	Asp	Pro	Thr	Asp	Glu	Asp	Val	Ile	Asn	Pro	Lys	
				145					150					155		
cca	gga	act	ctt	cg	cac	gcg	ggt	atc	caa	gat	gag	cct	cta	tgg	att	529
Pro	Gly	Thr	Leu	Arg	His	Ala	Val	Ile	Gln	Asp	Glu	Pro	Leu	Trp	Ile	
			160					165					170			
gtg	ttc	aag	aga	gat	atg	gtg	ata	gag	ctg	aaa	caa	gag	ctg	att	atg	577
Val	Phe	Lys	Arg	Asp	Met	Val	Ile	Glu	Leu	Lys	Gln	Glu	Leu	Ile	Met	
		175					180					185				
aac	agt	ttc	aag	acc	att	gat	ggt	cg	ggt	gct	aat	gtc	cat	ata	gct	625
Asn	Ser	Phe	Lys	Thr	Ile	Asp	Gly	Arg	Gly	Ala	Asn	Val	His	Ile	Ala	
	190					195					200					
aac	ggt	gct	tgc	atc	acc	ctc	cag	ttt	atc	acc	gac	gtc	atc	atc	cat	673
Asn	Gly	Ala	Cys	Ile	Thr	Leu	Gln	Phe	Ile	Thr	Asn	Val	Ile	Ile	His	
205				210					215						220	
ggt	ctt	cac	att	cat	gat	tgc	aag	cct	act	gga	aac	gcc	atg	ggt	aga	721
Gly	Leu	His	Ile	His	Asp	Cys	Lys	Pro	Thr	Gly	Asn	Ala	Met	Val	Arg	
				225					230					235		
agc	tcg	cca	tct	cat	ttt	ggc	tgg	agg	aca	atg	gct	gat	ggt	gat	gca	769
Ser	Ser	Pro	Ser	His	Phe	Gly	Trp	Arg	Thr	Met	Ala	Asp	Gly	Asp	Ala	
			240					245					250			
gtc	tct	atc	ttt	cag	tca	tct	cat	atc	tgg	att	gat	cat	aac	tct	ctc	817
Val	Ser	Ile	Phe	Gln	Ser	Ser	His	Ile	Trp	Ile	Asp	His	Asn	Ser	Leu	
		255					260					265				
tct	cac	tgt	gct	gat	ggc	ctt	gtg	gat	gct	gtc	atg	ggt	tct	act	gct	865
Ser	His	Cys	Ala	Asp	Gly	Leu	Val	Asp	Ala	Val	Met	Gly	Ser	Thr	Ala	
	270					275					280					
att	acc	ggt	tcc	aat	aat	cac	ttt	aca	cac	cac	aat	gag	gtc	atg	ttg	913
Ile	Thr	Val	Ser	Asn	Asn	His	Phe	Thr	His	His	Asn	Glu	Val	Met	Leu	
285				290					295						300	
ctc	ggc	cac	agt	gat	tcc	tac	aca	ata	gac	aag	ctg	atg	caa	gtg	acc	961
Leu	Gly	His	Ser	Asp	Ser	Tyr	Thr	Ile	Asp	Lys	Leu	Met	Gln	Val	Thr	
				305					310					315		
att	gct	tac	aac	cat	ttt	gga	gaa	gga	ttg	ggt	cag	aga	atg	cca	agg	1009
Ile	Ala	Tyr	Asn	His	Phe	Gly	Glu	Gly	Leu	Val	Gln	Arg	Met	Pro	Arg	
			320					325					330			
tgc	aga	cat	ggg	tat	ttc	cat	gtg	gtc	aac	aac	gac	tac	aca	cac	tgg	1057
Cys	Arg	His	Gly	Tyr	Phe	His	Val	Val	Asn	Asn	Asp	Tyr	Thr	His	Trp	
		335					340					345				
gag	atg	tac	gca	att	ggt	ggg	agt	gca	gat	cca	acc	ata	aac	agt	caa	1105
Glu	Met	Tyr	Ala	Ile	Gly	Gly	Ser	Ala	Asp	Pro	Thr	Ile	Asn	Ser	Gln	
	350					355					360					
gga	aac	aga	tat	gct	gct	cct	aag	aac	cct	ttc	gcc	aaa	gag	gtg	acg	1153
Gly	Asn	Arg	Tyr	Ala	Ala	Pro	Lys	Asn	Pro	Phe	Ala	Lys	Glu	Val	Thr	
365				370					375						380	
aaa	aga	gta	gag	aca	gat	gca	agt	gaa	tgg	cag	aag	tgg	aat	tgg	aga	1201
Lys	Arg	Val	Glu	Thr	Asp	Ala	Ser	Glu	Trp	Gln	Lys	Trp	Asn	Trp	Arg	
				385					390					395		
tca	gaa	gga	gat	ctg	cta	ctg	aat	gga	gca	ttc	ttc	aag	gca	tca	gga	1249
Ser	Glu	Gly	Asp	Leu	Leu	Leu	Asn	Gly	Ala	Phe	Phe	Lys	Ala	Ser	Gly	
			400					405					410			

PF59082SeqList_PF59082.txt

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gca gaa gcc tca gct agc tat gga cga gcc tca agc tta gca gct aaa 1297
Ala Glu Ala Ser Ala Ser Tyr Gly Arg Ala Ser Ser Leu Ala Ala Lys
      415      420      425
cca tca tca atg gtc cac acc ata acc tct act gca gga gca cta ggt 1345
Pro Ser Ser Met Val His Thr Ile Thr Ser Thr Ala Gly Ala Leu Gly
      430      435      440
tgc cgc aga ggc aga cct tgt tag ttctctctat accacccgta gtaactaacc 1399
Cys Arg Arg Gly Arg Pro Cys
      445      450
aaccctaaac cctttcccca tatctatgga aagtggaata tatagtagtc tttctgcttt 1459

ctcgtttcgt tgtggtcgta tcattgtttc ggcagatccc gctcagtttt cttacgggtg 1519

gtaggaattg gtcaacctca gcttgctttt tctttaaaaa tgggtgttggg ggaaacaaag 1579

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ctcactccct tgcgtctgta gtctttttgg gttttctctt tcaagttagt ggtcatagta 1759

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tgtcttttaa gaaaaaaaaa aaaaaa 1845

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<210> 1816
 <211> 451
 <212> PRT
 <213> Brassica napus

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<400> 1816
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Ser Ser Arg Lys Val Lys Thr Glu Glu Leu Gln Ser Ser Lys Asn Thr
      35      40      45
Ser Thr Met Ala Ala Asn Arg Leu Glu Gly Val Glu Leu Asn Glu Gln
      50      55      60
His Ala Val Asp Asp Pro Asp Lys Val Ala Asp Glu Val Ser Thr Leu
65      70      75      80
Val Gln Met Ser Glu His Asn Ile Thr Ala Arg Arg Lys Leu Gly Phe
      85      90      95
Phe Ser Cys Gly Thr Gly Asn Pro Ile Asp Asp Cys Trp Arg Cys Asp
      100      105      110
Arg Asn Trp His Lys Asn Arg Lys Arg Leu Ala Asp Cys Gly Ile Gly
      115      120      125
Phe Gly Arg Asn Ala Val Gly Gly Arg Asp Gly Arg Phe Tyr Val Val
      130      135      140
Thr Asp Pro Thr Asp Glu Asp Val Ile Asn Pro Lys Pro Gly Thr Leu
145      150      155      160
Arg His Ala Val Ile Gln Asp Glu Pro Leu Trp Ile Val Phe Lys Arg
      165      170      175
Asp Met Val Ile Glu Leu Lys Gln Glu Leu Ile Met Asn Ser Phe Lys
      180      185      190
Thr Ile Asp Gly Arg Gly Ala Asn Val His Ile Ala Asn Gly Ala Cys
      195      200      205
Ile Thr Leu Gln Phe Ile Thr Asn Val Ile Ile His Gly Leu His Ile
      210      215      220
His Asp Cys Lys Pro Thr Gly Asn Ala Met Val Arg Ser Ser Pro Ser

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PF59082SeqList_PF59082.txt

225 230 235 240
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Gln Ser Ser His Ile Trp Ile Asp His Asn Ser Leu Ser His Cys Ala
Asp Gly Leu Val Asp Ala Val Met Gly Ser Thr Ala Ile Thr Val Ser
Asn Asn His Phe Thr His His Asn Glu Val Met Leu Leu Gly His Ser
Asp Ser Tyr Thr Ile Asp Lys Leu Met Gln Val Thr Ile Ala Tyr Asn
His Phe Gly Glu Gly Leu Val Gln Arg Met Pro Arg Cys Arg His Gly
Tyr Phe His Val Val Asn Asn Asp Tyr Thr His Trp Glu Met Tyr Ala
Ile Gly Gly Ser Ala Asp Pro Thr Ile Asn Ser Gln Gly Asn Arg Tyr
Ala Ala Pro Lys Asn Pro Phe Ala Lys Glu Val Thr Lys Arg Val Glu
Thr Asp Ala Ser Glu Trp Gln Lys Trp Asn Trp Arg Ser Glu Gly Asp
Leu Leu Leu Asn Gly Ala Phe Phe Lys Ala Ser Gly Ala Glu Ala Ser
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<210> 1817
<211> 1559
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (37)..(1470)

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Ile Ile Leu Phe Ser Val Val Ala Ile Phe Leu Pro His Gly Thr Ala
10 15 20
atg ctc aac ctc act ctc cca gga caa cac cca gac cct gaa gcc gtt 150
Met Leu Asn Leu Thr Leu Pro Gly Gln His Pro Asp Pro Glu Ala Val
25 30 35
gct cga gaa gtt cat agg aaa gtg aat gct tca atg gca aga agg gaa 198
Ala Arg Glu Val His Arg Lys Val Asn Ala Ser Met Ala Arg Arg Glu
40 45 50
atg ctg gga gtg tca gag aaa gag gtg gca tca tgt cta aca ggg aat 246
Met Leu Gly Val Ser Glu Lys Glu Val Ala Ser Cys Leu Thr Gly Asn
55 60 65 70
ccc ata gat gat tgt tgg aaa tgt gac cca gat tgg gcc aac aac agg 294
Pro Ile Asp Asp Cys Trp Lys Cys Asp Pro Asp Trp Ala Asn Asn Arg
75 80 85
cag agg cta gca gat tgt gca ata ggg ttc ggg cag aac gca aag gga 342
Gln Arg Leu Ala Asp Cys Ala Ile Gly Phe Gly Gln Asn Ala Lys Gly
90 95 100
gga aaa ggt ggc caa ttt tac ata gtc act gat tcc tca gat gag gac 390
Gly Lys Gly Gly Gln Phe Tyr Ile Val Thr Asp Ser Ser Asp Glu Asp
105 110 115
cct gtg aac cca aaa cct gga aca ctt aga tat gca gtg ata cag aac 438
Pro Val Asn Pro Lys Pro Gly Thr Leu Arg Tyr Ala Val Ile Gln Asn
120 125 130
gag cca ctg tgg ata gtg ttc ccc agt aac atg atg att aag ctg tct 486
Glu Pro Leu Trp Ile Val Phe Pro Ser Asn Met Met Ile Lys Leu Ser

PF59082SeqList_PF59082.txt

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	gac	gtg	cac	att	gtg	ggt	gga	ggc	tcg	att	act	ctt	cag	tat	att	agc	582
	Asp	Val	His	Ile	Val	Gly	Gly	Gly	Cys	Ile	Thr	Leu	Gln	Tyr	Ile	Ser	
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	aat	gtc	att	att	cac	aac	att	cac	atc	cac	cat	tgc	cat	ccc	tct	ggc	630
	Asn	Val	Ile	Ile	His	Asn	Ile	His	Ile	His	His	Cys	His	Pro	Ser	Gly	
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	aac	gct	aac	gtg	cgg	tcg	agc	ccg	gaa	cat	tat	ggg	tac	cgc	acg	gag	678
	Asn	Ala	Asn	Val	Arg	Ser	Ser	Pro	Glu	His	Tyr	Gly	Tyr	Arg	Thr	Glu	
		200					205					210					
	tcg	gac	ggc	gac	ggg	atc	tcc	atc	ttc	ggc	tcg	cgt	gac	att	tgg	atc	726
	Ser	Asp	Gly	Asp	Gly	Ile	Ser	Ile	Phe	Gly	Ser	Arg	Asp	Ile	Trp	Ile	
		215				220					225					230	
	gac	cac	tgc	acc	ctc	tcc	cgg	tgc	aag	gac	ggc	ctg	atc	gat	gca	gtg	774
	Asp	His	Cys	Thr	Leu	Ser	Arg	Cys	Lys	Asp	Gly	Leu	Ile	Asp	Ala	Val	
				235					240					245			
	atg	ggt	tcc	agc	gct	atc	acg	atc	tcc	aac	cac	ttc	tcc	cac	cac	His	822
	Met	Gly	Ser	Ser	Ala	Ile	Thr	Ile	Ser	Asn	Asn	His	Phe	Ser	His	His	
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	aat	gac	gtg	atg	ctc	ctg	ggc	cac	agc	gac	cac	tac	ctc	cca	gac	tcc	870
	Asn	Asp	Val	Met	Leu	Leu	Gly	His	Ser	Asp	His	Tyr	Leu	Pro	Asp	Ser	
			265				270						275				
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	Gly	Met	Gln	Val	Thr	Ile	Gly	Phe	Asn	His	Phe	Gly	Glu	Gly	Leu	Val	
		280					285					290					
	cag	cgc	atg	ccg	cgt	tgc	cga	cga	ggt	tac	atc	cac	gtg	gtg	aac	aat	966
	Gln	Arg	Met	Pro	Arg	Cys	Arg	Arg	Gly	Tyr	Ile	His	Val	Val	Asn	Asn	
		295				300					305					310	
	gac	ttc	aca	cga	tgg	gag	atg	tac	gcc	atc	ggc	ggc	agt	gcg	gga	ccc	1014
	Asp	Phe	Thr	Arg	Trp	Glu	Met	Tyr	Ala	Ile	Gly	Gly	Ser	Ala	Gly	Pro	
				315					320					325			
	acc	att	aac	agc	cag	gga	aac	cgc	tac	acc	gcg	ccg	gag	gat	ccg	tac	1062
	Thr	Ile	Asn	Ser	Gln	Gly	Asn	Arg	Tyr	Thr	Ala	Pro	Glu	Asp	Pro	Tyr	
				330					335					340			
	gcg	aag	cag	ggt	acg	aag	agg	ctg	gat	gcc	gga	gaa	ggg	gag	tgg	agc	1110
	Ala	Lys	Gln	Val	Thr	Lys	Arg	Leu	Asp	Ala	Gly	Glu	Gly	Glu	Trp	Ser	
			345					350					355				
	ggg	tgg	aat	tgg	cgg	tcc	gaa	ggg	gat	ggt	ttg	ttg	aat	ggc	gcg	ttc	1158
	Gly	Trp	Asn	Trp	Arg	Ser	Glu	Gly	Asp	Val	Leu	Leu	Asn	Gly	Ala	Phe	
		360				365					370						
	ttc	ggt	gct	tcg	gga	gca	ggt	gct	gaa	cct	aac	tat	cag	aac	gcc	tac	1206
	Phe	Val	Ala	Ser	Gly	Ala	Val	Ala	Glu	Pro	Asn	Tyr	Gln	Asn	Ala	Tyr	
		375				380					385					390	
	agc	acc	caa	cct	aag	aac	gtg	gat	cgc	att	tcg	ctt	ctc	act	atg	tcc	1254
	Ser	Thr	Gln	Pro	Lys	Asn	Val	Asp	Arg	Ile	Ser	Leu	Leu	Thr	Met	Ser	
				395					400					405			
	gcc	ggt	ggt	ctc	ggc	ggt	gct	agg	gac	aat	ctg	gga	atg	tgg	atc		1302
	Ala	Gly	Val	Leu	Gly	Val	Ala	Arg	Asp	Asn	Asn	Leu	Gly	Met	Trp	Ile	
				410				415					420				
	aga	gga	ccc	aac	gat	ggc	act	gta	tat	ttt	tca	gat	tct	ggc	cca	gaa	1350
	Arg	Gly	Pro	Asn	Asp	Gly	Thr	Val	Tyr	Phe	Ser	Asp	Ser	Gly	Pro	Glu	
			425					430					435				
	tac	aca	gac	gaa	atg	tcc	cgg	agt	aca	atg	ccg	ttg	cta	cct	tca	cgt	1398
	Tyr	Thr	Asp	Glu	Met	Ser	Arg	Ser	Thr	Met	Pro	Leu	Leu	Pro	Ser	Arg	
		440				445						450					
	att	ttg	att	ctt	gta	tct	gca	ctc	tta	tgc	ttc	tta	ggt	cat	aca	aca	1446
	Ile	Leu	Ile	Leu	Val	Ser	Ala	Leu	Leu	Cys	Phe	Leu	Gly	His	Thr	Thr	
		455				460				465						470	
	acc	tta	aca	aca	cta	ccc	aat	tag	cgactt	caat	tcgat	gat	gc	ttcat	gtctc		1500
	Thr	Leu	Thr	Thr	Leu	Pro	Asn										
				475													
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PF59082SeqList_PF59082.txt

<211> 477

<212> PRT

<213> Glycine max

<400> 1818

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Pro Asp Pro Glu Ala Val Ala Arg Glu Val His Arg Lys Val Asn Ala
      35      40      45
Ser Met Ala Arg Arg Glu Met Leu Gly Val Ser Glu Lys Glu Val Ala
      50      55      60
Ser Cys Leu Thr Gly Asn Pro Ile Asp Asp Cys Trp Lys Cys Asp Pro
65      70      75      80
Asp Trp Ala Asn Asn Arg Gln Arg Leu Ala Asp Cys Ala Ile Gly Phe
      85      90      95
Gly Gln Asn Ala Lys Gly Gly Lys Gly Gly Gln Phe Tyr Ile Val Thr
      100      105      110
Asp Ser Ser Asp Glu Asp Pro Val Asn Pro Lys Pro Gly Thr Leu Arg
      115      120      125
Tyr Ala Val Ile Gln Asn Glu Pro Leu Trp Ile Val Phe Pro Ser Asn
      130      135      140
Met Met Ile Lys Leu Ser Gln Glu Leu Ile Phe Asn Ser Tyr Lys Thr
145      150      155      160
Ile Asp Gly Arg Gly Ala Asp Val His Ile Val Gly Gly Gly Cys Ile
      165      170      175
Thr Leu Gln Tyr Ile Ser Asn Val Ile Ile His Asn Ile His Ile His
      180      185      190
His Cys His Pro Ser Gly Asn Ala Asn Val Arg Ser Ser Pro Glu His
      195      200      205
Tyr Gly Tyr Arg Thr Glu Ser Asp Gly Asp Gly Ile Ser Ile Phe Gly
      210      215      220
Ser Arg Asp Ile Trp Ile Asp His Cys Thr Leu Ser Arg Cys Lys Asp
225      230      235      240
Gly Leu Ile Asp Ala Val Met Gly Ser Ser Ala Ile Thr Ile Ser Asn
      245      250      255
Asn His Phe Ser His His Asn Asp Val Met Leu Leu Gly His Ser Asp
      260      265      270
His Tyr Leu Pro Asp Ser Gly Met Gln Val Thr Ile Gly Phe Asn His
      275      280      285
Phe Gly Glu Gly Leu Val Gln Arg Met Pro Arg Cys Arg Arg Gly Tyr
      290      295      300
Ile His Val Val Asn Asn Asp Phe Thr Arg Trp Glu Met Tyr Ala Ile
305      310      315      320
Gly Gly Ser Ala Gly Pro Thr Ile Asn Ser Gln Gly Asn Arg Tyr Thr
      325      330      335
Ala Pro Glu Asp Pro Tyr Ala Lys Gln Val Thr Lys Arg Leu Asp Ala
      340      345      350
Gly Glu Gly Glu Trp Ser Gly Trp Asn Trp Arg Ser Glu Gly Asp Val
      355      360      365
Leu Leu Asn Gly Ala Phe Phe Val Ala Ser Gly Ala Val Ala Glu Pro
      370      375      380
Asn Tyr Gln Asn Ala Tyr Ser Thr Gln Pro Lys Asn Val Asp Arg Ile
385      390      395      400
Ser Leu Leu Thr Met Ser Ala Gly Val Leu Gly Val Ala Arg Asp Asn
      405      410      415
Asn Leu Gly Met Trp Ile Arg Gly Pro Asn Asp Gly Thr Val Tyr Phe
      420      425      430
Ser Asp Ser Gly Pro Glu Tyr Thr Asp Glu Met Ser Arg Ser Thr Met
      435      440      445
Pro Leu Leu Pro Ser Arg Ile Leu Ile Leu Val Ser Ala Leu Leu Cys
      450      455      460
Phe Leu Gly His Thr Thr Thr Leu Thr Thr Leu Pro Asn
465      470      475

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<210> 1819

<211> 1806

<212> DNA

PF59082SeqList_PF59082.txt

<213> Brassica napus

<220>

<221> CDS

<222> (62)..(1357)

<400> 1819

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a atg gtg gtt ctt ccg aca tgg att tta gct atg ata tgt cta ctc ttc	109
Met Val Val Leu Pro Thr Trp Ile Leu Ala Met Ile Cys Leu Leu Phe	
1 5 10 15	
ttc gtg gga gca atg gac aac agt aca cac gac aag atc tca tct cta	157
Phe Val Gly Ala Met Asp Asn Ser Thr His Asp Lys Ile Ser Ser Leu	
20 25 30	
tcc aga tcg gac gaa atc gaa tgg aac aag cat gca gtg acg aat ccg	205
Ser Arg Ser Asp Glu Ile Glu Trp Asn Lys His Ala Val Thr Asn Pro	
35 40 45	
gat gaa gta gct gac gaa gtt atc gcc ttg gct gaa atg agt gta aga	253
Asp Glu Val Ala Asp Glu Val Ile Ala Leu Ala Glu Met Ser Val Arg	
50 55 60	
aat cat acc gag agg agg aag cta ggt tac ttt act tgc gga aca ggc	301
Asn His Thr Glu Arg Arg Lys Leu Gly Tyr Phe Thr Cys Gly Thr Gly	
65 70 75 80	
aac cca atc gac gat tgc tgg cga tgc gat cgc aac tgg cac aag aac	349
Asn Pro Ile Asp Asp Cys Trp Arg Cys Asp Arg Asn Trp His Lys Asn	
85 90 95	
cgc aaa cgc cta gcg gac tgt ggt atc gga ttt gga aga aac gcg att	397
Arg Lys Arg Leu Ala Asp Cys Gly Ile Gly Phe Gly Arg Asn Ala Ile	
100 105 110	
ggc ggt cgc gac ggg cgt ttc tac gta gtc act gac cca aga gac gac	445
Gly Gly Arg Asp Gly Arg Phe Tyr Val Val Thr Asp Pro Arg Asp Asp	
115 120 125	
aac ccg gtt aac cct aga ccg gga aca tta cgt cac gcc gtg acc caa	493
Asn Pro Val Asn Pro Arg Pro Gly Thr Leu Arg His Ala Val Thr Gln	
130 135 140	
gac cga cca cta tgg atc gtc ttt aaa cgt gac atg gtg att cag tta	541
Asp Arg Pro Leu Trp Ile Val Phe Lys Arg Asp Met Val Ile Gln Leu	
145 150 155 160	
aaa caa gag cta atc gta aac agt ttc aaa acg atc gac gga cgt ggc	589
Lys Gln Glu Leu Ile Val Asn Ser Phe Lys Thr Ile Asp Gly Arg Gly	
165 170 175	
gca aac gtt cac atc gct aac ggc ggt tgc atc acg att cag tac gtg	637
Ala Asn Val His Ile Ala Asn Gly Gly Cys Ile Thr Ile Gln Tyr Val	
180 185 190	
acg aac gtc atc gtg cat gga ttg cat att cat gat tgt aaa ccg acg	685
Thr Asn Val Ile Val His Gly Leu His Ile His Asp Cys Lys Pro Thr	
195 200 205	
ggt aac gct atg gtt aga agc tca gag acg cac ttt ggg tgg aga acg	733
Gly Asn Ala Met Val Arg Ser Ser Glu Thr His Phe Gly Trp Arg Thr	
210 215 220	
atg gct gat ggt gac gcc att tcc atc ttt ggt tcg agt cat gtt tgg	781
Met Ala Asp Gly Asp Ala Ile Ser Ile Phe Gly Ser Ser His Val Trp	
225 230 235 240	
att gat cac aac tcg ttg tct cat tgc gct gat ggg ctt gtg gat gct	829
Ile Asp His Asn Ser Leu Ser His Cys Ala Asp Gly Leu Val Asp Ala	
245 250 255	
atc atg ggc tcc acc gcg att acg atc tct aac aac cac atg act cac	877
Ile Met Gly Ser Thr Ala Ile Thr Ile Ser Asn Asn His Met Thr His	
260 265 270	
cac aac gag gtt atg ttg ctc gga cat agt gat tct tac acg agg gac	925
His Asn Glu Val Met Leu Leu Gly His Ser Asp Ser Tyr Thr Arg Asp	
275 280 285	
aaa gct atg caa gtt acc att gct tat aac cat ttt gga gtc gga ctt	973
Lys Ala Met Gln Val Thr Ile Ala Tyr Asn His Phe Gly Val Gly Leu	
290 295 300	
att caa aga atg cca agg tgt cgg cat ggg tac ttc cat gtc gtg aac	1021
Ile Gln Arg Met Pro Arg Cys Arg His Gly Tyr Phe His Val Val Asn	

PF59082SeqList_PF59082.txt

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305          310          315          320
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Asn Asp Tyr Thr His Trp Glu Met Tyr Ala Ile Gly Gly Ser Ala Asn
          325          330          335
cca aca atc aac agt caa gga aac cgc tac gcc gcc cct aaa aat cct      1117
Pro Thr Ile Asn Ser Gln Gly Asn Arg Tyr Ala Ala Pro Lys Asn Pro
          340          345          350
ttt gcc aaa gag gta acg aag aga gtg aac aca cct acg ggt cat tgg      1165
Phe Ala Lys Glu Val Thr Lys Arg Val Asn Thr Pro Thr Gly His Trp
          355          360          365
aaa gga tgg aac tgg aga acc gaa gga gat ttg ctt cag aac gga gct      1213
Lys Gly Trp Asn Trp Arg Thr Glu Gly Asp Leu Leu Gln Asn Gly Ala
          370          375          380
tac ttc act gct tcg gga gtc gct gca tct ggt agc tac gca cgt gcc      1261
Tyr Phe Thr Ala Ser Gly Val Ala Ala Ser Gly Ser Tyr Ala Arg Ala
          385          390          395
tct agc ctc gcc gct aaa tct tct tca ttg gtc gat aca att act tct      1309
Ser Ser Leu Ala Ala Lys Ser Ser Ser Leu Val Asp Thr Ile Thr Ser
          405          410          415
gac gct gga gct cta cca tgt cgc cga gga cgt caa tgt acc tca tag      1357
Asp Ala Gly Ala Leu Pro Cys Arg Arg Gly Arg Gln Cys Thr Ser
          420          425          430
ttgttttttaa cctcctaccg acaccataac caccaaaatt cataaccatt ttctattata      1417

tttagacaaa agtgtacatt ctcacacatt tgtcaattaa aagcctattg tctcttcttt      1477

ttttcgtctg tgtttgtgtc aatttttcaa cctcggggttt tcttgcttca accgcaagtt      1537

aacacaagaa aaggaaataa aaaaactttt catgtaaaag agaaactccc gaagtgttgt      1597

tggttctgtc tgatcaactc gtatacccag aaaaaaacia gaatgttaat gtcttgtttt      1657

ttctttttgtg tgttcttctg gtttataatt aaatataatg tctaattgatt tgtgaatctt      1717

tctacttgtc tttgtaatag agtgttctaataaagtgtaat atagtggtcta ataaaagttt      1777

atagctttga tagcaaaaaa aaaaaaaaaa                                     1806

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<210> 1820
 <211> 431
 <212> PRT
 <213> Brassica napus

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Phe Val Gly Ala Met Asp Asn Ser Thr His Asp Lys Ile Ser Ser Leu
          20          25          30
Ser Arg Ser Asp Glu Ile Glu Trp Asn Lys His Ala Val Thr Asn Pro
          35          40          45
Asp Glu Val Ala Asp Glu Val Ile Ala Leu Ala Glu Met Ser Val Arg
          50          55          60
Asn His Thr Glu Arg Arg Lys Leu Gly Tyr Phe Thr Cys Gly Thr Gly
65          70          75          80
Asn Pro Ile Asp Asp Cys Trp Arg Cys Asp Arg Asn Trp His Lys Asn
          85          90          95
Arg Lys Arg Leu Ala Asp Cys Gly Ile Gly Phe Gly Arg Asn Ala Ile
          100          105          110
Gly Gly Arg Asp Gly Arg Phe Tyr Val Val Thr Asp Pro Arg Asp Asp
          115          120          125

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PF59082SeqList_PF59082.txt

Asn Pro Val Asn Pro Arg Pro Gly Thr Leu Arg His Ala Val Thr Gln
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 Asp Arg Pro Leu Trp Ile Val Phe Lys Arg Asp Met Val Ile Gln Leu
 145 150 155 160
 Lys Gln Glu Leu Ile Val Asn Ser Phe Lys Thr Ile Asp Gly Arg Gly
 165 170 175
 Ala Asn Val His Ile Ala Asn Gly Gly Cys Ile Thr Ile Gln Tyr Val
 180 185 190
 Thr Asn Val Ile Val His Gly Leu His Ile His Asp Cys Lys Pro Thr
 195 200 205
 Gly Asn Val Met Val Arg Ser Glu Thr His Phe Gly Trp Arg Thr
 210 215 220
 Met Ala Asp Gly Asp Ala Ile Ser Ile Phe Gly Ser Ser His Val Trp
 225 230 235 240
 Ile Asp His Asn Ser Leu Ser His Cys Ala Asp Gly Leu Val Asp Ala
 245 250 255
 Ile Met Gly Ser Thr Ala Ile Thr Ile Ser Asn Asn His Met Thr His
 260 265 270
 His Asn Glu Val Met Leu Leu Gly His Ser Asp Ser Tyr Thr Arg Asp
 275 280 285
 Lys Ala Met Gln Val Thr Ile Ala Tyr Asn His Phe Gly Val Gly Leu
 290 295 300
 Ile Gln Arg Met Pro Arg Cys Arg His Gly Tyr Phe His Val Val Asn
 305 310 315 320
 Asn Asp Tyr Thr His Trp Glu Met Tyr Ala Ile Gly Gly Ser Ala Asn
 325 330 335
 Pro Thr Ile Asn Ser Gln Gly Asn Arg Tyr Ala Ala Pro Lys Asn Pro
 340 345 350
 Phe Ala Lys Glu Val Thr Lys Arg Val Asn Thr Pro Thr Gly His Trp
 355 360 365
 Lys Gly Trp Asn Trp Arg Thr Glu Gly Asp Leu Leu Gln Asn Gly Ala
 370 375 380
 Tyr Phe Thr Ala Ser Gly Val Ala Ala Ser Gly Ser Tyr Ala Arg Ala
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 Ser Ser Leu Ala Ala Lys Ser Ser Ser Leu Val Asp Thr Ile Thr Ser
 405 410 415
 Asp Ala Gly Ala Leu Pro Cys Arg Arg Gly Arg Gln Cys Thr Ser
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<210> 1821
 <211> 1498
 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (59)..(1297)

<400> 1821
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58

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 Met Ala Thr Thr Gln Val Leu Val Leu Phe Ala Ser Ala Leu Leu Leu
 1 5 10 15
 aca atg ctc ttt gct ggc gtc gat tcc acc agg tcc aat gaa aca tgg
 Thr Met Leu Phe Ala Gly Val Asp Ser Thr Arg Ser Asn Glu Thr Trp
 20 25 30
 cat gaa cat gca gtt gag aat cca gac gaa gta gct gcc atg gtg gac
 His Glu His Ala Val Glu Asn Pro Asp Glu Val Ala Ala Met Val Asp
 35 40 45
 att acc atg cgg aga agg tta ggt tac ttc tct tgc tcc acc ggt aac
 Ile Thr Met Arg Arg Arg Leu Gly Tyr Phe Ser Cys Ser Thr Gly Asn
 50 55 60
 ccc atc gac gat tgc tgg cgt tgt gac cgg aaa tgg caa ctc cgg cga
 Pro Ile Asp Asp Cys Trp Arg Cys Asp Arg Lys Trp Gln Leu Arg Arg
 65 70 75 80
 aaa cac cta gcc gtc tgc gca atc gga ttc gga cgc aac gca ata ggc
 Lys His Leu Ala Val Cys Ala Ile Gly Phe Gly Arg Asn Ala Ile Gly
 85 90 95 100

106

154

202

250

298

346

PF59082SeqList_PF59082.txt

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ccg gtt aac cct aaa ccg ggt aca ctc cgt cac gcc gtg atc caa gtc	Pro Val Asn Pro Lys Pro Gly Thr Leu Arg His Ala Val Ile Gln Val	442		
gag cct ctt tgg atc gtc ttc aaa cgc gac atg gtc ata aca ctg aag	Glu Pro Leu Trp Ile Val Phe Lys Arg Asp Met Val Ile Thr Leu Lys	490		
caa gaa ctc atc atg aac agc ttc aag acg ata gat ggt cgt ggc gtc	Gln Glu Leu Ile Met Asn Ser Phe Lys Thr Ile Asp Gly Arg Gly Val	538		
aac gtc cac ata gct aac ggt gca tgc atc acg ata cag tac gtg acg	Asn Val His Ile Ala Asn Gly Ala Cys Ile Thr Ile Gln Tyr Val Thr	586		
aac att atc ata cat ggg att cat att cat gac tgt aaa cct act ggt	Asn Ile Ile Ile His Gly Ile His Ile His Asp Cys Lys Pro Thr Gly	634		
aag gct atg gtg aga agc tct ccg tcg cat tat ggg tgg agg acg atg	Lys Ala Met Val Arg Ser Ser Pro Ser His Tyr Gly Trp Arg Thr Met	682		
gct gac ggt gat ggg atc tcg atc ttt ggg tct agt cat att tgg att	Ala Asp Gly Asp Gly Ile Ser Ile Phe Gly Ser Ser His Ile Trp Ile	730		
gat cac aac tcg ctc tct agt tgc gct gat ggg ctc att gat gct gtt	Asp His Asn Ser Leu Ser Ser Cys Ala Asp Gly Leu Ile Asp Ala Val	778		
atg gct tcc acc gct att act atc tct aac aat tac ttt acg cac cat	Met Ala Ser Thr Ala Ile Thr Ile Ser Asn Tyr Phe Thr His His	826		
aac gag gtt atg ttg ttg gga cat agt gat act tac aca agg gac aag	Asn Glu Val Met Leu Leu Gly His Ser Asp Thr Tyr Thr Arg Asp Lys	874		
gtg atg cag gtt act att gct tat aac cat ttt ggt aga ggt ctt atc	Val Met Gln Val Thr Ile Ala Tyr Asn His Phe Gly Arg Gly Leu Ile	922		
cag agg atg cca agg tgt agg cat gga tac ttc cat gta gta aac aat	Gln Arg Met Pro Arg Cys Arg His Gly Tyr Phe His Val Val Asn Asn	970		
gac tac aca cat tgg gaa atg tat gca att ggt ggc agt gca agt ccc	Asp Tyr Thr His Trp Glu Met Tyr Ala Ile Gly Gly Ser Ala Ser Pro	1018		
acc atc aat agt caa gga aac aga tat ctt gcc cct aga aac cgc ttt	Thr Ile Asn Ser Gln Gly Asn Arg Tyr Leu Ala Pro Arg Asn Arg Phe	1066		
gct aaa gag gtg aca aag aga gac tat gca gga cac tgg caa tgg aag	Ala Lys Glu Val Thr Lys Arg Asp Tyr Ala Gly His Trp Gln Trp Lys	1114		
cat tgg aac tgg aga tca gaa gga gat ctt ttc cta aac ggt gct ttc	His Trp Asn Trp Arg Ser Glu Gly Asp Leu Phe Leu Asn Gly Ala Phe	1162		
ttc aca cgt tct ggt tca gga cgt gga gct agc tac gct aga gct tca	Phe Thr Arg Ser Gly Ser Gly Arg Gly Ala Ser Tyr Ala Arg Ala Ser	1210		
agt ttg gca gcc aaa tcg tca tcc ctt gtt ggc gtc att acc tct aat	Ser Leu Ala Ala Lys Ser Ser Ser Leu Val Gly Val Ile Thr Ser Asn	1258		
gct ggc gct ctt aat tgc aga ggt ggt cgc tgt taa tacttgctca	Ala Gly Ala Leu Asn Cys Arg Gly Gly Arg Cys	1307		
ttagtcctttc ttttggttc ttgcatttta tacatggcaa tagcactatt ggagtgttga		1367		
ggcttgatta aaaactgcct caactgtagt gtaaattgttg gatgattaca ttcttgtttt		1427		
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1498

<210> 1822
 <211> 412
 <212> PRT
 <213> Brassica napus

<400> 1822
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 35 40 45
 Ile Thr Met Arg Arg Arg Leu Gly Tyr Phe Ser Cys Ser Thr Gly Asn
 50 55 60
 Pro Ile Asp Asp Cys Trp Arg Cys Asp Arg Lys Trp Gln Leu Arg Arg
 65 70 75 80
 Lys His Leu Ala Val Cys Ala Ile Gly Phe Gly Arg Asn Ala Ile Gly
 85 90 95
 Gly Arg Asp Gly Arg Tyr Tyr Val Val Ser Asp Pro Asn Asp Asp Asn
 100 105 110
 Pro Val Asn Pro Lys Pro Gly Thr Leu Arg His Ala Val Ile Gln Val
 115 120 125
 Glu Pro Leu Trp Ile Val Phe Lys Arg Asp Met Val Ile Thr Leu Lys
 130 135 140
 Gln Glu Leu Ile Met Asn Ser Phe Lys Thr Ile Asp Gly Arg Gly Val
 145 150 155 160
 Asn Val His Ile Ala Asn Gly Ala Cys Ile Thr Ile Gln Tyr Val Thr
 165 170 175
 Asn Ile Ile Ile His Gly Ile His Ile His Asp Cys Lys Pro Thr Gly
 180 185 190
 Lys Ala Met Val Arg Ser Ser Pro Ser His Tyr Gly Trp Arg Thr Met
 195 200 205
 Ala Asp Gly Asp Gly Ile Ser Ile Phe Gly Ser Ser His Ile Trp Ile
 210 215 220
 Asp His Asn Ser Leu Ser Cys Ala Asp Gly Leu Ile Asp Ala Val
 225 230 235 240
 Met Ala Ser Thr Ala Ile Thr Ile Ser Asn Asn Tyr Phe Thr His His
 245 250 255
 Asn Glu Val Met Leu Leu Gly His Ser Asp Thr Tyr Thr Arg Asp Lys
 260 265 270
 Val Met Gln Val Thr Ile Ala Tyr Asn His Phe Gly Arg Gly Leu Ile
 275 280 285
 Gln Arg Met Pro Arg Cys Arg His Gly Tyr Phe His Val Val Asn Asn
 290 295 300
 Asp Tyr Thr His Trp Glu Met Tyr Ala Ile Gly Gly Ser Ala Ser Pro
 305 310 315 320
 Thr Ile Asn Ser Gln Gly Asn Arg Tyr Leu Ala Pro Arg Asn Arg Phe
 325 330 335
 Ala Lys Glu Val Thr Lys Arg Asp Tyr Ala Gly His Trp Gln Trp Lys
 340 345 350
 His Trp Asn Trp Arg Ser Glu Gly Asp Leu Phe Leu Asn Gly Ala Phe
 355 360 365
 Phe Thr Arg Ser Gly Ser Gly Arg Gly Ala Ser Tyr Ala Arg Ala Ser
 370 375 380
 Ser Leu Ala Ala Lys Ser Ser Leu Val Gly Val Ile Thr Ser Asn
 385 390 395 400
 Ala Gly Ala Leu Asn Cys Arg Gly Gly Arg Arg Cys
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<210> 1823
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 <212> DNA
 <213> Brassica napus

PF59082SeqList_PF59082.txt

<220>

<221> CDS

<222> (53)..(1429)

<400> 1823

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Ala Ala Val Leu Asn Ile Gly Gly Tyr Leu Phe Val Phe Cys Leu Ser	
	5 10 15
tta tta gca aca ttg act cca cac gtt gga gcc aat gtt gct gtc ttc	154
Leu Leu Ala Thr Leu Thr Pro His Val Gly Ala Asn Val Ala Val Phe	
	20 25 30
gac aat tac tgg tta caa cgt caa ggc gat gcg ttg aaa caa acc att	202
Asp Asn Tyr Trp Leu Gln Arg Gln Gly Asp Ala Leu Lys Gln Thr Ile	
	35 40 45 50
gcc tct ttc gat cct aat cct ctt aac gtc acc gac cat ttg aat tac	250
Ala Ser Phe Asp Pro Asn Pro Leu Asn Val Thr Asp His Leu Asn Tyr	
	55 60 65
cat gtc gct tta gcc gtg gac gcc acg gaa tca acc aac agc aca agg	298
His Val Ala Leu Ala Val Asp Ala Thr Glu Ser Thr Asn Ser Thr Arg	
	70 75 80
aga gag ctc tca cag gtg aga aat ggt cgg aaa cta aag aga agc gga	346
Arg Glu Leu Ser Gln Val Arg Asn Gly Arg Lys Leu Lys Arg Ser Gly	
	85 90 95
aaa tgc gta gcg tac aac cct ata gac aga tgc tgg cga tgc aac ggt	394
Lys Cys Val Ala Tyr Asn Pro Ile Asp Arg Cys Trp Arg Cys Asn Gly	
	100 105 110
gac tgg gag aag aac cgt aag aaa cta gcg gat tgt gta ctc ggg ttc	442
Asp Trp Glu Lys Asn Arg Lys Lys Leu Ala Asp Cys Val Leu Gly Phe	
	115 120 125 130
ggc agg aga acc acc gga ggc aaa gac gga cct atc tac gtc gtc aac	490
Gly Arg Arg Thr Thr Gly Gly Lys Asp Gly Pro Ile Tyr Val Val Asn	
	135 140 145
gac gcc tcc gat gac gat ctt atc aac cct aag cca gga acg tta agg	538
Asp Ala Ser Asp Asp Asp Leu Ile Asn Pro Lys Pro Gly Thr Leu Arg	
	150 155 160
cac gcg gtg aca aga gac gga ccg ctt tgg atc ata ttc gga agc agc	586
His Ala Val Thr Arg Asp Gly Pro Leu Trp Ile Ile Phe Gly Ser Ser	
	165 170 175
atg atc ata aac ttg caa caa gaa ctg atc ata acg agc gat aaa aca	634
Met Ile Ile Asn Leu Gln Gln Glu Leu Ile Ile Thr Ser Asp Lys Thr	
	180 185 190
ata gat gga cgt gga gct agg gtt tac atc atg gaa gga gct gga tta	682
Ile Asp Gly Arg Gly Ala Arg Val Tyr Ile Met Glu Gly Ala Gly Leu	
	195 200 205 210
acg ctg cag ttt gtg aac aat gtg atc ata cac aat att tat gtc aag	730
Thr Leu Gln Phe Val Asn Asn Val Ile Ile His Asn Ile Tyr Val Lys	
	215 220 225
cac gtt gtt cct aag agc ggt ggt ttg atc aga gac tct gag cag cat	778
His Val Val Pro Lys Ser Gly Gly Leu Ile Arg Asp Ser Glu Gln His	
	230 235 240
ata ggg ctt agg acg gta agc gat ggt gat gga atc agt ttg ttt ggt	826
Ile Gly Leu Arg Thr Val Ser Asp Gly Asp Gly Ile Ser Leu Phe Gly	
	245 250 255
gca acg aat gtt tgg atc gat cat gtc tcg atg act aga tgt tca gat	874
Ala Thr Asn Val Trp Ile Asp His Val Ser Met Thr Arg Cys Ser Asp	
	260 265 270
ggt atg att gat gcg att ctt ggc tcc act gct ata act att tcc aac	922
Gly Met Ile Asp Ala Ile Leu Gly Ser Thr Ala Ile Thr Ile Ser Asn	
	275 280 285 290
agc cat ttc acc gac cat gaa gag gtg atg cta ttt ggg gcc aat gac	970
Ser His Phe Thr Asp His Glu Glu Val Met Leu Phe Gly Ala Asn Asp	
	295 300 305
aag cac gtg atc gac aag aaa atg cag ata acg gtt gcg ttc aac cac	1018
Lys His Val Ile Asp Lys Lys Met Gln Ile Thr Val Ala Phe Asn His	
	310 315 320
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PF59082SeqList_PF59082.txt

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		325					330					335					
atc	cat	gtg	gtg	aac	aat	gac	tac	aca	cat	tgg	gag	atg	tac	aca	att		1114
Ile	His	Val	Val	Asn	Asn	Asp	Tyr	Thr	His	Trp	Glu	Met	Tyr	Thr	Ile		
		340				345					350						
ggt	gga	aac	atg	aac	cct	aca	atc	att	agc	caa	ggc	aac	cgt	ttc	att		1162
Gly	Gly	Asn	Met	Asn	Pro	Thr	Ile	Ile	Ser	Gln	Gly	Asn	Arg	Phe	Ile		
		355			360					365					370		
gct	cct	cct	aac	gaa	caa	gcc	aaa	cag	att	aca	aag	aga	gag	tac	aca		1210
Ala	Pro	Pro	Asn	Glu	Gln	Ala	Lys	Gln	Ile	Thr	Lys	Arg	Glu	Tyr	Thr		
				375				380						385			
cct	tac	gtt	aac	tgg	aaa	atg	tgg	aac	tgg	caa	tca	gaa	gga	gat	tac		1258
Pro	Tyr	Val	Asn	Trp	Lys	Met	Trp	Asn	Trp	Gln	Ser	Glu	Gly	Asp	Tyr		
			390				395						400				
ttc	ttg	aat	gga	gct	tac	ttt	gtg	caa	tcc	gga	aaa	caa	aat	gca	tgg		1306
Phe	Leu	Asn	Gly	Ala	Tyr	Phe	Val	Gln	Ser	Gly	Lys	Gln	Asn	Ala	Trp		
		405				410						415					
agc	cct	aaa	ccg	att	aac	cct	gtc	ccg	aaa	aag	ttt	gcc	ata	cga	cct		1354
Ser	Pro	Lys	Pro	Ile	Asn	Pro	Val	Pro	Lys	Lys	Phe	Ala	Ile	Arg	Pro		
		420				425					430						
caa	ccg	gga	act	atg	gtc	cgt	aaa	ctc	acc	atg	gac	gca	gga	gca	ctt		1402
Gln	Pro	Gly	Thr	Met	Val	Arg	Lys	Leu	Thr	Met	Asp	Ala	Gly	Ala	Leu		
		435			440					445					450		
ggc	tgc	aag	ccg	ggt	aca	ccc	tgc	tga	ttaaa	actac	catttt	gtcc					1449
Gly	Cys	Lys	Pro	Gly	Thr	Pro	Cys										
			455														
ccttccagcc	aaaaaaaaag	cttatgcttt	gtagttgctt	gtcgtccaag	aaaagagaga												1509
aagtaagcag	aagggagtgt	ttcctatgag	tggggttaat	tattcttttt	agaattcagg												1569
ttcacgacac	gcag																1583

<210> 1824
 <211> 458
 <212> PRT
 <213> Brassica napus

<400> 1824

Met	Thr	Ala	Ala	Val	Leu	Asn	Ile	Gly	Gly	Tyr	Leu	Phe	Val	Phe	Cys
1				5					10					15	
Leu	Ser	Leu	Leu	Ala	Thr	Leu	Thr	Pro	His	Val	Gly	Ala	Asn	Val	Ala
			20					25					30		
Val	Phe	Asp	Asn	Tyr	Trp	Leu	Gln	Arg	Gln	Gly	Asp	Ala	Leu	Lys	Gln
		35				40						45			
Thr	Ile	Ala	Ser	Phe	Asp	Pro	Asn	Pro	Leu	Asn	Val	Thr	Asp	His	Leu
	50					55					60				
Asn	Tyr	His	Val	Ala	Leu	Ala	Val	Asp	Ala	Thr	Glu	Ser	Thr	Asn	Ser
65					70				75					80	
Thr	Arg	Arg	Glu	Leu	Ser	Gln	Val	Arg	Asn	Gly	Arg	Lys	Leu	Lys	Arg
			85					90					95		
Ser	Gly	Lys	Cys	Val	Ala	Tyr	Asn	Pro	Ile	Asp	Arg	Cys	Trp	Arg	Cys
			100					105					110		
Asn	Gly	Asp	Trp	Glu	Lys	Asn	Arg	Lys	Lys	Leu	Ala	Asp	Cys	Val	Leu
		115					120					125			
Gly	Phe	Gly	Arg	Arg	Thr	Thr	Gly	Gly	Lys	Asp	Gly	Pro	Ile	Tyr	Val
	130					135					140				
Val	Asn	Asp	Ala	Ser	Asp	Asp	Asp	Leu	Ile	Asn	Pro	Lys	Pro	Gly	Thr
145					150					155				160	
Leu	Arg	His	Ala	Val	Thr	Arg	Asp	Gly	Pro	Leu	Trp	Ile	Ile	Phe	Gly
			165					170						175	
Ser	Ser	Met	Ile	Asn	Leu	Gln	Gln	Glu	Leu	Ile	Ile	Thr	Ser	Asp	
			180				185					190			
Lys	Thr	Ile	Asp	Gly	Arg	Gly	Ala	Arg	Val	Tyr	Ile	Met	Glu	Gly	Ala
		195					200					205			
Gly	Leu	Thr	Leu	Gln	Phe	Val	Asn	Asn	Val	Ile	Ile	His	Asn	Ile	Tyr

PF59082SeqList_PF59082.txt

210 215 220
Val Lys His Val Val Pro Lys Ser Gly Gly Leu Ile Arg Asp Ser Glu
225 Gln His Ile Gly Leu 230 Arg Thr Val Ser Asp Gly Asp Gly Ile Ser 240
Phe Gly Ala Thr 245 Val Trp Ile Asp 250 Val Ser Met Thr Arg Cys
Ser Asp Gly Met Ile Asp Ala Ile Leu Gly Ser Thr Ala Ile Thr Ile
Ser Asn Ser His Phe Thr Asp 280 His Glu Glu Val Met Leu Phe Gly Ala
Asn Asp Lys His Val Ile Asp Lys Lys Met Gln Ile Thr Val Ala Phe
305 Asn His Phe Gly Lys Arg Leu Asp Gln Arg Met Pro Arg Cys Arg Phe
Gly Thr Ile His 325 Val Asn Asn Asp Tyr Thr His Trp Glu Met Tyr
Thr Ile Gly Gly Asn Met Asn Pro Thr Ile Ile Ser Gln Gly Asn Arg
Phe Ile Ala Pro Pro Asn Glu Gln Ala Lys Gln Ile Thr Lys Arg Glu
Tyr Thr Pro Tyr Val Asn Trp Lys Met Trp Asn Trp Gln Ser Glu Gly
385 Asp Tyr Phe Leu Asn Gly Ala Tyr Phe Val Gln Ser Gly Lys Gln Asn
Ala Trp Ser Pro Lys Pro Ile Asn Pro Val Pro Lys Lys Phe Ala Ile
Arg Pro Gln Pro Gly Thr Met Val Arg Lys Leu Thr Met Asp Ala Gly
Ala Leu Gly Cys Lys Pro Gly Thr Pro Cys
450 455

<210> 1825
<211> 1617
<212> DNA
<213> Brassica napus

<220>
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<222> (51)..(1271)

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Met Thr Lys Leu Phe Ile Ser Ile Val Ser Phe Leu Leu Tyr Ala His
5 10 15
ttg atc tta tct tca cca gta cca gac cca gaa gct atc gtc gaa gaa 152
Leu Ile Leu Ser Ser Pro Val Pro Asp Pro Glu Ala Ile Val Glu Glu
20 25 30
gtt cac aag agc att aat gcg tcg gtt gct gga aga agg aag cta ggt 200
Val His Lys Ser Ile Asn Ala Ser Val Ala Gly Arg Arg Lys Leu Gly
35 40 45 50
tac ctc tca tgc acc act ggt aac ccc atc gac gac tgt tgg cga tgc 248
Tyr Leu Ser Cys Thr Thr Gly Asn Pro Ile Asp Asp Cys Trp Arg Cys
55 60 65
gat cca cac tgg gag acc aac cgt caa cgt ctc gca gac tgc gcc ata 296
Asp Pro His Trp Glu Thr Asn Arg Gln Arg Leu Ala Asp Cys Ala Ile
70 75 80
ggg ttc ggc aag aac gct ata ggt ggc cga gat ggt cgt atc tac gtg 344
Gly Phe Gly Lys Asn Ala Ile Gly Gly Arg Asp Gly Arg Ile Tyr Val
85 90 95
gtg aca gac tca gga aac gac gac cca gtg acc ccc aaa ccc gga acg 392
Val Thr Asp Ser Gly Asn Asp Asp Pro Val Thr Pro Lys Pro Gly Thr
100 105 110
tta aga tac gct gtg gtt caa gac gag cca cta tgg atc att ttc caa 440
Leu Arg Tyr Ala Val Val Gln Asp Glu Pro Leu Trp Ile Ile Phe Gln
115 120 125 130

PF59082SeqList_PF59082.txt

cga gac atg acc att cag ctc aaa gaa gag ctg atc atg aac tct ttc	488
Arg Asp Met Thr Ile Gln Leu Lys Glu Glu Leu Ile Met Asn Ser Phe	
135 140 145	
aag acc ata gac ggt cgt ggc gcg tca gta cac ata gct ggt ggg cca	536
Lys Thr Ile Asp Gly Arg Gly Ala Ser Val His Ile Ala Gly Gly Pro	
150 155 160	
tgc att acg atc cag tac gtg act aac atc atc atc cat ggt atc cat	584
Cys Ile Thr Ile Gln Tyr Val Thr Asn Ile Ile Ile His Gly Ile His	
165 170 175	
atc cat gat tgt aag cca ggt ggt aac gct atg gtg cgg agc tca cca	632
Ile His Asp Cys Lys Pro Gly Asn Ala Met Val Arg Ser Ser Pro	
180 185 190	
cgg cat tac gga tgg aga acg ata tcg gac ggt gac ggt gtc tcc atc	680
Arg His Tyr Gly Trp Arg Thr Ile Ser Asp Gly Asp Gly Val Ser Ile	
195 200 210	
ttt gga gga agt cat gtt tgg gtt gac cat tgt tcg tta tct aat tgc	728
Phe Gly Gly Ser His Val Trp Val Asp His Cys Ser Leu Ser Asn Cys	
215 220 225	
gaa gac ggg ctt att gat gct ata ata ggc tcg acg gct att act ctg	776
Glu Asp Gly Leu Ile Asp Ala Ile Ile Gly Ser Thr Ala Ile Thr Leu	
230 235 240	
tct aac aat tac atg acg cat cat gat aag gtc atg ttg ctt ggt cat	824
Ser Asn Asn Tyr Met Thr His His Asp Lys Val Met Leu Leu Gly His	
245 250 255	
agt gac act tac act cgt gac aag aac atg caa atc acc att gct ttt	872
Ser Asp Thr Tyr Thr Arg Asp Lys Asn Met Gln Ile Thr Ile Ala Phe	
260 265 270	
aac cat ttt ggc gaa ggt ctt gtt caa aga atg cca agg tgt aga cat	920
Asn His Phe Gly Glu Gly Leu Val Gln Arg Met Pro Arg Cys Arg His	
275 280 285 290	
ggg tac ttc cat gtg gtg aac aac gac tat aca cat tgg gag atg tat	968
Gly Tyr Phe His Val Val Asn Asn Asp Tyr Thr His Trp Glu Met Tyr	
295 300 305	
gct att ggt gga agt gct aac cct aca atc aat agt caa ggg aac aga	1016
Ala Ile Gly Ser Ala Asn Pro Thr Ile Asn Ser Gln Gly Asn Arg	
310 315 320	
ttt ttg gcc cca gat att aga ttt agc aaa gaa gtg act aag cat gag	1064
Phe Leu Ala Pro Asp Ile Arg Phe Ser Lys Glu Val Thr Lys His Glu	
325 330 335	
gac gcc cca gag agt gag tgg aag agc tgg aac tgg aga tcc tct ggt	1112
Asp Ala Pro Glu Ser Glu Trp Lys Ser Trp Asn Trp Arg Ser Ser Gly	
340 345 350	
gat tta ttg cta aac ggt gca ttt ttt acg cct tcg ggt ggt gct acc	1160
Asp Leu Leu Leu Asn Gly Ala Phe Phe Thr Pro Ser Gly Gly Ala Thr	
355 360 365 370	
tcg tct agc tat gcc aag gct tcg agt ctt ggg gct aga ccg tct tct	1208
Ser Ser Ser Tyr Ala Lys Ala Ser Ser Leu Gly Ala Arg Pro Ser Ser	
375 380 385	
ctt gtt gga ccg ttg acg gtt ggt tct ggt gca ttg aat tgc cgt aag	1256
Leu Val Gly Pro Leu Thr Val Gly Ser Gly Ala Leu Asn Cys Arg Lys	
390 395 400	
ggt tcc cgt tgc tga ttgtggtggc tcacttaagt gtatttagcc aatttaaaaa	1311
Gly Ser Arg Cys	
405	
atgatataga aaaggcaatt aaagccatca attaaggggt taagttataa ctttcattac	1371
cccccttttaa ttagtctctt ttgatttttc ttcttttttg ggtaaagtta aggagaatac	1431
aacctctggc ttcacttctc ttaggaccca tctaaggaat tttctgtttt aaggtatctt	1491
ttatggcccc atctttttatt aggttaaagt gtagtaacaa gtgcagatgt gttgatcttc	1551
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aaaaaa

1617

<210> 1826
 <211> 406
 <212> PRT
 <213> Brassica napus

<400> 1826
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 Glu Glu Val His Lys Ser Ile Asn Ala Ser Val Ala Gly Arg Arg Lys
 35 40 45
 Leu Gly Tyr Leu Ser Cys Thr Thr Gly Asn Pro Ile Asp Asp Cys Trp
 50 55 60
 Arg Cys Asp Pro His Trp Glu Thr Asn Arg Gln Arg Leu Ala Asp Cys
 65 70 75 80
 Ala Ile Gly Phe Gly Lys Asn Ala Ile Gly Gly Arg Asp Gly Arg Ile
 85 90 95
 Tyr Val Val Thr Asp Ser Gly Asn Asp Asp Pro Val Thr Pro Lys Pro
 100 105 110
 Gly Thr Leu Arg Tyr Ala Val Val Gln Asp Glu Pro Leu Trp Ile Ile
 115 120 125
 Phe Gln Arg Asp Met Thr Ile Gln Leu Lys Glu Glu Leu Ile Met Asn
 130 135 140
 Ser Phe Lys Thr Ile Asp Gly Arg Gly Ala Ser Val His Ile Ala Gly
 145 150 155 160
 Gly Pro Cys Ile Thr Ile Gln Tyr Val Thr Asn Ile Ile Ile His Gly
 165 170 175
 Ile His Ile His Asp Cys Lys Pro Gly Gly Asn Ala Met Val Arg Ser
 180 185 190
 Ser Pro Arg His Tyr Gly Trp Arg Thr Ile Ser Asp Gly Asp Gly Val
 195 200 205
 Ser Ile Phe Gly Gly Ser His Val Trp Val Asp His Cys Ser Leu Ser
 210 215 220
 Asn Cys Glu Asp Gly Leu Ile Asp Ala Ile Ile Gly Ser Thr Ala Ile
 225 230 235 240
 Thr Leu Ser Asn Asn Tyr Met Thr His His Asp Lys Val Met Leu Leu
 245 250 255
 Gly His Ser Asp Thr Tyr Thr Arg Asp Lys Asn Met Gln Ile Thr Ile
 260 265 270
 Ala Phe Asn His Phe Gly Glu Gly Leu Val Gln Arg Met Pro Arg Cys
 275 280 285
 Arg His Gly Tyr Phe His Val Val Asn Asn Asp Tyr Thr His Trp Glu
 290 295 300
 Met Tyr Ala Ile Gly Gly Ser Ala Asn Pro Thr Ile Asn Ser Gln Gly
 305 310 315 320
 Asn Arg Phe Leu Ala Pro Asp Ile Arg Phe Ser Lys Glu Val Thr Lys
 325 330 335
 His Glu Asp Ala Pro Glu Ser Glu Trp Lys Ser Trp Asn Trp Arg Ser
 340 345 350
 Ser Gly Asp Leu Leu Leu Asn Gly Ala Phe Phe Thr Pro Ser Gly Gly
 355 360 365
 Ala Thr Ser Ser Ser Tyr Ala Lys Ala Ser Ser Leu Gly Ala Arg Pro
 370 375 380
 Ser Ser Leu Val Gly Pro Leu Thr Val Gly Ser Gly Ala Leu Asn Cys
 385 390 395 400
 Arg Lys Gly Ser Arg Cys
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 <211> 1876
 <212> DNA
 <213> Glycine max

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PF59082SeqList_PF59082.txt

<221> CDS

<222> (88)..(1434)

<400> 1827

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agagcgaggg gaattcaact ttctgca atg gcg gtt tct tct tct tct gca aca      114
                    Met Ala Val Ser Ser Ser Ser Ala Thr
                    1          5
aaa tgg gtc gtc ttc ttg ctt ctg gcg ctg ctt att cga gaa gaa gct      162
Lys Trp Val Val Phe Leu Leu Leu Ala Leu Leu Ile Arg Glu Glu Ala
10          15          20          25
atg gct aca cca cag atc tct gac ctc agg aat ctt gaa gtt gaa aga      210
Met Ala Thr Pro Gln Ile Ser Asp Leu Arg Asn Leu Glu Val Glu Arg
30          35          40
cac agg ttg ccg agc ttg acg aac tcg tca atg gcg gag agg gca aaa      258
His Arg Leu Pro Ser Leu Thr Asn Ser Ser Met Ala Glu Arg Ala Lys
45          50          55
gag gct gag aaa tta aat gaa caa gct gca gtg gct aac cca gag gaa      306
Glu Ala Glu Lys Leu Asn Glu Gln Ala Ala Val Ala Asn Pro Glu Glu
60          65          70
gtg gtt tca atg gtt gag atg agc atc caa aac agt aca gag agg agg      354
Val Val Ser Met Val Glu Met Ser Ile Gln Asn Ser Thr Glu Arg Arg
75          80          85
aag ttg gga ttt ttc tct tgt gga act ggc aac ccc att gat gat tgc      402
Lys Leu Gly Phe Phe Ser Cys Gly Thr Gly Asn Pro Ile Asp Asp Cys
90          95          100
tgg cgt tgc gac ccc aac tgg caa cgc aat cgg aag cgt ctt gca gat      450
Trp Arg Cys Asp Pro Asn Trp Gln Arg Asn Arg Lys Arg Leu Ala Asp
110          115          120
tgt ggc att ggt ttt ggc cga aac gcc atc ggt ggc cgt gat gga aaa      498
Cys Gly Ile Gly Phe Gly Arg Asn Ala Ile Gly Gly Arg Asp Gly Lys
125          130          135
ttc tat gtg gtg act gac ccc agg gat gat gac cct gtg aac ccg aaa      546
Phe Tyr Val Val Thr Asp Pro Arg Asp Asp Pro Val Asn Pro Lys
140          145          150
ccc ggc act ctt cgc cat gct gtg atc cag gat aag cca ttg tgg att      594
Pro Gly Thr Leu Arg His Ala Val Ile Gln Asp Lys Pro Leu Trp Ile
155          160          165
gtg ttc aag agg gac atg gtt att cag ctg aaa caa gag ctg atc atg      642
Val Phe Lys Arg Asp Met Val Ile Gln Leu Lys Gln Glu Leu Ile Met
170          175          180
aac agc ttc aag aca att gat ggt aga gga gtc aat gtg cac att gct      690
Asn Ser Phe Lys Thr Ile Asp Gly Arg Gly Val Asn Val His Ile Ala
190          195          200
aat gga gca tgc atc aca att cag ttt gtt acc aat gtc atc atc cat      738
Asn Gly Ala Cys Ile Thr Ile Gln Phe Val Thr Asn Val Ile Ile His
205          210          215
ggc ttg cac att cat gat tgc aaa cct act gga aat gct atg gtg aga      786
Gly Leu His Ile His Asp Cys Lys Pro Thr Gly Asn Ala Met Val Arg
220          225          230
agc tcc cca acc cac ttt ggt tgg agg aca atg gct gat aga gat gcc      834
Ser Ser Pro Thr His Phe Gly Trp Arg Thr Met Ala Asp Arg Asp Ala
235          240          245
atc tcc ata ttt ggc tca agc cac att tgg gtt gac cac aac tcc ttg      882
Ile Ser Ile Phe Gly Ser Ser His Ile Trp Val Asp His Asn Ser Leu
250          255          260
tca cac tgt gct gat ggc ctt gtg gat gct gtc ctg ggc tca aca gcc      930
Ser His Cys Ala Asp Gly Leu Val Asp Ala Val Leu Gly Ser Thr Ala
265          270          275
ata act att tcc aac aac cac ttc acc cac cac aat gag gtg att ctg      978
Ile Thr Ile Ser Asn Asn His Phe Thr His His Asn Glu Val Ile Leu
285          290          295
ctg ggc cat agt gac tct tac aca aga gac aag cag atg caa gtg acc      1026
Leu Gly His Ser Asp Ser Tyr Thr Arg Asp Lys Gln Met Gln Val Thr
300          305          310
att gca tac aac cat ttt gga gag gga ctt atc cag aga atg cca cgt      1074
Ile Ala Tyr Asn His Phe Gly Glu Gly Leu Ile Arg Met Pro Arg

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PF59082SeqList_PF59082.txt

315	320	325		
tgt aga cat gga tat ttc cac gtg gtg aac aat gac tac act cac tgg				1122
Cys Arg His Gly Tyr Phe His Val Val Asn Asn Asp Tyr Thr His Trp				
330	335	340	345	
gag atg tat gct att ggt gga agt gct aac ccc acc atc aac agc cag				1170
Glu Met Tyr Ala Ile Gly Gly Ser Ala Asn Pro Thr Ile Asn Ser Gln				
350	355	360		
ggc aac aga tac aat gct cct act aac cgt ttt gcc aag gag gtg aca				1218
Gly Asn Arg Tyr Asn Ala Pro Thr Asn Arg Phe Ala Lys Glu Val Thr				
365	370	375		
aag aga gtg gaa aca gca gaa agt cag tgg aag ggt tgg aat tgg agg				1266
Lys Arg Val Glu Thr Ala Glu Ser Gln Trp Lys Gly Trp Asn Trp Arg				
380	385	390		
tca gag gga gat ttg ttg ctg aat ggt gcc tat ttc aca cca tct ggt				1314
Ser Glu Gly Asp Leu Leu Leu Asn Gly Ala Tyr Phe Thr Pro Ser Gly				
395	400	405		
gct gga gcc tca gca agc tat gca aga gcc tct agc tta gga gca aaa				1362
Ala Gly Ala Ser Ala Ser Tyr Ala Arg Ala Ser Ser Leu Gly Ala Lys				
410	415	420	425	
tct tct tcc atg gtt ggt tcc atg act tcc aat gct ggt gca cta ggt				1410
Ser Ser Ser Met Val Gly Ser Met Thr Ser Asn Ala Gly Ala Leu Gly				
430	435	440		
tgc aaa aga ggc agt cag tgc tag catatatattat catcaaccac aaccatgtga				1464
Cys Lys Arg Gly Ser Gln Cys				
445				
atgaaagagg tcatccatta tttttctttt gttgtttgat tctcaagggtt ttacatatt				1524
atagtagaac atcatcatca tcatatatcc ataatccatt gctttctttc ctcacacctc				1584
catcatcata tcttcgagta ttcttgacaa gtgtacatta aattacacat gtcaatatgg				1644
ttttatgtgt tacccttttg ccacaccgtg tgtattgttg ttggtcaacc ttagctgctc				1704
gacttgctcc agctgaaaca agcaatgcaa ttgtaggagc aggtgcagaa gcgccatcca				1764
ttgttttctt ccctttttca ttcttactct tttttttttt tgcctttttc ttcctttggt				1824
ccttcccatc tcatcccccc ccccccacacc aattcatatg catatttttc gc				1876

<210> 1828
 <211> 448
 <212> PRT
 <213> Glycine max

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 20 25 30
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 35 40 45
 Asn Ser Ser Met Ala Glu Arg Ala Lys Glu Ala Glu Lys Leu Asn Glu
 50 55 60
 Gln Ala Ala Val Ala Asn Pro Glu Glu Val Val Ser Met Val Glu Met
 65 70 75 80
 Ser Ile Gln Asn Ser Thr Glu Arg Arg Lys Leu Gly Phe Phe Ser Cys
 85 90 95
 Gly Thr Gly Asn Pro Ile Asp Asp Cys Trp Arg Cys Asp Pro Asn Trp
 100 105 110
 Gln Arg Asn Arg Lys Arg Leu Ala Asp Cys Gly Ile Gly Phe Gly Arg
 115 120 125

PF59082SeqList_PF59082.txt

Asn Ala Ile Gly Gly Arg Asp Gly Lys Phe Tyr Val Val Thr Asp Pro
 130 135 140
 Arg Asp Asp Asp Pro Val Asn Pro Lys Pro Gly Thr Leu Arg His Ala
 145 150 155 160
 Val Ile Gln Asp Lys Pro Leu Trp Ile Val Phe Lys Arg Asp Met Val
 165 170 175
 Ile Gln Leu Lys Gln Glu Leu Ile Met Asn Ser Phe Lys Thr Ile Asp
 180 185 190
 Gly Arg Gly Val Asn Val His Ile Ala Asn Gly Ala Cys Ile Thr Ile
 195 200 205
 Gln Phe Val Thr Asn Val Ile Ile His Gly Leu His Ile His Asp Cys
 210 215 220
 Lys Pro Thr Gly Asn Ala Met Val Arg Ser Ser Pro Thr His Phe Gly
 225 230 235 240
 Trp Arg Thr Met Ala Asp Arg Asp Ala Ile Ser Ile Phe Gly Ser Ser
 245 250 255
 His Ile Trp Val Asp His Asn Ser Leu Ser His Cys Ala Asp Gly Leu
 260 265 270
 Val Asp Ala Val Leu Gly Ser Thr Ala Ile Thr Ile Ser Asn Asn His
 275 280 285
 Phe Thr His His Asn Glu Val Ile Leu Leu Gly His Ser Asp Ser Tyr
 290 295 300
 Thr Arg Asp Lys Gln Met Gln Val Thr Ile Ala Tyr Asn His Phe Gly
 305 310 315 320
 Glu Gly Leu Ile Gln Arg Met Pro Arg Cys Arg His Gly Tyr Phe His
 325 330 335
 Val Val Asn Asn Asp Tyr Thr His Trp Glu Met Tyr Ala Ile Gly Gly
 340 345 350
 Ser Ala Asn Pro Thr Ile Asn Ser Gln Gly Asn Arg Tyr Asn Ala Pro
 355 360 365
 Thr Asn Arg Phe Ala Lys Glu Val Thr Lys Arg Val Glu Thr Ala Glu
 370 375 380
 Ser Gln Trp Lys Gly Trp Asn Trp Arg Ser Glu Gly Asp Leu Leu Leu
 385 390 395 400
 Asn Gly Ala Tyr Phe Thr Pro Ser Gly Ala Gly Ala Ser Ala Ser Tyr
 405 410 415
 Ala Arg Ala Ser Ser Leu Gly Ala Lys Ser Ser Ser Met Val Gly Ser
 420 425 430
 Met Thr Ser Asn Ala Gly Ala Leu Gly Cys Lys Arg Gly Ser Gln Cys
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 <211> 2076
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (343)..(1857)

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 tttccatcct agaataatta cccgaccatt actattataa atctagttat tataaaaacc 180

 cctcctatitt ccccaaatt ttcgagcttc ataagtaatt gtgcattcaa gaggaaaaca 240

 tcatccaag ccaagcatca ttttacaaca caaaaaaaca gacaaaacaa accccttccc 300

 aaacccaac tcaatcataa ttgtttgttc cttgaaagaa ca atg ctc ccc atc 354
 Met Leu Pro Ile
 1

PF59082SeqList_PF59082.txt

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Thr	Cys	Ile	Leu	Phe	Met	Cys	Leu	Leu	Ser	Ser	Phe	Ser	Pro	Pro	Ile	
5					10				15						20	
aac	gct	ctt	ctc	aac	ctc	aac	ctc	acc	ctg	ccc	cat	caa	tac	cct	cac	450
Asn	Ala	Leu	Leu	Asn	Leu	Asn	Leu	Thr	Leu	Pro	His	Gln	Tyr	Pro	His	
				25					30					35		
ccc	gaa	tcc	gtc	gtc	caa	gat	atc	caa	cgg	aag	gtg	aat	gcc	tca	cta	498
Pro	Glu	Ser	Val	Val	Gln	Asp	Ile	Gln	Arg	Lys	Val	Asn	Ala	Ser	Leu	
			40					45					50			
cgg	aga	agg	gaa	atg	ctg	tca	aag	gac	gaa	caa	caa	ggc	atg	tct	tcg	546
Arg	Arg	Arg	Glu	Met	Leu	Ser	Lys	Asp	Glu	Gln	Gln	Gly	Met	Ser	Ser	
		55					60					65				
tgt	ctg	aca	gga	aac	ccc	atc	gac	gac	tgc	tgg	cgg	tgc	gag	ccg	aac	594
Cys	Leu	Thr	Gly	Asn	Pro	Ile	Asp	Asp	Cys	Trp	Arg	Cys	Glu	Pro	Asn	
	70					75					80					
tgg	gcg	gcg	gag	cgg	cag	aag	ctg	gcg	gag	tgc	ggc	ctc	ggg	ttc	ggc	642
Trp	Ala	Ala	Glu	Arg	Gln	Lys	Leu	Ala	Glu	Cys	Gly	Leu	Gly	Phe	Gly	
85					90					95					100	
aaa	tac	gcc	atg	ggc	ggc	aaa	ggc	ggg	cag	atc	tac	atc	gtg	acg	gac	690
Lys	Tyr	Ala	Met	Gly	Gly	Lys	Gly	Gly	Gln	Ile	Tyr	Ile	Val	Thr	Asp	
				105					110					115		
tcc	tcg	gac	cgc	gac	cct	gcc	aac	ccc	att	ccg	ggc	acc	ctc	cgc	cac	738
Ser	Ser	Asp	Arg	Asp	Pro	Ala	Asn	Pro	Ile	Pro	Gly	Thr	Leu	Arg	His	
			120					125					130			
gcc	gtc	atc	caa	gac	gag	gca	ctc	tgg	ata	gtc	ttc	gcc	gcc	gac	atg	786
Ala	Val	Ile	Gln	Asp	Glu	Ala	Leu	Trp	Ile	Val	Phe	Ala	Ala	Asp	Met	
		135					140					145				
acc	atc	aac	cta	aaa	cac	gag	ctc	ata	ttc	aac	agc	tac	aag	acc	ctg	834
Thr	Ile	Asn	Leu	Lys	His	Glu	Leu	Ile	Phe	Asn	Ser	Tyr	Lys	Thr	Leu	
	150					155					160					
gac	ggc	cgc	gga	gcc	aac	gtc	cac	gtc	acc	ggc	cac	ggc	tgc	atc	acg	882
Asp	Gly	Arg	Gly	Ala	Asn	Val	His	Val	Thr	Gly	His	Gly	Cys	Ile	Thr	
165					170				175						180	
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Leu	Gln	Tyr	Val	Ser	Asn	Ile	Ile	Ile	His	Asn	Ile	His	Ile	His	His	
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tgc	act	ccc	tcc	ggg	aac	acc	aac	ata	cga	gcc	agt	cca	acg	cac	gta	978
Cys	Thr	Pro	Ser	Gly	Asn	Thr	Asn	Ile	Arg	Ala	Ser	Pro	Thr	His	Val	
			200					205					210			
ggg	tgg	aga	ggc	aaa	tcg	gac	ggt	gat	ggg	att	tcg	att	ttt	ggc	tcg	1026
Gly	Trp	Arg	Gly	Lys	Ser	Asp	Gly	Asp	Gly	Ile	Ser	Ile	Phe	Gly	Ser	
		215					220					225				
cgg	aag	atc	tgg	atc	gac	cat	tgc	tcg	ctg	tct	tat	tgc	acg	gac	ggc	1074
Arg	Lys	Ile	Trp	Ile	Asp	His	Cys	Ser	Leu	Ser	Tyr	Cys	Thr	Asp	Gly	
	230					235					240					
ttg	atc	gat	gct	att	atg	ggg	tcc	act	ggg	att	act	att	tcg	aat	agt	1122
Leu	Ile	Asp	Ala	Ile	Met	Gly	Ser	Thr	Gly	Ile	Thr	Ile	Ser	Asn	Ser	
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cat	ttt	gcg	cac	cat	gat	gag	gtg	atg	ctt	gga	cac	gat	gat	aag		1170
His	Phe	Ala	His	His	Asp	Glu	Val	Met	Leu	Gly	His	Asp	Asp	Lys		
				265					270					275		
tac	ttg	gtg	gat	agg	ggc	atg	cag	gtt	aca	atc	acg	ttt	aat	cac	ttc	1218
Tyr	Leu	Val	Asp	Arg	Gly	Met	Gln	Val	Thr	Ile	Thr	Phe	Asn	His	Phe	
			280					285					290			
ggc	gag	ggt	ttg	gtg	cag	cgc	atg	cca	cga	tgc	agg	ctc	ggt	tat	atc	1266
Gly	Glu	Gly	Leu	Val	Gln	Arg	Met	Pro	Arg	Cys	Arg	Leu	Gly	Tyr	Ile	
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His	Val	Val	Asn	Asn	Asp	Phe	Thr	Gln	Trp	Arg	Met	Tyr	Ala	Ile	Gly	
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ggt	agc	gct	aac	ccc	acc	atc	aac	agc	cag	ggc	aac	cgt	tac	acg	gct	1362
Gly	Ser	Ala	Asn	Pro	Thr	Ile	Asn	Ser	Gln	Gly	Asn	Arg	Tyr	Thr	Ala	
325					330				335						340	
ccc	gga	gac	cct	gat	gcc	aag	gag	gtg	acg	aag	cgc	gtg	gac	aca	gac	1410
Pro	Gly	Asp	Pro	Asp	Ala	Lys	Glu	Val	Thr	Lys	Arg	Val	Asp	Thr	Asp	
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gat	aga	gag	tgg	agt	ggt	tgg	aat	tgg	agg	acg	gaa	ggg	gac	ata	atg	1458
Asp	Arg	Glu	Trp	Ser	Gly	Trp	Asn	Trp	Arg	Thr	Glu	Gly	Asp	Ile	Met	
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PF59082SeqList_PF59082.txt

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Val Asn Gly Ala Phe Phe Val Pro Ser Gly Ala Ala Gly Gln Ser Gly	
375 380 385	
cag tac caa gag gcc acc agt gtg caa gcc aaa tcc gcc gtg caa ata	1554
Gln Tyr Gln Glu Ala Thr Ser Val Gln Ala Lys Ser Ala Val Gln Ile	
390 395 400	
gac cag ctc act atg tac tcc ggt gtc ttg ggt gat ccc agg gat aat	1602
Asp Gln Leu Thr Met Tyr Ser Gly Val Leu Gly Asp Pro Arg Asp Asn	
405 410 415 420	
ggg gat tta tat ccc ggc ttc aac ggc ggt ggg acc gtg acc gga gcc	1650
Gly Asp Leu Tyr Pro Gly Phe Asn Gly Gly Thr Val Thr Gly Ala	
425 430 435	
acc agc aaa ggc aac act gac ggg tcc agc agt gac gat ggg ggg gac	1698
Thr Ser Lys Gly Asn Thr Asp Gly Ser Ser Ser Asp Asp Gly Gly Asp	
440 445 450	
ttc ttc ggg atg ata ttc aga ggt ggc agc agc agc agc agc agc	1746
Phe Phe Gly Met Ile Phe Arg Gly Gly Ser Ser Ser Ser Ser Ser	
455 460 465	
caa gca gcg cca cca tcg tcc gtt cta ttt gtt tca atc ttt ttg tct	1794
Gln Ala Ala Pro Pro Ser Ser Val Leu Phe Val Ser Ile Phe Leu Ser	
470 475 480	
ctt tta att att ttt gtt ttg gac act acc acc aac cat gcc ttt tta	1842
Leu Leu Ile Ile Phe Val Leu Asp Thr Thr Thr Asn His Ala Phe Leu	
485 490 495 500	
tta tca tta cta tga tcacacaatt gggaaagggg aaaaacaaaa aaactccctt	1897
Leu Ser Leu Leu	
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aaatttagaa actaggaatc gtgttttaggt atgtacacag ctcttcaaag ttattattaa	2017
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Gln Tyr Pro His Pro Glu Ser Val Val Gln Asp Ile Gln Arg Lys Val	35 40 45
Asn Ala Ser Leu Arg Arg Arg Glu Met Leu Ser Lys Asp Glu Gln Gln	50 55 60
Gly Met Ser Ser Cys Leu Thr Gly Asn Pro Ile Asp Asp Cys Trp Arg	65 70 75 80
Cys Glu Pro Asn Trp Ala Ala Glu Arg Gln Lys Leu Ala Glu Cys Gly	85 90 95
Leu Gly Phe Gly Lys Tyr Ala Met Gly Gly Lys Gly Gly Gln Ile Tyr	100 105 110
Ile Val Thr Asp Ser Ser Asp Arg Asp Pro Ala Asn Pro Ile Pro Gly	115 120 125
Thr Leu Arg His Ala Val Ile Asn Leu Lys His Glu Leu Ile Phe Asn Ser	130 135 140 145 150 155 160
Ala Ala Asp Met Thr Ile Asn Leu Lys His Glu Val His Val Thr Gly His	165 170 175
Tyr Lys Thr Leu Asp Gly Arg Gly Ala Asn Ile Ile Ile His Asn Ile	180 185 190
Gly Cys Ile Thr Leu Gln Tyr Val Ser Asn Thr Asn Ile Arg Ala Ser	195 200 205
His Ile His His Cys Thr Pro Ser Gly Asn Thr Asn Ile Arg Ala Ser	

PF59082SeqList_PF59082.txt

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ccg tta tgg atc ata ttt gca cat gac atg acc att cga ctc aaa gaa	439							
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gaa ctc ttg atg aac tca ttc aag acc atc gat ggt cgt ggg gcc aat	487							
Glu Leu Leu Met Asn Ser Phe Lys Thr Ile Asp Gly Arg Gly Ala Asn								
gtt cat ata gcc ggt gga cca tgc atc acc ata caa tat gtg aca aac	535							
Val His Ile Ala Gly Gly Pro Cys Ile Thr Ile Gln Tyr Val Thr Asn								
atc atc ata cat ggt gtc aac ata cat gat tgt aag caa ggg ggg aac	583							
Ile Ile Ile His Gly Val Asn Ile His Asp Cys Lys Gln Gly Gly Asn								
acc gat gtt agg gac tca ccg gac cat tat ggg ttc cgc aca ata tcg	631							
Thr Asp Val Arg Asp Ser Pro Asp His Tyr Gly Phe Arg Thr Ile Ser								
gat ggt gat ggg atc tcc atc ttt ggt gga agt cat gta tgg gtg gat	679							
Asp Gly Asp Gly Ile Ser Ile Phe Gly Gly Ser His Val Trp Val Asp								
cat tgt tca ttg gct aat tgt cat gat ggt tta att gat gcc ata cat	727							
His Cys Ser Leu Ala Asn Cys His Asp Gly Leu Ile Asp Ala Ile His								
gga tcc aca gcc ata acc ata tcc aat aac tac atg aca cat cat gat	775							
Gly Ser Thr Ala Ile Thr Ile Ser Asn Asn Tyr Met Thr His His Asp								
aag gtc atg tta ttg gga cat agt gac act tta ctt caa gac aag aat	823							
Lys Val Met Leu Leu Gly His Ser Asp Thr Leu Leu Gln Asp Lys Asn								
atg caa gtc aca att gca ttt aac cat ttt ggt gaa ggc ctt gta caa	871							
Met Gln Val Thr Ile Ala Phe Asn His Phe Gly Glu Gly Leu Val Gln								
agg atg cca aga tgt agg ggg tat ttc cat gtg gtt aac aat gac	919							
Arg Met Pro Arg Cys Arg His Gly Tyr Phe His Val Val Asn Asn Asp								
tat acc cat tgg gaa atg tat gca att gga gga agt gct tca cca acc	967							
Tyr Thr His Trp Glu Met Tyr Ala Ile Gly Gly Ser Ala Ser Pro Thr								
atc aat agt caa ggg aat aga ttt cta gct ccc aat aca tat gat aat	1015							
Ile Asn Ser Gln Gly Asn Arg Phe Leu Ala Pro Asn Thr Tyr Asp Asn								
aaa gaa gtg aca aaa cga gag gag gcg tca gaa agc gaa tgg aaa aac	1063							
Lys Glu Val Thr Lys Arg Glu Glu Ala Ser Glu Ser Glu Trp Lys Asn								
tgg aat tgg cgt tca gaa ggc gac ctc atg tta aac ggt gcc tat ttc	1111							
Trp Asn Trp Arg Ser Glu Gly Asp Leu Met Leu Asn Gly Ala Tyr Phe								
act cca tca ggc gca ggg gct tct aaa agt tat gca cga gca tca agc	1159							
Thr Pro Ser Gly Ala Gly Ala Ser Lys Ser Tyr Ala Arg Ala Ser Ser								
tta agt gca aga cca tct tcc att gtg ggg ttt gtc aca gct aac gca	1207							
Leu Ser Ala Arg Pro Ser Ser Ile Val Gly Phe Val Thr Ala Asn Ala								
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Gly Val Leu Arg Cys Thr Arg Gly Ser Arg Cys								
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PF59082SeqList_PF59082.txt

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His Val His Arg Ser Ile Asn Glu Ser Arg Arg Asn Leu Gly Ser Leu
35      40      45
Ser Cys Gly Thr Gly Asn Pro Ile Asp Asp Cys Trp Arg Cys Asp Lys
50      55      60
Ser Trp Glu Lys Asn Arg Gln Arg Leu Ala Asp Cys Ala Ile Gly Phe
65      70      75      80
Gly Lys His Ala Ile Gly Gly Arg Asp Gly Lys Ile Tyr Val Val Thr
85      90      95
Asp Ser Lys Asn Asp Asp Pro Val Asn Pro Lys Pro Gly Thr Leu Arg
100     105     110
Tyr Gly Val Ile Gln Asn Glu Pro Leu Trp Ile Ile Phe Ala His Asp
115     120     125
Met Thr Ile Arg Leu Lys Glu Glu Leu Leu Met Asn Ser Phe Lys Thr
130     135     140
Ile Asp Gly Arg Gly Ala Asn Val His Ile Ala Gly Pro Cys Ile
145     150     155     160
Thr Ile Gln Tyr Val Thr Asn Ile Ile Ile His Gly Val Asn Ile His
165     170     175
Asp Cys Lys Gln Gly Gly Asn Thr Asp Val Arg Asp Ser Pro Asp His
180     185     190
Tyr Gly Phe Arg Thr Ile Ser Asp Gly Asp Gly Ile Ser Ile Phe Gly
195     200     205
Gly Ser His Val Trp Val Asp His Cys Ser Leu Ala Asn Cys His Asp
210     215     220
Gly Leu Ile Asp Ala Ile His Gly Ser Thr Ala Ile Thr Ile Ser Asn
225     230     235     240
Asn Tyr Met Thr His His Asp Lys Val Met Leu Leu Gly His Ser Asp
245     250     255
Thr Leu Leu Gln Asp Lys Asn Met Gln Val Thr Ile Ala Phe Asn His
260     265     270
Phe Gly Glu Gly Leu Val Gln Arg Met Pro Arg Cys Arg His Gly Tyr
275     280     285
Phe His Val Val Asn Asn Asp Tyr Thr His Trp Glu Met Tyr Ala Ile
290     295     300
Gly Gly Ser Ala Ser Pro Thr Ile Asn Ser Gln Gly Asn Arg Phe Leu
305     310     315     320
Ala Pro Asn Thr Tyr Asp Asn Lys Glu Val Thr Lys Arg Glu Glu Ala
325     330     335
Ser Glu Ser Glu Trp Lys Asn Trp Asn Trp Arg Ser Glu Gly Asp Leu
340     345     350
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355     360     365
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atg aaa cag agg aag aac agt aat ctc tca atc ttc gtc gta gtc ttc      96
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PF59082SeqList_PF59082.txt

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Ser	Val	Phe	Leu	Phe	Gly	Ile	Phe	Met	Tyr	Asn	Glu	Asp	Val	Lys	Ser
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atc	gca	gag	ttt	cct	ttc	tcc	acc	tca	aaa	cct	cac	gac	gtc	cac	gac
Ile	Ala	Glu	Phe	Pro	Phe	Ser	Thr	Ser	Lys	Pro	His	Asp	Val	His	Asp
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gaa	gcg	aca	ccg	atc	aca	gag	atc	aca	aca	cta	ccg	ggt	caa	gag	tcg
Glu	Ala	Thr	Pro	Ile	Thr	Glu	Ile	Thr	Thr	Leu	Pro	Val	Gln	Glu	Ser
	65				70					75				80	
atc	aag	aac	tca	gac	cca	att	cag	gaa	tcg	atc	aaa	aac	gca	gac	tca
Ile	Lys	Asn	Ser	Asp	Pro	Ile	Gln	Glu	Ser	Ile	Lys	Asn	Ala	Asp	Ser
				85				90					95		
ggt	caa	gat	tca	ggt	aaa	gac	gta	gca	gaa	cca	ggt	caa	gag	gag	gta
Val	Gln	Asp	Ser	Val	Lys	Asp	Val	Ala	Glu	Pro	Val	Gln	Glu	Glu	Val
			100				105					110			
tcg	aaa	aca	gag	gaa	ggt	aaa	aag	att	gag	ctt	ttc	gct	gcg	acg	gag
Ser	Lys	Thr	Glu	Glu	Val	Lys	Lys	Ile	Glu	Leu	Phe	Ala	Ala	Thr	Glu
		115				120					125				
gat	gaa	gac	gtg	gaa	ttg	ccg	ccg	gag	gaa	tgc	gat	ttg	ttc	acc	
Asp	Glu	Glu	Asp	Val	Glu	Leu	Pro	Pro	Glu	Glu	Cys	Asp	Leu	Phe	Thr
	130				135					140					
gga	gaa	tgg	ggt	ttt	gat	aac	gag	acg	cat	cca	ttg	tat	aaa	gag	gat
Gly	Glu	Trp	Val	Phe	Asp	Asn	Glu	Thr	His	Pro	Leu	Tyr	Lys	Glu	Asp
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Gln	Cys	Glu	Phe	Leu	Thr	Ala	Gln	Val	Thr	Cys	Met	Arg	Asn	Gly	Arg
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Arg	Asp	Ser	Leu	Tyr	Gln	Asn	Trp	Arg	Trp	Gln	Pro	Arg	Asp	Cys	Ser
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tta	cca	aag	ttc	aaa	gcg	aaa	ttg	ctg	ttg	gag	aag	cta	agg	aac	aag
Leu	Pro	Lys	Phe	Lys	Ala	Lys	Leu	Leu	Leu	Glu	Lys	Leu	Arg	Asn	Lys
		195					200				205				
aga	atg	atg	ttc	ggt	gga	gat	tcc	cta	aac	cgg	aac	caa	tgg	gaa	tca
Arg	Met	Met	Phe	Val	Gly	Asp	Ser	Leu	Asn	Arg	Asn	Gln	Trp	Glu	Ser
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Met	Val	Cys	Leu	Val	Gln	Ser	Val	Val	Pro	Pro	Gly	Arg	Lys	Ser	Leu
	225				230				235					240	
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Asn	Lys	Thr	Gly	Ser	Leu	Ser	Val	Phe	Arg	Val	Glu	Asp	Tyr	Asn	Ala
			245					250					255		
acg	gtg	gag	ttt	tat	tgg	gca	cca	ttt	ttg	gtg	gaa	tcg	aat	tca	gat
Thr	Val	Glu	Phe	Tyr	Trp	Ala	Pro	Phe	Leu	Val	Glu	Ser	Asn	Ser	Asp
			260			265					270				
gat	cca	aat	atg	cat	agt	ata	ctt	aac	cgt	ata	ata	atg	cct	gag	tcc
Asp	Pro	Asn	Met	His	Ser	Ile	Leu	Asn	Arg	Ile	Ile	Met	Pro	Glu	Ser
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Ile	Glu	Lys	His	Gly	Val	Asn	Trp	Lys	Gly	Val	Asp	Phe	Leu	Val	Phe
	290				295					300					
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Asn	Thr	Tyr	Ile	Trp	Trp	Met	Asn	Thr	Phe	Ala	Met	Lys	Val	Leu	Arg
	305				310				315					320	
gga	tcg	ttc	gat	aaa	gga	gac	acc	gag	tat	gag	gag	atc	gaa	cgg	cca
Gly	Ser	Phe	Asp	Lys	Gly	Asp	Thr	Glu	Tyr	Glu	Glu	Ile	Glu	Arg	Pro
			325					330					335		
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Val	Ala	Tyr	Arg	Arg	Val	Met	Arg	Thr	Trp	Gly	Asp	Trp	Val	Glu	Arg
			340			345					350				
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Asn	Ile	Asp	Pro	Leu	Arg	Thr	Thr	Val	Phe	Phe	Ala	Ser	Met	Ser	Pro
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Leu	His	Ile	Lys	Ser	Leu	Asp	Trp	Glu	Asn	Pro	Asp	Gly	Ile	Lys	Cys
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PF59082SeqList_PF59082.txt

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Gly	Thr	Asp	Tyr	Arg 405	Leu	Phe	Ser	Val	Ala 410	Glu	Asn	Val	Thr	His 415	Ser	
ctt	aat	gtt	ccg	gtt	tac	ttt	ctc	aac	att	acc	aaa	ctc	tcc	gaa	tac	1296
Leu	Asn	Val	Pro	Val	Tyr	Phe	Leu	Asn	Ile	Thr	Lys	Leu	Ser	Glu	Tyr	
			420					425					430			
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Arg	Lys	Asp	Ala	His	Thr	Ser	Val	His	Thr	Ile	Arg	Gln	Gly	Lys	Met	
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Leu	Thr	Pro	Glu	Gln	Gln	Ala	Asp	Pro	Asn	Thr	Tyr	Ala	Asp	Cys	Ile	
	450					455					460					
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His	Trp	Cys	Leu	Pro	Gly	Leu	Pro	Asp	Thr	Trp	Asn	Glu	Phe	Leu	Tyr	
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Thr	Arg	Ile	Ile	Ser	Arg	Ser										
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<211> 487

<212> PRT

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<400> 1834

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Ser	Val	Phe	Leu	Phe	Gly	Ile	Phe	Met	Tyr	Asn	Glu	Asp	Val 45	Lys	Ser	
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Ile	Lys	Asn	Ser	Asp 85	Pro	Ile	Gln	Glu	Ser 90	Ile	Lys	Asn	Ala	Asp 95	Ser	
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Ser	Lys	Thr	Glu	Glu	Val	Lys	Lys	Ile	Glu	Leu	Phe	Ala	Ala	Thr	Glu	
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Gln	Cys	Glu	Phe	Leu	Thr	Ala	Gln	Val	Thr	Cys	Met	Arg	Asn	Gly	Arg	
				165					170					175		
Arg	Asp	Ser	Leu	Tyr	Gln	Asn	Trp	Arg	Trp	Gln	Pro	Arg	Asp	Cys	Ser	
			180					185					190			
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Arg	Met	Met	Phe	Val	Gly	Asp	Ser	Leu	Asn	Arg	Asn	Gln	Trp	Glu	Ser	
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Met	Val	Cys	Leu	Val	Gln	Ser	Val	Val	Pro	Pro	Gly	Arg	Lys	Ser	Leu	
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Asn	Lys	Thr	Gly	Ser	Leu	Ser	Val	Phe	Arg	Val	Glu	Asp	Tyr	Asn	Ala	
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Thr	Val	Glu	Phe	Tyr	Trp	Ala	Pro	Phe	Leu	Val	Glu	Ser	Asn	Ser	Asp	
				260				265						270		
Asp	Pro	Asn	Met	His	Ser	Ile	Leu	Asn	Arg	Ile	Ile	Met	Pro	Glu	Ser	
	275						280					285				
Ile	Glu	Lys	His	Gly	Val	Asn	Trp	Lys	Gly	Val	Asp	Phe	Leu	Val	Phe	
	290					295					300					
Asn	Thr	Tyr	Ile	Trp	Trp	Met	Asn	Thr	Phe	Ala	Met	Lys	Val	Leu	Arg	
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Gly	Ser	Phe	Asp	Lys	Gly	Asp	Thr	Glu	Tyr	Glu	Glu	Ile	Glu	Arg	Pro	
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PF59082SeqList_PF59082.txt

Val Ala Tyr Arg Arg Val Met Arg Thr Trp Gly Asp Trp Val Glu Arg
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 Asn Ile Asp Pro Leu Arg Thr Thr Val Phe Phe Ala Ser Met Ser Pro
 355 360 365
 Leu His Ile Lys Ser Leu Asp Trp Glu Asn Pro Asp Gly Ile Lys Cys
 370 375 380
 Ala Leu Glu Thr Thr Pro Ile Leu Asn Met Ser Met Pro Phe Ser Val
 385 390 395 400
 Gly Thr Asp Tyr Arg Leu Phe Ser Val Ala Glu Asn Val Thr His Ser
 405 410 415
 Leu Asn Val Pro Val Tyr Phe Leu Asn Ile Thr Lys Leu Ser Glu Tyr
 420 425 430
 Arg Lys Asp Ala His Thr Ser Val His Thr Ile Arg Gln Gly Lys Met
 435 440 445
 Leu Thr Pro Glu Gln Gln Ala Asp Pro Asn Thr Tyr Ala Asp Cys Ile
 450 455 460
 His Trp Cys Leu Pro Gly Leu Pro Asp Thr Trp Asn Glu Phe Leu Tyr
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 Thr Arg Ile Ile Ser Arg Ser
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 <211> 1647
 <212> DNA
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tcaaaattca aaatcaaaat caaccacaac cctccaacac cacc atg cag agc tgg 176
 Met Gln Ser Trp

aag tgg aac agg aag aaa cca cct gtt ttc cct ttg ctt gtg ctt att 224
 Lys Trp Asn Arg Lys Lys Pro Pro Val Phe Pro Leu Leu Val Leu Ile
 5 10 15 20

tta ctg ttc ttc ata gcc ttc tca acc ctc cac agt gaa cac att ata 272
 Leu Leu Phe Phe Ile Ala Phe Ser Thr Leu His Ser Glu His Ile Ile
 25 30 35

caa cga atc cat gaa aat cca gat cat gtt cac aac cac caa gaa gtt 320
 Gln Arg Ile His Glu Asn Pro Asp His Val His Asn His Gln Glu Val
 40 45 50

tct tca gcc acc ttt gtc aaa ccc aac ctc tct ggt cac cta aag caa 368
 Ser Ser Ala Thr Phe Val Lys Pro Asn Leu Ser Gly His Leu Lys Gln
 55 60 65

gct gca gag gtt ttg gat aga ttc agt aga tgc aac tcc act gta gag 416
 Ala Ala Glu Val Leu Asp Arg Phe Ser Arg Cys Asn Ser Thr Val Glu
 70 75 80

tac aat ggc cgc aaa gtt gct tgg ctc ggc gat tct cag cat tcc ggt 464
 Tyr Asn Gly Arg Lys Val Ala Trp Leu Gly Asp Ser Gln His Ser Gly
 85 90 95 100

cac tgg agt gcg agg ccg gaa agt tgt gat gtt ttt tca ggc aaa tgg 512
 His Trp Ser Ala Arg Pro Glu Ser Cys Asp Val Phe Ser Gly Lys Trp
 105 110 115

ggt ttt gat aat gtt tca cat cca ctt tac aac gag tca gat tgc cct 560
 Val Phe Asp Asn Val Ser His Pro Leu Tyr Asn Glu Ser Asp Cys Pro
 120 125 130

tac atg tct gac caa ttg gcc tgt cac aag cat gga agg tct gat ttg 608
 Tyr Met Ser Asp Gln Leu Ala Cys His Lys His Gly Arg Ser Asp Leu
 135 140 145

ggg tac cag tac tgg aga tgg caa cca cat aac tgc aat ttg aaa agg 656
 Gly Tyr Gln Tyr Trp Arg Trp Gln Pro His Asn Cys Asn Leu Lys Arg

PF59082SeqList_PF59082.txt

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165	170	175	180
ttt gtt gga gat tca cta	aat aga ggg caa ttg	ata tct atg gta tgt	752
Phe Val Gly Asp Ser	Leu Asn Arg Gly Gln Trp	Ile Ser Met Val Cys	
185	190	195	
ttg tta caa tca gta att	cct gct gat aag aga tca atg tca cca aat	800	
Leu Leu Gln Ser Val Ile	Pro Ala Asp Lys Arg Ser Met Ser Pro Asn		
200	205	210	
gct cat ctc acc att ttc	aga gca gag gaa tac aat gca act gtg gaa	848	
Ala His Leu Thr Ile Phe	Arg Ala Glu Glu Tyr Asn Ala Thr Val Glu		
215	220	225	
ttt ctc tgg gct cct ctt	ctt gtt gaa tct aat tct gat gac cca gta	896	
Phe Leu Trp Ala Pro Leu	Leu Val Glu Ser Asn Ser Asp Asp Pro Val		
230	235	240	
aat cac aga cta gat gaa	cgg ata att cgt cct gat acg gtt ctt aga	944	
Asn His Arg Leu Asp Glu	Arg Ile Ile Arg Pro Asp Thr Val Leu Arg		
245	250	255	260
cat gca tca ctg tgg gaa	aat gct gat ata ctt gtt ttt aac aca tac	992	
His Ala Ser Leu Trp	Glu Asn Ala Asp Ile Leu Val Phe Asn Thr Tyr		
265	270	275	
tta tgg tgg aga caa ggc	cca gtc aag cta tta tgg aca gct gaa gaa	1040	
Leu Trp Trp Arg Gln Gly	Pro Val Lys Leu Leu Trp Thr Ala Glu Glu		
280	285	290	
aat gga gct tgt gaa gaa	ttg gat ggg cat gga gcc atg gag tta gcc	1088	
Asn Gly Ala Cys Glu Glu	Leu Asp Gly His Gly Ala Met Glu Leu Ala		
295	300	305	
atg gga gcc tgg gca gat	tgg gta tct tca aaa gtt gac cca ctc atg	1136	
Met Gly Ala Trp Ala Asp	Trp Val Ser Ser Lys Val Asp Pro Leu Met		
310	315	320	
aag cgt gtc ttt ttt gtg	aca atg tcg cca act cat ctc tgg agc cga	1184	
Lys Arg Val Phe Phe Val	Thr Met Ser Pro Thr His Leu Trp Ser Arg		
325	330	335	340
gag tgg aaa cca gga agc	aag ggt aac tgt tat ggg gag aag gat ccc	1232	
Glu Trp Lys Pro Gly Ser	Lys Gly Asn Cys Tyr Gly Glu Lys Asp Pro		
345	350	355	
att gac ctt gag ggc tac	tgg gga agt ggt tca gat ttg cct aca atg	1280	
Ile Asp Leu Glu Gly Tyr	Trp Gly Ser Gly Ser Asp Leu Pro Thr Met		
360	365	370	
agc acc gtg gag aag atc	cta aga cat ttg aac tca aaa gtt tct gtc	1328	
Ser Thr Val Glu Lys Ile	Leu Arg His Leu Asn Ser Lys Val Ser Val		
375	380	385	
atc aac att act caa cta	tca gag tat aga aag gat ggt cat cct tcc	1376	
Ile Asn Ile Thr Gln Leu	Ser Glu Tyr Arg Lys Asp Gly His Pro Ser		
390	395	400	
att ttt cgc aaa ttt tgg	gag ccc ctt cgg ccg gaa caa ttg tca aat	1424	
Ile Phe Arg Lys Phe Trp	Glu Pro Leu Arg Pro Glu Gln Leu Ser Asn		
405	410	415	420
ccc ccg tct tac tct gat	tgc att cat tgg tgc ttg cct ggg gta cct	1472	
Pro Pro Ser Tyr Ser Asp	Cys Ile His Trp Cys Leu Pro Gly Val Pro		
425	430	435	
gat gtg tgg aat gag tta	ctc ttc cat ttt ttg tag aaattgttta	1518	
Asp Val Trp Asn Glu Leu	Leu Leu Phe His Phe Leu		
440	445		
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 <211> 447
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PF59082SeqList_PF59082.txt

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Glu His Ile Ile Gln Arg Ile His Glu Asn Pro Asp His Val His Asn
35      40      45
His Gln Glu Val Ser Ser Ala Thr Phe Val Lys Pro Asn Leu Ser Gly
50      55      60
His Leu Lys Gln Ala Ala Glu Val Leu Asp Arg Phe Ser Arg Cys Asn
65      70      75      80
Ser Thr Val Glu Tyr Asn Gly Arg Lys Val Ala Trp Leu Gly Asp Ser
85      90      95
Gln His Ser Gly His Trp Ser Ala Arg Pro Glu Ser Cys Asp Val Phe
100     105     110
Ser Gly Lys Trp Val Phe Asp Asn Val Ser His Pro Leu Tyr Asn Glu
115     120     125
Ser Asp Cys Pro Tyr Met Ser Asp Gln Leu Ala Cys His Lys His Gly
130     135     140
Arg Ser Asp Leu Gly Tyr Gln Tyr Trp Arg Trp Gln Pro His Asn Cys
145     150     155     160
Asn Leu Lys Arg Trp Asn Val Lys Glu Met Trp Glu Lys Leu Arg Gly
165     170     175
Lys Arg Leu Met Phe Val Gly Asp Ser Leu Asn Arg Gly Gln Trp Ile
180     185     190
Ser Met Val Cys Leu Leu Gln Ser Val Ile Pro Ala Asp Lys Arg Ser
195     200     205
Met Ser Pro Asn Ala His Leu Thr Ile Phe Arg Ala Glu Glu Tyr Asn
210     215     220
Ala Thr Val Glu Phe Leu Trp Ala Pro Leu Leu Val Glu Ser Asn Ser
225     230     235     240
Asp Asp Pro Val Asn His Arg Leu Asp Glu Arg Ile Ile Arg Pro Asp
245     250     255
Thr Val Leu Arg His Ala Ser Leu Trp Glu Asn Ala Asp Ile Leu Val
260     265     270
Phe Asn Thr Tyr Leu Trp Trp Arg Gln Gly Pro Val Lys Leu Leu Trp
275     280     285
Thr Ala Glu Glu Asn Gly Ala Cys Glu Glu Leu Asp Gly His Gly Ala
290     295     300
Met Glu Leu Ala Met Gly Ala Trp Ala Asp Trp Val Ser Ser Lys Val
305     310     315     320
Asp Pro Leu Met Lys Arg Val Phe Phe Val Thr Met Ser Pro Thr His
325     330     335
Leu Trp Ser Arg Glu Trp Lys Pro Gly Ser Lys Gly Asn Cys Tyr Gly
340     345     350
Glu Lys Asp Pro Ile Asp Leu Glu Gly Tyr Trp Gly Ser Gly Ser Asp
355     360     365
Leu Pro Thr Met Ser Thr Val Glu Lys Ile Leu Arg His Leu Asn Ser
370     375     380
Lys Val Ser Val Ile Asn Ile Thr Gln Leu Ser Glu Tyr Arg Lys Asp
385     390     395     400
Gly His Pro Ser Ile Phe Arg Lys Phe Trp Glu Pro Leu Arg Pro Glu
405     410     415
Gln Leu Ser Asn Pro Pro Ser Tyr Ser Asp Cys Ile His Trp Cys Leu
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Pro Gly Val Pro Asp Val Trp Asn Glu Leu Leu Phe His Phe Leu
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<222> (20)..(1474)

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<400> 1837

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His	Val	Cys	Leu	Cys	Asn	Thr	Arg	His	Gly	Lys	Glu	Cys	Pro	His	Tyr	
			15					20					25			
aat	aaa	aga	ggg	gac	agc	gcc	aca	gcc	gat	tca	cca	gag	aaa	atg	aag	148
Asn	Lys	Arg	Gly	Asp	Ser	Ala	Thr	Ala	Asp	Ser	Pro	Glu	Lys	Met	Lys	
			30					35				40				
ccg	gag	cag	gcc	acc	cac	aac	aag	atg	acc	acg	gcg	acg	tcc	tcc	ccg	196
Pro	Glu	Gln	Ala	Thr	His	Asn	Lys	Met	Thr	Thr	Ala	Thr	Ser	Ser	Pro	
			45					50				55				
tcc	cct	gtc	gtc	ggc	ctg	cgg	ggc	gtg	gtg	agc	tcc	ctc	gtc	gcc	ttc	244
Ser	Pro	Val	Val	Gly	Leu	Arg	Gly	Val	Val	Ser	Ser	Leu	Val	Ala	Phe	
					65					70					75	
ttc	atc	gtc	gtc	agc	acc	gtc	tcc	ctg	ctg	ttc	gac	cgc	ggc	cac	gag	292
Phe	Ile	Val	Val	Ser	Thr	Val	Ser	Leu	Leu	Phe	Asp	Arg	Gly	His	Glu	
					80					85					90	
tcg	cag	gtg	cag	ctg	acg	gtc	cag	cac	cgg	cac	cag	gag	gtg	aag	gtg	340
Ser	Gln	Val	Gln	Leu	Thr	Val	Gln	His	Arg	His	Gln	Glu	Val	Lys	Val	
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gcg	gag	gcc	ggg	ggc	cac	gag	gag	cag	gtg	cag	tgg	acg	gac	gag	ctc	388
Ala	Ala	Ala	Gly	Gly	His	Glu	Ala	Gln	Val	Gln	Trp	Thr	Asp	Glu	Leu	
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atg	ggc	gag	gcc	atg	agg	ggc	tcc	ggc	gag	gag	tgc	aac	tgg	tcc	ttg	436
Met	Gly	Glu	Ala	Met	Arg	Gly	Ser	Gly	Glu	Glu	Cys	Asn	Trp	Ser	Leu	
							130				135					
gga	cgg	tgg	gtg	tac	gac	aac	acc	tcc	cag	ccg	ctc	tac	tcc	ggc	ctc	484
Gly	Arg	Trp	Val	Tyr	Asp	Asn	Thr	Ser	Gln	Pro	Leu	Tyr	Ser	Gly	Leu	
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aac	tgc	tcc	ttc	atc	ttc	gac	gag	gtc	gcc	tgc	gag	aag	tat	ggc	cgg	532
Asn	Cys	Ser	Phe	Ile	Phe	Asp	Glu	Val	Ala	Cys	Glu	Lys	Tyr	Gly	Arg	
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Asn	Asp	Thr	Arg	Tyr	Gln	Tyr	Trp	Arg	Trp	Gln	Pro	Asp	Gly	Cys	Asp	
										180						
ctt	cca	agg	ttc	aac	gcc	acg	aaa	ctg	ctc	gaa	aag	ctg	agg	aac	aag	628
Leu	Pro	Arg	Phe	Asn	Ala	Thr	Lys	Leu	Leu	Glu	Lys	Leu	Arg	Asn	Lys	
								195				200				
agg	atg	gtc	ttc	gtc	ggc	gac	tca	atc	aac	agg	aac	caa	tgg	gtc	tcc	676
Arg	Met	Val	Phe	Val	Gly	Asp	Ser	Ile	Asn	Arg	Asn	Gln	Trp	Val	Ser	
											215					
atg	gtg	tgc	atg	gtg	gag	gcc	tcc	atc	cct	gaa	ggc	cag	aag	atg	cgc	724
Met	Val	Cys	Met	Val	Glu	Ala	Ser	Ile	Pro	Glu	Gly	Gln	Lys	Met	Arg	
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gtt	tac	aac	ggc	tca	ctc	atc	tcc	ttc	acg	gca	ttc	gaa	tac	aat	gcg	772
Val	Tyr	Asn	Gly	Ser	Leu	Ile	Ser	Phe	Thr	Ala	Phe	Glu	Tyr	Asn	Ala	
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aca	atc	gac	ttc	tac	tgg	tcg	ccg	ctg	ata	cta	gaa	tcc	aac	agc	gac	820
Thr	Ile	Asp	Phe	Tyr	Trp	Ser	Pro	Leu	Ile	Leu	Glu	Ser	Asn	Ser	Asp	
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Asn	Pro	Ile	Ile	His	Arg	Val	Glu	Tyr	Arg	Ile	Ile	Arg	Ala	Glu	Lys	
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Ile	Glu	Lys	His	Ala	Arg	Ala	Trp	Gly	Asn	Ala	Asp	Val	Ile	Val	Phe	
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aac	tct	tac	ctt	tgg	tgg	agg	aag	cag	aag	ccc	gat	atg	aag	atg	aag	964
Asn	Ser	Tyr	Leu	Trp	Trp	Arg	Lys	Gln	Lys	Pro	Asp	Met	Lys	Met	Lys	
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gtc	atg	tat	ggc	tca	ttt	gag	gat	ggg	gat	gca	aag	cta	gac	gaa	gtg	1012
Val	Met	Tyr	Gly	Ser	Phe	Glu	Asp	Gly	Asp	Ala	Lys	Leu	Asp	Glu	Val	
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Glu	Met	Val	Glu	Gly	Phe	Glu	Ile	Ala	Leu	Lys	Lys	Leu	Thr	Glu	Trp	
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Val	Gly	Ala	Asn	Val	Asn	Asn	Lys	Thr	Lys	Ile	Tyr	Phe	Ala	Gly	Ser	
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PF59082SeqList_PF59082.txt

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Lys Cys Leu Asn Glu Ser Glu Pro Ile Gln Lys Val Gly Tyr Lys Gly	
380 385 390 395	
gcg acc acg gac tac agc atg atg gac aag gcg aag cag atc ttc aga	1252
Ala Thr Thr Asp Tyr Ser Met Met Asp Lys Ala Lys Gln Ile Phe Arg	
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cca ctg gag cag aaa ggc ata aac gtt cag ata ctc aac ttc acc cag	1300
Pro Leu Glu Gln Lys Gly Ile Asn Val Gln Ile Leu Asn Phe Thr Gln	
415 420 425	
ctg acc gac tac cgc atc gac gcg cac ccc acc gtg ttc cgg cgg cag	1348
Leu Thr Asp Tyr Arg Ile Asp Ala His Pro Thr Val Phe Arg Arg Gln	
430 435 440	
ttc acc ccc ctc acg aag gag cag atc gcc aac ccg agc agc tac gcc	1396
Phe Thr Pro Leu Thr Lys Glu Gln Ile Ala Asn Pro Ser Ser Tyr Ala	
445 450 455	
gac tgc acg cac tgg tgc ctc ccc ggc gtc cct gac gtg tgg aac cac	1444
Asp Cys Thr His Trp Cys Leu Pro Gly Val Pro Asp Val Trp Asn His	
460 465 470 475	
ttc ctc tac tgc tat ctc gtg cag aaa tga tgtaaatata catatacatg	1494
Phe Leu Tyr Ser Tyr Leu Val Gln Lys	
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 <212> PRT
 <213> Triticum aestivum

<400> 1838

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His Asn Lys Met Thr Thr Ala Thr Ser Ser Pro Ser Pro Val Val Gly	50 55 60
Leu Arg Gly Val Val Ser Ser Leu Val Ala Phe Phe Ile Val Val Ser	65 70 75 80
Thr Val Ser Leu Leu Phe Asp Arg Gly His Glu Ser Gln Val Gln Leu	85 90 95
Thr Val Gln His Arg His Gln Glu Val Lys Val Ala Ala Ala Gly Gly	100 105 110
His Glu Ala Gln Val Gln Trp Thr Asp Glu Leu Met Gly Glu Ala Met	115 120 125
Arg Gly Ser Gly Glu Glu Cys Asn Trp Ser Leu Gly Arg Trp Val Tyr	130 135 140
Asp Asn Thr Ser Gln Pro Leu Tyr Ser Gly Leu Asn Cys Ser Phe Ile	145 150 155 160
Phe Asp Glu Val Ala Cys Glu Lys Tyr Gly Arg Asn Asp Thr Arg Tyr	165 170 175
Gln Tyr Trp Arg Trp Gln Pro Asp Gly Cys Asp Leu Pro Arg Phe Asn	180 185 190
Ala Thr Lys Leu Leu Glu Lys Leu Arg Asn Lys Arg Met Val Phe Val	195 200 205

PF59082SeqList_PF59082.txt

Gly Asp Ser Ile Asn Arg Asn Gln Trp Val Ser Met Val Cys Met Val
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 Glu Ala Ser Ile Pro Glu Gly Gln Lys Met Arg Val Tyr Asn Gly Ser
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 245 250 255
 Trp Ser Pro Leu Ile Leu Glu Ser Asn Ser Asp Asn Pro Ile Ile His
 260 265 270
 Arg Val Glu Tyr Arg Ile Ile Arg Ala Glu Lys Ile Glu Lys His Ala
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 Arg Ala Trp Gly Asn Ala Asp Val Ile Val Phe Asn Ser Tyr Leu Trp
 290 295 300
 Trp Arg Lys Gln Lys Pro Asp Met Lys Met Lys Val Met Tyr Gly Ser
 305 310 315 320
 Phe Glu Asp Gly Asp Ala Lys Leu Asp Glu Val Glu Met Val Glu Gly
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 Phe Glu Ile Ala Leu Lys Lys Leu Thr Glu Trp Val Gly Ala Asn Val
 340 345 350
 Asn Asn Lys Thr Lys Ile Tyr Phe Ala Gly Ser Ser Pro Thr His Thr
 355 360 365
 Trp Ala Ser Asp Trp Gly Gly Asp Asp Ser Asn Lys Cys Leu Asn Glu
 370 375 380
 Ser Glu Pro Ile Gln Lys Val Gly Tyr Lys Gly Ala Thr Thr Asp Tyr
 385 390 395 400
 Ser Met Met Asp Lys Ala Lys Gln Ile Phe Arg Pro Leu Glu Gln Lys
 405 410 415
 Gly Ile Asn Val Gln Ile Leu Asn Phe Thr Gln Leu Thr Asp Tyr Arg
 420 425 430
 Ile Asp Ala His Pro Thr Val Phe Arg Arg Gln Phe Thr Pro Leu Thr
 435 440 445
 Lys Glu Gln Ile Ala Asn Pro Ser Ser Tyr Ala Asp Cys Thr His Trp
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 Leu Val Gln Lys

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 <213> Arabidopsis thaliana

<220>
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 Lys Ser Asp Leu Gly Ile Ser Ser Phe Pro Lys Ser Ser Gln Ile Ser
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 att cat cga tgt cag aag aaa tcg atc tca cgg aag att gtt tcc gtt 144
 Ile His Arg Cys Gln Lys Lys Ser Ile Ser Arg Lys Ile Val Ser Val
 35 40 45
 atg gct cct caa aag gat cgg tct cct gga act aca gga tcg gtg aaa 192
 Met Ala Pro Gln Lys Asp Arg Ser Pro Gly Thr Thr Gly Ser Val Lys
 50 55 60
 act ggg atg aca atg acg gag aag att cta gct aga gct tcg gag aag 240
 Thr Gly Met Thr Met Thr Glu Lys Ile Leu Ala Arg Ala Ser Glu Lys
 65 70 75 80
 tca tta gtg gtt cct ggt gat aac att tgg gtt aat gtt gat gtt ctt 288
 Ser Leu Val Val Pro Gly Asp Asn Ile Trp Val Asn Val Asp Val Leu
 85 90 95
 atg act cat gat gtt tgt ggt cct ggt gct ttt ggt atc ttc aag aga 336
 Met Thr His Asp Val Cys Gly Pro Gly Ala Phe Gly Ile Phe Lys Arg
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 gag ttt ggt gaa aaa gcc aag gtt tgg gat ccg gag aag att gtt gtg 384

PF59082SeqList_PF59082.txt

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Ile	Pro	Asp	His	Tyr	Ile	Phe	Thr	Ala	Asp	Lys	Arg	Ala	Asn	Arg	Asn	
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Tyr	Asp	Ile	Thr	Asp	Leu	Gly	Asn	Phe	Lys	Ala	Asn	Pro	Asp	Tyr	Lys	
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ggg	gtt	tgc	cat	gtt	gca	ctt	gca	caa	gaa	ggg	cat	tgc	agg	cca	gga	576
Gly	Val	Cys	His	Val	Ala	Leu	Ala	Gln	Glu	Gly	His	Cys	Arg	Pro	Gly	
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Glu	Val	Leu	Leu	Gly	Thr	Asp	Ser	His	Thr	Cys	Thr	Ala	Gly	Ala	Phe	
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Gly	Gln	Phe	Ala	Thr	Gly	Ile	Gly	Asn	Thr	Asp	Ala	Gly	Phe	Val	Leu	
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Gly	Thr	Gly	Lys	Ile	Leu	Leu	Lys	Val	Pro	Pro	Thr	Met	Arg	Phe	Ile	
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Leu	Asp	Gly	Glu	Met	Pro	Ser	Tyr	Leu	Gln	Ala	Lys	Asp	Leu	Ile	Leu	
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Gln	Ile	Ile	Gly	Glu	Ile	Ser	Val	Ala	Gly	Ala	Thr	Tyr	Lys	Thr	Met	
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Tyr	Arg	Phe	Asp	Val	Ser	Lys	Leu	Glu	Pro	Val	Val	Ala	Lys	Pro	His	
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Ser	Pro	Asp	Asn	Arg	Ala	Leu	Ala	Arg	Glu	Cys	Lys	Asp	Val	Lys	Ile	
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gac	aga	gta	tac	atc	ggg	tct	tgt	act	ggg	ggg	aag	aca	gag	gat	ttt	1152
Asp	Arg	Val	Tyr	Ile	Gly	Ser	Cys	Thr	Gly	Gly	Lys	Thr	Glu	Asp	Phe	
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Pro	Thr	Phe	Leu	Val	Pro	Ala	Thr	Gln	Lys	Val	Trp	Met	Asp	Val	Tyr	
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Ala	Leu	Pro	Val	Pro	Gly	Ala	Gly	Gly	Lys	Thr	Cys	Ala	Gln	Ile	Phe	
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gaa	gaa	gct	ggc	tgt	gac	aca	cca	gcc	agc	cct	agc	tgt	ggg	gct	tgc	1344
Glu	Glu	Ala	Gly	Cys	Asp	Thr	Pro	Ala	Ser	Pro	Ser	Cys	Gly	Ala	Cys	
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Leu	Gly	Gly	Pro	Ala	Asp	Thr	Tyr	Ala	Arg	Leu	Asn	Glu	Pro	Gln	Val	
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Cys	Val	Ser	Thr	Thr	Asn	Arg	Asn	Phe	Pro	Gly	Arg	Met	Gly	His	Lys	
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PF59082SeqList_PF59082.txt

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1530

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 Thr Gly Met Thr Met Thr Glu Lys Ile Leu Ala Arg Ala Ser Glu Lys
 65 70 75 80
 Ser Leu Val Val Pro Gly Asp Asn Ile Trp Val Asn Val Asp Val Leu
 85 90 95
 Met Thr His Asp Val Cys Gly Pro Gly Ala Phe Gly Ile Phe Lys Arg
 100 105 110
 Glu Phe Gly Glu Lys Ala Lys Val Trp Asp Pro Glu Lys Ile Val Val
 115 120 125
 Ile Pro Asp His Tyr Ile Phe Thr Ala Asp Lys Arg Ala Asn Arg Asn
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 Val Asp Ile Met Arg Glu His Cys Arg Glu Gln Asn Ile Lys Tyr Phe
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 Gly Val Cys His Val Ala Leu Ala Gln Glu Gly His Cys Arg Pro Gly
 180 185 190
 Glu Val Leu Leu Gly Thr Asp Ser His Thr Cys Thr Ala Gly Ala Phe
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 Gly Gln Phe Ala Thr Gly Ile Gly Asn Thr Asp Ala Gly Phe Val Leu
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 Gly Thr Gly Lys Ile Leu Leu Lys Val Pro Pro Thr Met Arg Phe Ile
 225 230 235 240
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 Gln Ile Ile Gly Glu Ile Ser Val Ala Gly Ala Thr Tyr Lys Thr Met
 260 265 270
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 325 330 335
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 370 375 380
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 385 390 395 400
 Pro Thr Phe Leu Val Pro Ala Thr Gln Lys Val Trp Met Asp Val Tyr
 405 410 415
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PF59082SeqList_PF59082.txt

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 Ser Ser Pro Phe Val Cys Lys Ser Pro Ala Lys Lys Asp Leu Gly Val 10 15 20
 tct tcg ttc cgt aaa gca tcg cag att tcg att cat gga tgc cag agg 149
 Ser Ser Phe Arg Lys Ala Ser Gln Ile Ser Ile His Gly Cys Gln Arg 25 30 35
 aaa tcg att tct cgg aag atc gtc tcc gtc atg gct ccg cag cgc tca 197
 Lys Ser Ile Ser Arg Lys Ile Val Ser Val Met Ala Pro Gln Arg Ser 40 45 50 55
 tcg tcc acc tca gga tcg gtg aaa act ggg atg acg atg acg gag aag 245
 Ser Ser Thr Ser Gly Ser Val Lys Thr Gly Met Thr Met Thr Glu Lys 60 65 70
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 Ile Trp Val Asn Val Asp Val Leu Met Thr His Asp Val Cys Gly Pro 90 95 100
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 Gly Ala Phe Gly Ile Phe Lys Arg Glu Phe Gly Asp Asn Ala Lys Val 105 110 115
 tgg gac tcg gag aag atc gtt gtt ata cca gac cat tac ata ttc aca 437
 Trp Asp Ser Glu Lys Ile Val Val Ile Pro Asp His Tyr Ile Phe Thr 120 125 130 135
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 Ser Asp Lys Arg Ala Asn Arg Asn Val Asp Ile Met Arg Glu His Cys 140 145 150
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 Arg Glu Gln Asn Ile Lys Tyr Phe Tyr Asp Ile Thr Asp Leu Gly Asp 155 160 165
 ttt agg gct aat cct gac tac aaa ggt gtt tgc cat gtt gcg ctt gca 581
 Phe Arg Ala Asn Pro Asp Tyr Lys Gly Val Cys His Val Ala Leu Ala 170 175 180
 caa gaa ggt cat tgc agg cct gga gag gtt ttg tta gga aca gac tca 629
 Gln Glu Gly His Cys Arg Pro Gly Glu Val Leu Leu Gly Thr Asp Ser 185 190 195
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 His Thr Cys Thr Ala Gly Ala Phe Gly Gln Phe Ala Thr Gly Ile Gly 200 205 210 215
 aac act gat gca ggc ttt gtg tta ggc act gga aaa atc ctc ctt aag 725
 Asn Thr Asp Ala Gly Phe Val Leu Gly Thr Gly Lys Ile Leu Leu Lys 220 225 230
 gtt cca cca act atg agg ttt atc ttg gat ggt gaa atg ccc agt tat 773
 Val Pro Pro Thr Met Arg Phe Ile Leu Asp Gly Glu Met Pro Ser Tyr 235 240 245
 ttg caa gca aag gat ctg att ctg cag atc att ggt gaa ata tct gtt 821
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Ser	Leu	Thr	Met	Glu	Glu	Arg	Met	Thr	Leu	Cys	Asn	Met	Val	Val	Glu	
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Tyr	Val	Glu	Asn	Arg	Thr	Ser	Val	Pro	Phe	Gln	Pro	Val	Tyr	Ser	Asp	
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Ala	Asn	Ala	Ser	Phe	Val	Ala	Asp	Tyr	Arg	Phe	Asp	Val	Ser	Lys	Leu	
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Glu	Pro	Val	Val	Ala	Lys	Pro	His	Ser	Pro	Asp	Asn	Arg	Ala	Leu	Ala	
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Arg	Glu	Cys	Lys	Asp	Val	Lys	Ile	Asp	Arg	Val	Tyr	Ile	Gly	Ser	Cys	
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Ala	Ala	Gly	Lys	Gln	Val	Lys	Val	Pro	Thr	Phe	Leu	Val	Pro	Ala	Thr	
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Gln	Lys	Val	Trp	Met	Asp	Val	Tyr	Ala	Leu	Pro	Val	Pro	Gly	Ala	Gly	
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Thr	Ser	Pro	Ser	Cys	Gly	Ala	Cys	Leu	Gly	Pro	Ala	Asp	Thr	Tyr		
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Ala	Arg	Leu	Asn	Glu	Pro	Gln	Val	Cys	Val	Ser	Thr	Thr	Asn	Arg	Asn	
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Phe	Pro	Gly	Arg	Met	Gly	His	Lys	Glu	Gly	Gln	Ile	Tyr	Leu	Ala	Ser	
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 35 40 45 50

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Pro	Asp	His	Tyr	Ile	Phe	Thr	Ser	Asp	Lys	Arg	Ala	Asn	Arg	Asn	Val
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Val	Ser	Thr	Thr	Asn	Arg	Asn	Phe	Pro	Gly	Arg	Met	Gly	His	Lys	Glu
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Glu Lys Ser Gln Val Val Pro Gly Asp Asn Ile Trp Val Asn Val Asp
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Val Leu Met Thr His Asp Val Cys Gly Pro Gly Ala Phe Gly Ile Phe
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Lys Arg Gln Phe Gly Glu Asn Ala Lys Val Trp Asp Ser Glu Lys Ile
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Val Val Ile Pro Asp His Tyr Ile Phe Thr Thr Asp Lys Arg Ala Asn
125          130          135
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gca ttc ggt cag ttt gct aca ggg att gga aac act gat gca ggc ttt      676
Ala Phe Gly Gln Phe Ala Thr Gly Ile Gly Asn Thr Asp Ala Gly Phe
200          205          210
gtg tta ggc act gga aaa atc ctc ctt aag gtt cca cca act atg agg      724
Val Leu Gly Thr Gly Lys Ile Leu Leu Val Pro Pro Thr Met Arg
215          220          225
ttt atc ttg gat ggt gaa atg ccc agt tat ttg caa gca aag gat ctg      772
Phe Ile Leu Asp Gly Glu Met Pro Ser Tyr Leu Gln Ala Lys Asp Leu
230          235          240
att ctg cag atc att ggt gaa ata tct gtt gct ggt gca act tac aag      820
Ile Leu Gln Ile Ile Gly Glu Ile Ser Val Ala Gly Ala Thr Tyr Lys
245          250          255
acg atg gag ttc agt ggt aca act att gaa agt ctg act atg gaa gaa      868
Thr Met Gln Phe Ser Gly Thr Thr Ile Glu Ser Leu Thr Met Glu Glu
260          265          270
cga atg aca ttg tgc aac atg gtt gtg gaa gct ggg gga aag aat ggt      916
Arg Met Thr Leu Cys Asn Met Val Val Glu Ala Gly Gly Lys Asn Gly
275          280          285
gtc atc cct cct gat gcg acg aca ttc aat tac gtt gag aat agg aca      964
Val Ile Pro Pro Asp Ala Thr Thr Phe Asn Tyr Val Glu Asn Arg Thr
290          295          300
tct gta ccc ttt cag cct gta tat agt gat gga aat gca agc ttt gtg      1012
Ser Val Pro Phe Gln Pro Val Tyr Ser Asp Gly Asn Ala Ser Phe Val
305          310          315
gca gat tat aga ttt gat gtg tca aag cta gag cct gtg gtt gct aag      1060
Ala Asp Tyr Arg Phe Asp Val Ser Lys Leu Glu Pro Val Val Ala Lys
320          325          330
cct cat tct cct gat aat cgt gct cta gcg aga gaa tgc aaa gat gtg      1108
Pro His Ser Pro Asp Asn Arg Ala Leu Ala Arg Glu Cys Lys Asp Val
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PF59082SeqList_PF59082.txt

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gat ttt atg gct gca gct aaa ctt ttc cat gca gca gga aag caa gtc      1204
Asp Phe Met Ala Ala Lys Leu Phe His Ala Ala Gly Lys Gln Val
          385          390          395
aaa gtt cca act ttc ctt gtc ccg gcc act cag aag gtg tgg atg gac      1252
Lys Val Pro Thr Phe Leu Val Pro Ala Thr Gln Lys Val Trp Met Asp
          400          405          410
gtg tat gca ctc cca gta cct gga gcg ggt gga aag aca tgt gcg cag      1300
Val Tyr Ala Leu Pro Val Pro Gly Ala Gly Gly Lys Thr Cys Ala Gln
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att ttt gaa gaa gct gga tgt gac aca cca acc agt cct agc tgt ggt      1348
Ile Phe Glu Glu Ala Gly Cys Asp Thr Pro Thr Ser Pro Ser Cys Gly
          430          435          440
gcc tgc ctt ggt ggc cca gca gac acc tac gct cgt ttg aat gaa cct      1396
Ala Cys Leu Gly Gly Pro Ala Asp Thr Tyr Ala Arg Leu Asn Glu Pro
          445          450          455          460
caa gtg tgt gtc tcg aca acg aac agg aac ttc ccc ggt cgg atg gga      1444
Gln Val Cys Val Ser Thr Asn Arg Asn Phe Pro Gly Arg Met Gly
          465          470          475
cac aaa gaa ggg cag ata tac ttg gct tct cct tac act gct gca gcc      1492
His Lys Glu Gly Gln Ile Tyr Leu Ala Ser Pro Tyr Thr Ala Ala Ala
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tcg gct cta acc ggc cat gtc acc gac cca aga gag ttc ttg cag tag      1540
Ser Ala Leu Thr Gly His Val Thr Asp Pro Arg Glu Phe Leu Gln
          495          500          505
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aagtgatgtg cattgtgaac tatagtgtgt attttccttg cttcgctgtt gaactttgat      1660

agtttgaaca agcagtatatt tctgttttga gtttgaaaga acaaaggata atcatataag      1720

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<210> 1844
 <211> 507
 <212> PRT
 <213> Brassica napus

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<400> 1844
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35      40      45
Met Ala Pro Gln Arg Ser Ser Thr Ser Gly Ser Val Lys Thr Gly
50      55      60
Met Thr Met Thr Glu Lys Ile Leu Ala Lys Ala Ala Glu Lys Ser Gln
65      70      75      80
Val Val Pro Gly Asp Asn Ile Trp Val Asn Val Asp Val Leu Met Thr
85      90      95
His Asp Val Cys Gly Pro Gly Ala Phe Gly Ile Phe Lys Arg Glu Phe
100      105      110
Gly Glu Asn Ala Lys Val Trp Asp Ser Glu Lys Ile Val Val Ile Pro
115      120      125
Asp His Tyr Ile Phe Thr Thr Asp Lys Arg Ala Asn Arg Asn Val Asp
130      135      140
Ile Met Arg Glu His Cys Arg Glu Gln Asn Ile Lys Tyr Phe Tyr Asp
145      150      155      160
Ile Thr Asp Leu Gly Asp Phe Arg Ala Asn Pro Asp Tyr Lys Gly Val
165      170      175

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PF59082SeqList_PF59082.txt

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 Leu Leu Gly Thr Asp Ser His Thr Cys Thr Ala Gly Ala Phe Gly Gln
 195 200 205
 Phe Ala Thr Gly Ile Gly Asn Thr Asp Ala Gly Phe Val Leu Gly Thr
 210 215 220
 Gly Lys Ile Leu Leu Lys Val Pro Pro Thr Met Arg Phe Ile Leu Asp
 225 230 235 240
 Gly Glu Met Pro Ser Tyr Leu Gln Ala Lys Asp Leu Ile Leu Gln Ile
 245 250 255
 Ile Gly Glu Ile Ser Val Ala Gly Ala Thr Tyr Lys Thr Met Glu Phe
 260 265 270
 Ser Gly Thr Thr Ile Glu Ser Leu Thr Met Glu Glu Arg Met Thr Leu
 275 280 285
 Cys Asn Met Val Val Glu Ala Gly Gly Lys Asn Gly Val Ile Pro Pro
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 Asp Ala Thr Thr Phe Asn Tyr Val Glu Asn Arg Thr Ser Val Pro Phe
 305 310 315 320
 Gln Pro Val Tyr Ser Asp Gly Asn Ala Ser Phe Val Ala Asp Tyr Arg
 325 330 335
 Phe Asp Val Ser Lys Leu Glu Pro Val Val Ala Lys Pro His Ser Pro
 340 345 350
 Asp Asn Arg Ala Leu Ala Arg Glu Cys Lys Asp Val Lys Ile Asp Arg
 355 360 365
 Val Tyr Ile Gly Ser Cys Thr Gly Gly Lys Thr Glu Asp Phe Met Ala
 370 375 380
 Ala Ala Lys Leu Phe His Ala Ala Gly Lys Gln Val Lys Val Pro Thr
 385 390 395 400
 Phe Leu Val Pro Ala Thr Gln Lys Val Trp Met Asp Val Tyr Ala Leu
 405 410 415
 Pro Val Pro Gly Ala Gly Gly Lys Thr Cys Ala Gln Ile Phe Glu Glu
 420 425 430
 Ala Gly Cys Asp Thr Pro Thr Ser Pro Ser Cys Gly Ala Cys Leu Gly
 435 440 445
 Gly Pro Ala Asp Thr Tyr Ala Arg Leu Asn Glu Pro Gln Val Cys Val
 450 455 460
 Ser Thr Thr Asn Arg Asn Phe Pro Gly Arg Met Gly His Lys Glu Gly
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<211> 1805

<212> DNA

<213> Linum usitatissimum

<220>

<221> CDS

<222> (27)..(1559)

<400> 1845

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 Ser Thr Ser Phe Leu Pro Gly Lys Glu Leu Gly Arg Ser Val Phe Ala
 10 15 20 25
 caa cca ccc tcc tct atc tcg gtt ccc aaa tgc agg aat tcg atc tcc 149
 Gln Pro Pro Ser Ser Ile Ser Val Pro Lys Cys Arg Asn Ser Ile Ser
 30 35 40
 aag aaa att gtt tcc gtc atg gct cca cat caa tca gag cgc aag cct 197
 Lys Lys Ile Val Ser Val Met Ala Pro His Gln Ser Glu Arg Lys Pro
 45 50 55
 tca act act ggc acg gtg aag act gct atg aca atg aca gaa aaa atc 245
 Ser Thr Thr Gly Thr Val Lys Thr Ala Met Thr Met Thr Glu Lys Ile
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 ttg gct atg gct gca gag aag tcc cag ttg agc ccc ggt gaa aat gtt 293
 75 80 85 90 95

PF59082SeqList_PF59082.txt

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Trp	Val	Asn	Val	Asp	Val	Leu	Met	Thr	His	Asp	Val	Cys	Gly	Pro	Gly	
90					95					100					105	
tct	ttt	gat	atc	ttc	aag	aaa	gag	ttt	ggg	cag	aat	gct	aag	ggt	tgg	389
Ser	Phe	Asp	Ile	Phe	Lys	Lys	Glu	Phe	Gly	Gln	Asn	Ala	Lys	Val	Trp	
				110					115					120		
gat	cgt	gag	aag	att	gtg	gtg	ata	cct	gaa	cat	tac	ata	ttc	acc	aac	437
Asp	Arg	Glu	Lys	Ile	Val	Val	Ile	Pro	Glu	His	Tyr	Ile	Phe	Thr	Asn	
				125				130					135			
gac	aaa	cgt	gcg	aat	agg	aat	gtg	gat	atc	ttg	aga	gaa	ttc	tgc	acg	485
Asp	Lys	Arg	Ala	Asn	Arg	Asn	Val	Asp	Ile	Leu	Arg	Glu	Phe	Cys	Thr	
		140				145						150				
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Glu	Gln	Asn	Ile	Lys	Tyr	Phe	Tyr	Asp	Ile	Gln	Asp	Arg	Ala	Asn	Phe	
	155					160				165						
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Lys	Ala	Asn	Pro	Asp	Tyr	Lys	Gly	Val	Cys	His	Ile	Ala	Leu	Ala	Gln	
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Glu	Gly	His	Cys	Arg	Pro	Gly	Glu	Val	Leu	Leu	Gly	Thr	Asp	Ser	His	
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Thr	Cys	Thr	Ala	Gly	Ala	Phe	Gly	Gln	Phe	Ala	Thr	Gly	Ile	Gly	Asn	
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Thr	Asp	Ala	Gly	Phe	Val	Leu	Gly	Thr	Gly	Lys	Ala	Leu	Leu	Lys	Val	
		220				225						230				
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Pro	Pro	Thr	Leu	Arg	Phe	Val	Met	Asp	Gly	Glu	Met	Pro	Asp	Cys	Ile	
	235					240				245						
ctt	gct	aag	gat	ttg	att	ttg	caa	atc	att	ggg	gaa	ata	tct	gtg	gcg	821
Leu	Ala	Lys	Asp	Leu	Ile	Leu	Gln	Ile	Ile	Gly	Glu	Ile	Ser	Val	Ala	
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Gly	Ala	Thr	Tyr	Lys	Ser	Met	Glu	Phe	Val	Gly	Thr	Thr	Val	Glu	Gly	
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Leu	Ser	Met	Glu	Arg	Met	Thr	Leu	Cys	Asn	Met	Val	Ile	Glu	Ala		
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Gly	Gly	Lys	Asn	Gly	Val	Val	Pro	Ala	Asp	Asn	Thr	Thr	Phe	Asn	Tyr	
		300				305						310				
ctt	gag	gac	aag	gta	tct	gtt	ccc	tat	gag	cca	gtt	tac	agt	gac	caa	1013
Leu	Glu	Asp	Lys	Val	Ser	Val	Pro	Tyr	Glu	Pro	Val	Tyr	Ser	Asp	Gln	
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Gln	Ala	Arg	Tyr	Leu	Ser	Glu	Tyr	Arg	Phe	Asp	Val	Ser	Lys	Leu	Glu	
330					335					340					345	
cca	cta	ggt	gct	aag	ccc	cat	tct	cct	gat	aac	cga	gct	tta	gca	aga	1109
Pro	Leu	Val	Ala	Lys	Pro	His	Ser	Pro	Asp	Asn	Arg	Ala	Leu	Ala	Arg	
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gag	tgc	aaa	gat	gtc	aag	att	gac	aga	gta	tat	att	gga	tct	tgt	act	1157
Glu	Cys	Lys	Asp	Val	Lys	Ile	Asp	Arg	Val	Tyr	Ile	Gly	Ser	Cys	Thr	
				365				370					375			
gga	gga	aaa	act	gag	gat	ttt	atg	gct	gcg	gca	aaa	ggt	ttt	tta	gct	1205
Gly	Gly	Lys	Thr	Glu	Asp	Phe	Met	Ala	Ala	Ala	Lys	Val	Phe	Leu	Ala	
		380				385						390				
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Ser	Gly	Tyr	Lys	Lys	Val	Lys	Ala	Pro	Thr	Phe	Leu	Val	Pro	Ala	Thr	
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Gln	Lys	Val	Trp	Met	Asp	Val	Tyr	Ser	Leu	Pro	Val	Pro	Gly	Ser	Gly	
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Gly	Lys	Thr	Cys	Ser	Gln	Ile	Phe	Glu	Glu	Val	Gly	Cys	Asp	Thr	Pro	
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PF59082SeqList_PF59082.txt

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Phe	Pro	Gly	Arg	Met	Gly	His	Lys	Glu	Gly	Glu	Ile	Tyr	Leu	Ala	Ser		
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Pro	Tyr	Thr	Ala	Ala	Ala	Ser	Ala	Leu	Thr	Gly	Tyr	Val	Thr	Asp	Pro		
	490				495					500					505		
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Arg	Glu	Phe	Leu	His													
			510														
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<211> 510

<212> PRT

<213> Linum usitatissimum

<400> 1846

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Val	Pro	Lys	Cys	Arg	Asn	Ser	Ile	Ser	Lys	Lys	Ile	Val	Ser	Val	Met		
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Val	Asp	Ile	Leu	Arg	Glu	Phe	Cys	Thr	Glu	Gln	Asn	Ile	Lys	Tyr	Phe		
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Glu	Val	Leu	Leu	Gly	Thr	Asp	Ser	His	Thr	Cys	Thr	Ala	Gly	Ala	Phe		
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Gln	Ile	Ile	Gly	Glu	Ile	Ser	Val	Ala	Gly	Ala	Thr	Tyr	Lys	Ser	Met		
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PF59082SeqList_PF59082.txt

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 Ser Pro Asp Asn Arg Ala Leu Ala Arg Glu Cys Lys Asp Val Lys Ile
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 Asp Arg Val Tyr Ile Gly Ser Cys Thr Gly Gly Lys Thr Glu Asp Phe
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 Tyr Ser Leu Pro Val Pro Gly Ser Gly Gly Lys Thr Cys Ser Gln Ile
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 Phe Glu Glu Val Gly Cys Asp Thr Pro Ala Ser Pro Ser Cys Gly Ala
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 Cys Leu Gly Gly Pro Lys Asp Thr Tyr Gly Arg Leu Asn Glu Pro Lys
 450 455 460
 Val Cys Val Ser Thr Thr Asn Arg Asn Phe Pro Gly Arg Met Gly His
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<210> 1847

<211> 1929

<212> DNA

<213> Arabidopsis thaliana

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<222> (1)..(1929)

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Phe Asn Ile Ser Thr Gly Gly Phe Asp Tyr Val Leu Ala Pro Leu Val	
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gat cct tcg tat agg ccg agc ttg gtg gaa gga aat ggt gta gat act	192
Asp Pro Ser Tyr Arg Pro Ser Leu Val Glu Gly Asn Gly Val Asp Thr	
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tgg agc agt cat gtt gtt gga aaa att agt tcg tgg att gac ttg gat	288
Trp Ser Ser His Val Val Gly Lys Ile Ser Ser Trp Ile Asp Leu Asp	
85 90 95	
tct gaa gat gag gtc tta cgg atg gat tca gaa acc aca ttg aag caa	336
Ser Glu Asp Glu Val Leu Arg Met Asp Ser Glu Thr Thr Leu Lys Gln	
100 105 110	
gaa ata gct tgg gct act cat ctc tcc tta cag gca tgc ctt ctt ccc	384
Glu Ile Ala Trp Ala Thr His Leu Ser Leu Gln Ala Cys Leu Leu Pro	
115 120 125	
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130 135 140	
atc tta caa ggc ctc act acc ttg cag tta tgg cta agg gtt cca ctg	480
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PF59082SeqList_PF59082.txt

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gat	tcc	tgg	gag	ctg	tgg	aat	tcg	ttt	cgt	ctt	ctt	tgt	gag	cat	gac	576
Asp	Ser	Trp	Glu	Leu	Trp	Asn	Ser	Phe	Arg	Leu	Leu	Cys	Glu	His	Asp	
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Ser	Lys	Leu	Ser	Val	Ala	Leu	Asp	Val	Leu	Ser	Thr	Leu	Pro	Ser	Glu	
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Thr	Ser	Leu	Gly	Arg	Trp	Met	Gly	Glu	Ser	Val	Arg	Ala	Ala	Ile	Leu	
	210					215					220					
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Ser	Thr	Asp	Ala	Phe	Leu	Thr	Asn	Ala	Arg	Gly	Tyr	Pro	Cys	Leu	Ser	
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Val	Val	Ile	Cys	Gly	Lys	Pro	Val	His	Asn	Leu	Gln	Lys	Pro	Leu	Asp	
			260					265					270			
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Ser	Ser	Ser	Glu	Gly	Thr	Glu	Lys	Asn	Pro	Leu	Arg	Ile	Tyr	Leu	Asp	
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Tyr	Val	Ala	Tyr	Leu	Phe	Gln	Lys	Met	Glu	Ser	Leu	Ser	Glu	Gln	Glu	
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ctt	atg	gac	aac	ctc	gaa	gcc	caa	acc	tat	gag	acg	ttt	gag	aga	gac	1008
Leu	Met	Asp	Asn	Leu	Glu	Ala	Gln	Thr	Tyr	Glu	Thr	Phe	Glu	Arg	Asp	
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Ser	Val	Lys	Tyr	Ile	Gln	Tyr	Gln	Arg	Ala	Val	Glu	Lys	Ala	Leu	Val	
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Val	Val	Gly	Ala	Gly	Arg	Gly	Pro	Leu	Val	Arg	Ala	Ser	Leu	Gln	Ala	
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Ala	Glu	Glu	Thr	Asp	Arg	Lys	Leu	Lys	Val	Tyr	Ala	Val	Glu	Lys	Asn	
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cct	aat	gcc	gtt	gta	aca	ctc	cat	aat	ttg	gtt	aag	atg	gaa	gga	tgg	1248
Pro	Asn	Ala	Val	Val	Thr	Leu	His	Asn	Leu	Val	Lys	Met	Glu	Gly	Trp	
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Glu	Asp	Val	Val	Thr	Ile	Ile	Ser	Cys	Asp	Met	Arg	Phe	Trp	Asn	Ala	
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Pro	Glu	Gln	Ala	Asp	Ile	Leu	Val	Ser	Glu	Leu	Leu	Gly	Ser	Phe	Gly	
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Asp	Asn	Glu	Leu	Ser	Pro	Glu	Cys	Leu	Asp	Gly	Ala	Gln	Arg	Phe	Leu	
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Lys	Pro	Asp	Gly	Ile	Ser	Ile	Pro	Ser	Ser	Tyr	Thr	Ser	Phe	Ile	Gln	
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Pro	Ile	Thr	Ala	Ser	Lys	Leu	Tyr	Asn	Asp	Val	Lys	Ala	His	Lys	Asp	
			485					490					495			
ctt	gcg	cac	ttt	gaa	act	gct	tat	gtt	gtc	aag	ctg	cat	agt	gta	gca	1536
Leu	Ala	His	Phe	Glu	Thr	Ala	Tyr	Val	Val	Lys	Leu	His	Ser	Val	Ala	
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Lys	Leu	Ala	Pro	Ser	Gln	Ser	Val	Phe	Thr	Phe	Thr	His	Pro	Asn	Phe	
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PF59082SeqList_PF59082.txt

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Pro	Ser	Asp	Ala	Gly	Ser	Ala	Leu	Val	His	Gly	Phe	Ala	Gly	Tyr	Phe	
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Asp	Ser	Val	Leu	Tyr	Lys	Asp	Val	His	Leu	Gly	Ile	Glu	Pro	Thr	Thr	
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gca	aca	cca	aac	atg	ttc	agc	tgg	ttc	cca	atc	ttt	ttc	cca	ttg	agg	1776
Ala	Thr	Pro	Asn	Met	Phe	Ser	Trp	Phe	Pro	Ile	Phe	Phe	Pro	Leu	Arg	
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Lys	Pro	Val	Glu	Val	His	Pro	Asp	Thr	Pro	Leu	Glu	Val	His	Phe	Trp	
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Arg	Cys	Cys	Gly	Ser	Ser	Lys	Val	Trp	Tyr	Glu	Trp	Ser	Val	Ser	Ser	
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cct	act	cca	tct	ccg	atg	cat	aac	acc	aat	ggc	cgt	tcg	tac	tgg	gtt	1920
Pro	Thr	Pro	Ser	Pro	Met	His	Asn	Thr	Asn	Gly	Arg	Ser	Tyr	Trp	Val	
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<211> 642

<212> PRT

<213> Arabidopsis thaliana

<400> 1848

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Phe	Asn	Ile	Ser	Thr	Gly	Gly	Phe	Asp	Tyr	Val	Leu	Ala	Pro	Leu	Val	
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Asp	Pro	Ser	Tyr	Arg	Pro	Ser	Leu	Val	Glu	Gly	Asn	Gly	Val	Asp	Thr	
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Gln	Val	Leu	Pro	Val	Cys	Gly	Ser	Asp	Leu	Val	Leu	Ser	Pro	Ser	Gln	
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Trp	Ser	Ser	His	Val	Val	Gly	Lys	Ile	Ser	Ser	Trp	Ile	Asp	Leu	Asp	
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Ser	Glu	Asp	Glu	Val	Leu	Arg	Met	Asp	Ser	Glu	Thr	Thr	Leu	Lys	Gln	
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Glu	Ile	Ala	Trp	Ala	Thr	His	Leu	Ser	Leu	Gln	Ala	Cys	Leu	Leu	Pro	
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Ile	Leu	Gln	Gly	Leu	Thr	Thr	Leu	Gln	Leu	Trp	Leu	Arg	Val	Pro	Leu	
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Val	Lys	Ser	Glu	Gly	Asp	Ser	Met	Asp	Asp	Thr	Ser	Glu	Gly	Leu	Asn	
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		180						185					190			
Ser	Lys	Leu	Ser	Val	Ala	Leu	Asp	Val	Leu	Ser	Thr	Leu	Pro	Ser	Glu	
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Lys	Arg	His	Gln	Lys	Leu	Ile	Ala	Gly	Phe	Phe	Asp	His	Ala	Ala	Gln	
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Ser	Ser	Ser	Glu	Gly	Thr	Glu	Lys	Asn	Pro	Leu	Arg	Ile	Tyr	Leu	Asp	
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PF59082SeqList_PF59082.txt

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 340 345 350
 Asp Arg Val Pro Asp Glu Lys Ala Ser Glu Leu Thr Thr Val Leu Met
 355 360 365
 Val Val Gly Ala Gly Arg Gly Pro Leu Val Arg Ala Ser Leu Gln Ala
 370 375 380
 Ala Glu Glu Thr Asp Arg Lys Leu Lys Val Tyr Ala Val Glu Lys Asn
 385 390 395 400
 Pro Asn Ala Val Val Thr Leu His Asn Leu Val Lys Met Glu Gly Trp
 405 410 415
 Glu Asp Val Val Thr Ile Ile Ser Cys Asp Met Arg Phe Trp Asn Ala
 420 425 430
 Pro Glu Gln Ala Asp Ile Leu Val Ser Glu Leu Leu Gly Ser Phe Gly
 435 440 445
 Asp Asn Glu Leu Ser Pro Glu Cys Leu Asp Gly Ala Gln Arg Phe Leu
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 Lys Pro Asp Gly Ile Ser Ile Pro Ser Ser Tyr Thr Ser Phe Ile Gln
 465 470 475 480
 Pro Ile Thr Ala Ser Lys Leu Tyr Asn Asp Val Lys Ala His Lys Asp
 485 490 495
 Leu Ala His Phe Glu Thr Ala Tyr Val Val Lys Leu His Ser Val Ala
 500 505 510
 Lys Leu Ala Pro Ser Gln Ser Val Phe Thr Phe Thr His Pro Asn Phe
 515 520 525
 Ser Thr Lys Val Asn Asn Gln Arg Tyr Lys Lys Leu Gln Phe Ser Leu
 530 535 540
 Pro Ser Asp Ala Gly Ser Ala Leu Val His Gly Phe Ala Gly Tyr Phe
 545 550 555 560
 Asp Ser Val Leu Tyr Lys Asp Val His Leu Gly Ile Glu Pro Thr Thr
 565 570 575
 Ala Thr Pro Asn Met Phe Ser Trp Phe Pro Ile Phe Phe Pro Leu Arg
 580 585 590
 Lys Pro Val Glu Val His Pro Asp Thr Pro Leu Glu Val His Phe Trp
 595 600 605
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 Gly Leu

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tcgtacggag gagaagcgct gtttacaccc gtctggcagg g atg ccg ctg ggg cag 176
 Met Pro Leu Gly Gln 5

cgt tcg ggg gac aag agc gac tcc cgc tac tgc ggg gtg gag gtt ctc 224
 Arg Ser Gly Asp Lys Ser Asp Ser Arg Tyr Cys Gly Val Glu Val Leu 10 15 20

gac ttc ccc gcc ggg gag ggc ctc cct gcc gtc ctc aat cac tcc ctc 272
 Asp Phe Pro Ala Gly Glu Gly Leu Pro Ala Val Leu Asn His Ser Leu

PF59082SeqList_PF59082.txt

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atc aaa ttg gag ggt tgg gaa agc ctg gtt act gta att tct agt gac					1472
Ile Lys Leu Glu Gly Trp Glu Ser Leu Val Thr Val Ile Ser Asp					
	425	430	435		
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Met Arg Cys Trp Asp Ala Pro Glu Lys Ala Asp Ile Leu Val Ser Glu					
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Leu Leu Gly Ser Phe Gly Asp Asn Glu Leu Ser Pro Glu Cys Leu Asp					
	455	460	465		
ggg gct caa cga ttc ttg aag cct gat ggg att tcc att cct tca tca					1616
Gly Ala Gln Arg Phe Leu Lys Pro Asp Gly Ile Ser Ile Pro Ser Ser					
	470	475	480		
tac acc agc ttc atc caa cca ata aca gcg tca aaa ttg cac gac gac					1664
Tyr Thr Ser Phe Ile Gln Pro Ile Thr Ala Ser Lys Leu His Asp Asp					
	490	495	500		
atc aaa gca cac aaa gat att gca cat ttt gaa acg gca tat gtt gtg					1712
Ile Lys Ala His Lys Asp Ile Ala His Phe Glu Thr Ala Tyr Val Val					
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aaa cta cac cgc ata gcg aca ctt gca cct cca caa cag gtt ttt act					1760
Lys Leu His Arg Ile Ala Thr Leu Ala Pro Pro Gln Gln Val Phe Thr					
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Phe Thr His Pro Asn Phe Ser Pro Asn Ala Ser Asn Gln Arg Tyr Thr					
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aag ttg caa ttt gaa atg ctg cca gac atg ggt tca tgc ctt gtg cac					1856
Lys Leu Gln Phe Glu Met Leu Pro Asp Met Gly Ser Cys Leu Val His					
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Gly Phe Ala Gly Tyr Phe Asp Ser Val Leu Tyr Lys Asp Val His Leu					
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gga atc gag cca aac acc gct aca cca aac atg ttc agc tgg ttc ccg					1952
Gly Ile Glu Pro Asn Thr Ala Thr Pro Asn Met Phe Ser Trp Phe Pro					
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Ile Phe Phe Pro Leu Arg Lys Pro Ile Tyr Val Pro Glu Gly Ser Pro					
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Ile Glu Val His Phe Trp Arg Cys Cys Ala Pro Thr Lys Val Trp Tyr					
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Glu Trp Ala Val Thr Thr Pro Thr Pro Ser Pro Ile His Asn Ser Asn					
	630	635	640		
ggc cgg tcc tat tgg gtt ggt cta taa taaggcatca agatcatctt					2143
Gly Arg Ser Tyr Trp Val Gly Leu					
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gcagtgtgct tagtgctact gggtttctgcc tggagagctg atcaaaggat atatgtagcg					2263
tggtgttatc tgatctgaaa gggagtgctt gacccccaac gttgttctac tcgattttgc					2323
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PF59082SeqList_PF59082.txt

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35      40      45
Val Asp Pro Asn Tyr Arg Pro Ala Pro Gly Ala Val Leu Pro Val Ser
50      55      60
Ala Ser Asp Leu Val Leu Gly Pro Ser Gln Trp Ser Asn His Val Val
65      70      75      80
Gly Lys Ile Ser Glu Trp Ile Asp Leu Asp Ala Glu Asp Glu Arg Leu
85      90      95
Arg Leu Asp Ser Glu Leu Thr Leu Lys Gln Glu Ile Ala Trp Ala Ser
100     105     110
His Val Ser Leu Gln Ala Cys Val Ile Pro Ala Pro Arg Arg Ser Phe
115     120     125
Cys Gly Asn Tyr Ala Arg Val Val Asn Gln Ile Leu Gln Gly Leu Thr
130     135     140
Asn Met Asn Leu Trp Leu Arg Leu Pro Leu Glu Lys Ser Glu Pro Met
145     150     155     160
Asp Gly Asp Leu Asp Lys Ile Lys Asn Asn Asn His Thr Leu Gln Ser
165     170     175
Glu Ile Ala Asp Ser Trp Glu Leu Trp Asn Ser Phe Arg Leu Leu Cys
180     185     190
Asp His Ser Ser Gln Leu Cys Val Ala Leu Asp Ile Ser Gly Thr Leu
195     200     205
Pro Ser Met Asn Ser Leu Gly Arg Trp Phe Gly Glu Pro Val Arg Ala
210     215     220
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225     230     235     240
Cys Leu Ser Lys Arg His Gln Arg Leu Leu Thr Gly Leu Phe Asn His
245     250     255
Ser Val Gln Ala Ile Ile Ser Gly Arg Ser Asn His Asn Val Phe Pro
260     265     270
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275     280     285
Tyr Val Arg His Ala Leu Ala Pro Tyr Leu Glu Tyr Ile Ala Tyr Leu
290     295     300
Tyr Gln Lys Met Asp Pro Leu Pro Glu Gln Glu Arg Phe Glu Ile Asn
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Tyr Arg Asp Phe Leu Gln Ser Pro Pro Gln Pro Leu Met Asp Asn Leu
325     330     335
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Asp Ala Val Ser Thr Thr Arg Thr Val Leu Met Val Val Gly Ala Gly
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Arg Gly Pro Leu Val Arg Ala Ser Leu Gln Ala Ala Glu Glu Thr Gly
385     390     395     400
Arg Lys Leu Lys Val Tyr Ala Val Glu Lys Asn Pro Asn Ala Val Ile
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Thr Leu His Ser Leu Ile Lys Leu Glu Gly Trp Glu Ser Leu Val Thr
420     425     430
Val Ile Ser Ser Asp Met Arg Cys Trp Asp Ala Pro Glu Lys Ala Asp
435     440     445
Ile Leu Val Ser Glu Leu Leu Gly Ser Phe Gly Asp Asn Glu Leu Ser
450     455     460
Pro Glu Cys Leu Asp Gly Ala Gln Arg Phe Leu Lys Pro Asp Gly Ile
465     470     475     480
Ser Ile Pro Ser Ser Tyr Thr Ser Phe Ile Gln Pro Ile Thr Ala Ser
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Lys Leu His Asp Asp Ile Lys Ala His Lys Asp Ile Ala His Phe Glu
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 580 585 590
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 595 600 605
 Pro Glu Gly Ser Pro Ile Glu Val His Phe Trp Arg Cys Cys Ala Pro
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gat ctg gat ctg gtt ggt gca gct ttc aaa tgc aca aag tca tca gat	144
Asp Leu Asp Leu Val Gly Ala Ala Phe Lys Cys Thr Lys Ser Ser Asp	
35 40 45	
tgt gat tac ttc ttg cac aag tca tgt ttt gaa ctt cca cgt gaa acc	192
Cys Asp Tyr Phe Leu His Lys Ser Cys Phe Glu Leu Pro Arg Glu Thr	
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Asn His Lys Ser His Gln Pro His Thr Leu Thr Leu Ile Tyr Ser Pro	
65 70 75 80	
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Lys Ser Thr Tyr Thr Cys Asn Ala Cys Gly Glu Tyr Gly Ser Ser Phe	
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acg tac aac tgt tca atc tgt cag tac gat gta cat gtc gga tgt gtt	336
Thr Tyr Asn Cys Ser Ile Cys Gln Tyr Asp Val His Val Gly Cys Val	
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Ser Met Pro Glu Thr Val Lys Arg Glu Asp His Pro His Pro Leu Thr	
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ctt ctt tac ggt tct cct tat aac caa ccc ggt tta gtt tcc aaa tgc	432
Leu Leu Tyr Gly Ser Pro Tyr Asn Gln Pro Gly Leu Val Ser Lys Cys	
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Glu Ala Lys Lys Glu Asp Gln Lys Gly Glu Gly Ser Lys Asn Ser Met	
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aat tcg gag tta gct gca atg tta gag gct caa aga gaa gtg gag agg	624
Asn Ser Glu Leu Ala Ala Met Leu Glu Ala Gln Arg Glu Val Glu Arg	
195 200 205	
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<211> 234
<212> PRT
<213> Arabidopsis thaliana

<400> 1852
Met Ser Ser Arg Gln Ser Val Arg His Pro Ser His Asn His Pro Leu
1 5 10 15
Arg Gly His Lys Cys Glu Ala Lys Asp Glu Ile Ile Cys Ser Gly Cys
20 25 30
Asp Leu Asp Leu Val Gly Ala Ala Phe Lys Cys Thr Lys Ser Ser Asp
35 40 45
Cys Asp Tyr Phe Leu His Lys Ser Cys Phe Glu Leu Pro Arg Glu Thr
50 55 60
Asn His Lys Ser His Gln Pro His Thr Leu Thr Leu Ile Tyr Ser Pro
65 70 75 80
Lys Ser Thr Tyr Thr Cys Asn Ala Cys Gly Glu Tyr Gly Ser Ser Phe
85 90 95
Thr Tyr Asn Cys Ser Ile Cys Gln Tyr Asp Val His Val Gly Cys Val
100 105 110
Ser Met Pro Glu Thr Val Lys Arg Glu Asp His Pro His Pro Leu Thr
115 120 125
Leu Leu Tyr Gly Ser Pro Tyr Asn Gln Pro Gly Leu Val Ser Lys Cys
130 135 140
Asp Val Cys Glu Asp Ile Val Pro Asp Asn Leu Trp Ser Tyr Tyr Cys
145 150 155 160
Lys Glu Cys Asp Tyr Ala Thr His Leu His Ser Cys Lys Lys Glu Glu
165 170 175
Glu Ala Lys Lys Glu Asp Gln Lys Gly Glu Gly Ser Lys Asn Ser Met
180 185 190
Asn Ser Glu Leu Ala Ala Met Leu Glu Ala Gln Arg Glu Val Glu Arg
195 200 205
Met Gln Ile Glu Met His Leu Ala Met Gln Ser Ala Leu Ile Ser Lys
210 215 220
Lys Ala Asn Lys Ala Ala Leu Asn Cys Ile
225 230

<210> 1853
<211> 952
<212> DNA
<213> Brassica napus

<220>
<221> CDS
<222> (13)..(747)

<400> 1853
attttaccta ca atg gct tca aga aaa cca tcg gtg agg cac cct agc cac 51
Met Ala Ser Arg Lys Pro Ser Val Arg His Pro Ser His
1 5 10
aac cat cca ttg cgc ggt cac aaa gcc cta gct gaa gaa gag acc atc 99
Asn His Pro Leu Arg Gly His Lys Ala Leu Ala Glu Glu Glu Thr Ile
15 20 25
tgc tcc ggc tgc gac cta gac cta ata ggt gca gct ttc aaa tgc aca 147
Cys Ser Gly Cys Asp Leu Asp Leu Ile Gly Ala Ala Phe Lys Cys Thr
30 35 40 45
aag tca gaa tgt gat tac ttc ttg cac aag tca tgt ttc gat ctt cca 195
Lys Ser Glu Cys Asp Tyr Phe Leu His Lys Ser Cys Phe Asp Leu Pro
50 55 60
cgt gag aca cgc cac aag tct cac cct gat cac cct ctg acc ctg ctt 243
Arg Glu Thr Arg His Lys Ser His Pro Asp His Pro Leu Thr Leu Leu
65 70 75
tat tcg cca ccg tac gag tcc tca act tac gag tgc agc gcg tgc agt 291
Tyr Ser Pro Pro Tyr Glu Ser Ser Thr Tyr Glu Cys Ser Ala Cys Ser
80 85 90
gag tat gga tca ggg ttc gtt tac aac tgc tct atc tgc cag ttt gat 339

PF59082SeqList_PF59082.txt

Glu	Tyr	Gly	Ser	Gly	Phe	Val	Tyr	Asn	Cys	Ser	Ile	Cys	Gln	Phe	Asp	
95						100					105					
tta	cat	gtc	ggg	tgc	ata	tct	atg	cct	gag	tcc	gtg	gag	cgt	gaa	gga	387
Leu	His	Val	Gly	Cys	Ile	Ser	Met	Pro	Glu	Ser	Val	Glu	Arg	Glu	Gly	
110					115					120					125	
cat	gag	cat	ccg	cta	acg	ttg	ctt	tac	tgt	tct	cct	tac	acg	aac	ggt	435
His	Glu	His	Pro	Leu	Thr	Leu	Leu	Tyr	Cys	Ser	Pro	Tyr	Thr	Asn	Gly	
				130					135					140		
ttg	atc	gtc	aag	tgt	gac	gta	tgt	caa	gag	acg	gtt	ccg	gat	cat	cta	483
Leu	Ile	Val	Lys	Cys	Asp	Val	Cys	Gln	Glu	Thr	Val	Pro	Asp	His	Leu	
			145					150					155			
tgg	tct	tat	tac	tgc	aag	gaa	tgt	gac	tac	ggc	acg	cat	tta	cat	tct	531
Trp	Ser	Tyr	Tyr	Cys	Lys	Glu	Cys	Asp	Tyr	Gly	Thr	His	Leu	His	Ser	
		160					165				170					
tgt	gaa	gta	gaa	gaa	gtg	gtg	gag	cca	aag	aga	gga	gga	gga	aag	gcg	579
Cys	Glu	Val	Glu	Glu	Val	Val	Glu	Pro	Lys	Arg	Gly	Gly	Gly	Lys	Ala	
	175				180						185					
agt	aca	agt	ggt	aat	aaa	gga	gga	gga	aga	ggc	tcg	gct	gct	tcg	gag	627
Ser	Thr	Ser	Gly	Asn	Lys	Gly	Gly	Gly	Arg	Gly	Ser	Ala	Ala	Ser	Glu	
190					195					200					205	
tta	gct	gca	atg	ctt	gaa	gct	caa	agg	gag	atg	gat	agg	atg	cag	att	675
Leu	Ala	Ala	Met	Leu	Glu	Ala	Gln	Arg	Glu	Met	Asp	Arg	Met	Gln	Ile	
			210						215					220		
gag	ttg	cat	atg	gag	atg	cag	aga	gct	aag	att	gcg	aag	aaa	gcg	aga	723
Glu	Leu	His	Met	Glu	Met	Gln	Arg	Ala	Lys	Ile	Ala	Lys	Lys	Ala	Arg	
			225					230					235			
aaa	gct	tgt	ctc	aag	ttg	ata	taa	aaatatgata	aagttgaaaa	cgtttatgtt						777
Lys	Ala	Cys	Leu	Lys	Leu	Ile										
	240															
tctctc	gagc	tttctt	ggat	tctt	ggagct	ctgaaactat	atgattgttg	tttttctt	gtt							837
gttttg	gttc	ttgtttt	tca	ttgattt	gtt	ttatttg	ctata	atttcat	gtt	attttct	tttt					897
gaataattat	taataatctg	aaataaaaag	atctttaact	aaaaaaaaaa	aaaaa											952

<210> 1854
 <211> 244
 <212> PRT
 <213> Brassica napus

<400> 1854
 Met Ala Ser Arg Lys Pro Ser Val Arg His Pro Ser His Asn His Pro
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 Leu Arg Gly His Lys Ala Leu Ala Glu Glu Thr Ile Cys Ser Gly
 20 25 30
 Cys Asp Leu Asp Leu Ile Gly Ala Phe Lys Cys Thr Lys Ser Glu
 35 40 45
 Cys Asp Tyr Phe Leu His Lys Ser Cys Phe Asp Leu Pro Arg Glu Thr
 50 55 60
 Arg His Lys Ser His Pro Asp His Pro Leu Thr Leu Leu Tyr Ser Pro
 65 70 75 80
 Pro Tyr Glu Ser Ser Thr Tyr Glu Cys Ser Ala Cys Ser Glu Tyr Gly
 85 90 95
 Ser Gly Phe Val Tyr Asn Cys Ser Ile Cys Gln Phe Asp Leu His Val
 100 105 110
 Gly Cys Ile Ser Met Pro Glu Ser Val Glu Arg Glu Gly His Glu His
 115 120 125
 Pro Leu Thr Leu Leu Tyr Cys Ser Pro Tyr Thr Asn Gly Leu Ile Val
 130 135 140
 Lys Cys Asp Val Cys Gln Glu Thr Val Pro Asp His Leu Trp Ser Tyr
 145 150 155 160
 Tyr Cys Lys Glu Cys Asp Tyr Gly Thr His Leu His Ser Cys Glu Val
 165 170 175
 Glu Glu Val Val Glu Pro Lys Arg Gly Gly Gly Lys Ala Ser Thr Ser
 180 185 190

PF59082SeqList_PF59082.txt

Gly Asn Lys Gly Gly Gly Arg Gly Ser Ala Ala Ser Glu Leu Ala Ala
 195 200 205
 Met Leu Glu Ala Gln Arg Glu Met Asp Arg Met Gln Ile Glu Leu His
 210 215 220
 Met Glu Met Gln Arg Ala Lys Ile Ala Lys Lys Ala Arg Lys Ala Cys
 225 230 235 240
 Leu Lys Leu Ile

<210> 1855
 <211> 950
 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (11)..(745)

<400> 1855
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 1 5 10
 aac cat cca ttg cgc ggt cac aaa gcc cta gct gaa gaa gag acc atc 97
 Asn His Pro Leu Arg Gly His Lys Ala Leu Ala Glu Glu Glu Thr Ile
 15 20 25
 tgc tcc ggc tgc gac cta gac cta ata ggt gca gct ttc aaa tgc aca 145
 Cys Ser Gly Cys Asp Leu Asp Leu Ile Gly Ala Ala Phe Lys Cys Thr
 30 35 40 45
 aag tca gaa tgt gat tac ttc ttg cac aag tca tgt gtc gat ctt cca 193
 Lys Ser Glu Cys Asp Tyr Phe Leu His Lys Ser Cys Val Asp Leu Pro
 50 55 60
 cgt gag aca cgc cac aag tct cac cct gat cac cct ctg acc ctg ctt 241
 Arg Glu Thr Arg His Lys Ser His Pro Asp His Pro Leu Thr Leu Leu
 65 70 75
 tat tcg cca ccg tac gag tcc tca act tac gag tgc agc gcg tgc agt 289
 Tyr Ser Pro Pro Tyr Glu Ser Ser Thr Tyr Glu Cys Ser Ala Cys Ser
 80 85 90
 gag tat gga tca ggg ttc gtt tac aac tgc tct atc tgc cag ttt gat 337
 Glu Tyr Gly Ser Gly Phe Val Tyr Asn Cys Ser Ile Cys Gln Phe Asp
 95 100 105
 tta cat gtc ggg tgc ata tct atg cct gag tcc gtg gag cgt gaa gga 385
 Leu His Val Gly Cys Ile Ser Met Pro Glu Ser Val Glu Arg Glu Gly
 110 115 120 125
 cat gag cat ccg cta acg ttg ctt tac tgt tct cct tac acg aac ggt 433
 His Glu His Pro Leu Thr Leu Leu Tyr Cys Ser Pro Tyr Thr Asn Gly
 130 135 140
 ttg atc gtc aag tgt gac gta tgt caa gag acg gtt ccg gat cat cta 481
 Leu Ile Val Lys Cys Asp Val Cys Gln Glu Thr Val Pro Asp His Leu
 145 150 155
 tgg tct tat tac tgc aag gaa tgt gac tac ggc acg cat tta cat tct 529
 Trp Ser Tyr Tyr Cys Lys Glu Cys Asp Tyr Gly Thr His Leu His Ser
 160 165 170
 tgt gaa gta gaa gaa gtg gtg gag cca aag aga gga gga gga aag gcg 577
 Cys Glu Val Glu Glu Val Val Glu Pro Lys Arg Gly Gly Gly Lys Ala
 175 180 185
 agt aca agt ggt aat aaa gga gga gga aga ggc tcg gct gct tcg gag 625
 Ser Thr Ser Gly Asn Lys Gly Gly Gly Arg Gly Ser Ala Ala Ser Glu
 190 195 200 205
 tta gct gca atg ctt gaa gct caa agg gag atg gat agg atg cag att 673
 Leu Ala Ala Met Leu Glu Ala Gln Arg Glu Met Asp Arg Met Gln Ile
 210 215 220
 gag ttg cat atg gag atg cag aga gct aag att gcg aag aaa gcg aga 721
 Glu Leu His Met Glu Met Gln Arg Ala Lys Ile Ala Lys Lys Ala Arg
 225 230 235
 aaa gct tgt ctc aag ttg ata taa aaatatgata aagttgaaaa cgtttatgtt 775
 Lys Ala Cys Leu Lys Leu Ile
 240
 tctctcgagc tttcttgat tcttgagct ctgaaactat atgattgttg ttttcttgt 835

PF59082SeqList_PF59082.txt

gttttggttc ttgtttttca ttgatttggt ttatttgcta atttcatgtt attttctttt 895

gaataattat taataatctg aaataaaaag atctttaacc aaaaaaaaaa aaaaa 950

<210> 1856
<211> 244
<212> PRT
<213> Brassica napus

<400> 1856
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Leu Arg Gly His Lys Ala Leu Ala Glu Glu Glu Thr Ile Cys Ser Gly
20 25 30
Cys Asp Leu Asp Leu Ile Gly Ala Ala Phe Lys Cys Thr Lys Ser Glu
35 40 45
Cys Asp Tyr Phe Leu His Lys Ser Cys Val Asp Leu Pro Arg Glu Thr
50 55 60
Arg His Lys Ser His Pro Asp His Pro Leu Thr Leu Leu Tyr Ser Pro
65 70 75 80
Pro Tyr Glu Ser Ser Thr Tyr Glu Cys Ser Ala Cys Ser Glu Tyr Gly
85 90 95
Ser Gly Phe Val Tyr Asn Cys Ser Ile Cys Gln Phe Asp Leu His Val
100 105 110
Gly Cys Ile Ser Met Pro Glu Ser Val Glu Arg Glu Gly His Glu His
115 120 125
Pro Leu Thr Leu Leu Tyr Cys Ser Pro Tyr Thr Asn Gly Leu Ile Val
130 135 140
Lys Cys Asp Val Cys Gln Glu Thr Val Pro Asp His Leu Trp Ser Tyr
145 150 155 160
Tyr Cys Lys Glu Cys Asp Tyr Gly Thr His Leu His Ser Cys Glu Val
165 170 175
Glu Glu Val Val Glu Pro Lys Arg Gly Gly Gly Lys Ala Ser Thr Ser
180 185 190
Gly Asn Lys Gly Gly Gly Arg Gly Ser Ala Ala Ser Glu Leu Ala Ala
195 200 205
Met Leu Glu Ala Gln Arg Glu Met Asp Arg Met Gln Ile Glu Leu His
210 215 220
Met Glu Met Gln Arg Ala Lys Ile Ala Lys Lys Ala Arg Lys Ala Cys
225 230 235 240
Leu Lys Leu Ile

<210> 1857
<211> 579
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)..(579)

<400> 1857
atg ata gat ttc agt cga atc cag aaa gag ctt cag gac tgc gag aga 48
Met Ile Asp Phe Ser Arg Ile Gln Lys Glu Leu Gln Asp Cys Glu Arg
1 5 10 15
aac cag gat tct tcg ggt atc cgg gtc tgc ccc aaa tcc gat aac ctc 96
Asn Gln Asp Ser Ser Gly Ile Arg Val Cys Pro Lys Ser Asp Asn Leu
20 25 30
acc cga ctc acc gga acc att cct ggt cca atc ggt act cct tac gaa 144
Thr Arg Leu Thr Gly Thr Ile Pro Gly Pro Ile Gly Thr Pro Tyr Glu
35 40 45
ggc ggt aca ttt cag atc gat atc act atg cca gat ggg tat cca ttt 192
Gly Gly Thr Phe Gln Ile Asp Ile Thr Met Pro Asp Gly Tyr Pro Phe
50 55 60

PF59082SeqList_PF59082.txt

gag	cct	cca	aag	atg	cag	ttt	tca	act	aaa	gtt	tgg	cat	ccg	aat	att	240
Glu	Pro	Pro	Lys	Met	Gln	Phe	Ser	Thr	Lys	Val	Trp	His	Pro	Asn	Ile	
65					70					75					80	
agt	agc	caa	agc	ggg	gca	ata	tgc	ttg	gat	atc	ttg	aaa	gac	cag	tgg	288
Ser	Ser	Gln	Ser	Gly	Ala	Ile	Cys	Leu	Asp	Ile	Leu	Lys	Asp	Gln	Trp	
				85					90					95		
agt	cca	gct	ctt	act	ctg	aag	aca	gct	ctt	gtt	tca	att	cag	gct	tta	336
Ser	Pro	Ala	Leu	Thr	Leu	Lys	Thr	Ala	Leu	Val	Ser	Ile	Gln	Ala	Leu	
			100					105					110			
ctc	tct	gca	cct	gag	ccc	aaa	gac	cct	caa	gat	gct	gtt	gta	gct	gaa	384
Leu	Ser	Ala	Pro	Glu	Pro	Lys	Asp	Pro	Gln	Asp	Ala	Val	Val	Ala	Glu	
		115					120					125				
cag	tac	atg	aag	aac	tat	caa	gtg	ttt	gta	tca	aca	gct	cgt	tac	tgg	432
Gln	Tyr	Met	Lys	Asn	Tyr	Gln	Val	Phe	Val	Ser	Thr	Ala	Arg	Tyr	Trp	
	130					135					140					
act	gaa	act	ttc	gcc	aag	aaa	tct	tct	cta	gag	gaa	aaa	gtc	aag	aga	480
Thr	Glu	Thr	Phe	Ala	Lys	Lys	Ser	Ser	Leu	Glu	Glu	Lys	Val	Lys	Arg	
145					150					155					160	
ctt	gtg	gag	atg	ggg	ttt	gga	gac	gct	caa	gtt	agg	agt	gca	att	gaa	528
Leu	Val	Glu	Met	Gly	Phe	Gly	Asp	Ala	Gln	Val	Arg	Ser	Ala	Ile	Glu	
				165					170					175		
tca	agt	ggg	ggg	gat	gag	aat	ctg	gct	ctg	gaa	aag	ctc	tgt	tct	gct	576
Ser	Ser	Gly	Gly	Asp	Glu	Asn	Leu	Ala	Leu	Glu	Lys	Leu	Cys	Ser	Ala	
			180					185					190			
tag																579

<210> 1858
 <211> 192
 <212> PRT
 <213> Arabidopsis thaliana

<400> 1858
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 20 25 30
 Thr Arg Leu Thr Gly Thr Ile Pro Gly Pro Ile Gly Thr Pro Tyr Glu
 35 40 45
 Gly Gly Thr Phe Gln Ile Asp Ile Thr Met Pro Asp Gly Tyr Pro Phe
 50 55 60
 Glu Pro Pro Lys Met Gln Phe Ser Thr Lys Val Trp His Pro Asn Ile
 65 70 75 80
 Ser Ser Gln Ser Gly Ala Ile Cys Leu Asp Ile Leu Lys Asp Gln Trp
 85 90 95
 Ser Pro Ala Leu Thr Leu Lys Thr Ala Leu Val Ser Ile Gln Ala Leu
 100 105 110
 Leu Ser Ala Pro Glu Pro Lys Asp Pro Gln Asp Ala Val Val Ala Glu
 115 120 125
 Gln Tyr Met Lys Asn Tyr Gln Val Phe Val Ser Thr Ala Arg Tyr Trp
 130 135 140
 Thr Glu Thr Phe Ala Lys Lys Ser Ser Leu Glu Glu Lys Val Lys Arg
 145 150 155 160
 Leu Val Glu Met Gly Phe Gly Asp Ala Gln Val Arg Ser Ala Ile Glu
 165 170 175
 Ser Ser Gly Gly Asp Glu Asn Leu Ala Leu Glu Lys Leu Cys Ser Ala
 180 185 190

<210> 1859
 <211> 869
 <212> DNA
 <213> Oryza sativa

<220>
 <221> CDS
 <222> (193)..(639)

<400> 1859

PF59082SeqList_PF59082.txt

ccaaccaca cggtccagtc ctctcctcgc cgtagacgcg gcggccgagg aacaagtccg 60

tcacgcgaac cttccagaac ctcacacgtc acgcaacctc ctctctttta ttacgactac 120

taccaccccc tctctcctct ccgttccacc gccggattca gattcggaga gagctactcc 180

tcgtcgttag cc atg gcg tcc aag cgg atc ctc aag gag ctc aag gac ctg 231
Met Ala Ser Lys Arg Ile Leu Lys Glu Leu Lys Asp Leu

cag aag gat ccc ccc acc tcc tgc agc gcc ggc cct gtg gca gaa gat 279
Gln Lys Asp Pro Pro Thr Ser Cys Ser Ala Gly Pro Val Ala Glu Asp

atg ttc cac tgg cag gca aca ctg atg ggt cca tca gat agc cct tat 327
Met Phe His Trp Gln Ala Thr Leu Met Gly Pro Ser Asp Ser Pro Tyr

gct gga ggc gtg ttt ttg gtt acc att cat ttt cct cct gat tat cca 375
Ala Gly Gly Val Phe Leu Val Thr Ile His Phe Pro Pro Asp Tyr Pro

ttc aaa ccg cct aag gtg gca ttg aag aca aag gtg ttc cac cca aac 423
Phe Lys Pro Pro Lys Val Ala Leu Lys Thr Lys Val Phe His Pro Asn

att aat agc aac gga agc ata tgc ctt gat atc ttg aag gag cag tgg 471
Ile Asn Ser Asn Gly Ser Ile Cys Leu Asp Ile Leu Lys Glu Gln Trp

agt cct gca ttg act att tca aag gtg cta ctc tca att tgc tcg ctg 519
Ser Pro Ala Leu Thr Ile Ser Lys Val Leu Leu Ser Ile Cys Ser Leu

ttg acg gat cca aat cct gat gat cca ttg gtt cca gag att gct cac 567
Leu Thr Asp Pro Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala His

atg tac aag act gat cgg gcc aag tac gag tcc acc gca agg agc tgg 615
Met Tyr Lys Thr Asp Arg Ala Lys Tyr Glu Ser Thr Ala Arg Ser Trp

acc cag aaa tat gct atg ggc tag aatgggtaac aataagaaat gtgagatatg 669
Thr Gln Lys Tyr Ala Met Gly

ccattgtatt gccttgtatt ctctgtaac tctttcaaca ttttaagaaac agcaagaatc 729

aaattgaact ctcgagttgt tgtatggaat cctactatag atgttcagct attgtaaatt 789

atgtagtggg tggttctatt gattgttcga tgagcacttg gaatgggtact tttatgttcc 849

agagtaaaaa aaaaaaaaaa 869

<210> 1860
<211> 148
<212> PRT
<213> Oryza sativa

<400> 1860
Met Ala Ser Lys Arg Ile Leu Lys Glu Leu Lys Asp Leu Gln Lys Asp
1 5 10 15
Pro Pro Thr Ser Cys Ser Ala Gly Pro Val Ala Glu Asp Met Phe His
20 25 30
Trp Gln Ala Thr Leu Met Gly Pro Ser Asp Ser Pro Tyr Ala Gly Gly
35 40 45
Val Phe Leu Val Thr Ile His Phe Pro Pro Asp Tyr Pro Phe Lys Pro
50 55 60
Pro Lys Val Ala Leu Lys Thr Lys Val Phe His Pro Asn Ile Asn Ser
65 70 75 80
Asn Gly Ser Ile Cys Leu Asp Ile Leu Lys Glu Gln Trp Ser Pro Ala

PF59082SeqList_PF59082.txt

85 90 95
 Leu Thr Ile Ser Lys Val Leu Leu Ser Ile Cys Ser Leu Leu Thr Asp
 100 105 110
 Pro Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala His Met Tyr Lys
 115 120 125
 Thr Asp Arg Ala Lys Tyr Glu Ser Thr Ala Arg Ser Trp Thr Gln Lys
 130 135 140
 Tyr Ala Met Gly
 145

<210> 1861
 <211> 663
 <212> DNA
 <213> Oryza sativa

<220>
 <221> CDS
 <222> (61)..(507)

<400> 1861
 cgcttttctca tcgctgatca aacttcaaac cctagctagg atttcaaggt acacttaacg 60

atg gct tca aaa cgc att act aag gag ttg aag gat ctg cag cag gac 108
 Met Ala Ser Lys Arg Ile Thr Lys Glu Leu Lys Asp Leu Gln Gln Asp
 1 5 10 15
 cct cct gtt tcc tgc agt gct ggc cct gtt ggt gat gac atg ttt cat 156
 Pro Pro Val Ser Cys Ser Ala Gly Pro Val Gly Asp Asp Met Phe His
 20 25 30
 tgg caa gct aca att atg ggt cca act gac agt cct tat gct ggt ggt 204
 Trp Gln Ala Thr Ile Met Gly Pro Thr Asp Ser Pro Tyr Ala Gly Gly
 35 40 45
 gta ttc ctg gtg acc att cac ttc cca cca gat tat cca ttt aag cca 252
 Val Phe Leu Val Thr Ile His Phe Pro Pro Asp Tyr Pro Phe Lys Pro
 50 55 60
 cca aag gtt tcc ttc cga acc aag gta ttt cac cct aac ata aac agc 300
 Pro Lys Val Ser Phe Arg Thr Lys Val Phe His Pro Asn Ile Asn Ser
 65 70 75 80
 aat gga agt atc tgt ctg gac att ctg aaa gag cag tgg agt cct gcc 348
 Asn Gly Ser Ile Cys Leu Asp Ile Leu Lys Glu Gln Trp Ser Pro Ala
 85 90 95
 ctt aca gtt tcc aag gtg cta ctt tca att tgc tcc ctg ctg aca gat 396
 Leu Thr Val Ser Lys Val Leu Leu Ser Ile Cys Ser Leu Leu Thr Asp
 100 105 110
 ccc aac ccg gat gat cct ttg gtg cct gat att gct cac atg tac aag 444
 Pro Asn Pro Asp Asp Pro Leu Val Pro Asp Ile Ala His Met Tyr Lys
 115 120 125
 act gac aga gac aag tac gag agc act gcc cgt tct tgg act cag aaa 492
 Thr Asp Arg Asp Lys Tyr Glu Ser Thr Ala Arg Ser Trp Thr Gln Lys
 130 135 140
 tac gcc atg agc tag aagaaaatat ctttattgtt ctggtgacag cttatgtgcg 547
 Tyr Ala Met Ser
 145
 caaaacaagt tgtttgggga tatgtcagta tataatatac atatacaagt agttctgctt 607

 tgatacttta taataattaa aaccctggat tttttttttc taaaaaaaaa aaaaaa 663

<210> 1862
 <211> 148
 <212> PRT
 <213> Oryza sativa

<400> 1862
 Met Ala Ser Lys Arg Ile Thr Lys Glu Leu Lys Asp Leu Gln Gln Asp
 1 5 10 15
 Pro Pro Val Ser Cys Ser Ala Gly Pro Val Gly Asp Asp Met Phe His
 Seite 2439

PF59082SeqList_PF59082.txt

20 25 30
 Trp Gln Ala Thr Ile Met Gly Pro Thr Asp Ser Pro Tyr Ala Gly Gly
 35 40 45
 Val Phe Leu Val Thr Ile His Phe Pro Pro Asp Tyr Pro Phe Lys Pro
 50 55 60
 Pro Lys Val Ser Phe Arg Thr Lys Val Phe His Pro Asn Ile Asn Ser
 65 70 75 80
 Asn Gly Ser Ile Cys Leu Asp Ile Leu Lys Glu Gln Trp Ser Pro Ala
 85 90 95
 Leu Thr Val Ser Lys Val Leu Leu Ser Ile Cys Ser Leu Leu Thr Asp
 100 105 110
 Pro Asn Pro Asp Asp Pro Leu Val Pro Asp Ile Ala His Met Tyr Lys
 115 120 125
 Thr Asp Arg Asp Lys Tyr Glu Ser Thr Ala Arg Ser Trp Thr Gln Lys
 130 135 140
 Tyr Ala Met Ser
 145

<210> 1863

<211> 642

<212> DNA

<213> Oryza sativa

<220>

<221> CDS

<222> (23)..(469)

<400> 1863

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 Met Ala Ser Lys Arg Ile Leu Lys Glu Leu
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 aag gac ctg cag aag gat ccc cca acc tcc tgc agc gct ggc cct gtg 100
 Lys Asp Leu Gln Lys Asp Pro Pro Thr Ser Cys Ser Ala Gly Pro Val
 15 20 25
 gga gaa gat atg ttc cac tgg caa gct acg att atg ggt cca gca gat 148
 Gly Glu Asp Met Phe His Trp Gln Ala Thr Ile Met Gly Pro Ala Asp
 30 35 40
 agt cca tat gca ggt ggc gtc ttc ttg gtt tct att cac ttc cct cca 196
 Ser Pro Tyr Ala Gly Gly Val Phe Leu Val Ser Ile His Phe Pro Pro
 45 50 55
 gac tat ccg ttc aaa ccg ccc aag gtt gca ttt aag aca aag gtt ttc 244
 Asp Tyr Pro Phe Lys Pro Pro Lys Val Ala Phe Lys Thr Lys Val Phe
 60 65 70
 cac cca aac atc aac agt aac gga agc atc tgc ctt gat atc ctg aag 292
 His Pro Asn Ile Asn Ser Asn Gly Ser Ile Cys Leu Asp Ile Leu Lys
 75 80 85 90
 gaa cag tgg agc cct gca ttg aca gtg tca aag gta ctc ctc tca att 340
 Glu Gln Trp Ser Pro Ala Leu Thr Val Ser Lys Val Leu Leu Ser Ile
 95 100 105
 tgt tct cta ctg acg gac cca aac cca gac gac ccg cta gtt ccg gag 388
 Cys Ser Leu Leu Thr Asp Pro Asn Pro Asp Asp Pro Leu Val Pro Glu
 110 115 120
 att gcg cac atg tac aag act gat cgg gcc aaa tat gaa tca act gcg 436
 Ile Ala His Met Tyr Lys Thr Asp Arg Ala Lys Tyr Glu Ser Thr Ala
 125 130 135
 agg ggc tgg acc cag aaa tat gca atg ggc tga acgacgtagg ccgatagtgt 489
 Arg Gly Trp Thr Gln Lys Tyr Ala Met Gly
 140 145
 tctctagcga tatatgttat ctgttgatc tagtgttcat gtcctgctac atgcctacat 549
 ggggtgtaat ttcttctgtc actgaattta tgtcaaattc tcgattgatg gtagaagtta 609
 ttgagaaaaa tttcaattaa aaaaaaaaaa aaa 642

<210> 1864

PF59082SeqList_PF59082.txt

<211> 148
<212> PRT
<213> Oryza sativa

<400> 1864
Met Ala Ser Lys Arg Ile Leu Lys Glu Leu Lys Asp Leu Gln Lys Asp
1 5 10 15
Pro Pro Thr Ser Cys Ser Ala Gly Pro Val Gly Glu Asp Met Phe His
20 25 30
Trp Gln Ala Thr Ile Met Gly Pro Ala Asp Ser Pro Tyr Ala Gly Gly
35 40 45
Val Phe Leu Val Ser Ile His Phe Pro Pro Asp Tyr Pro Phe Lys Pro
50 55 60
Pro Lys Val Ala Phe Lys Thr Lys Val Phe His Pro Asn Ile Asn Ser
65 70 75 80
Asn Gly Ser Ile Cys Leu Asp Ile Leu Lys Glu Gln Trp Ser Pro Ala
85 90 95
Leu Thr Val Ser Lys Val Leu Leu Ser Ile Cys Ser Leu Leu Thr Asp
100 105 110
Pro Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala His Met Tyr Lys
115 120 125
Thr Asp Arg Ala Lys Tyr Glu Ser Thr Ala Arg Gly Trp Thr Gln Lys
130 135 140
Tyr Ala Met Gly
145

<210> 1865
<211> 737
<212> DNA
<213> Brassica napus

<220>
<221> CDS
<222> (64)..(510)

<400> 1865
cgattcgatc atcgtttctc agctcaccga tcattcttcct agaagcagcg agtacagttc

60

aag atg gct tgc aaa aga atc aac aaa gag ctt agg gac ctc caa agg	108
Met Ala Ser Lys Arg Ile Asn Lys Glu Leu Arg Asp Leu Gln Arg	
1 5 10 15	
gat cct cct gtc tca tgc agt gcc ggt cct gtg ggt gat gat atg ttc	156
Asp Pro Pro Val Ser Cys Ser Ala Gly Pro Val Gly Asp Asp Met Phe	
20 25 30	
cac tgg caa gcg act atc atg ggc cca act gat agc cca ttc tcc gga	204
His Trp Gln Ala Thr Ile Met Gly Pro Thr Asp Ser Pro Phe Ser Gly	
35 40 45	
ggg gtg ttt ctt gtt tcc att cac ttc cct cca gat tac ccc ttc aag	252
Gly Val Phe Leu Val Ser Ile His Phe Pro Pro Asp Tyr Pro Phe Lys	
50 55 60	
cca cca aag gtt tct ttc cgc acc aag gtt tac cac ccg aat gtc aac	300
Pro Pro Lys Val Ser Phe Arg Thr Lys Val Tyr His Pro Asn Val Asn	
65 70 75	
agc aat ggc agc atc tgt ctt gac att ctg aaa gag cag tgg agc cct	348
Ser Asn Gly Ser Ile Cys Leu Asp Ile Leu Lys Glu Gln Trp Ser Pro	
80 85 90 95	
gcg ctt acc ata tcc aag gtc ctt ctg tgc tca ctg ctg aca	396
Ala Leu Thr Ile Ser Lys Val Leu Leu Ser Ile Cys Ser Leu Leu Thr	
100 105 110	
gat cca aac cct gat gac cct ctg gtt cca gaa ata gct cac acc tac	444
Asp Pro Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala His Thr Tyr	
115 120 125	
aag aca gac cga gtc aag tac gag agc act gcc cga tcc tgg acc cag	492
Lys Thr Asp Arg Val Lys Tyr Glu Ser Thr Ala Arg Ser Trp Thr Gln	
130 135 140	
aag tat gca atg gga tga tgatgattgg caataataat ccgcaccaat	540
Lys Tyr Ala Met Gly	
145	

PF59082SeqList_PF59082.txt

acattgcgca ttgtctaaga atatgagaaa taagattgaa aaaaaacaga gtgtggcggtt 600

ttgcttggtt gctttattag ttttatcatc atcttaagcc gtgtgttggt ttgtgtacat 660

gagctttata ttgagacatt ttgagagctt gcaatgctat aaagccaata actgggttatt 720

ataaaaaaaaa aaaaaaa 737

<210> 1866
 <211> 148
 <212> PRT
 <213> Brassica napus

<400> 1866
 Met Ala Ser Lys Arg Ile Asn Lys Glu Leu Arg Asp Leu Gln Arg Asp
 1 5 10 15
 Pro Pro Val Ser Cys Ser Ala Gly Pro Val Gly Asp Asp Met Phe His
 20 25 30
 Trp Gln Ala Thr Ile Met Gly Pro Thr Asp Ser Pro Phe Ser Gly Gly
 35 40 45
 Val Phe Leu Val Ser Ile His Phe Pro Pro Asp Tyr Pro Phe Lys Pro
 50 55 60
 Pro Lys Val Ser Phe Arg Thr Lys Val Tyr His Pro Asn Val Asn Ser
 65 70 75 80
 Asn Gly Ser Ile Cys Leu Asp Ile Leu Lys Glu Gln Trp Ser Pro Ala
 85 90 95
 Leu Thr Ile Ser Lys Val Leu Leu Ser Ile Cys Ser Leu Leu Thr Asp
 100 105 110
 Pro Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala His Thr Tyr Lys
 115 120 125
 Thr Asp Arg Val Lys Tyr Glu Ser Thr Ala Arg Ser Trp Thr Gln Lys
 130 135 140
 Tyr Ala Met Gly
 145

<210> 1867
 <211> 702
 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (57)..(485)

<400> 1867
 cttgagattt cccaagatca aatctaaaaa cccttagtag ctgactattc aagctt atg 59
 Met
 1
 gca tcg aga aga att aac agc gag ctt agg gac ctg caa aag gac cct 107
 Ala Ser Arg Arg Ile Asn Ser Glu Leu Arg Asp Leu Gln Lys Asp Pro
 5 10 15
 cca ctg tct tgc agt gcc ggt cct gtg ggt gat gat atg tac cac tgg 155
 Pro Leu Ser Cys Ser Ala Gly Pro Val Gly Asp Asp Met Tyr His Trp
 20 25 30
 caa gca act atc atg ggt cca act gat agc cca ttc acc ggt ggt gta 203
 Gln Ala Thr Ile Met Gly Pro Thr Asp Ser Pro Phe Thr Gly Gly Val
 35 40 45
 ttt ctt gtt tcc att cac ttc cct cca gat tac ccc ttc aag cca cca 251
 Phe Leu Val Ser Ile His Phe Pro Pro Asp Tyr Pro Phe Lys Pro Pro
 50 55 60 65
 aag gtc tat cac ccg aat gtc aac agt aat ggc agc atc tgt ctt gac 299
 Lys Val Tyr His Pro Asn Val Asn Ser Asn Gly Ser Ile Cys Leu Asp
 70 75 80
 att ctg aaa gag cag tgg agc cct gct ctt acc ata tcc aag gtt ctt 347

PF59082SeqList_PF59082.txt

```

Ile Leu Lys Glu Gln Trp Ser Pro Ala Leu Thr Ile Ser Lys Val Leu
      85          90          95
ctg tcg ata tgc tca ttg ctg aca gat cca aac cct gat gat cct ctg      395
Leu Ser Ile Cys Ser Leu Leu Thr Asp Pro Asn Pro Asp Asp Pro Leu
      100          105          110
gtt cca gag ata gct aac atc tac aag tca gac cgt acc aag tac gag      443
Val Pro Glu Ile Ala Asn Ile Tyr Lys Ser Asp Arg Thr Lys Tyr Glu
      115          120          125
aac act gcc cga tcc tgg acc cag aag tat gca atg gga tga tatgatggtt      495
Asn Thr Ala Arg Ser Trp Thr Gln Lys Tyr Ala Met Gly
      130          135          140
ggcaataatg atccgcacca gttaaattgcg catttgtcta agaattgggg aaataagaaa      555

aacctggatt tggcttttgc ttggctgctt gatttaatta gttttattat cttcttatta      615

agccatgtgt acatgagcgc tatttaagcc ttattgaaca tttgatgtct ttcttttaat      675

ccagtaattg gcaaaaaaaaa aaaaaaa      702

```

<210> 1868
 <211> 142
 <212> PRT
 <213> Brassica napus

```

<400> 1868
Met Ala Ser Arg Arg Ile Asn Ser Glu Leu Arg Asp Leu Gln Lys Asp
1      5      10      15
Pro Pro Leu Ser Cys Ser Ala Gly Pro Val Gly Asp Asp Met Tyr His
      20      25      30
Trp Gln Ala Thr Ile Met Gly Pro Thr Asp Ser Pro Phe Thr Gly Gly
      35      40      45
Val Phe Leu Val Ser Ile His Phe Pro Pro Asp Tyr Pro Phe Lys Pro
      50      55      60
Pro Lys Val Tyr His Pro Asn Val Asn Ser Asn Gly Ser Ile Cys Leu
65      70      75      80
Asp Ile Leu Lys Glu Gln Trp Ser Pro Ala Leu Thr Ile Ser Lys Val
      85      90      95
Leu Leu Ser Ile Cys Ser Leu Leu Thr Asp Pro Asn Pro Asp Asp Pro
      100      105      110
Leu Val Pro Glu Ile Ala Asn Ile Tyr Lys Ser Asp Arg Thr Lys Tyr
      115      120      125
Glu Asn Thr Ala Arg Ser Trp Thr Gln Lys Tyr Ala Met Gly
      130      135      140

```

<210> 1869
 <211> 569
 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (73)..(519)

```

<400> 1869
aagaaggcgg cgaaaacctc gccaaagtctg agatacgcg acccaaaaga gatcgtattg      60

taggttttgg at atg gcg tcg aag cgg atc ttg aag gaa ctg aag gat ctg      111
      Met Ala Ser Lys Arg Ile Leu Lys Glu Leu Lys Asp Leu
      1      5      10
cag aag gat cca ccc acc tct tgt agc gca gga cct gtt gct gaa gac      159
Gln Lys Asp Pro Pro Thr Ser Cys Ser Ala Gly Pro Val Ala Glu Asp
      15      20      25
atg ttt cat tgg cag gca acg ata atg ggt cct tca gac agt cct tac      207

```

PF59082SeqList_PF59082.txt

Met	Phe	His	Trp	Gln	Ala	Thr	Ile	Met	Gly	Pro	Ser	Asp	Ser	Pro	Tyr		
30					35				40					45			
gct	ggt	ggt	ggt	ttc	ctt	ggt	acc	att	cat	ttc	cct	cca	gat	tac	cct		255
Ala	Gly	Gly	Val	Phe	Leu	Val	Thr	Ile	His	Phe	Pro	Pro	Asp	Tyr	Pro		
				50					55					60			
ttc	aaa	cct	cct	aag	ggt	gcc	ttt	agg	acg	aag	gtg	ttc	cat	ccc	aac		303
Phe	Lys	Pro	Pro	Lys	Val	Ala	Phe	Arg	Thr	Lys	Val	Phe	His	Pro	Asn		
				65				70					75				
atc	aac	agc	aac	gga	agt	att	tgc	ctt	gac	atc	ttg	aag	gag	caa	tgg		351
Ile	Asn	Ser	Asn	Gly	Ser	Ile	Cys	Leu	Asp	Ile	Leu	Lys	Glu	Gln	Trp		
				80			85					90					
agt	cct	gct	ctc	acc	atc	tcc	aag	gtg	ttg	tta	tcg	atc	tgt	tca	ttg		399
Ser	Pro	Ala	Leu	Thr	Ile	Ser	Lys	Val	Leu	Leu	Ser	Ile	Cys	Ser	Leu		
				95		100				105							
ttg	acc	gat	cca	aac	cct	gat	gat	cct	ttg	gtg	cct	gag	ata	gct	cat		447
Leu	Thr	Asp	Pro	Asn	Pro	Asp	Asp	Pro	Leu	Val	Pro	Glu	Ile	Ala	His		
110				115				120						125			
atg	tat	aag	act	gac	aag	aac	aag	tat	gag	tca	act	gca	cgg	agc	tgg		495
Met	Tyr	Lys	Thr	Asp	Lys	Asn	Lys	Tyr	Glu	Ser	Thr	Ala	Arg	Ser	Trp		
				130				135						140			
act	cag	aag	tat	gcc	atg	ggc	tga	aat	gga	aacc	cca	atc	taca	aa	act	ctc	549
Thr	Gln	Lys	Tyr	Ala	Met	Gly											
				145													
ttt	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	569

<210> 1870
 <211> 148
 <212> PRT
 <213> Brassica napus

<400> 1870
 Met Ala Ser Lys Arg Ile Leu Lys Glu Leu Lys Asp Leu Gln Lys Asp
 1 5 10 15
 Pro Pro Thr Ser Cys Ser Ala Gly Pro Val Ala Glu Asp Met Phe His
 20 25 30
 Trp Gln Ala Thr Ile Met Gly Pro Ser Asp Ser Pro Tyr Ala Gly Gly
 35 40 45
 Val Phe Leu Val Thr Ile His Phe Pro Pro Asp Tyr Pro Phe Lys Pro
 50 55 60
 Pro Lys Val Ala Phe Arg Thr Lys Val Phe His Pro Asn Ile Asn Ser
 65 70 75 80
 Asn Gly Ser Ile Cys Leu Asp Ile Leu Lys Glu Gln Trp Ser Pro Ala
 85 90 95
 Leu Thr Ile Ser Lys Val Leu Leu Ser Ile Cys Ser Leu Leu Thr Asp
 100 105 110
 Pro Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala His Met Tyr Lys
 115 120 125
 Thr Asp Lys Asn Lys Tyr Glu Ser Thr Ala Arg Ser Trp Thr Gln Lys
 130 135 140
 Tyr Ala Met Gly
 145

<210> 1871
 <211> 757
 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (132)..(578)

<400> 1871
 cctcttgaga tttccaaga tcaaatctaa aaacccttag taaatccacc cacgtgtgtg 60
 tgtgtgtgtg tgtggggggg ggttctatta tcgtatttct agaatattct ggtagctgac 120

PF59082SeqList_PF59082.txt

```

tattcaagct t atg gct tcg aga aga att aac agc gag ctt agg gac ctg 170
          Met Ala Ser Arg Arg Ile Asn Ser Glu Leu Arg Asp Leu
          1          5          10
caa aag gac cct cct ctg tct tgc agt gcc ggt cct gtg ggt gat gat 218
Gln Lys Asp Pro Pro Leu Ser Cys Ser Ala Gly Pro Val Gly Asp Asp
          15          20          25
atg tac cac tgg caa gca act atc atg ggt cca act gat agc cca ttc 266
Met Tyr His Trp Gln Ala Thr Ile Met Gly Pro Thr Asp Ser Pro Phe
          30          35          40          45
acc ggt ggt gta ttt ctt gtt tcc att cac ttc cct cca gat tac ccc 314
Thr Gly Gly Val Phe Leu Val Ser Ile His Phe Pro Pro Asp Tyr Pro
          50          55          60
ttc aag cca cca aag gtt tct ttc cgc acc aag gtc tat cac ccg aat 362
Phe Lys Pro Pro Lys Val Ser Phe Arg Thr Lys Val Tyr His Pro Asn
          65          70          75
gtc aac agt aat ggc agc atc tgt ctt gac att ctg aaa gag cag tgg 410
Val Asn Ser Asn Gly Ser Ile Cys Leu Asp Ile Leu Lys Glu Gln Trp
          80          85          90
agc cct gct ctt acc ata tcc aag gtt ctt ctg tcg ata tcc tca ttg 458
Ser Pro Ala Leu Thr Ile Ser Lys Val Leu Leu Ser Ile Ser Ser Leu
          95          100          105
ctg aca gat cca aac cct gat gat cct ctg gtt cca gag ata gct aac 506
Leu Thr Asp Pro Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala Asn
          110          115          120          125
atc tac aag tca gac cgt acc aag tac gag aac act gcc cga tcc tgg 554
Ile Tyr Lys Ser Asp Arg Thr Lys Tyr Glu Asn Thr Ala Arg Ser Trp
          130          135          140
acc cag aag tat gca atg gga tga tatgatgatg gttggcaata atgatccgca 608
Thr Gln Lys Tyr Ala Met Gly
          145
ccagtaaatt gcgcatttgt ctaagaattg gggaaataag aagaaaaaaa catggatttg 668

gcttttgctt gcctgcttga ttttaattagt tttattatct tcctatgtgt tgggtgtgta 728

catgagcaga taagaaaaaa aaaaaaaaaa 757

```

<210> 1872
 <211> 148
 <212> PRT
 <213> Brassica napus

```

<400> 1872
Met Ala Ser Arg Arg Ile Asn Ser Glu Leu Arg Asp Leu Gln Lys Asp
1          5          10          15
Pro Pro Leu Ser Cys Ser Ala Gly Pro Val Gly Asp Asp Met Tyr His
          20          25          30
Trp Gln Ala Thr Ile Met Gly Pro Thr Asp Ser Pro Phe Thr Gly Gly
          35          40          45
Val Phe Leu Val Ser Ile His Phe Pro Pro Asp Tyr Pro Phe Lys Pro
          50          55          60
Pro Lys Val Ser Phe Arg Thr Lys Val Tyr His Pro Asn Val Asn Ser
          65          70          75          80
Asn Gly Ser Ile Cys Leu Asp Ile Leu Lys Glu Gln Trp Ser Pro Ala
          85          90          95
Leu Thr Ile Ser Lys Val Leu Leu Ser Ile Ser Ser Leu Leu Thr Asp
          100          105          110
Pro Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala Asn Ile Tyr Lys
          115          120          125
Ser Asp Arg Thr Lys Tyr Glu Asn Thr Ala Arg Ser Trp Thr Gln Lys
          130          135          140
Tyr Ala Met Gly
          145

```

<210> 1873

PF59082SeqList_PF59082.txt

<211> 450
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (1)..(447)

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<400> 1873
atg gca tcc aag aga ata ctg aag gag ctc aag gac tta cag aga gat      48
Met Ala Ser Lys Arg Ile Leu Lys Glu Leu Lys Asp Leu Gln Arg Asp
1      5      10      15
cca cca act tca tgc agt gca ggc cct gtg ggc gag gac atg ttc cat      96
Pro Pro Thr Ser Cys Ser Ala Gly Pro Val Gly Glu Asp Met Phe His
20      25      30
tgg caa gca acc atc att ggt cca aat gac agt ccc tat gct ggt ggt      144
Trp Gln Ala Thr Ile Ile Gly Pro Asn Asp Ser Pro Tyr Ala Gly Gly
35      40      45
gtt ttc ctt gtg acc atc cat ttc cct ccc gat tat ccc ttc aaa cct      192
Val Phe Leu Val Thr Ile His Phe Pro Pro Asp Tyr Pro Phe Lys Pro
50      55      60
ccc aag gta gca ttc agg acc aag gtg ttc cat ccc aac att aac agc      240
Pro Lys Val Ala Phe Arg Thr Lys Val Phe His Pro Asn Ile Asn Ser
65      70      75      80
aat ggc aat att tgc ctg gac ata ctc aaa gaa caa tgg agt cct gct      288
Asn Gly Asn Ile Cys Leu Asp Ile Leu Lys Glu Gln Trp Ser Pro Ala
85      90      95
ctc acc ata tcc aag gtg ctg ctc tct ata tgt tct ctg cta acg gat      336
Leu Thr Ile Ser Lys Val Leu Leu Ser Ile Cys Ser Leu Leu Thr Asp
100      105      110
cca aat cct gat gac cct tta gtg cct gaa att gct cat ttg tgc aag      384
Pro Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala His Leu Cys Lys
115      120      125
acc gac aaa ttc aag tat gag tct act gct aga agc tgg acc cag aag      432
Thr Asp Lys Phe Lys Tyr Glu Ser Thr Ala Arg Ser Trp Thr Gln Lys
130      135      140
tat gcc atg ggc taa aac
Tyr Ala Met Gly
145
```

<210> 1874
<211> 148
<212> PRT
<213> Glycine max

```
<400> 1874
Met Ala Ser Lys Arg Ile Leu Lys Glu Leu Lys Asp Leu Gln Arg Asp
1      5      10      15
Pro Pro Thr Ser Cys Ser Ala Gly Pro Val Gly Glu Asp Met Phe His
20      25      30
Trp Gln Ala Thr Ile Ile Gly Pro Asn Asp Ser Pro Tyr Ala Gly Gly
35      40      45
Val Phe Leu Val Thr Ile His Phe Pro Pro Asp Tyr Pro Phe Lys Pro
50      55      60
Pro Lys Val Ala Phe Arg Thr Lys Val Phe His Pro Asn Ile Asn Ser
65      70      75      80
Asn Gly Asn Ile Cys Leu Asp Ile Leu Lys Glu Gln Trp Ser Pro Ala
85      90      95
Leu Thr Ile Ser Lys Val Leu Leu Ser Ile Cys Ser Leu Leu Thr Asp
100      105      110
Pro Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala His Leu Cys Lys
115      120      125
Thr Asp Lys Phe Lys Tyr Glu Ser Thr Ala Arg Ser Trp Thr Gln Lys
130      135      140
Tyr Ala Met Gly
145
```

<210> 1875
<211> 745

PF59082SeqList_PF59082.txt

<212> DNA

<213> Triticum aestivum

<220>

<221> CDS

<222> (53)..(499)

<400> 1875

```

gggaccgaag gcagaggaga gaacaatcca aagccttccc agacctacag at atg gcg      58
                                     Met Ala
                                     1
aac aaa agg att cag aag gag ctc atg gat ttg caa aag gat cca cca      106
Asn Lys Arg Ile Gln Lys Glu Leu Met Asp Leu Gln Lys Asp Pro Pro
      5      10      15
aca tca tgc agc gct ggg cct gct ggg gcg gat cta ttc cac tgg cag      154
Thr Ser Cys Ser Ala Gly Pro Ala Gly Ala Asp Leu Phe His Trp Gln
      20      25      30
gcc aca atc atg ggc cct ggt gac agc ccc tac tca gga ggg gtg ttc      202
Ala Thr Ile Met Gly Pro Gly Asp Ser Pro Tyr Ser Gly Gly Val Phe
      35      40      45      50
ttc gtc aac atc cat ttc cct cct gat tac ccc ttt aag cct cca aaa      250
Phe Val Asn Ile His Phe Pro Pro Asp Tyr Pro Phe Lys Pro Pro Lys
      55      60      65
gtg aat ttc caa aca aag gtg tat cac ccg aac atc aac tcc aac ggc      298
Val Asn Phe Gln Thr Lys Val Tyr His Pro Asn Ile Asn Ser Asn Gly
      70      75      80
agc atc tgc ctg gac atc ctc aag gag cag tgg agc ccg gca ctg acc      346
Ser Ile Cys Leu Asp Ile Leu Lys Glu Gln Trp Ser Pro Ala Leu Thr
      85      90      95
ata tcc aag gtc cta ctc tcc atc agc tcc ctg ctc acc gac ccc aac      394
Ile Ser Lys Val Leu Leu Ser Ile Ser Ser Leu Leu Thr Asp Pro Asn
      100      105      110
ccc gac gac ccc ctt gtc ccg gag atc gcg cag ctc tac aag aac cag      442
Pro Asp Asp Pro Leu Val Pro Glu Ile Ala Gln Leu Tyr Lys Asn Gln
      115      120      125      130
aga ggc cgc tac gag gag acc gcg agg gcc tgg acc cag aag tac gcc      490
Arg Gly Arg Tyr Glu Glu Thr Ala Arg Ala Trp Thr Gln Lys Tyr Ala
      135      140      145
atg ggc tga tcgctgcaaa gatgaccgtg gcatcgtgta agacaacttc tgtgtcgcgc      549
Met Gly

cggtttcccg ccctctgagt ttcgaccca tatctggcct tctctgaacc agttttactt      609

gtgtacagtt gtcaaaactg ggtgatgttt gcatttctgt ttccaaactt tgggtgtacg      669

ccctgtccct gaagacctgt atgtatcaac acagaacatt tttaagaatt tgtggtgttt      729

taaaaaaaaa aaaaaa      745

```

<210> 1876

<211> 148

<212> PRT

<213> Triticum aestivum

<400> 1876

```

Met Ala Asn Lys Arg Ile Gln Lys Glu Leu Met Asp Leu Gln Lys Asp
1      5      10      15
Pro Pro Thr Ser Cys Ser Ala Gly Pro Ala Gly Ala Asp Leu Phe His
      20      25      30
Trp Gln Ala Thr Ile Met Gly Pro Gly Asp Ser Pro Tyr Ser Gly Gly
      35      40      45
Val Phe Phe Val Asn Ile His Phe Pro Pro Asp Tyr Pro Phe Lys Pro
      50      55      60
Pro Lys Val Asn Phe Gln Thr Lys Val Tyr His Pro Asn Ile Asn Ser

```

PF59082SeqList_PF59082.txt

```

65          70          75          80
Asn Gly Ser Ile Cys Leu Asp Ile Leu Lys Glu Gln Trp Ser Pro Ala
          85          90          95
Leu Thr Ile Ser Lys Val Leu Leu Ser Ile Ser Ser Leu Leu Thr Asp
          100          105          110
Pro Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala Gln Leu Tyr Lys
          115          120          125
Asn Gln Arg Gly Arg Tyr Glu Glu Thr Ala Arg Ala Trp Thr Gln Lys
          130          135          140
Tyr Ala Met Gly
145

```

<210> 1877

<211> 849

<212> DNA

<213> Triticum aestivum

<220>

<221> CDS

<222> (84)..(674)

<400> 1877

cctattccca ccgccaccgc gccccaccg gccgcctcca gggacagcga gcgagagagg 60

aggaggagggg ctcgtcggag aag atg gtg gac gtg tcg cgc gtg cag aag gag 113
Met Val Asp Val Ser Arg Val Gln Lys Glu 10

ctg acg gag tgc aac cgg gac tcg gac atc tcc ggc gtc tcc atc gcg 161
Leu Thr Glu Cys Asn Arg Asp Ser Asp Ile Ser Gly Val Ser Ile Ala 25

ctc cac gac ggg ggc tcc agc atc acc cac ctc acc ggc acc atc gcc 209
Leu His Asp Gly Gly Ser Ser Ile Thr His Leu Thr Gly Thr Ile Ala 40

ggg ccc cgc gac agc ccc tac gag ggc ggc acc ttc cgc atc gac atc 257
Gly Pro Arg Asp Ser Pro Tyr Glu Gly Gly Thr Phe Arg Ile Asp Ile 55

cgc cta cca ggt ggc tat ccc ttt gag cct cct aag atg cag ttc atc 305
Arg Leu Pro Gly Gly Tyr Pro Phe Glu Pro Pro Lys Met Gln Phe Ile 70

acc aaa gta tgg cac ccg aat att agc agc cag aat gga gca att tgc 353
Thr Lys Val Trp His Pro Asn Ile Ser Ser Gln Asn Gly Ala Ile Cys 90

ttg gac ata ctg aaa gat cag tgg agc cca gcc ctt acc ttg aag acg 401
Leu Asp Ile Leu Lys Asp Gln Trp Ser Pro Ala Leu Thr Leu Lys Thr 105

gca ttg cta tcc ctt caa gct ctt ctt tct gct cct gcc cct gat gat 449
Ala Leu Leu Ser Leu Gln Ala Leu Leu Ser Ala Pro Ala Pro Asp Asp 120

cct cag gat gct gtt gtt gca caa cag tat ctg cgt gac aag gcc aca 497
Pro Gln Asp Ala Val Val Ala Gln Gln Tyr Leu Arg Asp Lys Ala Thr 135

ttt gtt agt act gct cgt tac tgg acc gag gca ttc gca aag agc gac 545
Phe Val Ser Thr Ala Arg Tyr Trp Thr Glu Ala Phe Ala Lys Ser Asp 150

tcc act ggc atg gaa gaa aag gtg cag aag ctg gtc gag atg ggc ttc 593
Ser Thr Gly Met Glu Glu Lys Val Gln Lys Leu Val Glu Met Gly Phe 170

ccc gag gac atg gtg aga agc gcc ctg ctg agt gtg aat ggc gac gag 641
Pro Glu Asp Met Val Arg Ser Ala Leu Leu Ser Val Asn Gly Asp Glu 185

aac atg gct ctc gag aag ctc tgc tct ggc tga aggccctatg tggcctataa 694
Asn Met Ala Leu Glu Lys Leu Cys Ser Gly 195

gaagtgtaaa ttgcgagccc attcattatg gaacaacgat cctagctaata gctcctgtta 754

tgccattccg gtttggccta taggaacaat atatatatag tggactgaac catgggactg 814

PF59082SeqList_PF59082.txt

aactgaagag tgcctatcgt aaaaaaaaaa aaaaa

849

<210> 1878
<211> 196
<212> PRT
<213> Triticum aestivum

<400> 1878
Met Val Asp Val Ser Arg Val Gln Lys Glu Leu Thr Glu Cys Asn Arg
1 5 10 15
Asp Ser Asp Ile Ser Gly Val Ser Ile Ala Leu His Asp Gly Gly Ser
20 25 30
Ser Ile Thr His Leu Thr Gly Thr Ile Ala Gly Pro Arg Asp Ser Pro
35 40 45
Tyr Glu Gly Gly Thr Phe Arg Ile Asp Ile Arg Leu Pro Gly Gly Tyr
50 55 60
Pro Phe Glu Pro Pro Lys Met Gln Phe Ile Thr Lys Val Trp His Pro
65 70 75 80
Asn Ile Ser Ser Gln Asn Gly Ala Ile Cys Leu Asp Ile Leu Lys Asp
85 90 95
Gln Trp Ser Pro Ala Leu Thr Leu Lys Thr Ala Leu Leu Ser Leu Gln
100 105 110
Ala Leu Leu Ser Ala Pro Ala Pro Asp Asp Pro Gln Asp Ala Val Val
115 120 125
Ala Gln Gln Tyr Leu Arg Asp Lys Ala Thr Phe Val Ser Thr Ala Arg
130 135 140
Tyr Trp Thr Glu Ala Phe Ala Lys Ser Asp Ser Thr Gly Met Glu Glu
145 150 155 160
Lys Val Gln Lys Leu Val Glu Met Gly Phe Pro Glu Asp Met Val Arg
165 170 175
Ser Ala Leu Leu Ser Val Asn Gly Asp Glu Asn Met Ala Leu Glu Lys
180 185 190
Leu Cys Ser Gly
195

<210> 1879
<211> 854
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (180)..(626)

<400> 1879
agagagagag cgagcgagcg agcagtttca aagagaggat ttgggattgg gaaggcgagg

60

gattgcgctg cgtctcttcc tcttctcttt cgattcatcc ctcatcdata atcttccaat

120

ccaacaacct cagcctcaca ctacacata cacacatctg aacgcgtatc gtccctccc

179

atg gct tca aag cgc atc ctc aag gag ctc aag gac ttg cag aaa gac
Met Ala Ser Lys Arg Ile Leu Lys Glu Leu Lys Asp Leu Gln Lys Asp
1 5 10 15
cca cca act tct tgc agc gct ggt cca gta gct gag gac atg ttc cat
Pro Pro Thr Ser Cys Ser Ala Gly Pro Val Ala Glu Asp Met Phe His
20 25 30
tgg caa gca acg att atg ggt cct gct gat agt cct tat gct gga ggt
Trp Gln Ala Thr Ile Met Gly Pro Ala Asp Ser Pro Tyr Ala Gly Gly
35 40 45
gta ttc cta gtc act att cac ttt cct ccg gat tat cct ttc aaa cct
Val Phe Leu Val Thr Ile His Phe Pro Pro Asp Tyr Pro Phe Lys Pro
50 55 60

227

275

323

371

PF59082SeqList_PF59082.txt

```

ccc aag gtt gcc ttt agg act aag gtg ttt cat ccg aac atc aac agc      419
Pro Lys Val Ala Phe Arg Thr Lys Val Phe His Pro Asn Ile Asn Ser
 65      70      75      80
aat ggt agc att tgt ctt gat atc ctt aag gag cag tgg agc cct gca      467
Asn Gly Ser Ile Cys Leu Asp Ile Leu Lys Glu Gln Trp Ser Pro Ala
      85      90      95
ctc acc atc tct aag gta ctg ctt tct atc tgc tca ttg ctg act gat      515
Leu Thr Ile Ser Lys Val Leu Leu Ser Ile Cys Ser Leu Leu Thr Asp
      100      105      110
cca aat cct gat gat cca ctt gtt ccg gaa atc gct cac atg tac aaa      563
Pro Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala His Met Tyr Lys
      115      120      125
act aac cgg gcc aag tat gag gcc act gca cgc agc tgg acc cag aag      611
Thr Asn Arg Ala Lys Tyr Glu Ala Thr Ala Arg Ser Trp Thr Gln Lys
      130      135      140
tat gcc atg ggc tga tttgtgttta gataatgtat attgaaatgg atggcatcta      666
Tyr Ala Met Gly
145
tgaaaacttt tgtgggtttg cttttctctt cctgtttttc tggggtaaga ttatgtttgt      726

tatgagggga tagggaaggg cggtgtctta atttgataaa aataactatg ttcaacaacc      786

actgtgatgt ttttatcatg atgcgaacgc atgaacaaga tgttatttgt gtcaaaaaaa      846

aaaaaaaaa                                                                854

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<210> 1880
 <211> 148
 <212> PRT
 <213> Glycine max

<400> 1880
 Met Ala Ser Lys Arg Ile Leu Lys Glu Leu Lys Asp Leu Gln Lys Asp
 1 5 10 15
 Pro Pro Thr Ser Cys Ser Ala Gly Pro Val Ala Glu Asp Met Phe His
 20 25 30
 Trp Gln Ala Thr Ile Met Gly Pro Ala Asp Ser Pro Tyr Ala Gly Gly
 35 40 45
 Val Phe Leu Val Thr Ile His Phe Pro Pro Asp Tyr Pro Phe Lys Pro
 50 55 60
 Pro Lys Val Ala Phe Arg Thr Lys Val Phe His Pro Asn Ile Asn Ser
 65 70 75 80
 Asn Gly Ser Ile Cys Leu Asp Ile Leu Lys Glu Gln Trp Ser Pro Ala
 85 90 95
 Leu Thr Ile Ser Lys Val Leu Leu Ser Ile Cys Ser Leu Leu Thr Asp
 100 105 110
 Pro Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala His Met Tyr Lys
 115 120 125
 Thr Asn Arg Ala Lys Tyr Glu Ala Thr Ala Arg Ser Trp Thr Gln Lys
 130 135 140
 Tyr Ala Met Gly
 145

<210> 1881
 <211> 450
 <212> DNA
 <213> Linum usitatissimum

<220>
 <221> CDS
 <222> (1)..(447)

<400> 1881
 atg gct tct aag cgt atc ctc aag gag ctc aag gat ttg cag aag gat 48
 seite 2450

PF59082SeqList_PF59082.txt

```

Met Ala Ser Lys Arg Ile Leu Lys Glu Leu Lys Asp Leu Gln Lys Asp
1      5      10      15
cct ccc tct tcc tgc agc gca ggt cct gtg gcg gag gac atg ttc cac      96
Pro Pro Ser Ser Cys Ser Ala Gly Pro Val Ala Glu Asp Met Phe His
20
tgg cag gca acg atc atg gga ccc tct gac agt cct tat tct gga ggt      144
Trp Gln Ala Thr Ile Met Gly Pro Ser Asp Ser Pro Tyr Ser Gly Gly
35
gtt ttc ctg gtt aca atc cat ttc cct cca gat tat cct ttc aag cct      192
Val Phe Leu Val Thr Ile His Phe Pro Pro Asp Tyr Pro Phe Lys Pro
50
ccc aag gta gca ttt agg acc aag gtc ttt cac ccc aat gta aac agc      240
Pro Lys Val Ala Phe Arg Thr Lys Val Phe His Pro Asn Val Asn Ser
65
aat ggg agc att tgt ctt gat atc ctg aaa gag cag tgg agc cca gct      288
Asn Gly Ser Ile Cys Leu Asp Ile Leu Lys Glu Gln Trp Ser Pro Ala
85
ctt acc att tca aag gta ctg ctg tca ata tgc tca cta ttg acg gat      336
Leu Thr Ile Ser Lys Val Leu Leu Ser Ile Cys Ser Leu Leu Thr Asp
100
ccc aac ccg gac gac cct ctg gtg cca gag att gca cac atg tac aag      384
Pro Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala His Met Tyr Lys
115
aca gac cgt gcc aaa tac gag gcg act gca tgc agc tgg act cag aaa      432
Thr Asp Arg Ala Lys Tyr Glu Ala Thr Ala Cys Ser Trp Thr Gln Lys
130
tat gcc atg gga tga cga
Tyr Ala Met Gly
145

```

<210> 1882

<211> 148

<212> PRT

<213> Linum usitatissimum

<400> 1882

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Met Ala Ser Lys Arg Ile Leu Lys Glu Leu Lys Asp Leu Gln Lys Asp
1      5      10      15
Pro Pro Ser Ser Cys Ser Ala Gly Pro Val Ala Glu Asp Met Phe His
20
Trp Gln Ala Thr Ile Met Gly Pro Ser Asp Ser Pro Tyr Ser Gly Gly
35
Val Phe Leu Val Thr Ile His Phe Pro Pro Asp Tyr Pro Phe Lys Pro
50
Pro Lys Val Ala Phe Arg Thr Lys Val Phe His Pro Asn Val Asn Ser
65
Asn Gly Ser Ile Cys Leu Asp Ile Leu Lys Glu Gln Trp Ser Pro Ala
85
Leu Thr Ile Ser Lys Val Leu Leu Ser Ile Cys Ser Leu Leu Thr Asp
100
Pro Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala His Met Tyr Lys
115
Thr Asp Arg Ala Lys Tyr Glu Ala Thr Ala Cys Ser Trp Thr Gln Lys
130
Tyr Ala Met Gly
145

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<210> 1883

<211> 827

<212> DNA

<213> Linum usitatissimum

<220>

<221> CDS

<222> (224)..(670)

<400> 1883

gcaaagccaa aaaagaaaaa agtagacgaa tcgggaactg cgtgcatggc aaggactccc 60

PF59082SeqList_PF59082.txt

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ccgcaaattt agcgccgaac ctttctccgt tgtataaata caatctacag ttgctgagtt      120

gatcttcaat ctctccccgc cgtcgttcca cactctctcg gagtcagctg agtttcgccg      180

gagttcactg ccgatattcc ttatagactt ctgaagctgg aag atg gct tca aag      235
               Met Ala Ser Lys
               1
agg att aac aag gag ctc aag gac ttg cag aag gat cct cct gca tca      283
Arg Ile Asn Lys Glu Leu Lys Asp Leu Gln Lys Asp Pro Pro Ala Ser
5 10 15 20
tgc agt gca gga cct gct ggt gat gat atg ttc cat tgg caa gca act      331
Cys Ser Ala Gly Pro Ala Gly Asp Asp Met Phe His Trp Gln Ala Thr
25 30 35
ata atg ggt cct cca gat agc cct tat gcc ggt ggt gtt ttc ttg gtc      379
Ile Met Gly Pro Pro Asp Ser Pro Tyr Ala Gly Gly Val Phe Leu Val
40 45 50
acc att aac ttc cct cca gat tat cca ttc aag cca ccc aag tgc tcg      427
Thr Ile Asn Phe Pro Pro Asp Tyr Pro Phe Lys Pro Pro Lys Cys Ser
55 60 65
ttc aag acc aaa gtt tat cac ccg aac atc aac agc aac gga agc atc      475
Phe Lys Thr Lys Val Tyr His Pro Asn Ile Asn Ser Asn Gly Ser Ile
70 75 80
tgc ctc gac atc ctc aaa gaa cag tgg agt cca gct ctc acc gta tcg      523
Cys Leu Asp Ile Leu Lys Glu Gln Trp Ser Pro Ala Leu Thr Val Ser
85 90 95 100
aag gtg ctg ctg tct att tgc tcg ctg ctg acg gac ccc aac ccg gac      571
Lys Val Leu Leu Ser Ile Cys Ser Leu Leu Thr Asp Pro Asn Pro Asp
105 110 115
gat cca ctg gtg cct gag att gct cac atg tac aag aac gac aga acc      619
Asp Pro Leu Val Pro Glu Ile Ala His Met Tyr Lys Asn Asp Arg Thr
120 125 130
aag tat gag aac acc gct cgt gcc tgg acc cag aag tac gca atg ggt      667
Lys Tyr Glu Asn Thr Ala Arg Ala Trp Thr Gln Lys Tyr Ala Met Gly
135 140 145
taa acatctcgtc gagttcggat gatataagaa aagaggaatt tgtagtcttt      720

ctccagctga aaaaccattc tatgaacttg aatctcctca ttgtataaat aaattgctac      780

ttggatttct taaggtttcg gagtttcgaa ctaaaaaaaaa aaaaaaa      827

```

<210> 1884
 <211> 148
 <212> PRT
 <213> Linum usitatissimum

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<400> 1884
Met Ala Ser Lys Arg Ile Asn Lys Glu Leu Lys Asp Leu Gln Lys Asp
1 5 10 15
Pro Pro Ala Ser Cys Ser Ala Gly Pro Ala Gly Asp Asp Met Phe His
20 25 30
Trp Gln Ala Thr Ile Met Gly Pro Pro Asp Ser Pro Tyr Ala Gly Gly
35 40 45
Val Phe Leu Val Thr Ile Asn Phe Pro Pro Asp Tyr Pro Phe Lys Pro
50 55 60
Pro Lys Cys Ser Phe Lys Thr Lys Val Tyr His Pro Asn Ile Asn Ser
65 70 75 80
Asn Gly Ser Ile Cys Leu Asp Ile Leu Lys Glu Gln Trp Ser Pro Ala
85 90 95
Leu Thr Val Ser Lys Val Leu Leu Ser Ile Cys Ser Leu Leu Thr Asp
100 105 110
Pro Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala His Met Tyr Lys
115 120 125

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PF59082SeqList_PF59082.txt

Asn Asp Arg Thr Lys Tyr Glu Asn Thr Ala Arg Ala Trp Thr Gln Lys
 130 135 140
 Tyr Ala Met Gly
 145

<210> 1885
 <211> 1157
 <212> DNA
 <213> Linum usitatissimum

<220>
 <221> CDS
 <222> (308)..(889)

<400> 1885
 ggcccaaaca tgagggattt tctatgttaa ctacccttcc catttaccct acacaacctc 60

 catccgctcc aaactctctc ctctccgata agtctgaact ccggcgctcta ctggagcctt 120

 ccccggcgtc cagcttcctt ctccgaagtg gcggtgctgg tttgagatca ggggaaagat 180

 agagaccatt tgctgtctcc ttcaaccag taaacagtgg actaggtggt gaagtacttc 240

 ccggagaaga ctgctgctcg attaggggttc catcgatttc tcccagttga gtagagtgg 300

 tgctact atg atc gac ttc gct cga gtt cag aag gag ctc caa gaa tgc 349
 Met Ile Asp Phe Ala Arg Val Gln Lys Glu Leu Gln Glu Cys
 1 5 10
 agc aga gac att gga gct tcc ggc atc aag gtt tcc ccc aac tcc gac 397
 Ser Arg Asp Ile Gly Ala Ser Gly Ile Lys Val Ser Pro Asn Ser Asp
 15 20 25 30
 agc cta gct cgc ctc agt ggc acc att cct ggc cct att ggc act cct 445
 Ser Leu Ala Arg Leu Ser Gly Thr Ile Pro Gly Pro Ile Gly Thr Pro
 35 40 45
 tat gaa ggt ggc tct ttc caa att gac atc tcc ctt cca gat ggg tac 493
 Tyr Glu Gly Gly Ser Phe Gln Ile Asp Ile Ser Leu Pro Asp Gly Tyr
 50 55 60
 ccg ttc gag cct cct aga atg aag ttc gtg acg aaa gtc tgg cac cca 541
 Pro Phe Glu Pro Pro Arg Met Lys Phe Val Thr Lys Val Trp His Pro
 65 70 75
 aat att agc agt cag agc gga gct att tgc ctt gat ata ttg aaa gac 589
 Asn Ile Ser Ser Gln Ser Gly Ala Ile Cys Leu Asp Ile Leu Lys Asp
 80 85 90
 caa tgg agc cct gct cta act ctg aag aca gct cta ctc tcc gtt caa 637
 Gln Trp Ser Pro Ala Leu Thr Leu Lys Thr Ala Leu Leu Ser Val Gln
 95 100 105 110
 gca ctg ctc tct gct cct gag cct gat gac cct caa gat gca gta gta 685
 Ala Leu Leu Ser Ala Pro Glu Pro Asp Asp Pro Gln Asp Ala Val Val
 115 120 125
 gca cag cag tat ctc aag gat tac cag acc ttt gtt ggg aca gct cgc 733
 Ala Gln Gln Tyr Leu Lys Asp Tyr Gln Thr Phe Val Gly Thr Ala Arg
 130 135 140
 tac tgg aca gaa act ttt gct aag gtc tca tct ctc ggt gtt gaa gaa 781
 Tyr Trp Thr Glu Thr Phe Ala Lys Val Ser Ser Leu Gly Val Glu Glu
 145 150 155
 aag gta cag aaa ctt gtt gaa atg gga ttc cct gaa gct ttg gtg agg 829
 Lys Val Gln Lys Leu Val Glu Met Gly Phe Pro Glu Ala Leu Val Arg
 160 165 170
 agt aca ctg gat tca gtt ggt ggg gac gag aac ttg gct ctg gag agg 877
 Ser Thr Leu Asp Ser Val Gly Gly Asp Glu Asn Leu Ala Leu Glu Arg
 175 180 185 190
 ctg tgt tct tga aggatcccag ggttaagggt tgatatgaag aatgtataga 929
 Leu Cys Ser

PF59082SeqList_PF59082.txt

ggctctccta agtaactagt tatttttgta agctacttcc ttttgtttat gatatacctcc 989

tgaattgcga gaagtgaaca tctgtgtgag acgattgatg acccacaact gtagggcatc 1049

catttatcgg caacttattc agcaagggct gaagagttgc ctaaactgat taatatatat 1109

atgggcccgt ttgataattt tgggcttatt tggaaaaaaaa aaaaaaaaa 1157

<210> 1886
<211> 193
<212> PRT
<213> Linum usitatissimum

<400> 1886
Met Ile Asp Phe Ala Arg Val Gln Lys Glu Leu Gln Glu Cys Ser Arg
1 5 10 15
Asp Ile Gly Ala Ser Gly Ile Lys Val Ser Pro Asn Ser Asp Ser Leu
20 25 30
Ala Arg Leu Ser Gly Thr Ile Pro Gly Pro Ile Gly Thr Pro Tyr Glu
35 40 45
Gly Gly Ser Phe Gln Ile Asp Ile Ser Leu Pro Asp Gly Tyr Pro Phe
50 55 60
Glu Pro Pro Arg Met Lys Phe Val Thr Lys Val Trp His Pro Asn Ile
65 70 75 80
Ser Ser Gln Ser Gly Ala Ile Cys Leu Asp Ile Leu Lys Asp Gln Trp
85 90 95
Ser Pro Ala Leu Thr Leu Lys Thr Ala Leu Leu Ser Val Gln Ala Leu
100 105 110
Leu Ser Ala Pro Glu Pro Asp Asp Pro Gln Asp Ala Val Val Ala Gln
115 120 125
Gln Tyr Leu Lys Asp Tyr Gln Thr Phe Val Gly Thr Ala Arg Tyr Trp
130 135 140
Thr Glu Thr Phe Ala Lys Val Ser Ser Leu Gly Val Glu Glu Lys Val
145 150 155 160
Gln Lys Leu Val Glu Met Gly Phe Pro Glu Ala Leu Val Arg Ser Thr
165 170 175
Leu Asp Ser Val Gly Gly Asp Glu Asn Leu Ala Leu Glu Arg Leu Cys
180 185 190
Ser

<210> 1887
<211> 875
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (91)..(537)

<400> 1887
cctccttcaa agccctctgg cgatcgagat tcttccccct ccgtctccag gtatacccat 60

cggagcagca cagacaagag ttctcctgat atg gca aac aaa agg att cag aag 114
Met Ala Asn Lys Arg Ile Gln Lys
1 5
gaa ctc atg gat ctg caa aag gac cca ccg aca tca tgc agt gca ggg 162
Glu Leu Met Asp Leu Gln Lys Asp Pro Pro Thr Ser Cys Ser Ala Gly
10 15 20
cca gct gga gag gat cta ttc cac tgg cag gcc aca atc atg ggt cct 210
Pro Ala Gly Glu Asp Leu Phe His Trp Gln Ala Thr Ile Met Gly Pro
25 30 35 40
agc gac agc ccc tat gca gga ggg gtt ttc gtt aat atc cat ttt 258

PF59082SeqList_PF59082.txt

```

Ser Asp Ser Pro Tyr Ala Gly Gly Val Phe Phe Val Asn Ile His Phe
      45      50      55
cct cct gac tac ccg ttt aag cct cca aaa gtg aac ttc caa aca aaa      306
Pro Pro Asp Tyr Pro Phe Lys Pro Pro Lys Val Asn Phe Gln Thr Lys
      60      65      70
gtt tat cac ccg aac atc aac tct aac ggg agc atc tgc ctt gat atc      354
Val Tyr His Pro Asn Ile Asn Ser Asn Gly Ser Ile Cys Leu Asp Ile
      75      80      85
ctc aag gag cag tgg agc cct gca ctg acc ata tca aag gtc ctc ctc      402
Leu Lys Glu Gln Trp Ser Pro Ala Leu Thr Ile Ser Lys Val Leu Leu
      90      95      100
tcc atc agc tcg ctt ctg act gac ccc aac cca gac gac ccc ctc gtc      450
Ser Ile Ser Ser Leu Leu Thr Asp Pro Asn Pro Asp Asp Pro Leu Val
      105      110      115      120
ccc gag atc gcc cac atg tac aag aac cag agg ccg cgc tac gag aaa      498
Pro Glu Ile Ala His Met Tyr Lys Asn Gln Arg Pro Arg Tyr Glu Lys
      125      130      135
acc gca cgg gcc tgg acc cag aag tac gcg atg ggc tag ctgattctgt      547
Thr Ala Arg Ala Trp Thr Gln Lys Tyr Ala Met Gly
      140      145
ctcgccgaac aatactgtca ctggcaagaa gatcatcatc acgatgttgt aagaattaag      607

ttgaaccggt ttccccgtcg tgtgatggta ttaagaccaa agttcttgtg cgtgtacagt      667

acttttgaag ctggatagtc tgaatcctgt gccagtacca aaggctcttcg ctttgttccc      727

tgaagagcgt ttgtgaccat agaatctgca tgcgtaacct tgccagccaa gaaaacagta      787

gctgcttgta tgatgtcgag atgatatagt tcagatgggt ggaaccgtgc agatgaaaca      847

gtccagtggt cttgcgcaaa aaaaaaaaaa      875

```

<210> 1888
 <211> 148
 <212> PRT
 <213> Zea mays

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<400> 1888
Met Ala Asn Lys Arg Ile Gln Lys Glu Leu Met Asp Leu Gln Lys Asp
1      5      10      15
Pro Pro Thr Ser Cys Ser Ala Gly Pro Ala Gly Glu Asp Leu Phe His
      20      25      30
Trp Gln Ala Thr Ile Met Gly Pro Ser Asp Ser Pro Tyr Ala Gly Gly
      35      40      45
Val Phe Phe Val Asn Ile His Phe Pro Pro Asp Tyr Pro Phe Lys Pro
      50      55      60
Pro Lys Val Asn Phe Gln Thr Lys Val Tyr His Pro Asn Ile Asn Ser
      65      70      75      80
Asn Gly Ser Ile Cys Leu Asp Ile Leu Lys Glu Gln Trp Ser Pro Ala
      85      90      95
Leu Thr Ile Ser Lys Val Leu Leu Ser Ile Ser Ser Leu Leu Thr Asp
      100      105      110
Pro Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala His Met Tyr Lys
      115      120      125
Asn Gln Arg Pro Arg Tyr Glu Lys Thr Ala Arg Ala Trp Thr Gln Lys
      130      135      140
Tyr Ala Met Gly
      145

```

<210> 1889
 <211> 755
 <212> DNA

PF59082SeqList_PF59082.txt

<213> Linum usitatissimum

<220>

<221> CDS

<222> (17)..(478)

<400> 1889

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aagaaaagaa acctca atg gcg aac agt aac ctt cct cgg aga att atc aag      52
                Met Ala Asn Ser Asn Leu Pro Arg Arg Ile Ile Lys
                1      5      10
gaa acg cag cgg ctg ctc agt gaa cca gcc cct gga att agt gct tcc      100
Glu Thr Gln Arg Leu Leu Ser Glu Pro Ala Pro Gly Ile Ser Ala Ser
                15      20      25
cct tct gaa gaa aac atg cga tac ttc aat gtt atg att ctt ggt cca      148
Pro Ser Glu Glu Asn Met Arg Tyr Phe Asn Val Met Ile Leu Gly Pro
                30      35      40
aca caa tca cct tat gaa ggt ggt gtt ttt aag ttg gaa ttg ttc ttg      196
Thr Gln Ser Pro Tyr Glu Gly Gly Val Phe Lys Leu Glu Leu Phe Leu
                45      50      55      60
ccc gaa gaa tac cca atg gca cct ccc aag gtt cgc ttc ttg acg aaa      244
Pro Glu Glu Tyr Pro Met Ala Pro Pro Lys Val Arg Phe Leu Thr Lys
                65      70      75
att tat cac cct aat att gac aag ctt gga aga att tgc ctt gat att      292
Ile Tyr His Pro Asn Ile Asp Lys Leu Gly Arg Ile Cys Leu Asp Ile
                80      85      90
ctg aaa gat aaa tgg agc cct gca ctc cag atc cga act gtt ctg cta      340
Leu Lys Asp Lys Trp Ser Pro Ala Leu Gln Ile Arg Thr Val Leu Leu
                95      100      105
agt atc caa gct ctc ttg agc gca cca aat cct gat gat cct ctg tct      388
Ser Ile Gln Ala Leu Leu Ser Ala Pro Asn Pro Asp Asp Pro Leu Ser
                110      115      120
gag aac att gca aag cac tgg aag tca aat gaa gct gaa gct gtt gaa      436
Glu Asn Ile Ala Lys His Trp Lys Ser Asn Glu Ala Glu Ala Val Glu
                125      130      135      140
aca gct aaa gaa tgg agc cgc tta tat gca agt ggt gca tga ggaggcaagc      488
Thr Ala Lys Glu Trp Ser Arg Leu Tyr Ala Ser Gly Ala
                145      150
tggagcagtg caaatgatct atgttggtttc ttgttacatt ggtaaataatga atttgaaatg      548

taatgtctgt tggttcctaa aatgggaaat atgcttcaat gtatgctctg aacactatca      608

gatacatgaa tccttaaaga gtctcgagtc ttgaatcgca gcagtactct cttttcagta      668

tactggacct gtatcataca gcgtcattgg aagcttcctt ttaattgact tgcgataatg      728

actgattgac tgaaaaaaaa aaaaaaa      755

```

<210> 1890

<211> 153

<212> PRT

<213> Linum usitatissimum

<400> 1890

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Met Ala Asn Ser Asn Leu Pro Arg Arg Ile Ile Lys Glu Thr Gln Arg
1      5      10      15
Leu Leu Ser Glu Pro Ala Pro Gly Ile Ser Ala Ser Pro Ser Glu Glu
                20      25      30
Asn Met Arg Tyr Phe Asn Val Met Ile Leu Gly Pro Thr Gln Ser Pro
                35      40      45
Tyr Glu Gly Gly Val Phe Lys Leu Glu Leu Phe Leu Pro Glu Glu Tyr
                50      55      60
Pro Met Ala Pro Pro Lys Val Arg Phe Leu Thr Lys Ile Tyr His Pro
65      70      75      80

```

PF59082SeqList_PF59082.txt

Asn Ile Asp Lys Leu Gly Arg Ile Cys Leu Asp Ile Leu Lys Asp Lys
 85 90 95
 Trp Ser Pro Ala Leu Gln Ile Arg Thr Val Leu Leu Ser Ile Gln Ala
 100 105 110
 Leu Leu Ser Ala Pro Asn Pro Asp Pro Leu Ser Glu Asn Ile Ala
 115 120 125
 Lys His Trp Lys Ser Asn Glu Ala Glu Ala Val Glu Thr Ala Lys Glu
 130 135 140
 Trp Ser Arg Leu Tyr Ala Ser Gly Ala
 145 150

<210> 1891

<211> 834

<212> DNA

<213> Linum usitatissimum

<220>

<221> CDS

<222> (88)..(534)

<400> 1891

cgccccaact ctcttcgcga gaaatctccg tttcgccggc gacgaggagg atccgatctc 60

tagctttctc tccacagggt ctcggcg atg gcg tcc aag cgc atc ttg aag gag 114
 Met Ala Ser Lys Arg Ile Leu Lys Glu
 1 5

ctc aag gat ttg cag aag gat cct ccc acg tct tgc agc gct ggt cct 162
 Leu Lys Asp Leu Gln Lys Asp Pro Pro Thr Ser Cys Ser Ala Gly Pro
 10 15 20 25

gtt gcg gag gac atg ttc cac tgg caa gca acg atc atg ggt cct cca 210
 Val Ala Glu Asp Met Phe His Trp Gln Ala Thr Ile Met Gly Pro Pro
 30 35 40

gat agc cct tat tct ggt ggt gtt ttc ctg gtc act atc cat ttc cct 258
 Asp Ser Pro Tyr Ser Gly Gly Val Phe Leu Val Thr Ile His Phe Pro
 45 50 55

ccg gat tat cca ttc aag cct ccc aag gtg gct ttc aga aca aag gtg 306
 Pro Asp Tyr Pro Phe Lys Pro Pro Lys Val Ala Phe Arg Thr Lys Val
 60 65 70

ttc cac ccg aat atc aac agc aac ggt agc atc tgt ctc gac atc ttg 354
 Phe His Pro Asn Ile Asn Ser Asn Gly Ser Ile Cys Leu Asp Ile Leu
 75 80 85

aaa gaa cag tgg agc cct gct ctt acc ata tcc aag gtg ttg ctc tcg 402
 Lys Glu Gln Trp Ser Pro Ala Leu Thr Ile Ser Lys Val Leu Leu Ser
 90 95 100 105

atc tgc tcg ttg ttg acg gat ccc aac ccg gac gac cca ttg gta ccc 450
 Ile Cys Ser Leu Leu Thr Asp Pro Asn Pro Asp Asp Pro Leu Val Pro
 110 115 120

gag att gcc cac atg tac aaa aca gac agg cac aag tac gag acg act 498
 Glu Ile Ala His Met Tyr Lys Thr Asp Arg His Lys Tyr Glu Thr Thr
 125 130 135

gca agg agc tgg acc cag aag tat gcc atg gga tga aaatttgaga 544
 Ala Arg Ser Trp Thr Gln Lys Tyr Ala Met Gly
 140 145

gaggaaaagg aacaagaact ctgctatcag tctatctctc tctctctcta tctcagttgg 604

tatgtattaa tttgtccttt gttgtgcttt gctcttcaga aactatgaac gaggggcttt 664

aaaagtttgg ctctccatta acatttcccc ccctcgtgaa gaaagaaaaa agaagagaga 724

cccaaagaaa gagatgtttg gtctcgttct ctcttctttg ttgtatggat aatttgatgt 784

tcgcaaacga ttcgaaaagt aaagtgttct tctccaaaaa aaaaaaaaaa 834

PF59082SeqList_PF59082.txt

<210> 1892
 <211> 148
 <212> PRT
 <213> Linum usitatissimum

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 20 25 30
 Trp Gln Ala Thr Ile Met Gly Pro Pro Asp Ser Pro Tyr Ser Gly Gly
 35 40 45
 Val Phe Leu Val Thr Ile His Phe Pro Pro Asp Tyr Pro Phe Lys Pro
 50 55 60
 Pro Lys Val Ala Phe Arg Thr Lys Val Phe His Pro Asn Ile Asn Ser
 65 70 75 80
 Asn Gly Ser Ile Cys Leu Asp Ile Leu Lys Glu Gln Trp Ser Pro Ala
 85 90 95
 Leu Thr Ile Ser Lys Val Leu Leu Ser Ile Cys Ser Leu Leu Thr Asp
 100 105 110
 Pro Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala His Met Tyr Lys
 115 120 125
 Thr Asp Arg His Lys Tyr Glu Thr Thr Ala Arg Ser Trp Thr Gln Lys
 130 135 140
 Tyr Ala Met Gly
 145

<210> 1893
 <211> 811
 <212> DNA
 <213> Helianthus annuus

<220>
 <221> CDS
 <222> (187)..(633)

<400> 1893
 attccaatgt cgccaaattc attcaaaacc ctaattttcc cccaatttca tctccattag 60

 ctctcaatct tctcattttc gatcccaaatt catccaattc ttccgttttc ccttgcttcc 120

 gcatctcctc gatcagggtt tggtttggtg acgtgagagg aaagtttcgg attgtaaggt 180

 gtgggtg atg gcg tca aag cgt atc att aag gaa ctc aag gat ttg cag 228
 Met Ala Ser Lys Arg Ile Ile Lys Glu Leu Lys Asp Leu Gln
 1 5 10
 aag gat cct cct acg tca tgc agt gct ggt cct gtt gct gag gac atg 276
 Lys Asp Pro Pro Thr Ser Cys Ser Ala Gly Pro Val Ala Glu Asp Met
 15 20 25 30
 ttt cat tgg caa gca aca ata atg gga cct tcg gat agc cct tac tct 324
 Phe His Trp Gln Ala Thr Ile Met Gly Pro Ser Asp Ser Pro Tyr Ser
 35 40 45
 ggt ggg gtg ttt ctc gtc aat att cat ttc ccc cct gat tac cca ttt 372
 Gly Gly Val Phe Leu Val Asn Ile His Phe Pro Pro Asp Tyr Pro Phe
 50 55 60
 aag ccc cca aag gtt gca ttt agg acg aag gtg ttt cat cca aac atc 420
 Lys Pro Pro Lys Val Ala Phe Arg Thr Lys Val Phe His Pro Asn Ile
 65 70 75
 aat agc aac ggt agc ata tgt ttg gat atc ctc aag gaa caa tgg agt 468
 Asn Ser Asn Gly Ser Ile Cys Leu Asp Ile Leu Lys Glu Gln Trp Ser
 80 85 90
 cca gca cta aca atc tcc aag gtg ttg ctt tcc atc tgc tca ctg ttg 516
 Pro Ala Leu Thr Ile Ser Lys Val Leu Leu Ser Ile Cys Ser Leu Leu
 95 100 105 110
 aca gac ccg aac cct gat gat ccg ttg gtg cca gag att gct cac atg 564

PF59082SeqList_PF59082.txt

Thr Asp Pro Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala His Met
 115 120 125
 tat aaa acc gac aag tcc aag tac gag gcc act gct cgt agc tgg acg 612
 Tyr Lys Thr Asp Lys Ser Lys Tyr Glu Ala Thr Ala Arg Ser Trp Thr
 130 135 140
 cag aag tat gcc atg ggc taa tctctcgagt ctcgtttgaa tcaaatcgat 663
 Gln Lys Tyr Ala Met Gly
 145
 tgttggaaga ataaaaaatg ttggtttttc actttttatt cttggaatgt ctcaatgaag 723
 aaatggttgt taagattgtc tcagtttgtg taatattgaa atgattttaa tcaaagagac 783
 tcattttaga aagaaaaaaa aaaaaaaa 811

<210> 1894
 <211> 148
 <212> PRT
 <213> Helianthus annuus

<400> 1894
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 20 25 30
 Trp Gln Ala Thr Ile Met Gly Pro Ser Asp Ser Pro Tyr Ser Gly Gly
 35 40 45
 Val Phe Leu Val Asn Ile His Phe Pro Pro Asp Tyr Pro Phe Lys Pro
 50 55 60
 Pro Lys Val Ala Phe Arg Thr Lys Val Phe His Pro Asn Ile Asn Ser
 65 70 75 80
 Asn Gly Ser Ile Cys Leu Asp Ile Leu Lys Glu Gln Trp Ser Pro Ala
 85 90 95
 Leu Thr Ile Ser Lys Val Leu Leu Ser Ile Cys Ser Leu Leu Thr Asp
 100 105 110
 Pro Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala His Met Tyr Lys
 115 120 125
 Thr Asp Lys Ser Lys Tyr Glu Ala Thr Ala Arg Ser Trp Thr Gln Lys
 130 135 140
 Tyr Ala Met Gly
 145

<210> 1895
 <211> 810
 <212> DNA
 <213> Helianthus annuus

<220>
 <221> CDS
 <222> (123)..(707)

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 ttgtgatttt atcccccaaa caaaacattc cctcacttca attccagttg ctcaaacaaa 120
 ac atg gtg gat ttc ggt aga gtg caa aag gag ctt caa gac tgc aac 167
 Met Val Asp Phe Gly Arg Val Gln Lys Glu Leu Gln Asp Cys Asn
 1 5 10 15
 aaa gac atc aat gtc tct ggt atc cgc gtt aac cct aag ctc gac aat 215
 Lys Asp Ile Asn Val Ser Gly Ile Arg Val Asn Pro Lys Leu Asp Asn
 20 25 30
 ctc atc aat ttg atc ggc acc att ccc ggc cct gtt ggc act cct tac 263
 Leu Ile Asn Leu Ile Gly Thr Ile Pro Gly Pro Val Gly Thr Pro Tyr
 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995

PF59082SeqList_PF59082.txt

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      35      40      45
gaa ggc gga acc ttc aaa atc gat atc gat ttg ccc gat gca tac cct 311
Glu Gly Gly Thr Phe Lys Ile Asp Ile Asp Leu Pro Asp Ala Tyr Pro
      50      55      60
ttt gag cca cca agg atg aaa ttt gct act aaa gtc tgg cac ccg aat 359
Phe Glu Pro Pro Arg Met Lys Phe Ala Thr Lys Val Trp His Pro Asn
      65      70      75
att agc agc caa agc ggg gcc att tgc tta gac att ttg aag gac cag 407
Ile Ser Ser Gln Ser Gly Ala Ile Cys Leu Asp Ile Leu Lys Asp Gln
      80      85      90
tgg agc cca gcc ctt act ctg aaa acg gca ctt tcc ata cag gct 455
Trp Ser Pro Ala Leu Thr Leu Lys Thr Ala Leu Leu Ser Ile Gln Ala
      100      105      110
tta ctc tcc gcc cct gaa cct gat gac cca caa gat gcg gtt gtg gca 503
Leu Leu Ser Ala Pro Glu Pro Asp Asp Pro Gln Asp Ala Val Val Ala
      115      120      125
cag cag tat ctt aaa gat tat caa act ttt gca agc act gct cgt tac 551
Gln Gln Tyr Leu Lys Asp Tyr Gln Thr Phe Ala Ser Thr Ala Arg Tyr
      130      135      140
tgg aca gaa tcg ttt gca aag aca tca tct cta ggg gtt gaa gat aag 599
Trp Thr Glu Ser Phe Ala Lys Thr Ser Ser Leu Gly Val Glu Asp Lys
      145      150      155
gtg caa aag ctc gtt gag atg gga ttt cct gaa ggc atg gtt agg agt 647
Val Gln Lys Leu Val Glu Met Gly Phe Pro Glu Gly Met Val Arg Ser
      160      165      170
acc ttg gaa gtg gtt ggt ggc gac gaa aat ttg gcg ttg gag aag ctt 695
Thr Leu Glu Val Val Gly Gly Asp Glu Asn Leu Ala Leu Glu Lys Leu
      180      185      190
tgt tcc ggc taa ttataattgt ttatgttttt tttaatcaac aaaggaagga 747
Cys Ser Gly

gaaccttgaa atcaaatgat aaatatgaaa tggaattgtg tgtttgtgaa aaaaaaaaaa 807

aaa 810

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<210> 1896
 <211> 194
 <212> PRT
 <213> Helianthus annuus

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<400> 1896
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      20      25      30
Ile Asn Leu Ile Gly Thr Ile Pro Gly Pro Val Gly Thr Pro Tyr Glu
      35      40      45
Gly Gly Thr Phe Lys Ile Asp Ile Asp Leu Pro Asp Ala Tyr Pro Phe
      50      55      60
Glu Pro Pro Arg Met Lys Phe Ala Thr Lys Val Trp His Pro Asn Ile
65      70      75
Ser Ser Gln Ser Gly Ala Ile Cys Leu Asp Ile Leu Lys Asp Gln Trp
      80      85      90
Ser Pro Ala Leu Thr Leu Lys Thr Ala Leu Leu Ser Ile Gln Ala Leu
      100      105      110
Leu Ser Ala Pro Glu Pro Asp Asp Pro Gln Asp Ala Val Val Ala Gln
      115      120      125
Gln Tyr Leu Lys Asp Tyr Gln Thr Phe Ala Ser Thr Ala Arg Tyr Trp
      130      135      140
Thr Glu Ser Phe Ala Lys Thr Ser Ser Leu Gly Val Glu Asp Lys Val
145      150      155
Gln Lys Leu Val Glu Met Gly Phe Pro Glu Gly Met Val Arg Ser Thr
      160      165      170
Leu Glu Val Val Gly Gly Asp Glu Asn Leu Ala Leu Glu Lys Leu Cys
      180      185      190
ser Gly

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PF59082SeqList_PF59082.txt

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<210> 1897
<211> 619
<212> DNA
<213> Helianthus annuus
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$\langle 220 \rangle$
 $\langle 221 \rangle$ CDS
 $\langle 222 \rangle$ (31) . . (477)

<400>	1897	
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gag ttg aag gac ttg caa aag gac ccc cct gct tca tgc agt gct ggc		102
Glu Leu Lys Asp Leu Gln Lys Asp Pro Pro Ala Ser Cys Ser Ala Gly		
	10 15 20	
cct gct ggt gaa gac atg ttc cat tgg caa gcg acc att ttg ggt cct		150
Pro Ala Gly Glu Asp Met Phe His Trp Gln Ala Thr Ile Leu Gly Pro		
	25 30 35 40	
tca gat agc ccg ttt tct gga gga gta ttt ctg atc tcc att cac ttc		198
Ser Asp Ser Pro Phe Ser Gly Gly Val Phe Leu Ile Ser Ile His Phe		
	45 50 55	
cct ccg gat tac cca ttt aag cca cca aag gtt tcc ttc cga acc aag		246
Pro Pro Asp Tyr Pro Phe Lys Pro Pro Lys Val Ser Phe Arg Thr Lys		
	60 65 70	
gta ttc cat cca aat ata aac agc aac ggt agc atc tgc ctt gac att		294
Val Phe His Pro Asn Ile Asn Ser Asn Gly Ser Ile Cys Leu Asp Ile		
	75 80 85	
ctc aaa gaa cac tgg agt cct gca ctt acc atc tct aag gtt ttg ctt		342
Leu Lys Glu Gln Trp Ser Pro Ala Leu Thr Ile Ser Lys Val Leu Leu		
	90 95 100	
tca att tgt tca ttg ttg aca gac ccg aac cct gat gat cca ttg gtg		390
Ser Ile Cys Ser Leu Leu Thr Asp Pro Asn Pro Asp Asp Pro Leu Val		
	105 110 115 120	
cct gag att gct cat atg tac aag aat gat agg gcc aag tat gag acc		438
Pro Glu Ile Ala His Met Tyr Lys Asn Asp Arg Ala Lys Tyr Glu Thr		
	125 130 135	
acc gct cga gct tgg acc cag aaa tat gcc atg ggt taa tcattagtta		487
Thr Ala Arg Ala Trp Thr Gln Lys Tyr Ala Met Gly		
	140 145	
gggtatgttg aatgctttct agtcgaataa aaaaaccaac tctttgacat aaaaatttgg		547
ttgagcactt gggcttgaca cctctagcaa ctttataaaa aacatatatc atgtggcaaa		607
aaaaaaaaaa aa		619

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<210> 1898
<211> 148
<212> PRT
<213> Helianthus annuus
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<400> 1898
Met Ala Ser Lys Arg Ile Gln Lys Glu Leu Lys Asp Leu Gln Lys Asp
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Pro Pro Ala Ser Cys Ser Ala Gly Pro Ala Gly Glu Asp Met Phe His
20 25 30
Trp Gln Ala Thr Ile Leu Gly Pro Ser Asp Ser Pro Phe Ser Gly Gly
35 40 45
Val Phe Leu Ile Ser Ile His Phe Pro Pro Asp Tyr Pro Phe Lys Pro
50 55 60
Pro Lys Val Ser Phe Arg Thr Lys Val Phe His Pro Asn Ile Asn Ser
65 70 75 80
Asn Gly Ser Ile Cys Leu Asp Ile Leu Lys Glu Gln Trp Ser Pro Ala
seite 2461

PF59082SeqList_PF59082.txt

				85					90					95			
Leu	Thr	Ile	Ser	Lys	Val	Leu	Leu	Ser	Ile	Cys	Ser	Leu	Leu	Thr	Asp		
			100					105					110				
Pro	Asn	Pro	Asp	Asp	Pro	Leu	Val	Pro	Glu	Ile	Ala	His	Met	Tyr	Lys		
		115					120					125					
Asn	Asp	Arg	Ala	Lys	Tyr	Glu	Thr	Thr	Ala	Arg	Ala	Trp	Thr	Gln	Lys		
	130					135					140						
Tyr	Ala	Met	Gly														
145																	