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SEQUENCE LISTING

<110> BASF Plant Science GmbH

<120> Use of genes for increasing the resistance in
Arabidopsis regarding phytopatogenic fungi

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<141> 2008 08 27

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<170> Biomax PatentTool according to PatentIN 3.1 format

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aatatcggga 120

aacctcctcg gattccattg cccagctatc tgtcacttca tcaaaaggac
agtagaaaag 180

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gacgttccaa ccacgtcttc aaagcaagtg gattgatgtg aacatgggtg
agcacgacac 360

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ctattgagac 420

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attgcgataa 540

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gtacgggctaa 420

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tgaggaaact 540

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purposes

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purposes

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Tyr Arg                               10
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gaa aaa                               96
Trp Leu Lys Asn Asp Ile Ile Arg Gly Asn Phe Gln Pro Asp
Glu Lys                               20
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ggg ccg                               144
Leu Arg Met Ser Leu Leu Thr Ser Arg Tyr Ala Leu Gly Val
Gly Pro                               35
tta cgg gaa gct ctt tcg caa ctg gtg gcg gaa cgg ctg gtc
acg gtg                               192
Leu Arg Glu Ala Leu Ser Gln Leu Val Ala Glu Arg Leu Val
Thr Val                               50
gtg aat caa aaa ggg tat cgg gtg gcg tct atg tca gag cag
gag ctg                               240
Val Asn Gln Lys Gly Tyr Arg Val Ala Ser Met Ser Glu Gln
Glu Leu                               65
65
70
80
ctc gat att ttc gac gcc cgc gcc aat atg gaa gcg atg tta
gtg agt                               288
Leu Asp Ile Phe Asp Ala Arg Ala Asn Met Glu Ala Met Leu
Val Ser                               85
95
ctg gcg att gcc cgc ggt ggc gat gag tgg gag gca gac gtt
ctc gca                               336
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Leu Ala                               100
105
110
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0070110

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Glu Lys
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gca att
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Ala Ile
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cgg ttg
Val Ala Gly Cys Gly Ser His Tyr Leu Leu Gln Met Arg Glu
Arg Leu
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Thr Val
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Leu Ser Val Glu Met Leu Glu Asp Lys His Asp Gln His Gln
Thr Leu
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tta atg
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Leu Met
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Gly Pro

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Thr Val

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Val Asn Gln Lys Gly Tyr Arg Val Ala Ser Met Ser Glu Gln
Glu Leu

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95

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Leu Ala

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Glu Lys

115 120 125

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Ala Ile

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Arg Leu

145 150 155

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Thr Val

165 170

175

Leu Ser Val Glu Met Leu Glu Asp Lys His Asp Gln His Gln
Thr Leu

180 185 190

0070110

Thr Ala Ala Val Leu Ala Arg Asp Thr Ala Arg Ala Ser Glu
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Gly Asn
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ctg cgg 96
Lys Asn Asp Ile Ile Arg Gly Thr Tyr Gln Pro Asp Glu Lys
Leu Arg 20 25 30
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ctg cgt 144
Met Ser Leu Leu Thr Ala Arg Tyr Ala Leu Gly Val Gly Pro
Leu Arg 35 40 45
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gtg aat 192
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Val Asn 50 55 60
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ctc gat 240
Gln Lys Gly Tyr Arg Val Ala Ser Met Ser Glu Ala Glu Leu
Leu Asp

0070110

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	85				90									
95														
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Arg	Ala													
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Met	Leu													
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Val	Ala													
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Phe	Asp													
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678

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Lys Asn Asp Ile Ile Arg Gly Thr Tyr Gln Pro Asp Glu Lys
Leu Arg
20 25 30

Met Ser Leu Leu Thr Ala Arg Tyr Ala Leu Gly Val Gly Pro
Leu Arg
35 40 45

Glu Ala Leu Ser Gln Leu Val Ala Glu Arg Leu Val Thr Val
Val Asn
50 55 60

Gln Lys Gly Tyr Arg Val Ala Ser Met Ser Glu Ala Glu Leu
Leu Asp
65 70 75
80

Ile Phe Asp Ala Arg Ala Asn Met Glu Ala Met Leu Val Arg
Leu Ala
85 90

95
Ile Glu Arg Gly Asp Asp Ala Trp Glu Ala Glu Ile Leu Ala
Arg Ala
100 105 110

His Met Leu Ser Lys Leu Glu Ala Ser Asp Ala Ser Glu His
Met Leu
115 120 125

Asp Glu Trp Asp Gln Arg His Gln Ala Phe His Ser Ala Ile
Seite 29

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Val	Ala													
130													140	
Gly	Cys	Gly	Ser	His	Tyr	Leu	Leu	Gln	Met	Arg	Glu	Arg	Leu	
Phe	Asp													
145					150					155				
160														
Leu	Ala	Ala	Arg	Tyr	Arg	Phe	Ile	Trp	Leu	Arg	Glu	Thr	Val	
Leu	Ser													
				165						170				
175														
Val	Glu	Met	Leu	Glu	Asp	Lys	His	Ile	Gln	His	His	Thr	Leu	
Thr	Glu													
			180					185					190	
Ala	Ile	Leu	Ala	Arg	Glu	Ala	Ala	Arg	Ala	Ser	Glu	Leu	Met	
Arg	Gln													
		195					200					205		
His	Leu	Leu	Thr	Pro	Ile	Pro	Ile	Ile	Arg	Gln	Ala	Met	Ala	
Gly	Lys													
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Met
225

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 <213> Shigella flexneri 2a str. 301

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Asp	Ile													
1				5					10					
15														
att	cgc	ggt	aat	ttt	caa	ccg	gat	gaa	aaa	tta	cgg	atg	agt	
tta	ctg			96										
Ile	Arg	Gly	Asn	Phe	Gln	Pro	Asp	Glu	Lys	Leu	Arg	Met	Ser	
Leu	Leu													
			20					25					30	

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aca	tcg	cgt	tat	gca	ctt	ggc	gtt	ggg	ccg	ttg	cag	gaa	gca
ctt	tct		144										
Thr	Ser	Arg	Tyr	Ala	Leu	Gly	Val	Gly	Pro	Leu	Gln	Glu	Ala
Leu	Ser												
		35				40					45		
caa	ctg	gtg	gcg	gaa	cgg	ctg	gtc	acg	gtg	gtg	aat	caa	aaa
ggg	tat		192										
Gln	Leu	Val	Ala	Glu	Arg	Leu	Val	Thr	Val	Val	Asn	Gln	Lys
Gly	Tyr												
	50					55					60		
cgg	gtg	gcg	tct	atg	tca	gag	cag	gag	ctg	ctc	gat	att	ttc
gac	gcc		240										
Arg	Val	Ala	Ser	Met	Ser	Glu	Gln	Glu	Leu	Leu	Asp	Ile	Phe
Asp	Ala												
65					70					75			
80													
cgc	gcc	aat	atg	gaa	gcg	atg	ctg	gtc	agt	ctg	gcg	att	gcc
cgc	ggt		288										
Arg	Ala	Asn	Met	Glu	Ala	Met	Leu	Val	Ser	Leu	Ala	Ile	Ala
Arg	Gly												
				85					90				
95													
ggc	gat	gaa	tgg	gag	gca	gac	gtt	ctc	gca	aaa	gcg	cat	ctg
ctc	agt		336										
Gly	Asp	Glu	Trp	Glu	Ala	Asp	Val	Leu	Ala	Lys	Ala	His	Leu
Leu	Ser												
		100						105				110	
aag	ctg	gaa	gcc	tgt	gac	gcc	agc	gag	aaa	atg	ctt	gat	gag
tgg	gat		384										
Lys	Leu	Glu	Ala	Cys	Asp	Ala	Ser	Glu	Lys	Met	Leu	Asp	Glu
Trp	Asp												
		115				120					125		
ctg	cgt	cat	cag	gcg	ttt	cat	aca	gca	att	gtg	gcg	ggc	tgt
ggt	tct		432										
Leu	Arg	His	Gln	Ala	Phe	His	Thr	Ala	Ile	Val	Ala	Gly	Cys
Gly	Ser												
	130					135					140		
cac	tat	ttg	ctg	caa	atg	cgt	gaa	cgg	ttg	ttt	gat	ctg	gcg
gcg	cgt		480										
His	Tyr	Leu	Leu	Gln	Met	Arg	Glu	Arg	Leu	Phe	Asp	Leu	Ala
Ala	Arg												
145					150					155			
160													
tat	cga	ttt	atc	tgg	ctg	cgg	cga	acg	gtg	ctt	tcg	gtg	gaa
atg	ctg		528										
Tyr	Arg	Phe	Ile	Trp	Leu	Arg	Arg	Thr	Val	Leu	Ser	Val	Glu
Met	Leu												

0070110

165

170

175

gag gat aaa cac gat cag cac cag acc ctg act gcg gcg gta
ctg ccg 576

Glu Asp Lys His Asp Gln His Gln Thr Leu Thr Ala Ala Val

Leu Pro

180

185

190

cga gat aca gcg cgc gcc agt gag tta atg cgc cag cat tta
ctg acg 624

Arg Asp Thr Ala Arg Ala Ser Glu Leu Met Arg Gln His Leu

Leu Thr

195

200

205

cca att ccc att atc cag cag gcg atg gct ggc aat taa

Pro Ile Pro Ile Ile Gln Gln Ala Met Ala Gly Asn

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215

220

<210> 14

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<212> PRT

<213> Shigella flexneri 2a str. 301

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Asp Ile

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15

Ile Arg Gly Asn Phe Gln Pro Asp Glu Lys Leu Arg Met Ser
Leu Leu

20

25

30

Thr Ser Arg Tyr Ala Leu Gly Val Gly Pro Leu Gln Glu Ala
Leu Ser

35

40

45

Gln Leu Val Ala Glu Arg Leu Val Thr Val Val Asn Gln Lys
Gly Tyr

50

55

60

Arg Val Ala Ser Met Ser Glu Gln Glu Leu Leu Asp Ile Phe
Asp Ala

65

70

75

80

Arg Ala Asn Met Glu Ala Met Leu Val Ser Leu Ala Ile Ala
Arg Gly

85

90

95

0070110

Gly Asp Glu Trp Glu Ala Asp Val Leu Ala Lys Ala His Leu
 Leu Ser
 100 105 110

Lys Leu Glu Ala Cys Asp Ala Ser Glu Lys Met Leu Asp Glu
 Trp Asp
 115 120 125

Leu Arg His Gln Ala Phe His Thr Ala Ile Val Ala Gly Cys
 Gly Ser
 130 135 140

His Tyr Leu Leu Gln Met Arg Glu Arg Leu Phe Asp Leu Ala
 Ala Arg
 145 150 155
 160

Tyr Arg Phe Ile Trp Leu Arg Arg Thr Val Leu Ser Val Glu
 Met Leu
 165 170

175
 Glu Asp Lys His Asp Gln His Gln Thr Leu Thr Ala Ala Val
 Leu Pro
 180 185 190

Arg Asp Thr Ala Arg Ala Ser Glu Leu Met Arg Gln His Leu
 Leu Thr
 195 200 205

Pro Ile Pro Ile Ile Gln Gln Ala Met Ala Gly Asn
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 <211> 696
 <212> DNA
 <213> Pseudomonas putida KT2440

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 <223> transl_table=11

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 tat gag 48
 Met Glu Ala Leu Ala Pro Arg Gln Asn Ser Ala Phe Ser Gly
 Tyr Glu
 1 5 10
 15

0070110

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

0070110

160

ttc gac cag gcc gag cgc tac cgc cac ctg tgg ctg acg cag
acg gtg 528
Phe Asp Gln Ala Glu Arg Tyr Arg His Leu Trp Leu Thr Gln
Thr Val

165

170

175

ttt tcc gaa gag gcg ctg gcg ctc aag cgc cag gag cat gcg
gca ctg 576
Phe Ser Glu Glu Ala Leu Ala Leu Lys Arg Gln Glu His Ala
Ala Leu

180

185

190

gtc gag gtg atc ctc gcc cgg gat gcc aaa acc gcc agc gcc
atg atg 624

val Glu val Ile Leu Ala Arg Asp Ala Lys Thr Ala Ser Ala
Met Met

195

200

205

cgc tcg cac ctg atg aca ccg gta ccg atc att gcg cag atc
atg cac 672
Arg Ser His Leu Met Thr Pro Val Pro Ile Ile Ala Gln Ile
Met His

210

215

220

gcc gaa ggc atc ggt gcc cgc tag
696

Ala Glu Gly Ile Gly Ala Arg
225 230

<210> 16

<211> 231

<212> PRT

<213> Pseudomonas putida KT2440

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Met Glu Ala Leu Ala Pro Arg Gln Asn Ser Ala Phe Ser Gly
Tyr Glu

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Arg Leu Lys Lys Asp Ile Ile Arg Gly Val Phe Lys Pro Gly
Glu Lys

20

25

30

Leu Leu Met Ser Thr Leu Lys Glu Arg Tyr Asp Leu Gly Val
Gly Pro

35

40

45

Leu Arg Glu Ala Leu Ser Gln Leu Val Ala Glu His Leu Val

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

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<212> DNA

<213> Escherichia coli CFT073

<220>

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Asp Ile
  1              5              10
15
att cgc ggc aat ttt cag ccg gat gaa aaa tta cgg atg agt
ttg ctg      96
Ile Arg Gly Asn Phe Gln Pro Asp Glu Lys Leu Arg Met Ser
Leu Leu
      20              25              30
aca tcg cgt tat gca ctt ggc gtc gga ccg ttg cgg gaa gcg
ctt tcg      144
Thr Ser Arg Tyr Ala Leu Gly Val Gly Pro Leu Arg Glu Ala
Leu Ser
      35              40              45
caa ctg gtg gca gaa cga ctg gtc acg gtg gtg aat caa aaa
ggg tat      192
Gln Leu Val Ala Glu Arg Leu Val Thr Val Val Asn Gln Lys
Gly Tyr
  50              55              60
cgg gtg gcg tct atg tca gag cag gag ctg ctc gat att ttc
gac gcc      240
Arg Val Ala Ser Met Ser Glu Gln Glu Leu Leu Asp Ile Phe
Asp Ala
  65              70              75
80
cgc gcc aat atg gaa gcg atg ctg gtg agt ctg gcg att gcc
cgc ggt      288
Arg Ala Asn Met Glu Ala Met Leu Val Ser Leu Ala Ile Ala
Arg Gly
      85              90
95
ggc gat gaa tgg gag gca gac gtt ctc gca aaa gcg cat ctg
ctc agt      336
Gly Asp Glu Trp Glu Ala Asp Val Leu Ala Lys Ala His Leu
Leu Ser
      100              105              110
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0070110

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aag ctt gag gcc tgt gac gcc agt gag aaa atg ctt gat gag
tgg gat
Lys Leu Glu Ala Cys Asp Ala Ser Glu Lys Met Leu Asp Glu
Trp Asp
115 120 125
ctg cgt cat cag gcg ttt cat act gca att gtg gcg ggc tgt
ggg tct
Leu Arg His Gln Ala Phe His Thr Ala Ile Val Ala Gly Cys
Gly Ser
130 135 140
tac tat ttg ctg caa atg cgt gaa cgg ttg ttt gat ctg gca
gcg cgt
Tyr Tyr Leu Leu Gln Met Arg Glu Arg Leu Phe Asp Leu Ala
Ala Arg
145 150 155
160
tat cga ttt atc tgg ctg cgg cga aca gtg ctt tcg gtg gaa
atg ctg
Tyr Arg Phe Ile Trp Leu Arg Arg Thr Val Leu Ser Val Glu
Met Leu
165 170
175
gaa gat aaa cac gat cag cac cag acc ctg act gcg gcg gta
ctg gcg
Glu Asp Lys His Asp Gln His Gln Thr Leu Thr Ala Ala Val
Leu Ala
180 185 190
cga gat acc gcg cgc gcc agt gag tta atg cgc cag cat tta
ctg acg
Arg Asp Thr Ala Arg Ala Ser Glu Leu Met Arg Gln His Leu
Leu Thr
195 200 205
cca att ccc att atc cag cag gcg atg gct ggc aat taa
663
Pro Ile Pro Ile Ile Gln Gln Ala Met Ala Gly Asn
210 215 220

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<211> 220

<212> PRT

<213> Escherichia coli CFT073

<400> 18

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Asp Ile

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

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Pro Ile Pro Ile Ile Gln Gln Ala Met Ala Gly Asn
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Ser Asp
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acg ctc agc gag cgc gcg gcc aac ctg ctc gag cgc gat atc
gtc tcg 96
Thr Leu Ser Glu Arg Ala Ala Asn Leu Leu Glu Arg Asp Ile
Val Ser
20 25 30
ggc gag ctg ccg ccg gga tcg aag ctc ggc atc gtc gag ctg
gcg cgc 144
Gly Glu Leu Pro Pro Gly Ser Lys Leu Gly Ile Val Glu Leu
Ala Arg
35 40 45
cgc tac gag atc ggc gcc acg ccg ctg cgc gag ggg ctg tcg
cgg ctg 192
Arg Tyr Glu Ile Gly Ala Thr Pro Leu Arg Glu Gly Leu Ser
Arg Leu
50 55 60
acg tcg cgc ggg ctg atc gtc gcg atc ggg cag cgc ggc ttc
cgc gtc 240
Thr Ser Arg Gly Leu Ile Val Ala Ile Gly Gln Arg Gly Phe
Arg Val
65 70 75
80
gcc gaa gtc agc cgc gac gat ctg ctc gac atc acg cgg atg
cgg acg 288
Ala Glu Val Ser Arg Asp Asp Leu Leu Asp Ile Thr Arg Met
Arg Thr
85 90
95
gtg atc gaa cgc gag gcg cta cgg ctc gcg atc gac aat ggc

0070110

ggc	gac			336										
Val	Ile	Glu	Arg	Glu	Ala	Leu	Arg	Leu	Ala	Ile	Asp	Asn	Gly	
Gly	Asp													
			100					105					110	
gcc	tgg	gag	gcc	ggg	atc	gtc	gcg	gcg	ttg	cac	cag	atg	cag	
cgc	tac			384										
Ala	Trp	Glu	Ala	Gly	Ile	Val	Ala	Ala	Leu	His	Gln	Met	Gln	
Arg	Tyr													
		115					120					125		
gtg	gag	cgc	aac	gcc	aac	gat	ttc	cga	gaa	ggc	gcg	ccg	gag	
ttc	gat			432										
Val	Glu	Arg	Asn	Ala	Asn	Asp	Phe	Arg	Glu	Gly	Ala	Pro	Glu	
Phe	Asp													
		130				135					140			
cgg	ctg	cac	aag	gcg	ttt	cac	acc	agc	ctg	ctt	gca	gcc	tgc	
ggc	tct			480										
Arg	Leu	His	Lys	Ala	Phe	His	Thr	Ser	Leu	Leu	Ala	Ala	Cys	
Gly	Ser													
145					150					155				
160														
cct	cgc	ctg	ctg	gca	gcg	cat	tcg	gac	ctg	tac	gat	cag	gcc	
tat	cgc			528										
Pro	Arg	Leu	Leu	Ala	Ala	His	Ser	Asp	Leu	Tyr	Asp	Gln	Ala	
Tyr	Arg													
				165						170				
175														
tat	cgg	cgg	gtg	atg	atg	cgc	agc	att	gaa	agc	ggc	cgg	tac	
ttc	atc			576										
Tyr	Arg	Arg	Val	Met	Met	Arg	Ser	Ile	Glu	Ser	Gly	Arg	Tyr	
Phe	Ile													
			180					185					190	
gcc	gcg	cat	cgc	gaa	ttg	gcc	gac	ctc	gtg	ctc	gca	cgc	gac	
gcc	gag			624										
Ala	Ala	His	Arg	Glu	Leu	Ala	Asp	Leu	Val	Leu	Ala	Arg	Asp	
Ala	Glu													
		195					200					205		
gcc	gca	gag	acc	aag	ctc	gac	cag	cat	ctg	cgc	gcg	acg	ctg	
act	acc			672										
Ala	Ala	Glu	Thr	Lys	Leu	Asp	Gln	His	Leu	Arg	Ala	Thr	Leu	
Thr	Thr													
		210				215					220			
gtc	tat	ccg	ccg	ggc	aag	agc	cag	ccg	cca	tcc	cgc	tga		
			711											
Val	Tyr	Pro	Pro	Gly	Lys	Ser	Gln	Pro	Pro	Ser	Arg			
225					230					235				

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<211> 236
<212> PRT
<213> Rhodopseudomonas palustris CGA009

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Ser Asp
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15
Thr Leu Ser Glu Arg Ala Ala Asn Leu Leu Glu Arg Asp Ile
Val Ser
20 25 30

Gly Glu Leu Pro Pro Gly Ser Lys Leu Gly Ile Val Glu Leu
Ala Arg
35 40 45

Arg Tyr Glu Ile Gly Ala Thr Pro Leu Arg Glu Gly Leu Ser
Arg Leu
50 55 60

Thr Ser Arg Gly Leu Ile Val Ala Ile Gly Gln Arg Gly Phe
Arg Val
65 70 75

80
Ala Glu Val Ser Arg Asp Asp Leu Leu Asp Ile Thr Arg Met
Arg Thr
85 90

95
Val Ile Glu Arg Glu Ala Leu Arg Leu Ala Ile Asp Asn Gly
Gly Asp
100 105 110

Ala Trp Glu Ala Gly Ile Val Ala Ala Leu His Gln Met Gln
Arg Tyr
115 120 125

Val Glu Arg Asn Ala Asn Asp Phe Arg Glu Gly Ala Pro Glu
Phe Asp
130 135 140

Arg Leu His Lys Ala Phe His Thr Ser Leu Leu Ala Ala Cys
Gly Ser
145 150 155

160
Pro Arg Leu Leu Ala Ala His Ser Asp Leu Tyr Asp Gln Ala

0070110

Tyr	Arg													
				165					170					
175														
Tyr	Arg	Arg	Val	Met	Met	Arg	Ser	Ile	Glu	Ser	Gly	Arg	Tyr	
Phe	Ile													
				180				185					190	
Ala	Ala	His	Arg	Glu	Leu	Ala	Asp	Leu	Val	Leu	Ala	Arg	Asp	
Ala	Glu													
		195					200					205		
Ala	Ala	Glu	Thr	Lys	Leu	Asp	Gln	His	Leu	Arg	Ala	Thr	Leu	
Thr	Thr													
	210					215					220			
Val	Tyr	Pro	Pro	Gly	Lys	Ser	Gln	Pro	Pro	Ser	Arg			
225					230					235				

<210> 21
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 <212> DNA
 <213> Klebsiella pneumoniae subsp. pneumoniae MGH 78578

<220>
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 <222> (1)..(693)
 <223> transl_table=11

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tgg	tta			48										
Met	Thr	Ala	Ile	Pro	Gln	Ala	Thr	Ala	Ile	Asp	Gly	Tyr	Arg	
Trp	Leu													
1				5					10					
15														
aaa	aac	gac	atc	atc	cgc	ggg	gtt	tac	cac	ccc	gat	gag	aag	
ctg	cgg			96										
Lys	Asn	Asp	Ile	Ile	Arg	Gly	Val	Tyr	His	Pro	Asp	Glu	Lys	
Leu	Arg													
			20					25					30	
atg	agc	ctg	ctg	acg	tcg	cgc	tat	ggc	ctg	ggg	gtc	ggt	ccg	
ctg	cgc			144										
Met	Ser	Leu	Leu	Thr	Ser	Arg	Tyr	Gly	Leu	Gly	Val	Gly	Pro	
Leu	Arg													
		35				40					45			
gag	gcg	ctt	tcg	caa	ctg	gtg	gcc	gag	cgg	ctg	gtg	acg	gtg	
gtc	aat			192										
Glu	Ala	Leu	Ser	Gln	Leu	Val	Ala	Glu	Arg	Leu	Val	Thr	Val	

0070110

Val	Asn 50					55				60			
cag	aaa	ggc	tat	cgg	gtg	gcg	ccc	atg	tcg	gaa	cag	gag	ctt
ctc	gat			240									
Gln	Lys	Gly	Tyr	Arg	Val	Ala	Pro	Met	Ser	Glu	Gln	Glu	Leu
Leu	Asp												
65					70					75			
80													
atc	ttc	gac	gcg	cgc	gcc	aac	atg	gag	gcc	atg	ctg	gtg	cgt
ctc	gcc			288									
Ile	Phe	Asp	Ala	Arg	Ala	Asn	Met	Glu	Ala	Met	Leu	Val	Arg
Leu	Ala												
				85						90			
95													
att	gaa	cgc	ggc	ggc	gac	gag	tgg	gaa	gcc	gag	ctg	ctg	gcc
cgc	gcc			336									
Ile	Glu	Arg	Gly	Gly	Asp	Glu	Trp	Glu	Ala	Glu	Leu	Leu	Ala
Arg	Ala												
			100					105					110
cat	ctg	ctc	aac	aag	ctg	gag	tcg	tgc	gaa	gcg	agt	gag	cac
cta	ctc			384									
His	Leu	Leu	Asn	Lys	Leu	Glu	Ser	Cys	Glu	Ala	Ser	Glu	His
Leu	Leu												
		115					120					125	
gat	gaa	tgg	gac	cag	cgc	cat	cag	gcg	ttt	cac	acc	gcc	atc
gtc	gcc			432									
Asp	Glu	Trp	Asp	Gln	Arg	His	Gln	Ala	Phe	His	Thr	Ala	Ile
Val	Ala												
	130					135					140		
ggc	tgc	ggt	tcg	cag	tat	ctg	ctg	cag	atg	cgc	gaa	cgg	ctg
ttc	gat			480									
Gly	Cys	Gly	Ser	Gln	Tyr	Leu	Leu	Gln	Met	Arg	Glu	Arg	Leu
Phe	Asp												
145					150					155			
160													
ctg	gcg	gcg	cgc	tac	cgc	ttc	atc	tgg	ctg	cgc	acc	acc	gtg
ctg	tcg			528									
Leu	Ala	Ala	Arg	Tyr	Arg	Phe	Ile	Trp	Leu	Arg	Thr	Thr	Val
Leu	Ser												
				165						170			
175													
gtg	gag	atg	ctg	gaa	gat	aag	cat	gtc	cag	cat	cag	acc	ctg
gtg	gac			576									
Val	Glu	Met	Leu	Glu	Asp	Lys	His	Val	Gln	His	Gln	Thr	Leu
Val	Asp												
			180					185					190

0070110

gct att ctg gcg cgc gac gcc gaa cag gcc agc gcg ctg atg
 cgc gag 624
 Ala Ile Leu Ala Arg Asp Ala Glu Gln Ala Ser Ala Leu Met
 Arg Glu
 195 200 205
 cac tta ctg act ccg atc ccg att att caa cag gcg atg gct
 ggc aag 672
 His Leu Leu Thr Pro Ile Pro Ile Ile Gln Gln Ala Met Ala
 Gly Lys
 210 215 220
 ctg tcg ccg cag gca ggg tga
 693
 Leu Ser Pro Gln Ala Gly
 225 230

<210> 22

<211> 230

<212> PRT

<213> Klebsiella pneumoniae subsp. pneumoniae MGH 78578

<400> 22

Met Thr Ala Ile Pro Gln Ala Thr Ala Ile Asp Gly Tyr Arg
 Trp Leu
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 15
 Lys Asn Asp Ile Ile Arg Gly Val Tyr His Pro Asp Glu Lys
 Leu Arg
 20 25 30
 Met Ser Leu Leu Thr Ser Arg Tyr Gly Leu Gly Val Gly Pro
 Leu Arg
 35 40 45
 Glu Ala Leu Ser Gln Leu Val Ala Glu Arg Leu Val Thr Val
 Val Asn
 50 55 60
 Gln Lys Gly Tyr Arg Val Ala Pro Met Ser Glu Gln Glu Leu
 Leu Asp
 65 70 75
 80
 Ile Phe Asp Ala Arg Ala Asn Met Glu Ala Met Leu Val Arg
 Leu Ala
 85 90
 95
 Ile Glu Arg Gly Gly Asp Glu Trp Glu Ala Glu Leu Leu Ala
 Arg Ala
 100 105 110

0070110

His Leu Leu Asn Lys Leu Glu Ser Cys Glu Ala Ser Glu His
Leu Leu
115 120 125

Asp Glu Trp Asp Gln Arg His Gln Ala Phe His Thr Ala Ile
Val Ala
130 135 140

Gly Cys Gly Ser Gln Tyr Leu Leu Gln Met Arg Glu Arg Leu
Phe Asp
145 150 155
160

Leu Ala Ala Arg Tyr Arg Phe Ile Trp Leu Arg Thr Thr Val
Leu Ser
165 170

175
Val Glu Met Leu Glu Asp Lys His Val Gln His Gln Thr Leu
Val Asp
180 185 190

Ala Ile Leu Ala Arg Asp Ala Glu Gln Ala Ser Ala Leu Met
Arg Glu
195 200 205

His Leu Leu Thr Pro Ile Pro Ile Ile Gln Gln Ala Met Ala
Gly Lys
210 215 220

Leu Ser Pro Gln Ala Gly
225 230

<210> 23

<211> 732

<212> DNA

<213> Salmonella enterica subsp. arizonae serovar
62:z4,z23:--

<220>

<221> CDS

<222> (1)..(732)

<223> transl_table=11

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acc gcg 48
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Thr Ala

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1				5					10				
15	ctt	tcc	caa	ccg	acg	gcc	ata	gat	gga	tat	cgc	tgg	ctt
	aat	gac		96									aaa
	Leu	Ser	Gln	Pro	Thr	Ala	Ile	Asp	Gly	Tyr	Arg	Trp	Leu
	Asn	Asp											Lys
			20						25				30
	att	att	cgc	ggg	act	tat	cag	ccg	gat	gaa	aaa	ctg	cgg
	agt	tta	144										atg
	Ile	Ile	Arg	Gly	Thr	Tyr	Gln	Pro	Asp	Glu	Lys	Leu	Arg
	Ser	Leu											Met
			35						40				45
	tta	acc	tcc	cgc	tat	gcg	ctc	ggc	gta	gga	ccg	cta	cgc
	gcg	ctg	192										gag
	Leu	Thr	Ser	Arg	Tyr	Ala	Leu	Gly	Val	Gly	Pro	Leu	Arg
	Ala	Leu											Glu
		50							55				60
	tca	caa	ctg	gtg	gcg	gaa	cgg	ctg	gtc	acc	gtg	gtg	aat
	aaa	ggc	240										caa
	Ser	Gln	Leu	Val	Ala	Glu	Arg	Leu	Val	Thr	Val	Val	Asn
	Lys	Gly											Gln
	65								70				75
	80												
	tat	cgt	gtg	gcg	tcc	atg	tca	gag	atg	gaa	ctt	ctc	gat
	ttt	gac	288										att
	Tyr	Arg	Val	Ala	Ser	Met	Ser	Glu	Met	Glu	Leu	Leu	Asp
	Phe	Asp											Ile
			85										90
	95												
	gcg	cgc	gcc	aat	atg	gaa	gca	atg	ctg	gtg	cgt	ctg	gcg
	gaa	cgc	336										att
	Ala	Arg	Ala	Asn	Met	Glu	Ala	Met	Leu	Val	Arg	Leu	Ala
	Glu	Arg											Ile
			100						105				110
	ggc	gat	gat	gcg	tgg	gag	gcg	gag	atc	ctg	gcc	cga	gcg
	atg	ctc	384										cat
	Gly	Asp	Asp	Ala	Trp	Glu	Ala	Glu	Ile	Leu	Ala	Arg	Ala
	Met	Leu											His
			115						120				125
	agt	aaa	ctg	gaa	gcc	agc	gat	gcc	agt	gaa	cat	atg	ctc
	gaa	tgg	432										gat
	Ser	Lys	Leu	Glu	Ala	Ser	Asp	Ala	Ser	Glu	His	Met	Leu
	Glu	Trp											Asp
		130							135				140
	gat	cag	cgc	cac	cag	gcg	ttt	cat	tcc	gca	att	gtc	gcc
	tgc	ggc	480										ggt
	Asp	Gln	Arg	His	Gln	Ala	Phe	His	Ser	Ala	Ile	Val	Ala
													Gly

0070110

Cys Gly
 145 150 155
 160
 tcc cac tac ctg cta cag atg cgc gaa cgg tta ttc gat ctg
 gcg gcg 528
 Ser His Tyr Leu Leu Gln Met Arg Glu Arg Leu Phe Asp Leu
 Ala Ala
 165 170
 175
 cgc tac cgc ttt att tgg tta cgt gaa acc gtc ctg tct gtc
 gag atg 576
 Arg Tyr Arg Phe Ile Trp Leu Arg Glu Thr Val Leu Ser Val
 Glu Met
 180 185 190
 ctg gaa gat aaa cat atc cag cat cac acg ctg aca gaa gcg
 att ctg 624
 Leu Glu Asp Lys His Ile Gln His His Thr Leu Thr Glu Ala
 Ile Leu
 195 200 205
 gcg cgc gag gcg gca cgc gcc agc gag tta atg cgt cag cat
 ttg ctg 672
 Ala Arg Glu Ala Ala Arg Ala Ser Glu Leu Met Arg Gln His
 Leu Leu
 210 215 220
 acg ccg att ccc att att cgt cag gcg atg acg gga aaa atg
 aag cca 720
 Thr Pro Ile Pro Ile Ile Arg Gln Ala Met Thr Gly Lys Met
 Lys Pro
 225 230 235
 240
 gga gcg gcc tga
 732
 Gly Ala Ala

<210> 24
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 <212> PRT
 <213> Salmonella enterica subsp. arizonae serovar
 62:z4,z23:--

<400> 24
 Met Pro Gly Ala Ser Arg Asp Ala Ser Gln Glu Lys Lys Met
 Thr Ala
 1 5 10
 15
 Leu Ser Gln Pro Thr Ala Ile Asp Gly Tyr Arg Trp Leu Lys

0070110

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

0070110

Leu Leu
210 215 220
Thr Pro Ile Pro Ile Ile Arg Gln Ala Met Thr Gly Lys Met
Lys Pro
225 230 235
240
Gly Ala Ala

<210> 25
<211> 696
<212> DNA
<213> Pseudomonas putida GB-1

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<222> (1)..(696)
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Tyr Glu
1 5 10
15
agg ctc aag aag gac atc atc cgc ggc gtg ttc aaa ccc ggt
gaa aaa 96
Arg Leu Lys Lys Asp Ile Ile Arg Gly Val Phe Lys Pro Gly
Glu Lys
20 25 30
ctg ttg atg agc gcc ctc aag gaa cgc tac gac ctg ggc gtg
ggc ccg 144
Leu Leu Met Ser Ala Leu Lys Glu Arg Tyr Asp Leu Gly Val
Gly Pro
35 40 45
ctg cgc gaa gca ctg tca caa ctg gtg gca gag cac ctg gtc
aac gcg 192
Leu Arg Glu Ala Leu Ser Gln Leu Val Ala Glu His Leu Val
Asn Ala
50 55 60
ata agc cag aaa ggc tac cgg gtg gcg ccc atg tcg ctg gac
gag atg 240
Ile Ser Gln Lys Gly Tyr Arg Val Ala Pro Met Ser Leu Asp
Glu Met
65 70 75
80

0070110

aac gac atc tat gat gcc cgc gcc aac ctg gaa gcg atg atc
 atc gcc 288
 Asn Asp Ile Tyr Asp Ala Arg Ala Asn Leu Glu Ala Met Ile
 Ile Ala

85

90

95

ctg gcc atc gaa cgc ggc gac gac gcc tgg gag gcc tcg gtg
 ctg gcc 336
 Leu Ala Ile Glu Arg Gly Asp Asp Ala Trp Glu Ala Ser Val
 Leu Ala

100

105

110

cac tcg cac acc ctg gcc aaa gtg gtg gag gtg aaa acc cgt
 gaa cag 384
 His Ser His Thr Leu Ala Lys Val Val Glu Val Lys Thr Arg
 Glu Gln

115

120

125

cgc ctg gac gtg tgg gac gaa cgg cac aag gcg ttc cat acc
 gcc atc 432
 Arg Leu Asp Val Trp Asp Glu Arg His Lys Ala Phe His Thr
 Ala Ile

130

135

140

gcc tcg ggc tgc ggc tcc aag cac ctg ctg caa gcg cgc acc
 tac ctg 480
 Ala Ser Gly Cys Gly Ser Lys His Leu Leu Gln Ala Arg Thr
 Tyr Leu

145

150

155

160

ttc gac cag gcc gaa cgc tac cgc cat ctg tgg ctg acg cag
 acg gtg 528
 Phe Asp Gln Ala Glu Arg Tyr Arg His Leu Trp Leu Thr Gln
 Thr Val

165

170

175

ttt tcc gag cag gcg ctg gag ctc aag cgc cag gag cat gca
 gcg ctg 576
 Phe Ser Glu Gln Ala Leu Glu Leu Lys Arg Gln Glu His Ala
 Ala Leu

180

185

190

gtc gag gtg att ctc gcc cgt gat gcc aag cgc gcc agc gcc
 atg atg 624
 Val Glu Val Ile Leu Ala Arg Asp Ala Lys Arg Ala Ser Ala
 Met Met

195

200

205

cgc tcg cac ctg atg acc ccg gtg ccg atc att gcg cag atc
 atg cat 672
 Arg Ser His Leu Met Thr Pro Val Pro Ile Ile Ala Gln Ile

0070110

Met His
 210 215 220
 gct gaa ggt atc ggc gca cgc tag
 696
 Ala Glu Gly Ile Gly Ala Arg
 225 230

<210> 26
 <211> 231
 <212> PRT
 <213> Pseudomonas putida GB-1

<400> 26

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

Leu Leu Met Ser Ala Leu Lys Glu Arg Tyr Asp Leu Gly Val
 Gly Pro
 35 40 45

Leu Arg Glu Ala Leu Ser Gln Leu Val Ala Glu His Leu Val
 Asn Ala
 50 55 60

Ile Ser Gln Lys Gly Tyr Arg Val Ala Pro Met Ser Leu Asp
 Glu Met
 65 70 75
 80

Asn Asp Ile Tyr Asp Ala Arg Ala Asn Leu Glu Ala Met Ile
 Ile Ala
 85 90

95
 Leu Ala Ile Glu Arg Gly Asp Asp Ala Trp Glu Ala Ser Val
 Leu Ala
 100 105 110

His Ser His Thr Leu Ala Lys Val Val Glu Val Lys Thr Arg
 Glu Gln
 115 120 125

Arg Leu Asp Val Trp Asp Glu Arg His Lys Ala Phe His Thr
 Ala Ile
 130 135 140

0070110

```

Ala Ser Gly Cys Gly Ser Lys His Leu Leu Gln Ala Arg Thr
Tyr Leu
145                      150                      155
160
Phe Asp Gln Ala Glu Arg Tyr Arg His Leu Trp Leu Thr Gln
Thr Val
                      165                      170
175
Phe Ser Glu Gln Ala Leu Glu Leu Lys Arg Gln Glu His Ala
Ala Leu
                      180                      185                      190
Val Glu Val Ile Leu Ala Arg Asp Ala Lys Arg Ala Ser Ala
Met Met
                      195                      200                      205
Arg Ser His Leu Met Thr Pro Val Pro Ile Ile Ala Gln Ile
Met His
                      210                      215                      220
Ala Glu Gly Ile Gly Ala Arg
225                      230

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<210> 27
 <211> 783
 <212> DNA
 <213> Ralstonia eutropha JMP134

<220>
 <221> CDS
 <222> (1)..(783)
 <223> transl_table=11

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gtc cag
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Val Gln
1                      5                      10
15
gag tcg ccg gac ctc ggc ggg cgc acg tgg gca tcc gtc ctc
gaa cag
Glu Ser Pro Asp Leu Gly Gly Arg Thr Trp Ala Ser Val Leu
Glu Gln
                      20                      25                      30
gcg gtt cgc gaa gac atc atc agc ggg cgt ctg ccg gcg ggc
agc aaa
                      144

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0070110

Ala	Val	Arg	Glu	Asp	Ile	Ile	Ser	Gly	Arg	Leu	Pro	Ala	Gly
Ser	Lys												
		35					40					45	
ctg	cgc	ctg	aag	gaa	ctg	gcc	gag	cat	tac	cag	gcc	ggt	gtg
atc	cca		192										
Leu	Arg	Leu	Lys	Glu	Leu	Ala	Glu	His	Tyr	Gln	Ala	Gly	Val
Ile	Pro												
	50					55					60		
ctg	cgc	gag	gcc	ctg	tcc	cgg	ttg	tgc	acg	acc	ggc	ttt	gta
ctg	gca		240										
Leu	Arg	Glu	Ala	Leu	Ser	Arg	Leu	Cys	Thr	Thr	Gly	Phe	Val
Leu	Ala												
65					70					75			
80													
atc	gac	cag	aag	ggc	ttc	cgg	gtg	gcg	gag	ctg	tcc	ccc	gag
gaa	ttg		288										
Ile	Asp	Gln	Lys	Gly	Phe	Arg	Val	Ala	Glu	Leu	Ser	Pro	Glu
Glu	Leu												
				85					90				
95													
ctc	gac	gtc	acg	cgc	gtg	cgc	cag	cag	ata	gaa	tgc	cag	gct
ctg	cgc		336										
Leu	Asp	Val	Thr	Arg	Val	Arg	Gln	Gln	Ile	Glu	Cys	Gln	Ala
Leu	Arg												
				100				105				110	
gac	gcc	atc	agg	ctc	gcg	gac	atc	gct	tgg	gaa	agc	gat	gtg
gta	gcg		384										
Asp	Ala	Ile	Arg	Leu	Ala	Asp	Ile	Ala	Trp	Glu	Ser	Asp	Val
Val	Ala												
		115					120					125	
gcg	cac	cat	cgc	ctg	acg	cgc	atc	ccg	atg	gtg	ttg	cgc	gac
caa	cgc		432										
Ala	His	His	Arg	Leu	Thr	Arg	Ile	Pro	Met	Val	Leu	Arg	Asp
Gln	Arg												
	130					135					140		
ggc	gcg	ctg	aac	cca	gag	tgg	gaa	gcc	gca	cat	gtg	gct	ttt
cac	gat		480										
Gly	Ala	Leu	Asn	Pro	Glu	Trp	Glu	Ala	Ala	His	Val	Ala	Phe
His	Asp												
145					150					155			
160													
gcg	ctg	atc	tgg	ggc	tgc	cac	tcc	cca	tgg	ctg	cgg	cgg	ttc
tcg	gcc		528										
Ala	Leu	Ile	Trp	Gly	Cys	His	Ser	Pro	Trp	Leu	Arg	Arg	Phe
Ser	Ala												
				165					170				
175													

0070110

gta ctg cgc gac cag acg gcg cgc tat cgg ttc ctc tcg ctc
gcc gta 576
Val Leu Arg Asp Gln Thr Ala Arg Tyr Arg Phe Leu Ser Leu
Ala Val
180 185 190

ccc aag gcc gaa cgg agc cgg gac gtg gcg gcg gaa cac gag
gcc atc 624
Pro Lys Ala Glu Arg Ser Arg Asp Val Ala Ala Glu His Glu
Ala Ile
195 200 205

gtc agc gcc gtg gtc gca cgc aac gct gac cgc gcc tgc aaa
ctg ctg 672
Val Ser Ala Val Val Ala Arg Asn Ala Asp Arg Ala Cys Lys
Leu Leu
210 215 220

tcg gac cat ttc cag cac acc acc gac ctg gtg ctc cag tac
ctt gcc 720
Ser Asp His Phe Gln His Thr Thr Asp Leu Val Leu Gln Tyr
Leu Ala
225 230 235
240

cgg cag aaa ggc ggc gcc gcg ccg acg cgc aaa cgc agg gca
gcg gcc 768
Arg Gln Lys Gly Gly Ala Ala Pro Thr Arg Lys Arg Arg Ala
Ala Ala
245 250

255
gaa gcc cct gtc tga
783
Glu Ala Pro Val
260

<210> 28
<211> 260
<212> PRT
<213> Ralstonia eutropha JMP134

<400> 28
Met Pro Ala Lys Pro Ala Lys Pro Val Thr Ile Asp Thr Ala
Val Gln
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15
Glu Ser Pro Asp Leu Gly Gly Arg Thr Trp Ala Ser Val Leu
Glu Gln
20 25 30

Ala Val Arg Glu Asp Ile Ile Ser Gly Arg Leu Pro Ala Gly
Seite 55

0070110

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

0070110

Leu Ala
225 230 235
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Arg Gln Lys Gly Gly Ala Ala Pro Thr Arg Lys Arg Arg Ala
Ala Ala
245 250
255
Glu Ala Pro Val
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<210> 29
<211> 738
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<213> Mesorhizobium sp. BNC1

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gcc tat 48
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Ala Tyr
1 5 10
15
cgc ctg atc cgg aaa gct atc ttg cgg ggc gac att gag cct
ggc tca 96
Arg Leu Ile Arg Lys Ala Ile Leu Arg Gly Asp Ile Glu Pro
Gly Ser
20 25 30
cgc ttg aaa ata gat atg ctt cag cgc cag ttt tcg ttc tcc
agc agc 144
Arg Leu Lys Ile Asp Met Leu Gln Arg Gln Phe Ser Phe Ser
Ser Ser
35 40 45
cca ttg cgt gaa gct ctg aac cgg ctc gtc tcc gaa gat ctt
gtt gag 192
Pro Leu Arg Glu Ala Leu Asn Arg Leu Val Ser Glu Asp Leu
Val Glu
50 55 60
att gat aat cgc cgc ggc ttt cgg gcg gcg gcc gtt tcg ctg
cga gat 240
Ile Asp Asn Arg Arg Gly Phe Arg Ala Ala Ala Val Ser Leu
Arg Asp
65 70 75
80

0070110

atg aaa gac ctg acg gcc ttc cgc ctg aac ata gag ccg att
 tcg tta 288
 Met Lys Asp Leu Thr Ala Phe Arg Leu Asn Ile Glu Pro Ile
 Ser Leu

85

90

95

cgc gag tcg atc gag cat ggc gac gac gaa tgg gag gcg cag
 gtg ctt 336
 Arg Glu Ser Ile Glu His Gly Asp Asp Glu Trp Glu Ala Gln
 Val Leu

100

105

110

gcc gcc tat cat cgc ctt gac ctt ctg gag gcg cga gag gat
 gag cag 384
 Ala Ala Tyr His Arg Leu Asp Leu Leu Glu Ala Arg Glu Asp
 Glu Gln

115

120

125

gcg ccc tac agc gac gaa tgg gct gag cgg cat aga gcc ttc
 cac gca 432
 Ala Pro Tyr Ser Asp Glu Trp Ala Glu Arg His Arg Ala Phe
 His Ala

130

135

140

gca ctt atc gcc gcc tgt cct tcc tcc cgg cag att tcg gtc
 tgc ctg 480
 Ala Leu Ile Ala Ala Cys Pro Ser Ser Arg Gln Ile Ser Val
 Cys Leu

145

150

155

160

aac ctt ttc gat cat gta gag cgc tac cgg cgg ctt tcg atc
 tgt tgg 528
 Asn Leu Phe Asp His Val Glu Arg Tyr Arg Arg Leu Ser Ile
 Cys Trp

165

170

175

cga aaa tcc aaa cgc gac cgt tca aac gaa cac agg gag atc
 atg gat 576
 Arg Lys Ser Lys Arg Asp Arg Ser Asn Glu His Arg Glu Ile
 Met Asp

180

185

190

gcc gcc ttg gcg cgt gat cat gaa aga gca gtc tcg aag ctg
 acg gag 624
 Ala Ala Leu Ala Arg Asp His Glu Arg Ala Val Ser Lys Leu
 Thr Glu

195

200

205

cat atc gag cgg aca acg ctg cat gtg gcg agg atg cta aag
 gcg ctg 672
 His Ile Glu Arg Thr Thr Leu His Val Ala Arg Met Leu Lys

0070110

Ala Leu
210 215 220
gaa aca gaa aaa act gcc aca gga cag gag cag gtc gaa ggt
ctc ggt 720
Glu Thr Glu Lys Thr Ala Thr Gly Gln Glu Gln Val Glu Gly
Leu Gly
225 230 235
240
cgg gca atg aag gcc tga
738
Arg Ala Met Lys Ala
245

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<212> PRT
<213> Mesorhizobium sp. BNC1

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Ala Tyr
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Arg Leu Ile Arg Lys Ala Ile Leu Arg Gly Asp Ile Glu Pro
Gly Ser
20 25 30
Arg Leu Lys Ile Asp Met Leu Gln Arg Gln Phe Ser Phe Ser
Ser Ser
35 40 45
Pro Leu Arg Glu Ala Leu Asn Arg Leu Val Ser Glu Asp Leu
Val Glu
50 55 60
Ile Asp Asn Arg Arg Gly Phe Arg Ala Ala Ala Val Ser Leu
Arg Asp
65 70 75
80
Met Lys Asp Leu Thr Ala Phe Arg Leu Asn Ile Glu Pro Ile
Ser Leu
85 90
95
Arg Glu Ser Ile Glu His Gly Asp Asp Glu Trp Glu Ala Gln
Val Leu
100 105 110
Ala Ala Tyr His Arg Leu Asp Leu Leu Glu Ala Arg Glu Asp
Seite 59

0070110

Glu	Gln													
		115					120					125		
Ala	Pro	Tyr	Ser	Asp	Glu	Trp	Ala	Glu	Arg	His	Arg	Ala	Phe	
His	Ala													
		130				135					140			
Ala	Leu	Ile	Ala	Ala	Cys	Pro	Ser	Ser	Arg	Gln	Ile	Ser	Val	
Cys	Leu													
					150					155				
		160												
Asn	Leu	Phe	Asp	His	Val	Glu	Arg	Tyr	Arg	Arg	Leu	Ser	Ile	
Cys	Trp													
				165					170					
		175												
Arg	Lys	Ser	Lys	Arg	Asp	Arg	Ser	Asn	Glu	His	Arg	Glu	Ile	
Met	Asp													
			180					185					190	
Ala	Ala	Leu	Ala	Arg	Asp	His	Glu	Arg	Ala	Val	Ser	Lys	Leu	
Thr	Glu													
		195					200					205		
His	Ile	Glu	Arg	Thr	Thr	Leu	His	Val	Ala	Arg	Met	Leu	Lys	
Ala	Leu													
		210				215					220			
Glu	Thr	Glu	Lys	Thr	Ala	Thr	Gly	Gln	Glu	Gln	Val	Glu	Gly	
Leu	Gly													
		225			230					235				
		240												
Arg	Ala	Met	Lys	Ala										
				245										

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 <212> DNA
 <213> Azoarcus sp. BH72

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 ccc aag 48

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Met	Leu	Asn	Asp	Val	Ala	Pro	Ala	Glu	Leu	Pro	Thr	Ala	Glu
Pro	Lys												
1				5					10				
15													
acc	ctg	gtc	gag	gcc	gcc	tac	aac	cag	ctg	cgc	cgc	gac	atc
atc	gaa		96										
Thr	Leu	val	Glu	Ala	Ala	Tyr	Asn	Gln	Leu	Arg	Arg	Asp	Ile
Ile	Glu												
		20						25					30
ggc	gtt	cat	ccg	ccg	ggc	gaa	aaa	ctg	cgc	gtc	gag	cat	cta
aag	gac		144										
Gly	Val	His	Pro	Pro	Gly	Glu	Lys	Leu	Arg	Val	Glu	His	Leu
Lys	Asp												
		35					40					45	
cag	tac	gag	gtc	ggc	gcc	gga	acc	ctg	cgc	gag	gcc	ttg	ctg
ctg	ctg		192										
Gln	Tyr	Glu	Val	Gly	Ala	Gly	Thr	Leu	Arg	Glu	Ala	Leu	Leu
Leu	Leu												
	50					55				60			
gtc	acc	gat	gcg	ctg	gtg	gtg	gcc	cag	ggc	cag	cgc	ggc	ttc
cgc	gtg		240										
Val	Thr	Asp	Ala	Leu	Val	Val	Ala	Gln	Gly	Gln	Arg	Gly	Phe
Arg	Val												
65					70					75			
80													
gcc	ccc	atc	tcc	gtg	gcc	gac	ttc	gag	gac	atc	acc	cgc	acc
cgc	gtg		288										
Ala	Pro	Ile	Ser	Val	Ala	Asp	Phe	Glu	Asp	Ile	Thr	Arg	Thr
Arg	Val												
			85							90			
95													
ctg	ctg	gaa	acc	gag	gca	ctg	cgc	cag	tcg	atc	gcg	ctc	ggc
gac	gac		336										
Leu	Leu	Glu	Thr	Glu	Ala	Leu	Arg	Gln	Ser	Ile	Ala	Leu	Gly
Asp	Asp												
		100						105				110	
gcc	tgg	gag	gcc	gat	ctg	gtc	gcc	gcc	ttc	cac	cgt	ctg	tcg
cgc	gcc		384										
Ala	Trp	Glu	Ala	Asp	Leu	Val	Ala	Ala	Phe	His	Arg	Leu	Ser
Arg	Ala												
		115					120					125	
gaa	cag	aag	ctg	gct	gac	cac	gac	gcc	aac	acc	acc	gag	gaa
tgg	gag		432										
Glu	Gln	Lys	Leu	Ala	Asp	His	Asp	Ala	Asn	Thr	Thr	Glu	Glu
Trp	Glu												
	130					135					140		
aag	cgc	aac	cgc	gcc	ttc	cac	gag	gcg	ctg	atc	gcc	gcc	tgc

0070110

```

ccc tcg          480
Lys Arg Asn Arg Ala Phe His Glu Ala Leu Ile Ala Ala Cys
Pro Ser
145          150          155
160
cgc tgg atc cgc cat ttt cag cac atc ctc tat cag cag tcc
gag cgc          528
Arg Trp Ile Arg His Phe Gln His Ile Leu Tyr Gln Gln Ser
Glu Arg
          165          170
175
tac cgc cgc atc agc ctg ttc cgc cag ccc atc gcg cgc gac
atc cac          576
Tyr Arg Arg Ile Ser Leu Phe Arg Gln Pro Ile Ala Arg Asp
Ile His
          180          185          190

gcc gaa cac cag gcc atc ttc gac gcc acg ctc gcg cgc gac
gcc acc          624
Ala Glu His Gln Ala Ile Phe Asp Ala Thr Leu Ala Arg Asp
Ala Thr
          195          200          205
cgc gcc acc tcc atc ctc acc gag cac atc ctg cgc acg ctg
gat gcg          672
Arg Ala Thr Ser Ile Leu Thr Glu His Ile Leu Arg Thr Leu
Asp Ala
          210          215          220
gtg aag cgg atg ccg gag gat ttc ttc agc aag cct ggg cag
cgg          717
Val Lys Arg Met Pro Glu Asp Phe Phe Ser Lys Pro Gly Gln
Arg
225          230          235
tga
          720

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<210> 32
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 <212> PRT
 <213> Azoarcus sp. BH72

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 Met Leu Asn Asp Val Ala Pro Ala Glu Leu Pro Thr Ala Glu
 Pro Lys
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 Thr Leu Val Glu Ala Ala Tyr Asn Gln Leu Arg Arg Asp Ile
 Seite 62

0070110

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

0070110

Asp	Ala												
210						215					220		
Val	Lys	Arg	Met	Pro	Glu	Asp	Phe	Phe	Ser	Lys	Pro	Gly	Gln
Arg													
225					230					235			

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 <212> DNA
 <213> Neptuniibacter caesariensis

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 <222> (1)..(702)
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Phe	Ala												
1				5					10				
15													
aca	cag	gtt	ctc	ggc	cag	tta	aag	caa	gat	att	ctg	act	ggg
tac	ttt		96										
Thr	Gln	Val	Leu	Gly	Gln	Leu	Lys	Gln	Asp	Ile	Leu	Thr	Gly
Tyr	Phe												
			20					25					30
aat	ccg	ggt	gaa	aag	ctg	aag	atg	acc	cgc	ctg	aaa	gaa	cgc
tat	cag		144										
Asn	Pro	Gly	Glu	Lys	Leu	Lys	Met	Thr	Arg	Leu	Lys	Glu	Arg
Tyr	Gln												
		35				40						45	
gta	ggg	gtc	agc	cct	ttg	cgg	gaa	gcg	ctg	tcg	caa	ctt	ctg
gtc	gaa		192										
Val	Gly	Val	Ser	Pro	Leu	Arg	Glu	Ala	Leu	Ser	Gln	Leu	Leu
Val	Glu												
		50				55						60	
cag	ctc	gta	gtt	gtt	gag	aac	cag	cgt	ggc	ttc	aaa	gta	cat
cca	atc		240										
Gln	Leu	Val	Val	Val	Glu	Asn	Gln	Arg	Gly	Phe	Lys	Val	His
Pro	Ile												
		65			70					75			
		80											
tcg	gct	gaa	gag	atg	gaa	gat	att	tat	cat	acc	cgt	gca	gag
ata	gag		288										

0070110

Ser	Ala	Glu	Glu	Met	Glu	Asp	Ile	Tyr	His	Thr	Arg	Ala	Glu
Ile	Glu												
				85					90				
95													
gcc	ctg	tgt	gtg	agt	cag	gcc	att	gac	cgc	ggt	gat	gat	gcc
tgg	gag			336									
Ala	Leu	Cys	Val	Ser	Gln	Ala	Ile	Asp	Arg	Gly	Asp	Asp	Ala
Trp	Glu												
			100					105					110
gcc	ggt	att	ctg	gcc	gct	gcc	cat	cag	ctt	aaa	aaa	tca	gca
gaa	ctg			384									
Ala	Gly	Ile	Leu	Ala	Ala	Ala	His	Gln	Leu	Lys	Lys	Ser	Ala
Glu	Leu												
		115					120					125	
ctt	gaa	gaa	gag	aac	ccg	gaa	aag	atc	cag	cgc	tgg	gag	gcc
ctt	cat			432									
Leu	Glu	Glu	Glu	Asn	Pro	Glu	Lys	Ile	Gln	Arg	Trp	Glu	Ala
Leu	His												
		130				135					140		
cag	gcc	ttt	cac	aga	gcg	att	gcc	gag	ggc	tgt	ggc	tcc	cct
agc	ctg			480									
Gln	Ala	Phe	His	Arg	Ala	Ile	Ala	Glu	Gly	Cys	Gly	Ser	Pro
Ser	Leu												
145					150					155			
160													
ctc	cat	gtc	cgc	ctg	tcc	ctt	tat	gag	aaa	gct	tcg	cgc	tac
cgc	aac			528									
Leu	His	Val	Arg	Leu	Ser	Leu	Tyr	Glu	Lys	Ala	Ser	Arg	Tyr
Arg	Asn												
				165						170			
175													
cac	tgg	ctt	aaa	gag	aat	atg	ctg	gac	cgc	tct	atc	ttt	gat
gcc	aac			576									
His	Trp	Leu	Lys	Glu	Asn	Met	Leu	Asp	Arg	Ser	Ile	Phe	Asp
Ala	Asn												
			180					185					190
cag	aaa	gag	cat	gaa	gca	tta	acc	gaa	gca	ctg	ctc	aac	agg
gat	aaa			624									
Gln	Lys	Glu	His	Glu	Ala	Leu	Thr	Glu	Ala	Leu	Leu	Asn	Arg
Asp	Lys												
		195				200						205	
gaa	aag	gcg	gta	gag	att	atc	cgc	cag	cat	att	ctc	agc	cct
tac	cga			672									
Glu	Lys	Ala	Val	Glu	Ile	Ile	Arg	Gln	His	Ile	Leu	Ser	Pro
Tyr	Arg												
	210					215					220		

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ctg ctg aaa gat tcg att agc ttc gat tga
702
Leu Leu Lys Asp Ser Ile Ser Phe Asp
225 230

<210> 34
<211> 233
<212> PRT
<213> *Neptuniibacter caesariensis*

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Phe Ala
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Thr Gln Val Leu Gly Gln Leu Lys Gln Asp Ile Leu Thr Gly
Tyr Phe
20 25 30
Asn Pro Gly Glu Lys Leu Lys Met Thr Arg Leu Lys Glu Arg
Tyr Gln
35 40 45
Val Gly Val Ser Pro Leu Arg Glu Ala Leu Ser Gln Leu Leu
Val Glu
50 55 60
Gln Leu Val Val Val Glu Asn Gln Arg Gly Phe Lys Val His
Pro Ile
65 70 75
80
Ser Ala Glu Glu Met Glu Asp Ile Tyr His Thr Arg Ala Glu
Ile Glu
85 90
95
Ala Leu Cys Val Ser Gln Ala Ile Asp Arg Gly Asp Asp Ala
Trp Glu
100 105 110
Ala Gly Ile Leu Ala Ala Ala His Gln Leu Lys Lys Ser Ala
Glu Leu
115 120 125
Leu Glu Glu Glu Asn Pro Glu Lys Ile Gln Arg Trp Glu Ala
Leu His
130 135 140
Gln Ala Phe His Arg Ala Ile Ala Glu Gly Cys Gly Ser Pro
Seite 66

0070110

Ser Leu
145 150 155
160
Leu His Val Arg Leu Ser Leu Tyr Glu Lys Ala Ser Arg Tyr
Arg Asn
165 170
175
His Trp Leu Lys Glu Asn Met Leu Asp Arg Ser Ile Phe Asp
Ala Asn
180 185 190
Gln Lys Glu His Glu Ala Leu Thr Glu Ala Leu Leu Asn Arg
Asp Lys
195 200 205
Glu Lys Ala Val Glu Ile Ile Arg Gln His Ile Leu Ser Pro
Tyr Arg
210 215 220
Leu Leu Lys Asp Ser Ile Ser Phe Asp
225 230

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<212> DNA
<213> Marinobacter sp. ELB17

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<222> (1)..(711)
<223> transl_table=11

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gag aac 48
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Glu Asn
1 5 10
15
ctc ggt gtc cgc gct tac aag ctg cta aag aat gac att att
agg ggt 96
Leu Gly Val Arg Ala Tyr Lys Leu Leu Lys Asn Asp Ile Ile
Arg Gly
20 25 30
cag ttc cgc ccc gac gag aag cta cgc atg agc atc ttg aaa
gag cgc 144
Gln Phe Arg Pro Asp Glu Lys Leu Arg Met Ser Ile Leu Lys

0070110

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

0070110

caa aag 576

Val	Trp	Leu	Lys	Glu	Thr	Val	Phe	Ser	Ser	Glu	Ala	Leu	Asp
Gln	Lys												
			180					185					190

cgc	aaa	gag	cac	gct	gcg	ctg	gtg	gaa	gtt	act	ctt	gcc	cgc
cgc	aaa		624										
Arg	Lys	Glu	His	Ala	Ala	Leu	Val	Glu	Val	Thr	Leu	Ala	Arg
Arg	Lys												
		195				200						205	

gac	gag	gcc	gag	aag	atg	atg	cgc	gaa	cac	ctg	atg	acg	cct
gtg	ccg		672										
Asp	Glu	Ala	Glu	Lys	Met	Met	Arg	Glu	His	Leu	Met	Thr	Pro
Val	Pro												
		210				215					220		

att	att	act	gcc	gtc	atg	caa	cag	caa	gga	act	gcc	tga	
			711										

Ile	Ile	Thr	Ala	Val	Met	Gln	Gln	Gln	Gly	Thr	Ala		
225					230					235			

<210> 36

<211> 236

<212> PRT

<213> Marinobacter sp. ELB17

<400> 36

Met	Asn	Pro	Lys	Thr	His	Gln	Glu	Glu	Leu	Ala	Asp	Ile	Arg
Glu	Asn												
1				5					10				

15													
Leu	Gly	Val	Arg	Ala	Tyr	Lys	Leu	Leu	Lys	Asn	Asp	Ile	Ile
Arg	Gly												
			20					25				30	

Gln	Phe	Arg	Pro	Asp	Glu	Lys	Leu	Arg	Met	Ser	Ile	Leu	Lys
Glu	Arg												
		35					40					45	

Tyr	Asp	Leu	Gly	Ile	Gly	Pro	Leu	Arg	Glu	Ala	Leu	Ser	Gln
Leu	Val												
	50					55					60		

Ala	Glu	Gln	Leu	Val	Val	Ala	Ile	Ser	Gln	Arg	Gly	Tyr	Arg
Val	Ser												
65					70					75			

80													
Pro	Met	Ser	Leu	Ala	Glu	Leu	His	Asp	Ile	Tyr	Asp	Ala	Arg

0070110

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Ala Glu
      85      90
95
Leu Glu Ala Met Met Leu Gly Leu Ala Ile Glu Arg Gly Asp
Asp Asn
      100      105      110
Trp Glu Ala Glu Ile Leu Ala Arg Asn Tyr Gln Leu Ala Lys
Val Ser
      115      120      125
Glu Ala His Thr Pro Asp Ser Leu Leu Glu Ile Trp Asp Ala
Arg His
      130      135      140
Ser Gln Phe His Ile Ala Leu Val Cys Gly Cys Arg Ser Pro
Gln Leu
      145      150      155
      160
Met Lys Val Arg Asp Gly Leu Phe Asp Lys Val Gln Arg Tyr
Arg His
      165      170
      175
Val Trp Leu Lys Glu Thr Val Phe Ser Ser Glu Ala Leu Asp
Gln Lys
      180      185      190
Arg Lys Glu His Ala Ala Leu Val Glu Val Thr Leu Ala Arg
Arg Lys
      195      200      205
Asp Glu Ala Glu Lys Met Met Arg Glu His Leu Met Thr Pro
Val Pro
      210      215      220
Ile Ile Thr Ala Val Met Gln Gln Gln Gly Thr Ala
225      230      235

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Pro Lys
  1              5              10
15
acc ctc gtc gag ggg gcc tac cag cgc ctg cgc cgg gac atc
atc gag          96
Thr Leu Val Glu Gly Ala Tyr Gln Arg Leu Arg Arg Asp Ile
Ile Glu
          20              25              30
ggc gtt cac ccg ccc ggc gag aaa ctt cgc gtc gaa cat ctc
aag gac          144
Gly Val His Pro Pro Gly Glu Lys Leu Arg Val Glu His Leu
Lys Asp
          35              40              45
cgc tac gag gtc ggc gcc ggc acc ctg cgc gag gcc ctc ctc
ctg ctc          192
Arg Tyr Glu Val Gly Ala Gly Thr Leu Arg Glu Ala Leu Leu
Leu Leu
          50              55              60
gtc acc gac gcc ctg gtg gtc gcc cag gga caa cgc ggc ttc
cgc gtc          240
Val Thr Asp Ala Leu Val Val Ala Gln Gly Gln Arg Gly Phe
Arg Val
  65              70              75
80
tcg ccg att tcc atc gag gac ttc gag gac atc acc cgc acc
cgc ctg          288
Ser Pro Ile Ser Ile Glu Asp Phe Glu Asp Ile Thr Arg Thr
Arg Leu
          85              90
95
ctg ctc gag acc gaa gcc ctg cgc cag tcg ctg cag ctc ggc
ggc gag          336
Leu Leu Glu Thr Glu Ala Leu Arg Gln Ser Leu Gln Leu Gly
Gly Glu
          100              105              110
gac tgg gag gcc tcc gtg gtc gcg gct ttc cac cgc ctc tct
cgc gcc          384
Asp Trp Glu Ala Ser Val Val Ala Ala Phe His Arg Leu Ser
Arg Ala
          115              120              125
gag caa aag ctc ggc gac cac gac tcg ctg gcc gcc gag gag
tgg gag          432
Glu Gln Lys Leu Gly Asp His Asp Ser Leu Ala Ala Glu Glu

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0070110

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Trp Glu
130
cgg cgc aac cgc gcc ttc 135 gag gca ctg atc 140 gcc gcg tcg
ccc tcg 480
Arg Arg Asn Arg Ala Phe His Glu Ala Leu Ile Ala Ala Ser
Pro Ser
145 150 155
160
cgc tgg atc cgt cat ttc cag cac atc ctc tac cag cag tcc
gag cgc 528
Arg Trp Ile Arg His Phe Gln His Ile Leu Tyr Gln Gln Ser
Glu Arg
165 170
175
tac cgg cgc ctg agc ctg ttc agc cat ccg atc ccg cgc gac
atc cac 576
Tyr Arg Arg Leu Ser Leu Phe Ser His Pro Ile Pro Arg Asp
Ile His
180 185 190
gcc gag cac cag gcc ttg ttc aac gcc agc ctg gca cgc gac
acc acg 624
Ala Glu His Gln Ala Leu Phe Asn Ala Ser Leu Ala Arg Asp
Thr Thr
195 200 205
cgc gcg acc tcc atc ctc acc gag cac gtg ctg cgc acg ctc
gac gcg 672
Arg Ala Thr Ser Ile Leu Thr Glu His Val Leu Arg Thr Leu
Asp Ala
210 215 220
gtg aag ctg ctt ccg gcg gag ttc ttc gcc ggc aag cac aag
tcc 717
Val Lys Leu Leu Pro Ala Glu Phe Phe Ala Gly Lys His Lys
Ser
225 230 235
tga
720

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<210> 38
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 <212> PRT
 <213> Thauera sp. MZ1T

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 Met Asn Glu Ala Val Pro Gln Arg Thr Pro Glu Ala Val Glu
 Pro Lys

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

0070110

Thr	Thr													
		195					200				205			
Arg	Ala	Thr	Ser	Ile	Leu	Thr	Glu	His	Val	Leu	Arg	Thr	Leu	
Asp	Ala						215				220			
	210													
Val	Lys	Leu	Leu	Pro	Ala	Glu	Phe	Phe	Ala	Gly	Lys	His	Lys	
Ser														
225					230					235				

<210> 39
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 <212> DNA
 <213> Escherichia coli 06

<220>
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 tat cgc 48

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Tyr	Arg													
1				5					10					
15														
tgg	ctg	aag	aac	gat	att	att	cgc	ggc	aat	ttt	cag	ccg	gat	
gaa	aaa		96											
Trp	Leu	Lys	Asn	Asp	Ile	Ile	Arg	Gly	Asn	Phe	Gln	Pro	Asp	
Glu	Lys													
			20					25					30	
tta	cgg	atg	agt	ttg	ctg	aca	tcg	cgt	tat	gca	ctt	ggc	gtc	
gga	ccg		144											
Leu	Arg	Met	Ser	Leu	Leu	Thr	Ser	Arg	Tyr	Ala	Leu	Gly	Val	
Gly	Pro													
		35					40					45		
ttg	cgg	gaa	gcg	ctt	tcg	caa	ctg	gtg	gca	gaa	cga	ctg	gtc	
acg	gtg		192											
Leu	Arg	Glu	Ala	Leu	Ser	Gln	Leu	Val	Ala	Glu	Arg	Leu	Val	
Thr	Val													
	50					55				60				
gtg	aat	caa	aaa	ggg	tat	cgg	gtg	gcg	tct	atg	tca	gag	cag	
gag	ctg		240											
Val	Asn	Gln	Lys	Gly	Tyr	Arg	Val	Ala	Ser	Met	Ser	Glu	Gln	

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Glu 65	Leu 80													
		70					75							
ctc	gat	att	ttc	gac	gcc	cgc	gcc	aat	atg	gaa	gcg	atg	ctg	
gtg	agt	288												
Leu	Asp	Ile	Phe	Asp	Ala	Arg	Ala	Asn	Met	Glu	Ala	Met	Leu	
Val	Ser	85					90							
95														
ctg	gcg	att	gcc	cgc	ggc	ggc	gat	gaa	tgg	gag	gca	gac	gtt	
ctc	gca	336												
Leu	Ala	Ile	Ala	Arg	Gly	Gly	Asp	Glu	Trp	Glu	Ala	Asp	Val	
Leu	Ala	100					105							
110														
aaa	gcg	cat	ctg	ctc	agt	aag	ctt	gag	gcc	tgt	gac	gcc	agt	
gag	aaa	384												
Lys	Ala	His	Leu	Leu	Ser	Lys	Leu	Glu	Ala	Cys	Asp	Ala	Ser	
Glu	Lys	115					120				125			
atg	ctt	gat	gag	tgg	gat	ctg	cgt	cat	cag	gcg	ttt	cat	act	
gca	att	432												
Met	Leu	Asp	Glu	Trp	Asp	Leu	Arg	His	Gln	Ala	Phe	His	Thr	
Ala	Ile	130					135				140			
gtg	gcg	ggc	tgt	ggc	tct	tac	tat	ttg	ctg	caa	atg	cgt	gaa	
cgg	ttg	480												
Val	Ala	Gly	Cys	Gly	Ser	Tyr	Tyr	Leu	Leu	Gln	Met	Arg	Glu	
Arg	Leu	145					150				155			
160														
ttt	gat	ctg	gca	gcg	cgt	tat	cga	ttt	atc	tgg	ctg	cgg	cga	
aca	gtg	528												
Phe	Asp	Leu	Ala	Ala	Arg	Tyr	Arg	Phe	Ile	Trp	Leu	Arg	Arg	
Thr	Val	165					170							
175														
ctt	tcg	gtg	gaa	atg	ctg	gaa	gat	aaa	cac	gat	cag	cac	cag	
acc	ctg	576												
Leu	Ser	Val	Glu	Met	Leu	Glu	Asp	Lys	His	Asp	Gln	His	Gln	
Thr	Leu	180					185							
190														
act	gcg	gcg	gta	ctg	gcg	cga	gat	acc	gcg	cgc	gcc	agt	gag	
tta	atg	624												
Thr	Ala	Ala	Val	Leu	Ala	Arg	Asp	Thr	Ala	Arg	Ala	Ser	Glu	
Leu	Met	195					200				205			

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cgc cag cat tta ctg acg cca att ccc att atc cag cag gcg
 atg gct 672
 Arg Gln His Leu Leu Thr Pro Ile Pro Ile Ile Gln Gln Ala
 Met Ala
 210 215 220
 ggc aat taa
 681
 Gly Asn
 225

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 <212> PRT
 <213> Escherichia coli 06

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 Tyr Arg
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 15
 Trp Leu Lys Asn Asp Ile Ile Arg Gly Asn Phe Gln Pro Asp
 Glu Lys
 20 25 30
 Leu Arg Met Ser Leu Leu Thr Ser Arg Tyr Ala Leu Gly Val
 Gly Pro
 35 40 45
 Leu Arg Glu Ala Leu Ser Gln Leu Val Ala Glu Arg Leu Val
 Thr Val
 50 55 60
 Val Asn Gln Lys Gly Tyr Arg Val Ala Ser Met Ser Glu Gln
 Glu Leu
 65 70 75
 80
 Leu Asp Ile Phe Asp Ala Arg Ala Asn Met Glu Ala Met Leu
 Val Ser
 85 90
 95
 Leu Ala Ile Ala Arg Gly Gly Asp Glu Trp Glu Ala Asp Val
 Leu Ala
 100 105 110
 Lys Ala His Leu Leu Ser Lys Leu Glu Ala Cys Asp Ala Ser
 Glu Lys
 115 120 125

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Met Leu Asp Glu Trp Asp Leu Arg His Gln Ala Phe His Thr
Ala Ile
130 135 140

Val Ala Gly Cys Gly Ser Tyr Tyr Leu Leu Gln Met Arg Glu
Arg Leu
145 150 155

160
Phe Asp Leu Ala Ala Arg Tyr Arg Phe Ile Trp Leu Arg Arg
Thr Val
165 170

175
Leu Ser Val Glu Met Leu Glu Asp Lys His Asp Gln His Gln
Thr Leu
180 185 190

Thr Ala Ala Val Leu Ala Arg Asp Thr Ala Arg Ala Ser Glu
Leu Met
195 200 205

Arg Gln His Leu Leu Thr Pro Ile Pro Ile Ile Gln Gln Ala
Met Ala
210 215 220

Gly Asn
225

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<211> 663
<212> DNA
<213> Escherichia coli

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gat att 48
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Asp Ile
1 5 10
15
att cgc ggt aat ttt caa ccg gat gaa aaa tta cga atg agt
ttg ctg 96
Ile Arg Gly Asn Phe Gln Pro Asp Glu Lys Leu Arg Met Ser
Leu Leu

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			20				25					30	
aca	tcg	cgt	tat	gca	ctt	ggc	ggt	ggg	ccg	tta	cgg	gaa	gct
ctt	tcg		144										
Thr	Ser	Arg	Tyr	Ala	Leu	Gly	Val	Gly	Pro	Leu	Arg	Glu	Ala
Leu	Ser												
		35					40					45	
caa	ctg	gtg	gcg	gaa	cgg	ctg	gtc	acg	gtg	gtg	aat	caa	aaa
ggg	tat		192										
Gln	Leu	Val	Ala	Glu	Arg	Leu	Val	Thr	Val	Val	Asn	Gln	Lys
Gly	Tyr												
	50					55					60		
cgg	gtg	gcg	tct	atg	tca	gag	cag	gag	ctg	ctc	gat	att	ttc
gac	gcc		240										
Arg	Val	Ala	Ser	Met	Ser	Glu	Gln	Glu	Leu	Leu	Asp	Ile	Phe
Asp	Ala												
65					70					75			
80													
cgc	gcc	aat	atg	gaa	gcg	atg	tta	gtg	agt	ctg	gcg	att	gcc
cgc	ggt		288										
Arg	Ala	Asn	Met	Glu	Ala	Met	Leu	Val	Ser	Leu	Ala	Ile	Ala
Arg	Gly												
			85						90				
95													
ggc	gat	gag	tgg	gag	gca	gac	ggt	ctc	gca	aaa	gcg	cat	ctg
ctg	agt		336										
Gly	Asp	Glu	Trp	Glu	Ala	Asp	Val	Leu	Ala	Lys	Ala	His	Leu
Leu	Ser												
		100						105				110	
aag	ctt	gag	gcc	tgt	gac	gcc	agc	gag	aaa	atg	ctt	gat	gag
tgg	gat		384										
Lys	Leu	Glu	Ala	Cys	Asp	Ala	Ser	Glu	Lys	Met	Leu	Asp	Glu
Trp	Asp												
		115					120				125		
ctg	cgt	cat	cag	gcg	ttt	cat	acg	gca	att	gtg	gcg	ggc	tgt
ggg	tct		432										
Leu	Arg	His	Gln	Ala	Phe	His	Thr	Ala	Ile	Val	Ala	Gly	Cys
Gly	Ser												
	130					135					140		
cac	tat	ttg	ctg	caa	atg	cgt	gaa	cgg	ttg	ttt	gat	ctg	gcg
gcg	cgt		480										
His	Tyr	Leu	Leu	Gln	Met	Arg	Glu	Arg	Leu	Phe	Asp	Leu	Ala
Ala	Arg												
145					150					155			
160													
tat	cga	ttt	atc	tgg	ctg	cgg	cga	acg	gtg	ctt	tcg	gtg	gaa
atg	ctg		528										
Tyr	Arg	Phe	Ile	Trp	Leu	Arg	Arg	Thr	Val	Leu	Ser	Val	Glu

0070110

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Met Leu
175
gag gat aaa cac gat cag cac cag acc ctg act gcg gcg gta
ctg gcg
Glu Asp Lys His Asp Gln His Gln Thr Leu Thr Ala Ala Val
Leu Ala
180 185 190

cga gat acc gcg cgc gcc agt gag tta atg cgc cag cat tta
ctg acg
Arg Asp Thr Ala Arg Ala Ser Glu Leu Met Arg Gln His Leu
Leu Thr
195 200 205
cca att ccc att atc cag cag gcg atg gct ggc aat taa
Pro Ile Pro Ile Ile Gln Gln Ala Met Ala Gly Asn
210 215 220

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<211> 220
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<213> Escherichia coli

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Asp Ile
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Ile Arg Gly Asn Phe Gln Pro Asp Glu Lys Leu Arg Met Ser
Leu Leu
20 25 30

Thr Ser Arg Tyr Ala Leu Gly Val Gly Pro Leu Arg Glu Ala
Leu Ser
35 40 45

Gln Leu Val Ala Glu Arg Leu Val Thr Val Val Asn Gln Lys
Gly Tyr
50 55 60

Arg Val Ala Ser Met Ser Glu Gln Glu Leu Leu Asp Ile Phe
Asp Ala
65 70 75
80
Arg Ala Asn Met Glu Ala Met Leu Val Ser Leu Ala Ile Ala
Arg Gly
85 90

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95

Gly Asp Glu Trp Glu Ala Asp Val Leu Ala Lys Ala His Leu
Leu Ser
100 105 110

Lys Leu Glu Ala Cys Asp Ala Ser Glu Lys Met Leu Asp Glu
Trp Asp
115 120 125

Leu Arg His Gln Ala Phe His Thr Ala Ile Val Ala Gly Cys
Gly Ser
130 135 140

His Tyr Leu Leu Gln Met Arg Glu Arg Leu Phe Asp Leu Ala
Ala Arg
145 150 155

160
Tyr Arg Phe Ile Trp Leu Arg Arg Thr Val Leu Ser Val Glu
Met Leu
165 170

175
Glu Asp Lys His Asp Gln His Gln Thr Leu Thr Ala Ala Val
Leu Ala
180 185 190

Arg Asp Thr Ala Arg Ala Ser Glu Leu Met Arg Gln His Leu
Leu Thr
195 200 205

Pro Ile Pro Ile Ile Gln Gln Ala Met Ala Gly Asn
210 215 220

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<213> Artificial sequence

<220>
<223> primer

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atgatcagga gtcacaccat ga
22

<210> 44
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21

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<222> (12)..(14)

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<222> (16)..(16)

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<222> (20)..(23)

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<222> (32)..(33)
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<221> variant

<222> (139)..(140)

<223> Xaa in position 139 to 140 is any amino acid

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<221> variant

<222> (142)..(147)

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 <222> (157)..(159)
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 <222> (173)..(176)
 <223> Xaa in position 173 to 176 is any or no amino acid

<220>
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 <222> (178)..(179)
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<220>
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<220>
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 <222> (188)..(191)
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 <222> (193)..(198)
 <223> Xaa in position 193 to 198 is any amino acid

<400> 45
 Tyr Xaa Xaa Leu Xaa Xaa Asp Ile Ile Xaa Gly Xaa Xaa Xaa
 Pro Xaa
 1 5 10
 15
 Glu Lys Leu Xaa Xaa Xaa Xaa Leu Xaa Xaa Arg Tyr Xaa Xaa
 Gly Xaa

0070110

20

25

30

Xaa Pro Leu Arg Glu Ala Leu Ser Xaa Leu Val Xaa Xaa Xaa
Leu Val

35

40

45

Xaa Xaa Xaa Xaa Gln Xaa Gly Xaa Arg Val Ala Xaa Xaa Ser
Xaa Xaa

50

55

60

Xaa Xaa Xaa Asp Ile Xaa Xaa Xaa Arg Xaa Xaa Xaa Glu Xaa
Xaa Xaa

65

70

75

80

Xaa Xaa Xaa Ala Ile Xaa Xaa Gly Xaa Asp Xaa Trp Glu Ala
Xaa Xaa

85

90

95

Xaa Ala Xaa Xaa His Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa
Xaa Xaa

100

105

110

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp Xaa Xaa Arg His Xaa
Ala Phe

115

120

125

His Xaa Ala Xaa Xaa Xaa Xaa Cys Xaa Ser Xaa Xaa Leu Xaa
Xaa Xaa

130

135

140

Xaa Xaa Xaa Leu Xaa Asp Xaa Xaa Xaa Arg Tyr Arg Xaa Xaa
Xaa Leu

145

150

155

160

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
Xaa Xaa

165

170

175

His Xaa Xaa Leu Xaa Xaa Xaa Xaa Leu Ala Arg Xaa Xaa Xaa
Xaa Ala

180

185

190

Xaa Xaa Xaa Xaa Xaa Xaa His
195

<210> 46

<211> 57

0070110

<212> PRT

<213> Artificial sequence

<220>

<223> protein pattern

<220>

<221> variant

<222> (3)..(3)

<223> Xaa in position 3 is Ile or Leu

<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> (7)..(7)

<223> Xaa in position 7 is Phe, His or Tyr

<220>

<221> variant

<222> (8)..(8)

<223> Xaa in position 8 is any amino acid

<220>

<221> variant

<222> (10)..(10)

<223> Xaa in position 10 is Asp or Gly

<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 Met or Val

<220>

<221> variant

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<222> (16)..(16)

<223> Xaa in position 16 is Glu, Ser or Thr

<220>

<221> variant

<222> (17)..(17)

<223> Xaa in position 17 is any amino acid

<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, Asp, Glu or Ser

<220>

<221> variant

<222> (21)..(21)

<223> Xaa in position 21 is Gln or Arg

<220>

<221> variant

<222> (23)..(23)

<223> Xaa in position 23 is Ala, Asp, Glu, Gly or Gln

<220>

<221> variant

<222> (24)..(24)

<223> Xaa in position 24 is Leu or Val

<220>

<221> variant

<222> (26)..(26)

<223> Xaa in position 26 is Ala, Ile or Val

<220>

<221> variant

<222> (27)..(27)

<223> Xaa in position 27 is Gly or Ser

<220>

<221> variant

<222> (28)..(28)

<223> Xaa in position 28 is Pro or Thr

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<220>

<221> Variant

<222> (30)..(30)

<223> Xaa in position 30 is Gln or Arg

<220>

<221> Variant

<222> (34)..(35)

<223> Xaa in position 34 to 35 is any amino acid

<220>

<221> Variant

<222> (37)..(37)

<223> Xaa in position 37 is any or no amino acid

<220>

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<222> (39)..(40)

<223> Xaa in position 39 to 40 is any amino acid

<220>

<221> Variant

<222> (41)..(41)

<223> Xaa in position 41 is any or no amino acid

<220>

<221> Variant

<222> (44)..(44)

<223> Xaa in position 44 is Asn, Thr or Val

<220>

<221> Variant

<222> (45)..(45)

<223> Xaa in position 45 is Ala or Val

<220>

<221> Variant

<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 Gly, Asn or Ser

<220>

<221> Variant

<222> (49)..(49)

0070110

<223> Xaa in position 49 is Lys or Arg

<220>

<221> Variant

<222> (51)..(51)

<223> Xaa in position 51 is Phe or Tyr

<220>

<221> Variant

<222> (52)..(52)

<223> Xaa in position 52 is Lys or Arg

<220>

<221> Variant

<222> (54)..(54)

<223> Xaa in position 54 is any amino acid

<220>

<221> Variant

<222> (55)..(55)

<223> Xaa in position 55 is Pro or Ser

<220>

<221> Variant

<222> (56)..(56)

<223> Xaa in position 56 is Ile or Met

<400> 46

Asp Ile Xaa Xaa Gly Xaa Xaa Xaa Pro Xaa Glu Lys Leu Xaa
Xaa Xaa

1 5 10

15

Xaa Leu Xaa Xaa Xaa Tyr Xaa Xaa Gly Xaa Xaa Xaa Leu Xaa
Glu Ala

20 25 30

Leu Xaa Xaa Leu Xaa Val Xaa Xaa Xaa Leu Val Xaa Xaa Xaa
Xaa Gln

35 40 45

Xaa Gly Xaa Xaa Val Xaa Xaa Xaa Ser
50 55

<210> 47

<211> 37

<212> PRT

<213> Artificial sequence

<220>
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<223> Xaa in position 2 is any amino acid

<220>
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<222> (3)..(3)
<223> Xaa in position 3 is any or no amino acid

<220>
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<222> (5)..(8)
<223> Xaa in position 5 to 8 is any or no amino acid

<220>
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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 Ile or Leu

<220>
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<222> (14)..(14)
<223> Xaa in position 14 is Ala, Ile or Val

<220>
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<222> (15)..(15)
<223> Xaa in position 15 is Ala, Glu or Ser

<220>
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<222> (16)..(16)
<223> Xaa in position 16 is Ala or Gly

<220>
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<222> (17)..(17)
<223> Xaa in position 17 is Cys or Ser

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<220>
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<222> (18)..(18)
<223> Xaa in position 18 is Gly or Pro

<220>
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<222> (20)..(28)
<223> Xaa in position 20 to 28 is any amino acid

<220>
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<222> (30)..(30)
<223> Xaa in position 30 is Phe or Tyr

<220>
<221> Variant
<222> (31)..(31)
<223> Xaa in position 31 is Asp, Glu or Gln

<220>
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<222> (32)..(32)
<223> Xaa in position 32 is any amino acid

<220>
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<222> (33)..(33)
<223> Xaa in position 33 is Ala, Ser or Val

<220>
<221> Variant
<222> (34)..(34)
<223> Xaa in position 34 is Ala, Glu or Ser

<400> 47
Arg Xaa Xaa Ala Xaa Xaa Xaa Xaa Phe His Xaa Ala Xaa Xaa
Xaa Xaa
1 5 10
15
Xaa Xaa Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa
Xaa Xaa
20 25 30
Xaa Xaa Arg Tyr Arg
35

<210> 48
<211> 41
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<213> Artificial sequence

<220>
<223> protein pattern

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<222> (2)..(4)
<223> Xaa in position 2 to 4 is any or no amino acid

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

<220>
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<222> (7)..(7)
<223> Xaa in position 7 is Asp, His 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, Thr or Val

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

<220>
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<222> (12)..(12)
<223> Xaa in position 12 is Ile, Leu or Met

<220>
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<222> (14)..(16)
<223> Xaa in position 14 to 16 is any amino acid

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<222> (17)..(17)
<223> Xaa in position 17 is Ile, Leu or Val

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<222> (18)..(19)
<223> Xaa in position 18 to 19 is any amino acid

<220>
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<222> (20)..(20)
<223> Xaa in position 20 is Ala or Ser

<220>
<221> Variant
<222> (22)..(22)
<223> Xaa in position 22 is Ala, Asp or Glu

<220>
<221> Variant
<222> (23)..(23)
<223> Xaa in position 23 is any amino acid

<220>
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<222> (25)..(25)
<223> Xaa in position 25 is Asp or Gly

<220>
<221> Variant
<222> (27)..(27)
<223> Xaa in position 27 is Ala, Glu or Asn

<220>
<221> Variant
<222> (31)..(31)
<223> Xaa in position 31 is Asp, Glu, Gly or Ser

<220>
<221> Variant
<222> (32)..(32)
<223> Xaa in position 32 is Ile, Leu or Val

<220>
<221> Variant

0070110

<222> (33)..(33)

<223> Xaa in position 33 is Leu or Val

<220>

<221> variant

<222> (35)..(36)

<223> Xaa in position 35 to 36 is any amino acid

<220>

<221> variant

<222> (37)..(37)

<223> Xaa in position 37 is His or Tyr

<220>

<221> variant

<222> (38)..(38)

<223> Xaa in position 38 is any amino acid

<220>

<221> variant

<222> (39)..(39)

<223> Xaa in position 39 is Leu or Met

<220>

<221> variant

<222> (40)..(40)

<223> Xaa in position 40 is any amino acid

<220>

<221> variant

<222> (41)..(41)

<223> Xaa in position 41 is Lys or Arg

<400> 48

Asp Xaa Xaa Xaa Ile Xaa Xaa Xaa Arg Xaa Xaa Xaa Glu Xaa
Xaa Xaa

1 5 10

15

Xaa Xaa Xaa Xaa Ile Xaa Xaa Gly Xaa Asp Xaa Trp Glu Ala
Xaa Xaa

20 25 30

Xaa Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35 40

<210> 49

0070110

<211> 37
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<213> Artificial sequence

<220>
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<220>
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<223> Xaa in position 2 to 6 is any or no amino acid

<220>
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<222> (8)..(8)
<223> Xaa in position 8 is any amino acid

<220>
<221> Variant
<222> (9)..(9)
<223> Xaa in position 9 is Ala or Thr

<220>
<221> Variant
<222> (10)..(10)
<223> Xaa in position 10 is Ile or Leu

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

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<221> Variant
<222> (12)..(12)
<223> Xaa in position 12 is Ala, Asp, Glu or Asn

<220>
<221> Variant
<222> (13)..(13)
<223> Xaa in position 13 is Ala 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> (16)..(16)
<223> Xaa in position 16 is Ala, Asn or Pro

<220>
<221> Variant
<222> (18)..(18)
<223> Xaa in position 18 is Asp, Glu or Arg

<220>
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<222> (19)..(21)
<223> Xaa in position 19 to 21 is any amino acid

<220>
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<222> (23)..(24)
<223> Xaa in position 23 to 24 is any amino acid

<220>
<221> Variant
<222> (25)..(26)
<223> Xaa in position 25 to 26 is Ile, Leu or Met

<220>
<221> Variant
<222> (27)..(27)
<223> Xaa in position 27 is any amino acid

<220>
<221> Variant
<222> (28)..(28)
<223> Xaa in position 28 is Glu, Gln or Ser

<220>
<221> Variant
<222> (30)..(30)
<223> Xaa in position 30 is Ile, Leu or Val

<220>
<221> Variant
<222> (31)..(31)
<223> Xaa in position 31 is Leu or Met

<220>
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<222> (32)..(32)

0070110

<223> xaa in position 32 is any amino acid

<220>

<221> variant

<222> (33)..(33)

<223> xaa in position 33 is Pro or Thr

<220>

<221> variant

<222> (34)..(35)

<223> xaa in position 34 to 35 is any amino acid

<220>

<221> variant

<222> (36)..(36)

<223> xaa in position 36 is Ala, Ile or Leu

<220>

<221> variant

<222> (37)..(37)

<223> xaa in position 37 is Ile, Leu or Val

<400> 49

Glu xaa xaa xaa xaa xaa His xaa xaa xaa xaa xaa xaa xaa
Leu xaa

1 5 10

15

Arg xaa xaa xaa xaa Ala xaa xaa xaa xaa xaa xaa His xaa
xaa xaa

20

25

30

xaa xaa xaa xaa xaa
35

<210> 50

<211> 579

<212> DNA

<213> Saccharomyces cerevisiae

<220>

<221> CDS

<222> (1)..(579)

<400> 50

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gat ggt 48

Met Ser Glu Lys Ala Val Arg Arg Lys Leu Val Ile Ile Gly
Asp Gly

0070110

1		5		10
15				
gct	tgt	ggc	aag	acc
aaa	ttc		96	
Ala	Cys	Gly	Lys	Thr
Lys	Phe		Ser	Leu
			Leu	Tyr
			Val	Phe
			Thr	Leu
			Gly	
		20		25
cct	gaa	caa	tat	cat
gat	tgc		144	
Pro	Glu	Gln	Tyr	His
Asp	Cys		Pro	Thr
			Val	Phe
			Glu	Asn
			Tyr	Val
			Thr	
		35		40
aga	gtt	gac	gga	ata
gcg	gga		192	
Arg	Val	Asp	Gly	Ile
Ala	Gly		Lys	Val
			Ser	Leu
			Thr	Leu
			Trp	Asp
			Thr	
		50		55
caa	gag	gaa	tat	gaa
gca	gat		240	
Gln	Glu	Glu	Tyr	Glu
Ala	Asp		Arg	Leu
			Arg	Pro
			Phe	Ser
			Tyr	Ser
			Lys	
65			70	
80				75
ata	ata	tta	att	ggg
att	aac		288	
Ile	Ile	Leu	Ile	Gly
Ile	Asn		Phe	Ala
			Val	Asp
			Asn	Phe
			Glu	Ser
			Leu	
		85		90
95				
gca	agg	acg	aaa	tgg
gac	gca		336	
Ala	Arg	Thr	Lys	Trp
Asp	Ala		Ala	Asp
			Glu	Ala
			Leu	Arg
			Tyr	Cys
			Pro	
		100		105
				110
cca	atc	gtt	ctt	gta
gcc	cat		384	
Pro	Ile	Val	Leu	Val
Ala	His		Gly	Leu
			Lys	Lys
			Asp	Leu
			Arg	Gln
			Glu	
		115		120
ttt	aaa	gag	aat	gct
gca	aaa		432	
Phe	Lys	Glu	Asn	Ala
Ala	Lys		Thr	Asp
			Glu	Met
			Val	Pro
			Ile	Glu
			Asp	
		130		135
caa	gtt	gca	agg	gcc
agt	gca		480	
Gln	Val	Ala	Arg	Ala
			Ile	Gly
			Ala	Lys
			Lys	Lys
			Tyr	Met
			Glu	Cys

0070110

Ser Ala
 145 150 155
 160
 ctg act ggt gag ggt gtg gat gat gtc ttt gaa gta gct aca
 aga acc 528
 Leu Thr Gly Glu Gly Val Asp Asp Val Phe Glu Val Ala Thr
 Arg Thr
 165 170
 175
 agt ttg ctt atg aag aag gaa cca ggg gct aac tgt tgc ata
 att tta 576
 Ser Leu Leu Met Lys Lys Glu Pro Gly Ala Asn Cys Cys Ile
 Ile Leu
 180 185 190
 taa
 579

<210> 51
 <211> 192
 <212> PRT
 <213> Saccharomyces cerevisiae

<400> 51
 Met Ser Glu Lys Ala Val Arg Arg Lys Leu Val Ile Ile Gly
 Asp Gly
 1 5 10
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 Ala Cys Gly Lys Thr Ser Leu Leu Tyr Val Phe Thr Leu Gly
 Lys Phe
 20 25 30
 Pro Glu Gln Tyr His Pro Thr Val Phe Glu Asn Tyr Val Thr
 Asp Cys
 35 40 45
 Arg Val Asp Gly Ile Lys Val Ser Leu Thr Leu Trp Asp Thr
 Ala Gly
 50 55 60
 Gln Glu Glu Tyr Glu Arg Leu Arg Pro Phe Ser Tyr Ser Lys
 Ala Asp
 65 70 75
 80
 Ile Ile Leu Ile Gly Phe Ala Val Asp Asn Phe Glu Ser Leu
 Ile Asn

0070110

85

90

95

Ala Arg Thr Lys Trp Ala Asp Glu Ala Leu Arg Tyr Cys Pro
Asp Ala

100

105

110

Pro Ile Val Leu Val Gly Leu Lys Lys Asp Leu Arg Gln Glu
Ala His

115

120

125

Phe Lys Glu Asn Ala Thr Asp Glu Met Val Pro Ile Glu Asp
Ala Lys
130

135

140

Gln Val Ala Arg Ala Ile Gly Ala Lys Lys Tyr Met Glu Cys
Ser Ala
145

150

155

160

Leu Thr Gly Glu Gly Val Asp Asp Val Phe Glu Val Ala Thr
Arg Thr

165

170

175

Ser Leu Leu Met Lys Lys Glu Pro Gly Ala Asn Cys Cys Ile
Ile Leu

180

185

190

<210> 52

<211> 564

<212> DNA

<213> *Eremothecium gossypii*

<220>

<221> CDS

<222> (1)..(564)

<400> 52

atg acg gtc aac gtt gtg aga cgg aag ttg gta atc ata ggg
gat ggg 48

Met Thr Val Asn Val Val Arg Arg Lys Leu Val Ile Ile Gly
Asp Gly

1

5

10

15

gca tgc ggc aag acg tcg tta cta cat gtg ttc acg ctg ggg
aag ttc 96

Ala Cys Gly Lys Thr Ser Leu Leu His Val Phe Thr Leu Gly
Lys Phe

20

25

30

0070110

cct	gag	gaa	tat	ctg	ccc	acg	gtt	ttc	gag	aac	tac	gtt	acg
gat	tgc												
Pro	Glu	Glu	Tyr	Leu	Pro	Thr	Val	Phe	Glu	Asn	Tyr	Val	Thr
Asp	Cys												
		35					40					45	
cgt	gta	gac	ggc	ata	aaa	gtg	cag	ttg	gcg	cta	tgg	gat	act
gct	ggt												
Arg	Val	Asp	Gly	Ile	Lys	Val	Gln	Leu	Ala	Leu	Trp	Asp	Thr
Ala	Gly												
		50					55				60		
cag	gaa	gaa	tac	gag	cgt	ctg	cgc	ccc	atg	tcc	tac	tcg	aag
gcg	gac												
Gln	Glu	Glu	Tyr	Glu	Arg	Leu	Arg	Pro	Met	Ser	Tyr	Ser	Lys
Ala	Asp												
65					70					75			
80													
atc	ata	tta	atc	ggg	ttt	gcc	ata	gac	gac	ccg	ggg	tcg	ttg
tcc	aat												
Ile	Ile	Leu	Ile	Gly	Phe	Ala	Ile	Asp	Asp	Pro	Gly	Ser	Leu
Ser	Asn												
					85					90			
95													
gcg	cgg	gag	aag	tgg	acg	gtc	gag	gcg	ctg	cgc	tac	tgt	ccc
aac	gcc												
Ala	Arg	Glu	Lys	Trp	Thr	Val	Glu	Ala	Leu	Arg	Tyr	Cys	Pro
Asn	Ala												
					100					105			110
ccg	atc	atc	ctc	gtg	ggg	ctc	aaa	aag	gac	ctt	cgc	cgc	ccc
ggg	acg												
Pro	Ile	Ile	Leu	Val	Gly	Leu	Lys	Lys	Asp	Leu	Arg	Arg	Pro
Gly	Thr												
		115					120				125		
cag	tgc	gcg	atg	gta	gcg	cct	tcg	cag	gca	caa	gag	gtg	gtg
cg	gcc												
Gln	Cys	Ala	Met	Val	Ala	Pro	Ser	Gln	Ala	Gln	Glu	Val	Val
Arg	Ala												
		130				135					140		
atc	ggc	gca	aag	aaa	tac	atg	gag	tgc	agc	gca	ctt	acg	ggg
gag	ggc												
Ile	Gly	Ala	Lys	Lys	Tyr	Met	Glu	Cys	Ser	Ala	Leu	Thr	Gly
Glu	Gly												
145					150						155		
160													
gtg	gac	gat	gtg	ttc	gag	ctg	gcc	acg	aga	aca	agt	ctt	ctg
gtg	aac												
Val	Asp	Asp	Val	Phe	Glu	Leu	Ala	Thr	Arg	Thr	Ser	Leu	Leu
Val	Asn												

0070110

165

170

175

aag gag ccg ggt caa ggc tgt tgc att atc tca tga

Lys Glu Pro Gly Gln Gly Cys Cys Ile Ile Ser

<210> 53

<211> 187

<212> PRT

<213> Eremanthecium gossypii

<400> 53

Met Thr Val Asn Val Val Arg Arg Lys Leu Val Ile Ile Gly
Asp Gly

1 5 10

Ala Cys Gly Lys Thr Ser Leu Leu His Val Phe Thr Leu Gly
Lys Phe

20 25 30

Pro Glu Glu Tyr Leu Pro Thr Val Phe Glu Asn Tyr Val Thr
Asp Cys

35 40 45

Arg Val Asp Gly Ile Lys Val Gln Leu Ala Leu Trp Asp Thr
Ala Gly

50 55 60

Gln Glu Glu Tyr Glu Arg Leu Arg Pro Met Ser Tyr Ser Lys
Ala Asp

65 70 75

Ile Ile Leu Ile Gly Phe Ala Ile Asp Asp Pro Gly Ser Leu
Ser Asn

85 90

Ala Arg Glu Lys Trp Thr Val Glu Ala Leu Arg Tyr Cys Pro
Asn Ala

100 105 110

Pro Ile Ile Leu Val Gly Leu Lys Lys Asp Leu Arg Arg Pro
Gly Thr

115 120 125

Gln Cys Ala Met Val Ala Pro Ser Gln Ala Gln Glu Val Val
Arg Ala

0070110

130

135

140

Ile Gly Ala Lys Lys Tyr Met Glu Cys Ser Ala Leu Thr Gly
Glu Gly

145

150

155

160

Val Asp Asp Val Phe Glu Leu Ala Thr Arg Thr Ser Leu Leu
Val Asn

165

170

175

Lys Glu Pro Gly Gln Gly Cys Cys Ile Ile Ser
180 185

<210> 54

<211> 594

<212> DNA

<213> Glycine max

<220>

<221> CDS

<222> (1)..(594)

<400> 54

atg agt gca tgc agg ttc att aag tgc gtc acc gtc ggc gac
ggc gct 48
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala

1

5

10

15

gtc ggc aaa acc tgc ttg ttg att tcc tac acc agc aac act
ttt ccc 96
Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro

20

25

30

acg gac tac gtg ccc acg gtt ttt gac aat ttc agt gct aat
gtt gtg 144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val

35

40

45

gtg gat gga agc acc gta aac ctg ggc ttg tgg gat act gct
ggt cag 192
Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln

50

55

60

gag gat tat aat agg ctt aga ccc ttg agt tat cga gga gct
gat gta 240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val

0070110

65					70							75	
80													
ttt	ata	ctt	gcc	ttt	tct	ctc	ata	agc	aag	gct	agc	tat	gaa
aat	att			288									
Phe	Ile	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Lys	Ala	Ser	Tyr	Glu
Asn	Ile												
				85						90			
95													
gca	aag	aag	tgg	atc	cct	gaa	cta	agg	cat	tat	gcc	cct	ggt
ggt	cca		336										
Ala	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Arg	His	Tyr	Ala	Pro	Gly
Val	Pro												
			100					105				110	
ata	att	ctc	ggt	gga	aca	aag	tta	gat	ctt	cga	gaa	gat	aag
caa	ttt		384										
Ile	Ile	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Glu	Asp	Lys
Gln	Phe												
		115					120				125		
ttt	ata	gac	cac	cct	ggt	gca	gta	cca	ata	act	aca	aca	cag
gga	gaa		432										
Phe	Ile	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Thr	Thr	Thr	Gln
Gly	Glu												
		130				135					140		
gaa	tta	aga	aaa	ctg	att	ggt	gct	cct	gct	tac	atc	gag	tgt
agt	tca		480										
Glu	Leu	Arg	Lys	Leu	Ile	Gly	Ala	Pro	Ala	Tyr	Ile	Glu	Cys
Ser	Ser												
145					150					155			
160													
aaa	aca	cag	cag	aat	ggt	aaa	gct	gtc	ttt	gac	gct	gcc	atc
aaa	gtg		528										
Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile
Lys	Val												
				165						170			
175													
ggt	ctt	caa	cca	cca	aag	caa	aag	aaa	aag	aag	aga	aaa	gca
cag	aaa		576										
Val	Leu	Gln	Pro	Pro	Lys	Gln	Lys	Lys	Lys	Lys	Arg	Lys	Ala
Gln	Lys												
			180					185				190	
gct	tgc	tca	ata	ttg	tga								
			594										
Ala	Cys	Ser	Ile	Leu									
		195											

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<211> 197

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<213> Glycine max

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Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala

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Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro

20 25 30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val

35 40 45

Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln

50 55 60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val

65 70 75

80

Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Ile

85 90

95

Ala Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Gly
Val Pro

100 105 110

Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Glu Asp Lys
Gln Phe

115 120 125

Phe Ile Asp His Pro Gly Ala Val Pro Ile Thr Thr Thr Gln
Gly Glu

130 135 140

Glu Leu Arg Lys Leu Ile Gly Ala Pro Ala Tyr Ile Glu Cys
Ser Ser

145 150 155

160

Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Lys Val

165 170

0070110

175
Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Arg Lys Ala
Gln Lys
180 185 190

Ala Cys Ser Ile Leu
195

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gga gct 48
Met Asn Ala Ser Lys Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10
15
gtt ggg aaa acc tgc atg ctc att tgc tac acc agc aac aag
ttc ccc 96
Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser Asn Lys
Phe Pro
20 25 30
act gat tac ata cca aca gta ttt gac aat ttc agt gcc aat
gtt gct 144
Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Ala
35 40 45
gtg gat gga agc att gtc aat ttg ggg cta tgg gac aca gca
ggc cag 192
Val Asp Gly Ser Ile Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60
gaa gac tat agc agg ttg agg cca ctg agc tat aga gga gca
gac att 240
Glu Asp Tyr Ser Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Ile
65 70 75
80
ttt gtc tta gca ttc tca ctg att agc aga gct agc tat gaa
aat gtt 288
Phe Val Leu Ala Phe Ser Leu Ile Ser Arg Ala Ser Tyr Glu
Seite 107

Asn	Val	85						90						
95														
ctc	aag	aag	tgg	atg	ccg	gaa	ttg	cgt	aga	ttt	gca	cct	aat	
ggt	cca	336												
Leu	Lys	Lys	Trp	Met	Pro	Glu	Leu	Arg	Arg	Phe	Ala	Pro	Asn	
Val	Pro	100						105				110		
att	ggt	ctt	ggt	ggt	acg	aag	cta	gat	ctt	cgt	gaa	gac	cgg	
ggt	tat	384												
Ile	Val	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Glu	Asp	Arg	
Gly	Tyr	115						120				125		
gta	gct	gat	cac	atg	gga	tct	aat	gtc	ata	aca	tct	gct	gag	
ggg	gaa	432												
Val	Ala	Asp	His	Met	Gly	Ser	Asn	Val	Ile	Thr	Ser	Ala	Glu	
Gly	Glu	130						135				140		
gaa	ctg	agg	aaa	caa	att	ggt	gca	gct	gct	tac	att	gag	tgc	
agt	tca	480												
Glu	Leu	Arg	Lys	Gln	Ile	Gly	Ala	Ala	Ala	Tyr	Ile	Glu	Cys	
Ser	Ser	145						150				155		
160														
aag	act	caa	cag	aat	gtc	aaa	gca	gtg	ttt	gac	act	gca	att	
aag	ggt	528												
Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Thr	Ala	Ile	
Lys	Val	165						170						
175														
ggt	ctc	caa	cct	caa	cct	cca	agg	agg	aaa	gaa	atg	gca	agg	
aag	aaa	576												
Val	Leu	Gln	Pro	Gln	Pro	Pro	Arg	Arg	Lys	Glu	Met	Ala	Arg	
Lys	Lys	180						185				190		
agg	cat	aga	agg	tct	ggt	tgc	tca	ttt	gta	agt	att	atg	tgc	
gga	ggc	624												
Arg	His	Arg	Arg	Ser	Gly	Cys	Ser	Phe	Val	Ser	Ile	Met	Cys	
Gly	Gly	195						200				205		
tgt	gct	gct	taa											
Cys	Ala	Ala	636											
210														

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<212> PRT
<213> Glycine max

<400> 57

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

0070110

				165						170				
175	Val	Leu	Gln	Pro	Gln	Pro	Pro	Arg	Arg	Lys	Glu	Met	Ala	Arg
	Lys	Lys												
				180				185					190	
	Arg	His	Arg	Arg	Ser	Gly	Cys	Ser	Phe	Val	Ser	Ile	Met	Cys
	Gly	Gly												
			195					200					205	
	Cys	Ala	Ala											
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<220>
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 <222> (36)..(665)

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 gct tca 53

Met Ala Ala Thr

Ala Ser

1

5	agg	ttt	atc	aag	tgt	gtg	aca	gtt	ggg	gat	gga	gct	gta	ggc
	aaa	act		101										
	Arg	Phe	Ile	Lys	Cys	Val	Thr	Val	Gly	Asp	Gly	Ala	Val	Gly
	Lys	Thr												
			10					15					20	
	tgc	atg	ctc	att	tgc	tat	act	agc	aac	aaa	ttc	ccc	acg	gac
	tat	att		149										
	Cys	Met	Leu	Ile	Cys	Tyr	Thr	Ser	Asn	Lys	Phe	Pro	Thr	Asp
	Tyr	Ile												
			25					30					35	
	cca	acg	gtg	ttt	gat	aat	ttc	agt	gca	aat	gta	gtt	gtg	gaa
	ggc	aca		197										
	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn	Val	Val	Val	Glu
	Gly	Thr												
			40				45					50		
	act	gtc	aat	tta	ggc	ctc	tgg	gac	act	gct	gga	caa	gag	gat
	tac	aac		245										
	Thr	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala	Gly	Gln	Glu	Asp
	Tyr	Asn												

0070110

55					60						65			
70														
aga	ctg	agg	cct	ttg	agc	tac	agg	ggg	gca	gat	gtc	ttt	gtc	
ttg	gct		293											
Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala	Asp	Val	Phe	Val	
Leu	Ala													
					75						80			
85														
ttc	tct	tta	gtc	agt	cat	gca	agc	tat	gaa	aat	gtg	ttg	aag	
aag	tgg		341											
Phe	Ser	Leu	Val	Ser	His	Ala	Ser	Tyr	Glu	Asn	Val	Leu	Lys	
Lys	Trp													
					90						95			100
ggt	cct	gag	ctg	cag	cat	ttt	gct	ccc	ggc	att	cca	gtg	gtg	
cta	ggt		389											
Val	Pro	Glu	Leu	Gln	His	Phe	Ala	Pro	Gly	Ile	Pro	Val	Val	
Leu	Val													
		105					110					115		
ggc	acc	aaa	ttg	gat	ctc	cga	gaa	gac	aag	cac	tat	ttg	gct	
gat	cat		437											
Gly	Thr	Lys	Leu	Asp	Leu	Arg	Glu	Asp	Lys	His	Tyr	Leu	Ala	
Asp	His													
		120				125					130			
cct	ggt	ctg	gtg	cct	gtg	act	tct	gag	caa	ggt	gag	gaa	ttg	
cgt	aaa		485											
Pro	Gly	Leu	Val	Pro	Val	Thr	Ser	Glu	Gln	Gly	Glu	Glu	Leu	
Arg	Lys													
135					140						145			
150														
ctg	gtg	gga	gct	aca	tat	tat	ata	gag	tgc	agc	tca	aaa	act	
cag	cag		533											
Leu	Val	Gly	Ala	Thr	Tyr	Tyr	Ile	Glu	Cys	Ser	Ser	Lys	Thr	
Gln	Gln													
					155						160			
165														
aat	gtg	aag	tca	ggt	ttt	gat	gct	gct	ata	aag	gtg	gtc	att	
aag	cct		581											
Asn	Val	Lys	Ser	Val	Phe	Asp	Ala	Ala	Ile	Lys	Val	Val	Ile	
Lys	Pro													
					170						175			180
cca	caa	aaa	caa	gag	aag	aaa	aaa	cca	cgt	cga	ggg	tgt	cta	
cta	aat		629											
Pro	Gln	Lys	Gln	Glu	Lys	Lys	Lys	Pro	Arg	Arg	Gly	Cys	Leu	
Leu	Asn													
		185				190					195			
gtc	atc	tgt	gga	agg	aat	ata	ggt	cgt	ttt	aaa	tgaaacattt			

0070110

cgtccaaagg 682
Val Ile Cys Gly Arg Asn Ile Val Arg Phe Lys

200 205
cttttcttgg gagggagaag cactgtcatc atcattctgt agaatttttt
aaattgacct 742

gggtcctttg gctttttaat ttcattg
768

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<211> 209
<212> PRT
<213> Glycine max

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Met Ala Ala Thr Ala Ser Arg Phe Ile Lys Cys Val Thr Val
Gly Asp
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15
Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser
Asn Lys
20 25 30
Phe Pro Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser
Ala Asn
35 40 45
Val Val Val Glu Gly Thr Thr Val Asn Leu Gly Leu Trp Asp
Thr Ala
50 55 60
Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg
Gly Ala
65 70 75
80
Asp Val Phe Val Leu Ala Phe Ser Leu Val Ser His Ala Ser
Tyr Glu
85 90
95
Asn Val Leu Lys Lys Trp Val Pro Glu Leu Gln His Phe Ala
Pro Gly
100 105 110

0070110

Ile	Pro	Val	Val	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Glu
Asp	Lys												
		115					120					125	

His	Tyr	Leu	Ala	Asp	His	Pro	Gly	Leu	Val	Pro	Val	Thr	Ser
Glu	Gln												
	130					135					140		

Gly	Glu	Glu	Leu	Arg	Lys	Leu	Val	Gly	Ala	Thr	Tyr	Tyr	Ile
Glu	Cys												
145					150					155			

		160											
Ser	Ser	Lys	Thr	Gln	Gln	Asn	Val	Lys	Ser	Val	Phe	Asp	Ala
Ala	Ile												
				165						170			

		175											
Lys	Val	Val	Ile	Lys	Pro	Pro	Gln	Lys	Gln	Glu	Lys	Lys	Lys
Pro	Arg												
			180					185					190

Arg	Gly	Cys	Leu	Leu	Asn	Val	Ile	Cys	Gly	Arg	Asn	Ile	Val
Arg	Phe												
		195					200					205	

Lys

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 <211> 639
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (1)..(639)

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gtt	ggc			48									
Met	Ala	Ala	Ala	Thr	Ala	Pro	Arg	Phe	Ile	Lys	Cys	Val	Thr
Val	Gly												
	1			5					10				
15													
gat	gga	gct	gta	ggg	aag	acc	tgc	atg	ctc	att	tgc	tat	acc
agc	aac			96									
Asp	Gly	Ala	Val	Gly	Lys	Thr	Cys	Met	Leu	Ile	Cys	Tyr	Thr
Ser	Asn												
			20					25					30

0070110

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

0070110

165

170

175

atc aga atg gtc atc aag cct cca caa aag caa aac gag aaa
 agg aag
 Ile Arg Met Val Ile Lys Pro Pro Gln Lys Gln Asn Glu Lys
 Arg Lys

180

185

190

aaa aaa cca cgt ggc tgt ttc cta aat gtc ctc tgt gga agg
 aac att
 Lys Lys Pro Arg Gly Cys Phe Leu Asn Val Leu Cys Gly Arg
 Asn Ile

195

200

205

gtt cgt ctt aag tga
 Val Arg Leu Lys
 210

<210> 61

<211> 212

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<213> Glycine max

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Met Ala Ala Ala Thr Ala Pro Arg Phe Ile Lys Cys Val Thr
 Val Gly

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15

Asp Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr
 Ser Asn

20

25

30

Lys Phe Pro Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe
 Ser Ala

35

40

45

Asn Val Val Val Glu Gly Ile Thr Val Asn Leu Gly Leu Trp
 Asp Thr
 50 55 60

Ala Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr
 Arg Gly

65

70

75

80

Ala Asp Val Phe Val Leu Ala Phe Ser Leu Val Ser Arg Ala
 Ser Tyr

85

90

95

0070110

Glu Asn Val Leu Lys Lys Trp Ile Pro Glu Leu Gln His Phe
Ala Pro
100 105 110

Gly Ile Pro Leu Val Leu Val Gly Thr Lys Leu Asp Leu Arg
Glu Asp
115 120 125

Arg His Tyr Met Ala Asp His Pro Gly Leu Val Pro Val Thr
Thr Glu
130 135 140

Gln Gly Glu Glu Leu Arg Lys His Ile Gly Ala Thr Tyr Tyr
Ile Glu
145 150 155
160

Cys Ser Ser Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp
Ala Ala
165 170

175
Ile Arg Met Val Ile Lys Pro Pro Gln Lys Gln Asn Glu Lys
Arg Lys
180 185 190

Lys Lys Pro Arg Gly Cys Phe Leu Asn Val Leu Cys Gly Arg
Asn Ile
195 200 205

Val Arg Leu Lys
210

<210> 62
<211> 594
<212> DNA
<213> Glycine max

<220>
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<222> (1)..(594)

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ggt gcc 48
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Gly Ala
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15
gtt ggc aag act tgc atg ctc atc tcc tac acc agc aac act

0070110

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

0070110

aaa aca caa cag aat gtg aag gct gtt ttt gat gca gcc atc
 aag gta 528
 Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
 Lys Val

165

170

175

gtt ctc cag ccc cca aag cag aag aaa aag aag aga aag gga
 caa aag 576
 Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Arg Lys Gly
 Gln Lys

180

185

190

gcc tgt tcc att ttg tga
 594
 Ala Cys Ser Ile Leu
 195

<210> 63

<211> 197

<212> PRT

<213> Glycine max

<400> 63

Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala

1

5

10

15

Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
 Phe Pro

20

25

30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
 Val Val

35

40

45

Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
 Gly Gln

50

55

60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
 Asp Val

65

70

75

80

Phe Leu Leu Ala Phe Ser Leu Ile Ser Arg Ala Ser Tyr Glu
 Asn Val

85

90

95

Ala Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Gly
 Seite 118

0070110

Val	Pro													
			100					105					110	
Ile	Ile	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys	
Gln	Phe													
			115					120					125	
Phe	Gln	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Thr	Thr	Ala	Gln	
Gly	Glu													
	130					135						140		
Glu	Leu	Arg	Lys	Leu	Ile	Gly	Ala	Pro	Ile	Tyr	Ile	Glu	Cys	
Ser	Ser													
145					150					155				
160														
Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile	
Lys	Val													
				165						170				
175														
Val	Leu	Gln	Pro	Pro	Lys	Gln	Lys	Lys	Lys	Lys	Arg	Lys	Gly	
Gln	Lys													
			180					185					190	
Ala	Cys	Ser	Ile	Leu										
		195												

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 <213> Glycine max

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ggt	gct			48										
Met	Ser	Ala	Ser	Arg	Phe	Ile	Lys	Cys	Val	Thr	Val	Gly	Asp	
Gly	Ala													
1				5					10					
15														
gtg	ggc	aaa	acc	tgt	ttg	ctt	att	tcc	tac	acc	agc	aac	act	
ttt	ccc			96										
Val	Gly	Lys	Thr	Cys	Leu	Leu	Ile	Ser	Tyr	Thr	Ser	Asn	Thr	
Phe	Pro													
			20					25					30	

0070110

acc	gat	tat	gtg	ccg	act	gtt	ttt	gac	aat	ttc	agc	gca	aat
gtg	gtt		144										
Thr	Asp	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn
Val	Val												
		35				40						45	
gtc	aat	ggg	agc	att	gtg	aat	ctg	ggt	ttg	tgg	gat	act	gct
gga	caa		192										
Val	Asn	Gly	Ser	Ile	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala
Gly	Gln												
	50					55					60		
gag	gat	tat	aac	aga	tta	aga	cct	ttg	agt	tac	cgt	ggt	gcc
gat	gtt		240										
Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala
Asp	Val												
65					70					75			
80													
ttc	ata	ctg	gct	ttc	tct	ctc	ata	agc	aag	gcc	agt	tat	gaa
aat	gtc		288										
Phe	Ile	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Lys	Ala	Ser	Tyr	Glu
Asn	Val												
			85						90				
95													
tct	aaa	aag	tgg	att	ccg	gag	ttg	aag	cat	tat	gct	cct	ggt
gtc	ccc		336										
Ser	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Lys	His	Tyr	Ala	Pro	Gly
Val	Pro												
			100					105				110	
att	att	ctg	gtt	ggc	aca	aag	ctt	gac	ctt	cgg	gat	gat	aag
cag	ttc		384										
Ile	Ile	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys
Gln	Phe												
		115				120						125	
tgc	att	gac	cat	cct	ggt	gcc	gta	cct	att	acc	aca	gct	cag
gga	gaa		432										
Cys	Ile	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Thr	Thr	Ala	Gln
Gly	Glu												
	130					135					140		
gag	ctt	agg	aag	ctg	att	aat	gcg	cca	gct	tac	att	gaa	tgc
agt	tca		480										
Glu	Leu	Arg	Lys	Leu	Ile	Asn	Ala	Pro	Ala	Tyr	Ile	Glu	Cys
Ser	Ser												
145					150					155			
160													
aaa	aca	cag	gag	aac	gtg	aag	gca	gtc	ttt	gat	gca	gcc	ata
aga	gtt		528										
Lys	Thr	Gln	Glu	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile
Arg	Val												

0070110

165

170

175

gtc ctt caa cca cct aag cag aag aaa aag aag ggt aaa gca

caa aag 576

Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Gly Lys Ala

Gln Lys

180

185

190

gcc tgt tcg ata ttg tga

594

Ala Cys Ser Ile Leu

195

<210> 65

<211> 197

<212> PRT

<213> Glycine max

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Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp

Gly Ala

1

5

10

15

Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr

Phe Pro

20

25

30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn

Val Val

35

40

45

Val Asn Gly Ser Ile Val Asn Leu Gly Leu Trp Asp Thr Ala

Gly Gln

50

55

60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala

Asp Val

65

70

75

80

Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu

Asn Val

85

90

95

Ser Lys Lys Trp Ile Pro Glu Leu Lys His Tyr Ala Pro Gly

Val Pro

100

105

110

Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys

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0070110

Gln	Phe													
		115						120						125
Cys	Ile	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Thr	Thr	Ala	Gln	
Gly	Glu													
	130						135						140	
Glu	Leu	Arg	Lys	Leu	Ile	Asn	Ala	Pro	Ala	Tyr	Ile	Glu	Cys	
Ser	Ser													
145						150						155		
	160													
Lys	Thr	Gln	Glu	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile	
Arg	Val													
						165						170		
175														
Val	Leu	Gln	Pro	Pro	Lys	Gln	Lys	Lys	Lys	Lys	Gly	Lys	Ala	
Gln	Lys													
							180						185	190
Ala	Cys	Ser	Ile	Leu										
		195												

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<213> Glycine max

<220>
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<222> (1) .. (594)

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gga	gcc			48									
Met	Ser	Ala	Ser	Arg	Phe	Ile	Lys	Cys	Val	Thr	Val	Gly	Asp
Gly	Ala			5					10				
1													
15													
gtg	ggc	aaa	act	tgt	ttg	cta	atc	tcc	tac	acc	agc	aac	acc
ttc	ccc			96									
Val	Gly	Lys	Thr	Cys	Leu	Leu	Ile	Ser	Tyr	Thr	Ser	Asn	Thr
Phe	Pro			20				25					30
act	gat	tat	gtg	cca	act	gtt	ttc	gac	aat	ttc	agc	gca	aat
gtg	ggt			144									
Thr	Asp	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn
Val	Val												
		35					40					45	

0070110

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

0070110

Gln Lys 180 185 190

gca tgt tca ata ttg tga
594

Ala Cys Ser Ile Leu
195

<210> 67
<211> 197
<212> PRT
<213> Glycine max

<400> 67
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala

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Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro 20 25 30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val 35 40 45

Val Asn Gly Ala Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln 50 55 60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val 65 70 75

80
Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val 85 90

95
Ser Lys Lys Trp Ile Pro Glu Leu Lys His Tyr Ala Pro Asp
Val Pro 100 105 110

Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe 115 120 125

Phe Ile Asp His Pro Gly Ala Val Pro Ile Thr Thr Val Gln
Gly Glu

0070110

130

135

140

Glu Leu Met Lys Leu Ile Asn Ala Pro Ala Tyr Ile Glu Cys
Ser Ser

145

150

155

160

Lys Ser Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Arg Val

165

170

175

Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Ser Lys Ala
Gln Lys

180

185

190

Ala Cys Ser Ile Leu
195

<210> 68

<211> 594

<212> DNA

<213> Glycine max

<220>

<221> CDS

<222> (1)..(594)

<400> 68

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ggt gcc 48

Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala

1

5

10

15

gtt ggc aag act tgc atg ctc atc tcc tac acc agc aac act
ttt cct 96

Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro

20

25

30

acg gac tac gtg cca act gtc ttt gac aat ttc agt gca aat
gta gtt 144

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val

35

40

45

gtg gat gga agc act gtg aat ctt ggg ttg tgg gat act gct
ggc caa 192

Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln

50

55

60

0070110

gaa	gat	tac	aat	aga	tta	aga	ccc	tta	agc	tat	cgt	gga	gca
gat	gta			240									
Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala
Asp	Val												
65					70					75			
80													
ttc	ctg	ctt	gct	ttc	tct	ctc	ata	agc	agg	gct	agc	tat	gaa
aat	gtt			288									
Phe	Leu	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Arg	Ala	Ser	Tyr	Glu
Asn	Val												
				85						90			
95													
gcc	aag	aaa	tgg	att	cct	gag	ttg	agg	cat	tat	gct	cct	ggt
ggt	cca			336									
Ala	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Arg	His	Tyr	Ala	Pro	Gly
Val	Pro												
				100						105			110
att	att	ctt	ggt	gga	aca	aaa	ctt	gat	ctt	cgg	gat	gat	aag
cag	ttc			384									
Ile	Ile	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys
Gln	Phe												
		115						120					125
ttt	caa	gac	cat	cct	ggt	gca	gtg	cct	atc	acc	aca	gca	cag
ggt	gag			432									
Phe	Gln	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Thr	Thr	Ala	Gln
Gly	Glu												
		130				135					140		
gag	ctg	aga	aag	ctt	atc	ggt	gct	cca	ggt	tac	att	gaa	tgt
agt	tca			480									
Glu	Leu	Arg	Lys	Leu	Ile	Gly	Ala	Pro	Val	Tyr	Ile	Glu	Cys
Ser	Ser												
145					150						155		
160													
aaa	acg	caa	cag	aat	gtg	aag	gct	ggt	ttt	gat	gcg	gcc	atc
aag	gta			528									
Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile
Lys	Val												
				165						170			
175													
ggt	ctc	cag	ccc	cca	aaa	cag	aag	aaa	aag	aag	aga	aag	ggg
caa	aag			576									
Val	Leu	Gln	Pro	Pro	Lys	Gln	Lys	Lys	Lys	Lys	Arg	Lys	Gly
Gln	Lys												
				180						185			190
gcc	tgt	tcc	att	ttg	tga								
			594										

0070110

Ala Cys Ser Ile Leu
195

<210> 69
<211> 197
<212> PRT
<213> Glycine max

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

0070110

160
 Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
 Lys Val
 165 170
 175
 Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Arg Lys Gly
 Gln Lys
 180 185 190
 Ala Cys Ser Ile Leu
 195

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 <211> 564
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (1)..(564)

<400> 70
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 ggt gct 48
 Met Ser Thr Ala Arg Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala
 1 5 10
 15
 gtg gga aag aca tgc atg ctt ata tcc tat acc agc aat acc
 ttt ccc 96
 Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
 Phe Pro
 20 25 30
 acg gat tat gtt cca aca gtg ttt gac aat ttc agt gct aat
 gta acc 144
 Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
 Val Thr
 35 40 45
 gtg gat ggt agt acg gtt aat ctt ggt tta tgg gac act gca
 ggg caa 192
 Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
 Gly Gln
 50 55 60
 gaa gat tac aat agg ctg agg cct tta agc tat aga gga gct
 gat gtg 240
 Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
 Asp Val
 65 70 75

0070110

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      80
ttt ttg ttg tgc tat tct ctc atc agc aaa gcc agt tat gag
aac atc      288
Phe Leu Leu Cys Tyr Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Ile

      85                      90
95
tcc aaa aag tgg ata cct gag ctg aga cat tat gct cca aat
gtg cct      336
Ser Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Asn
Val Pro

      100                      105                      110
ata gtg ctg gtg gga aca aaa cta gat ttg cga gat gac aag
caa ttt      384
Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe

      115                      120                      125
ctg att gat cat ccg gga tcc gca cga ata aca act gct cag
gca ttc      432
Leu Ile Asp His Pro Gly Ser Ala Arg Ile Thr Thr Ala Gln
Ala Phe

      130                      135                      140
act tat att gag tgc agc tcc aaa aca cag cag aat gtg aag
aca gtt      480
Thr Tyr Ile Glu Cys Ser Ser Lys Thr Gln Gln Asn Val Lys
Thr Val

      145                      150                      155
      160
ttt gat gct gca ata aag gtt gca ttg agg cca cca aag cca
aag aag      528
Phe Asp Ala Ala Ile Lys Val Ala Leu Arg Pro Pro Lys Pro
Lys Lys

      165                      170
175
aaa cca cgc aag aaa aag acc tgt cct ttc ctc tga
      564
Lys Pro Arg Lys Lys Lys Thr Cys Pro Phe Leu
      180                      185

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<210> 71
 <211> 187
 <212> PRT
 <213> Glycine max

<400> 71
 Met Ser Thr Ala Arg Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala

0070110

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15													
Val	Gly	Lys	Thr	Cys	Met	Leu	Ile	Ser	Tyr	Thr	Ser	Asn	Thr
Phe	Pro												
			20					25				30	
Thr	Asp	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn
Val	Thr												
		35					40					45	
Val	Asp	Gly	Ser	Thr	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala
Gly	Gln												
	50					55					60		
Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala
Asp	Val												
65					70					75			
	80												
Phe	Leu	Leu	Cys	Tyr	Ser	Leu	Ile	Ser	Lys	Ala	Ser	Tyr	Glu
Asn	Ile												
				85					90				
95													
Ser	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Arg	His	Tyr	Ala	Pro	Asn
Val	Pro												
		100						105				110	
Ile	Val	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys
Gln	Phe												
		115					120					125	
Leu	Ile	Asp	His	Pro	Gly	Ser	Ala	Arg	Ile	Thr	Thr	Ala	Gln
Ala	Phe												
	130					135					140		
Thr	Tyr	Ile	Glu	Cys	Ser	Ser	Lys	Thr	Gln	Gln	Asn	Val	Lys
Thr	Val												
145					150					155			
	160												
Phe	Asp	Ala	Ala	Ile	Lys	Val	Ala	Leu	Arg	Pro	Pro	Lys	Pro
Lys	Lys												
				165					170				
175													
Lys	Pro	Arg	Lys	Lys	Lys	Thr	Cys	Pro	Phe	Leu			
			180					185					

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 <211> 594
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<213> Glycine max

<220>

<221> CDS

<222> (1)..(594)

<400> 72

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atg agc aca aca cgg ttt att aag tgt gtc aca gtt ggt gat
ggg gct          48
Met Ser Thr Thr Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
  1              5              10
15
gtg gga aag act tgc atg ctt atc tct tac act agc aac act
ttc ccc          96
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
      20              25              30
acg gat tat gtt cct aca gtt ttc gac aat ttc agt gca aat
gtt gtg          144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
      35              40              45
gtt gat ggc agc aca gtt aac ctg gga ttg tgg gac act gct
gga cag          192
Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
      50              55              60
gaa gat tac aac agg ctt agg cca ttg agt tac aga gga gca
gat gtg          240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
      65              70              75
80
ttc ttg ctg gcc ttt tcc ctc atc agc aaa gcc agc tat gaa
aat ata          288
Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Ile
      85              90
95
tct aaa aag tgg att cct gaa ttg aga cat tat gcc cca act
gtg cct          336
Ser Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Thr
Val Pro
      100              105              110
att gta ctg gtt gga act aaa ctt gat ttg agg gaa gac agg
caa tat          384

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Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Glu Asp Arg
Gln Tyr

gga gaa 432
Leu Ile Asp His Pro Gly Thr Thr Ala Ile Ala Thr Ala Gln
Gly Glu

agc tca 480
Glu Leu Lys Lys Ala Ile Gly Ala Ala Val Tyr Ile Glu Cys
Ser Ser

aag act cag cag aat gtg aag gcc gtg ttt gat gct gca atc
aag gtt 528

175 165 170

Val Leu Gln Pro Pro Lys Ser Lys Lys Lys Gly Lys Lys Lys
Asn Thr 122 125 128

cct tgt gtt ttc ctc tga
594

<210> 73

<213> Glycine max

Gly Ala	5	10
1	5	10

Phe Pro 20 25 30

val	val	val	val
35	40	45	

0070110

Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65 70 75
80

Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Ile
85 90

95
Ser Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Thr
Val Pro
100 105 110

Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Glu Asp Arg
Gln Tyr
115 120 125

Leu Ile Asp His Pro Gly Thr Thr Ala Ile Ala Thr Ala Gln
Gly Glu
130 135 140

Glu Leu Lys Lys Ala Ile Gly Ala Ala Val Tyr Ile Glu Cys
Ser Ser
145 150 155
160

Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Lys Val
165 170

175
Val Leu Gln Pro Pro Lys Ser Lys Lys Lys Gly Lys Lys Lys
Asn Thr
180 185 190

Pro Cys Val Phe Leu
195

<210> 74
<211> 630
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (1)..(630)

0070110

<400> 74

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gga	gct			48									
Met	Asn	Ala	Ser	Lys	Phe	Ile	Lys	Cys	Val	Thr	Val	Gly	Asp
Gly	Ala												
1				5					10				
15													
ggt	ggg	aaa	acc	tgc	atg	ctc	att	tgc	tac	acc	agc	aac	aag
ttc	ccc			96									
Val	Gly	Lys	Thr	Cys	Met	Leu	Ile	Cys	Tyr	Thr	Ser	Asn	Lys
Phe	Pro												
			20					25					30
act	gat	tac	ata	cca	aca	gta	ttt	gat	aat	ttt	agt	gcc	aat
ggt	gct			144									
Thr	Asp	Tyr	Ile	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn
Val	Ala												
		35					40					45	
gtg	gat	gga	agc	att	gtc	aat	ttg	ggg	cta	tgg	gac	aca	gca
ggc	cag			192									
Val	Asp	Gly	Ser	Ile	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala
Gly	Gln												
		50				55					60		
gaa	gac	tac	agc	agg	ttg	agg	cca	ttg	agt	tat	aga	gga	gca
gac	att			240									
Glu	Asp	Tyr	Ser	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala
Asp	Ile												
65					70					75			
80													
ttt	gtc	tta	gca	ttc	tca	ctg	att	agc	aga	gct	agc	tat	gaa
aat	ggt			288									
Phe	Val	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Arg	Ala	Ser	Tyr	Glu
Asn	Val												
				85						90			
95													
ctc	aag	aag	tgg	atg	ccg	gaa	ttg	cgt	aga	ttt	gca	cct	aat
ggt	cca			336									
Leu	Lys	Lys	Trp	Met	Pro	Glu	Leu	Arg	Arg	Phe	Ala	Pro	Asn
Val	Pro												
			100					105					110
att	ggt	ctt	ggt	ggg	aca	aag	tta	gat	ctt	cgt	gaa	gac	cgg
ggg	tat			384									
Ile	Val	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Glu	Asp	Arg
Gly	Tyr												
		115					120					125	
gta	gct	gat	cac	atg	gga	tct	agc	gtc	ata	aca	tct	gct	gag
ggg	gaa			432									

0070110

Val	Ala	Asp	His	Met	Gly	Ser	Ser	Val	Ile	Thr	Ser	Ala	Glu
Gly	Glu												
	130					135					140		
gaa	ctg	agg	aaa	caa	att	ggt	gca	gta	gct	tac	ata	gag	tgc
agt	tca		480										
Glu	Leu	Arg	Lys	Gln	Ile	Gly	Ala	Val	Ala	Tyr	Ile	Glu	Cys
Ser	Ser												
145					150					155			
160													
aag	act	caa	cag	aat	gtc	aaa	gca	gtg	ttt	gac	act	gca	att
aag	ggt		528										
Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Thr	Ala	Ile
Lys	Val												
					165					170			
175													
ggt	ctc	caa	cct	cca	agg	agg	aaa	gaa	atg	gct	agg	aag	aaa
agg	cat		576										
Val	Leu	Gln	Pro	Pro	Arg	Arg	Lys	Glu	Met	Ala	Arg	Lys	Lys
Arg	His												
			180					185				190	
agg	agg	tct	ggt	tgc	tca	ttt	gta	agt	atc	atg	tgt	gga	ggc
tgt	gct		624										
Arg	Arg	Ser	Gly	Cys	Ser	Phe	Val	Ser	Ile	Met	Cys	Gly	Gly
Cys	Ala												
		195					200				205		
gct	taa												
			630										
Ala													

<210> 75
 <211> 209
 <212> PRT
 <213> Glycine max

<400> 75													
Met	Asn	Ala	Ser	Lys	Phe	Ile	Lys	Cys	Val	Thr	Val	Gly	Asp
Gly	Ala												
1				5					10				
15													
Val	Gly	Lys	Thr	Cys	Met	Leu	Ile	Cys	Tyr	Thr	Ser	Asn	Lys
Phe	Pro												
			20					25				30	
Thr	Asp	Tyr	Ile	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn
Val	Ala												
		35					40					45	

0070110

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

Ala

<210> 76
 <211> 591
 <212> DNA
 <213> Glycine max

0070110

<220>

<221> CDS

<222> (1)..(591)

<400> 76

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gga gcc 48
Met Ser Thr Ala Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10

15

gtg gga aag acc tgt atg ctc atc tct tac acc agc aac aca
ttc ccc 96
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro

20 25 30
acg gat tat gtt cct aca gtt ttt gac aac ttc agt gca aat
gtg gtg 144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val

35 40 45
gtt gat gga agc aca gtt aat ctc gga tta tgg gac act gct
gga cag 192
Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln

50 55 60
gag gat tac aac agg ctt agg ccc ttg agc tac aga gga gca
gat gtg 240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65 70 75

80

ttt ttg ctt gca ttt tcc ctc ctc agc aga gcc agc tat gaa
aat atc 288
Phe Leu Leu Ala Phe Ser Leu Leu Ser Arg Ala Ser Tyr Glu
Asn Ile

95

85 90
tct aag aag tgg att cct gaa ctg aga cat tat gcc ccc act
gtg cca 336
Ser Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Thr
Val Pro

100 105 110

att gta ctt gtg gga acc aaa ctt gat ttg agg gaa gat agg
cag tat 384
Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Glu Asp Arg

0070110

Gln	Tyr															
		115						120						125		
ttg	att	gat	cat	cct	gga	gcc	aca	cct	ata	act	act	gct	cag			
gca	gaa	432														
Leu	Ile	Asp	His	Pro	Gly	Ala	Thr	Pro	Ile	Thr	Thr	Ala	Gln			
Ala	Glu															
	130						135						140			
gag	ctg	aag	aag	gca	att	ggt	gct	gct	gtg	tac	ata	gaa	tgc			
agc	tca	480														
Glu	Leu	Lys	Lys	Ala	Ile	Gly	Ala	Ala	Val	Tyr	Ile	Glu	Cys			
Ser	Ser															
145						150						155				
160																
aag	act	cag	cag	aat	gtg	aag	gct	gtg	ttt	gat	gct	gca	atc			
aag	gtt	528														
Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile			
Lys	Val															
					165						170					
175																
gtt	ttg	cag	cca	cca	aag	cca	aag	aaa	aaa	aga	aag	aag	aac			
agg	aca	576														
Val	Leu	Gln	Pro	Pro	Lys	Pro	Lys	Lys	Lys	Arg	Lys	Lys	Asn			
Arg	Thr															
					180						185					
190																
tgc	gtt	ttc	ctt	taa												
		591														
Cys	Val	Phe	Leu													
		195														

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<210> 77
<211> 196
<212> PRT
<213> Glycine max
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<400> 77
Met Ser Thr Ala Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1          5          10
15
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
          20          25          30
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
          35          40          45

```

0070110

Val	Asp	Gly	Ser	Thr	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala
Gly	Gln												
	50					55					60		

Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala
Asp	Val												
65					70					75			

	80												
Phe	Leu	Leu	Ala	Phe	Ser	Leu	Leu	Ser	Arg	Ala	Ser	Tyr	Glu
Asn	Ile												

				85					90				
95													
Ser	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Arg	His	Tyr	Ala	Pro	Thr
Val	Pro												

			100					105				110	
Ile	Val	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Glu	Asp	Arg
Gln	Tyr												

			115				120					125	
Leu	Ile	Asp	His	Pro	Gly	Ala	Thr	Pro	Ile	Thr	Thr	Ala	Gln
Ala	Glu												

						135					140		
Glu	Leu	Lys	Lys	Ala	Ile	Gly	Ala	Ala	Val	Tyr	Ile	Glu	Cys
Ser	Ser												

						150				155			
160													
Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile
Lys	Val												

						165				170			
175													
Val	Leu	Gln	Pro	Pro	Lys	Pro	Lys	Lys	Lys	Arg	Lys	Lys	Asn
Arg	Thr												

0070110

<400> 78

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

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0070110

[illegible]

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<210> 79
<211> 212
<212> PRT
<213> Glycine max
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<400> 79
Met Ala Ser Ala Thr Ala Pro Arg Phe Ile Lys Cys Val Thr
Val Gly
1          5          10
15
Asp Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr
Ser Asn
          20          25          30
Lys Phe Pro Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe
Ser Ala
          35          40          45

```

0070110

Asn Val Val Val Glu Gly Ile Thr Val Asn Leu Gly Leu Trp
 Asp Thr
 50 55 60

Ala Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr
 Arg Gly
 65 70 75

80
 Ala Asp Val Phe Val Leu Ala Phe Ser Leu Val Ser Arg Ala
 Ser Tyr
 85 90

95
 Glu Asn Val Leu Lys Lys Trp Ile Pro Glu Leu Gln His Phe
 Ala Pro
 100 105 110

Gly Ile Pro Leu Val Leu Val Gly Thr Lys Leu Asp Leu Arg
 Glu Asp
 115 120 125

Lys His Tyr Met Ala Asp His Pro Ser Leu Val Pro Val Thr
 Thr Asp
 130 135 140

Gln Gly Glu Glu Leu Arg Lys His Ile Gly Ala Thr Tyr Tyr
 Ile Glu
 145 150 155

160
 Cys Ser Ser Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp
 Ala Ala
 165 170

175
 Ile Arg Met Val Ile Lys Pro Pro Gln Lys Gln Asn Glu Lys
 Arg Lys
 180 185 190

Lys Lys Pro Arg Gly Cys Phe Leu Asn Val Leu Cys Arg Arg
 Asn Ile
 195 200 205

Val Arg Leu Lys
 210

<210> 80
 <211> 745
 <212> DNA
 <213> Glycine max

0070110

<220>

<221> CDS

<222> (19)..(612)

<400> 80

tagatctctg atctgaag atg agt gcg tcg agg ttc att aag tgc
gtc acc 51

Met Ser Ala Ser Arg Phe Ile Lys Cys
Val Thr

1

5

10

gtc ggc gac ggc gct gtc ggc aaa acc tgc ttg ttg att tcc
tac acc 99

Val Gly Asp Gly Ala Val Gly Lys Thr Cys Leu Leu Ile Ser
Tyr Thr

15

20

25

agc aac act ttt ccc acg gac tac gtg ccc acg gtt ttt gac
aat ttc 147

Ser Asn Thr Phe Pro Thr Asp Tyr Val Pro Thr Val Phe Asp
Asn Phe

30

35

40

agt gct aat gtt gtg gtg gat gga agc acc gta aac ttg gca
ttg tgg 195

Ser Ala Asn Val Val Val Asp Gly Ser Thr Val Asn Leu Ala
Leu Trp

45

50

55

gat act gct ggt cag gaa gat tat aat agg ctt aga ccc ttg
agc tat 243

Asp Thr Ala Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu
Ser Tyr

60

65

70

75

cga gga gct gat gtt ttt ata ctt gcc ttt tct ctc ata agc
aag gct 291

Arg Gly Ala Asp Val Phe Ile Leu Ala Phe Ser Leu Ile Ser
Lys Ala

80

85

90

agc tat gaa aat att gca aag aag tgg atc cct gaa cta agg
cat tat 339

Ser Tyr Glu Asn Ile Ala Lys Lys Trp Ile Pro Glu Leu Arg
His Tyr

95

100

105

gcc cct ggt gtt cca ata att ctc gtt gga aca aag tta gat
ctt cgg 387

Ala Pro Gly Val Pro Ile Ile Leu Val Gly Thr Lys Leu Asp
Leu Arg

0070110

	110		115		120
gaa	gat	aag	caa	ttt	ttt
att	act		435	atg	gac
Glu	Asp	Lys	Gln	Phe	Phe
Ile	Thr			Met	Asp
	125		130		135
aca	gca	cag	gga	gaa	gaa
gcc	tac		483	tta	aga
Thr	Ala	Gln	Gly	Glu	Glu
Ala	Tyr			Leu	Arg
140			145		150
155					
atc	gag	tgt	agt	tca	aaa
ttt	gac		531	aca	cag
Ile	Glu	Cys	Ser	Ser	Lys
Phe	Asp			Thr	Gln
			160		165
170					
gct	gcc	atc	aaa	gtg	ggt
aag	aag		579	ctt	caa
Ala	Ala	Ile	Lys	Val	Val
Lys	Lys			Leu	Gln
			175		180
					185

aga aag gca caa aaa gct tgc tca ata ttg tgattaagaa
tcagaaggct 629
Arg Lys Ala Gln Lys Ala Cys Ser Ile Leu

190	195
tgctcaatag	tatgatttaa
tctggccaac	689
	gaaccagaga
	ttaataggag
	gtattgactg

ctttaatgct gcctcccat tggtttttct tgttttgggtc gctatccttt
gtagcg 745

<210> 81
<211> 197
<212> PRT
<213> Glycine max

<400> 81
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala

0070110

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

0070110

<210> 82
<211> 591
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (1)..(591)

<400> 82
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ggt gct 48
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10
15
gtc ggc aaa acc tgc ttg ttg att tcc tac acc agc aac act
ttt ccc 96
Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
20 25 30
acg gac tat gtg ccc acc gtt ttt gac aat ttc agt gct aat
gtg gtg 144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
35 40 45
gtg gat gga agc acc gta aac cta gga ttg tgg gat aca gct
ggt cag 192
Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60
gag gat tac aat aga tta aga ccc ttg agc tat cga gga gct
gat gtc 240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65 70 75
80
ttc ata ctt gcc ttt tct ctc ata agc aag gct agc tat gaa
aat att 288
Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Ile
85 90
95
gca aag aag tgg atc cct gaa cta agg cat tat gcc cct ggt
gtt cca 336
Ala Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Gly
Val Pro

0070110

100

105

110

ata att ctc gtt gga aca aag tta gat ctt cgg gat gat aag
 caa ttt 384
 Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
 Gln Phe

115 120 125
 ttt atg gac cat cct ggt gca gtg cca att act aca gca cag
 gga gaa 432
 Phe Met Asp His Pro Gly Ala Val Pro Ile Thr Thr Ala Gln
 Gly Glu

130 135 140
 gaa ttg aga aag ctg att ggt gct ccg gcc tac att gag tgt
 agt tcc 480
 Glu Leu Arg Lys Leu Ile Gly Ala Pro Ala Tyr Ile Glu Cys
 Ser Ser

145 150 155
 160
 aaa acg caa cag aac gtg aaa gct gtc ttt gac gcg gca atc
 aaa gtg 528
 Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
 Lys Val

165 170
 175
 gtt atc caa cca cca aag cta aag aaa aag aga aaa aca cag
 aaa gct 576
 Val Ile Gln Pro Pro Lys Leu Lys Lys Lys Arg Lys Thr Gln
 Lys Ala

180 185 190
 tgc tcc ata tta tga
 591
 Cys Ser Ile Leu
 195

<210> 83
 <211> 196
 <212> PRT
 <213> Glycine max

<400> 83
 Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala
 1 5 10
 15
 Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
 Phe Pro

0070110

20

25

30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val 35 40 45

Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln 50 55 60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val 65 70 75

80
Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Ile 85 90

95
Ala Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Gly
Val Pro 100 105 110

Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe 115 120 125

Phe Met Asp His Pro Gly Ala Val Pro Ile Thr Thr Ala Gln
Gly Glu 130 135 140

Glu Leu Arg Lys Leu Ile Gly Ala Pro Ala Tyr Ile Glu Cys
Ser Ser 145 150 155

160
Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Lys Val 165 170

175
Val Ile Gln Pro Pro Lys Leu Lys Lys Lys Arg Lys Thr Gln
Lys Ala 180 185 190

Cys Ser Ile Leu
195

<210> 84
<211> 582
<212> DNA

<213> *Ciona intestinalis*

<220>

<221> CDS

<222> (1)..(582)

<400> 84

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atg gct tca att cgt aag aag ctg gta ata gtt ggt gat ggt
gct tgt          48
Met Ala Ser Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly
Ala Cys
  1              5              10
15
ggg aaa act tgc tta ctc atc gtg ttt agc aaa gat caa ttc
cca gaa          96
Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Asp Gln Phe
Pro Glu
      20              25              30
gtt tac gtc cca act gtt ttt gaa aac tat gtg gct gat att
gaa gta          144
Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Ile
Glu Val
      35              40              45
gac tct aaa cag gtt gag ctt gct ttg tgg gat aca gct ggt
caa gaa          192
Asp Ser Lys Gln Val Glu Leu Ala Leu Trp Asp Thr Ala Gly
Gln Glu
      50              55              60
gat tac gac agg ctt cgt cca ctt tcc tac ccc gat act gat
gtt att          240
Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Thr Asp
Val Ile
      65              70              75
80
ctt atg tgt ttc tca atc gac agc cca gat tca ctt gag aac
att ccc          288
Leu Met Cys Phe Ser Ile Asp Ser Pro Asp Ser Leu Glu Asn
Ile Pro
      85              90
95
gaa aaa tgg acc cct gag gta agg cat ttt tgc cca agt gtt
cca atc          336
Glu Lys Trp Thr Pro Glu Val Arg His Phe Cys Pro Ser Val
Pro Ile
      100              105              110
att ttg gtt gga aac aaa aaa gat ctt cgt aac gac agt tca
aca ata          384

```

0070110

Ile	Leu	Val	Gly	Asn	Lys	Lys	Asp	Leu	Arg	Asn	Asp	Ser	Ser
Thr	Ile												
		115					120					125	
aag	gaa	ctt	gct	aaa	atg	aaa	caa	tct	gcc	ggt	agt	aac	gaa
gat	gga		432										
Lys	Glu	Leu	Ala	Lys	Met	Lys	Gln	Ser	Ala	Val	Ser	Asn	Glu
Asp	Gly												
	130					135					140		
atg	gcg	atg	gca	gag	aag	att	ggc	gct	tac	gga	tat	atg	gaa
tgt	tca		480										
Met	Ala	Met	Ala	Glu	Lys	Ile	Gly	Ala	Tyr	Gly	Tyr	Met	Glu
Cys	Ser												
145					150					155			
160													
gcg	cgc	acc	aaa	gaa	ggc	ggt	ggt	cgg	gaa	gtg	ttt	gag	ctt
act	aaa		528										
Ala	Arg	Thr	Lys	Glu	Gly	Val	Arg	Glu	Val	Phe	Glu	Leu	Ala
Thr	Lys												
			165						170				
175													
gca	gct	tta	caa	acc	aag	aaa	aga	aag	aaa	aag	agt	gga	tgt
gaa	gtc		576										
Ala	Ala	Leu	Gln	Thr	Lys	Lys	Arg	Lys	Lys	Lys	Ser	Gly	Cys
Glu	Val												
			180					185				190	
ttg	taa												
Leu			582										

<210> 85
 <211> 193
 <212> PRT
 <213> Ciona intestinalis

<400> 85													
Met	Ala	Ser	Ile	Arg	Lys	Lys	Leu	Val	Ile	Val	Gly	Asp	Gly
Ala	Cys												
1				5					10				
15													
Gly	Lys	Thr	Cys	Leu	Leu	Ile	Val	Phe	Ser	Lys	Asp	Gln	Phe
Pro	Glu												
			20					25				30	
Val	Tyr	Val	Pro	Thr	Val	Phe	Glu	Asn	Tyr	Val	Ala	Asp	Ile
Glu	Val												
		35					40					45	

0070110

Asp Ser Lys Gln Val Glu Leu Ala Leu Trp Asp Thr Ala Gly
Gln Glu
50 55 60

Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Thr Asp
Val Ile
65 70 75
80

Leu Met Cys Phe Ser Ile Asp Ser Pro Asp Ser Leu Glu Asn
Ile Pro
85 90

95
Glu Lys Trp Thr Pro Glu Val Arg His Phe Cys Pro Ser Val
Pro Ile
100 105 110

Ile Leu Val Gly Asn Lys Lys Asp Leu Arg Asn Asp Ser Ser
Thr Ile
115 120 125

Lys Glu Leu Ala Lys Met Lys Gln Ser Ala Val Ser Asn Glu
Asp Gly
130 135 140

Met Ala Met Ala Glu Lys Ile Gly Ala Tyr Gly Tyr Met Glu
Cys Ser
145 150 155
160

Ala Arg Thr Lys Glu Gly Val Arg Glu Val Phe Glu Leu Ala
Thr Lys
165 170

175
Ala Ala Leu Gln Thr Lys Lys Arg Lys Lys Lys Ser Gly Cys
Glu Val
180 185 190

Leu

<210> 86
<211> 576
<212> DNA
<213> Ciona intestinalis

<220>
<221> CDS
<222> (1)..(576)

0070110

<400> 86

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

```

0070110

```

Leu Ser Lys Asn Lys Gln Lys Ala Ile Thr Gln Asp Met Gly
Asp Lys
130 135 140
ctt gca agg gaa tta aaa gct gta aaa tat gtt gaa tgt tca
gct ctg 480
Leu Ala Arg Glu Leu Lys Ala Val Lys Tyr Val Glu Cys Ser
Ala Leu
145 150 155
160
act cag aaa gga tta aag aat gta ttt gat gaa gcc ata tta
gct gct 528
Thr Gln Lys Gly Leu Lys Asn Val Phe Asp Glu Ala Ile Leu
Ala Ala
165 170
175
ttg gaa cct cct gaa ccg aag cgt cgt cga cgt tgt caa gtc
ttg 573
Leu Glu Pro Pro Glu Pro Lys Arg Arg Arg Arg Cys Gln Val
Leu
180 185 190
tga
576

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<210> 87
 <211> 191
 <212> PRT
 <213> Ciona intestinalis

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<400> 87
Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys
1 5 10
15
Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe Pro Gln
Glu Tyr
20 25 30
Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val Met Ile
Gly Gly
35 40 45
Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu
Asp Tyr
50 55 60

```

0070110

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

<210> 88
 <211> 579
 <212> DNA
 <213> Ciona intestinalis

<220>
 <221> CDS
 <222> (1)..(579)

<400> 88
 atg cag gcg atc aag tgt gtt gtg gtt gga gat gga gct gtt
 ggt aaa 48
 Met Gln Ala Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
 Gly Lys
 1 5 10

0070110

```

15
acc tgt ttg ctg atc agc tac aca acc aat gct ttc cct gga
gaa tat          96
Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Ala Phe Pro Gly
Glu Tyr

          20          25          30
att ccc act gtg ttt gat aac tac tct gcc aat gtc atg gta
gat ggc          144
Ile Pro Thr Val Phe Asp Asn Tyr Ser Ala Asn Val Met Val
Asp Gly

          35          40          45
cgc cct gtc aac ttg gga tta tgg gat aca gca ggg cag gag
gat tac          192
Arg Pro Val Asn Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu
Asp Tyr

          50          55          60
gac aga ctt cgg cct ctc tcc tac cca caa acg gac gtt ttt
ctg atc          240
Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
Leu Ile

          65          70          75
          80
tgt ttc tca ctc gtg tca cca gcc tca ttc gaa aac gtg cgc
gca aag          288
Cys Phe Ser Leu Val Ser Pro Ala Ser Phe Glu Asn Val Arg
Ala Lys

          85          90
95
tgg tat cca gaa gtc gca cac cac tgt cca gat aca ccg gtc
att ctc          336
Trp Tyr Pro Glu Val Ala His His Cys Pro Asp Thr Pro Val
Ile Leu

          100          105          110
gtg gga aca aaa ctt gat tta cgt gac gac cag gaa acc atc
caa aag          384
Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Gln Glu Thr Ile
Gln Lys

          115          120          125
ctg aaa gaa aag aaa ctt gcc cca atc ctc tac cca caa ggg
ttg cag          432
Leu Lys Glu Lys Lys Leu Ala Pro Ile Leu Tyr Pro Gln Gly
Leu Gln

          130          135          140
atg gcg aaa gaa gtg aac gcc gta aag tac ctg gag tgc tcg
gct ctc          480
Met Ala Lys Glu Val Asn Ala Val Lys Tyr Leu Glu Cys Ser
Ala Leu

```

				150				155					
160													
acc	caa	aaa	ggc	ctg	aaa	acc	gtt	ttc	gac	gag	gcg	atc	cgc
gcc	gtc		528										
Thr	Gln	Lys	Gly	Leu	Lys	Thr	Val	Phe	Asp	Glu	Ala	Ile	Arg
Ala	Val												
				165				170					
175													
ctg	tgc	cct	gag	caa	aag	ccg	aag	aaa	aag	aag	ccc	tgc	gag
ctt	ttg		576										
Leu	Cys	Pro	Glu	Gln	Lys	Pro	Lys	Lys	Lys	Lys	Pro	Cys	Glu
Leu	Leu												
				180				185				190	
tga													
				579									

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<210> 89
<211> 192
<212> PRT
<213> Ciona intestinalis
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<400> 89
Met Gln Ala Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys
1          5          10
15
Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Ala Phe Pro Gly
Glu Tyr
20          25          30
Ile Pro Thr Val Phe Asp Asn Tyr Ser Ala Asn Val Met Val
Asp Gly
35          40          45
Arg Pro Val Asn Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu
Asp Tyr
50          55          60
Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
Leu Ile
65          70          75
80
Cys Phe Ser Leu Val Ser Pro Ala Ser Phe Glu Asn Val Arg
Ala Lys
85          90

```


0070110

```

95
Trp Tyr Pro Glu Val Ala His His Cys Pro Asp Thr Pro Val
Ile Leu
      100                      105                      110

Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Gln Glu Thr Ile
Gln Lys
      115                      120                      125

Leu Lys Glu Lys Lys Leu Ala Pro Ile Leu Tyr Pro Gln Gly
Leu Gln
      130                      135                      140

Met Ala Lys Glu Val Asn Ala Val Lys Tyr Leu Glu Cys Ser
Ala Leu
      145                      150                      155
      160
Thr Gln Lys Gly Leu Lys Thr Val Phe Asp Glu Ala Ile Arg
Ala Val
      165                      170

175
Leu Cys Pro Glu Gln Lys Pro Lys Lys Lys Lys Pro Cys Glu
Leu Leu
      180                      185                      190

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<210> 90
 <211> 582
 <212> DNA
 <213> *Ciona intestinalis*

<220>
 <221> CDS
 <222> (1)..(582)

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<400> 90
atg gct agc atg tta agg tgt gta gtg gta gga gac ggc gca
gtg ggt
Met Ala Ser Met Leu Arg Cys Val Val Val Gly Asp Gly Ala
Val Gly
      1                      5                      10
15
aag acc agt atg ctt atc agt tac aca aaa ggg ggt ttc cca
gac gaa
Lys Thr Ser Met Leu Ile Ser Tyr Thr Lys Gly Gly Phe Pro
Asp Glu
      20                      25                      30
tat gtt cca acg ata ctt gat cag tat gcg gca acg att act

```

0070110

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

0070110

175
 gtg ttg tac cca gag gaa aaa tct agc gag aaa aag aat tgt
 aca ata 576
 Val Leu Tyr Pro Glu Glu Lys Ser Ser Glu Lys Lys Asn Cys
 Thr Ile
 180 185 190

tct taa
 582
 Ser

<210> 91
 <211> 193
 <212> PRT
 <213> Ciona intestinalis

<400> 91
 Met Ala Ser Met Leu Arg Cys Val Val Val Gly Asp Gly Ala
 Val Gly
 1 5 10
 15
 Lys Thr Ser Met Leu Ile Ser Tyr Thr Lys Gly Gly Phe Pro
 Asp Glu
 20 25 30

Tyr Val Pro Thr Ile Leu Asp Gln Tyr Ala Ala Thr Ile Thr
 Val Gly
 35 40 45

Gly Thr Pro Tyr Val Leu Glu Leu Ile Asp Thr Ala Gly Gln
 Glu Asp
 50 55 60

Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Asn Lys Ala Asp Val
 Phe Leu
 65 70 75

80
 Val Cys Tyr Ser Val Val Val Pro Ser Ser Phe Thr Asn Ile
 Lys Glu
 85 90

95
 Thr Trp Ile Pro Glu Leu Lys Gln His Ser Thr Lys Val Pro
 Tyr Ile
 100 105 110

Leu Val Gly Thr Gln Thr Asp Leu Arg Asp Asp Pro Arg Val
 Leu Gln

						0070110							
		115				120						125	
Glu	Leu	His	Lys	Lys	Lys	Gln	Lys	Pro	Val	Asn	Val	Glu	Ser
Gly	Gln												
	130					135						140	
Arg	Arg	Ala	Ala	Lys	Leu	Gly	Ala	Ala	Ala	Tyr	Lys	Glu	Cys
Ser	Ala												
145					150					155			
160													
Val	Thr	Met	Asn	Gly	Ile	Lys	Asp	Val	Phe	Asp	Glu	Ala	Ile
His	Thr												
				165					170				
175													
Val	Leu	Tyr	Pro	Glu	Glu	Lys	Ser	Ser	Glu	Lys	Lys	Asn	Cys
Thr	Ile												
			180					185				190	

Ser

<210> 92
 <211> 579
 <212> DNA
 <213> Ciona intestinalis

<220>
 <221> CDS
 <222> (1)..(579)

<400> 92
 atg caa gcg ata aag tgc gtt gtg gtt gga gat gga gct gtt
 ggt aaa 48
 Met Gln Ala Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
 Gly Lys 1 5 10
 15
 acc tgt ttg ctg atc agc tac aca act aac gct ttc cct gga
 gaa tat 96
 Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Ala Phe Pro Gly
 Glu Tyr 20 25 30
 att ccc act gtg ttt gat aac tac tct gcc aat gtc atg gta
 gat ggc 144
 Ile Pro Thr Val Phe Asp Asn Tyr Ser Ala Asn Val Met Val
 Asp Gly 35 40 45
 cgc cct gtc aac ttg gga tta tgg gat aca gca gga cag gag

0070110

gat	tat		192											
Arg	Pro	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala	Gly	Gln	Glu	
Asp	Tyr													
	50					55					60			
gac	aga	ctc	cga	cct	ctc	tcc	tac	cca	caa	acc	gat	gtt	ttt	
ctc	att		240											
Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Pro	Gln	Thr	Asp	Val	Phe	
Leu	Ile													
65					70					75				
80														
tgt	ttc	tct	gtg	gct	tct	ccc	gct	tcc	tac	gaa	aac	gtg	cgc	
gca	aag		288											
Cys	Phe	Ser	Val	Ala	Ser	Pro	Ala	Ser	Tyr	Glu	Asn	Val	Arg	
Ala	Lys													
			85						90					
95														
tgg	cac	ccg	gag	gtc	gca	cac	cac	tgc	ccg	gaa	acg	ccc	gta	
ctt	ctc		336											
Trp	His	Pro	Glu	Val	Ala	His	His	Cys	Pro	Glu	Thr	Pro	Val	
Leu	Leu													
			100					105					110	
gtg	gga	aca	aaa	ctt	gat	tta	cgt	gac	gat	gcg	gac	act	gtg	
aac	aag		384											
Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Ala	Asp	Thr	Val	
Asn	Lys													
		115					120					125		
cta	gct	gag	aaa	aag	ctc	tcc	acc	att	act	act	acc	caa	ggt	
tta	caa		432											
Leu	Ala	Glu	Lys	Lys	Leu	Ser	Thr	Ile	Thr	Thr	Thr	Gln	Gly	
Leu	Gln													
		130				135					140			
atg	gcg	aag	gaa	ctg	ggg	gcg	ggt	aaa	tac	caa	gag	tgc	tct	
gct	ctg		480											
Met	Ala	Lys	Glu	Leu	Gly	Ala	Val	Lys	Tyr	Gln	Glu	Cys	Ser	
Ala	Leu													
145					150					155				
160														
acg	caa	aag	ggg	ctg	aaa	aat	ggt	ttc	gac	gaa	gcg	att	cgg	
gcg	ggt		528											
Thr	Gln	Lys	Gly	Leu	Lys	Asn	Val	Phe	Asp	Glu	Ala	Ile	Arg	
Ala	Val													
			165						170					
175														
ctt	aac	cca	aca	aga	aga	gtc	gtc	cga	acg	aag	aac	tgc	gaa	
att	cta		576											
Leu	Asn	Pro	Thr	Arg	Arg	Val	Val	Arg	Thr	Lys	Asn	Cys	Glu	
Ile	Leu													

0070110

180

185

190

tga

579

<210> 93

<211> 192

<212> PRT

<213> Ciona intestinalis

<400> 93

Met Gln Ala Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys

1 5 10

15

Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Ala Phe Pro Gly
Glu Tyr

20

25

30

Ile Pro Thr Val Phe Asp Asn Tyr Ser Ala Asn Val Met Val
Asp Gly

35

40

45

Arg Pro Val Asn Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu
Asp Tyr

50

55

60

Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
Leu Ile

65

70

75

80

Cys Phe Ser Val Ala Ser Pro Ala Ser Tyr Glu Asn Val Arg
Ala Lys

85

90

95

Trp His Pro Glu Val Ala His His Cys Pro Glu Thr Pro Val
Leu Leu

100

105

110

Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Ala Asp Thr Val
Asn Lys

115

120

125

Leu Ala Glu Lys Lys Leu Ser Thr Ile Thr Thr Thr Gln Gly
Leu Gln

130

135

140

0070110

Met Ala Lys Glu Leu Gly Ala Val Lys Tyr Gln Glu Cys Ser
Ala Leu
145 150 155
160
Thr Gln Lys Gly Leu Lys Asn Val Phe Asp Glu Ala Ile Arg
Ala Val
165 170
175
Leu Asn Pro Thr Arg Arg Val Val Arg Thr Lys Asn Cys Glu
Ile Leu
180 185 190

<210> 94
<211> 582
<212> DNA
<213> *Ciona intestinalis*

<220>
<221> CDS
<222> (1)..(582)

<400> 94
atg cag tcc gtg aaa tgt gtt gtg gtt gga gat gga gct gtt
ggt aaa 48
Met Gln ser val Lys Cys val val val Gly Asp Gly Ala val
Gly Lys 5 10
15
acc tgt ttg ctg atc agc tac aca acc aat gct ttc cct gga
gaa tat 96
Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Ala Phe Pro Gly
Glu Tyr 20 25 30
att ccc act gtg ttt gaa agc tat gct gca aat gtt gtg gtg
gat ggg 144
Ile Pro Thr val Phe Glu Ser Tyr Ala Ala Asn val val val
Asp Gly 35 40 45
aac cca gtg aac atc ggt tta tgg gac aca gct ggc cag gaa
gat tac 192
Asn Pro val Asn Ile Gly Leu Trp Asp Thr Ala Gly Gln Glu
Asp Tyr 50 55 60
gat aaa ctt cga ccg cta tca tac cca cag tca gat gtc ttt
gtc atg 240
Asp Lys Leu Arg Pro Leu Ser Tyr Pro Gln Ser Asp val Phe

0070110

Val Met													
65					70					75			
80													
tgc ttc	tcg ttg gta	aac cca aca	tct tat	gaa aac	att gca								
gaa aaa	288												
Cys Phe	Ser Leu Val	Asn Pro Thr	Ser Tyr	Glu Asn	Ile Ala								
Glu Lys													
	85									90			
95													
tgg tat	ccg gaa gtt	cat gaa cac	tgt ccc	gac atc	ccc att								
gta ctc	336												
Trp Tyr	Pro Glu Val	His Glu His	Cys Pro	Asp Ile	Pro Ile								
Val Leu													
	100									105			110
gtt ggg	aca aaa ctg	gat tta cgt	gaa gac	cca gaa	aca ctc								
aaa acg	384												
Val Gly	Thr Lys Leu	Asp Leu Arg	Glu Asp	Pro Glu	Thr Leu								
Lys Thr													
	115												
ttg ggt	gag aga aat	ctt gtt cca	ggt acc	aaa acc	cag ggc								
ctc cag	432												
Leu Gly	Glu Arg Asn	Leu Val Pro	Val Thr	Lys Thr	Gln Gly								
Leu Gln													
	130												
ttg gcg	aaa aaa gtt	ggg gca aag	aaa tat	ttt gag	tgc tcg								
gcg ctt	480												
Leu Ala	Lys Lys Val	Gly Ala Lys	Lys Tyr	Phe Glu	Cys Ser								
Ala Leu													
	145												
	150												
act cgt	gaa aac tta	gac gaa ctc	ttt ctt	gaa gca	atg cgc								
aat gcc	528												
Thr Arg	Glu Asn Leu	Asp Glu Leu	Phe Leu	Glu Ala	Met Arg								
Asn Ala													
	165												
175													
ctg aaa	gga ccg gac	aaa att	gta aaa	gag aaa	cca aat	tgt							
caa att	576												
Leu Lys	Gly Pro Asp	Lys Ile Val	Lys Glu	Lys Pro	Asn Cys								
Gln Ile													
	180												
atc taa													
	582												
Ile													

0070110

<210> 95
<211> 193
<212> PRT
<213> Ciona intestinalis

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

0070110

165

170

175
Leu Lys Gly Pro Asp Lys Ile Val Lys Glu Lys Pro Asn Cys
Gln Ile

180

185

190

Ile

<210> 96

<211> 582

<212> DNA

<213> *Ciona intestinalis*

<220>

<221> CDS

<222> (1)..(582)

<400> 96

atg cag agt gta aaa tgc gtt gtt gtt ggg gat ggt gca gtt
gga aaa 48
Met Gln ser Val Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys

1

5

10

15

acg agt atg ata ata acc tat aca acc aac gga ttt cca caa
gat aat 96
Thr Ser Met Ile Ile Thr Tyr Thr Thr Asn Gly Phe Pro Gln
Asp Asn

20

25

30

gta cca tcg gta ttg gat aat cat aca tca aat atc atg gta
gat gga 144
Val Pro Ser Val Leu Asp Asn His Thr Ser Asn Ile Met Val
Asp Gly

35

40

45

aag cca att aac ctt agt ttg aac gac acg gct tcg gca gaa
aaa tac 192
Lys Pro Ile Asn Leu Ser Leu Asn Asp Thr Ala Ser Ala Glu
Lys Tyr

50

55

60

gac agg ctt cgg cct ctt tcc ttt cca caa acg gac gtt ttt
ctg atc 240
Asp Arg Leu Arg Pro Leu Ser Phe Pro Gln Thr Asp Val Phe
Leu Ile

65

70

75

80

tgt ttc tca ctg gtg tca cca cct tca ttt gaa aac gtg cgc

0070110

gca aag 288
Cys Phe Ser Leu Val Ser Pro Pro Ser Phe Glu Asn Val Arg
Ala Lys

85

90

95

tgg ttc cca gac gta cat cat cat aat ccg acc aca ccc gtg
gta ctt 336
Trp Phe Pro Asp Val His His His Asn Pro Thr Thr Pro Val
Val Leu

100

105

110

gtc ggc acc aag ctc gat cta cga gat gac cag gaa ttc gtc
gca aag 384
Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Gln Glu Phe Val
Ala Lys

115

120

125

cta gag gag aag aat cta tca cct att gca aca gcg caa ggt
ttg cag 432
Leu Glu Glu Lys Asn Leu Ser Pro Ile Ala Thr Ala Gln Gly
Leu Gln

130

135

140

atg caa aac gat atc agg gct gtc aaa tat ttg gag tgt tct
gcc ctc 480
Met Gln Asn Asp Ile Arg Ala Val Lys Tyr Leu Glu Cys Ser
Ala Leu

145

150

155

160

act caa gca ggg ttg caa gcc gta ttt att gaa gcc gct gaa
gct gcc 528
Thr Gln Ala Gly Leu Gln Ala Val Phe Ile Glu Ala Ala Glu
Ala Ala

165

170

175

ttg aac cca gtt tac cag cag cct cca ttg aaa aag aaa tgt
ttg gtc 576

Leu Asn Pro Val Tyr Gln Gln Pro Pro Leu Lys Lys Lys Cys
Leu Val

180

185

190

cta taa

582

Leu

<210> 97
<211> 193
<212> PRT

0070110

<213> Ciona intestinalis

<400> 97

Met Gln Ser Val Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys

1 5 10

15

Thr Ser Met Ile Ile Thr Tyr Thr Thr Asn Gly Phe Pro Gln
Asp Asn

20 25 30

Val Pro Ser Val Leu Asp Asn His Thr Ser Asn Ile Met Val
Asp Gly

35 40 45

Lys Pro Ile Asn Leu Ser Leu Asn Asp Thr Ala Ser Ala Glu
Lys Tyr

50 55 60

Asp Arg Leu Arg Pro Leu Ser Phe Pro Gln Thr Asp Val Phe
Leu Ile

65 70 75

80

Cys Phe Ser Leu Val Ser Pro Pro Ser Phe Glu Asn Val Arg
Ala Lys

85 90

95

Trp Phe Pro Asp Val His His His Asn Pro Thr Thr Pro Val
Val Leu

100 105 110

Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Gln Glu Phe Val
Ala Lys

115 120 125

Leu Glu Glu Lys Asn Leu Ser Pro Ile Ala Thr Ala Gln Gly
Leu Gln

130 135 140

Met Gln Asn Asp Ile Arg Ala Val Lys Tyr Leu Glu Cys Ser
Ala Leu

145 150 155

160

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

165 170

175

Leu Asn Pro Val Tyr Gln Gln Pro Pro Leu Lys Lys Lys Cys

0070110

Leu Val 180 185 190

Leu

<210> 98
 <211> 579
 <212> DNA
 <213> Ciona intestinalis

<220>
 <221> CDS
 <222> (1)..(579)

<400> 98
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 gga aaa 48
 Met Gln Pro Val Lys Ile Val Val Val Gly Asp Gly Ala Val
 Gly Lys 1 5 10
 15
 aca tgt atg tgc att act tat gca aac ggg gta ttt cct agt
 gac tat 96
 Thr Cys Met Cys Ile Thr Tyr Ala Asn Gly Val Phe Pro Ser
 Asp Tyr 20 25 30
 gtg ccc acc ata ttc gac aac tat gca gca aca agc acg ttt
 gag gga 144
 Val Pro Thr Ile Phe Asp Asn Tyr Ala Ala Thr Ser Thr Phe
 Glu Gly 35 40 45
 att tcc tat aac tta gca ctc tgg gac acg gca gga caa gaa
 gaa tat 192
 Ile Ser Tyr Asn Leu Ala Leu Trp Asp Thr Ala Gly Gln Glu
 Glu Tyr 50 55 60
 gac agg ttg aga ccg ttg agt tac cca cgc acc aat gtt ttt
 ctg tta 240
 Asp Arg Leu Arg Pro Leu Ser Tyr Pro Arg Thr Asn Val Phe
 Leu Leu 65 70 75
 80
 tgt ttc tca gtc gtt tcc cca gct tcg ttt ttc agc att tct
 tca aag 288
 Cys Phe Ser Val Val Ser Pro Ala Ser Phe Phe Ser Ile Ser
 Ser Lys 85 90

0070110

95

tgg cat cct gaa gtc agt cac cat tca ccc aaa act cct tgt
 att tta 336
 Trp His Pro Glu Val Ser His His Ser Pro Lys Thr Pro Cys
 Ile Leu

100

105

110

atc gga aca aag cag gat ctc aga gat gac gaa gaa acc gta
 aaa aag 384
 Ile Gly Thr Lys Gln Asp Leu Arg Asp Asp Glu Glu Thr Val
 Lys Lys

115

120

125

ctg aag aat act gat tca gcc ccg att cga tat gaa caa gga
 gaa gcg 432
 Leu Lys Asn Thr Asp Ser Ala Pro Ile Arg Tyr Glu Gln Gly
 Glu Ala

130

135

140

cta gca aag caa ctg gga gca gtc aaa tac gtg gag tgc tct
 gca ctg 480
 Leu Ala Lys Gln Leu Gly Ala Val Lys Tyr Val Glu Cys Ser
 Ala Leu

145

150

155

160

aag aaa gta ggg gta gac tct gta ttc caa gac gct att agt
 gca gtg 528
 Lys Lys Val Gly Val Asp Ser Val Phe Gln Asp Ala Ile Ser
 Ala Val

165

170

175

tta aat cct gct aaa cca cct aaa cca acg aag agg tgc gtg
 tta ctg 576
 Leu Asn Pro Ala Lys Pro Pro Lys Pro Thr Lys Arg Cys Val
 Leu Leu

180

185

190

taa

579

<210> 99

<211> 192

<212> PRT

<213> Ciona intestinalis

<400> 99

Met Gln Pro Val Lys Ile Val Val Val Gly Asp Gly Ala Val
 Gly Lys

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1				5					10					
15	Thr	Cys	Met	Cys	Ile	Thr	Tyr	Ala	Asn	Gly	Val	Phe	Pro	Ser
	Asp	Tyr												
				20					25					30
	Val	Pro	Thr	Ile	Phe	Asp	Asn	Tyr	Ala	Ala	Thr	Ser	Thr	Phe
	Glu	Gly												
			35					40					45	
	Ile	Ser	Tyr	Asn	Leu	Ala	Leu	Trp	Asp	Thr	Ala	Gly	Gln	Glu
	Glu	Tyr												
		50					55					60		
	Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Pro	Arg	Thr	Asn	Val	Phe
	Leu	Leu												
	65					70					75			
		80												
	Cys	Phe	Ser	Val	Val	Ser	Pro	Ala	Ser	Phe	Phe	Ser	Ile	Ser
	Ser	Lys												
					85					90				
	95													
	Trp	His	Pro	Glu	Val	Ser	His	His	Ser	Pro	Lys	Thr	Pro	Cys
	Ile	Leu												
					100				105					110
	Ile	Gly	Thr	Lys	Gln	Asp	Leu	Arg	Asp	Asp	Glu	Glu	Thr	Val
	Lys	Lys												
	Leu	Lys	Asn	Thr	Asp	Ser	Ala	Pro	Ile	Arg	Tyr	Glu	Gln	Gly
	Glu	Ala												
		130					135					140		
	Leu	Ala	Lys	Gln	Leu	Gly	Ala	Val	Lys	Tyr	Val	Glu	Cys	Ser
	Ala	Leu												
	145					150						155		
		160												
	Lys	Lys	Val	Gly	Val	Asp	Ser	Val	Phe	Gln	Asp	Ala	Ile	Ser
	Ala	Val												
					165					170				
	175													
	Leu	Asn	Pro	Ala	Lys	Pro	Pro	Lys	Pro	Thr	Lys	Arg	Cys	Val
	Leu	Leu												
					180				185					190

<210> 100

0070110

<211> 585
 <212> DNA
 <213> Ciona intestinalis

<220>
 <221> CDS
 <222> (1)..(585)

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

0070110

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gtg ggt acg aag ctt gac ttg aga gaa gac acc gaa att cta
caa cag          384
Val Gly Thr Lys Leu Asp Leu Arg Glu Asp Thr Glu Ile Leu
Gln Gln
      115              120              125
ctt tcc tcg aaa aat cta aaa cca ata aca cca gaa gaa ggg
gcg aaa          432
Leu Ser Ser Lys Asn Leu Lys Pro Ile Thr Pro Glu Glu Gly
Ala Lys
      130              135              140
atg gcg aaa gat att aaa gca gtt aaa tat tta gag tgt tct
gct cta          480
Met Ala Lys Asp Ile Lys Ala Val Lys Tyr Leu Glu Cys Ser
Ala Leu
145              150              155
      160
act cag gag tgt ctc agc caa gta ttt gat gac gct gtt att
gca gtg          528
Thr Gln Glu Cys Leu Ser Gln Val Phe Asp Asp Ala Val Ile
Ala Val
      165              170
175
cta aac cca tca cac ttt tca agt aac aat gac aac agc tgt
tgt aag          576
Leu Asn Pro Ser His Phe Ser Ser Asn Asn Asp Asn Ser Cys
Cys Lys
      180              185              190

atc gtt taa
ile val          585

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<210> 101
 <211> 194
 <212> PRT
 <213> Ciona intestinalis

<400> 101
 Met Gln Ser Ile Lys Leu Val Val Val Gly Asp Gly Ala Val
 Gly Lys
 1 5 10
 15
 Thr Cys Leu Leu Ile Ser Tyr Thr Ala Asn Ala Phe Pro Arg
 Glu Tyr
 20 25 30
 Val Pro Thr Val Phe Glu Asn Tyr Met Ala Asn Ile Thr Val

0070110

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

<210> 102
 <211> 645
 <212> DNA
 <213> Zea mays

<220>

0070110

<221> CDS

<222> (1)..(645)

<400> 102

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atg gcg tcc agc gcc tct cgg ttc atc aag tgc gtc acg gtc
ggc gac
Met Ala Ser Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val
Gly Asp
1 5 10
15
ggg gcc gtg ggc aag aca tgt atg ctc atc tgc tac acc agc
aac aag
Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser
Asn Lys
20 25 30
ttc ccc act gac tac ata cct acg gtg ttc gac aat ttc agt
gca aat
Phe Pro Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser
Ala Asn
35 40 45
gta gtt gtg gat ggc acc act gtg aat ttg ggc ctt tgg gat
acc gct
Val Val Val Asp Gly Thr Thr Val Asn Leu Gly Leu Trp Asp
Thr Ala
50 55 60
ggg cag gaa gat tac aac cgc ctg agg cct cta agc tac cga
ggg gca
Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg
Gly Ala
65 70 75
80
gat gtt ttc gtg ctt gca ttc tca ctt gtg agc cga gct agc
tat gag
Asp Val Phe Val Leu Ala Phe Ser Leu Val Ser Arg Ala Ser
Tyr Glu
85 90
95
aat atc atg aag aag tgg ata cca gag ctt caa cat tat gca
cct ggg
Asn Ile Met Lys Lys Trp Ile Pro Glu Leu Gln His Tyr Ala
Pro Gly
100 105 110
115
gtg ccc gtt gtt ttg gca ggc aca aaa ttg gat ctt cgt gaa
gac aag
Val Pro Val Val Leu Ala Gly Thr Lys Leu Asp Leu Arg Glu
Asp Lys
120 125

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0070110

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cac tac ttg atg gac cat cct gga ttg gtg cct gtt acc act
gca cag      432
His Tyr Leu Met Asp His Pro Gly Leu Val Pro Val Thr Thr
Ala Gln
      130      135      140
ggg gag gaa ctt cgt aga caa att ggt gct atg tat tac att
gaa tgc      480
Gly Glu Glu Leu Arg Arg Gln Ile Gly Ala Met Tyr Tyr Ile
Glu Cys
145      150      155
      160
agc tca aag aca cag cag aat gtc aaa gct gtg ttc gat gct
gcc atc      528
Ser Ser Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala
Ala Ile
      165      170
175
aag gta gta atc cag cct cca act aaa ata aga gaa aag aag
aag aaa      576
Lys Val Val Ile Gln Pro Pro Thr Lys Ile Arg Glu Lys Lys
Lys Lys
      180      185      190
aaa tca cgc aaa gga tgt tct atg atg aac atc ttc ggt gga
aga aaa      624
Lys Ser Arg Lys Gly Cys Ser Met Met Asn Ile Phe Gly Gly
Arg Lys
      195      200      205
atg cta tgc ttc aag tcc tga
      645
Met Leu Cys Phe Lys Ser
      210

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<210> 103
 <211> 214
 <212> PRT
 <213> Zea mays

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<400> 103
Met Ala Ser Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val
Gly Asp
1      5      10
15
Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser
Asn Lys
      20      25      30

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0070110

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

<210> 104

0070110

<211> 663
 <212> DNA
 <213> Zea mays

<220>
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 <222> (1)..(663)

<400> 104

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atg agc gcg gcg gca gcg gcg gcg gcg agc tcg gtc acc aag
ttc atc                               48
Met Ser Ala Ala Ala Ala Ala Ala Ala Ser Ser Val Thr Lys
Phe Ile                               10
1
15
aag tgc gtc acg gtc ggc gat ggg gcc gtc ggg aag acc tgc
atg ctc                               96
Lys Cys Val Thr Val Gly Asp Gly Ala Val Gly Lys Thr Cys
Met Leu                               20
atc tgc tac acc tgc aac aag ttc ccc acg gat tac atc ccc
acc gta                               144
Ile Cys Tyr Thr Cys Asn Lys Phe Pro Thr Asp Tyr Ile Pro
Thr Val                               35
ttt gac aac ttc agc gcc aat gtc tcc gtg ggt ggg agc atc
gtc aac                               192
Phe Asp Asn Phe Ser Ala Asn Val Ser Val Gly Gly Ser Ile
Val Asn                               50
ttg ggc ctc tgg gac acg gca ggc cag gag gat tac agc agg
ttg agg                               240
Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu Asp Tyr Ser Arg
Leu Arg                               65
65
70
80
cct ctc agc tac agg ggt gct gat gtg ttc atc ctc tcc ttc
tcc ctg                               288
Pro Leu Ser Tyr Arg Gly Ala Asp Val Phe Ile Leu Ser Phe
Ser Leu                               85
95
gtc agc agg gcg agc tat gag aac gtc ctg aag aag tgg atg
cca gag                               336
Val Ser Arg Ala Ser Tyr Glu Asn Val Leu Lys Lys Trp Met
Pro Glu                               100
105
110
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0070110

```

ctt cgc cga ttt tca cct act gtt cct gta gtt ctt gtt gga
acc aaa
Leu Arg Arg Phe Ser Pro Thr Val Pro Val Val Leu Val Gly
Thr Lys
115
cta gat ctc cgt gaa gac aga tct tac ctt gct gac cat tct
gct gct
Leu Asp Leu Arg Glu Asp Arg Ser Tyr Leu Ala Asp His Ser
Ala Ala
130
tcc atc atc tct act gaa cag gga gaa gag ctc agg aag cag
ata ggt
Ser Ile Ile Ser Thr Glu Gln Gly Glu Glu Leu Arg Lys Gln
Ile Gly
145
150
155
160
gct gtg gcg tac ata gaa tgc agc tca aag aca cag agg aac
gta aag
Ala Val Ala Tyr Ile Glu Cys Ser Ser Lys Thr Gln Arg Asn
Val Lys
165
170
175
gct gtg ttc gac act gca att aaa gta gtg ctg caa cca ccg
agg aga
Ala Val Phe Asp Thr Ala Ile Lys Val Val Leu Gln Pro Pro
Arg Arg
180
185
190
aga gaa gtt acc agg aag aaa atg aag aca agt tcg aat cag
tct ctg
Arg Glu Val Thr Arg Lys Lys Met Lys Thr Ser Ser Asn Gln
Ser Leu
195
200
205
aga aga tac ctc tgt gga agc gga tgt ttc aca tcg taa
663
Arg Arg Tyr Leu Cys Gly Ser Gly Cys Phe Thr Ser
210 215 220

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<210> 105
 <211> 220
 <212> PRT
 <213> Zea mays

<400> 105
 Met Ser Ala Ala Ala Ala Ala Ala Ala Ser Ser Val Thr Lys
 Phe Ile
 1 5 10
 15

0070110

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

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Arg Arg Tyr Leu Cys Gly Ser Gly Cys Phe Thr Ser
210 215 220

<210> 106
<211> 645
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (1)..(645)

<400> 106

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ggc gac          48
Met Ala Ser Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val
Gly Asp
1          5          10
15
ggg gcc gtg ggc aag aca tgt atg ctc atc tgc tac acc agc
aac aag          96
Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser
Asn Lys
20          25          30
ttc ccc act gat tac ata ccc acg gtg ttc gac aat ttc agt
gca aat          144
Phe Pro Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser
Ala Asn
35          40          45
gtc gtt gtg gat ggc acc acg gtg aat ttg ggc ctg tgg gat
acc gca          192
Val Val Val Asp Gly Thr Thr Val Asn Leu Gly Leu Trp Asp
Thr Ala
50          55          60
ggg cag gaa gat tac aac cga ctg agg cct cta agc tac cgt
ggt gca          240
Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg
Gly Ala
65          70          75
80
gat gtt ttc gtg ctt gca ttc tca ctt gtg agt cga gct agc
tat gag          288
Asp Val Phe Val Leu Ala Phe Ser Leu Val Ser Arg Ala Ser
Tyr Glu
85          90
95
aat atc atg aag aag tgg ata ccg gag ctt cag cat tat gca
cgt ggg          336

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0070110

Asn	Ile	Met	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Gln	His	Tyr	Ala
Arg	Gly												
			100					105					110

gtg	cct	ggt	gtg	ttg	gta	ggc	aca	aaa	ttt	gat	ctt	cgt	gaa
gac	aag			384									
Val	Pro	Val	Val	Leu	Val	Gly	Thr	Lys	Phe	Asp	Leu	Arg	Glu
Asp	Lys												

		115				120						125	
cac	tac	ttg	atg	gac	cat	cct	ggg	ttg	gtg	cct	ggt	acc	aca
gca	caa		432										
His	Tyr	Leu	Met	Asp	His	Pro	Gly	Leu	Val	Pro	Val	Thr	Thr
Ala	Gln												

	130					135					140		
ggg	gag	gaa	ctt	cgt	aga	caa	att	ggt	gct	atg	tat	tac	atc
gaa	tgc		480										
Gly	Glu	Glu	Leu	Arg	Arg	Gln	Ile	Gly	Ala	Met	Tyr	Tyr	Ile
Glu	Cys												
145					150					155			

	160												
agt	tcg	aag	aca	cag	cag	aat	gtc	aaa	gct	gtg	ttc	gat	gct
gcc	atc		528										
Ser	Ser	Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala
Ala	Ile												

			165							170			
175													
aag	ggt	gta	atc	cag	cct	cca	act	aaa	cta	aga	gaa	aag	aag
aaa	aag		576										
Lys	Val	Val	Ile	Gln	Pro	Pro	Thr	Lys	Leu	Arg	Glu	Lys	Lys
Lys	Lys												
			180							185			190

aaa	tca	cgc	aag	gga	tgt	tcg	atg	gtg	aac	atc	tta	tct	gga
aga	aaa		624										
Lys	Ser	Arg	Lys	Gly	Cys	Ser	Met	Val	Asn	Ile	Leu	Ser	Gly
Arg	Lys												

		195				200					205		
atg	cta	tgc	ttc	aag	tcc	tga							
			645										
Met	Leu	Cys	Phe	Lys	Ser								
	210												

<210> 107
 <211> 214
 <212> PRT
 <213> Zea mays

0070110

<400> 107

Met Ala Ser Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val
Gly Asp

1 5 10

15

Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser
Asn Lys

20 25 30

Phe Pro Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser
Ala Asn

35 40 45

Val Val Val Asp Gly Thr Thr Val Asn Leu Gly Leu Trp Asp
Thr Ala

50 55 60

Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg
Gly Ala

65 70 75

80

Asp Val Phe Val Leu Ala Phe Ser Leu Val Ser Arg Ala Ser
Tyr Glu

85 90

95

Asn Ile Met Lys Lys Trp Ile Pro Glu Leu Gln His Tyr Ala
Arg Gly

100 105 110

Val Pro Val Val Leu Val Gly Thr Lys Phe Asp Leu Arg Glu
Asp Lys

115 120 125

His Tyr Leu Met Asp His Pro Gly Leu Val Pro Val Thr Thr
Ala Gln

130 135 140

Gly Glu Glu Leu Arg Arg Gln Ile Gly Ala Met Tyr Tyr Ile
Glu Cys

145 150 155

160

Ser Ser Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala
Ala Ile

165 170

175

Lys Val Val Ile Gln Pro Pro Thr Lys Leu Arg Glu Lys Lys
Lys Lys

180 185 190

0070110

Lys Ser Arg Lys Gly Cys Ser Met Val Asn Ile Leu Ser Gly
Arg Lys
195 200 205

Met Leu Cys Phe Lys Ser
210

<210> 108
<211> 639
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (1)..(639)

<400> 108
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ggc gcg 48
Met Ser Val Thr Lys Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10
15
gtg ggc aag acc tgc atg ctc atc tgc tac acc agc aac aag
ttc ccc 96
Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser Asn Lys
Phe Pro
20 25 30
acg gat tac atc ccc acg gtg ttc gac aac ttc agc gcc aac
gtc tcc 144
Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Ser
35 40 45
gtg gac ggc agc atc gtc aac ctg ggc ctc tgg gac act gca
gga caa 192
Val Asp Gly Ser Ile Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60
gag gac tac agc aga ttg cgg cca ctg agc tac agg ggc gcg
gac gtg 240
Glu Asp Tyr Ser Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65 70 75
80
ttc gtg ctg gcc ttc tcc ttg atc agc agg gcg agc tat gag
aac gtc 288
Phe Val Leu Ala Phe Ser Leu Ile Ser Arg Ala Ser Tyr Glu
Seite 184

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Asn	Val													
				85						90				
95														
ctt	aag	aag	tgg	gtg	cca	gag	ctt	cgc	aga	ttc	gcg	ccc	gac	
gtc	ccg		336											
Leu	Lys	Lys	Trp	Val	Pro	Glu	Leu	Arg	Arg	Phe	Ala	Pro	Asp	
Val	Pro													
			100					105					110	
gtc	gtt	ctt	gtc	ggg	acc	aag	tta	gat	ctc	cgt	gac	cac	agg	
gcc	tac		384											
Val	Val	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	His	Arg	
Ala	Tyr													
		115					120					125		
ctt	gct	gac	cat	cct	gga	gcg	tcg	acg	atc	acg	acg	gca	cag	
ggc	gaa		432											
Leu	Ala	Asp	His	Pro	Gly	Ala	Ser	Thr	Ile	Thr	Thr	Ala	Gln	
Gly	Glu													
	130					135					140			
gaa	ctg	agg	agg	cag	atc	ggc	gct	gcg	gct	tac	atc	gag	tgc	
agt	tcc		480											
Glu	Leu	Arg	Arg	Gln	Ile	Gly	Ala	Ala	Ala	Tyr	Ile	Glu	Cys	
Ser	Ser													
145					150						155			
160														
aaa	acg	cag	cag	aat	gtc	aag	tcg	gtc	ttc	gac	aca	gcc	atc	
aaa	gtg		528											
Lys	Thr	Gln	Gln	Asn	Val	Lys	Ser	Val	Phe	Asp	Thr	Ala	Ile	
Lys	Val													
			165									170		
175														
gtc	ctt	cag	ccc	ccg	cgg	agg	agg	gag	gcg	acg	cct	gcc	agg	
agg	aag		576											
Val	Leu	Gln	Pro	Pro	Arg	Arg	Arg	Glu	Ala	Thr	Pro	Ala	Arg	
Arg	Lys													
			180										190	
aac	agg	cgt	ggc	tcc	ggg	tgc	tct	atc	atg	aac	ctc	atg	tgt	
ggc	agc		624											
Asn	Arg	Arg	Gly	Ser	Gly	Cys	Ser	Ile	Met	Asn	Leu	Met	Cys	
Gly	Ser													
		195						200				205		
acg	tgc	gct	gct	tag										
			639											
Thr	Cys	Ala	Ala											
	210													

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0070110

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

<400> 109

Met Ser Val Thr Lys Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala

1 5 10

15

Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser Asn Lys
Phe Pro

20 25 30

Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Ser

35 40 45

Val Asp Gly Ser Ile Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln

50 55 60

Glu Asp Tyr Ser Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val

65 70 75

80

Phe Val Leu Ala Phe Ser Leu Ile Ser Arg Ala Ser Tyr Glu
Asn Val

85 90

95

Leu Lys Lys Trp Val Pro Glu Leu Arg Arg Phe Ala Pro Asp
Val Pro

100 105 110

Val Val Leu Val Gly Thr Lys Leu Asp Leu Arg Asp His Arg
Ala Tyr

115 120 125

Leu Ala Asp His Pro Gly Ala Ser Thr Ile Thr Thr Ala Gln
Gly Glu

130 135 140

Glu Leu Arg Arg Gln Ile Gly Ala Ala Ala Tyr Ile Glu Cys
Ser Ser

145 150 155

160

Lys Thr Gln Gln Asn Val Lys Ser Val Phe Asp Thr Ala Ile
Lys Val

165 170

0070110

175
Val Leu Gln Pro Pro Arg Arg Arg Glu Ala Thr Pro Ala Arg
Arg Lys
180 185 190
Asn Arg Arg Gly Ser Gly Cys Ser Ile Met Asn Leu Met Cys
Gly Ser
195 200 205
Thr Cys Ala Ala
210

<210> 110
<211> 594
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (1)..(594)

<400> 110
atg agc gcg tcc agg ttc ata aag tgc gtc acg gtc ggg gac
ggc gcc 48
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10
15
gtc ggc aag acc tgc atg ctc atc tcc tac acc tcc aac acc
ttc ccc 96
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
20 25 30
acc gac tat gtt ccg aca gtg ttt gat aac ttc agt gcc aac
gtt gtg 144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
35 40 45
gtt gat ggt aat act gtc aac ctc ggc ctc tgg gac act gca
ggt caa 192
Val Asp Gly Asn Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60
gag gat tac aac aga ctg aga cca ctg agc tat cgt gga gct
gat gtt 240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65 70 75

0070110

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      80
ttt ctt ctg gct ttc tca ctg atc agt aag gcc agc tat gag
aat gtt      288
Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val

      85                      90
95
tcg aag aag tgg ata cct gaa ctg aag cat tat gca cct ggt
gtg cca      336
Ser Lys Lys Trp Ile Pro Glu Leu Lys His Tyr Ala Pro Gly
Val Pro

      100                      105                      110

att att ctc gta ggg aca aag ctt gat ctt cga gac gac aag
cag ttc      384
Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe

      115                      120                      125
ttt gtg gac cat cct ggt gct gtc cct atc act act gct cag
gga gag      432
Phe Val Asp His Pro Gly Ala Val Pro Ile Thr Thr Ala Gln
Gly Glu

      130                      135                      140
gag cta aga aag caa ata ggc gct cca tac tac atc gaa tgc
agc tcg      480
Glu Leu Arg Lys Gln Ile Gly Ala Pro Tyr Tyr Ile Glu Cys
Ser Ser

      145                      150                      155
      160
aag acc caa cta aac gtg aag ggc gtc ttc gat gcg gcg ata
aag gtt      528
Lys Thr Gln Leu Asn Val Lys Gly Val Phe Asp Ala Ala Ile
Lys Val

      165                      170
175
gtg ctg cag ccg cct aag gcg aag aag aag aaa aag gtg cag
agg ggg      576
Val Leu Gln Pro Pro Lys Ala Lys Lys Lys Lys Val Gln
Arg Gly

      180                      185                      190

gcg tgc tcc att ttg tga
      594
Ala Cys Ser Ile Leu
      195

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<210> 111

<211> 197

0070110

<212> PRT

<213> Zea mays

<400> 111

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

0070110

Val Leu Gln Pro Pro Lys Ala Lys Lys Lys Lys Lys Val Gln
 Arg Gly
 180 185 190

Ala Cys Ser Ile Leu
 195

<210> 112
 <211> 594
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (1)..(594)

<400> 112
 atg agc gcg tct cgg ttc atc aag tgc gtc acc gtg ggg gac
 ggt gcc 48
 Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala
 1 5 10
 15
 gtc gga aag acc tgc atg ctc atc tcc tac aca tcc aac act
 ttc ccc 96
 Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
 Phe Pro
 20 25 30
 act gac tat gtt cca act gtg ttc gac aac ttc agt gcc aat
 gtt gtg 144
 Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
 Val Val
 35 40 45
 gtt gac ggg agc act gtc aac ttg ggt ctg tgg gat aca gca
 gga caa 192
 Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
 Gly Gln
 50 55 60
 gaa gat tac aat aga ctg cgt ccg ttg agc tat cgt ggt gct
 gat gtt 240
 Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
 Asp Val
 65 70 75
 80
 ttt ctg ctc gcc ttt tct ctt atc agc aaa gca agc tat gag
 aat gtc 288
 Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
 Asn Val

0070110

85

90

95
tct aag aag tgg gtt cct gaa tta agg cac tat gct cct ggc
gtg ccc 336
Ser Lys Lys Trp Val Pro Glu Leu Arg His Tyr Ala Pro Gly
Val Pro
100 105 110

ata atc ctt gtt ggg aca aaa ctt gat ctg cgt gat gat aag
cag ttt 384
Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe
115 120 125

ttt gtt gat cac cct ggt gct gtt cca att tcc act gcc cag
ggc gaa 432
Phe Val Asp His Pro Gly Ala Val Pro Ile Ser Thr Ala Gln
Gly Glu
130 135 140

gag ctg agg aag cta att ggt gct gcc gcc tac atc gaa tgc
agt tca 480
Glu Leu Arg Lys Leu Ile Gly Ala Ala Ala Tyr Ile Glu Cys
Ser Ser
145 150 155

160
aaa atc cag cag aac ata aaa gca gtg ttt gac gca gca att
aag gtg 528
Lys Ile Gln Gln Asn Ile Lys Ala Val Phe Asp Ala Ala Ile
Lys Val
165 170

175
gtt ctc cag cca cca aag caa aag aag agg aag aag aag gtg
cag aag 576
Val Leu Gln Pro Pro Lys Gln Lys Lys Arg Lys Lys Lys Val
Gln Lys
180 185 190

gga tgc acc att ttg taa
594
Gly Cys Thr Ile Leu
195

<210> 113
<211> 197
<212> PRT
<213> Zea mays

<400> 113
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Seite 191

0070110

Gly	Ala													
1				5					10					
15														
Val	Gly	Lys	Thr	Cys	Met	Leu	Ile	Ser	Tyr	Thr	Ser	Asn	Thr	
Phe	Pro													
			20					25					30	
Thr	Asp	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn	
Val	Val													
		35					40					45		
Val	Asp	Gly	Ser	Thr	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala	
Gly	Gln													
	50					55					60			
Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala	
Asp	Val													
65					70					75				
	80													
Phe	Leu	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Lys	Ala	Ser	Tyr	Glu	
Asn	Val													
				85					90					
95														
Ser	Lys	Lys	Trp	Val	Pro	Glu	Leu	Arg	His	Tyr	Ala	Pro	Gly	
Val	Pro													
			100					105					110	
Ile	Ile	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys	
Gln	Phe													
		115					120					125		
Phe	Val	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Ser	Thr	Ala	Gln	
Gly	Glu													
	130					135					140			
Glu	Leu	Arg	Lys	Leu	Ile	Gly	Ala	Ala	Ala	Tyr	Ile	Glu	Cys	
Ser	Ser													
145					150					155				
	160													
Lys	Ile	Gln	Gln	Asn	Ile	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile	
Lys	Val													
				165					170					
175														
Val	Leu	Gln	Pro	Pro	Lys	Gln	Lys	Lys	Arg	Lys	Lys	Lys	Val	
Gln	Lys													
			180					185					190	
Gly	Cys	Thr	Ile	Leu										

<210> 114
 <211> 648
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (1)..(648)

<400> 114
 atg gcc tcc agc gcc tcc cgg ttc atc aag tgc gtc aca gtg
 ggg gac 48
 Met Ala Ser Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val
 Gly Asp
 1 5 10
 15
 ggc gcc gtg gga aag acc tgc atg ctc atc tgc tac acc agc
 aac aag 96
 Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser
 Asn Lys
 20 25 30
 ttc ccc act gat tac ata ccc act gtc ttc gat aac ttc agt
 gca aac 144
 Phe Pro Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser
 Ala Asn
 35 40 45
 gtg gta gtc gac ggt acc acg gtg aat ttg ggc ctt tgg gat
 act gca 192
 Val Val Val Asp Gly Thr Thr Val Asn Leu Gly Leu Trp Asp
 Thr Ala
 50 55 60
 ggg cag gaa gat tac aac aga ctg agg cca ctg agc tac cgc
 gga gca 240
 Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg
 Gly Ala
 65 70 75
 80
 gat gtg ttc gtg ctc gcc ttc tcg ctt gtc agc cga gct agc
 tac gag 288
 Asp Val Phe Val Leu Ala Phe Ser Leu Val Ser Arg Ala Ser
 Tyr Glu
 85 90
 95
 aat gtt atg aag aag tgg cta ccg gag ctt cag cat tat gca
 ccg ggt 336
 Asn Val Met Lys Lys Trp Leu Pro Glu Leu Gln His Tyr Ala

0070110

Pro Gly													
		100					105					110	
gtc ccc ata gtg ttg gcc gga act aaa ttg gat ctt cgt gaa													
gac agg			384										
Val Pro Ile Val Leu Ala Gly Thr Lys Leu Asp Leu Arg Glu													
Asp Arg													
		115					120					125	
cac tac tta gtt gac cat cct ggt gcg gta cct gtt act aca													
gca cag			432										
His Tyr Leu Val Asp His Pro Gly Ala Val Pro Val Thr Thr													
Ala Gln													
		130					135					140	
ggg gag gaa ctg cgc aag cac att ggc gca act tgc tac atc													
gaa tgc			480										
Gly Glu Glu Leu Arg Lys His Ile Gly Ala Thr Cys Tyr Ile													
Glu Cys													
145						150						155	
160													
agc tca aaa act cag cag aat gtg aaa gct gtg ttt gat gct													
gcc atc			528										
Ser Ser Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala													
Ala Ile													
		165										170	
175													
aag gta gta atc agg cct ccg acg aag cag cga gaa agg aag													
aaa aag			576										
Lys Val Val Ile Arg Pro Pro Thr Lys Gln Arg Glu Arg Lys													
Lys Lys													
		180										185	
aaa gaa cgg cga gga tgc tca ata ttc tgc agc cgt atc atg													
cac gca			624										
Lys Glu Arg Arg Gly Cys Ser Ile Phe Cys Ser Arg Ile Met													
His Ala													
		195										200	
aga aga cta gga tgc ttc aag tga													
			648										
Arg Arg Leu Gly Cys Phe Lys													
210							215						

<210> 115
 <211> 215
 <212> PRT
 <213> Zea mays

<400> 115
 Met Ala Ser Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val
 Seite 194

0070110

Gly	Asp													
1				5					10					
15														
Gly	Ala	Val	Gly	Lys	Thr	Cys	Met	Leu	Ile	Cys	Tyr	Thr	Ser	
Asn	Lys													
			20					25					30	
Phe	Pro	Thr	Asp	Tyr	Ile	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	
Ala	Asn													
		35					40					45		
Val	Val	Val	Asp	Gly	Thr	Thr	Val	Asn	Leu	Gly	Leu	Trp	Asp	
Thr	Ala													
	50					55					60			
Gly	Gln	Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	
Gly	Ala													
65					70					75				
	80													
Asp	Val	Phe	Val	Leu	Ala	Phe	Ser	Leu	Val	Ser	Arg	Ala	Ser	
Tyr	Glu													
			85						90					
95														
Asn	Val	Met	Lys	Lys	Trp	Leu	Pro	Glu	Leu	Gln	His	Tyr	Ala	
Pro	Gly													
			100					105					110	
Val	Pro	Ile	Val	Leu	Ala	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Glu	
Asp	Arg													
		115					120					125		
His	Tyr	Leu	Val	Asp	His	Pro	Gly	Ala	Val	Pro	Val	Thr	Thr	
Ala	Gln													
	130					135					140			
Gly	Glu	Glu	Leu	Arg	Lys	His	Ile	Gly	Ala	Thr	Cys	Tyr	Ile	
Glu	Cys													
145					150					155				
	160													
Ser	Ser	Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	
Ala	Ile													
			165					170						
175														
Lys	Val	Val	Ile	Arg	Pro	Pro	Thr	Lys	Gln	Arg	Glu	Arg	Lys	
Lys	Lys													
			180					185					190	
Lys	Glu	Arg	Arg	Gly	Cys	Ser	Ile	Phe	Cys	Ser	Arg	Ile	Met	

0070110

His Ala 195 200 205

Arg Arg Leu Gly Cys Phe Lys
210 215

<210> 116
<211> 576
<212> DNA
<213> Acyrthosiphon pisum

<220>
<221> CDS
<222> (1)..(576)

<400> 116
atg cag acc atc aag tgc gtg gtt gtt ggt gat gga gct gtt
ggt aag 48
Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys 1 5 10
15
act tgt ctg ctc ata tcg tac acg aca aac aag ttt cct tca
gaa tat 96
Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe Pro Ser
Glu Tyr 20 25 30
gta ccg act gtt ttt gac aat tat gca gtg acc gtt atg att
ggc gga 144
Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val Met Ile
Gly Gly 35 40 45
gag cca tac aca tta ggt tta ttt gat aca gca ggt cag gaa
gat tat 192
Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu
Asp Tyr 50 55 60
gat cgc ctc aga cct ttg agt tat cca caa act gat gtg ttt
ctt gtt 240
Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
Leu Val 65 70 75
80
tgt ttc tcc gtg gtt tca cca tct tcg ttt gaa aat gtc aaa
gaa aaa 288
Cys Phe Ser Val Val Ser Pro Ser Ser Phe Glu Asn Val Lys
Glu Lys 85 90

0070110

```

95
tgg gtt cca gag ata acg cat cac tgt caa aaa aca cca ttc
ctg ttg          336
Trp Val Pro Glu Ile Thr His His Cys Gln Lys Thr Pro Phe
Leu Leu
          100          105          110

gtt ggc aca caa ata gac ctt aga gaa gat gcc aca act gta
gag aaa          384
Val Gly Thr Gln Ile Asp Leu Arg Glu Asp Ala Thr Thr Val
Glu Lys
          115          120          125

cta gcc aaa aat aaa caa aaa tca ata tca tct gaa caa gga
gag aag          432
Leu Ala Lys Asn Lys Gln Lys Ser Ile Ser Ser Glu Gln Gly
Glu Lys
          130          135          140

cta gct aaa gaa ctt aaa gct gta aaa tat gtt gaa tgc tca
gca ctt          480
Leu Ala Lys Glu Leu Lys Ala Val Lys Tyr Val Glu Cys Ser
Ala Leu
145          150          155
160
aca caa aaa gga cta aaa aat gta ttt gat gaa gct att ctt
gca gct          528
Thr Gln Lys Gly Leu Lys Asn Val Phe Asp Glu Ala Ile Leu
Ala Ala
          165          170

175
tta gag cct cct gag cca gtc aag aag agg aag tgt gtt ata
ttg          573
Leu Glu Pro Pro Glu Pro Val Lys Lys Arg Lys Cys Val Ile
Leu
          180          185          190

taa
          576

```

<210> 117
 <211> 191
 <212> PRT
 <213> Acyrthosiphon pisum

<400> 117
 Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
 Gly Lys

0070110

1				5					10					
15	Thr	Cys	Leu	Leu	Ile	Ser	Tyr	Thr	Thr	Asn	Lys	Phe	Pro	Ser
	Glu	Tyr												
				20					25					30
	Val	Pro	Thr	Val	Phe	Asp	Asn	Tyr	Ala	Val	Thr	Val	Met	Ile
	Gly	Gly												
			35					40					45	
	Glu	Pro	Tyr	Thr	Leu	Gly	Leu	Phe	Asp	Thr	Ala	Gly	Gln	Glu
	Asp	Tyr												
		50					55					60		
	Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Pro	Gln	Thr	Asp	Val	Phe
	Leu	Val												
	65					70					75			
	80													
	Cys	Phe	Ser	Val	Val	Ser	Pro	Ser	Ser	Phe	Glu	Asn	Val	Lys
	Glu	Lys												
					85					90				
	95													
	Trp	Val	Pro	Glu	Ile	Thr	His	His	Cys	Gln	Lys	Thr	Pro	Phe
	Leu	Leu												
				100					105					110
	Val	Gly	Thr	Gln	Ile	Asp	Leu	Arg	Glu	Asp	Ala	Thr	Thr	Val
	Glu	Lys												
			115					120					125	
	Leu	Ala	Lys	Asn	Lys	Gln	Lys	Ser	Ile	Ser	Ser	Glu	Gln	Gly
	Glu	Lys												
		130					135					140		
	Leu	Ala	Lys	Glu	Leu	Lys	Ala	Val	Lys	Tyr	Val	Glu	Cys	Ser
	Ala	Leu												
	145					150					155			
	160													
	Thr	Gln	Lys	Gly	Leu	Lys	Asn	Val	Phe	Asp	Glu	Ala	Ile	Leu
	Ala	Ala												
				165						170				
	175													
	Leu	Glu	Pro	Pro	Glu	Pro	Val	Lys	Lys	Arg	Lys	Cys	Val	Ile
	Leu													
				180					185					190

<210> 118

0070110

<211> 588
 <212> DNA
 <213> *Drosophila melanogaster*

<220>
 <221> CDS
 <222> (1)..(588)

<400> 118
 atg tca acc gga agg ccc ata aag tgt gta gtc gtt ggt gac
 ggc acc 48
 Met Ser Thr Gly Arg Pro Ile Lys Cys Val Val Val Gly Asp
 Gly Thr
 1 5 10
 15
 gtc gga aag acc tgc atg cta atc tcc tac acg aca gac tgc
 ttt ccc 96
 Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Thr Asp Cys
 Phe Pro
 20 25 30
 ggc gaa tat gtg ccc aca gtc ttc gac aac tac tcg gcg ccc
 atg caa 144
 Gly Glu Tyr Val Pro Thr Val Phe Asp Asn Tyr Ser Ala Pro
 Met Gln
 35 40 45
 gtg gac aca ata cag gtc tcg ctg gga ctg tgg gat acg gcg
 ggt cag 192
 Val Asp Thr Ile Gln Val Ser Leu Gly Leu Trp Asp Thr Ala
 Gly Gln
 50 55 60
 gag gac tac gac cgc ctg aga ccg cta tcc tac ccg cag aca
 gac gtt 240
 Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr
 Asp Val
 65 70 75
 80
 ttc ctg ata tgc tac agc gtg gcg agt ccc tcg tcc ttt gag
 aac gtc 288
 Phe Leu Ile Cys Tyr Ser Val Ala Ser Pro Ser Ser Phe Glu
 Asn Val
 85 90
 95
 acc tcg aaa tgg tat ccg gag ata aag cac cac tgt ccc gat
 gcg ccc 336
 Thr Ser Lys Trp Tyr Pro Glu Ile Lys His His Cys Pro Asp
 Ala Pro
 100 105 110

0070110

```

atc att cta gtt ggc acc aaa atc gat ttg cgc gaa gat cga
gag aca      384
Ile Ile Leu Val Gly Thr Lys Ile Asp Leu Arg Glu Asp Arg
Glu Thr
      115      120      125
ctc agc ggc ctg gca gag cag gga ctg acg ccg ctg aag cgc
gag cag      432
Leu Ser Gly Leu Ala Glu Gln Gly Leu Thr Pro Leu Lys Arg
Glu Gln
      130      135      140
ggc cag aag ctg gca aac aag ata cgc gct gtg aaa tac atg
gag tgc      480
Gly Gln Lys Leu Ala Asn Lys Ile Arg Ala Val Lys Tyr Met
Glu Cys
145      150      155
      160
tcc gcc ttg acg cag cgc ggt ctc aag ccg gtg ttc gag gaa
gcg gtg      528
Ser Ala Leu Thr Gln Arg Gly Leu Lys Pro Val Phe Glu Glu
Ala Val
      165      170
175
cgc gcg gtg ctc aga cca gag ccg cta aag cga cgc cag cga
aag tgt      576
Arg Ala Val Leu Arg Pro Glu Pro Leu Lys Arg Arg Gln Arg
Lys Cys
      180      185      190

tta ata atg taa
      588
Leu Ile Met
      195

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<210> 119
 <211> 195
 <212> PRT
 <213> Drosophila melanogaster

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<400> 119
Met Ser Thr Gly Arg Pro Ile Lys Cys Val Val Val Gly Asp
Gly Thr
1      5      10
15
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Thr Asp Cys
Phe Pro
      20      25      30

Gly Glu Tyr Val Pro Thr Val Phe Asp Asn Tyr Ser Ala Pro

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

<220>

0070110

<221> CDS

<222> (1)..(576)

<400> 120

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atg cag acg ata aaa tgt gta gta gta ggg gat gga gct gtg
gga aag          48
Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys
  1              5              10
15
acc tgt cta ctt atc tca tat aca aca aat aaa ttc cct tca
gaa tat          96
Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe Pro Ser
Glu Tyr
          20              25              30
gta cca acg gtt ttc gat aat tat gca gta act gtt atg atc
ggt gga          144
Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val Met Ile
Gly Gly
          35              40              45
gag ccg tac acg ttg ggt ctc ttt gat aca gca gga caa gaa
gat tac          192
Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu
Asp Tyr
          50              55              60
gac aga ctt cga cct ctc agc tac ccc cag acg gat gtc ttc
ctc gtc          240
Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
Leu Val
          65              70              75
80
tgt ttt tca gtt gta gcg cca tct tca ttt gaa aat gtc aaa
gaa aag          288
Cys Phe Ser Val Val Ala Pro Ser Ser Phe Glu Asn Val Lys
Glu Lys
          85              90
95
tgg gta cca gag atc acc cac cac tgt cag aaa aca cca ttc
ctg ctg          336
Trp Val Pro Glu Ile Thr His His Cys Gln Lys Thr Pro Phe
Leu Leu
          100              105              110
gtg ggg acc cag ata gat ctg cgt gac gac cca gcc acc att
gag aag          384
Val Gly Thr Gln Ile Asp Leu Arg Asp Asp Pro Ala Thr Ile
Glu Lys
          115              120              125

```

0070110

```

ctc atg aag aac aag cag aag ccc acg acg gga gag gct ggt
gag agg          432
Leu Met Lys Asn Lys Gln Lys Pro Thr Thr Gly Glu Ala Gly
Glu Arg
130          135          140
atg gcc aaa gag ctg cgt gcc gtt aaa tac gtt gag tgc tct
gca ctt          480
Met Ala Lys Glu Leu Arg Ala Val Lys Tyr Val Glu Cys Ser
Ala Leu
145          150          155
160
aca cag aaa gga cta aag aac gtc ttt gac gag gcc atc cta
gcg gct          528
Thr Gln Lys Gly Leu Lys Asn Val Phe Asp Glu Ala Ile Leu
Ala Ala
165          170
175
ctt gag ccc cct gaa cca gtc aag aag aag agg tgt cga ctc
ctt          573
Leu Glu Pro Pro Glu Pro Val Lys Lys Lys Arg Cys Arg Leu
Leu
180          185          190

taa
576

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<210> 121
 <211> 191
 <212> PRT
 <213> Strongylocentrotus purpuratus

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<400> 121
Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys
1          5          10
15
Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe Pro Ser
Glu Tyr
20          25          30

Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val Met Ile
Gly Gly
35          40          45

Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu
Asp Tyr

```

0070110

50

55

60

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

<210> 122
 <211> 579
 <212> DNA
 <213> Strongylocentrotus purpuratus

<220>
 <221> CDS
 <222> (1)..(579)

<400> 122
 atg gct gct ata agg aaa aag ttg gtt atc gtt gga gat ggt
 gct tgt 48
 Met Ala Ala Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly

0070110

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

0070110

Gln Thr Met Ser Asp Lys Ile Asn Ala Tyr Lys Tyr Leu Glu
 Cys Ser
 145 150 155
 160
 gcc aag tct aac gat ggt gtc cgg gaa gtg ttt gag acg gca
 acc aga 528
 Ala Lys Ser Asn Asp Gly Val Arg Glu Val Phe Glu Thr Ala
 Thr Arg
 165 170
 175
 gca gca cta caa gtc aaa aag aag aag tca tca aaa tgc agc
 atc ttt 576
 Ala Ala Leu Gln Val Lys Lys Lys Lys Ser Ser Lys Cys Ser
 Ile Phe
 180 185 190
 taa
 579

<210> 123
 <211> 192
 <212> PRT
 <213> Strongylocentrotus purpuratus

<400> 123
 Met Ala Ala Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly
 Ala Cys
 1 5 10
 15
 Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Asp Gln Phe
 Pro Glu
 20 25 30
 Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Ile
 Glu Val
 35 40 45
 Asp Gly Lys Gln Val Glu Leu Ala Leu Trp Asp Thr Ala Gly
 Gln Glu
 50 55 60
 Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Thr Asp
 Val Ile
 65 70 75
 80

0070110

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

<210> 124
 <211> 582
 <212> DNA
 <213> Strongylocentrotus purpuratus

<220>
 <221> CDS
 <222> (1)..(582)

<400>	124												
atg	gct	gcg	att	agg	aaa	aag	ttg	gtc	atc	ggt	gga	gat	ggt
gct	tgt		48										
Met	Ala	Ala	Ile	Arg	Lys	Lys	Leu	Val	Ile	Val	Gly	Asp	Gly
Ala	Cys												
1			5						10				
15													
gga	aag	aca	tgt	ctg	ctc	ata	gta	ttt	agc	aaa	gac	cag	ttc
cct	gaa		96										
Gly	Lys	Thr	Cys	Leu	Leu	Ile	Val	Phe	Ser	Lys	Asp	Gln	Phe

0070110

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

0070110

Ala Lys Thr Asn Asp Gly Val Arg Glu Val Phe Glu Thr Ala
Thr Arg

165

170

175

gca gca ctg cag agt aag aag cgc aag aag aag ctc tca tgc

aag atc 576

Ala Ala Leu Gln Ser Lys Lys Arg Lys Lys Lys Leu Ser Cys

Lys Ile

180

185

190

ttc taa

582

Phe

<210> 125

<211> 193

<212> PRT

<213> Strongylocentrotus purpuratus

<400> 125

Met Ala Ala Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly

Ala Cys

1 5

10

15

Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Asp Gln Phe

Pro Glu

20

25

30

Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Ile

Glu Val

35

40

45

Asp Ser Lys Gln Val Glu Leu Ala Leu Trp Asp Thr Ala Gly

Gln Glu

50

55

60

Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Thr Asp

Val Ile

65

70

75

80

Leu Met Cys Phe Ala Ile Asp Asn Pro Asp Ser Leu Glu Asn

Ile Pro

85

90

95

Glu Lys Trp Thr Pro Glu Val Lys His Phe Cys Pro Asn Val

Pro Ile

100

105

110

0070110

Ile	Leu	Val	Gly	Asn	Lys	Lys	Asp	Leu	Arg	Asn	Asp	Asp	Asn
Thr	Lys												
		115					120					125	

Met	Glu	Leu	Gln	Arg	Thr	Lys	Gln	Thr	Pro	Val	Thr	Tyr	Asp
Glu	Gly												
	130					135					140		

His	Gln	Met	Ser	Val	Lys	Ile	Asn	Ala	Ala	Lys	Tyr	Met	Glu
Cys	Ser												
145					150					155			
160													

Ala	Lys	Thr	Asn	Asp	Gly	Val	Arg	Glu	Val	Phe	Glu	Thr	Ala
Thr	Arg												
				165					170				

175													
Ala	Ala	Leu	Gln	Ser	Lys	Lys	Arg	Lys	Lys	Lys	Leu	Ser	Cys
Lys	Ile												
			180				185					190	

Phe

<210> 126
<211> 609
<212> DNA
<213> Strongylocentrotus purpuratus

<220>
<221> CDS
<222> (1)..(609)

<400>	126												
atg	gct	gcg	att	agg	aaa	aag	ttg	gtc	atc	ggt	gga	gat	ggt
gct	tgt		48										
Met	Ala	Ala	Ile	Arg	Lys	Lys	Leu	Val	Ile	Val	Gly	Asp	Gly
Ala	Cys												
1				5					10				
15													
gga	gcg	acc	tgt	ctg	ctc	aca	gta	ttt	agc	aaa	gac	cag	ttc
cct	gaa		96										
Gly	Ala	Thr	Cys	Leu	Leu	Thr	Val	Phe	Ser	Lys	Asp	Gln	Phe
Pro	Glu												
			20				25					30	
gtc	tac	gtc	cca	aca	gta	ttt	gag	agc	tat	gaa	gct	tat	ata
gaa	gta		144										
Val	Tyr	Val	Pro	Thr	Val	Phe	Glu	Ser	Tyr	Glu	Ala	Tyr	Ile

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0070110

Glu	Val	35			40				45				
gat	agc	aaa	cag	ggt	gaa	tta	gca	tta	tgg	gaa	aca	gca	ggt
cag	gaa	192											
Asp	Ser	Lys	Gln	Val	Glu	Leu	Ala	Leu	Trp	Glu	Thr	Ala	Gly
Gln	Glu				55				60				
gcc	tac	gac	aga	atg	aga	tcg	ctc	tca	tat	cca	gac	aca	gac
ggt	ata	240											
Ala	Tyr	Asp	Arg	Met	Arg	Ser	Leu	Ser	Tyr	Pro	Asp	Thr	Asp
Val	Ile				70				75				
65													
80													
ctc	atg	tgc	ttt	gat	atc	tac	cgt	cca	ggc	act	ttg	gtg	aat
atc	tgg	288											
Leu	Met	Cys	Phe	Asp	Ile	Tyr	Arg	Pro	Gly	Thr	Leu	Val	Asn
Ile	Trp				85				90				
95													
gag	aaa	tgg	aca	cca	gag	gtc	aag	cat	ttc	tgt	ccc	aac	gtg
ccc	atc	336											
Glu	Lys	Trp	Thr	Pro	Glu	Val	Lys	His	Phe	Cys	Pro	Asn	Val
Pro	Ile				100				105				
												110	
atc	ctc	gtg	ggt	aac	aag	aag	gac	ctt	cgt	aac	gac	gac	aac
acc	aag	384											
Ile	Leu	Val	Gly	Asn	Lys	Lys	Asp	Leu	Arg	Asn	Asp	Asp	Asn
Thr	Lys				115				120				
atg	gag	ctg	cag	cag	acc	aag	cag	acc	ccc	gtc	acg	tac	gac
gaa	ggt	432											
Met	Glu	Leu	Gln	Gln	Thr	Lys	Gln	Thr	Pro	Val	Thr	Tyr	Asp
Glu	Gly				130				135				
cac	cag	atg	gcg	gtc	aag	atc	aat	gct	gcc	aag	tac	atg	gag
tgt	tcg	480											
His	Gln	Met	Ala	Val	Lys	Ile	Asn	Ala	Ala	Lys	Tyr	Met	Glu
Cys	Ser				140				145				
145													
160													
gcc	aag	acc	aac	gat	ggg	gtg	agg	gag	gtc	ttt	gaa	acg	gcc
aca	agg	528											
Ala	Lys	Thr	Asn	Asp	Gly	Val	Arg	Glu	Val	Phe	Glu	Thr	Ala
Thr	Arg				165				170				
175													
gca	gca	ctg	cag	agc	att	gag	agc	att	gag	agc	att	gag	agc

0070110

aag aag 576
Ala Ala Leu Gln Ser Ile Glu Ser Ile Glu Ser Ile Glu Ser
Lys Lys 180 185 190

cgc aag aag aag ctt tca tgc aag atc ttc taa
609
Arg Lys Lys Lys Leu Ser Cys Lys Ile Phe
195 200

<210> 127
<211> 202
<212> PRT
<213> Strongylocentrotus purpuratus

<400> 127
Met Ala Ala Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly
Ala Cys
1 5 10
15

Gly Ala Thr Cys Leu Leu Thr Val Phe Ser Lys Asp Gln Phe
Pro Glu 20 25 30

Val Tyr Val Pro Thr Val Phe Glu Ser Tyr Glu Ala Tyr Ile
Glu Val 35 40 45

Asp Ser Lys Gln Val Glu Leu Ala Leu Trp Glu Thr Ala Gly
Gln Glu 50 55 60

Ala Tyr Asp Arg Met Arg Ser Leu Ser Tyr Pro Asp Thr Asp
Val Ile 65 70 75

80
Leu Met Cys Phe Asp Ile Tyr Arg Pro Gly Thr Leu Val Asn
Ile Trp 85 90

95
Glu Lys Trp Thr Pro Glu Val Lys His Phe Cys Pro Asn Val
Pro Ile 100 105 110

Ile Leu Val Gly Asn Lys Lys Asp Leu Arg Asn Asp Asp Asn
Thr Lys 115 120 125

0070110

Met Glu Leu Gln Gln Thr Lys Gln Thr Pro Val Thr Tyr Asp
 Glu Gly
 130 135 140

His Gln Met Ala Val Lys Ile Asn Ala Ala Lys Tyr Met Glu
 Cys Ser
 145 150 155

160
 Ala Lys Thr Asn Asp Gly Val Arg Glu Val Phe Glu Thr Ala
 Thr Arg
 165 170

175
 Ala Ala Leu Gln Ser Ile Glu Ser Ile Glu Ser Ile Glu Ser
 Lys Lys
 180 185 190

Arg Lys Lys Lys Leu Ser Cys Lys Ile Phe
 195 200

<210> 128
 <211> 585
 <212> DNA
 <213> Anopheles gambiae str. PEST

<220>
 <221> CDS
 <222> (1)..(585)

<400> 128
 atg acg atc act ggt acg agt aat ggt ggt ggc ggt gga atg
 cgg ccc 48
 Met Thr Ile Thr Gly Thr Ser Asn Gly Gly Gly Gly Gly Met
 Arg Pro
 1 5 10

15
 ctg aag gta acg acg gtc ggc gac ggt atg gtc ggg aag acc
 tgc atg 96
 Leu Lys Val Thr Thr Val Gly Asp Gly Met Val Gly Lys Thr
 Cys Met

20 25 30
 ctc atc acc tac acg cag aac gag ttc ccg agc gag tac gtc
 ccg acc 144
 Leu Ile Thr Tyr Thr Gln Asn Glu Phe Pro Ser Glu Tyr Val
 Pro Thr

35 40 45
 gtg ttc gac aat cac gcg tgc aac att gtg gtg gac ggg gcc
 gat tac 192
 Val Phe Asp Asn His Ala Cys Asn Ile Val Val Asp Gly Ala

0070110

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

0070110

ata cta tag

585

Ile Leu

<210> 129

<211> 194

<212> PRT

<213> Anopheles gambiae str. PEST

<400> 129

Met Thr Ile Thr Gly Thr Ser Asn Gly Gly Gly Gly Gly Met
Arg Pro

1 5 10

15

Leu Lys Val Thr Thr Val Gly Asp Gly Met Val Gly Lys Thr
Cys Met

20 25 30

Leu Ile Thr Tyr Thr Gln Asn Glu Phe Pro Ser Glu Tyr Val
Pro Thr

35 40 45

Val Phe Asp Asn His Ala Cys Asn Ile Val Val Asp Gly Ala
Asp Tyr

50 55 60

Ala Leu Thr Leu Trp Asp Thr Ala Gly Gln Glu Asp Tyr Glu
Arg Leu

65 70 75

80

Arg Pro Leu Ser Tyr Pro Asn Thr Asp Cys Phe Leu Ile Cys
Tyr Ser

85 90

95

Ile Ser Asn Arg Thr Ser Phe Asp Asn Val Leu Ser Lys Trp
Tyr Pro

100 105 110

Glu Ile Arg His Phe Ala Pro Ser Val Pro Ile Val Leu Val
Gly Thr

115 120 125

Lys Ser Asp Leu Arg Val Pro Gly Ser Glu Lys Phe Val Thr
Thr Ala

130 135 140

Glu Gly Lys Lys Leu Lys His Lys Ile Lys Ala Tyr Ala Leu

Seite 215

0070110

Val Glu
145 150 155
160
Cys Ser Ala Lys Arg Lys Leu Asn Leu Ala Glu Val Phe Asp
Glu Ala
165 170
175
Val Arg Ala Val Glu Lys Lys Pro His Ala Gly Pro Arg Met
Cys Thr
180 185 190

Ile Leu

<210> 130
<211> 600
<212> DNA
<213> Magnaporthe grisea 70-15

<220>
<221> CDS
<222> (1)..(600)

<400> 130
atg gcc gcc cct ggg gtt cag tct ttg aag tgt gtc gtc act
ggc gac 48
Met Ala Ala Pro Gly Val Gln Ser Leu Lys Cys Val Val Thr
Gly Asp
1 5 10
15
ggt gct gtc gga aag aca tgc ctt ctc atc tcc tac acc aca
aac gcc 96
Gly Ala Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Thr
Asn Ala
20 25 30
ttc ccc ggc gag tac atc ccc aca gta ttc gac aac tac tcg
gct agt 144
Phe Pro Gly Glu Tyr Ile Pro Thr Val Phe Asp Asn Tyr Ser
Ala Ser
35 40 45
gtt atg gtc gat gga aag ccc atc agc ttg gga ctt tgg gat
acc gct 192
Val Met Val Asp Gly Lys Pro Ile Ser Leu Gly Leu Trp Asp
Thr Ala
50 55 60
gga cag gag gac tac gac aga ctg agg ccg cta tca tac ccg
cag aca 240
Gly Gln Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro
Seite 216

0070110

Gln Thr
65
80

70

75

gat gtc ttc cta att tgc ttc tcg atc gtt agc ccg ccg tca
ttc gac 288
Asp Val Phe Leu Ile Cys Phe Ser Ile Val Ser Pro Pro Ser
Phe Asp

85

90

95

aac gtc aag gcg aag tgg tac cca gag atc gac cat cac gcg
ccc aac 336
Asn Val Lys Ala Lys Trp Tyr Pro Glu Ile Asp His His Ala
Pro Asn

100

105

110

gtg ccc atc atc ctc gtc gga acc aag ctc gat ctt cgt gaa
gac ccc 384
Val Pro Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Glu
Asp Pro

115

120

125

tcc acc ctc gag agt ctt cgc tcc aag agg atg gag cct gtt
tcg tac 432
Ser Thr Leu Glu Ser Leu Arg Ser Lys Arg Met Glu Pro Val
Ser Tyr

130

135

140

gac cag gca ctt atc tgc gca aag gag att agg gcg cac aag
tac ctt 480
Asp Gln Ala Leu Ile Cys Ala Lys Glu Ile Arg Ala His Lys
Tyr Leu

145

150

155

160

gag tgc tct gca ttg acg caa agg aac ctg aag agt gtg ttc
gat gag 528
Glu Cys Ser Ala Leu Thr Gln Arg Asn Leu Lys Ser Val Phe
Asp Glu

165

170

175

gcc att agg gct gtc ctc aac ccc cga ccc cag ccg gcg aag
gtt aag 576
Ala Ile Arg Ala Val Leu Asn Pro Arg Pro Gln Pro Ala Lys
Val Lys

180

185

190

aag tca aag tgc acc att ctg tga
600

Lys Ser Lys Cys Thr Ile Leu
195

0070110

<210> 131
<211> 199
<212> PRT
<213> Magnaporthe grisea 70-15

<400> 131
Met Ala Ala Pro Gly Val Gln Ser Leu Lys Cys Val Val Thr
Gly Asp
1 5 10
15
Gly Ala Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Thr
Asn Ala
20 25 30
Phe Pro Gly Glu Tyr Ile Pro Thr Val Phe Asp Asn Tyr Ser
Ala Ser
35 40 45
Val Met Val Asp Gly Lys Pro Ile Ser Leu Gly Leu Trp Asp
Thr Ala
50 55 60
Gly Gln Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro
Gln Thr
65 70 75
80
Asp Val Phe Leu Ile Cys Phe Ser Ile Val Ser Pro Pro Ser
Phe Asp
85 90
95
Asn Val Lys Ala Lys Trp Tyr Pro Glu Ile Asp His His Ala
Pro Asn
100 105 110
Val Pro Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Glu
Asp Pro
115 120 125
Ser Thr Leu Glu Ser Leu Arg Ser Lys Arg Met Glu Pro Val
Ser Tyr
130 135 140
Asp Gln Ala Leu Ile Cys Ala Lys Glu Ile Arg Ala His Lys
Tyr Leu
145 150 155
160
Glu Cys Ser Ala Leu Thr Gln Arg Asn Leu Lys Ser Val Phe
Seite 218

0070110

Asp Glu
165 170
175
Ala Ile Arg Ala Val Leu Asn Pro Arg Pro Gln Pro Ala Lys
Val Lys
180 185 190
Lys Ser Lys Cys Thr Ile Leu
195

<210> 132
<211> 609
<212> DNA
<213> *Nasonia vitripennis*

<220>
<221> CDS
<222> (1)..(609)

<400> 132
atg aag aag aga aac atc acc atg agt tca ggt aga cca atc
aag tgc 48
Met Lys Lys Arg Asn Ile Thr Met Ser Ser Gly Arg Pro Ile
Lys Cys
1 5 10
15
gtg gtt gtg gga gat ggc aca gtg gga aaa act tgt atg ctg
ata tct 96
Val Val Val Gly Asp Gly Thr Val Gly Lys Thr Cys Met Leu
Ile Ser
20 25 30
tac acg acg gac agc ttt cct gga gaa tac gtg cct acg gtg
ttt gac 144
Tyr Thr Thr Asp Ser Phe Pro Gly Glu Tyr Val Pro Thr Val
Phe Asp
35 40 45
aat tac tct gca cca atg gta gtg gat ggt att cca gta agc
ctt ggc 192
Asn Tyr Ser Ala Pro Met Val Val Asp Gly Ile Pro Val Ser
Leu Gly
50 55 60
tta tgg gat aca gca ggt caa gaa gat tac gac agg ctc cga
cca ctc 240
Leu Trp Asp Thr Ala Gly Gln Glu Asp Tyr Asp Arg Leu Arg
Pro Leu
65 70 75
80
tct tat cca cag aca gat gtg ttt ctc att tgt ttt tcc gtg

0070110

```

aca agt      288
Ser Tyr Pro Gln Thr Asp Val Phe Leu Ile Cys Phe Ser Val
Thr Ser

          85                      90
95
cca tca tcg ttt gag aat gtc acc agc aag tgg tat cca gaa
ata aaa      336
Pro Ser Ser Phe Glu Asn Val Thr Ser Lys Trp Tyr Pro Glu
Ile Lys
          100                      105                      110

cat cac tgt cca gac gca cca atg att ctt gtg gga acc aaa
att gat      384

His His Cys Pro Asp Ala Pro Met Ile Leu Val Gly Thr Lys
Ile Asp
          115                      120                      125
ctg cga gat gat cgt gaa aca tta act gcc ttg gct gaa caa
ggg ctc      432
Leu Arg Asp Asp Arg Glu Thr Leu Thr Ala Leu Ala Glu Gln
Gly Leu
          130                      135                      140
agt gcc att aaa cgt gaa caa gga cag aaa tta gct aat aag
att cga      480
Ser Ala Ile Lys Arg Glu Gln Gly Gln Lys Leu Ala Asn Lys
Ile Arg
          145                      150                      155
          160
gct gtt aaa tat atg gaa tgt tct gct ttg aca caa cgt ggc
tta aag      528
Ala Val Lys Tyr Met Glu Cys Ser Ala Leu Thr Gln Arg Gly
Leu Lys
          165                      170
          175
caa gtg ttt gat gag gct gtt cgc tca gta ctt cga cct gaa
ccc caa      576
Gln Val Phe Asp Glu Ala Val Arg Ser Val Leu Arg Pro Glu
Pro Gln
          180                      185                      190

aaa cgc aga caa cga agg tgc atc gtg atg taa
          609
Lys Arg Arg Gln Arg Arg Cys Ile Val Met
          195                      200

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<210> 133
 <211> 202
 <212> PRT

0070110

Gln Val Phe Asp Glu Ala Val Arg Ser Val Leu Arg Pro Glu
Pro Gln
180 185 190

Lys Arg Arg Gln Arg Arg Cys Ile Val Met
195 200

<210> 134

<211> 576

<212> DNA

<213> Nasonia vitripennis

<220>

<221> CDS

<222> (1)..(576)

<400> 134

atg cag aca ata aag tgc gtg gtg gtc gga gat gga gct gtg
ggt aaa 48
Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys
1 5 10

15
act tgc ctg ctg att tcc tac acg acg aac aaa ttt ccc tcc
gag tat 96
Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe Pro Ser
Glu Tyr

20 25 30
gta cct aca gtc ttc gac aac tat gca gtc aca gtg atg att
gga gga 144
Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val Met Ile
Gly Gly

35 40 45
gag cct tat act tta gga ctt ttt gat aca gct ggt cag gaa
gat tat 192
Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu
Asp Tyr

50 55 60
gat aga ctt aga cca ctg agc tat cct caa aca gat gtt ttt
cta gtc 240
Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
Leu Val

65 70 75
80

tgt ttt tca gtg gta tcg cct tca tct ttt gaa aac gta aaa
gag aag 288
Cys Phe Ser Val Val Ser Pro Ser Ser Phe Glu Asn Val Lys
Glu Lys

0070110

85

90

95

tgg gtg cca gaa ata acg cat cac tgt caa aag acg ccg ttc
 ttg ctg 336

Trp Val Pro Glu Ile Thr His His Cys Gln Lys Thr Pro Phe
 Leu Leu

100

105

110

gtc gga acg caa atc gat ctg agg gac gac gcg gcg acc atc
 gag aag 384

Val Gly Thr Gln Ile Asp Leu Arg Asp Asp Ala Ala Thr Ile
 Glu Lys

115

120

125

ctc gcg aaa aac aaa cag aag cct ata acg gga gaa cag gga
 gag aaa 432

Leu Ala Lys Asn Lys Gln Lys Pro Ile Thr Gly Glu Gln Gly
 Glu Lys

130

135

140

cta gcg aag gaa ctt aaa gct gtg aaa tac gtc gag tgc agt
 gca ttg 480

Leu Ala Lys Glu Leu Lys Ala Val Lys Tyr Val Glu Cys Ser
 Ala Leu

145

150

155

160

acg cag aaa gga cta aaa aac gtt ttt gac gaa gcg atc tta
 gca gct 528

Thr Gln Lys Gly Leu Lys Asn Val Phe Asp Glu Ala Ile Leu
 Ala Ala

165

170

175

ctc gag ccc cca gaa cca gtg agg aga agg cga tgc atc gtt
 ttg 573

Leu Glu Pro Pro Glu Pro Val Arg Arg Arg Arg Cys Ile Val
 Leu

180

185

190

tag

576

<210> 135

<211> 191

<212> PRT

<213> Nasonia vitripennis

<400> 135

Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val

0070110

Gly	Lys													
1				5					10					
15														
Thr	Cys	Leu	Leu	Ile	Ser	Tyr	Thr	Thr	Asn	Lys	Phe	Pro	Ser	
Glu	Tyr													
			20					25					30	
Val	Pro	Thr	Val	Phe	Asp	Asn	Tyr	Ala	Val	Thr	Val	Met	Ile	
Gly	Gly													
		35					40					45		
Glu	Pro	Tyr	Thr	Leu	Gly	Leu	Phe	Asp	Thr	Ala	Gly	Gln	Glu	
Asp	Tyr													
	50					55						60		
Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Pro	Gln	Thr	Asp	Val	Phe	
Leu	Val													
65					70					75				
	80													
Cys	Phe	Ser	Val	Val	Ser	Pro	Ser	Ser	Phe	Glu	Asn	Val	Lys	
Glu	Lys													
				85					90					
95														
Trp	Val	Pro	Glu	Ile	Thr	His	His	Cys	Gln	Lys	Thr	Pro	Phe	
Leu	Leu													
			100					105					110	
Val	Gly	Thr	Gln	Ile	Asp	Leu	Arg	Asp	Asp	Ala	Ala	Thr	Ile	
Glu	Lys													
		115					120					125		
Leu	Ala	Lys	Asn	Lys	Gln	Lys	Pro	Ile	Thr	Gly	Glu	Gln	Gly	
Glu	Lys													
	130					135					140			
Leu	Ala	Lys	Glu	Leu	Lys	Ala	Val	Lys	Tyr	Val	Glu	Cys	Ser	
Ala	Leu													
145					150					155				
	160													
Thr	Gln	Lys	Gly	Leu	Lys	Asn	Val	Phe	Asp	Glu	Ala	Ile	Leu	
Ala	Ala													
			165					170						
175														
Leu	Glu	Pro	Pro	Glu	Pro	Val	Arg	Arg	Arg	Arg	Cys	Ile	Val	
Leu														
			180					185					190	

0070110

<210> 136
<211> 576
<212> DNA
<213> *Nasonia vitripennis*

<220>
<221> CDS
<222> (1)..(576)

<400> 136
atg caa aca atc aag tgc gta gtt gtg gga gat ggt gcg gta
ggt aaa 48
Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys 1 5 10
15
acc tgc ctg ctg atc tcc tac act acc aat aaa ttt ccc tcc
gaa tat 96
Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe Pro Ser
Glu Tyr 20 25 30
gta cct act gta ttc gac aat tat gca gta aca gta atg atc
gga gga 144
Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val Met Ile
Gly Gly 35 40 45
gat ccc tac acc ctg gga tta ttt gac aca gct ggt cag gaa
gat tat 192
Asp Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu
Asp Tyr 50 55 60
gat cgg ctg cgt cct cta agc tat cca caa acg gat gtt ttt
tta gtc 240
Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
Leu Val 65 70 75
80
tgt ttt tca gtt gta tcg cct tca tca ttt gaa aat gtg aaa
gaa aaa 288
Cys Phe Ser Val Val Ser Pro Ser Ser Phe Glu Asn Val Lys
Glu Lys 85 90
95
tgg gta cca gaa ata aca cat cac tgt caa agg act cca ttc
ctg ctg 336
Trp Val Pro Glu Ile Thr His His Cys Gln Arg Thr Pro Phe
Leu Leu 100 105 110

0070110

```

gta ggc act caa gtt gat tta aga gac gac gtt gct act att
gaa aaa          384
Val Gly Thr Gln Val Asp Leu Arg Asp Asp Val Ala Thr Ile
Glu Lys
      115          120          125
cta gca aag aac aag caa aag cct ata tca gtg gag cag gga
gaa aaa          432
Leu Ala Lys Asn Lys Gln Lys Pro Ile Ser Val Glu Gln Gly
Glu Lys
      130          135          140
ctt gca aag gaa ctg aag gcc gtg aag tac gtc gaa tgc agc
gct ctt          480
Leu Ala Lys Glu Leu Lys Ala Val Lys Tyr Val Glu Cys Ser
Ala Leu
145          150          155
      160
act cag aaa ggc ttg aag aat gta ttt gac gaa gca att tta
gct gca          528
Thr Gln Lys Gly Leu Lys Asn Val Phe Asp Glu Ala Ile Leu
Ala Ala
      165          170
175
ctg gag cca cca gag cct ccg aag ggt aga aag tgt ttc ctt
ctg          573
Leu Glu Pro Pro Glu Pro Pro Lys Gly Arg Lys Cys Phe Leu
Leu
      180          185          190

taa
      576

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<210> 137
 <211> 191
 <212> PRT
 <213> *Nasonia vitripennis*

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<400> 137
Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys
1          5          10
15
Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe Pro Ser
Glu Tyr
      20          25          30

```

0070110

Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val Met Ile
Gly Gly 35 40 45

Asp Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu
Asp Tyr 50 55 60

Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
Leu Val 65 70 75

Cys Phe Ser Val Val Ser Pro Ser Ser Phe Glu Asn Val Lys
Glu Lys 80 85 90

95
Trp Val Pro Glu Ile Thr His His Cys Gln Arg Thr Pro Phe
Leu Leu 100 105 110

Val Gly Thr Gln Val Asp Leu Arg Asp Asp Val Ala Thr Ile
Glu Lys 115 120 125

Leu Ala Lys Asn Lys Gln Lys Pro Ile Ser Val Glu Gln Gly
Glu Lys 130 135 140

Leu Ala Lys Glu Leu Lys Ala Val Lys Tyr Val Glu Cys Ser
Ala Leu 145 150 155

160
Thr Gln Lys Gly Leu Lys Asn Val Phe Asp Glu Ala Ile Leu
Ala Ala 165 170

175
Leu Glu Pro Pro Glu Pro Pro Lys Gly Arg Lys Cys Phe Leu
Leu 180 185 190

<210> 138

<211> 579

<212> DNA

<213> Nasonia vitripennis

<220>

<221> CDS

<222> (1)..(579)

<400> 138

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atg gca gct ata agg aag aaa ttg gtg atc gtt ggc gat ggt
gcc tgt          48
Met Ala Ala Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly
Ala Cys
  1              5              10
15
ggt aaa act tgc ttg ctg att gtg ttc agt aag gat cag ttt
cct gag          96
Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Asp Gln Phe
Pro Glu
          20              25              30
gtg tat gtg cct act gtt ttt gaa aac tat gta gct gat att
gaa gta          144
Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Ile
Glu Val
          35              40              45
gat gga aag caa gtc gag ctc gcc ctg tgg gat act gca ggg
caa gaa          192
Asp Gly Lys Gln Val Glu Leu Ala Leu Trp Asp Thr Ala Gly
Gln Glu
          50              55              60
gac tac gac aga ctt cgc cca cta tcc tat cct gac aca gat
gtc atc          240
Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Thr Asp
Val Ile
  65              70              75
80
ttg atg tgc ttc tcc att gac agt ccc gat tcc ctt gag aac
att ccg          288
Leu Met Cys Phe Ser Ile Asp Ser Pro Asp Ser Leu Glu Asn
Ile Pro
          85              90
95
gaa aag tgg aca cca gag gtc aag cat ttt tgc cct aat gta
cca atc          336
Glu Lys Trp Thr Pro Glu Val Lys His Phe Cys Pro Asn Val
Pro Ile
          100              105              110
att ttg gtt ggt aac aaa aag gat ctg cgc aat gat cca agc
acc atc          384
Ile Leu Val Gly Asn Lys Lys Asp Leu Arg Asn Asp Pro Ser
Thr Ile
  115              120              125
aag gaa ctt ggc aag atg aag cag gag ccc gtc aag ccc gaa

```


0070110

```

gaa ggc      432
Lys Glu Leu Gly Lys Met Lys Gln Glu Pro Val Lys Pro Glu
Glu Gly
      130
cgc gcc atg gct gaa aag atc agt gct ttt gcc tac ctt gag
tgc tct      480
Arg Ala Met Ala Glu Lys Ile Ser Ala Phe Ala Tyr Leu Glu
Cys Ser
145      150      155
      160
gcc aag agc aag gaa ggt gtc aga gag gtc ttt gaa aca gcg
acc aga      528
Ala Lys Ser Lys Glu Gly Val Arg Glu Val Phe Glu Thr Ala
Thr Arg
      165      170
175
gct gca tta cag gtc aag aag aag aag aag gga agg tgt agg
ctg ctt      576
Ala Ala Leu Gln Val Lys Lys Lys Lys Lys Gly Arg Cys Arg
Leu Leu
      180      185      190

taa
      579

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<210> 139
 <211> 192
 <212> PRT
 <213> *Nasonia vitripennis*

```

<400> 139
Met Ala Ala Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly
Ala Cys
1      5      10
15
Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Asp Gln Phe
Pro Glu
      20      25      30

Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Ile
Glu Val
      35      40      45

Asp Gly Lys Gln Val Glu Leu Ala Leu Trp Asp Thr Ala Gly
Gln Glu
      50      55      60

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0070110

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

<210> 140

<211> 561

<212> DNA

<213> Aedes aegypti

<220>

<221> CDS

<222> (1)..(561)

<400> 140

atg	acg	atg	ggc	aat	atg	cgt	ccg	cta	aaa	atc	acc	act	gtc
ggc	gat		48										
Met	Thr	Met	Gly	Asn	Met	Arg	Pro	Leu	Lys	Ile	Thr	Thr	Val
Gly	Asp												

0070110

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

0070110

Leu Asn
 145 150 155
 160
 ctc ggg gaa gtg ttt gac gaa gcc gtg cga gcg gtg gag aaa
 aag ccc 528
 Leu Gly Glu Val Phe Asp Glu Ala Val Arg Ala Val Glu Lys
 Lys Pro
 165 170
 175
 cac gcc aaa cca cgt gtc tgt acg ata ctc tag
 561
 His Ala Lys Pro Arg Val Cys Thr Ile Leu
 180 185

<210> 141
 <211> 186
 <212> PRT
 <213> Aedes aegypti

<400> 141
 Met Thr Met Gly Asn Met Arg Pro Leu Lys Ile Thr Thr Val
 Gly Asp
 1 5 10
 15
 Gly Met Val Gly Lys Thr Cys Met Leu Ile Thr Tyr Thr Gln
 Asn Glu
 20 25 30
 Phe Pro Val Glu Tyr Val Pro Thr Val Phe Asp Asn His Ala
 Cys Asn
 35 40 45
 Ile Thr Val Asp Glu Lys Glu Tyr Ala Leu Thr Leu Trp Asp
 Thr Ala
 50 55 60
 Gly Gln Glu Asp Tyr Glu Arg Leu Arg Pro Leu Ser Tyr Pro
 Asn Thr
 65 70 75
 80
 Asp Cys Phe Leu Ile Cys Tyr Ser Ile Ser Ser Lys Thr Ser
 Phe Asp
 85 90
 95
 Asn Val Leu Ser Lys Trp Tyr Pro Glu Ile Arg His Tyr Ala
 Pro His
 100 105 110

0070110

Val Pro Ile Val Leu Val Gly Thr Lys Ser Asp Leu Arg Val
His Gly 115 120 125

Ser Glu Lys Phe Val Thr Thr Ala Glu Gly Lys Lys Leu Lys
His Lys 130 135 140

Ile Lys Ala Tyr Ser Leu Val Glu Cys Ser Ala Lys Lys Lys
Leu Asn 145 150 155

160
Leu Gly Glu Val Phe Asp Glu Ala Val Arg Ala Val Glu Lys
Lys Pro 165 170

175
His Ala Lys Pro Arg Val Cys Thr Ile Leu
180 185

<210> 142

<211> 624

<212> DNA

<213> Aedes aegypti

<220>

<221> CDS

<222> (1)..(624)

<400> 142

atg tgg tgt ttt tca tgc gtt tct gct cca gct aat tca gaa
caa atg 48
Met Trp Cys Phe Ser Cys Val Ser Ala Pro Ala Asn Ser Glu
Gln Met 1 5 10

15
gca gcc atc cgg aag aag ctc gta atc gtc ggc gac ggt gcc
tgc ggt 96
Ala Ala Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly Ala
Cys Gly 20 25 30

aag acg tgt ctg ctg atc gtc ttc agc aag gat cag ttc ccg
gag gtt 144
Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Asp Gln Phe Pro
Glu Val 35 40 45

tac gtc ccc acc gtg ttc gag aac tat gtg gcc gac atc gag
gtc gac 192
Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Ile Glu

0070110

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

0070110

gcg tta cag gtc aaa aag aag aag aag agt aaa tgt gtt ttg
 ctc 621
 Ala Leu Gln Val Lys Lys Lys Lys Lys Ser Lys Cys Val Leu
 Leu
 195 200 205
 taa
 624

<210> 143
 <211> 207
 <212> PRT
 <213> Aedes aegypti

<400> 143
 Met Trp Cys Phe Ser Cys Val Ser Ala Pro Ala Asn Ser Glu
 Gln Met
 1 5 10
 15
 Ala Ala Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly Ala
 Cys Gly
 20 25 30
 Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Asp Gln Phe Pro
 Glu Val
 35 40 45
 Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Ile Glu
 Val Asp
 50 55 60
 Gly Lys Gln Val Glu Leu Ala Leu Trp Asp Thr Ala Gly Gln
 Glu Asp
 65 70 75
 80
 Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Thr Asp Val
 Ile Leu
 85 90
 95
 Met Cys Phe Ser Val Asp Ser Pro Asp Ser Leu Glu Asn Ile
 Pro Glu
 100 105 110
 Lys Trp Thr Pro Glu Val Lys His Phe Cys Pro Asn Val Pro
 Ile Ile
 115 120 125

0070110

Leu Val Gly Asn Lys Lys Asp Leu Arg Asn Asp Pro His Thr
 Ile Lys
 130 135 140

Glu Leu Ala Lys Met Lys Gln Glu Pro Val Lys Pro Gln Glu
 Gly Arg
 145 150 155

160
 Ala Met Ala Glu Lys Ile Asn Ala Phe Ala Tyr Leu Glu Cys
 Ser Ala
 165 170

175
 Lys Ser Lys Glu Gly Val Arg Glu Val Phe Glu Thr Ala Thr
 Arg Ala
 180 185 190

Ala Leu Gln Val Lys Lys Lys Lys Lys Ser Lys Cys Val Leu
 Leu
 195 200 205

<210> 144
 <211> 579
 <212> DNA
 <213> Aedes aegypti

<220>
 <221> CDS
 <222> (1)..(579)

<400> 144
 atg cag gcc atc aag tgc gtc gta gtc gga gat ggt gcc gtg
 ggt aag 48
 Met Gln Ala Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
 Gly Lys
 1 5 10
 15
 acc tgt ctg ttg atc agc tac acg acc aat gcc ttc ccg gga
 gaa tac 96
 Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Ala Phe Pro Gly
 Glu Tyr
 20 25 30
 att ccg acc gtg ttc gac aac tat tcg gcc aac gtc atg gtc
 gac ggg 144
 Ile Pro Thr Val Phe Asp Asn Tyr Ser Ala Asn Val Met Val
 Asp Gly
 35 40 45
 aag cca atc aat ctg gga ctg tgg gat acg gct gga cag gaa
 Seite 236

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gat	tac			192										
Lys	Pro	Ile	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala	Gly	Gln	Glu	
Asp	Tyr													
	50					55					60			
gat	cgt	ctc	cgg	cca	ctt	tcc	tac	cca	cag	acg	gac	gtg	ttt	
ctc	ata			240										
Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Pro	Gln	Thr	Asp	Val	Phe	
Leu	Ile													
65					70					75				
80														
tgc	ttc	tcg	ctg	gta	aat	ccg	gcc	tcg	ttt	gaa	aac	gtt	cgg	
gcc	aag			288										
Cys	Phe	Ser	Leu	Val	Asn	Pro	Ala	Ser	Phe	Glu	Asn	Val	Arg	
Ala	Lys													
				85						90				
95														
tgg	tac	ccg	gag	gta	cgt	cac	cat	tgt	ccg	aac	ata	ccg	ata	
atc	ctc			336										
Trp	Tyr	Pro	Glu	Val	Arg	His	His	Cys	Pro	Asn	Ile	Pro	Ile	
Ile	Leu													
				100				105					110	
gtt	gga	acc	aag	ctc	gat	ctt	cgg	gat	gac	aag	caa	acc	gtg	
gat	aag			384										
Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys	Gln	Thr	Val	
Asp	Lys													
		115					120					125		
cta	cgc	gaa	aag	aag	ctc	tcg	ccc	atc	acc	tac	ccc	cag	gga	
ttg	gcc			432										
Leu	Arg	Glu	Lys	Lys	Leu	Ser	Pro	Ile	Thr	Tyr	Pro	Gln	Gly	
Leu	Ala													
		130				135					140			
atg	gcc	aag	gaa	atc	ggc	gcc	gtc	aag	tat	ttg	gaa	tgt	tct	
gcc	ctg			480										
Met	Ala	Lys	Glu	Ile	Gly	Ala	Val	Lys	Tyr	Leu	Glu	Cys	Ser	
Ala	Leu													
145					150					155				
160														
aca	cag	aag	ggg	ctc	aaa	acc	gtt	ttc	gac	gaa	gcg	atc	cgt	
gcc	gtt			528										
Thr	Gln	Lys	Gly	Leu	Lys	Thr	Val	Phe	Asp	Glu	Ala	Ile	Arg	
Ala	Val													
				165						170				
175														
ctc	tgt	ccc	atc	ata	ccg	gtg	aaa	aac	aaa	cgt	aaa	tgt	tca	
att	ctg			576										
Leu	Cys	Pro	Ile	Ile	Pro	Val	Lys	Asn	Lys	Arg	Lys	Cys	Ser	
Ile	Leu													

0070110

180

185

190

taa

579

<210> 145

<211> 192

<212> PRT

<213> Aedes aegypti

<400> 145

Met Gln Ala Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys

1

5

10

15

Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Ala Phe Pro Gly
Glu Tyr

20

25

30

Ile Pro Thr Val Phe Asp Asn Tyr Ser Ala Asn Val Met Val
Asp Gly

35

40

45

Lys Pro Ile Asn Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu
Asp Tyr

50

55

60

Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
Leu Ile

65

70

75

80

Cys Phe Ser Leu Val Asn Pro Ala Ser Phe Glu Asn Val Arg
Ala Lys

85

90

95

Trp Tyr Pro Glu Val Arg His His Cys Pro Asn Ile Pro Ile
Ile Leu

100

105

110

Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys Gln Thr Val
Asp Lys

115

120

125

Leu Arg Glu Lys Lys Leu Ser Pro Ile Thr Tyr Pro Gln Gly
Leu Ala

130

135

140

0070110

Met Ala Lys Glu Ile Gly Ala Val Lys Tyr Leu Glu Cys Ser
Ala Leu
145 150 155
160
Thr Gln Lys Gly Leu Lys Thr Val Phe Asp Glu Ala Ile Arg
Ala Val
165 170
175
Leu Cys Pro Ile Ile Pro Val Lys Asn Lys Arg Lys Cys Ser
Ile Leu
180 185 190

<210> 146
<211> 624
<212> DNA
<213> Anopheles gambiae str. PEST

<220>
<221> CDS
<222> (1)..(624)

<400> 146
atg tgg tgt ctt tca tgc gtc tct tct cca act aat tca gaa
cca atg 48
Met Trp Cys Leu Ser Cys Val Ser Ser Pro Thr Asn Ser Glu
Pro Met
1 5 10
15
gct gct ata agg aaa aag ctt gtg atc gtc ggc gat ggt gcc
tgc ggt 96
Ala Ala Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly Ala
Cys Gly
20 25 30
aaa acc tgt ctg ctg atc gtc ttc agc aag gat cag ttc ccg
gag gtg 144
Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Asp Gln Phe Pro
Glu Val
35 40 45
tac gtg ccg acc gtg ttc gaa aac tac gtg gcc gac atc gaa
gtc gac 192
Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Ile Glu
Val Asp
50 55 60
ggc aag cag gtt gag ctg gca ctg tgg gat acg gcc ggg caa
gaa gat 240
Gly Lys Gln Val Glu Leu Ala Leu Trp Asp Thr Ala Gly Gln

Glu 65	Asp 80	70						75							
tac	gac	aga	ctg	agg	ccg	ctg	agc	tac	cca	gac	acc	gat	gtt		
att	ctc	288													
Tyr	Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Pro	Asp	Thr	Asp	Val		
Ile	Leu	85						90							
95	atg	tgc	ttc	tct	gtc	gat	tca	ccc	gac	tcg	ctg	gag	aac	atc	
ccc	gaa	336													
Met	Cys	Phe	Ser	Val	Asp	Ser	Pro	Asp	Ser	Leu	Glu	Asn	Ile		
Pro	Glu	100						105						110	
aag	tgg	acc	cct	gag	gta	aaa	cat	ttc	tgt	cct	aat	gta	ccc		
atc	atc	384													
Lys	Trp	Thr	Pro	Glu	Val	Lys	His	Phe	Cys	Pro	Asn	Val	Pro		
Ile	Ile	115						120						125	
tta	gtc	ggc	aac	aaa	aaa	gat	ctc	aga	aat	gac	cca	cac	aca		
ata	aag	432													
Leu	Val	Gly	Asn	Lys	Lys	Asp	Leu	Arg	Asn	Asp	Pro	His	Thr		
Ile	Lys	130						135						140	
gaa	ttg	gct	aaa	atg	aag	cag	gag	ccc	gtc	aag	cca	cag	gag		
gga	cgt	480													
Glu	Leu	Ala	Lys	Met	Lys	Gln	Glu	Pro	Val	Lys	Pro	Gln	Glu		
Gly	Arg	145						150						155	
160	gcg	atg	gcc	gaa	aaa	att	aat	gct	ttc	gct	tat	tta	gag	tgt	
tcg	gcc	528													
Ala	Met	Ala	Glu	Lys	Ile	Asn	Ala	Phe	Ala	Tyr	Leu	Glu	Cys		
Ser	Ala	165						170							
175	aaa	tcg	aag	gag	ggc	gtg	cgt	gaa	gtt	ttc	gag	act	gct	acg	
aga	gca	576													
Lys	Ser	Lys	Glu	Gly	Val	Arg	Glu	Val	Phe	Glu	Thr	Ala	Thr		
Arg	Ala	180						185						190	
gcg	tta	cag	gtg	aaa	aag	aag	aag	aag	agt	aaa	tgt	gtt	ctg		
ctc	621														
Ala	Leu	Gln	Val	Lys	Lys	Lys	Lys	Lys	Ser	Lys	Cys	Val	Leu		
Leu	195						200						205		

taa

624

<210> 147

<211> 207

<212> PRT

<213> Anopheles gambiae str. PEST

<400> 147

Met Trp Cys Leu Ser Cys Val Ser Ser Pro Thr Asn Ser Glu
Pro Met

1 5 10

15

Ala Ala Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly Ala
Cys Gly

20 25 30

Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Asp Gln Phe Pro
Glu Val

35 40 45

Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Ile Glu
Val Asp
50 55 60

Gly Lys Gln Val Glu Leu Ala Leu Trp Asp Thr Ala Gly Gln
Glu Asp
65 70 75

80

Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Thr Asp Val
Ile Leu

85 90

95

Met Cys Phe Ser Val Asp Ser Pro Asp Ser Leu Glu Asn Ile
Pro Glu

100 105 110

Lys Trp Thr Pro Glu Val Lys His Phe Cys Pro Asn Val Pro
Ile Ile

115 120 125

Leu Val Gly Asn Lys Lys Asp Leu Arg Asn Asp Pro His Thr
Ile Lys

130 135 140

Glu Leu Ala Lys Met Lys Gln Glu Pro Val Lys Pro Gln Glu
Seite 241

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Gly Arg
145 150 155
160
Ala Met Ala Glu Lys Ile Asn Ala Phe Ala Tyr Leu Glu Cys
Ser Ala
165 170
175
Lys Ser Lys Glu Gly Val Arg Glu Val Phe Glu Thr Ala Thr
Arg Ala
180 185 190
Ala Leu Gln Val Lys Lys Lys Lys Lys Ser Lys Cys Val Leu
Leu
195 200 205

<210> 148
<211> 579
<212> DNA
<213> Anopheles gambiae str. PEST

<220>
<221> CDS
<222> (1)..(579)

<400> 148
atg gct gct ata agg aaa aag ctt gtg atc gtc ggc gat ggt
gcc tgc 48
Met Ala Ala Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly
Ala Cys
1 5 10
15
ggt aaa acc tgt ctg ctg atc gtc ttc agc aag gat cag ttc
ccg gag 96
Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Asp Gln Phe
Pro Glu
20 25 30
gtg tac gtg ccg acc gtg ttc gaa aac tac gtg gcc gac atc
gaa gtc 144
Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Ile
Glu Val
35 40 45
gac ggc aag cag gtt gag ctg gca ctg tgg gat acg gcc ggg
caa gaa 192
Asp Gly Lys Gln Val Glu Leu Ala Leu Trp Asp Thr Ala Gly
Gln Glu
50 55 60
gat tac gac aga ctg agg ccg ctg agc tac cca gac acc gat
Seite 242

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gtt att      240
Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Thr Asp
Val Ile
65      70      75
80
ctc atg tgc ttc tct gtc gat tca ccc gac tcg ctg gag aac
atc ccc      288
Leu Met Cys Phe Ser Val Asp Ser Pro Asp Ser Leu Glu Asn
Ile Pro
85      90
95
gaa aag tgg acc cct gag gta aaa cat ttc tgt cct aat gta
ccc atc      336
Glu Lys Trp Thr Pro Glu Val Lys His Phe Cys Pro Asn Val
Pro Ile
100      105      110
atc tta gtc ggc aac aaa aaa gat ctc aga aat gac cca cac
aca ata      384
Ile Leu Val Gly Asn Lys Lys Asp Leu Arg Asn Asp Pro His
Thr Ile
115      120      125
aag gaa ttg gct aaa atg aag cag gag ccc gtc aag cca cag
gag gga      432
Lys Glu Leu Ala Lys Met Lys Gln Glu Pro Val Lys Pro Gln
Glu Gly
130      135      140
cgt gcg atg gcc gaa aaa att aat gct ttc gct tat tta gag
tgt tcg      480
Arg Ala Met Ala Glu Lys Ile Asn Ala Phe Ala Tyr Leu Glu
Cys Ser
145      150      155
160
gcc aaa tcg aag gag ggc gtg cgt gaa gtt ttc gag act gct
acg aga      528
Ala Lys Ser Lys Glu Gly Val Arg Glu Val Phe Glu Thr Ala
Thr Arg
165      170
175
gca gcg tta cag gtg aaa aag aag aag aag agt aaa tgt gtt
ctg ctc      576
Ala Ala Leu Gln Val Lys Lys Lys Lys Lys Ser Lys Cys Val
Leu Leu
180      185      190
taa
579

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0070110

<210> 149
<211> 192
<212> PRT
<213> Anopheles gambiae str. PEST

<400> 149
Met Ala Ala Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly
Ala Cys
1 5 10
15
Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Asp Gln Phe
Pro Glu
20 25 30
Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Ile
Glu Val
35 40 45
Asp Gly Lys Gln Val Glu Leu Ala Leu Trp Asp Thr Ala Gly
Gln Glu
50 55 60
Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Thr Asp
Val Ile
65 70 75
80
Leu Met Cys Phe Ser Val Asp Ser Pro Asp Ser Leu Glu Asn
Ile Pro
85 90
95
Glu Lys Trp Thr Pro Glu Val Lys His Phe Cys Pro Asn Val
Pro Ile
100 105 110
Ile Leu Val Gly Asn Lys Lys Asp Leu Arg Asn Asp Pro His
Thr Ile
115 120 125
Lys Glu Leu Ala Lys Met Lys Gln Glu Pro Val Lys Pro Gln
Glu Gly
130 135 140
Arg Ala Met Ala Glu Lys Ile Asn Ala Phe Ala Tyr Leu Glu
Cys Ser
145 150 155
160

0070110

Ala Lys Ser Lys Glu Gly Val Arg Glu Val Phe Glu Thr Ala
Thr Arg

165

170

175

Ala Ala Leu Gln Val Lys Lys Lys Lys Lys Ser Lys Cys Val
Leu Leu

180

185

190

<210> 150

<211> 591

<212> DNA

<213> Physcomitrella patens subsp. patens

<220>

<221> CDS

<222> (1)..(591)

<400> 150

atg agc act tca cgg ttt atc aag tgc gtg act gtt gga gat
gga gct 48

Met Ser Thr Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala

1

5

10

15

gtc ggg aag acg tgc atg ctt att tca tac acc agc aac aca
ttt cct 96

Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro

20

25

30

act gat tac gtt cct acc gtg ttt gac aac ttc agc gca aat
gta gtg 144

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val

35

40

45

gtc gat gga aat acc gtc aac ctc ggg tta tgg gat aca gca
ggt caa 192

Val Asp Gly Asn Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln

50

55

60

gaa gat tac aac agg ctt cgt cct ctg agt tac agg ggt gct
gat gtt 240

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val

65

70

75

80

ttt ctc ctg gcg ttc tcc ctc atc agc aag gct agt tat gaa
aac ata 288

0070110

Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Ile

85

90

95

tca aag aag tgg atc ccg gaa ctg aga cat tac gcg cca tct
gtg cca
Ser Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Ser
Val Pro

100

105

110

atc att ctc gtc gga aca aaa ctt gat ctt cgc gat gac aaa
caa ttc
Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe

115

120

125

ttt gct gat cat cct gga gcg gct cca ata act act tct caa
ggg gag
Phe Ala Asp His Pro Gly Ala Ala Pro Ile Thr Thr Ser Gln
Gly Glu

130

135

140

gag ctc agg aag tcg att ggg gcg gcc tcg tac ata gag tgc
agc tca
Glu Leu Arg Lys Ser Ile Gly Ala Ala Ser Tyr Ile Glu Cys
Ser Ser

145

150

155

160

aag act cag cag aat gta aaa gca gtt ttt gac gca gca atc
aag gtg
Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Lys Val

165

170

175

gtt ctc caa cca cca aag cag aag aag aag aag aaa aaa caa
aag aat
Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Lys Lys Gln
Lys Asn

180

185

190

tgc gtc att ctg tga
Cys Val Ile
195

<210> 151

<211> 196

<212> PRT

<213> Physcomitrella patens subsp. patens

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<400> 151
Met Ser Thr Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1          5          10
15
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
          20          25          30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
          35          40          45

Val Asp Gly Asn Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
          50          55          60

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

Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe
          115          120          125

Phe Ala Asp His Pro Gly Ala Ala Pro Ile Thr Thr Ser Gln
Gly Glu
          130          135          140

Glu Leu Arg Lys Ser Ile Gly Ala Ala Ser Tyr Ile Glu Cys
Ser Ser
145          150          155
160
Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Lys Val
          165          170
175
Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Lys Gln
Lys Asn

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0070110

180

185

190

Cys Val Ile Leu
195

<210> 152

<211> 591

<212> DNA

<213> Physcomitrella patens subsp. patens

<220>

<221> CDS

<222> (1)..(591)

<400> 152

atg agc aca tct cgg ttt atc aag tgc gtt act gta gga gat
gga gca 48
Met Ser Thr Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10

15
gtc gga aag acg tgc atg ctt att tct tat acc agc aat aca
ttt cct 96
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro

20 25 30
act gat tac gtt cct acc gtt ttt gat aac ttc agc gcg aat
gtc gtt 144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val

35 40 45
gtc gat gga aac act gta aac ctt gga cta tgg gat aca gca
ggc cag 192
Val Asp Gly Asn Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln

50 55 60
gaa gat tat aac agg ctt cga cct ctg agt tac agg ggt gct
gat gtt 240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val

65 70 75
80
ttt cta cta gca ttc tct ctt atc agc aaa gct agt tat gag
aac atc 288
Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Ile

85

90

0070110

95
tca aag aag tgg att cct gaa ctg aga cac tac gct cca tct
gta cct 336
Ser Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Ser
Val Pro
100 105 110

att atc ctc gtc gga acg aag cta gat ctt cga gat gac aag
caa ttt 384
Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe
115 120 125

ttc gcc gac cat cct gga gcg gct ccg atc aca acc tcc caa
ggt gaa 432
Phe Ala Asp His Pro Gly Ala Ala Pro Ile Thr Thr Ser Gln
Gly Glu
130 135 140

gaa ctc aga aag gcg att gga gca gcc tct tac att gag tgt
agc tct 480
Glu Leu Arg Lys Ala Ile Gly Ala Ala Ser Tyr Ile Glu Cys
Ser Ser
145 150 155

160
aag act cag cag aat gtg aaa gca gtt ttt gat gct gcc atc
aag gtt 528
Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Lys Val
165 170

175
gtt ctt cag cca ccc aag cag aag aag aag aag aaa aaa caa
aag aac 576
Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Lys Lys Gln
Lys Asn
180 185 190

tgt gtt att ctc tga
591
Cys Val Ile Leu
195

<210> 153

<211> 196

<212> PRT

<213> Physcomitrella patens subsp. patens

<400> 153

Met Ser Thr Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala

0070110

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

0070110

<210> 154
<211> 591
<212> DNA
<213> Physcomitrella patens subsp. patens

<220>
<221> CDS
<222> (1)..(591)

<400> 154
atg agc act tct cgc ttt atc aag tgc gtt act gta gga gat
gga gct 48
Met Ser Thr Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10
15
gtg ggg aag acg tgc atg ctt att tca tat acc agc aat aca
ttt cct 96
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
20 25 30
act gat tac gtc cct act gta ttc gac aac ttc agc gcg aat
gtc gtg 144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
35 40 45
gtc gat ggg aat acc gtc aac ctg gga cta tgg gat aca gca
ggt caa 192
Val Asp Gly Asn Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60
gaa gat tac aac aga ctc cga cct ctt agt tac agg ggt gcc
gat gtg 240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65 70 75
80
ttt tta ctg gca ttc tct ctc atc agc aag gct agt tat gaa
aac atc 288
Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Ile
85 90
95
tct aag aag tgg att cct gaa cta aga cat tat gcg cca tct
gtg cct 336
Ser Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Ser
Val Pro

0070110

100

105

110

atc atc ctc gtg gga acg aaa cta gat ctt cga gac gac aag
 cag ttc 384
 Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
 Gln Phe

115 120 125
 ttc gct gat cat cca gga gcg gct cca ata act acc tct caa
 ggt gaa 432
 Phe Ala Asp His Pro Gly Ala Ala Pro Ile Thr Thr Ser Gln
 Gly Glu

130 135 140
 gag ctc agg agg tca att gga gca gcc tca tac att gag tgt
 agc tca 480
 Glu Leu Arg Arg Ser Ile Gly Ala Ala Ser Tyr Ile Glu Cys
 Ser Ser

145 150 155
 160
 aag act cag cag aat gtg aaa gca gtt ttt gat gcc gcc ata
 aag gtg 528
 Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
 Lys Val

165 170
 175
 gtt ctt cag cca ccc aag cag aag aag aag aaa aag aag caa
 aag aac 576
 Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Lys Lys Gln
 Lys Asn

180 185 190
 tgt gtc att ctc taa
 591
 Cys Val Ile Leu
 195

<210> 155

<211> 196

<212> PRT

<213> Physcomitrella patens subsp. patens

<400> 155

Met Ser Thr Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala
 1 5 10
 15
 Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
 Phe Pro

20

25

30

0070110

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

<210> 156

<211> 597

<212> DNA

<213> Coprinopsis cinerea okayama7#130

0070110

<220>

<221> CDS

<222> (1)..(597)

<400> 156

atg gac tcg cga cga cca gat ttg aaa cgg aag ctc gtc gtt
gtt ggg 48
Met Asp Ser Arg Arg Pro Asp Leu Lys Arg Lys Leu Val Val
Val Gly
1 5 10

15
gac gga ggc tgt gga aag acg tgt ctg tta atc gtc tac gcc
gag aac 96
Asp Gly Gly Cys Gly Lys Thr Cys Leu Leu Ile Val Tyr Ala
Glu Asn

20 25 30
cga ttt cca gag gcc tat ata cca aca gtg ttt gag aac tac
gtg acc 144
Arg Phe Pro Glu Ala Tyr Ile Pro Thr Val Phe Glu Asn Tyr
Val Thr

35 40 45
cag gtg cag ttt gaa ggc aaa ttg gtt gag ttg gcg cta tgg
gat acc 192
Gln Val Gln Phe Glu Gly Lys Leu Val Glu Leu Ala Leu Trp
Asp Thr

50 55 60
gcg gga caa gag gaa tac gac cga cta cga ccg tta tcg tac
cct gaa 240
Ala Gly Gln Glu Glu Tyr Asp Arg Leu Arg Pro Leu Ser Tyr
Pro Glu

65 70 75
80
agc aac gtt atc ctc atc gtc ttc tcc atc gac ttt cca aca
tca ctt 288
Ser Asn Val Ile Leu Ile Val Phe Ser Ile Asp Phe Pro Thr
Ser Leu

85 90
95
gcc aat gtc cag gac aag tgg tat ccc gag gta gcc cac ttt
tgc gaa 336
Ala Asn Val Gln Asp Lys Trp Tyr Pro Glu Val Ala His Phe
Cys Glu

100 105 110
aat acc ccg cta atc ctc gtg ggc aca aag acc gat ttg cga
cgt gac 384
Asn Thr Pro Leu Ile Leu Val Gly Thr Lys Thr Asp Leu Arg

0070110

```

Arg Asp
115
gag caa acc agg cgt atg ctg agc gca cag gga caa gcc cct
atc acc
432
Glu Gln Thr Arg Arg Met Leu Ser Ala Gln Gly Gln Ala Pro
Ile Thr
130
ccc gag caa ggc gcc gcc gtt gca aag gag atc gga gct aaa
tac atc
480
Pro Glu Gln Gly Ala Ala Val Ala Lys Glu Ile Gly Ala Lys
Tyr Ile
145
150
155
160
gaa tgc tca gca aag gct ggt acc ggc gta cat gaa gtc ttt
gaa ctc
528
Glu Cys Ser Ala Lys Ala Gly Thr Gly Val His Glu Val Phe
Glu Leu
165
170
175
gcg ttg agg gag agc atg aag ggt cgc tgg ggg aag att gtc
aat cag
576
Ala Leu Arg Glu Ser Met Lys Gly Arg Trp Gly Lys Ile Val
Asn Gln
180
185
190

aaa cga tgc gtt atc atc tag
597
Lys Arg Cys Val Ile Ile
195

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<210> 157

<211> 198

<212> PRT

<213> Coprinopsis cinerea okayama7#130

<400> 157

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Met Asp Ser Arg Arg Pro Asp Leu Lys Arg Lys Leu Val Val
Val Gly

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1 5 10

15

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Asp Gly Gly Cys Gly Lys Thr Cys Leu Leu Ile Val Tyr Ala
Glu Asn

```

20

25

30

```

Arg Phe Pro Glu Ala Tyr Ile Pro Thr Val Phe Glu Asn Tyr
Val Thr

```

35

40

45

0070110

Gln Val Gln Phe Glu Gly Lys Leu Val Glu Leu Ala Leu Trp
 Asp Thr
 50 55 60

Ala Gly Gln Glu Glu Tyr Asp Arg Leu Arg Pro Leu Ser Tyr
 Pro Glu
 65 70 75

80
 Ser Asn Val Ile Leu Ile Val Phe Ser Ile Asp Phe Pro Thr
 Ser Leu
 85 90

95
 Ala Asn Val Gln Asp Lys Trp Tyr Pro Glu Val Ala His Phe
 Cys Glu
 100 105 110

Asn Thr Pro Leu Ile Leu Val Gly Thr Lys Thr Asp Leu Arg
 Arg Asp
 115 120 125

Glu Gln Thr Arg Arg Met Leu Ser Ala Gln Gly Gln Ala Pro
 Ile Thr
 130 135 140

Pro Glu Gln Gly Ala Ala Val Ala Lys Glu Ile Gly Ala Lys
 Tyr Ile
 145 150 155

160
 Glu Cys Ser Ala Lys Ala Gly Thr Gly Val His Glu Val Phe
 Glu Leu
 165 170

175
 Ala Leu Arg Glu Ser Met Lys Gly Arg Trp Gly Lys Ile Val
 Asn Gln
 180 185 190

Lys Arg Cys Val Ile Ile
 195

<210> 158

<211> 597

<212> DNA

<213> Coprinopsis cinerea okayama7#130

<220>

<221> CDS

<222> (1)..(597)

0070110

<400> 158

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

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0070110

```

Pro Arg Val Ile Glu Glu Leu Arg Lys Thr Ser Gln Arg Pro
Val Ser
130
ccc gag gag ggt atg gcg gtt gca cag aag att gga gca cga
cac tac
480
Pro Glu Glu Gly Met Ala Val Ala Gln Lys Ile Gly Ala Arg
His Tyr
145
150
155
160
ctc gaa tgc tca gcc aag act ggc gaa ggc gtc cgc gaa gtc
ttc cag
528
Leu Glu Cys Ser Ala Lys Thr Gly Glu Gly Val Arg Glu Val
Phe Gln
165
170
175
tac gca acc cga gca gct ctc ctc agc aag cct gga aag aga
aag cac
576
Tyr Ala Thr Arg Ala Ala Leu Leu Ser Lys Pro Gly Lys Arg
Lys His
180
185
190
agc cac tgc att gtc ctc taa
597
Ser His Cys Ile Val Leu
195

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<210> 159

<211> 198

<212> PRT

<213> Coprinopsis cinerea okayama7#130

<400> 159

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

```

0070110

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

<210> 160
 <211> 561
 <212> DNA
 <213> Culex quinquefasciatus

<220>
 <221> CDS
 <222> (1)..(561)

<400> 160
 atg acg atg ggc aac atg cgg ccg ctg aag atc aca acc gtc
 ggg gac 48
 Met Thr Met Gly Asn Met Arg Pro Leu Lys Ile Thr Thr Val

0070110

Gly	Asp													
1				5					10					
15														
gga	atg	gtg	ggc	aag	acg	tgc	ctg	cta	atc	acc	tac	gtc	cgc	
aac	gag		96											
Gly	Met	Val	Gly	Lys	Thr	Cys	Leu	Leu	Ile	Thr	Tyr	Val	Arg	
Asn	Glu													
			20					25					30	
ttc	ccc	agc	gag	tac	gtc	ccg	acg	gtg	ttt	gac	aac	cac	gcc	
tgc	aac		144											
Phe	Pro	Ser	Glu	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	His	Ala	
Cys	Asn													
		35				40						45		
atc	acc	gtg	gac	gaa	aag	gag	tac	gcc	ctc	acg	ctg	tgg	gac	
acg	gcc		192											
Ile	Thr	Val	Asp	Glu	Lys	Glu	Tyr	Ala	Leu	Thr	Leu	Trp	Asp	
Thr	Ala													
		50				55					60			
ggc	cag	gag	gac	tac	gag	cga	cta	cgg	ccc	ctc	agc	tac	cca	
aat	acc		240											
Gly	Gln	Glu	Asp	Tyr	Glu	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Pro	
Asn	Thr													
65				70						75				
80														
gat	tgt	ttt	ctc	ata	tgc	tac	tca	ata	tcg	agc	aag	aca	tct	
ttc	gat		288											
Asp	Cys	Phe	Leu	Ile	Cys	Tyr	Ser	Ile	Ser	Ser	Lys	Thr	Ser	
Phe	Asp													
			85											
95														
aac	gtt	att	tca	aaa	tgg	tac	cca	gag	ata	agg	cac	ttt	gcc	
cct	aac		336											
Asn	Val	Ile	Ser	Lys	Trp	Tyr	Pro	Glu	Ile	Arg	His	Phe	Ala	
Pro	Asn													
			100					105					110	
gtg	ccc	gtt	gta	ctc	gta	ggc	acc	aaa	agt	gat	ctc	cga	gtg	
cac	ggc		384											
Val	Pro	Val	Val	Leu	Val	Gly	Thr	Lys	Ser	Asp	Leu	Arg	Val	
His	Gly													
		115				120						125		
tcc	gag	aag	ttt	gtc	acg	acg	gtc	gag	ggc	aaa	aag	ctc	aag	
cac	aaa		432											
Ser	Glu	Lys	Phe	Val	Thr	Thr	Val	Glu	Gly	Lys	Lys	Leu	Lys	
His	Lys													
		130				135					140			
atc	aaa	gct	tac	tca	ctg	gtg	gag	tgt	tcc	gcg	aag	aag	aaa	
ctc	aac		480											

0070110

Ile Lys Ala Tyr Ser Leu Val Glu Cys Ser Ala Lys Lys Lys
Leu Asn

145 150 155

160

ctg ggt gac gtg ttc gac gaa gcc gtc cgg gcc gtg gag aag

aaa ccc 528

Leu Gly Asp Val Phe Asp Glu Ala Val Arg Ala Val Glu Lys

Lys Pro 165 170

175

cac cac aag cca cgt gtc tgc acg ata ctc tag

561

His His Lys Pro Arg Val Cys Thr Ile Leu

180 185

<210> 161

<211> 186

<212> PRT

<213> Culex quinquefasciatus

<400> 161

Met Thr Met Gly Asn Met Arg Pro Leu Lys Ile Thr Thr Val

Gly Asp 5 10

1 15

Gly Met Val Gly Lys Thr Cys Leu Leu Ile Thr Tyr Val Arg

Asn Glu 20 25 30

Phe Pro Ser Glu Tyr Val Pro Thr Val Phe Asp Asn His Ala

Cys Asn 35 40 45

Ile Thr Val Asp Glu Lys Glu Tyr Ala Leu Thr Leu Trp Asp

Thr Ala 50 55 60

Gly Gln Glu Asp Tyr Glu Arg Leu Arg Pro Leu Ser Tyr Pro

Asn Thr 65 70 75

80

Asp Cys Phe Leu Ile Cys Tyr Ser Ile Ser Ser Lys Thr Ser

Phe Asp 85 90

95

Asn Val Ile Ser Lys Trp Tyr Pro Glu Ile Arg His Phe Ala

Pro Asn 100 105 110

0070110

Val Pro Val Val Leu Val Gly Thr Lys Ser Asp Leu Arg Val
His Gly 115 120 125

Ser Glu Lys Phe Val Thr Thr Val Glu Gly Lys Lys Leu Lys
His Lys 130 135 140

Ile Lys Ala Tyr Ser Leu Val Glu Cys Ser Ala Lys Lys Lys
Leu Asn 145 150 155
160

Leu Gly Asp Val Phe Asp Glu Ala Val Arg Ala Val Glu Lys
Lys Pro 165 170

175
His His Lys Pro Arg Val Cys Thr Ile Leu
180 185

<210> 162
<211> 588
<212> DNA
<213> Culex quinquefasciatus

<220>
<221> CDS
<222> (1)..(588)

<400> 162
atg gcc tcg gga aga ccc att aag tgt gtt gta gtc ggc gac
gga acg 48
Met Ala Ser Gly Arg Pro Ile Lys Cys Val Val Val Gly Asp
Gly Thr 1 5 10
15
gtc ggc aag act tgc atg ctc att tca tac act acc gac agc
ttt ccc 96
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Thr Asp Ser
Phe Pro 20 25 30
ggc gaa tac gtt ccc acg gtg ttc gat aac tat tcc gca ccg
atg gta 144
Gly Glu Tyr Val Pro Thr Val Phe Asp Asn Tyr Ser Ala Pro
Met Val 35 40 45
gtg gac gga gta caa gtc tcg ctg gga ctg tgg gat acg gct
gga cag 192

Val Gly	Asp Gln 50	Gly	Val	Gln	Val	Ser	Leu	Gly	Leu	Trp	Asp	Thr	Ala
						55					60		
gag	gac	tac	gac	cgg	tta	cga	cca	ctg	tcg	tac	cca	cag	act
gac	gtg		240										
Glu	Asp	Tyr	Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Pro	Gln	Thr
Asp	Val				70					75			
65													
80													
ttc	ctc	atc	tgc	ttc	agc	gtt	gcc	agc	cca	tcc	tcg	ttc	gaa
aat	gtg		288										
Phe	Leu	Ile	Cys	Phe	Ser	Val	Ala	Ser	Pro	Ser	Ser	Phe	Glu
Asn	Val			85					90				
95													
act	tcc	aaa	tgg	tac	cca	gaa	atc	aaa	cat	cac	tgc	ccg	gat
gca	cca		336										
Thr	Ser	Lys	Trp	Tyr	Pro	Glu	Ile	Lys	His	His	Cys	Pro	Asp
Ala	Pro												
			100					105					110
att	att	cta	gtt	gga	acc	aag	att	gat	ttg	cgc	gag	gac	cgg
gaa	act		384										
Ile	Ile	Leu	Val	Gly	Thr	Lys	Ile	Asp	Leu	Arg	Glu	Asp	Arg
Glu	Thr												
		115					120					125	
ctc	agc	gca	cta	gcc	gag	cag	ggc	ctg	tcg	gca	ctc	aaa	cgg
gaa	cag		432										
Leu	Ser	Ala	Leu	Ala	Glu	Gln	Gly	Leu	Ser	Ala	Leu	Lys	Arg
Glu	Gln												
	130					135					140		
gga	caa	aaa	cta	gcc	aac	aaa	gta	cgc	gcc	gtc	aag	tat	atg
gaa	tgt		480										
Gly	Gln	Lys	Leu	Ala	Asn	Lys	Val	Arg	Ala	Val	Lys	Tyr	Met
Glu	Cys												
145					150					155			
160													
tca	gca	ctg	acc	cag	cgt	ggc	ctc	aag	cag	gta	ttc	gac	gag
gcc	gta		528										
Ser	Ala	Leu	Thr	Gln	Arg	Gly	Leu	Lys	Gln	Val	Phe	Asp	Glu
Ala	Val												
				165					170				
175													
cgg	gct	gta	ctc	cga	ccg	gaa	ccc	ctc	aaa	cga	cgt	caa	cga
aag	tgt		576										
Arg	Ala	Val	Leu	Arg	Pro	Glu	Pro	Leu	Lys	Arg	Arg	Gln	Arg
Lys	Cys												
			180					185					190

0070110

gtt gtg atg taa
588

val val Met
195

<210> 163

<211> 195

<212> PRT

<213> Culex quinquefasciatus

<400> 163

Met Ala Ser Gly Arg Pro Ile Lys Cys val val val Gly Asp
Gly Thr

1 5 10

15

Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Thr Asp Ser
Phe Pro

20 25 30

Gly Glu Tyr Val Pro Thr Val Phe Asp Asn Tyr Ser Ala Pro
Met Val

35 40 45

val Asp Gly val Gln val Ser Leu Gly Leu Trp Asp Thr Ala
Gly Gln

50 55 60

Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr
Asp Val

65 70 75

80

Phe Leu Ile Cys Phe Ser Val Ala Ser Pro Ser Ser Phe Glu
Asn Val

85 90

95

Thr Ser Lys Trp Tyr Pro Glu Ile Lys His His Cys Pro Asp
Ala Pro

100 105 110

Ile Ile Leu Val Gly Thr Lys Ile Asp Leu Arg Glu Asp Arg
Glu Thr

115 120 125

Leu Ser Ala Leu Ala Glu Gln Gly Leu Ser Ala Leu Lys Arg
Glu Gln

130 135 140

0070110

Gly Gln Lys Leu Ala Asn Lys Val Arg Ala Val Lys Tyr Met
 Glu Cys
 145 150 155
 160
 Ser Ala Leu Thr Gln Arg Gly Leu Lys Gln Val Phe Asp Glu
 Ala Val
 165 170
 175
 Arg Ala Val Leu Arg Pro Glu Pro Leu Lys Arg Arg Gln Arg
 Lys Cys
 180 185 190
 Val Val Met
 195

<210> 164
 <211> 588
 <212> DNA
 <213> Acyrthosiphon pisum

<220>
 <221> CDS
 <222> (1)..(588)

<400> 164
 atg tca gca gga cga cca att aag tgt gtg gtt gtt ggc gat
 ggt aca 48
 Met Ser Ala Gly Arg Pro Ile Lys Cys Val Val Val Gly Asp
 Gly Thr
 1 5 10
 15
 gtg ggc aag act tgt atg tta ata tcg tat act acc gac agc
 ttt cca 96
 Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Thr Asp Ser
 Phe Pro
 20 25 30
 gga gaa tac gta cct act gta ttt gat aac tac tct gca ccc
 atg gtg 144
 Gly Glu Tyr Val Pro Thr Val Phe Asp Asn Tyr Ser Ala Pro
 Met Val
 35 40 45
 gtt gac agt att cct gtc agc ctt ggt cta tgg gat acg gct
 ggc caa 192
 Val Asp Ser Ile Pro Val Ser Leu Gly Leu Trp Asp Thr Ala
 Gly Gln
 50 55 60
 gaa gat tac gac cgt cta aga cca ctt tcc tat cca cag act
 gac gta 240

0070110

Glu	Asp	Tyr	Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Pro	Gln	Thr
Asp	Val												
65					70					75			
80													
ttt	ttg	gtc	tgc	ttt	agt	ggt	gct	agt	cca	tct	tct	ttt	gaa
aat	gtg			288									
Phe	Leu	Val	Cys	Phe	Ser	Val	Ala	Ser	Pro	Ser	Ser	Phe	Glu
Asn	Val												
				85					90				
95													
ggt	tcc	aaa	tgg	tat	ccg	gaa	att	aaa	cat	cac	tgt	cca	gat
gct	cct		336										
Val	Ser	Lys	Trp	Tyr	Pro	Glu	Ile	Lys	His	His	Cys	Pro	Asp
Ala	Pro												
			100					105					110
atg	att	tta	ggt	ggc	acg	aaa	ata	gat	tta	aga	gaa	gac	aaa
gaa	aca		384										
Met	Ile	Leu	Val	Gly	Thr	Lys	Ile	Asp	Leu	Arg	Glu	Asp	Lys
Glu	Thr												
		115					120					125	
tta	aat	ggt	ttg	tct	gaa	caa	gga	ctg	tcc	cca	atc	aaa	cgt
gaa	cag		432										
Leu	Asn	Val	Leu	Ser	Glu	Gln	Gly	Leu	Ser	Pro	Ile	Lys	Arg
Glu	Gln												
	130					135				140			
gga	caa	aag	ttg	gcc	aat	aaa	ata	aga	gct	gta	aaa	tat	ctc
gaa	tgt		480										
Gly	Gln	Lys	Leu	Ala	Asn	Lys	Ile	Arg	Ala	Val	Lys	Tyr	Leu
Glu	Cys												
145					150					155			
160													
tct	gca	ttg	act	caa	aga	gga	tta	aaa	ctg	gta	ttt	gat	gaa
gcc	gta		528										
Ser	Ala	Leu	Thr	Gln	Arg	Gly	Leu	Lys	Leu	Val	Phe	Asp	Glu
Ala	Val												
				165						170			
175													
aga	gcc	ggt	tta	cga	cca	gta	cca	ctc	aaa	cac	cag	caa	agg
aaa	tgc		576										
Arg	Ala	Val	Leu	Arg	Pro	Val	Pro	Leu	Lys	His	Gln	Gln	Arg
Lys	Cys												
			180					185					190
act	ata	gct	tag										
			588										
Thr	Ile	Ala											
		195											

0070110

<210> 165
<211> 195
<212> PRT
<213> Acyrthosiphon pisum

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

0070110

Ser Ala Leu Thr Gln Arg Gly Leu Lys Leu Val Phe Asp Glu
Ala Val

165

170

175

Arg Ala Val Leu Arg Pro Val Pro Leu Lys His Gln Gln Arg
Lys Cys

180

185

190

Thr Ile Ala
195

<210> 166

<211> 579

<212> DNA

<213> Acyrthosiphon pisum

<220>

<221> CDS

<222> (1)..(579)

<400> 166

atg caa gcc atc aag tgt gtc gta gtc ggc gat gga gcg gtt
ggt aaa 48
Met Gln Ala Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys
1 5 10

15

aca tgt tta ctc att agt tat acc agc aat gca ttt cct gga
gaa tac 96
Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Ala Phe Pro Gly
Glu Tyr

20

25

30

ata ccc act gta ttt gac aac tat tcg gcc aat gtt atg gtt
gat gga 144
Ile Pro Thr Val Phe Asp Asn Tyr Ser Ala Asn Val Met Val
Asp Gly

35

40

45

aaa cct ata aac tta gga ttg tgg gat act gct ggt caa gaa
gat tat 192
Lys Pro Ile Asn Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu
Asp Tyr
50

55

60

gat agg ctt agg cct ctt tca tat cca caa aca gat gtg ttt
ctt ata 240
Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
Leu Ile
65 70 75

80

0070110

tgt ttt tca cta gta aat cct gca tca ttt gaa aat gtg cgg
gcg aaa 288
Cys Phe Ser Leu Val Asn Pro Ala Ser Phe Glu Asn Val Arg
Ala Lys

85

90

95

tgg tat cct gaa gtt cga cac cat tgt cca agt act cca att
att tta 336
Trp Tyr Pro Glu Val Arg His His Cys Pro Ser Thr Pro Ile
Ile Leu

100

105

110

gtt ggt act aaa ctt gat tta cga gaa gat aaa gaa aca att
gat aaa 384
Val Gly Thr Lys Leu Asp Leu Arg Glu Asp Lys Glu Thr Ile
Asp Lys

115

120

125

ctc aaa gaa aaa aag tta act gct att aca tat cca cag ggt
tta tca 432
Leu Lys Glu Lys Lys Leu Thr Ala Ile Thr Tyr Pro Gln Gly
Leu Ser

130

135

140

atg gcc aaa gaa att gga gca gtg aaa tac ttg gaa tgt agt
gct ttg 480
Met Ala Lys Glu Ile Gly Ala Val Lys Tyr Leu Glu Cys Ser
Ala Leu

145

150

155

160

act caa aaa ggt cta aaa att gta ttt gat gaa gcc att aga
gca gtt 528
Thr Gln Lys Gly Leu Lys Ile Val Phe Asp Glu Ala Ile Arg
Ala Val

165

170

175

tta tgt cct gta ctg cca gtt aag cct aaa cgt aaa tgc aca
ata att 576
Leu Cys Pro Val Leu Pro Val Lys Pro Lys Arg Lys Cys Thr
Ile Ile

180

185

190

taa

579

<210> 167

<211> 192

<212> PRT

0070110

<213> Acyrthosiphon pisum

<400> 167

Met Gln Ala Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys

1 5 10

15

Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Ala Phe Pro Gly
Glu Tyr

20 25 30

Ile Pro Thr Val Phe Asp Asn Tyr Ser Ala Asn Val Met Val
Asp Gly

35 40 45

Lys Pro Ile Asn Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu
Asp Tyr

50 55 60

Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
Leu Ile

65 70 75

80

Cys Phe Ser Leu Val Asn Pro Ala Ser Phe Glu Asn Val Arg
Ala Lys

85 90

95

Trp Tyr Pro Glu Val Arg His His Cys Pro Ser Thr Pro Ile
Ile Leu

100 105 110

Val Gly Thr Lys Leu Asp Leu Arg Glu Asp Lys Glu Thr Ile
Asp Lys

115 120 125

Leu Lys Glu Lys Lys Leu Thr Ala Ile Thr Tyr Pro Gln Gly
Leu Ser

130 135 140

Met Ala Lys Glu Ile Gly Ala Val Lys Tyr Leu Glu Cys Ser
Ala Leu

145 150 155

160

Thr Gln Lys Gly Leu Lys Ile Val Phe Asp Glu Ala Ile Arg
Ala Val

165 170

175

Leu Cys Pro Val Leu Pro Val Lys Pro Lys Arg Lys Cys Thr

0070110

Ile Ile

180

185

190

<210> 168

<211> 579

<212> DNA

<213> Acyrthosiphon pisum

<220>

<221> CDS

<222> (1)..(579)

<400> 168

atg gcg gcc att cga aaa aaa ctc gtc atc gtt ggt gac ggt

gcc tgc 48

Met Ala Ala Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly

Ala Cys

1

5

10

15

gga aaa act tgt ctg ctc att gtg ttt tcc aaa gat caa ttc

cca gaa 96

Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Asp Gln Phe

Pro Glu

20

25

30

gtt tat gta cct acc gta ttt gag aac tat gta gct gat ata

gaa gta 144

Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Ile

Glu Val

35

40

45

gat ggc aaa caa gta gaa cta gca ctg tgg gat aca gca ggt

caa gaa 192

Asp Gly Lys Gln Val Glu Leu Ala Leu Trp Asp Thr Ala Gly

Gln Glu

50

55

60

gat tat gat aga cta aga cca ttg tcc tat cct gac acg gat

gtt atc 240

Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Thr Asp

Val Ile

65

70

75

80

ctc atg tgt ttc tcc ata gat tca cca gat tca tta gag aat

atc cca 288

Leu Met Cys Phe Ser Ile Asp Ser Pro Asp Ser Leu Glu Asn

Ile Pro

85

90

95

gag aaa tgg aca ccg gaa gtg aaa cat ttc tgt cct aat gtg

0070110

ccg att 336
 Glu Lys Trp Thr Pro Glu Val Lys His Phe Cys Pro Asn Val
 Pro Ile
 100 105 110

ata ttg gtt ggt aac aaa aaa gac ttg cgt aat gat cca aat
 act att 384
 Ile Leu Val Gly Asn Lys Lys Asp Leu Arg Asn Asp Pro Asn
 Thr Ile
 115 120 125

cgc gag ttg agc aaa atg aaa caa gag ccc gtg agg cca gaa
 gag ggg 432
 Arg Glu Leu Ser Lys Met Lys Gln Glu Pro Val Arg Pro Glu
 Glu Gly
 130 135 140

cga gca atg gcc gaa aag ata aat gca ttt gct tat ttg gaa
 tgt tca 480
 Arg Ala Met Ala Glu Lys Ile Asn Ala Phe Ala Tyr Leu Glu
 Cys Ser
 145 150 155
 160

gct aaa agt aag gag ggt gtc cgt gaa gta ttt gaa act tca
 act aga 528
 Ala Lys Ser Lys Glu Gly Val Arg Glu Val Phe Glu Thr Ser
 Thr Arg
 165 170

175
 gca gct tta cag gtt aaa aag aaa aag aag ggg cga tgc cgt
 cta ctt 576
 Ala Ala Leu Gln Val Lys Lys Lys Lys Lys Gly Arg Cys Arg
 Leu Leu
 180 185 190

taa
 579

<210> 169
 <211> 192
 <212> PRT
 <213> Acyrthosiphon pisum

<400> 169
 Met Ala Ala Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly
 Ala Cys
 1 5 10
 15

0070110

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

<210> 170
 <211> 579
 <212> DNA

0070110

<213> Acyrthosiphon pisum

<220>

<221> CDS

<222> (1)..(579)

<400> 170

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atg gca gca atc cgt aag aaa ctt gtc atc gtc ggc gac ggt
gcc tgc          48
Met Ala Ala Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly
Ala Cys
  1              5              10
15
gga aaa act tgt ctg ctc att gtg ttt tcc aaa gat caa ttc
cca gaa          96
Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Asp Gln Phe
Pro Glu
      20              25              30
gta tat gtt ccc act gtg ttt gag aac tat gta gct gat ata
gaa gtc          144
Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Ile
Glu Val
      35              40              45
gat ggc aaa caa gta gaa tta gca ctg tgg gat aca gcg ggt
caa gaa          192
Asp Gly Lys Gln Val Glu Leu Ala Leu Trp Asp Thr Ala Gly
Gln Glu
      50              55              60
gat tat gat aga cta aga cca ttg tcc tat cct gac acg gat
gtt atc          240
Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Thr Asp
Val Ile
      65              70              75
80
ctc atg tgt ttc tcc ata gat tca cca gat tcg tta gag aat
atc cca          288
Leu Met Cys Phe Ser Ile Asp Ser Pro Asp Ser Leu Glu Asn
Ile Pro
      85              90
95
gag aaa tgg aca ccg gaa gtg aaa cat ttc tgt cca aat gtg
ccg att          336
Glu Lys Trp Thr Pro Glu Val Lys His Phe Cys Pro Asn Val
Pro Ile
      100              105              110
ata ttg gtt ggt aac aaa aaa gac ttg cgt aat gat cca aat
acg att          384

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0070110

Ile	Leu	Val	Gly	Asn	Lys	Lys	Asp	Leu	Arg	Asn	Asp	Pro	Asn
Thr	Ile												
		115					120					125	
cgc	gag	ttg	aac	aag	atg	aaa	caa	gag	ccc	gtg	agg	cca	gaa
gag	ggg		432										
Arg	Glu	Leu	Asn	Lys	Met	Lys	Gln	Glu	Pro	Val	Arg	Pro	Glu
Glu	Gly												
	130					135					140		
cga	gca	atg	gcc	gaa	aag	atc	aat	gca	ttt	gct	tat	ttg	gaa
tgt	tca		480										
Arg	Ala	Met	Ala	Glu	Lys	Ile	Asn	Ala	Phe	Ala	Tyr	Leu	Glu
Cys	Ser												
145					150					155			
160													
gct	aaa	agc	aaa	gaa	gga	gtt	cgt	gaa	gtt	ttt	gaa	aca	tca
aca	aga		528										
Ala	Lys	Ser	Lys	Glu	Gly	Val	Arg	Glu	Val	Phe	Glu	Thr	Ser
Thr	Arg												
			165						170				
175													
gct	gca	cta	caa	gtc	aag	aaa	aag	aag	aaa	ggc	aaa	tgt	gcc
ttg	ttg		576										
Ala	Ala	Leu	Gln	Val	Lys	Lys	Lys	Lys	Lys	Gly	Lys	Cys	Ala
Leu	Leu												
			180					185				190	
taa													
			579										

<210> 171
 <211> 192
 <212> PRT
 <213> Acyrthosiphon pisum

<400> 171													
Met	Ala	Ala	Ile	Arg	Lys	Lys	Leu	Val	Ile	Val	Gly	Asp	Gly
Ala	Cys												
1				5					10				
15													
Gly	Lys	Thr	Cys	Leu	Leu	Ile	Val	Phe	Ser	Lys	Asp	Gln	Phe
Pro	Glu												
			20					25				30	
Val	Tyr	Val	Pro	Thr	Val	Phe	Glu	Asn	Tyr	Val	Ala	Asp	Ile
Glu	Val												
		35					40					45	

0070110

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

<210> 172
 <211> 576
 <212> DNA
 <213> Acyrthosiphon pisum

<220>
 <221> CDS
 <222> (1)..(576)

<400> 172

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atg	tct	cct	att	aag	aag	aaa	gta	gtg	atc	gtc	ggg	gac	ggc
gag	agt		48										
Met	Ser	Pro	Ile	Lys	Lys	Lys	Val	Val	Ile	Val	Gly	Asp	Gly
Glu	Ser			5					10				
1													
15													
ggg	aag	aca	tgc	cta	ttg	cgc	gtg	ttt	ttt	gag	gat	att	ttc
cca	gaa		96										
Gly	Lys	Thr	Cys	Leu	Leu	Arg	Val	Phe	Phe	Glu	Asp	Ile	Phe
Pro	Glu												
			20					25					30
gta	tac	gtg	cca	act	gtg	ttt	gac	tac	tat	tca	act	gtg	atc
gaa	gtt		144										
Val	Tyr	Val	Pro	Thr	Val	Phe	Asp	Tyr	Tyr	Ser	Thr	Val	Ile
Glu	Val												
		35				40						45	
gaa	ggg	aaa	aag	gtg	gcg	ctc	gac	cta	tgg	gac	act	gct	ggg
caa	gag		192										
Glu	Gly	Lys	Lys	Val	Ala	Leu	Asp	Leu	Trp	Asp	Thr	Ala	Gly
Gln	Glu												
		50				55					60		
gat	tat	gac	aga	ctg	cga	cca	ctg	tca	tat	ggg	gcc	gct	gat
gta	gtg		240										
Asp	Tyr	Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Gly	Ala	Ala	Asp
Val	Val												
65					70					75			
80													
atc	ata	tgc	tat	tca	atc	gat	act	ccc	aaa	tcg	ttg	att	aac
gta	att		288										
Ile	Ile	Cys	Tyr	Ser	Ile	Asp	Thr	Pro	Lys	Ser	Leu	Ile	Asn
Val	Ile												
			85						90				
95													
gat	aaa	tgg	gtg	ccg	gaa	gtg	cgg	tat	ttt	tgc	aag	gaa	gtg
ccg	gtg		336										
Asp	Lys	Trp	Val	Pro	Glu	Val	Arg	Tyr	Phe	Cys	Lys	Glu	Val
Pro	Val												
			100					105				110	
ata	ttg	gtt	ggc	aat	aag	aag	gac	ctc	cgc	gat	agc	ccg	aga
aaa	act		384										
Ile	Leu	Val	Gly	Asn	Lys	Lys	Asp	Leu	Arg	Asp	Ser	Pro	Arg
Lys	Thr												
		115				120					125		
acc	att	cgg	ata	cct	gaa	cat	aat	gtc	atg	aca	acc	aaa	gaa
att	ggg		432										
Thr	Ile	Arg	Ile	Pro	Glu	His	Asn	Val	Met	Thr	Thr	Lys	Glu
Ile	Gly												

0070110

130 135 140
 caa tca gtg gcc gaa gat atc aaa gct ttc gca ttt tta gaa
 tgt tct 480
 Gln Ser val Ala Glu Asp Ile Lys Ala Phe Ala Phe Leu Glu
 Cys Ser
 145 150 155
 160
 tcg aag acc aag gaa gga gtc cgt gat gtt ttc gtt gcc aca
 gtg aag 528
 Ser Lys Thr Lys Glu Gly val Arg Asp val Phe val Ala Thr
 val Lys
 165 170
 175
 gcg aca aga agg act tcc aaa cat agt acg cag tgt att tta
 ctt 573
 Ala Thr Arg Arg Thr Ser Lys His Ser Thr Gln Cys Ile Leu
 Leu
 180 185 190
 taa
 576

<210> 173
 <211> 191
 <212> PRT
 <213> Acyrthosiphon pisum

<400> 173
 Met Ser Pro Ile Lys Lys Lys val val Ile val Gly Asp Gly
 Glu Ser
 1 5 10
 15
 Gly Lys Thr Cys Leu Leu Arg val Phe Phe Glu Asp Ile Phe
 Pro Glu
 20 25 30
 val Tyr val Pro Thr val Phe Asp Tyr Tyr Ser Thr val Ile
 Glu val
 35 40 45
 Glu Gly Lys Lys val Ala Leu Asp Leu Trp Asp Thr Ala Gly
 Gln Glu
 50 55 60
 Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Gly Ala Ala Asp
 val val

0070110

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

<210> 174
 <211> 612
 <212> DNA
 <213> Acyrthosiphon pisum

<220>
 <221> CDS
 <222> (1)..(612)

<400> 174
 atg gga gcc gaa tca cat tac agc gac acc att aga tcg tcc
 aag aaa 48
 Met Gly Ala Glu Ser His Tyr Ser Asp Thr Ile Arg Ser Ser
 Lys Lys
 1 5 10
 15
 tgc agc aag ttg agg ccg ttg aag ata acc gcg gtc ggc gat

0070110

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ggg atg          96
Cys Ser Lys Leu Arg Pro Leu Lys Ile Thr Ala Val Gly Asp
Gly Met

          20          25          30
gtc gga aaa act tgc atg ctc atc acc tac acg acc aag caa
ttt cct          144
Val Gly Lys Thr Cys Met Leu Ile Thr Tyr Thr Thr Lys Gln
Phe Pro

          35          40          45
acc gaa tac gtg cct acc gta ttc gac aat tat gca gag aac
atg gtt          192
Thr Glu Tyr Val Pro Thr Val Phe Asp Asn Tyr Ala Glu Asn
Met Val

          50          55          60
atg gat ggt caa gag tac aac atg tgt ctg tgg gat act gcc
ggc caa          240
Met Asp Gly Gln Glu Tyr Asn Met Cys Leu Trp Asp Thr Ala
Gly Gln

          65          70          75
          80
gaa gat tac gaa aga ctt agg cca ctg tct tat cct aat acg
gat tgt          288
Glu Asp Tyr Glu Arg Leu Arg Pro Leu Ser Tyr Pro Asn Thr
Asp Cys

          85          90
95
ttt cta ctt tgc tat tca gtc ggt agt cgg agt tca ttc gaa
aac att          336
Phe Leu Leu Cys Tyr Ser Val Gly Ser Arg Ser Ser Phe Glu
Asn Ile

          100          105          110
gcc agt aaa tgg cat ccg gaa att caa cac cac tgt ccg aaa
ata cct          384
Ala Ser Lys Trp His Pro Glu Ile Gln His His Cys Pro Lys
Ile Pro

          115          120          125
gtg ata ttg atc ggt acg aaa acg gat tta agg ctg agc caa
aac gac          432
Val Ile Leu Ile Gly Thr Lys Thr Asp Leu Arg Leu Ser Gln
Asn Asp

          130          135          140
tgt ata aca cgg aaa aag ggc aag aaa atg atg aaa aag atc
ggg gcc          480
Cys Ile Thr Arg Lys Lys Gly Lys Lys Met Met Lys Lys Ile
Gly Ala

          145          150          155
          160

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0070110

gtc aag tac ctg gag tgt tca gct ctg acc aac gaa ggg ttg
 gac acc 528
 Val Lys Tyr Leu Glu Cys Ser Ala Leu Thr Asn Glu Gly Leu
 Asp Thr

165

170

175

ata ttc acg gaa tcg gtc cgc gcg gcc atc gaa agg cca aga
 aaa aac 576
 Ile Phe Thr Glu Ser Val Arg Ala Ala Ile Glu Arg Pro Arg
 Lys Asn

180

185

190

tgt ttc ggg ttc cct ttc atc caa tgc tgt aaa tag
 612
 Cys Phe Gly Phe Pro Phe Ile Gln Cys Cys Lys
 195 200

<210> 175

<211> 203

<212> PRT

<213> Acyrthosiphon pisum

<400> 175

Met Gly Ala Glu Ser His Tyr Ser Asp Thr Ile Arg Ser Ser
 Lys Lys

1

5

10

15

Cys Ser Lys Leu Arg Pro Leu Lys Ile Thr Ala Val Gly Asp
 Gly Met

20

25

30

Val Gly Lys Thr Cys Met Leu Ile Thr Tyr Thr Thr Lys Gln
 Phe Pro

35

40

45

Thr Glu Tyr Val Pro Thr Val Phe Asp Asn Tyr Ala Glu Asn
 Met Val
 50 55 60

Met Asp Gly Gln Glu Tyr Asn Met Cys Leu Trp Asp Thr Ala
 Gly Gln
 65 70 75

80

Glu Asp Tyr Glu Arg Leu Arg Pro Leu Ser Tyr Pro Asn Thr
 Asp Cys

85

90

95

Phe Leu Leu Cys Tyr Ser Val Gly Ser Arg Ser Ser Phe Glu
 Seite 281

0070110

Asn	Ile												
			100					105					110
Ala	Ser	Lys	Trp	His	Pro	Glu	Ile	Gln	His	His	Cys	Pro	Lys
Ile	Pro												
		115					120					125	
Val	Ile	Leu	Ile	Gly	Thr	Lys	Thr	Asp	Leu	Arg	Leu	Ser	Gln
Asn	Asp												
	130					135					140		
Cys	Ile	Thr	Arg	Lys	Lys	Gly	Lys	Lys	Met	Met	Lys	Lys	Ile
Gly	Ala												
145					150					155			
	160												
Val	Lys	Tyr	Leu	Glu	Cys	Ser	Ala	Leu	Thr	Asn	Glu	Gly	Leu
Asp	Thr												
				165					170				
175													
Ile	Phe	Thr	Glu	Ser	Val	Arg	Ala	Ala	Ile	Glu	Arg	Pro	Arg
Lys	Asn												
			180					185					190
Cys	Phe	Gly	Phe	Pro	Phe	Ile	Gln	Cys	Cys	Lys			
		195					200						

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<210> 176
<211> 579
<212> DNA
<213> Anopheles gambiae str. PEST
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<220>
<221> CDS
<222> (1) .. (579)

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<400> 176
atg  caa  gcg  atc  aaa  tgt  gtc  gtc  gtc  ggt  gac  ggt  gcc  gtc
ggt  aag                                     48
Met  Gln  Ala  Ile  Lys  Cys  Val  Val  Val  Gly  Asp  Gly  Ala  Val
Gly  Lys                                     10
15
acg  tgc  ctg  ctg  atc  agc  tac  aca  acg  aac  gcg  ttc  ccg  ggc
gag  tac                                     96
Thr  Cys  Leu  Leu  Ile  Ser  Tyr  Thr  Thr  Asn  Ala  Phe  Pro  Gly
Glu  Tyr                                     20
atc  ccg  acc  gtg  ttc  gac  aac  tac  tcc  gcg  aac  gtg  atg  gtc

```

0070110

gac Ile Asp	ggc Pro Gly		Thr	Val	Phe	Asp	Asn	Tyr	Ser	Ala	Asn	Val	Met	Val
		35						40					45	
aaa gat Lys Asp	cgc tac Pro Tyr	atc	aac	ctc	ggg	ctg	tgg	gat	acg	gcc	ggg	cag	gag	
			192											
		Ile	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala	Gly	Gln	Glu	
	50					55					60			
gat ctc Asp Leu	cgc ata Arg Ile	ctg	cgc	ccc	ctg	tcc	tac	ccg	cag	acg	gac	gtg	ttt	
			240											
		Leu	Arg	Pro	Leu	Ser	Tyr	Pro	Gln	Thr	Asp	Val	Phe	
65					70					75				
80														
tgc gcg Cys Ala	ttc aaa Phe Lys	tcg	ctc	gtc	aat	ccg	gcc	tcg	ttc	gag	aac	gtg	cgg	
			288											
		Ser	Leu	Val	Asn	Pro	Ala	Ser	Phe	Glu	Asn	Val	Arg	
				85					90					
95														
tgg ata Trp Ile	tac ctg Tyr Leu	ccg	gag	gtg	cgc	cac	cac	tgt	ccg	aac	ata	ccg	atc	
			336											
		Pro	Glu	Val	Arg	His	His	Cys	Pro	Asn	Ile	Pro	Ile	
			100					105					110	
gtc gac Val Asp	ggg aag Gly Lys	acg	aag	ctc	gat	ctg	cgg	gat	gac	aag	aac	acg	gtg	
			384											
		Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys	Asn	Thr	Val	
		115					120					125		
ctg ctg Leu Leu	cgc gcc Arg Ala	gac	aag	aag	ctg	tcg	ccg	atc	acg	tac	ccg	cag	ggg	
			432											
		Asp	Lys	Lys	Leu	Ser	Pro	Ile	Thr	Tyr	Pro	Gln	Gly	
	130					135					140			
atg gcg Met Ala	gcc ctg Ala Leu	aag	gag	atc	ggt	gcg	gtg	aag	tac	ctc	gag	tgt	tcg	
			480											
		Lys	Glu	Ile	Gly	Ala	Val	Lys	Tyr	Leu	Glu	Cys	Ser	
145					150					155				
160														
acg gcg Thr Ala	cag gtg Gln Val	aag	ggc	ctc	aag	acg	gtg	ttc	gac	gaa	gcg	atc	cgg	
			528											
		Lys	Gly	Leu	Lys	Thr	Val	Phe	Asp	Glu	Ala	Ile	Arg	
				165					170					

0070110

175

ctc tgt ccg atg att ccg ccg aag aag aaa ccc aag tgt aac
atc ctc 576
Leu Cys Pro Met Ile Pro Pro Lys Lys Lys Pro Lys Cys Asn
Ile Leu

180

185

190

taa

579

<210> 177

<211> 192

<212> PRT

<213> Anopheles gambiae str. PEST

<400> 177

Met Gln Ala Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys

1 5 10

15

Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Ala Phe Pro Gly
Glu Tyr

20

25

30

Ile Pro Thr Val Phe Asp Asn Tyr Ser Ala Asn Val Met Val
Asp Gly

35

40

45

Lys Pro Ile Asn Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu
Asp Tyr

50

55

60

Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
Leu Ile

65

70

75

80

Cys Phe Ser Leu Val Asn Pro Ala Ser Phe Glu Asn Val Arg
Ala Lys

85

90

95

Trp Tyr Pro Glu Val Arg His His Cys Pro Asn Ile Pro Ile
Ile Leu

100

105

110

0070110

Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys	Asn	Thr	Val
Asp	Lys												
		115					120					125	

Leu	Arg	Asp	Lys	Lys	Leu	Ser	Pro	Ile	Thr	Tyr	Pro	Gln	Gly
Leu	Ala												
	130					135					140		

Met	Ala	Lys	Glu	Ile	Gly	Ala	Val	Lys	Tyr	Leu	Glu	Cys	Ser
Ala	Leu												
145					150					155			

Thr	Gln	Lys	Gly	Leu	Lys	Thr	Val	Phe	Asp	Glu	Ala	Ile	Arg
Ala	Val												
				165					170				

175													
Leu	Cys	Pro	Met	Ile	Pro	Pro	Lys	Lys	Lys	Pro	Lys	Cys	Asn
Ile	Leu												
			180					185					190

<210> 178
 <211> 603
 <212> DNA
 <213> Magnaporthe grisea 70-15

<220>
 <221> CDS
 <222> (1)..(603)

<400> 178													
atg	gcg	gcc	gca	aat	aat	cag	aac	gtc	att	cgc	agg	aaa	ctg
gta	att		48										
Met	Ala	Ala	Ala	Asn	Asn	Gln	Asn	Val	Ile	Arg	Arg	Lys	Leu
Val	Ile												
1				5					10				

15													
ata	gga	gac	ggt	gca	tgc	gga	aag	aca	agt	tta	ctt	agc	gtg
ttc	act		96										
Ile	Gly	Asp	Gly	Ala	Cys	Gly	Lys	Thr	Ser	Leu	Leu	Ser	Val
Phe	Thr												

			20					25					30
ctt	ggg	tat	ttt	cca	aca	cat	tat	att	ccg	acc	gtc	ttc	gaa
aac	tac		144										
Leu	Gly	Tyr	Phe	Pro	Thr	His	Tyr	Ile	Pro	Thr	Val	Phe	Glu
Asn	Tyr												

		35				40					45		
gtg	aca	gat	tgc	agg	gtg	gat	ggc	aag	tcg	gtg	cag	cta	gca

0070110

tta	tgg			192										
Val	Thr	Asp	Cys	Arg	Val	Asp	Gly	Lys	Ser	Val	Gln	Leu	Ala	
Leu	Trp													
	50					55					60			
gat	acg	gca	ggc	cag	gag	gac	tac	gag	cga	tta	cgg	ccc	ttg	
gca	tac			240										
Asp	Thr	Ala	Gly	Gln	Glu	Asp	Tyr	Glu	Arg	Leu	Arg	Pro	Leu	
Ala	Tyr													
65					70						75			
80														
tca	aaa	gcg	cac	gtc	atc	cta	ata	ggg	ttt	tct	gtc	gac	acg	
ccg	gat			288										
Ser	Lys	Ala	His	Val	Ile	Leu	Ile	Gly	Phe	Ser	Val	Asp	Thr	
Pro	Asp													
				85						90				
95														
tca	ttg	gac	aat	gtg	aag	cac	aag	tgg	atc	gaa	gag	gct	acc	
gaa	aag			336										
Ser	Leu	Asp	Asn	Val	Lys	His	Lys	Trp	Ile	Glu	Glu	Ala	Thr	
Glu	Lys													
				100				105					110	
tgc	cct	ggg	gta	ccc	atc	atc	ctt	gtc	ggc	ctc	aag	aag	gac	
ctg	cgg			384										
Cys	Pro	Gly	Val	Pro	Ile	Ile	Leu	Val	Gly	Leu	Lys	Lys	Asp	
Leu	Arg													
		115					120					125		
gaa	gac	ccc	gtg	gcc	atc	gag	gag	atg	cgc	aag	aag	agc	atg	
cgc	ttt			432										
Glu	Asp	Pro	Val	Ala	Ile	Glu	Glu	Met	Arg	Lys	Lys	Ser	Met	
Arg	Phe													
		130				135						140		
gtc	acc	gag	cac	gac	ggg	gag	act	gcg	gcc	aag	gaa	gtc	ggg	
gcc	cgc			480										
Val	Thr	Glu	His	Asp	Gly	Glu	Thr	Ala	Ala	Lys	Glu	Val	Gly	
Ala	Arg													
145					150					155				
160														
aaa	tat	cta	gag	tgt	tcg	agc	ttg	tct	ggc	gaa	gga	gtc	gac	
gac	gtc			528										
Lys	Tyr	Leu	Glu	Cys	Ser	Ser	Leu	Ser	Gly	Glu	Gly	Val	Asp	
Asp	Val													
				165						170				
175														
ttt	gag	gca	gcc	acg	cgc	gca	gcc	ctc	ttg	aca	ttt	gaa	aag	
ggg	gag			576										
Phe	Glu	Ala	Ala	Thr	Arg	Ala	Ala	Leu	Leu	Thr	Phe	Glu	Lys	
Gly	Glu													

0070110

180

185

190

gga gcc gga tgc tgt gtg atc cta tag

603

Gly Ala Gly Cys Cys val Ile Leu

195

200

<210> 179

<211> 200

<212> PRT

<213> Magnaporthe grisea 70-15

<400> 179

Met Ala Ala Ala Asn Asn Gln Asn val Ile Arg Arg Lys Leu
val Ile

1

5

10

15

Ile Gly Asp Gly Ala Cys Gly Lys Thr Ser Leu Leu Ser val
Phe Thr

20

25

30

Leu Gly Tyr Phe Pro Thr His Tyr Ile Pro Thr val Phe Glu
Asn Tyr

35

40

45

val Thr Asp Cys Arg val Asp Gly Lys Ser val Gln Leu Ala
Leu Trp

50

55

60

Asp Thr Ala Gly Gln Glu Asp Tyr Glu Arg Leu Arg Pro Leu
Ala Tyr

65

70

75

80

Ser Lys Ala His val Ile Leu Ile Gly Phe Ser val Asp Thr
Pro Asp

85

90

95

Ser Leu Asp Asn val Lys His Lys Trp Ile Glu Glu Ala Thr
Glu Lys

100

105

110

Cys Pro Gly val Pro Ile Ile Leu val Gly Leu Lys Lys Asp
Leu Arg

115

120

125

Glu Asp Pro val Ala Ile Glu Glu Met Arg Lys Lys Ser Met
Arg Phe

130

135

140

0070110

Val Thr Glu His Asp Gly Glu Thr Ala Ala Lys Glu Val Gly
Ala Arg
145 150 155
160
Lys Tyr Leu Glu Cys Ser Ser Leu Ser Gly Glu Gly Val Asp
Asp Val
165 170
175
Phe Glu Ala Ala Thr Arg Ala Ala Leu Leu Thr Phe Glu Lys
Gly Glu
180 185 190
Gly Ala Gly Cys Cys Val Ile Leu
195 200

<210> 180
<211> 633
<212> DNA
<213> Magnaporthe grisea 70-15

<220>
<221> CDS
<222> (1)..(633)

<400> 180
atg cct tta tcg ctt tgc gga gga agc aaa acg gtc cag cgc
aag ctg 48
Met Pro Leu Ser Leu Cys Gly Gly Ser Lys Thr Val Gln Arg
Lys Leu
1 5 10
15
gta ttg ctt ggc gac ggt gct tgt gga aag aca tca ctg tta
aac gtc 96
Val Leu Leu Gly Asp Gly Ala Cys Gly Lys Thr Ser Leu Leu
Asn Val
20 25 30
ttc acg aga gga tac ttc ccg acc gtc tac gag cca aca gta
ttc gag 144
Phe Thr Arg Gly Tyr Phe Pro Thr Val Tyr Glu Pro Thr Val
Phe Glu
35 40 45
aac tat gtt cat gac atc ttt gta gat aat gtc cac atc gaa
ctg tca 192
Asn Tyr Val His Asp Ile Phe Val Asp Asn Val His Ile Glu
Leu Ser
50 55 60
cta tgg gat aca gca gga caa gag gaa ttc gac agg ttg agg
Seite 288

0070110

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agt ctt      240
Leu Trp Asp Thr Ala Gly Gln Glu Glu Phe Asp Arg Leu Arg
Ser Leu
65      70      75
80
tca tat gac gat acg gat ttg atc atg ctc tgc tat tcg gtc
gac agc      288
Ser Tyr Asp Asp Thr Asp Leu Ile Met Leu Cys Tyr Ser Val
Asp Ser
85      90
95
aag gac agt ctc gaa aac gtc gaa tca aaa tgg gtc ggc gag
ata gca      336
Lys Asp Ser Leu Glu Asn Val Glu Ser Lys Trp Val Gly Glu
Ile Ala
100      105      110
gac aac tgc ccg ggt gtc aag ttg gtg ctg gtt gcg ctc aag
tgc gac      384
Asp Asn Cys Pro Gly Val Lys Leu Val Leu Val Ala Leu Lys
Cys Asp
115      120      125
ttg cgc cag gag cag gct gat gac gcg gct gaa aac ggg aac
gcg aca      432
Leu Arg Gln Glu Gln Ala Asp Asp Ala Ala Glu Asn Gly Asn
Ala Thr
130      135      140
gat cct tcg cag cag cgc gag aag aag ccc atg atc acg tac
gac acg      480
Asp Pro Ser Gln Gln Arg Glu Lys Lys Pro Met Ile Thr Tyr
Asp Thr
145      150      155
160
ggg ctc gaa gtg gca cgg cgc atc aat gca ctg cgg tat ctc
gaa tgt      528
Gly Leu Glu Val Ala Arg Arg Ile Asn Ala Leu Arg Tyr Leu
Glu Cys
165      170
175
tcg gcc atg cgc aat cgc ggc gtc aac gag gcc ttt act gag
gcg gca      576
Ser Ala Met Arg Asn Arg Gly Val Asn Glu Ala Phe Thr Glu
Ala Ala
180      185      190
cgc gtg gca ctt agc gtg aag aag gac cgc gag gag agc aag
tgc acc      624
Arg Val Ala Leu Ser Val Lys Lys Asp Arg Glu Glu Ser Lys

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0070110

Cys Thr
 195
 gtc atg tag 200 205
 633
 val Met
 210

<210> 181
 <211> 210
 <212> PRT
 <213> Magnaporthe grisea 70-15

<400> 181

Met Pro Leu Ser Leu Cys Gly Gly Ser Lys Thr val Gln Arg
 Lys Leu
 1 5 10
 15
 val Leu Leu Gly Asp Gly Ala Cys Gly Lys Thr Ser Leu Leu
 Asn val
 20 25 30

Phe Thr Arg Gly Tyr Phe Pro Thr val Tyr Glu Pro Thr val
 Phe Glu
 35 40 45

Asn Tyr val His Asp Ile Phe val Asp Asn val His Ile Glu
 Leu Ser
 50 55 60

Leu Trp Asp Thr Ala Gly Gln Glu Glu Phe Asp Arg Leu Arg
 Ser Leu
 65 70 75
 80

Ser Tyr Asp Asp Thr Asp Leu Ile Met Leu Cys Tyr Ser val
 Asp Ser
 85 90

95
 Lys Asp Ser Leu Glu Asn val Glu Ser Lys Trp val Gly Glu
 Ile Ala
 100 105 110

Asp Asn Cys Pro Gly val Lys Leu val Leu val Ala Leu Lys
 Cys Asp
 115 120 125

Leu Arg Gln Glu Gln Ala Asp Asp Ala Ala Glu Asn Gly Asn
 Ala Thr
 130 135 140

0070110

Asp Pro Ser Gln Gln Arg Glu Lys Lys Pro Met Ile Thr Tyr
Asp Thr
145 150 155
160
Gly Leu Glu Val Ala Arg Arg Ile Asn Ala Leu Arg Tyr Leu
Glu Cys
165 170
175
Ser Ala Met Arg Asn Arg Gly Val Asn Glu Ala Phe Thr Glu
Ala Ala
180 185 190
Arg Val Ala Leu Ser Val Lys Lys Asp Arg Glu Glu Ser Lys
Cys Thr
195 200 205
Val Met
210

<210> 182
<211> 582
<212> DNA
<213> Magnaporthe grisea 70-15

<220>
<221> CDS
<222> (1)..(582)

<400> 182
atg gcc gaa atc cgc cgc aag ctg gtc atc gtc ggt gac ggt
gcc tgc 48
Met Ala Glu Ile Arg Arg Lys Leu Val Ile Val Gly Asp Gly
Ala Cys
1 5 10
15
ggt aag aca tgt ttg ttg att gtg ttc tct aag ggc acc ttc
ccc gag 96
Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Gly Thr Phe
Pro Glu
20 25 30
gtc tac gtc ccc acc gtc ttc gaa aac tac gtc gct gat gtg
gag gtc 144
Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Val
Glu Val
35 40 45
gat ggc aag cac gtc gag ttg gca cta tgg gat act gcc ggc
cag gag 192

0070110

Asp	Gly	Lys	His	Val	Glu	Leu	Ala	Leu	Trp	Asp	Thr	Ala	Gly
Gln	Glu												
	50					55				60			
gat	tac	gat	cgt	ctg	cgc	ccc	ttg	tcc	tac	ccc	gac	tct	cac
ggt	atc		240										
Asp	Tyr	Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Pro	Asp	Ser	His
Val	Ile												
65					70					75			
80													
ctg	att	tgc	ttc	gcc	atc	gac	tct	ccc	gac	tcc	ctt	gac	aac
gtc	caa		288										
Leu	Ile	Cys	Phe	Ala	Ile	Asp	Ser	Pro	Asp	Ser	Leu	Asp	Asn
Val	Gln												
				85						90			
95													
gag	aag	tgg	atc	tcc	gag	gtc	ctt	cac	ttc	tgc	tcg	ggc	ctg
cca	att		336										
Glu	Lys	Trp	Ile	Ser	Glu	Val	Leu	His	Phe	Cys	Ser	Gly	Leu
Pro	Ile												
			100				105						110
atc	ctt	ggt	ggt	tgc	aag	aag	gat	ctt	cgg	tat	gac	cag	aag
acc	att		384										
Ile	Leu	Val	Gly	Cys	Lys	Lys	Asp	Leu	Arg	Tyr	Asp	Gln	Lys
Thr	Ile												
		115					120					125	
gag	gag	ctt	cgc	aag	acc	agc	cag	aag	ccc	gtc	tca	cct	gag
gat	ggt		432										
Glu	Glu	Leu	Arg	Lys	Thr	Ser	Gln	Lys	Pro	Val	Ser	Pro	Glu
Asp	Gly												
	130					135					140		
gag	gag	att	aag	aag	aag	att	ggt	gcc	tac	aag	tac	ctc	gag
tgc	tcg		480										
Glu	Glu	Ile	Lys	Lys	Lys	Ile	Gly	Ala	Tyr	Lys	Tyr	Leu	Glu
Cys	Ser												
145					150					155			
160													
gcc	aag	acc	aac	gag	ggt	gtc	cgt	gag	gtg	ttc	gag	cat	gct
aca	cga		528										
Ala	Lys	Thr	Asn	Glu	Gly	Val	Arg	Glu	Val	Phe	Glu	His	Ala
Thr	Arg												
			165							170			
175													
gct	gcc	ctc	ctg	tct	cgc	cac	aag	acc	aag	aag	aag	aag	tgc
ctc	atc		576										
Ala	Ala	Leu	Leu	Ser	Arg	His	Lys	Thr	Lys	Lys	Lys	Lys	Cys
Leu	Ile												
			180						185				190

0070110

ctc taa

582

Leu

<210> 183

<211> 193

<212> PRT

<213> Magnaporthe grisea 70-15

<400> 183

Met Ala Glu Ile Arg Arg Lys Leu Val Ile Val Gly Asp Gly
Ala Cys

1 5 10

15

Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Gly Thr Phe
Pro Glu

20 25 30

Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Val
Glu Val

35 40 45

Asp Gly Lys His Val Glu Leu Ala Leu Trp Asp Thr Ala Gly
Gln Glu

50 55 60

Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Ser His
Val Ile

65 70 75

80

Leu Ile Cys Phe Ala Ile Asp Ser Pro Asp Ser Leu Asp Asn
Val Gln

85 90

95

Glu Lys Trp Ile Ser Glu Val Leu His Phe Cys Ser Gly Leu
Pro Ile

100 105 110

Ile Leu Val Gly Cys Lys Lys Asp Leu Arg Tyr Asp Gln Lys
Thr Ile

115 120 125

Glu Glu Leu Arg Lys Thr Ser Gln Lys Pro Val Ser Pro Glu
Asp Gly

130 135 140

0070110

Glu Glu Ile Lys Lys Lys Ile Gly Ala Tyr Lys Tyr Leu Glu
 Cys Ser
 145 150 155
 160
 Ala Lys Thr Asn Glu Gly Val Arg Glu Val Phe Glu His Ala
 Thr Arg
 165 170
 175
 Ala Ala Leu Leu Ser Arg His Lys Thr Lys Lys Lys Lys Cys
 Leu Ile
 180 185 190

Leu

<210> 184
 <211> 627
 <212> DNA
 <213> Gibberella zeae PH-1

<220>
 <221> CDS
 <222> (1)..(627)

<400> 184
 atg cct gct ctt tgt gga gga tcc aag act gtt cag cga aag
 ctg gtt 48
 Met Pro Ala Leu Cys Gly Gly Ser Lys Thr Val Gln Arg Lys
 Leu Val
 1 5 10
 15
 ctg ctg ggt gat ggt gct tgc gga aag aca tca ttg ctc aac
 gtc ttt 96
 Leu Leu Gly Asp Gly Ala Cys Gly Lys Thr Ser Leu Leu Asn
 Val Phe
 20 25 30
 act aga ggc tac ttc cca acg gtt tac gaa cct acg gtt ttc
 gag aat 144
 Thr Arg Gly Tyr Phe Pro Thr Val Tyr Glu Pro Thr Val Phe
 Glu Asn
 35 40 45
 tac gtt cac gac atc ttt gtg gat aat gtc cac atc gaa ctt
 tct ctc 192
 Tyr Val His Asp Ile Phe Val Asp Asn Val His Ile Glu Leu
 Ser Leu
 50 55 60
 tgg gat aca gcc ggc caa gaa gaa ttc gac cga tta cga tcc
 ctc tcc 240

0070110

Trp	Asp	Thr	Ala	Gly	Gln	Glu	Glu	Phe	Asp	Arg	Leu	Arg	Ser
Leu	Ser												
65					70					75			
80													
tac	gat	gac	aca	gat	ctc	atc	atg	ctc	tgc	tac	tca	gtc	gac
agc	aaa			288									
Tyr	Asp	Asp	Thr	Asp	Leu	Ile	Met	Leu	Cys	Tyr	Ser	Val	Asp
Ser	Lys												
				85					90				
95													
gac	tcg	ctc	gaa	aac	gta	gag	tcc	aag	tgg	gta	ggc	gaa	atc
gcc	gac			336									
Asp	Ser	Leu	Glu	Asn	Val	Glu	Ser	Lys	Trp	Val	Gly	Glu	Ile
Ala	Asp												
			100					105					110
aac	tgc	ccc	ggc	acg	aaa	ctc	gtg	ctc	gta	gcc	ctc	aag	tgc
gac	ctc			384									
Asn	Cys	Pro	Gly	Thr	Lys	Leu	Val	Leu	Val	Ala	Leu	Lys	Cys
Asp	Leu												
		115						120				125	
cgc	gag	cag	ggc	gaa	gac	gac	gaa	aac	gca	gca	gcg	ggc	ggc
gaa	tca			432									
Arg	Glu	Gln	Gly	Glu	Asp	Asp	Glu	Asn	Ala	Ala	Ala	Gly	Gly
Glu	Ser												
	130					135					140		
gaa	caa	ccc	cgg	gag	aag	aag	cca	atg	atc	aac	tac	gac	cag
ggc	ctc			480									
Glu	Gln	Pro	Arg	Glu	Lys	Lys	Pro	Met	Ile	Asn	Tyr	Asp	Gln
Gly	Leu												
145					150					155			
160													
gag	gtg	gcg	cgt	cgc	ata	ggc	gcc	cag	cga	tac	ctc	gag	tgc
tcc	gcc			528									
Glu	Val	Ala	Arg	Arg	Ile	Gly	Ala	Gln	Arg	Tyr	Leu	Glu	Cys
Ser	Ala												
				165						170			
175													
atg	aag	aac	agg	ggc	gtc	aac	gag	gcc	ttt	acc	gag	gct	gcg
cgc	gtt			576									
Met	Lys	Asn	Arg	Gly	Val	Asn	Glu	Ala	Phe	Thr	Glu	Ala	Ala
Arg	Val												
			180					185					190
gct	ctc	agc	gtc	aag	aag	gat	cgc	gag	gag	ggc	aag	tgc	atc
gtc	atg			624									
Ala	Leu	Ser	Val	Lys	Lys	Asp	Arg	Glu	Glu	Gly	Lys	Cys	Ile

0070110

Val Met
tga 195 200 205
627

<210> 185
<211> 208
<212> PRT
<213> Gibberella zeae PH-1

<400> 185
Met Pro Ala Leu Cys Gly Gly Ser Lys Thr Val Gln Arg Lys
Leu Val
1 5 10
15

Leu Leu Gly Asp Gly Ala Cys Gly Lys Thr Ser Leu Leu Asn
Val Phe
20 25 30

Thr Arg Gly Tyr Phe Pro Thr Val Tyr Glu Pro Thr Val Phe
Glu Asn
35 40 45

Tyr Val His Asp Ile Phe Val Asp Asn Val His Ile Glu Leu
Ser Leu
50 55 60

Trp Asp Thr Ala Gly Gln Glu Glu Phe Asp Arg Leu Arg Ser
Leu Ser
65 70 75
80

Tyr Asp Asp Thr Asp Leu Ile Met Leu Cys Tyr Ser Val Asp
Ser Lys
85 90

95
Asp Ser Leu Glu Asn Val Glu Ser Lys Trp Val Gly Glu Ile
Ala Asp
100 105 110

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

Arg Glu Gln Gly Glu Asp Asp Glu Asn Ala Ala Ala Gly Gly
Glu Ser
130 135 140

0070110

Glu	Gln	Pro	Arg	Glu	Lys	Lys	Pro	Met	Ile	Asn	Tyr	Asp	Gln
Gly	Leu												
145					150					155			
160													
Glu	Val	Ala	Arg	Arg	Ile	Gly	Ala	Gln	Arg	Tyr	Leu	Glu	Cys
Ser	Ala												
				165					170				
175													
Met	Lys	Asn	Arg	Gly	Val	Asn	Glu	Ala	Phe	Thr	Glu	Ala	Ala
Arg	Val												
			180					185					190
Ala	Leu	Ser	Val	Lys	Lys	Asp	Arg	Glu	Glu	Gly	Lys	Cys	Ile
Val	Met												
		195					200					205	

<210> 186
 <211> 594
 <212> DNA
 <213> Gibberella zeae PH-1

<220>
 <221> CDS
 <222> (1)..(594)

<400> 186													
atg	agc	gca	aat	ccg	agc	aac	gtt	atc	cgc	agg	aag	ctg	gtc
att	atc			48									
Met	Ser	Ala	Asn	Pro	Ser	Asn	Val	Ile	Arg	Arg	Lys	Leu	Val
Ile	Ile												
1				5					10				
15													
ggt	gat	ggt	gcc	tgc	ggc	aag	acc	agt	ttg	ttg	agc	gta	ttt
acg	cta			96									
Gly	Asp	Gly	Ala	Cys	Gly	Lys	Thr	Ser	Leu	Leu	Ser	Val	Phe
Thr	Leu												
			20					25					30
ggt	tac	ttt	cct	aca	att	ccc	aca	gtt	ttt	gag	aac	tac	gtg
acg	gac			144									
Gly	Tyr	Phe	Pro	Thr	Ile	Pro	Thr	Val	Phe	Glu	Asn	Tyr	Val
Thr	Asp												
		35					40					45	
tgc	aga	gtg	gac	ggc	aag	tct	gtc	cag	ctc	gct	ctt	tgg	gat
act	gct			192									
Cys	Arg	Val	Asp	Gly	Lys	Ser	Val	Gln	Leu	Ala	Leu	Trp	Asp
Thr	Ala												

0070110

<p>50 ggc cag gaa gac tac gag cga tta cga ccc ctt gca tat tcg aaa gcc Gly Gln Glu Asp Tyr Glu Arg Leu Arg Pro Leu Ala Tyr Ser Lys Ala 65</p> <p>80 cat gtc att ttg ata ggc ttt tct gtc gac acc cca gat tct ctc gac His Val Ile Leu Ile Gly Phe Ser Val Asp Thr Pro Asp Ser Leu Asp</p> <p>95 aac gtt aag cac aag tgg att gaa gaa gcc cag cga ctt tgc acc ggt Asn Val Lys His Lys Trp Ile Glu Glu Ala Gln Arg Leu Cys Thr Gly</p>	<p>240 70 288 85 336 100 384 115 432 130 480 145 160 528 165 576 180</p>	<p>55 75 90 105 110 120 125 135 140 150 155 170 185 190</p>	<p>60 gca tat tcg Ala Tyr Ser cca gat tct Pro Asp Ser cga ctt tgc Arg Leu Cys Leu Arg Glu Phe Val gca aaa cga Ala Lys Arg gac gat gtc ttc Asp Asp Val Phe gag ggc Glu Gly Glu Gly</p>
--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------	------------------------------------------------------------------------------------------------------------------------------------------	-----------------------------------------------------------------------------------------------------------------	-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------

tgc tgt gtc gtg ctg taa

0070110

Cys Cys Val Val⁵⁹⁴ Leu
195

<210> 187
<211> 197
<212> PRT
<213> Gibberella zeae PH-1

<400> 187

Met Ser Ala Asn Pro Ser Asn Val Ile Arg Arg Lys Leu Val
Ile Ile

1 5 10

15

Gly Asp Gly Ala Cys Gly Lys Thr Ser Leu Leu Ser Val Phe
Thr Leu

20 25 30

Gly Tyr Phe Pro Thr Ile Pro Thr Val Phe Glu Asn Tyr Val
Thr Asp

35 40 45

Cys Arg Val Asp Gly Lys Ser Val Gln Leu Ala Leu Trp Asp
Thr Ala
50 55 60

Gly Gln Glu Asp Tyr Glu Arg Leu Arg Pro Leu Ala Tyr Ser
Lys Ala

65 70 75

80

His Val Ile Leu Ile Gly Phe Ser Val Asp Thr Pro Asp Ser
Leu Asp

85 90

95

Asn Val Lys His Lys Trp Ile Glu Glu Ala Gln Arg Leu Cys
Thr Gly

100 105 110

Val Pro Ile Ile Leu Val Gly Leu Lys Lys Asp Leu Arg Glu
Asp Pro

115 120 125

Val Ala Ile Glu Glu Met Arg Lys Lys Ser Met Arg Phe Val
Ser Glu

130 135 140

His Asp Gly Glu Ser Ile Ala Arg Glu Ile Gly Ala Lys Arg
Tyr Leu

0070110

145		150		155
160				
Glu Cys Ser Ser Leu Ser Gly Glu Gly Val Asp Asp Val Phe				
Glu Ala				
	165		170	
175				
Ala Thr Arg Ala Ala Leu Leu Thr Phe Glu Lys Gly Glu Gly				
Gly Gly				
	180		185	190
Cys Cys Val Val Leu				
195				

<210> 188
 <211> 588
 <212> DNA
 <213> Gibberella zeae PH-1

<220>
 <221> CDS
 <222> (1)..(588)

<400> 188	
atg gct gag atc cgc cga aag ctc gtc att gtc ggc gat ggt	
gct tgt	48
Met Ala Glu Ile Arg Arg Lys Leu Val Ile Val Gly Asp Gly	
Ala Cys	
1	5 10
15	
ggt aaa acc tgt ttg ttg att gtt ttc tcc aag ggc act ttc	
ccc gag	96
Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Gly Thr Phe	
Pro Glu	
	20 25 30
ggt tac gtc ccc acc gtc ttc gag aac tat gtt gcc gat gtc	
gag gtt	144
Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Val	
Glu Val	
	35 40 45
gac ggc aag cac gtc gag ctc gcc cta tgg gat act gct ggt	
cag gag	192
Asp Gly Lys His Val Glu Leu Ala Leu Trp Asp Thr Ala Gly	
Gln Glu	
	50 55 60
gat tac gac cgt ctt cga cct ctt tct tac ccc gac tcc cac	
ggt atc	240
Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Ser His	
Val Ile	

0070110

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65      70      75
80
ttg atc tgc ttc gcc gtt gac tct ccc gac tcc ctc gac aac
gtc cag      288
Leu Ile Cys Phe Ala Val Asp Ser Pro Asp Ser Leu Asp Asn
Val Gln

85      90
95
gag aag tgg atc tct gag gtt ctg cac ttc tgc cag ggt ctc
cct atc      336
Glu Lys Trp Ile Ser Glu Val Leu His Phe Cys Gln Gly Leu
Pro Ile

100      105      110
atc ctt gtt ggc tgc aag aag gat ttg cga tac gac cag aag
atc att      384
Ile Leu Val Gly Cys Lys Lys Asp Leu Arg Tyr Asp Gln Lys
Ile Ile

115      120      125
gag gag ctc cga aag acc agc cag aag ccc gtc tcc cct gag
gag ggt      432
Glu Glu Leu Arg Lys Thr Ser Gln Lys Pro Val Ser Pro Glu
Glu Gly

130      135      140
gag gag atc cgc aag aag atc tct gct tac aag tac ctt gag
tgc tca      480
Glu Glu Ile Arg Lys Lys Ile Ser Ala Tyr Lys Tyr Leu Glu
Cys Ser

145      150      155
160
gcc aag acc aac gaa ggt gtc cgc gaa gtg ttc gag cac gct
act cgc      528
Ala Lys Thr Asn Glu Gly Val Arg Glu Val Phe Glu His Ala
Thr Arg

165      170
175
gct gct ctg ctg tcg cgc agc acc cga agc aag tct cac aag
aag tgt      576
Ala Ala Leu Leu Ser Arg Ser Thr Arg Ser Lys Ser His Lys
Lys Cys

180      185      190
ctt gtt ctg taa
Leu Val Leu      588
195

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<210> 189

0070110

<211> 195

<212> PRT

<213> Gibberella zeae PH-1

<400> 189

Met Ala Glu Ile Arg Arg Lys Leu Val Ile Val Gly Asp Gly
Ala Cys

1 5 10

15

Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Gly Thr Phe
Pro Glu

20 25 30

Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Val
Glu Val

35 40 45

Asp Gly Lys His Val Glu Leu Ala Leu Trp Asp Thr Ala Gly
Gln Glu

50 55 60

Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Ser His
Val Ile

65 70 75

80

Leu Ile Cys Phe Ala Val Asp Ser Pro Asp Ser Leu Asp Asn
Val Gln

85 90

95

Glu Lys Trp Ile Ser Glu Val Leu His Phe Cys Gln Gly Leu
Pro Ile

100 105 110

Ile Leu Val Gly Cys Lys Lys Asp Leu Arg Tyr Asp Gln Lys
Ile Ile

115 120 125

Glu Glu Leu Arg Lys Thr Ser Gln Lys Pro Val Ser Pro Glu
Glu Gly

130 135 140

Glu Glu Ile Arg Lys Lys Ile Ser Ala Tyr Lys Tyr Leu Glu
Cys Ser

145 150 155

160

Ala Lys Thr Asn Glu Gly Val Arg Glu Val Phe Glu His Ala
Thr Arg

165 170

0070110

175

Ala Ala Leu Leu Ser Arg Ser Thr Arg Ser Lys Ser His Lys
Lys Cys

180

185

190

Leu Val Leu
195

<210> 190

<211> 600

<212> DNA

<213> Gibberella zeae PH-1

<220>

<221> CDS

<222> (1)..(600)

<400> 190

atg gcc cag ccc ggc gtg caa tca ttg aag tgt gtg gtg acc
ggg gat 48

Met Ala Gln Pro Gly Val Gln Ser Leu Lys Cys Val Val Thr
Gly Asp

1

5

10

15

ggg gct gtt gga aag acc tgt cta ctc att tcc tac acc aca
aat gca 96

Gly Ala Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Thr
Asn Ala

20

25

30

ttc ccc ggc gaa tac atc cct aca gtc ttt gac aac tac tct
gct agt 144

Phe Pro Gly Glu Tyr Ile Pro Thr Val Phe Asp Asn Tyr Ser
Ala Ser

35

40

45

gtt atg gta gat ggc aag cct att agc ctt ggc ctc tgg gat
act gct 192

Val Met Val Asp Gly Lys Pro Ile Ser Leu Gly Leu Trp Asp
Thr Ala

50

55

60

ggg cag gag gat tac gac aga ctg cga ccc ctc tca tac ccc
cag acc 240

Gly Gln Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro
Gln Thr

65

70

75

80

gat gtc ttt ctc atc tgc ttc tcc atc gtc agc cct ccg tca
ttc gac 288

Asp Val Phe Leu Ile Cys Phe Ser Ile Val Ser Pro Pro Ser
Seite 303

0070110

Phe Asp

85

90

95

aac gta aag gca aag tgg tac ccc gag atc gac cat cat gcg
cca aac
Asn Val Lys Ala Lys Trp Tyr Pro Glu Ile Asp His His Ala
Pro Asn

100

105

110

atc ccc atc att ctc gtc gga acc aag ctc gat ctt cga gag
gac gca
Ile Pro Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Glu
Asp Ala

115

120

125

tcc acc ctc gag tct ctt cga cag aag cgc atg gag cct gtg
tca tac
Ser Thr Leu Glu Ser Leu Arg Gln Lys Arg Met Glu Pro Val
Ser Tyr

130

135

140

gag cag gcg ctg act tgc gcc aag gag atc aag gcc tac aag
tac ctc
Glu Gln Ala Leu Thr Cys Ala Lys Glu Ile Lys Ala Tyr Lys
Tyr Leu

145

150

155

160

gag tgt tct gct ttg acc caa aga aac ctc aag agc gtc ttt
gac gag
Glu Cys Ser Ala Leu Thr Gln Arg Asn Leu Lys Ser Val Phe
Asp Glu

165

170

175

gct atc cgg gcc gtt ctc aac ccc cga ccc aca cct tca aag
caa aag
Ala Ile Arg Ala Val Leu Asn Pro Arg Pro Thr Pro Ser Lys
Gln Lys

180

185

190

aag aac aaa tgc tcc atc ctg tag
600

Lys Asn Lys Cys Ser Ile Leu
195

<210> 191

<211> 199

<212> PRT

<213> Gibberella zeae PH-1

<400> 191

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Met	Ala	Gln	Pro	Gly	Val	Gln	Ser	Leu	Lys	Cys	Val	Val	Thr
Gly	Asp												
1				5					10				
15													
Gly	Ala	Val	Gly	Lys	Thr	Cys	Leu	Leu	Ile	Ser	Tyr	Thr	Thr
Asn	Ala												
			20					25					30
Phe	Pro	Gly	Glu	Tyr	Ile	Pro	Thr	Val	Phe	Asp	Asn	Tyr	Ser
Ala	Ser												
			35					40				45	
Val	Met	Val	Asp	Gly	Lys	Pro	Ile	Ser	Leu	Gly	Leu	Trp	Asp
Thr	Ala												
	50					55					60		
Gly	Gln	Glu	Asp	Tyr	Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Pro
Gln	Thr												
65					70					75			
80													
Asp	Val	Phe	Leu	Ile	Cys	Phe	Ser	Ile	Val	Ser	Pro	Pro	Ser
Phe	Asp												
				85					90				
95													
Asn	Val	Lys	Ala	Lys	Trp	Tyr	Pro	Glu	Ile	Asp	His	His	Ala
Pro	Asn												
			100					105					110
Ile	Pro	Ile	Ile	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Glu
Asp	Ala												
			115					120				125	
Ser	Thr	Leu	Glu	Ser	Leu	Arg	Gln	Lys	Arg	Met	Glu	Pro	Val
Ser	Tyr												
	130					135					140		
Glu	Gln	Ala	Leu	Thr	Cys	Ala	Lys	Glu	Ile	Lys	Ala	Tyr	Lys
Tyr	Leu												
145					150					155			
160													
Glu	Cys	Ser	Ala	Leu	Thr	Gln	Arg	Asn	Leu	Lys	Ser	Val	Phe
Asp	Glu												
				165					170				
175													
Ala	Ile	Arg	Ala	Val	Leu	Asn	Pro	Arg	Pro	Thr	Pro	Ser	Lys
Gln	Lys												
			180					185					190

0070110

Lys Asn Lys Cys Ser Ile Leu
195

<210> 192
<211> 642
<212> DNA
<213> Apis mellifera

<220>
<221> CDS
<222> (1)..(642)

<400> 192
atg gga tgc aat acg ggc cga tgc ctc ggt cca gac gat acg
ggg tac 48
Met Gly Cys Asn Thr Gly Arg Cys Leu Gly Pro Asp Asp Thr
Gly Tyr 1 5 10
15
cct gga tca gaa ttc atg gca gcc att aga aag aaa ttg gtt
att gtg 96
Pro Gly Ser Glu Phe Met Ala Ala Ile Arg Lys Lys Leu Val
Ile Val 20 25 30
ggg gat ggt gct tgt ggt aaa aca tgc tta ctt ata gtc ttc
agc aaa 144
Gly Asp Gly Ala Cys Gly Lys Thr Cys Leu Leu Ile Val Phe
Ser Lys 35 40 45
gac caa ttt cca gaa gtt tat gta cct aca gtg ttt gaa aat
tat gtt 192
Asp Gln Phe Pro Glu Val Tyr Val Pro Thr Val Phe Glu Asn
Tyr Val 50 55 60
gca gat att gaa gtt gat ggg aaa caa gtg gaa ctg gct ctt
tgg gac 240
Ala Asp Ile Glu Val Asp Gly Lys Gln Val Glu Leu Ala Leu
Trp Asp 65 70 75
80
aca gct gga caa gaa gat tat gat agg ttg cgt cca cta tca
tat cct 288
Thr Ala Gly Gln Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser
Tyr Pro 85 90
95
gac aca gat gta atc tta atg tgt ttc tct att gat agt cca
gat tcc 336

0070110

Asp	Thr	Asp	Val	Ile	Leu	Met	Cys	Phe	Ser	Ile	Asp	Ser	Pro
Asp	Ser												
			100					105					110

ctg	gaa	aac	att	cct	gag	aaa	tgg	aca	cca	gag	gtg	aag	cac
ttt	tgc			384									
Leu	Glu	Asn	Ile	Pro	Glu	Lys	Trp	Thr	Pro	Glu	Val	Lys	His
Phe	Cys												

		115					120					125	
cca	aat	gtg	ccc	att	atc	ctt	ggt	gga	aac	aaa	aaa	gac	tta
cg	aat		432										
Pro	Asn	Val	Pro	Ile	Ile	Leu	Val	Gly	Asn	Lys	Lys	Asp	Leu
Arg	Asn												

						135					140		
gat	cct	aat	aca	atc	aaa	gaa	ctt	agt	aag	atg	aaa	caa	gaa
cca	ggt		480										
Asp	Pro	Asn	Thr	Ile	Lys	Glu	Leu	Ser	Lys	Met	Lys	Gln	Glu
Pro	Val												

					150				155				
160													
aag	cca	gaa	gaa	gga	aga	gct	atg	gct	gaa	aaa	atc	aat	gcc
ttt	gct		528										
Lys	Pro	Glu	Glu	Gly	Arg	Ala	Met	Ala	Glu	Lys	Ile	Asn	Ala
Phe	Ala												

			165					170					
175													
tat	ctt	gaa	tgt	tct	gct	aaa	agt	aag	gaa	ggt	att	agg	gaa
gta	ttt		576										
Tyr	Leu	Glu	Cys	Ser	Ala	Lys	Ser	Lys	Glu	Gly	Ile	Arg	Glu
Val	Phe												

			180					185				190	
gaa	aca	gcc	act	cgg	gca	gca	tta	caa	gta	aaa	aag	aag	aag
aag	gga		624										
Glu	Thr	Ala	Thr	Arg	Ala	Ala	Leu	Gln	Val	Lys	Lys	Lys	Lys
Lys	Gly												

		195				200				205			
aga	tgt	tgg	ctc	cta	taa								
			642										
Arg	Cys	Trp	Leu	Leu									
	210												

<210> 193
 <211> 213
 <212> PRT
 <213> Apis mellifera

<400> 193

0070110

Met	Gly	Cys	Asn	Thr	Gly	Arg	Cys	Leu	Gly	Pro	Asp	Asp	Thr
Gly	Tyr												
1				5					10				
15													
Pro	Gly	Ser	Glu	Phe	Met	Ala	Ala	Ile	Arg	Lys	Lys	Leu	Val
Ile	Val												
			20					25					30
Gly	Asp	Gly	Ala	Cys	Gly	Lys	Thr	Cys	Leu	Leu	Ile	Val	Phe
Ser	Lys												
			35					40					45
Asp	Gln	Phe	Pro	Glu	Val	Tyr	Val	Pro	Thr	Val	Phe	Glu	Asn
Tyr	Val												
	50					55					60		
Ala	Asp	Ile	Glu	Val	Asp	Gly	Lys	Gln	Val	Glu	Leu	Ala	Leu
Trp	Asp												
65					70					75			
	80												
Thr	Ala	Gly	Gln	Glu	Asp	Tyr	Asp	Arg	Leu	Arg	Pro	Leu	Ser
Tyr	Pro												
				85					90				
95													
Asp	Thr	Asp	Val	Ile	Leu	Met	Cys	Phe	Ser	Ile	Asp	Ser	Pro
Asp	Ser												
			100					105					110
Leu	Glu	Asn	Ile	Pro	Glu	Lys	Trp	Thr	Pro	Glu	Val	Lys	His
Phe	Cys												
			115					120				125	
Pro	Asn	Val	Pro	Ile	Ile	Leu	Val	Gly	Asn	Lys	Lys	Asp	Leu
Arg	Asn												
	130					135					140		
Asp	Pro	Asn	Thr	Ile	Lys	Glu	Leu	Ser	Lys	Met	Lys	Gln	Glu
Pro	Val												
145					150					155			
	160												
Lys	Pro	Glu	Glu	Gly	Arg	Ala	Met	Ala	Glu	Lys	Ile	Asn	Ala
Phe	Ala												
				165					170				
175													
Tyr	Leu	Glu	Cys	Ser	Ala	Lys	Ser	Lys	Glu	Gly	Ile	Arg	Glu
Val	Phe												
			180					185					190

0070110

Glu Thr Ala Thr Arg Ala Ala Leu Gln Val Lys Lys Lys Lys
 Lys Gly
 195 200 205

Arg Cys Trp Leu Leu
 210

<210> 194
 <211> 576
 <212> DNA
 <213> Apis mellifera

<220>
 <221> CDS
 <222> (1)..(576)

<400> 194
 atg cag acg ata aaa tgc gtt gtg gtt gga gat gga gct gtg
 ggt aaa 48
 Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
 Gly Lys
 1 5 10
 15
 act tgt ctt ttg att tca tat aca acc aat aag ttt cca tcc
 gaa tat 96
 Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe Pro Ser
 Glu Tyr
 20 25 30
 gta cct aca gtg ttt gac aat tac gca gta aca gta atg atc
 ggt gga 144
 Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val Met Ile
 Gly Gly
 35 40 45
 gat cca tat aca ttg gga tta ttc gat act gct ggt cag gag
 gat tac 192
 Asp Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu
 Asp Tyr
 50 55 60
 gac aga ctt aga cca tta agt tat ccc caa acg gat gta ttt
 ctt gtt 240
 Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
 Leu Val
 65 70 75
 80
 tgt ttc tca gtt gtt tca cca tca tct ttt gaa aat gtt aaa
 gaa aag 288
 Cys Phe Ser Val Val Ser Pro Ser Ser Phe Glu Asn Val Lys
 Glu Lys

0070110

85

90

95

tgg gta ccc gaa ata aca cat cat tgt cca agg aca ccg ttt
tta ttg 336

Trp Val Pro Glu Ile Thr His His Cys Pro Arg Thr Pro Phe
Leu Leu

100

105

110

gtt ggt act caa atc gat ttg aga gat gat gtt gct act atc
gaa aag 384

Val Gly Thr Gln Ile Asp Leu Arg Asp Asp Val Ala Thr Ile
Glu Lys

115

120

125

ttg gca aag aat aaa caa aag cca ata tcc gcg gag caa ggg
gaa aag 432

Leu Ala Lys Asn Lys Gln Lys Pro Ile Ser Ala Glu Gln Gly
Glu Lys

130

135

140

ctt gcc aaa gaa tta aaa gca gtg aaa tac gta gaa tgt agt
gct ctt 480

Leu Ala Lys Glu Leu Lys Ala Val Lys Tyr Val Glu Cys Ser
Ala Leu

145

150

155

160

acg cag aaa ggt ttg aaa aat gtg ttt gat gaa gct att tta
gcc gcc 528

Thr Gln Lys Gly Leu Lys Asn Val Phe Asp Glu Ala Ile Leu
Ala Ala

165

170

175

tta gaa cct cca gaa cca gta aag aag aga aag tgt acg ctt
ttg 573

Leu Glu Pro Pro Glu Pro Val Lys Lys Arg Lys Cys Thr Leu
Leu

180

185

190

taa

576

<210> 195

<211> 191

<212> PRT

<213> Apis mellifera

<400> 195

Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val

0070110

Gly	Lys													
1				5					10					
15														
Thr	Cys	Leu	Leu	Ile	Ser	Tyr	Thr	Thr	Asn	Lys	Phe	Pro	Ser	
Glu	Tyr													
			20					25					30	
Val	Pro	Thr	Val	Phe	Asp	Asn	Tyr	Ala	Val	Thr	Val	Met	Ile	
Gly	Gly													
		35					40					45		
Asp	Pro	Tyr	Thr	Leu	Gly	Leu	Phe	Asp	Thr	Ala	Gly	Gln	Glu	
Asp	Tyr													
	50					55					60			
Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Pro	Gln	Thr	Asp	Val	Phe	
Leu	Val													
65					70					75				
	80													
Cys	Phe	Ser	Val	Val	Ser	Pro	Ser	Ser	Phe	Glu	Asn	Val	Lys	
Glu	Lys													
				85					90					
95														
Trp	Val	Pro	Glu	Ile	Thr	His	His	Cys	Pro	Arg	Thr	Pro	Phe	
Leu	Leu													
			100					105					110	
Val	Gly	Thr	Gln	Ile	Asp	Leu	Arg	Asp	Asp	Val	Ala	Thr	Ile	
Glu	Lys													
		115					120					125		
Leu	Ala	Lys	Asn	Lys	Gln	Lys	Pro	Ile	Ser	Ala	Glu	Gln	Gly	
Glu	Lys													
	130					135					140			
Leu	Ala	Lys	Glu	Leu	Lys	Ala	Val	Lys	Tyr	Val	Glu	Cys	Ser	
Ala	Leu													
145					150					155				
	160													
Thr	Gln	Lys	Gly	Leu	Lys	Asn	Val	Phe	Asp	Glu	Ala	Ile	Leu	
Ala	Ala													
				165					170					
175														
Leu	Glu	Pro	Pro	Glu	Pro	Val	Lys	Lys	Arg	Lys	Cys	Thr	Leu	
Leu														
			180					185					190	

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<210> 196
<211> 684
<212> DNA
<213> Candida glabrata CBS 138

<220>
<221> CDS
<222> (1)..(684)

<400> 196
atg gca ttt ctg tgt gga tcc tct tca tct caa tcc tca ggt
tct aag 48
Met Ala Phe Leu Cys Gly Ser Ser Ser Ser Gln Ser Ser Gly
Ser Lys 1 5 10
15
aaa cct gtc gag aga aag att gtt att cta ggt gat ggt gcg
tgt ggt 96
Lys Pro Val Glu Arg Lys Ile Val Ile Leu Gly Asp Gly Ala
Cys Gly 20 25 30
aaa acc tcg ctg ctg aac gtg ttc acc agg ggc tat ttc cca
gaa gtc 144
Lys Thr Ser Leu Leu Asn Val Phe Thr Arg Gly Tyr Phe Pro
Glu Val 35 40 45
tac gag ccc act gtc ttt gag aac tat att cat gac atc ttt
gtc gat 192
Tyr Glu Pro Thr Val Phe Glu Asn Tyr Ile His Asp Ile Phe
Val Asp 50 55 60
aac aga cac att acg ttg tcg ctg tgg gat acc gcg gga caa
gaa gaa 240
Asn Arg His Ile Thr Leu Ser Leu Trp Asp Thr Ala Gly Gln
Glu Glu 65 70 75
80
ttt gac agg tta cga tca tta tca tac tct gac acg cac acc
ata atg 288
Phe Asp Arg Leu Arg Ser Leu Ser Tyr Ser Asp Thr His Thr
Ile Met 85 90
95
ctg tgt ttc agt ata gac tct agg gac tcc ttg gag aac gtc
aag aat 336
Leu Cys Phe Ser Ile Asp Ser Arg Asp Ser Leu Glu Asn Val
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[illegible]

0070110

<212> PRT

<213> Candida glabrata CBS 138

<400> 197

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Met Ala Phe Leu Cys Gly Ser Ser Ser Ser Gln Ser Ser Gly
Ser Lys
1          5          10
15
Lys Pro Val Glu Arg Lys Ile Val Ile Leu Gly Asp Gly Ala
Cys Gly
          20          25          30

Lys Thr Ser Leu Leu Asn Val Phe Thr Arg Gly Tyr Phe Pro
Glu Val
          35          40          45

Tyr Glu Pro Thr Val Phe Glu Asn Tyr Ile His Asp Ile Phe
Val Asp
          50          55          60

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

Lys Trp Val Gly Glu Ile Thr Asp His Cys Glu Gly Val Asn
Leu Val
          115          120          125

Leu Val Ala Leu Lys Cys Asp Leu Arg Asn Asn Glu Asn Asn
Val Ile
          130          135          140

Thr Pro Asn Asn Ile Gln Asn Asn Arg Asn Asn Asn Asn
Asn Asn
145          150          155
160
Leu Ile Thr Tyr Glu Glu Gly Leu Ala Met Ala Lys Gln Ile
Gly Ala
          165          170
175

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Leu Arg Tyr Leu Glu Cys Ser Ala Lys Leu Asn Lys Gly Val
 Asn Glu
 180 185 190

Ala Phe Thr Glu Ala Ala Arg Val Ala Leu Thr Ala Lys Asn
 Ala Thr
 195 200 205

Asp Asn Ile Asn Ser Asn Ser Ser Ser Asn Glu Lys Asp Ser
 Phe Cys
 210 215 220

Thr Ile Cys
 225

<210> 198
 <211> 633
 <212> DNA
 <213> Candida glabrata CBS 138

<220>
 <221> CDS
 <222> (1)..(633)

<400> 198
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 att gtc 48
 Met Ser Gln Gln Val Gly Ala Ser Ile Arg Arg Lys Leu Val
 Ile Val
 1 5 10
 15
 ggt gat ggt gcc tgt ggt aag acc tgt ctt ttg att gtg ttt
 tcc aag 96
 Gly Asp Gly Ala Cys Gly Lys Thr Cys Leu Leu Ile Val Phe
 Ser Lys
 20 25 30
 ggt caa ttc cca gaa gtt tac gtt cca act gtt ttt gag aac
 tac gtt 144
 Gly Gln Phe Pro Glu Val Tyr Val Pro Thr Val Phe Glu Asn
 Tyr Val
 35 40 45
 gct gat gtt gag gtg gat ggc aga cgt gtt gag ttg gct ctg
 tgg gat 192
 Ala Asp Val Glu Val Asp Gly Arg Arg Val Glu Leu Ala Leu
 Trp Asp
 50 55 60
 acc gct ggc caa gaa gat tac gat aga cta aga cca ttg tcg
 tac cca 240

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Thr	Ala	Gly	Gln	Glu	Asp	Tyr	Asp	Arg	Leu	Arg	Pro	Leu	Ser
Tyr	Pro												
65					70					75			
80													
gac	tcc	aat	ggt	gtc	ttg	atc	tgt	ttc	tct	atc	gat	ctg	cca
gat	tcc		288										
Asp	Ser	Asn	Val	Val	Leu	Ile	Cys	Phe	Ser	Ile	Asp	Leu	Pro
Asp	Ser												
			85						90				
95													
cta	gag	aac	gtc	cag	gag	aag	tgg	att	gcc	gag	gtg	cta	cat
ttc	tgt		336										
Leu	Glu	Asn	Val	Gln	Glu	Lys	Trp	Ile	Ala	Glu	Val	Leu	His
Phe	Cys												
			100						105				110
caa	ggg	ggt	cca	atc	atc	ctt	gta	ggg	tgt	aaa	ggt	gat	cta
aga	aac		384										
Gln	Gly	Val	Pro	Ile	Ile	Leu	Val	Gly	Cys	Lys	Val	Asp	Leu
Arg	Asn												
		115					120					125	
gac	cca	caa	act	ttg	gaa	caa	ttg	aga	gct	gaa	ggc	cta	caa
cca	gtc		432										
Asp	Pro	Gln	Thr	Leu	Glu	Gln	Leu	Arg	Ala	Glu	Gly	Leu	Gln
Pro	Val												
		130				135				140			
gct	act	gcc	gat	ggg	caa	aac	ggt	gcc	gac	caa	att	ggg	gcc
act	ggc		480										
Ala	Thr	Ala	Asp	Gly	Gln	Asn	Val	Ala	Asp	Gln	Ile	Gly	Ala
Thr	Gly												
145					150					155			
160													
tac	tac	gaa	tgt	tcc	gcc	aag	acc	ggc	tac	ggg	gtg	cgt	gaa
gtc	ttt		528										
Tyr	Tyr	Glu	Cys	Ser	Ala	Lys	Thr	Gly	Tyr	Gly	Val	Arg	Glu
Val	Phe												
			165							170			
175													
gaa	gcc	gcc	act	aga	gcc	tct	ttg	atg	ggg	aag	caa	aag	aac
acc	ggg		576										
Glu	Ala	Ala	Thr	Arg	Ala	Ser	Leu	Met	Gly	Lys	Gln	Lys	Asn
Thr	Gly												
			180						185				190
aag	aag	aac	aag	aag	aac	tct	ggg	gaa	aag	aag	aag	aga	aag
tgt	gtt		624										
Lys	Lys	Asn	Lys	Lys	Asn	Ser	Gly	Glu	Lys	Lys	Lys	Arg	Lys
Cys	Val												

0070110
200

205

195
cta ttg taa
633
Leu Leu
210

<210> 199
<211> 210
<212> PRT
<213> Candida glabrata CBS 138

<400> 199
Met Ser Gln Gln Val Gly Ala Ser Ile Arg Arg Lys Leu Val
Ile Val
1 5 10
15
Gly Asp Gly Ala Cys Gly Lys Thr Cys Leu Leu Ile Val Phe
Ser Lys
20 25 30
Gly Gln Phe Pro Glu Val Tyr Val Pro Thr Val Phe Glu Asn
Tyr Val
35 40 45
Ala Asp Val Glu Val Asp Gly Arg Arg Val Glu Leu Ala Leu
Trp Asp
50 55 60
Thr Ala Gly Gln Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser
Tyr Pro
65 70 75
80
Asp Ser Asn Val Val Leu Ile Cys Phe Ser Ile Asp Leu Pro
Asp Ser
85 90
95
Leu Glu Asn Val Gln Glu Lys Trp Ile Ala Glu Val Leu His
Phe Cys
100 105 110
Gln Gly Val Pro Ile Ile Leu Val Gly Cys Lys Val Asp Leu
Arg Asn
115 120 125
Asp Pro Gln Thr Leu Glu Gln Leu Arg Ala Glu Gly Leu Gln
Pro Val
130 135 140

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Ala	Thr	Ala	Asp	Gly	Gln	Asn	Val	Ala	Asp	Gln	Ile	Gly	Ala
Thr	Gly												
145					150					155			
160													
Tyr	Tyr	Glu	Cys	Ser	Ala	Lys	Thr	Gly	Tyr	Gly	Val	Arg	Glu
Val	Phe												
				165						170			
175													
Glu	Ala	Ala	Thr	Arg	Ala	Ser	Leu	Met	Gly	Lys	Gln	Lys	Asn
Thr	Gly												
			180					185					190
Lys	Lys	Asn	Lys	Lys	Asn	Ser	Gly	Glu	Lys	Lys	Lys	Arg	Lys
Cys	Val												
		195					200					205	
Leu	Leu												
	210												

<210> 200
 <211> 567
 <212> DNA
 <213> Candida glabrata CBS 138

<220>
 <221> CDS
 <222> (1)..(567)

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gat	ggt			48									
Met	Ser	Glu	Lys	Ala	Ile	Arg	Arg	Lys	Leu	Val	Ile	Ile	Gly
Asp	Gly												
1				5					10				
15													
gcg	tgc	ggt	aaa	aca	tcg	tta	ctt	tat	gtg	ttt	acg	ctg	ggg
aaa	ttc			96									
Ala	Cys	Gly	Lys	Thr	Ser	Leu	Leu	Tyr	Val	Phe	Thr	Leu	Gly
Lys	Phe												
			20					25					30
cct	gaa	caa	tac	cat	cct	aca	gtg	ttt	gag	aac	tat	gta	aca
gat	tgt			144									
Pro	Glu	Gln	Tyr	His	Pro	Thr	Val	Phe	Glu	Asn	Tyr	Val	Thr
Asp	Cys												
		35					40					45	
cgc	gtt	gat	ggg	ata	aaa	gta	tct	ctg	gca	ttg	tgg	gat	aca
gca	gga			192									
Arg	Val	Asp	Gly	Ile	Lys	Val	Ser	Leu	Ala	Leu	Trp	Asp	Thr

Ala	Gly												
50						55					60		
caa	gaa	gaa	tac	gaa	aga	tta	aga	cca	ttt	tct	tat	tca	ggg
gca	gat			240									
Gln	Glu	Glu	Tyr	Glu	Arg	Leu	Arg	Pro	Phe	Ser	Tyr	Ser	Gly
Ala	Asp												
65					70					75			
80													
gta	ata	ctg	att	gct	ttt	tct	gtg	gac	aat	gtt	gaa	tct	cta
cat	aat			288									
Val	Ile	Leu	Ile	Ala	Phe	Ser	Val	Asp	Asn	Val	Glu	Ser	Leu
His	Asn												
				85					90				
95													
gcc	agg	aca	aaa	tgg	gcc	gaa	gaa	gcg	ttc	agg	tac	tgt	cca
gat	gca			336									
Ala	Arg	Thr	Lys	Trp	Ala	Glu	Glu	Ala	Phe	Arg	Tyr	Cys	Pro
Asp	Ala												
			100					105					110
cct	gtg	ata	ctt	gta	ggg	cta	aag	gaa	gat	ttg	agg	aaa	tca
aaa	caa			384									
Pro	Val	Ile	Leu	Val	Gly	Leu	Lys	Glu	Asp	Leu	Arg	Lys	Ser
Lys	Gln												
		115				120						125	
gaa	ggc	ata	gtt	ttc	gta	aat	aga	gaa	gat	gca	gaa	caa	gta
gcg	aag			432									
Glu	Gly	Ile	Val	Phe	Val	Asn	Arg	Glu	Asp	Ala	Glu	Gln	Val
Ala	Lys												
		130				135					140		
gcc	att	ggg	gct	aaa	aag	tat	ttg	gaa	tgc	agt	gcg	ttg	act
ggt	gaa			480									
Ala	Ile	Gly	Ala	Lys	Lys	Tyr	Leu	Glu	Cys	Ser	Ala	Leu	Thr
Gly	Glu												
145					150					155			
160													
ggg	gtc	gat	gat	gtt	ttt	gag	ttg	gcc	aca	aga	tca	agc	ttg
cta	atg			528									
Gly	Val	Asp	Asp	Val	Phe	Glu	Leu	Ala	Thr	Arg	Ser	Ser	Leu
Leu	Met												
				165					170				
175													
cac	aaa	gaa	ccg	gac	cat	ttt	tgt	tgt	tcg	ata	tct	tag	
			567										
His	Lys	Glu	Pro	Asp	His	Phe	Cys	Cys	Ser	Ile	Ser		
			180					185					

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<211> 188

<212> PRT

<213> Candida glabrata CBS 138

<400> 201

Met Ser Glu Lys Ala Ile Arg Arg Lys Leu Val Ile Ile Gly
Asp Gly

1 5 10

15

Ala Cys Gly Lys Thr Ser Leu Leu Tyr Val Phe Thr Leu Gly
Lys Phe

20 25 30

Pro Glu Gln Tyr His Pro Thr Val Phe Glu Asn Tyr Val Thr
Asp Cys

35 40 45

Arg Val Asp Gly Ile Lys Val Ser Leu Ala Leu Trp Asp Thr
Ala Gly

50 55 60

Gln Glu Glu Tyr Glu Arg Leu Arg Pro Phe Ser Tyr Ser Gly
Ala Asp

65 70 75

80

Val Ile Leu Ile Ala Phe Ser Val Asp Asn Val Glu Ser Leu
His Asn

85 90

95

Ala Arg Thr Lys Trp Ala Glu Glu Ala Phe Arg Tyr Cys Pro
Asp Ala

100 105 110

Pro Val Ile Leu Val Gly Leu Lys Glu Asp Leu Arg Lys Ser
Lys Gln

115 120 125

Glu Gly Ile Val Phe Val Asn Arg Glu Asp Ala Glu Gln Val
Ala Lys

130 135 140

Ala Ile Gly Ala Lys Lys Tyr Leu Glu Cys Ser Ala Leu Thr
Gly Glu

145 150 155

160

Gly Val Asp Asp Val Phe Glu Leu Ala Thr Arg Ser Ser Leu
Leu Met

165 170

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175

His Lys Glu Pro Asp His Phe Cys Cys Ser Ile Ser
180 185

<210> 202

<211> 657

<212> DNA

<213> Kluyveromyces lactis NRRL Y-1140

<220>

<221> CDS

<222> (1)..(657)

<400> 202

atg gca tta ata gtt gac aac ttt cgt aga acc cta ggt gat
att cct 48

Met Ala Leu Ile Val Asp Asn Phe Arg Arg Thr Leu Gly Asp
Ile Pro

1 5 10

15

cat tat tcc caa tgt ggt gtt aag ggt aga agc gca cag tat
cat ttg 96

His Tyr Ser Gln Cys Gly Val Lys Gly Arg Ser Ala Gln Tyr
His Leu

20 25 30
aaa ata gta gta gtt ggt gac ggt gct gtg ggg aag act tcg
tta ctt 144

Lys Ile Val Val Val Gly Asp Gly Ala Val Gly Lys Thr Ser
Leu Leu

35 40 45
att tcc tat aca caa ggt aaa ttt cct gaa gat tat gta ccc
acg ata 192

Ile Ser Tyr Thr Gln Gly Lys Phe Pro Glu Asp Tyr Val Pro
Thr Ile

50 55 60
ttt gaa aac tac gtg act aat tta gag gga cca aat ggt aag
ata gtt 240

Phe Glu Asn Tyr Val Thr Asn Leu Glu Gly Pro Asn Gly Lys
Ile Val

65 70 75

80
gaa ttg gca ttg tgg gac aca gca gga caa gaa gag tac agt
cga ctt 288

Glu Leu Ala Leu Trp Asp Thr Ala Gly Gln Glu Glu Tyr Ser
Arg Leu

85 90

95
aga cca ctg tcg tac acc gac gtt gat gta ttg atg ata tgc

0070110

tat	gcg		336											
Arg	Pro	Leu	Ser	Tyr	Thr	Asp	Val	Asp	Val	Leu	Met	Ile	Cys	
Tyr	Ala													
			100					105					110	

att	aac	agt	aaa	gta	tcc	ttt	tac	aac	att	gaa	gaa	atg	tgg	
tta	cct		384											
Ile	Asn	Ser	Lys	Val	Ser	Phe	Tyr	Asn	Ile	Glu	Glu	Met	Trp	
Leu	Pro													
		115						120				125		

gag	gtg	aaa	cat	ttc	tgt	cct	gac	gtt	cca	ata	atg	atc	gta	
ggt	ttg		432											
Glu	Val	Lys	His	Phe	Cys	Pro	Asp	Val	Pro	Ile	Met	Ile	Val	
Gly	Leu													
		130				135					140			

aag	agt	gat	ctg	tac	gct	gaa	gat	aac	att	tca	gac	ttt	gtc	
gat	gca		480											
Lys	Ser	Asp	Leu	Tyr	Ala	Glu	Asp	Asn	Ile	Ser	Asp	Phe	Val	
Asp	Ala													
145					150					155				
160														

ttt	aaa	gct	gaa	gaa	aca	gcg	aaa	aga	atc	gga	gca	ttc	gta	
cat	ctg		528											
Phe	Lys	Ala	Glu	Glu	Thr	Ala	Lys	Arg	Ile	Gly	Ala	Phe	Val	
His	Leu													
			165							170				

175														
caa	tgt	tcc	tca	aaa	tct	caa	caa	aag	gta	cgt	gaa	gtc	ttc	
gat	aca		576											
Gln	Cys	Ser	Ser	Lys	Ser	Gln	Gln	Lys	Val	Arg	Glu	Val	Phe	
Asp	Thr													
			180					185					190	

gct	atc	act	gct	gcc	ttg	tat	gac	gaa	ttg	aaa	cca	aag	aag	
aag	aaa		624											
Ala	Ile	Thr	Ala	Ala	Leu	Tyr	Asp	Glu	Leu	Lys	Pro	Lys	Lys	
Lys	Lys													
		195						200				205		

cta	aat	tca	cgt	cgg	aaa	tgt	gtg	att	att	tag				
			657											
Leu	Asn	Ser	Arg	Arg	Lys	Cys	Val	Ile	Ile					
	210					215								

<210> 203

<211> 218

<212> PRT

<213> Kluyveromyces lactis NRRL Y-1140

0070110

<400> 203

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Ile	Pro												
1				5					10				
15													
His	Tyr	Ser	Gln	Cys	Gly	Val	Lys	Gly	Arg	Ser	Ala	Gln	Tyr
His	Leu												
			20					25					30
Lys	Ile	Val	Val	Val	Gly	Asp	Gly	Ala	Val	Gly	Lys	Thr	Ser
Leu	Leu												
		35					40					45	
Ile	Ser	Tyr	Thr	Gln	Gly	Lys	Phe	Pro	Glu	Asp	Tyr	Val	Pro
Thr	Ile												
	50					55					60		
Phe	Glu	Asn	Tyr	Val	Thr	Asn	Leu	Glu	Gly	Pro	Asn	Gly	Lys
Ile	Val												
65					70					75			
80													
Glu	Leu	Ala	Leu	Trp	Asp	Thr	Ala	Gly	Gln	Glu	Glu	Tyr	Ser
Arg	Leu												
				85					90				
95													
Arg	Pro	Leu	Ser	Tyr	Thr	Asp	Val	Asp	Val	Leu	Met	Ile	Cys
Tyr	Ala												
			100					105					110
Ile	Asn	Ser	Lys	Val	Ser	Phe	Tyr	Asn	Ile	Glu	Glu	Met	Trp
Leu	Pro												
		115					120					125	
Glu	Val	Lys	His	Phe	Cys	Pro	Asp	Val	Pro	Ile	Met	Ile	Val
Gly	Leu												
	130					135				140			
Lys	Ser	Asp	Leu	Tyr	Ala	Glu	Asp	Asn	Ile	Ser	Asp	Phe	Val
Asp	Ala												
145					150					155			
160													
Phe	Lys	Ala	Glu	Glu	Thr	Ala	Lys	Arg	Ile	Gly	Ala	Phe	Val
His	Leu												
			165						170				
175													
Gln	Cys	Ser	Ser	Lys	Ser	Gln	Gln	Lys	Val	Arg	Glu	Val	Phe
Asp	Thr												
			180					185					190

0070110

Ala Ile Thr Ala Ala Leu Tyr Asp Glu Leu Lys Pro Lys Lys
Lys Lys
195 200 205

Leu Asn Ser Arg Arg Lys Cys Val Ile Ile
210 215

<210> 204

<211> 564

<212> DNA

<213> Kluyveromyces lactis NRRL Y-1140

<220>

<221> CDS

<222> (1)..(564)

<400> 204

atg tct acc aat cca gtt aaa agg aaa cta gtt att att ggt

gac gga 48

Met Ser Thr Asn Pro Val Lys Arg Lys Leu Val Ile Ile Gly

Asp Gly

1

5

10

15

gca tgt ggg aaa aca tct ttg tta tat gtt ttc act ttg gga

cag ttt 96

Ala Cys Gly Lys Thr Ser Leu Leu Tyr Val Phe Thr Leu Gly

Gln Phe

20

25

30

cca gaa gaa tat cat cca act gtc ttc gag aat tat gta acc

gac tgt 144

Pro Glu Glu Tyr His Pro Thr Val Phe Glu Asn Tyr Val Thr

Asp Cys

35

40

45

cga gtg gac ggt atc aaa gtt caa cta aca cta tgg gac aca

gct ggc 192

Arg Val Asp Gly Ile Lys Val Gln Leu Thr Leu Trp Asp Thr

Ala Gly

50

55

60

caa gag gaa tat gaa aga cta agg ccc ttc tcg tat tca aag

gcc gat 240

Gln Glu Glu Tyr Glu Arg Leu Arg Pro Phe Ser Tyr Ser Lys

Ala Asp

65

70

75

80

ata att ctc att ggt ttt gca atc gac gac ccg gaa tca ttg

gtg aat 288

Ile Ile Leu Ile Gly Phe Ala Ile Asp Asp Pro Glu Ser Leu

0070110

```

Val Asn
      85                      90
95
gca aga aat aaa tgg tca gaa gaa gtt ctc aga tat tgc cct
gaa gct      336
Ala Arg Asn Lys Trp Ser Glu Glu Val Leu Arg Tyr Cys Pro
Glu Ala
      100                      105                      110

cca gta gta cta gtt ggg ttg aag aaa gac tta aga tca ccg
gat aat      384
Pro Val Val Leu Val Gly Leu Lys Lys Asp Leu Arg Ser Pro
Asp Asn
      115                      120                      125
gaa cat cag atg gta aca cgg gag caa gcg gag caa gtt gcc
agg gcc      432
Glu His Gln Met Val Thr Arg Glu Gln Ala Glu Gln Val Ala
Arg Ala
      130                      135                      140
att ggt gct aaa aaa tat atg gaa tgc agt gca ttg aca gga
gaa aac      480
Ile Gly Ala Lys Lys Tyr Met Glu Cys Ser Ala Leu Thr Gly
Glu Asn
      145                      150                      155
      160
gtt gat gat gtt ttc gaa gta gcc aca agg aca agt ctc ttg
gta aat      528
Val Asp Asp Val Phe Glu Val Ala Thr Arg Thr Ser Leu Leu
Val Asn
      165                      170

175
aaa caa cca ggt cac ggg tgc tgc gta ata tgt tga
      564
Lys Gln Pro Gly His Gly Cys Cys Val Ile Cys
      180                      185

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<210> 205

<211> 187

<212> PRT

<213> Kluyveromyces lactis NRRL Y-1140

<400> 205

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Met Ser Thr Asn Pro Val Lys Arg Lys Leu Val Ile Ile Gly
Asp Gly
1      5      10
15
Ala Cys Gly Lys Thr Ser Leu Leu Tyr Val Phe Thr Leu Gly
Gln Phe

```

0070110

20

25

30

Pro Glu Glu Tyr His Pro Thr Val Phe Glu Asn Tyr Val Thr
Asp Cys

35

40

45

Arg Val Asp Gly Ile Lys Val Gln Leu Thr Leu Trp Asp Thr
Ala Gly
50

55

60

Gln Glu Glu Tyr Glu Arg Leu Arg Pro Phe Ser Tyr Ser Lys
Ala Asp
65

70

75

80

Ile Ile Leu Ile Gly Phe Ala Ile Asp Asp Pro Glu Ser Leu
Val Asn

85

90

95
Ala Arg Asn Lys Trp Ser Glu Glu Val Leu Arg Tyr Cys Pro
Glu Ala

100

105

110

Pro Val Val Leu Val Gly Leu Lys Lys Asp Leu Arg Ser Pro
Asp Asn

115

120

125

Glu His Gln Met Val Thr Arg Glu Gln Ala Glu Gln Val Ala
Arg Ala
130

135

140

Ile Gly Ala Lys Lys Tyr Met Glu Cys Ser Ala Leu Thr Gly
Glu Asn
145

150

155

160

Val Asp Asp Val Phe Glu Val Ala Thr Arg Thr Ser Leu Leu
Val Asn

165

170

175

Lys Gln Pro Gly His Gly Cys Cys Val Ile Cys
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185

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<211> 672

<212> DNA

<213> Kluyveromyces lactis NRRL Y-1140

<220>

<221> CDS

<222> (1)..(672)

<400> 206

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

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0070110

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att acc      432
Asp Leu Arg Asn Leu Glu Glu Phe Gly Asn Glu Ser Ala Ala
Ile Thr
130
cca ggc tct att cag aac agg aat agt aac gct aag gat aat
gga ttg      480
Pro Gly Ser Ile Gln Asn Arg Asn Ser Asn Ala Lys Asp Asn
Gly Leu
145      150      155
160
att agt tac gaa gaa ggt ttg gat atg gcg aag aaa atc ggt
gca ttg      528
Ile Ser Tyr Glu Glu Gly Leu Asp Met Ala Lys Lys Ile Gly
Ala Leu
      165      170
175
cgc tac ttg gaa tgc agc gcc aaa atg aat aga ggt gtc aac
gag gca      576
Arg Tyr Leu Glu Cys Ser Ala Lys Met Asn Arg Gly Val Asn
Glu Ala
      180      185      190

ttc acc gaa gct gct cgt tgt gca ttg act gca act cca aag
ggg gcg      624
Phe Thr Glu Ala Ala Arg Cys Ala Leu Thr Ala Thr Pro Lys
Gly Ala
      195      200      205
aat gat acc atc cct cag gat aaa gga agc agt tgt att att
atg      669
Asn Asp Thr Ile Pro Gln Asp Lys Gly Ser Ser Cys Ile Ile
Met
210      215      220
tga
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<210> 207

<211> 223

<212> PRT

<213> Kluyveromyces lactis NRRL Y-1140

<400> 207

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Met Pro Leu Cys Gly Gly Ser Ser Ser Lys Gln Pro Ile Glu
Arg Lys

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1 5 10

15

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Ile Val Ile Leu Gly Asp Gly Ala Cys Gly Lys Thr Ser Leu

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0070110

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

210

215

220

<210> 208

<211> 597

<212> DNA

<213> Debaryomyces hansenii CBS767

<220>

<221> CDS

<222> (1)..(597)

<223> transl_table=12

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ggt ggt 48

Met Val Pro Pro Pro Ala Glu Ile Arg Arg Lys Leu Val Ile

Val Gly

1

5

10

15

gat ggt gct tgt ggt aaa act tgt ttg ttg att gtg ttt tcc

aaa ggt 96

Asp Gly Ala Cys Gly Lys Thr Cys Leu Leu Ile Val Phe Ser

Lys Gly

20

25

30

aca ttc cca gaa gtt tac gtc cca act gtt ttc gaa aac tac

gtg gct 144

Thr Phe Pro Glu Val Tyr Val Pro Thr Val Phe Glu Asn Tyr

Val Ala

35

40

45

gac gtc gaa gtt gat ggc aga aag gtt gaa ttg gcc ttg tgg

gat act 192

Asp Val Glu Val Asp Gly Arg Lys Val Glu Leu Ala Leu Trp

Asp Thr

50

55

60

gcc ggt caa gaa gat tac gat aga ttg aga cct ttg tcc tac

cca gac 240

Ala Gly Gln Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr

Pro Asp

65

70

75

80

tcc aat gtt att tta ata tgt ttc tcc atc gac tcg cct gac

tcg ttg 288

Ser Asn Val Ile Leu Ile Cys Phe Ser Ile Asp Ser Pro Asp

Ser Leu

85

90

95

0070110

gat aac gta tta gaa aag tgg atc tcg gaa gtg tta cat ttc
 tgt caa 336
 Asp Asn Val Leu Glu Lys Trp Ile Ser Glu Val Leu His Phe
 Cys Gln
 100 105 110

ggt gtt cca atc atc ttg gtt ggt tgt aag tct gat tta aga
 aac gac 384
 Gly Val Pro Ile Ile Leu Val Gly Cys Lys Ser Asp Leu Arg
 Asn Asp
 115 120 125

caa aac act atc cat caa tta agt caa caa caa caa caa cct
 gtc tct 432
 Gln Asn Thr Ile His Gln Leu Ser Gln Gln Gln Gln Gln Pro
 Val Ser
 130 135 140

acc tcc gaa ggt caa gcg gtc gcc caa aag att ggt act agt
 tac tat 480
 Thr Ser Glu Gly Gln Ala Val Ala Gln Lys Ile Gly Thr Ser
 Tyr Tyr
 145 150 155

160
 ttg gaa tgt tcc gcc aga act gga gaa ggt gtc aga gaa gtg
 ttc gaa 528
 Leu Glu Cys Ser Ala Arg Thr Gly Glu Gly Val Arg Glu Val
 Phe Glu
 165 170

175
 gct gct acc aga gcc tcg ttg aag act aag gaa aag aag gaa
 aag aag 576
 Ala Ala Thr Arg Ala Ser Leu Lys Thr Lys Glu Lys Lys Glu
 Lys Lys
 180 185 190

aag aag tgt gtt gtg tta taa
 597
 Lys Lys Cys Val Val Leu
 195

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<212> PRT

<213> Debaryomyces hansenii CBS767

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Met Val Pro Pro Pro Ala Glu Ile Arg Arg Lys Leu Val Ile
 Val Gly

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

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<222> (1)..(564)
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gat gga 48
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Asp Gly
1 5 10
15
gca tgt ggg aaa act tcg ttg tta ttt gta ttc aca tta gga
gaa ttt 96
Ala Cys Gly Lys Thr Ser Leu Leu Phe Val Phe Thr Leu Gly
Glu Phe
20 25 30
cct act gaa tac cat ccc act gta ttt gag aat tat gtc act
gat tgc 144
Pro Thr Glu Tyr His Pro Thr Val Phe Glu Asn Tyr Val Thr
Asp Cys
35 40 45
aga gtc gat gga aaa gca gtt caa ttg gcc tta tgg gat acg
gct gga 192
Arg Val Asp Gly Lys Ala Val Gln Leu Ala Leu Trp Asp Thr
Ala Gly
50 55 60
caa gag gaa tac gaa aga ttg cgt cca ttg agc tat gcc aat
tcg cat 240
Gln Glu Glu Tyr Glu Arg Leu Arg Pro Leu Ser Tyr Ala Asn
Ser His
65 70 75
80
gta atc ttg atc ggc ttt gct ata gat gta cct gat tca ttg
gat aat 288
Val Ile Leu Ile Gly Phe Ala Ile Asp Val Pro Asp Ser Leu
Asp Asn
85 90
95
gct cga aca aaa tgg gtc gag gaa gtc acc aaa tat tgt ccc
aat acg 336
Ala Arg Thr Lys Trp Val Glu Glu Val Thr Lys Tyr Cys Pro
Asn Thr

0070110

100

105

110

cca tat tta tta att ggc tta aag aag gat ctt aga gtg gaa
 tct tcc 384
 Pro Tyr Leu Leu Ile Gly Leu Lys Lys Asp Leu Arg Val Glu
 Ser Ser

115 120 125
 aat aga aga aag tat gtc caa ttt cat cag ggc gag ata gca
 gcc aaa 432
 Asn Arg Arg Lys Tyr Val Gln Phe His Gln Gly Glu Ile Ala
 Ala Lys

130 135 140
 gag atg cat gct aaa aaa tac tta gag agt tca gca tta tac
 ggc gag 480
 Glu Met His Ala Lys Lys Tyr Leu Glu Ser Ser Ala Leu Tyr
 Gly Glu

145 150 155
 160
 ggt gta gac gat ata ttc gaa tat gcg aca aga aca agc tta
 ttg gtt 528
 Gly Val Asp Asp Ile Phe Glu Tyr Ala Thr Arg Thr Ser Leu
 Leu Val

165 170
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 caa aag gct aat caa aca tgc tgt act att tta taa
 564
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 180 185

<210> 211
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 <212> PRT
 <213> Debaryomyces hansenii CBS767

<400> 211
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 Glu Phe
 20 25 30

Pro Thr Glu Tyr His Pro Thr Val Phe Glu Asn Tyr Val Thr
 Asp Cys
 35 40 45

Arg Val Asp Gly Lys Ala Val Gln Leu Ala Leu Trp Asp Thr
 Seite 334

0070110

Ala	Gly													
	50						55					60		
Gln	Glu	Glu	Tyr	Glu	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Ala	Asn	
Ser	His													
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	80													
Val	Ile	Leu	Ile	Gly	Phe	Ala	Ile	Asp	Val	Pro	Asp	Ser	Leu	
Asp	Asn													
				85						90				
95														
Ala	Arg	Thr	Lys	Trp	Val	Glu	Glu	Val	Thr	Lys	Tyr	Cys	Pro	
Asn	Thr													
			100					105					110	
Pro	Tyr	Leu	Leu	Ile	Gly	Leu	Lys	Lys	Asp	Leu	Arg	Val	Glu	
Ser	Ser													
		115					120					125		
Asn	Arg	Arg	Lys	Tyr	Val	Gln	Phe	His	Gln	Gly	Glu	Ile	Ala	
Ala	Lys													
	130					135					140			
Glu	Met	His	Ala	Lys	Lys	Tyr	Leu	Glu	Ser	Ser	Ala	Leu	Tyr	
Gly	Glu													
145					150					155				
	160													
Gly	Val	Asp	Asp	Ile	Phe	Glu	Tyr	Ala	Thr	Arg	Thr	Ser	Leu	
Leu	Val													
				165					170					
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Gln	Lys	Ala	Asn	Gln	Thr	Cys	Cys	Thr	Ile	Leu				
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<211> 615

<212> DNA

<213> Yarrowia lipolytica CLIB122

<220>

<221> CDS

<222> (1)..(615)

<400> 212

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Gly	Asp													

0070110

1				5						10			
15													
gga	gcc	tgc	ggc	aag	acc	tgt	ctg	ctg	att	gtc	ttc	gcg	aag
ggc	acc		96										
Gly	Ala	Cys	Gly	Lys	Thr	Cys	Leu	Leu	Ile	Val	Phe	Ala	Lys
Gly	Thr												
			20					25					30
ttc	ccg	gag	gtg	tac	gtg	ccc	acc	gtg	ttt	gag	aac	tac	gtg
gcc	gac		144										
Phe	Pro	Glu	Val	Tyr	Val	Pro	Thr	Val	Phe	Glu	Asn	Tyr	Val
Ala	Asp												
		35				40						45	
gtg	gag	att	gac	ggc	cga	cga	gtg	gag	ctg	gcc	ctg	tgg	gat
acc	gcc		192										
Val	Glu	Ile	Asp	Gly	Arg	Arg	Val	Glu	Leu	Ala	Leu	Trp	Asp
Thr	Ala												
		50				55					60		
ggc	cag	gag	gat	tac	gac	cga	ctg	cga	ccc	ctg	tcc	tac	ccc
gac	gcc		240										
Gly	Gln	Glu	Asp	Tyr	Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Pro
Asp	Ala												
65					70					75			
80													
aac	gtc	atc	atc	atc	tgc	ttc	gcc	atc	gac	agc	ccc	gac	tcg
ctc	gac		288										
Asn	Val	Ile	Ile	Ile	Cys	Phe	Ala	Ile	Asp	Ser	Pro	Asp	Ser
Leu	Asp												
			85							90			
95													
aac	gtg	cag	gag	aag	tgg	atc	tcc	gag	gtg	ctg	cac	ttt	tgc
cag	ggc		336										
Asn	Val	Gln	Glu	Lys	Trp	Ile	Ser	Glu	Val	Leu	His	Phe	Cys
Gln	Gly												
			100							105			110
gtg	cct	att	ctg	ctg	gtc	ggc	tgc	aag	gtc	gac	ctg	cga	aac
gac	ccc		384										
Val	Pro	Ile	Leu	Leu	Val	Gly	Cys	Lys	Val	Asp	Leu	Arg	Asn
Asp	Pro												
		115				120						125	
aag	acc	atc	gag	gag	ctg	aga	aga	acg	tcc	cag	cga	ccc	gtc
acg	acc		432										
Lys	Thr	Ile	Glu	Glu	Leu	Arg	Arg	Thr	Ser	Gln	Arg	Pro	Val
Thr	Thr												
		130				135						140	
gag	gag	gga	aat	gcc	gtg	gcc	cag	aag	att	ggc	gcc	ggc	aag
tac	ctg		480										
Glu	Glu	Gly	Asn	Ala	Val	Ala	Gln	Lys	Ile	Gly	Ala	Gly	Lys

0070110

Tyr Leu
 145 150 155
 160
 gag tgc tct gcc cga acc cac gac gga gtg aga gag gtc ttc
 gag cat 528
 Glu Cys Ser Ala Arg Thr His Asp Gly Val Arg Glu Val Phe
 Glu His
 165 170
 175
 gcc acc cga gct gcc ctg act gcc cac ggc cag aag ggc tcc
 aag agc 576
 Ala Thr Arg Ala Ala Leu Thr Ala His Gly Gln Lys Gly Ser
 Lys Ser
 180 185 190
 tcc agc aga gag ggc aag aaa aag tgt ttg att ttg taa
 615
 Ser Ser Arg Glu Gly Lys Lys Lys Cys Leu Ile Leu
 195 200

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 <212> PRT
 <213> Yarrowia lipolytica CLIB122

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 Gly Asp
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 Gly Thr
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 Phe Pro Glu Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val
 Ala Asp
 35 40 45
 Val Glu Ile Asp Gly Arg Arg Val Glu Leu Ala Leu Trp Asp
 Thr Ala
 50 55 60
 Gly Gln Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro
 Asp Ala
 65 70 75
 80
 Asn Val Ile Ile Ile Cys Phe Ala Ile Asp Ser Pro Asp Ser
 Leu Asp

0070110

85

90

95
Asn Val Gln Glu Lys Trp Ile Ser Glu Val Leu His Phe Cys
Gln Gly
100 105 110

Val Pro Ile Leu Leu Val Gly Cys Lys Val Asp Leu Arg Asn
Asp Pro
115 120 125

Lys Thr Ile Glu Glu Leu Arg Arg Thr Ser Gln Arg Pro Val
Thr Thr
130 135 140

Glu Glu Gly Asn Ala Val Ala Gln Lys Ile Gly Ala Gly Lys
Tyr Leu
145 150 155
160

Glu Cys Ser Ala Arg Thr His Asp Gly Val Arg Glu Val Phe
Glu His
165 170

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Ala Thr Arg Ala Ala Leu Thr Ala His Gly Gln Lys Gly Ser
Lys Ser
180 185 190

Ser Ser Arg Glu Gly Lys Lys Lys Cys Leu Ile Leu
195 200

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<211> 612

<212> DNA

<213> Yarrowia lipolytica CLIB122

<220>

<221> CDS

<222> (1)..(612)

<400> 214

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gtg gga 48
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Val Gly
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15
gac gga gcc tgc gga aaa acc tgt ctg ctc att gtc ttt gcc
aag ggc 96
Asp Gly Ala Cys Gly Lys Thr Cys Leu Leu Ile Val Phe Ala

0070110

Lys	Gly													
			20				25						30	
acc	ttc	ccc	gag	gtc	tac	gtg	ccc	act	gtg	ttc	gac	aac	tac	
gtg	acc		144											
Thr	Phe	Pro	Glu	Val	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	Tyr	
Val	Thr													
		35					40					45		
gac	gtg	gag	att	gac	ggc	cga	cga	gtg	gag	ctg	gcc	ctg	tgg	
gat	acc		192											
Asp	Val	Glu	Ile	Asp	Gly	Arg	Arg	Val	Glu	Leu	Ala	Leu	Trp	
Asp	Thr													
	50					55					60			
gcc	ggc	cag	gaa	gac	tac	gac	cga	ctg	cga	ccc	ctg	tcg	tac	
ccc	gat		240											
Ala	Gly	Gln	Glu	Asp	Tyr	Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	
Pro	Asp													
65					70					75				
80														
tcc	aac	gtg	atc	atc	atc	tgc	ttt	gcc	atc	gac	tcg	ccc	gac	
tcg	ctg		288											
Ser	Asn	Val	Ile	Ile	Ile	Cys	Phe	Ala	Ile	Asp	Ser	Pro	Asp	
Ser	Leu													
		85								90				
95														
gac	aac	gtg	cag	gag	aag	tgg	att	tcc	gag	gtg	ctg	cac	ttt	
tgc	cag		336											
Asp	Asn	Val	Gln	Glu	Lys	Trp	Ile	Ser	Glu	Val	Leu	His	Phe	
Cys	Gln													
		100								105			110	
ggc	gtg	ccc	att	ctg	ctg	gtc	ggt	tgc	aag	gtg	gac	ctg	cga	
aac	gac		384											
Gly	Val	Pro	Ile	Leu	Leu	Val	Gly	Cys	Lys	Val	Asp	Leu	Arg	
Asn	Asp													
		115					120					125		
ccc	aag	acc	atc	gag	gag	ctc	aga	aga	acg	tcc	cag	cga	ccg	
gtc	acc		432											
Pro	Lys	Thr	Ile	Glu	Glu	Leu	Arg	Arg	Thr	Ser	Gln	Arg	Pro	
Val	Thr													
	130					135					140			
acc	gag	gag	gga	aac	gcc	gtg	gcc	cag	aag	att	ggc	gca	ctc	
aag	tac		480											
Thr	Glu	Glu	Gly	Asn	Ala	Val	Ala	Gln	Lys	Ile	Gly	Ala	Leu	
Lys	Tyr													
145					150					155				
160														
ctc	gag	tgc	tct	gcc	cga	acc	cac	gac	gga	gtg	cgg	gag	atc	
ttt	gag		528											

0070110

Leu Glu Cys Ser Ala Arg Thr His Asp Gly Val Arg Glu Ile
Phe Glu

165

170

175

cac gct acc cga gcc gct ctc att ggc ccc aag gga cga gag
ccc act

576

His Ala Thr Arg Ala Ala Leu Ile Gly Pro Lys Gly Arg Glu
Pro Thr

180

185

190

tca ggc aag aag aag aag aag tgc gtg atc ctc taa

612

Ser Gly Lys Lys Lys Lys Lys Cys Val Ile Leu

195

200

<210> 215

<211> 203

<212> PRT

<213> Yarrowia lipolytica CLIB122

<400> 215

Met Pro Ala Gln Pro Ala Asp Leu Arg Arg Lys Leu Val Ile
Val Gly

1

5

10

15

Asp Gly Ala Cys Gly Lys Thr Cys Leu Leu Ile Val Phe Ala
Lys Gly

20

25

30

Thr Phe Pro Glu Val Tyr Val Pro Thr Val Phe Asp Asn Tyr
Val Thr

35

40

45

Asp Val Glu Ile Asp Gly Arg Arg Val Glu Leu Ala Leu Trp
Asp Thr

50

55

60

Ala Gly Gln Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr
Pro Asp

65

70

75

80

Ser Asn Val Ile Ile Ile Cys Phe Ala Ile Asp Ser Pro Asp
Ser Leu

85

90

95

Asp Asn Val Gln Glu Lys Trp Ile Ser Glu Val Leu His Phe
Cys Gln

100

105

110

0070110

Gly	Val	Pro	Ile	Leu	Leu	Val	Gly	Cys	Lys	Val	Asp	Leu	Arg
Asn	Asp												
		115					120					125	

Pro	Lys	Thr	Ile	Glu	Glu	Leu	Arg	Arg	Thr	Ser	Gln	Arg	Pro
Val	Thr												
	130					135					140		

Thr	Glu	Glu	Gly	Asn	Ala	Val	Ala	Gln	Lys	Ile	Gly	Ala	Leu
Lys	Tyr												
145					150					155			
	160												

Leu	Glu	Cys	Ser	Ala	Arg	Thr	His	Asp	Gly	Val	Arg	Glu	Ile
Phe	Glu												
				165					170				

175													
His	Ala	Thr	Arg	Ala	Ala	Leu	Ile	Gly	Pro	Lys	Gly	Arg	Glu
Pro	Thr												
			180					185				190	

Ser	Gly	Lys	Lys	Lys	Lys	Lys	Cys	Val	Ile	Leu			
		195					200						

<210> 216
<211> 579
<212> DNA
<213> Yarrowia lipolytica CLIB122

<220>
<221> CDS
<222> (1)..(579)

<400> 216
atg cag agt ata aaa tgt gtc gtc act ggc gac ggt gcc gtc
ggt aaa 48
Met Gln Ser Ile Lys Cys Val Val Thr Gly Asp Gly Ala Val
Gly Lys 5 10
15
act tgc atg cta atc tca tac acc aca aac gcc ttc cca gga
gag tac 96
Thr Cys Met Leu Ile Ser Tyr Thr Thr Asn Ala Phe Pro Gly
Glu Tyr 20 25 30
atc ccc acc gtc ttc gac aac tac tct gcc aat gtc atg gtg
gat aac 144
Ile Pro Thr Val Phe Asp Asn Tyr Ser Ala Asn Val Met Val
Seite 341

0070110

Asp Asn

		35				40				45			
aaa	ccg	ata	aac	ctc	gga	ctt	tgg	gat	acc	gcg	ggc	cag	gaa
gat	tac		192										
Lys	Pro	Ile	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala	Gly	Gln	Glu
Asp	Tyr												
	50					55					60		
gac	cgg	ctg	cgg	cca	ctg	tca	tac	ccc	cag	acc	ggc	gtg	ttt
ctt	atc		240										
Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Pro	Gln	Thr	Gly	Val	Phe
Leu	Ile												
65					70					75			
80													
tgc	ttc	tcg	ctc	gtg	tcg	ccc	ccg	tcg	ttc	gag	aac	gtc	aaa
gct	aag		288										
Cys	Phe	Ser	Leu	Val	Ser	Pro	Pro	Ser	Phe	Glu	Asn	Val	Lys
Ala	Lys												
			85						90				
95													
tgg	cac	ccc	gaa	atc	tcg	cac	cac	gcc	ccc	aat	acg	ccc	atc
atc	ctc		336										
Trp	His	Pro	Glu	Ile	Ser	His	His	Ala	Pro	Asn	Thr	Pro	Ile
Ile	Leu												
		100						105				110	
gtc	ggc	acc	aag	ctc	gac	ctg	cgt	aac	gac	agt	gag	act	ctg
gcg	cgg		384										
Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asn	Asp	Ser	Glu	Thr	Leu
Ala	Arg												
		115					120				125		
ctc	gct	gaa	aag	cga	caa	gcc	ccc	atc	aca	tat	gca	gaa	ggc
gcc	aag		432										
Leu	Ala	Glu	Lys	Arg	Gln	Ala	Pro	Ile	Thr	Tyr	Ala	Glu	Gly
Ala	Lys												
	130					135					140		
tgt	gct	cgg	gac	att	ggc	gcc	gtc	aaa	tac	ttt	gag	tgc	tcg
gca	ttg		480										
Cys	Ala	Arg	Asp	Ile	Gly	Ala	Val	Lys	Tyr	Phe	Glu	Cys	Ser
Ala	Leu												
145					150					155			
160													
acc	caa	aag	gga	ctc	aaa	aca	gtg	ttt	gac	gag	gcc	att	cac
gcg	gtg		528										
Thr	Gln	Lys	Gly	Leu	Lys	Thr	Val	Phe	Asp	Glu	Ala	Ile	His
Ala	Val												
			165						170				
175													

0070110

ctg tcg cct ccc cag ccc aag aaa aag aag aag aac tgt gtg
att ctc 576
Leu Ser Pro Pro Gln Pro Lys Lys Lys Lys Lys Asn Cys Val
Ile Leu 180 185 190

taa
579

<210> 217
<211> 192
<212> PRT
<213> Yarrowia lipolytica CLIB122

<400> 217
Met Gln Ser Ile Lys Cys Val Val Thr Gly Asp Gly Ala Val
Gly Lys
1 5 10
15

Thr Cys Met Leu Ile Ser Tyr Thr Thr Asn Ala Phe Pro Gly
Glu Tyr 20 25 30

Ile Pro Thr Val Phe Asp Asn Tyr Ser Ala Asn Val Met Val
Asp Asn 35 40 45

Lys Pro Ile Asn Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu
Asp Tyr 50 55 60

Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Gly Val Phe
Leu Ile 65 70 75

80
Cys Phe Ser Leu Val Ser Pro Pro Ser Phe Glu Asn Val Lys
Ala Lys 85 90

95
Trp His Pro Glu Ile Ser His His Ala Pro Asn Thr Pro Ile
Ile Leu 100 105 110

Val Gly Thr Lys Leu Asp Leu Arg Asn Asp Ser Glu Thr Leu
Ala Arg 115 120 125

0070110

Leu Ala Glu Lys Arg Gln Ala Pro Ile Thr Tyr Ala Glu Gly
Ala Lys
130 135 140

Cys Ala Arg Asp Ile Gly Ala Val Lys Tyr Phe Glu Cys Ser
Ala Leu
145 150 155
160

Thr Gln Lys Gly Leu Lys Thr Val Phe Asp Glu Ala Ile His
Ala Val
165 170

175
Leu Ser Pro Pro Gln Pro Lys Lys Lys Lys Lys Asn Cys Val
Ile Leu
180 185 190

<210> 218
<211> 615
<212> DNA
<213> Yarrowia lipolytica CLIB122

<220>
<221> CDS
<222> (1)..(615)

<400> 218
atg gcc atc tgc ggc gga gcc ccc aag gct att tca aga aaa
att gtc 48
Met Ala Ile Cys Gly Gly Ala Pro Lys Ala Ile Ser Arg Lys
Ile Val
1 5 10
15
att cta ggt gat ggt gct tcc ggt aag acc tct ctg ctg aac
gtt ttc 96
Ile Leu Gly Asp Gly Ala Ser Gly Lys Thr Ser Leu Leu Asn
Val Phe
20 25 30
act cgg gga tac ttc ccc cac gtg tac gag ccc acc gtg ttt
gaa aac 144
Thr Arg Gly Tyr Phe Pro His Val Tyr Glu Pro Thr Val Phe
Glu Asn
35 40 45
tac gtg cat gac att ttc atc gac ggc cag ccc gta cag ctg
tct ctg 192
Tyr Val His Asp Ile Phe Ile Asp Gly Gln Pro Val Gln Leu
Ser Leu

0070110

50	55	60											
tgg gac act gct ggt cag gag gag ttt gac cga cta cga tct													
ctg tcg	240												
Trp Asp Thr Ala Gly Gln Glu Glu Phe Asp Arg Leu Arg Ser													
Leu Ser													
65	70	75											
80													
tac tca gat aca cac acc atc atg ctg tgt ttt tcc gtc gac													
tcg cgc	288												
Tyr Ser Asp Thr His Thr Ile Met Leu Cys Phe Ser Val Asp													
Ser Arg													
	85	90											
95													
gac tcg ctg gaa aac gtg cag acc aag tgg gtg ggt gag att													
gcc gac	336												
Asp Ser Leu Glu Asn Val Gln Thr Lys Trp Val Gly Glu Ile													
Ala Asp													
	100	105											110
cac tgt gag ggc gtc aag ttg gtg ctg gtg gct ctc aag tgc													
gat ctg	384												
His Cys Glu Gly Val Lys Leu Val Leu Val Ala Leu Lys Cys													
Asp Leu													
	115	120											125
cga aac aat gag gag ggc ggc gag ggc gcc aag aag acg tac													
gtc acc	432												
Arg Asn Asn Glu Glu Gly Gly Glu Gly Ala Lys Lys Thr Tyr													
Val Thr													
	130	135											140
tac gag cag ggc ctg gag gtg gcc aag aag att ggc gct ctt													
cga tac	480												
Tyr Glu Gln Gly Leu Glu Val Ala Lys Lys Ile Gly Ala Leu													
Arg Tyr													
	145	150											155
160													
ctc gag tgc tcg gcc aag atg aac cga gga gtc aac gag gct													
ttt acc	528												
Leu Glu Cys Ser Ala Lys Met Asn Arg Gly Val Asn Glu Ala													
Phe Thr													
	165	170											
175													
gag gct gct cga tgt gct ctg gga gct aag ccc aag ggc gct													
gca gcc	576												
Glu Ala Ala Arg Cys Ala Leu Gly Ala Lys Pro Lys Gly Ala													
Ala Ala													
	180	185											190
gat gac aag gag gag tct tcc aag tgc gtc atc atg tag													

0070110

Asp Asp Lys⁶¹⁵ Glu Glu Ser Ser Lys Cys Val Ile Met
195 200

<210> 219

<211> 204

<212> PRT

<213> Yarrowia lipolytica CLIB122

<400> 219

Met Ala Ile Cys Gly Gly Ala Pro Lys Ala Ile Ser Arg Lys
Ile Val

1 5 10

15

Ile Leu Gly Asp Gly Ala Ser Gly Lys Thr Ser Leu Leu Asn
Val Phe

20 25 30

Thr Arg Gly Tyr Phe Pro His Val Tyr Glu Pro Thr Val Phe
Glu Asn

35 40 45

Tyr Val His Asp Ile Phe Ile Asp Gly Gln Pro Val Gln Leu
Ser Leu
50 55 60

Trp Asp Thr Ala Gly Gln Glu Glu Phe Asp Arg Leu Arg Ser
Leu Ser
65 70 75

80

Tyr Ser Asp Thr His Thr Ile Met Leu Cys Phe Ser Val Asp
Ser Arg

85 90

95

Asp Ser Leu Glu Asn Val Gln Thr Lys Trp Val Gly Glu Ile
Ala Asp

100 105 110

His Cys Glu Gly Val Lys Leu Val Leu Val Ala Leu Lys Cys
Asp Leu

115 120 125

Arg Asn Asn Glu Glu Gly Gly Glu Gly Ala Lys Lys Thr Tyr
Val Thr

130 135 140

Tyr Glu Gln Gly Leu Glu Val Ala Lys Lys Ile Gly Ala Leu
Arg Tyr

0070110

145 150 155
 160
 Leu Glu Cys Ser Ala Lys Met Asn Arg Gly Val Asn Glu Ala
 Phe Thr
 165 170
 175
 Glu Ala Ala Arg Cys Ala Leu Gly Ala Lys Pro Lys Gly Ala
 Ala Ala
 180 185 190
 Asp Asp Lys Glu Glu Ser Ser Lys Cys Val Ile Met
 195 200

<210> 220
 <211> 573
 <212> DNA
 <213> Anopheles gambiae str. PEST

<220>
 <221> CDS
 <222> (1)..(573)

<400> 220
 atg tca tcc gga aga cct atc aaa tgt gtg gtg gtc ggc gac
 ggc acg 48
 Met Ser Ser Gly Arg Pro Ile Lys Cys Val Val Val Gly Asp
 Gly Thr
 1 5 10
 15
 gtg ggg aag acg tgc atg ttg atc agc tac acg acc gac agc
 ttt ccc 96
 Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Thr Asp Ser
 Phe Pro
 20 25 30
 ggc gaa tac gta ccc acg gtc ttc gac aac tac tcc gcc ccg
 atg gtg 144
 Gly Glu Tyr Val Pro Thr Val Phe Asp Asn Tyr Ser Ala Pro
 Met Val
 35 40 45
 gtg gac ggt gtg caa gtg tcg ctc ggg ctg tgg gat acg gcc
 ggg cag 192
 Val Asp Gly Val Gln Val Ser Leu Gly Leu Trp Asp Thr Ala
 Gly Gln
 50 55 60
 gaa gac tac gat cgg cta agg ccc ctg tcc tac cca cag acg
 gac gtg 240
 Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr
 Asp Val

0070110

65					70							75	
80													
ttc	ctc	ata	tgc	tac	agt	gtg	gcc	agc	ccg	tcg	tcg	ttc	gaa
aac	ggt			288									
Phe	Leu	Ile	Cys	Tyr	Ser	Val	Ala	Ser	Pro	Ser	Ser	Phe	Glu
Asn	Val												
				85						90			
95													
acc	tcc	aaa	tgg	tat	ccc	gag	atc	aag	cac	cac	tgc	ccg	gat
gcg	ccc		336										
Thr	Ser	Lys	Trp	Tyr	Pro	Glu	Ile	Lys	His	His	Cys	Pro	Asp
Ala	Pro												
				100				105					110
atc	att	tta	gtc	gga	acc	aaa	atc	gat	ctg	cgc	gag	gat	cgg
gaa	acg		384										
Ile	Ile	Leu	Val	Gly	Thr	Lys	Ile	Asp	Leu	Arg	Glu	Asp	Arg
Glu	Thr												
		115					120					125	
ata	agc	ttg	ctg	gcg	gac	cag	ggc	ctt	tcc	gcg	ctg	aag	cgc
gaa	cag		432										
Ile	Ser	Leu	Leu	Ala	Asp	Gln	Gly	Leu	Ser	Ala	Leu	Lys	Arg
Glu	Gln												
		130				135					140		
ggc	caa	aag	cta	gcg	aac	aag	ata	cgg	gcg	gta	aag	tat	atg
gaa	tgt		480										
Gly	Gln	Lys	Leu	Ala	Asn	Lys	Ile	Arg	Ala	Val	Lys	Tyr	Met
Glu	Cys												
145					150					155			
160													
tcg	gca	cta	acc	cag	cgg	ggc	cta	aag	cag	gtg	ttt	gac	gaa
gcg	ctt		528										
Ser	Ala	Leu	Thr	Gln	Arg	Gly	Leu	Lys	Gln	Val	Phe	Asp	Glu
Ala	Leu												
				165						170			
175													
tgc	gcc	acg	gaa	gag	aaa	gag	cga	atg	ccg	gta	gaa	gag	gag
tag			573										
Cys	Ala	Thr	Glu	Glu	Lys	Glu	Arg	Met	Pro	Val	Glu	Glu	Glu
				180				185					190

<210> 221
 <211> 190
 <212> PRT
 <213> Anopheles gambiae str. PEST

0070110

<400> 221

Met	Ser	Ser	Gly	Arg	Pro	Ile	Lys	Cys	Val	Val	Val	Gly	Asp
Gly	Thr												
1				5					10				
15													
Val	Gly	Lys	Thr	Cys	Met	Leu	Ile	Ser	Tyr	Thr	Thr	Asp	Ser
Phe	Pro												
			20					25					30
Gly	Glu	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	Tyr	Ser	Ala	Pro
Met	Val												
		35					40					45	
Val	Asp	Gly	Val	Gln	Val	Ser	Leu	Gly	Leu	Trp	Asp	Thr	Ala
Gly	Gln												
	50					55					60		
Glu	Asp	Tyr	Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Pro	Gln	Thr
Asp	Val												
65					70					75			
80													
Phe	Leu	Ile	Cys	Tyr	Ser	Val	Ala	Ser	Pro	Ser	Ser	Phe	Glu
Asn	Val												
			85						90				
95													
Thr	Ser	Lys	Trp	Tyr	Pro	Glu	Ile	Lys	His	His	Cys	Pro	Asp
Ala	Pro												
			100					105					110
Ile	Ile	Leu	Val	Gly	Thr	Lys	Ile	Asp	Leu	Arg	Glu	Asp	Arg
Glu	Thr												
		115					120					125	
Ile	Ser	Leu	Leu	Ala	Asp	Gln	Gly	Leu	Ser	Ala	Leu	Lys	Arg
Glu	Gln												
	130					135					140		
Gly	Gln	Lys	Leu	Ala	Asn	Lys	Ile	Arg	Ala	Val	Lys	Tyr	Met
Glu	Cys												
145					150					155			
160													
Ser	Ala	Leu	Thr	Gln	Arg	Gly	Leu	Lys	Gln	Val	Phe	Asp	Glu
Ala	Leu												
			165					170					
175													
Cys	Ala	Thr	Glu	Glu	Lys	Glu	Arg	Met	Pro	Val	Glu	Glu	Glu
			180					185					190

0070110

<210> 222
<211> 579
<212> DNA
<213> *Apis mellifera*

<220>
<221> CDS
<222> (1)..(579)

<400> 222
atg gca gcc att aga aag aaa ttg gtt att gtg ggt gat ggt
gct tgt 48
Met Ala Ala Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly
Ala Cys
1 5 10
15
ggg aaa aca tgc tta ctt ata gtc ttc agc aaa gac caa ttt
cca gaa 96
Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Asp Gln Phe
Pro Glu
20 25 30
gtt tat gta cct aca gtg ttt gaa aat tat gtt gca gat att
gaa gtt 144
Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Ile
Glu Val
35 40 45
gat ggg aaa caa gtg gaa ctg gct ctt tgg gac aca gct gga
caa gaa 192
Asp Gly Lys Gln Val Glu Leu Ala Leu Trp Asp Thr Ala Gly
Gln Glu
50 55 60
gat tat gat agg ttg cgt cca cta tca tat cct gac aca gat
gta atc 240
Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Thr Asp
Val Ile
65 70 75
80
tta atg tgt ttc tct att gat agt cca gat tcc ctg gaa aac
att cct 288
Leu Met Cys Phe Ser Ile Asp Ser Pro Asp Ser Leu Glu Asn
Ile Pro
85 90
95
gag aaa tgg aca cca gag gtg aag cac ttt tgc cca aat gtg
ccc att 336
Glu Lys Trp Thr Pro Glu Val Lys His Phe Cys Pro Asn Val
Pro Ile
100 105 110

0070110

```

atc ctt gtt gga aac aaa aaa gac tta cgc aat gat cct aat
aca atc      384
Ile Leu val Gly Asn Lys Lys Asp Leu Arg Asn Asp Pro Asn
Thr Ile
      115      120      125
aaa gaa ctt agt aag atg aaa caa gaa cca gtt aag cca gaa
gaa gga      432
Lys Glu Leu Ser Lys Met Lys Gln Glu Pro val Lys Pro Glu
Glu Gly
      130      135      140
aga gct atg gct gaa aaa atc aat gcc ttt gct tat ctt gaa
tgt tct      480
Arg Ala Met Ala Glu Lys Ile Asn Ala Phe Ala Tyr Leu Glu
Cys Ser
145      150      155
      160
gct aaa agt aag gaa ggt att agg gaa gta ttt gaa aca gcc
act cgg      528
Ala Lys Ser Lys Glu Gly Ile Arg Glu val Phe Glu Thr Ala
Thr Arg
      165      170
175
gca gca tta caa gta aaa aag aag aag aag gga aga tgt tgg
ctc cta      576
Ala Ala Leu Gln val Lys Lys Lys Lys Lys Gly Arg Cys Trp
Leu Leu
      180      185      190
taa
      579

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<210> 223
 <211> 192
 <212> PRT
 <213> Apis mellifera

<400> 223
 Met Ala Ala Ile Arg Lys Lys Leu val Ile val Gly Asp Gly
 Ala Cys
 1 5 10
 15
 Gly Lys Thr Cys Leu Leu Ile val Phe Ser Lys Asp Gln Phe
 Pro Glu
 20 25 30

0070110

Val	Tyr	Val	Pro	Thr	Val	Phe	Glu	Asn	Tyr	Val	Ala	Asp	Ile
Glu	Val												
		35					40					45	

Asp	Gly	Lys	Gln	Val	Glu	Leu	Ala	Leu	Trp	Asp	Thr	Ala	Gly
Gln	Glu												
	50					55					60		

Asp	Tyr	Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Pro	Asp	Thr	Asp
Val	Ile												
65					70					75			

	80												
Leu	Met	Cys	Phe	Ser	Ile	Asp	Ser	Pro	Asp	Ser	Leu	Glu	Asn
Ile	Pro												
				85					90				

95													
Glu	Lys	Trp	Thr	Pro	Glu	Val	Lys	His	Phe	Cys	Pro	Asn	Val
Pro	Ile												
			100				105					110	

Ile	Leu	Val	Gly	Asn	Lys	Lys	Asp	Leu	Arg	Asn	Asp	Pro	Asn
Thr	Ile												
		115					120				125		

Lys	Glu	Leu	Ser	Lys	Met	Lys	Gln	Glu	Pro	Val	Lys	Pro	Glu
Glu	Gly												
	130					135					140		

Arg	Ala	Met	Ala	Glu	Lys	Ile	Asn	Ala	Phe	Ala	Tyr	Leu	Glu
Cys	Ser												
145					150					155			

	160												
Ala	Lys	Ser	Lys	Glu	Gly	Ile	Arg	Glu	Val	Phe	Glu	Thr	Ala
Thr	Arg												
			165						170				

175													
Ala	Ala	Leu	Gln	Val	Lys	Lys	Lys	Lys	Lys	Gly	Arg	Cys	Trp
Leu	Leu												
			180					185				190	

<210> 224
 <211> 579
 <212> DNA
 <213> Apis mellifera

<220>
 <221> CDS

0070110

<222> (1)..(579)

<400> 224

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atg caa gct att aaa tgt gtt gtc gta gga gac gga gca gta
ggt aaa      48
Met Gln Ala Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys
  1              5              10
15
aca tgt ctc ctt ata agc tat act acc aat gcc ttt cct gga
gaa tat      96
Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Ala Phe Pro Gly
Glu Tyr
      20              25              30
att cca act gta ttt gat aat tat tct gca aat gtc atg gtg
gat ggt      144
Ile Pro Thr Val Phe Asp Asn Tyr Ser Ala Asn Val Met Val
Asp Gly
      35              40              45
aaa cca ata aat ctt ggt tta tgg gat aca gca ggt caa gaa
gat tat      192
Lys Pro Ile Asn Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu
Asp Tyr
      50              55              60
gac aga tta aga cca ttg tct tat cct caa aca gat gtt ttt
ttg atc      240
Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
Leu Ile
  65              70              75
80
tgc ttt tct ctc gtt aac cca gcc agt ttt gaa aat gtt cgt
gca aaa      288
Cys Phe Ser Leu Val Asn Pro Ala Ser Phe Glu Asn Val Arg
Ala Lys
      85              90
95
tgg tat cca gaa gta cgt cat cat tgt cca gct act cca att
att tta      336
Trp Tyr Pro Glu Val Arg His His Cys Pro Ala Thr Pro Ile
Ile Leu
      100              105              110
gta gga act aaa tta gat tta cgc gaa gat aaa gaa aca att
gag cga      384
Val Gly Thr Lys Leu Asp Leu Arg Glu Asp Lys Glu Thr Ile
Glu Arg
      115              120              125

```

0070110

```

tta aaa gat aag aaa ctt gca cca ata aca tat cct cag ggt
tta tcc          432
Leu Lys Asp Lys Lys Leu Ala Pro Ile Thr Tyr Pro Gln Gly
Leu Ser
    130          135          140
atg gca aaa gaa att ggt gct gta aaa tat tta gaa tgt tcg
gct ctt          480
Met Ala Lys Glu Ile Gly Ala Val Lys Tyr Leu Glu Cys Ser
Ala Leu
145          150          155
    160
act caa aaa gga tta aaa aca gta ttt gat gaa gca att cgc
gca gta          528
Thr Gln Lys Gly Leu Lys Thr Val Phe Asp Glu Ala Ile Arg
Ala Val
          165          170
175
ttg tgt cct gtt ctt caa gtg aaa cca aaa cgc aga tgt ttc
ctt cta          576
Leu Cys Pro Val Leu Gln Val Lys Pro Lys Arg Arg Cys Phe
Leu Leu
          180          185          190

```

taa

579

<210> 225
 <211> 192
 <212> PRT
 <213> Apis mellifera

```

<400> 225
Met Gln Ala Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys
1          5          10
15
Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Ala Phe Pro Gly
Glu Tyr
          20          25          30
Ile Pro Thr Val Phe Asp Asn Tyr Ser Ala Asn Val Met Val
Asp Gly
          35          40          45
Lys Pro Ile Asn Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu
Asp Tyr

```

0070110
55

50

60

Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Pro	Gln	Thr	Asp	Val	Phe
Leu	Ile												
65					70					75			
80													
Cys	Phe	Ser	Leu	Val	Asn	Pro	Ala	Ser	Phe	Glu	Asn	Val	Arg
Ala	Lys												
				85					90				
95													
Trp	Tyr	Pro	Glu	Val	Arg	His	His	Cys	Pro	Ala	Thr	Pro	Ile
Ile	Leu												
			100					105					110
Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Glu	Asp	Lys	Glu	Thr	Ile
Glu	Arg												
		115					120				125		
Leu	Lys	Asp	Lys	Lys	Leu	Ala	Pro	Ile	Thr	Tyr	Pro	Gln	Gly
Leu	Ser												
	130					135					140		
Met	Ala	Lys	Glu	Ile	Gly	Ala	Val	Lys	Tyr	Leu	Glu	Cys	Ser
Ala	Leu												
145					150					155			
160													
Thr	Gln	Lys	Gly	Leu	Lys	Thr	Val	Phe	Asp	Glu	Ala	Ile	Arg
Ala	Val												
			165					170					
175													
Leu	Cys	Pro	Val	Leu	Gln	Val	Lys	Pro	Lys	Arg	Arg	Cys	Phe
Leu	Leu												
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<210> 226
 <211> 588
 <212> DNA
 <213> Apis mellifera

<220>
 <221> CDS
 <222> (1)..(588)

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 gga aca 48
 Met Ser Ser Gly Arg Pro Ile Lys Cys Val Val Val Gly Asp
 Seite 355

0070110

Gly	Thr												
1				5				10					
15													
gta	gga	aaa	aca	tgt	atg	tta	ata	tca	tat	acc	act	gat	agt
ttt	cca		96										
Val	Gly	Lys	Thr	Cys	Met	Leu	Ile	Ser	Tyr	Thr	Thr	Asp	Ser
Phe	Pro												
			20					25					30
gga	gaa	tat	gtt	cct	aca	gtg	ttt	gat	aat	tac	tca	gca	cct
atg	ggt		144										
Gly	Glu	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	Tyr	Ser	Ala	Pro
Met	Val												
		35					40					45	
gtg	gat	gga	ata	cct	ggt	agt	ctt	gga	ctt	tgg	gat	aca	gca
ggt	caa		192										
Val	Asp	Gly	Ile	Pro	Val	Ser	Leu	Gly	Leu	Trp	Asp	Thr	Ala
Gly	Gln												
		50				55				60			
gaa	gat	tat	gac	agg	ctt	cgt	cca	ctt	tca	tat	cca	cag	act
gat	ggt		240										
Glu	Asp	Tyr	Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Pro	Gln	Thr
Asp	Val												
65					70					75			
80													
ttt	tta	att	tgt	ttc	tca	gta	aca	agt	cct	tca	tct	ttt	gaa
aat	ggt		288										
Phe	Leu	Ile	Cys	Phe	Ser	Val	Thr	Ser	Pro	Ser	Ser	Phe	Glu
Asn	Val												
				85						90			
95													
acc	agc	aaa	tgg	tat	cca	gag	att	aaa	cat	cac	tgc	cca	gat
gct	cca		336										
Thr	Ser	Lys	Trp	Tyr	Pro	Glu	Ile	Lys	His	His	Cys	Pro	Asp
Ala	Pro												
				100				105					110
atg	ata	ctt	ggt	gga	act	aaa	ata	gac	tta	cga	gat	gat	cgt
gaa	aca		384										
Met	Ile	Leu	Val	Gly	Thr	Lys	Ile	Asp	Leu	Arg	Asp	Asp	Arg
Glu	Thr												
		115					120					125	
ctt	act	gcc	tta	gct	gaa	caa	ggt	ctt	agt	gct	ata	aaa	cgt
gaa	caa		432										
Leu	Thr	Ala	Leu	Ala	Glu	Gln	Gly	Leu	Ser	Ala	Ile	Lys	Arg
Glu	Gln												
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gga	caa	aaa	ctg	gca	aat	aag	att	cgt	gct	gtg	aaa	tat	atg
gaa	tgt		480										

0070110

Gly Gln Lys Leu Ala Asn Lys Ile Arg Ala Val Lys Tyr Met
 Glu Cys
 145 150 155

160
 tct gca ctt aca caa cgt ggt cta aaa caa gtg ttt gat gaa
 gca gtt 528
 Ser Ala Leu Thr Gln Arg Gly Leu Lys Gln Val Phe Asp Glu
 Ala Val

165 170
 175
 cgt gct gtt tta aga cct gaa cct caa aaa cgc aga cag aga
 aga tgc 576
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 Arg Cys
 180 185 190

att atg tta taa
 588
 Ile Met Leu
 195

<210> 227
 <211> 195
 <212> PRT
 <213> Apis mellifera

<400> 227
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 Gly Thr
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 Phe Pro
 20 25 30

Gly Glu Tyr Val Pro Thr Val Phe Asp Asn Tyr Ser Ala Pro
 Met Val
 35 40 45

Val Asp Gly Ile Pro Val Ser Leu Gly Leu Trp Asp Thr Ala
 Gly Gln
 50 55 60

Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr
 Asp Val
 65 70 75
 80

0070110

Phe Leu Ile Cys Phe Ser Val Thr Ser Pro Ser Ser Phe Glu
Asn Val

85

90

95

Thr Ser Lys Trp Tyr Pro Glu Ile Lys His His Cys Pro Asp
Ala Pro

100

105

110

Met Ile Leu Val Gly Thr Lys Ile Asp Leu Arg Asp Asp Arg
Glu Thr

115

120

125

Leu Thr Ala Leu Ala Glu Gln Gly Leu Ser Ala Ile Lys Arg
Glu Gln
130

135

140

Gly Gln Lys Leu Ala Asn Lys Ile Arg Ala Val Lys Tyr Met
Glu Cys
145

150

155

160

Ser Ala Leu Thr Gln Arg Gly Leu Lys Gln Val Phe Asp Glu
Ala Val

165

170

175

Arg Ala Val Leu Arg Pro Glu Pro Gln Lys Arg Arg Gln Arg
Arg Cys

180

185

190

Ile Met Leu
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<210> 228

<211> 600

<212> DNA

<213> Aspergillus nidulans FGSC A4

<220>

<221> CDS

<222> (1)..(600)

<400> 228

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Met Ala Thr Gly Pro Ala Thr Gln Ser Leu Lys Cys Val Val
Thr Gly

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5

10

15

0070110

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

0070110

160

ctc gag tgc tct gcc cta acg caa cgc aac ctt aag agc gtg
ttc gac 528
Leu Glu Cys Ser Ala Leu Thr Gln Arg Asn Leu Lys Ser Val
Phe Asp

165

170

175

gaa gcc att cgt gct gtt ctg aac ccg cga cct gcg acg aaa
cag agg 576
Glu Ala Ile Arg Ala Val Leu Asn Pro Arg Pro Ala Thr Lys
Gln Arg

180

185

190

aac aag aag tgt acg att ctg tga
600

Asn Lys Lys Cys Thr Ile Leu
195

<210> 229

<211> 199

<212> PRT

<213> *Aspergillus nidulans* FGSC A4

<400> 229

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Thr Gly

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15

Asp Gly Ala Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr
Thr Asn

20

25

30

Ala Phe Pro Gly Glu Tyr Ile Pro Thr Val Phe Asp Asn Tyr
Thr Ala

35

40

45

Ser Val Met Val Asp Gly Arg Pro Ile Ser Leu Gly Leu Trp
Asp Thr

50

55

60

Ala Gly Gln Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr
Pro Gln

65

70

75

80

Thr Asp Val Phe Leu Ile Cys Phe Ser Ile Val Ser Pro Pro
Ser Phe

85

90

95

0070110

Asp Asn Val Lys Ser Lys Trp Phe Pro Glu Ile Glu His His
Ala Pro
100 105 110

Asn Val Pro Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg
Asp Asp
115 120 125

Pro Ala Gln Leu Glu Ser Leu Arg Met Arg Lys Gln Glu Pro
Val Thr
130 135 140

Tyr Glu Gln Ala Leu Ala Val Ala Lys Glu Ile Arg Ala His
Lys Tyr
145 150 155
160

Leu Glu Cys Ser Ala Leu Thr Gln Arg Asn Leu Lys Ser Val
Phe Asp
165 170

175
Glu Ala Ile Arg Ala Val Leu Asn Pro Arg Pro Ala Thr Lys
Gln Arg
180 185 190

Asn Lys Lys Cys Thr Ile Leu
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<210> 230
<211> 576
<212> DNA
<213> Aspergillus nidulans FGSC A4

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<222> (1)..(576)

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gtg ctc 48
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Val Leu
1 5 10
15
tta gga gat ggc gct tgc ggt aaa acc tcg gcc ctg aac gtg
ttc aca 96
Leu Gly Asp Gly Ala Cys Gly Lys Thr Ser Ala Leu Asn Val
Phe Thr
20 25 30

0070110

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

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0070110

165

170

175

aag gct caa aac acc ggc tcg tcg caa agc cgc tgc gtc att

cag

573

Lys Ala Gln Asn Thr Gly Ser Ser Gln Ser Arg Cys Val Ile

Gln

180

185

190

tga

576

<210> 231

<211> 191

<212> PRT

<213> *Aspergillus nidulans* FGSC A4

<400> 231

Met Asp Phe Cys Gly Arg Gln Lys Val Val Arg Arg Lys Met

Val Leu

1

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15

Leu Gly Asp Gly Ala Cys Gly Lys Thr Ser Ala Leu Asn Val

Phe Thr

20

25

30

Arg Gly Glu Pro Thr Val Phe Glu Asn Tyr Val His Asp Ile

Phe Val

35

40

45

Asp Asn Val His Met Glu Leu Ser Leu Trp Asp Thr Ala Gly

Gln Glu

50

55

60

Glu Phe Asp Arg Leu Arg Ala Leu Ser Tyr Glu Asp Thr His

Val Ile

65

70

75

80

Met Leu Cys Phe Ser Val Asp Ser Pro Asp Ser Phe Glu Asn

Val Ala

85

90

95

Ser Lys Trp Ile Glu Glu Ile Ser Glu Asn Val Pro Gly Val

Lys Leu

100

105

110

Val Leu Thr Ala Leu Lys Cys Asp Leu Arg Lys Asp Glu Tyr

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0070110

Met	Asn												
		115					120					125	
Asp	Asn	Pro	Asn	Val	Ile	Thr	Tyr	Glu	Gln	Gly	Leu	Ala	Lys
Ala	Lys												
	130					135					140		
Glu	Ile	Gly	Ala	Val	Lys	Tyr	Leu	Glu	Cys	Ser	Ala	Val	Gln
Asn	Arg												
145					150					155			
160													
Gly	Ile	Arg	Glu	Ala	Phe	Tyr	Glu	Ala	Ala	Lys	Val	Ala	Leu
Glu	Val												
				165					170				
175													
Lys	Ala	Gln	Asn	Thr	Gly	Ser	Ser	Gln	Ser	Arg	Cys	Val	Ile
Gln													
			180					185					190

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<210> 232
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<212> DNA
<213> Aspergillus nidulans FGSC A4
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Val	Ile												
1				5					10				
15													
atc	ggc	gac	ggc	gcc	tgt	ggg	aaa	acg	agt	ctg	ctg	agt	gtt
ttt	aca			96									
Ile	Gly	Asp	Gly	Ala	Cys	Gly	Lys	Thr	Ser	Leu	Leu	Ser	Val
Phe	Thr												
			20					25					30
ttg	ggc	tac	ttc	cct	aca	gtc	cca	acg	gtg	ttc	gag	agc	tat
gtg	aca			144									
Leu	Gly	Tyr	Phe	Pro	Thr	Val	Pro	Thr	Val	Phe	Glu	Ser	Tyr
Val	Thr												
		35					40					45	
gac	tgc	cgg	gta	gac	ggc	cgg	tca	gtc	cag	tta	gca	ttg	tgg
gat	aca			192									

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Asp	Cys	Arg	Val	Asp	Gly	Arg	Ser	Val	Gln	Leu	Ala	Leu	Trp
Asp	Thr												
	50					55					60		
gcc	ggt	cag	gaa	gat	tac	gag	cga	ctg	cgt	ccg	cta	gcc	tac
tcc	aaa			240									
Ala	Gly	Gln	Glu	Asp	Tyr	Glu	Arg	Leu	Arg	Pro	Leu	Ala	Tyr
Ser	Lys												
65					70					75			
80													
gcc	cac	gtt	atc	ctg	atc	gga	ttt	gct	gtc	gac	acg	cca	gat
tcg	ctc			288									
Ala	His	Val	Ile	Leu	Ile	Gly	Phe	Ala	Val	Asp	Thr	Pro	Asp
Ser	Leu												
				85						90			
95													
gag	aac	gtc	aag	atc	aag	tgg	atc	gaa	gaa	gcg	aat	gag	cga
tgc	ccc			336									
Glu	Asn	Val	Lys	Ile	Lys	Trp	Ile	Glu	Glu	Ala	Asn	Glu	Arg
Cys	Pro												
				100						105			110
ggc	gta	ccc	atc	atc	ctc	gtt	ggg	ctg	aag	aag	gac	ctc	cgc
gag	aac			384									
Gly	Val	Pro	Ile	Ile	Leu	Val	Gly	Leu	Lys	Lys	Asp	Leu	Arg
Glu	Asn												
				115				120				125	
ccc	gga	gag	atc	gag	gaa	atg	cga	aag	aag	tct	ctc	cga	ttt
gtg	tcg			432									
Pro	Gly	Ala	Ile	Glu	Glu	Met	Arg	Lys	Lys	Ser	Leu	Arg	Phe
Val	Ser												
								135				140	
ccc	aag	gaa	gga	agt	gaa	aca	gca	acg	cag	atc	aag	gcc	cga
aaa	tac			480									
Pro	Lys	Glu	Gly	Ser	Glu	Thr	Ala	Thr	Gln	Ile	Lys	Ala	Arg
Lys	Tyr												
145					150					155			
160													
ctt	gag	tgc	tct	tcg	cta	aca	ggc	gag	ggt	gtg	gac	gac	gtc
ttt	gaa			528									
Leu	Glu	Cys	Ser	Ser	Leu	Thr	Gly	Glu	Gly	Val	Asp	Asp	Val
Phe	Glu												
				165						170			
175													
gcc	gcc	acc	cgc	gcc	gag	ctc	ctc	acc	ttc	gat	aag	cgg	aaa
tcc	tca			576									
Ala	Ala	Thr	Arg	Ala	Ala	Leu	Leu	Thr	Phe	Asp	Lys	Arg	Lys
Ser	Ser												
				180						185			190

0070110

tgt tgc att gtg cta tga
594
Cys Cys Ile Val Leu
195

<210> 233
<211> 197
<212> PRT
<213> Aspergillus nidulans FGSC A4

<400> 233
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Val Ile
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Phe Thr 20 25 30
Leu Gly Tyr Phe Pro Thr Val Pro Thr Val Phe Glu Ser Tyr
Val Thr 35 40 45
Asp Cys Arg Val Asp Gly Arg Ser Val Gln Leu Ala Leu Trp
Asp Thr 50 55 60
Ala Gly Gln Glu Asp Tyr Glu Arg Leu Arg Pro Leu Ala Tyr
Ser Lys 65 70 75
80
Ala His Val Ile Leu Ile Gly Phe Ala Val Asp Thr Pro Asp
Ser Leu 85 90
95
Glu Asn Val Lys Ile Lys Trp Ile Glu Glu Ala Asn Glu Arg
Cys Pro 100 105 110
Gly Val Pro Ile Ile Leu Val Gly Leu Lys Lys Asp Leu Arg
Glu Asn 115 120 125
Pro Gly Ala Ile Glu Glu Met Arg Lys Lys Ser Leu Arg Phe
Val Ser 130 135 140

0070110

Pro Lys Glu Gly Ser Glu Thr Ala Thr Gln Ile Lys Ala Arg
 Lys Tyr
 145 150 155
 160
 Leu Glu Cys Ser Ser Leu Thr Gly Glu Gly Val Asp Asp Val
 Phe Glu
 165 170
 175
 Ala Ala Thr Arg Ala Ala Leu Leu Thr Phe Asp Lys Arg Lys
 Ser Ser
 180 185 190
 Cys Cys Ile Val Leu
 195

<210> 234
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 <212> DNA
 <213> Candida albicans SC5314

<220>
 <221> CDS
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 <223> transl_table=12

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 Gly Lys
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 15
 act tgt tta ttg ata tcc tat act acc aat act ttc cca aat
 gat tat 96
 Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Thr Phe Pro Asn
 Asp Tyr
 20 25 30
 att cca act gtt ttc gat aat tat tca gcc tca gtt atg att
 gat ggc 144
 Ile Pro Thr Val Phe Asp Asn Tyr Ser Ala Ser Val Met Ile
 Asp Gly
 35 40 45
 gaa cca atc aaa tta gga tta tgg gat acc gct ggt caa tca
 gaa tat 192
 Glu Pro Ile Lys Leu Gly Leu Trp Asp Thr Ala Gly Gln Ser
 Glu Tyr
 50 55 60
 gat aga tta aga ccg tta tcg tat cca caa aca gaa ata ttt
 Seite 367

0070110

tta	tgt			240										
Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Pro	Gln	Thr	Glu	Ile	Phe	
Leu	Cys													
65					70					75				
80														
tgt	ttc	tcc	gtg	ata	agt	cct	gac	tcg	ttc	caa	aat	gtc	aaa	
tct	aaa		288											
Cys	Phe	Ser	Val	Ile	Ser	Pro	Asp	Ser	Phe	Gln	Asn	Val	Lys	
Ser	Lys													
				85						90				
95														
tgg	ata	cct	gaa	ata	ttg	cat	cat	tgt	cca	aag	gat	att	tta	
att	tta		336											
Trp	Ile	Pro	Glu	Ile	Leu	His	His	Cys	Pro	Lys	Asp	Ile	Leu	
Ile	Leu													
				100					105				110	
ttg	att	ggt	acc	aag	gtc	gat	tta	cga	gac	gat	ttg	cat	gta	
ttg	gac		384											
Leu	Ile	Gly	Thr	Lys	Val	Asp	Leu	Arg	Asp	Asp	Leu	His	Val	
Leu	Asp													
		115					120					125		
gag	ttg	aca	gcc	agg	aat	ttg	agt	ccc	gtc	act	ttt	gac	cag	
gga	aac		432											
Glu	Leu	Thr	Ala	Arg	Asn	Leu	Ser	Pro	Val	Thr	Phe	Asp	Gln	
Gly	Asn													
		130				135					140			
aag	ttg	gct	aga	gag	att	ggt	gcc	ata	aaa	tat	atg	gaa	tgt	
tct	gct		480											
Lys	Leu	Ala	Arg	Glu	Ile	Gly	Ala	Ile	Lys	Tyr	Met	Glu	Cys	
Ser	Ala													
145					150					155				
160														
gct	act	caa	gtc	ggt	gtc	aag	gaa	ata	ttt	gat	tac	gca	ata	
agg	gca		528											
Ala	Thr	Gln	Val	Gly	Val	Lys	Glu	Ile	Phe	Asp	Tyr	Ala	Ile	
Arg	Ala													
				165						170				
175														
gtg	tta	gac	cca	cca	aac	gct	aac	aaa	ggt	gaa	tat	gtt	aca	
aat	gac		576											
Val	Leu	Asp	Pro	Pro	Asn	Ala	Asn	Lys	Gly	Glu	Tyr	Val	Thr	
Asn	Asp													
			180						185				190	
agt	gtg	cca	gga	atg	ggt	gtc	aac	aat	tcc	agt	ggt	agt	aag	
aaa	cat		624											

0070110

Ser	Val	Pro	Gly	Met	Gly	Val	Asn	Asn	Ser	Ser	Gly	Ser	Lys
Lys	His												
		195					200					205	
aac	gaa	aag	aat	ggg	tct	gga	aca	gca	act	gct	ggg	act	ggg
aag	aaa		672										
Asn	Glu	Lys	Asn	Gly	Ser	Gly	Thr	Ala	Thr	Ala	Gly	Thr	Gly
Lys	Lys												
	210					215					220		
aga	aaa	att	aag	aga	gct	aaa	aaa	tgt	act	ata	tta	taa	
		711											
Arg	Lys	Ile	Lys	Arg	Ala	Lys	Lys	Cys	Thr	Ile	Leu		
225					230					235			

<210> 235

<211> 236

<212> PRT

<213> Candida albicans SC5314

<400> 235

Met	Arg	Ser	Ile	Lys	Ser	Val	Val	Val	Gly	Asp	Gly	Gly	Val
Gly	Lys												
1				5					10				
15													
Thr	Cys	Leu	Leu	Ile	Ser	Tyr	Thr	Thr	Asn	Thr	Phe	Pro	Asn
Asp	Tyr												
			20					25					30
Ile	Pro	Thr	Val	Phe	Asp	Asn	Tyr	Ser	Ala	Ser	Val	Met	Ile
Asp	Gly												
			35				40					45	
Glu	Pro	Ile	Lys	Leu	Gly	Leu	Trp	Asp	Thr	Ala	Gly	Gln	Ser
Glu	Tyr												
	50					55					60		
Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Pro	Gln	Thr	Glu	Ile	Phe
Leu	Cys												
65					70					75			
	80												
Cys	Phe	Ser	Val	Ile	Ser	Pro	Asp	Ser	Phe	Gln	Asn	Val	Lys
Ser	Lys												
				85					90				
95													
Trp	Ile	Pro	Glu	Ile	Leu	His	His	Cys	Pro	Lys	Asp	Ile	Leu
Ile	Leu												
			100					105					110
Leu	Ile	Gly	Thr	Lys	Val	Asp	Leu	Arg	Asp	Asp	Leu	His	Val

0070110

Leu Asp	115	120	125
Glu Leu Thr Ala Arg Asn Leu Ser Pro Val Thr Phe Asp Gln			
Gly Asn	130	135	140
Lys Leu Ala Arg Glu Ile Gly Ala Ile Lys Tyr Met Glu Cys			
Ser Ala	145	150	155
Ala Thr Gln Val Gly Val Lys Glu Ile Phe Asp Tyr Ala Ile			
Arg Ala	160	165	170
Val Leu Asp Pro Pro Asn Ala Asn Lys Gly Glu Tyr Val Thr			
Asn Asp	175	180	185
Ser Val Pro Gly Met Gly Val Asn Asn Ser Ser Gly Ser Lys			
Lys His	195	200	205
Asn Glu Lys Asn Gly Ser Gly Thr Ala Thr Ala Gly Thr Gly			
Lys Lys	210	215	220
Arg Lys Ile Lys Arg Ala Lys Lys Cys Thr Ile Leu			
225	230	235	

<210> 236
 <211> 582
 <212> DNA
 <213> Ustilago maydis 521

<220>
 <221> CDS
 <222> (1)..(582)

<400> 236
 atg cag acc atc aag tgt gta gtc gtc gga gac ggt gcc gtc
 gga aag 48
 Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
 Gly Lys
 1 5 10
 15
 acg tgt ctt ctt atc tcg tat aca acc aac gcc ttc ccg ggc
 gaa tac 96

0070110

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

0070110

agc gtt 528
Thr Gln Lys Gly Leu Lys Gly Val Phe Asp Glu Ala Ile Arg
Ser Val

165

170

175

ttg gct cct gca cca gtc aag agt aag aag aag aac aac tgt
atg att 576
Leu Ala Pro Ala Pro Val Lys Ser Lys Lys Lys Asn Asn Cys
Met Ile

180

185

190

ctt taa

582

Leu

<210> 237

<211> 193

<212> PRT

<213> Ustilago maydis 521

<400> 237

Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys

1

5

10

15

Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Ala Phe Pro Gly
Glu Tyr

20

25

30

Ile Pro Thr Val Phe Asp Asn Tyr Ser Ala Asn Val Met Val
Asp Gly

35

40

45

Lys Pro Val Ser Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu
Asp Tyr

50

55

60

Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
Leu Val

65

70

75

80

Cys Phe Ser Leu Val Ser Pro Pro Ser Phe Glu Asn Val Arg
Thr Lys

85

90

95

Trp Trp Pro Glu Val Ser His His Ala Pro Asn Ile Pro Thr
Seite 372

0070110

Ile	Leu												
			100					105					110
Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Glu	Asp	Pro	Glu	Thr	Ile
Ala	Lys												
		115					120					125	
Leu	Arg	Asp	Arg	Arg	Met	Gln	Pro	Ile	Thr	Tyr	Ala	Gln	Gly
Asn	Gln												
		130				135					140		
Met	Ala	Arg	Asp	Ile	His	Ala	Thr	Lys	Tyr	Leu	Glu	Cys	Ser
Ala	Leu												
145					150					155			
160													
Thr	Gln	Lys	Gly	Leu	Lys	Gly	Val	Phe	Asp	Glu	Ala	Ile	Arg
Ser	Val												
				165					170				
175													
Leu	Ala	Pro	Ala	Pro	Val	Lys	Ser	Lys	Lys	Lys	Asn	Asn	Cys
Met	Ile												
			180					185					190

Leu

<210> 238
<211> 645
<212> DNA
<213> Ustilago maydis 521

<220>
<221> CDS
<222> (1)..(645)

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<400> 238
atg gca ccg gca gca att cgt agg aag ctc gta att gtc ggc
gac ggt
Met Ala Pro Ala Ala Ile Arg Arg Lys Leu Val Ile Val Gly
Asp Gly
1 5 10
15
gct tgc ggc aag acg agc ttg ctt tgc gtc ttt gcc att ggc
gag ttc
Ala Cys Gly Lys Thr Ser Leu Leu Cys Val Phe Ala Ile Gly
Glu Phe
20 25 30
ccg caa gag tat gaa ccc acc atc ttc gaa aac tac gtc gcc

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0070110

gag	atc			144										
Pro	Gln	Glu	Tyr	Glu	Pro	Thr	Ile	Phe	Glu	Asn	Tyr	Val	Ala	
Glu	Ile													
		35					40					45		
cgc	ctt	gat	ggc	aag	cct	gtc	cag	ctg	gcg	cta	tgg	gac	acc	
gcg	ggt		192											
Arg	Leu	Asp	Gly	Lys	Pro	Val	Gln	Leu	Ala	Leu	Trp	Asp	Thr	
Ala	Gly													
	50					55					60			
cag	gaa	gaa	tac	gag	cgt	ctt	cgt	cca	ctc	tcc	tac	tca	caa	
gca	cac		240											
Gln	Glu	Glu	Tyr	Glu	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Ser	Gln	
Ala	His													
65					70					75				
80														
gtc	atc	ttg	atc	gcc	ttt	gcc	atc	gat	aca	ccc	gac	tcg	ctc	
gaa	aac		288											
Val	Ile	Leu	Ile	Ala	Phe	Ala	Ile	Asp	Thr	Pro	Asp	Ser	Leu	
Glu	Asn													
				85					90					
95														
gtg	caa	gtc	aag	tgg	atg	gag	gag	gta	cgt	caa	ata	tgc	ggc	
ccc	tca		336											
Val	Gln	Val	Lys	Trp	Met	Glu	Glu	Val	Arg	Gln	Ile	Cys	Gly	
Pro	Ser													
		100						105					110	
gtg	cct	gtg	ctc	ctg	gta	ggc	tgc	aag	aag	gat	ctt	cgc	gaa	
gat	gcc		384											
Val	Pro	Val	Leu	Leu	Val	Gly	Cys	Lys	Lys	Asp	Leu	Arg	Glu	
Asp	Ala													
		115				120						125		
atc	gct	aag	ggc	aag	ccg	gtt	cag	ggt	cac	tat	gta	gag	aga	
caa	cag		432											
Ile	Ala	Lys	Gly	Lys	Pro	Val	Gln	Gly	His	Tyr	Val	Glu	Arg	
Gln	Gln													
	130					135						140		
gct	aaa	ctg	gta	gca	gca	cag	atc	ggc	gct	cga	tcg	tat	cac	
gaa	tgc		480											
Ala	Lys	Leu	Val	Ala	Ala	Gln	Ile	Gly	Ala	Arg	Ser	Tyr	His	
Glu	Cys													
145					150					155				
160														
tca	tca	ctc	aac	aac	caa	ggc	gtc	gac	gcc	gtg	ttc	gaa	gcc	
gcg	acg		528											
Ser	Ser	Leu	Asn	Asn	Gln	Gly	Val	Asp	Ala	Val	Phe	Glu	Ala	
Ala	Thr													
					165					170				

0070110

175

cgc gcg gcc atg ctt gtg cgc aat tcc ggt gct tct tca gga
ggc gcc
Arg Ala Ala Met Leu Val Arg Asn Ser Gly Ala Ser Ser Gly
Gly Ala

180

185

190

atc tcg cag agc aag acc aag gag gca tta cac aac gat gct
ggc tct
Ile Ser Gln Ser Lys Thr Lys Glu Ala Leu His Asn Asp Ala
Gly Ser

195

200

205

tgc aaa tgt atc gtc ctc tag
Cys Lys Cys Ile Val Leu
210

<210> 239

<211> 214

<212> PRT

<213> Ustilago maydis 521

<400> 239

Met Ala Pro Ala Ala Ile Arg Arg Lys Leu Val Ile Val Gly
Asp Gly

1

5

10

15

Ala Cys Gly Lys Thr Ser Leu Leu Cys Val Phe Ala Ile Gly
Glu Phe

20

25

30

Pro Gln Glu Tyr Glu Pro Thr Ile Phe Glu Asn Tyr Val Ala
Glu Ile

35

40

45

Arg Leu Asp Gly Lys Pro Val Gln Leu Ala Leu Trp Asp Thr
Ala Gly
50 55 60

Gln Glu Glu Tyr Glu Arg Leu Arg Pro Leu Ser Tyr Ser Gln
Ala His

65

70

75

80

Val Ile Leu Ile Ala Phe Ala Ile Asp Thr Pro Asp Ser Leu
Glu Asn

85

90

95

Val Gln Val Lys Trp Met Glu Glu Val Arg Gln Ile Cys Gly
Seite 375

0070110

Pro	Ser												
			100				105					110	
Val	Pro	Val	Leu	Leu	Val	Gly	Cys	Lys	Lys	Asp	Leu	Arg	Glu
Asp	Ala												
		115					120					125	
Ile	Ala	Lys	Gly	Lys	Pro	Val	Gln	Gly	His	Tyr	Val	Glu	Arg
Gln	Gln												
		130				135					140		
Ala	Lys	Leu	Val	Ala	Ala	Gln	Ile	Gly	Ala	Arg	Ser	Tyr	His
Glu	Cys												
145					150					155			
160													
Ser	Ser	Leu	Asn	Asn	Gln	Gly	Val	Asp	Ala	Val	Phe	Glu	Ala
Ala	Thr												
				165					170				
175													
Arg	Ala	Ala	Met	Leu	Val	Arg	Asn	Ser	Gly	Ala	Ser	Ser	Gly
Gly	Ala												
			180					185				190	
Ile	Ser	Gln	Ser	Lys	Thr	Lys	Glu	Ala	Leu	His	Asn	Asp	Ala
Gly	Ser												
		195					200					205	
Cys	Lys	Cys	Ile	Val	Leu								
		210											

<210> 240
 <211> 585
 <212> DNA
 <213> Ustilago maydis 521

<220>
 <221> CDS
 <222> (1)..(585)

<400> 240													
atg	tct	gaa	ctc	cgc	cga	aag	ctt	gtc	att	gtc	gga	gac	ggt
gct	tgt			48									
Met	Ser	Glu	Leu	Arg	Arg	Lys	Leu	Val	Ile	Val	Gly	Asp	Gly
Ala	Cys												
1				5					10				
15													
ggt	aag	act	tgt	ctt	ctt	atc	gtc	ttt	tcc	aag	ggc	acc	ttc
ccc	gag			96									

0070110

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

0070110

acg cgc 528
Ala Lys Thr Gly Glu Gly Val Arg Glu Val Phe Glu His Ala
Thr Arg

165

170

175

gcg gcg ctg gtt caa aga agc cgt ggc tcg agg aag aaa ggt
tgc acc 576
Ala Ala Leu Val Gln Arg Ser Arg Gly Ser Arg Lys Lys Gly
Cys Thr

180

185

190

gtt ctc taa

585

val Leu

<210> 241

<211> 194

<212> PRT

<213> Ustilago maydis 521

<400> 241

Met Ser Glu Leu Arg Arg Lys Leu Val Ile Val Gly Asp Gly
Ala Cys

1

5

10

15

Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Gly Thr Phe
Pro Glu

20

25

30

Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Val
Glu Val

35

40

45

Asp Gly Arg His Val Glu Leu Ala Leu Trp Asp Thr Ala Gly
Gln Glu 50 55 60

Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Ser His
Val Ile 65 70 75

80

Leu Ile Cys Phe Ala Val Asp Ser Pro Asp Ser Leu Asp Asn
Val Gln

85

90

95

Glu Lys Trp Ile Ser Glu Val Leu His Phe Cys His Ser Leu
Pro Ile

0070110

100

105

110

Ile Leu Val Gly Cys Lys Lys Asp Leu Arg His Asp Pro Lys
Ile Val

115

120

125

Asp Glu Leu Arg Lys Thr Ser Gln Arg Pro Val Ser Ala Glu
Glu Gly
130

135

140

Met Ala Val Ala Gln Lys Ile Gly Ala Val Arg Tyr Leu Glu
Cys Ser
145

150

155

160

Ala Lys Thr Gly Glu Gly Val Arg Glu Val Phe Glu His Ala
Thr Arg

165

170

175

Ala Ala Leu Val Gln Arg Ser Arg Gly Ser Arg Lys Lys Gly
Cys Thr

180

185

190

Val Leu

<210> 242

<211> 582

<212> DNA

<213> Cryptococcus neoformans var. neoformans B-3501A

<220>

<221> CDS

<222> (1)..(582)

<400> 242

atg cag aca atc aag tgt gtc gta gtc gga gac ggt gcc gtt
gga aag

48

Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys

1

5

10

15

acc tgc ttg ctc atc tcg tac act acc aat aag ttc cca tcc
gag tat

96

Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe Pro Ser
Glu Tyr

20

25

30

gtt cct acc gtc ttt gac aac tac gcc gtc agt gta act atc
ggt gac

144

0070110

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

0070110

tta gaa ccc cct atg gcg acc aag aaa aag tct aaa aag tgt
 ctc att 576
 Leu Glu Pro Pro Met Ala Thr Lys Lys Lys Ser Lys Lys Cys
 Leu Ile 180 185 190

ctt taa
 Leu 582

<210> 243
 <211> 193
 <212> PRT
 <213> Cryptococcus neoformans var. neoformans B-3501A

<400> 243
 Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
 Gly Lys 1 5 10
 15
 Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe Pro Ser
 Glu Tyr 20 25 30

Val Pro Thr Val Phe Asp Asn Tyr Ala Val Ser Val Thr Ile
 Gly Asp 35 40 45

Asp Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu
 Asp Tyr 50 55 60

Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
 Leu Val 65 70 75

80
 Cys Phe Ser Val Thr Ser Pro Ala Ser Phe Glu Asn Val Arg
 Glu Lys 85 90

95
 Trp Phe Pro Glu Ile Ala His His Cys Pro Gly Val Pro Ala
 Leu Ile 100 105 110

Val Gly Thr Gln Val Asp Leu Arg Asp Asp Pro Ala Gln Thr
 Glu Lys 115 120 125

0070110

Leu Gly Arg Gln Arg Met Lys Pro Ile Thr Gln Asp Met Gly
Glu Arg
130 135 140

Leu Ala Arg Glu Leu Gly Ala Val Lys Tyr Val Glu Cys Ser
Ala Leu
145 150 155

160
Thr Gln Arg Gly Leu Lys Asn Val Phe Asp Glu Ala Ile Val
Ala Ala
165 170

175
Leu Glu Pro Pro Met Ala Thr Lys Lys Lys Ser Lys Lys Cys
Leu Ile
180 185 190

Leu

<210> 244

<211> 651

<212> DNA

<213> Cryptococcus neoformans var. neoformans B-3501A

<220>

<221> CDS

<222> (1)..(651)

<400> 244

atg tcc gga gaa atc agg aga aag ctc gtt att gtc ggc gac
ggt gct 48
Met Ser Gly Glu Ile Arg Arg Lys Leu Val Ile Val Gly Asp
Gly Ala
1 5 10

15
tgt ggt aag aca tgt ctt ctt atc gtg ttc agc aag ggc atg
ttc ccc 96
Cys Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Gly Met
Phe Pro
20 25 30

gag gtg tac gtg ccc acc gtc ttt gaa aac tat gtc gcc gat
gta gag 144
Glu Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp
Val Glu
35 40 45

gtg gac ggg aag aag gtc gag ctg gcg ttg tgg gat act gct
gga cag 192

0070110

Val	Asp	Gly	Lys	Lys	Val	Glu	Leu	Ala	Leu	Trp	Asp	Thr	Ala
Gly	Gln												
	50					55					60		
gag	gac	tat	gac	cga	ctc	cga	cct	ctt	tct	tac	ccc	gac	tcc
cat	gtc		240										
Glu	Asp	Tyr	Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Pro	Asp	Ser
His	Val												
65					70					75			
80													
att	ctc	atc	tgt	ttc	gct	att	gac	tcc	ccc	gac	tcg	ctt	gac
aat	gtt		288										
Ile	Leu	Ile	Cys	Phe	Ala	Ile	Asp	Ser	Pro	Asp	Ser	Leu	Asp
Asn	Val												
				85					90				
95													
caa	gaa	aag	tgg	att	tcc	gag	gtc	ctt	cac	ttc	tgt	cag	ggc
ctc	ccc		336										
Gln	Glu	Lys	Trp	Ile	Ser	Glu	Val	Leu	His	Phe	Cys	Gln	Gly
Leu	Pro												
			100					105					110
atc	gtc	ctc	gtg	gcg	tgc	aag	aag	gat	ctc	cgc	gac	gat	ggc
aag	act		384										
Ile	Val	Leu	Val	Ala	Cys	Lys	Lys	Asp	Leu	Arg	Asp	Asp	Gly
Lys	Thr												
		115					120					125	
atc	cag	gac	ctt	gcc	agg	atg	aac	cag	agg	cct	gtt	tcc	cgg
gcc	gag		432										
Ile	Gln	Asp	Leu	Ala	Arg	Met	Asn	Gln	Arg	Pro	Val	Ser	Arg
Ala	Glu												
	130					135					140		
ggc	atg	gcc	gtt	gcc	caa	aag	att	ggg	gag	cag	ggc	tac	gtc
gag	tgc		480										
Gly	Met	Ala	Val	Ala	Gln	Lys	Ile	Gly	Ala	Gln	Gly	Tyr	Val
Glu	Cys												
145					150						155		
160													
agt	gcc	aag	acg	ggc	gag	ggc	gtc	agg	gaa	gtg	ttc	cag	act
gct	acc		528										
Ser	Ala	Lys	Thr	Gly	Glu	Gly	Val	Arg	Glu	Val	Phe	Gln	Thr
Ala	Thr												
			165								170		
175													
agg	cat	gct	ctc	cag	gtg	ggc	ctc	ttg	ccg	ctg	cat	cgt	aca
cca	ccg		576										
Arg	His	Ala	Leu	Gln	Val	Gly	Leu	Leu	Pro	Leu	His	Arg	Thr
Pro	Pro												
			180					185					190

0070110

ctg acc gtg cgc aga gca aaa agt cca agt ctg gca gag gga
aga agg 624
Leu Thr val Arg Arg Ala Lys Ser Pro Ser Leu Ala Glu Gly
Arg Arg 195 200 205
gtt gtg tgg tgc ttt agg gct cta taa
651
val val Trp Cys Phe Arg Ala Leu
210 215

<210> 245

<211> 216

<212> PRT

<213> Cryptococcus neoformans var. neoformans B-3501A

<400> 245

Met Ser Gly Glu Ile Arg Arg Lys Leu val Ile val Gly Asp
Gly Ala

1 5 10

15

Cys Gly Lys Thr Cys Leu Leu Ile val Phe Ser Lys Gly Met
Phe Pro

20 25 30

Glu val Tyr val Pro Thr val Phe Glu Asn Tyr val Ala Asp
val Glu

35 40 45

val Asp Gly Lys Lys val Glu Leu Ala Leu Trp Asp Thr Ala
Gly Gln

50 55 60

Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Ser
His val

65 70 75

80

Ile Leu Ile Cys Phe Ala Ile Asp Ser Pro Asp Ser Leu Asp
Asn val

85 90

95

Gln Glu Lys Trp Ile Ser Glu val Leu His Phe Cys Gln Gly
Leu Pro

100 105 110

Ile val Leu val Ala Cys Lys Lys Asp Leu Arg Asp Asp Gly
Lys Thr

115 120 125

0070110

Ile Gln Asp Leu Ala Arg Met Asn Gln Arg Pro Val Ser Arg
Ala Glu
130 135 140

Gly Met Ala Val Ala Gln Lys Ile Gly Ala Gln Gly Tyr Val
Glu Cys
145 150 155
160

Ser Ala Lys Thr Gly Glu Gly Val Arg Glu Val Phe Gln Thr
Ala Thr
165 170

175
Arg His Ala Leu Gln Val Gly Leu Leu Pro Leu His Arg Thr
Pro Pro
180 185 190

Leu Thr Val Arg Arg Ala Lys Ser Pro Ser Leu Ala Glu Gly
Arg Arg
195 200 205

Val Val Trp Cys Phe Arg Ala Leu
210 215

<210> 246

<211> 594

<212> DNA

<213> Cryptococcus neoformans var. neoformans B-3501A

<220>

<221> CDS

<222> (1)..(594)

<400> 246

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ggt gct 48
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Gly Ala
1 5 10

15
tgt ggt aag aca tgt ctt ctt atc gtg ttc agc aag ggc atg
ttc ccc 96
Cys Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Gly Met
Phe Pro

20 25 30
gag gtg tac gtg ccc acc gtc ttt gaa aac tat gtc gcc gat
gta gag 144

0070110

Glu	Val	Tyr	Val	Pro	Thr	Val	Phe	Glu	Asn	Tyr	Val	Ala	Asp
Val	Glu												
		35					40					45	
gtg	gac	ggg	aag	aag	gtc	gag	ctg	gcg	ttg	tgg	gat	act	gct
gga	cag		192										
Val	Asp	Gly	Lys	Lys	Val	Glu	Leu	Ala	Leu	Trp	Asp	Thr	Ala
Gly	Gln												
	50					55					60		
gag	gac	tat	gac	cga	ctc	cga	cct	ctt	tct	tac	ccc	gac	tcc
cat	gtc		240										
Glu	Asp	Tyr	Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Pro	Asp	Ser
His	Val												
65					70					75			
80													
att	ctc	atc	tgt	ttc	gct	att	gac	tcc	ccc	gac	tcg	ctt	gac
aat	gtt		288										
Ile	Leu	Ile	Cys	Phe	Ala	Ile	Asp	Ser	Pro	Asp	Ser	Leu	Asp
Asn	Val												
				85					90				
95													
caa	gaa	aag	tgg	att	tcc	gag	gtc	ctt	cac	ttc	tgt	cag	ggc
ctc	ccc		336										
Gln	Glu	Lys	Trp	Ile	Ser	Glu	Val	Leu	His	Phe	Cys	Gln	Gly
Leu	Pro												
				100				105					110
atc	gtc	ctc	gtg	gcg	tgc	aag	aag	gat	ctc	cgc	gac	gat	ggc
aag	act		384										
Ile	Val	Leu	Val	Ala	Cys	Lys	Lys	Asp	Leu	Arg	Asp	Asp	Gly
Lys	Thr												
		115				120					125		
atc	cag	gac	ctt	gcc	agg	atg	aac	cag	agg	cct	gtt	tcc	cgg
gcc	gag		432										
Ile	Gln	Asp	Leu	Ala	Arg	Met	Asn	Gln	Arg	Pro	Val	Ser	Arg
Ala	Glu												
	130					135					140		
ggc	atg	gcc	gtt	gcc	caa	aag	att	ggg	gcg	cag	ggc	tac	gtc
gag	tgc		480										
Gly	Met	Ala	Val	Ala	Gln	Lys	Ile	Gly	Ala	Gln	Gly	Tyr	Val
Glu	Cys												
145					150					155			
160													
agt	gcc	aag	acg	ggc	gag	ggc	gtc	agg	gaa	gtg	ttc	cag	act
gct	acc		528										
Ser	Ala	Lys	Thr	Gly	Glu	Gly	Val	Arg	Glu	Val	Phe	Gln	Thr
Ala	Thr												

165

170

0070110

175
 agg cat gct ctc cag agc aaa aag tcc aag tct ggc aga ggg
 aag aag 576
 Arg His Ala Leu Gln Ser Lys Lys Ser Lys Ser Gly Arg Gly
 Lys Lys
 180 185 190

ggg tgt gtg gtg ctt tag
 594
 Gly Cys Val Val Leu
 195

<210> 247
 <211> 197
 <212> PRT
 <213> Cryptococcus neoformans var. neoformans B-3501A

<400> 247
 Met Ser Gly Glu Ile Arg Arg Lys Leu Val Ile Val Gly Asp
 Gly Ala
 1 5 10
 15
 Cys Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Gly Met
 Phe Pro
 20 25 30

Glu Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp
 Val Glu
 35 40 45

Val Asp Gly Lys Lys Val Glu Leu Ala Leu Trp Asp Thr Ala
 Gly Gln
 50 55 60

Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Ser
 His Val
 65 70 75

80
 Ile Leu Ile Cys Phe Ala Ile Asp Ser Pro Asp Ser Leu Asp
 Asn Val
 85 90

95
 Gln Glu Lys Trp Ile Ser Glu Val Leu His Phe Cys Gln Gly
 Leu Pro
 100 105 110

Ile Val Leu Val Ala Cys Lys Lys Asp Leu Arg Asp Asp Gly
 Lys Thr

0070110
120

115

125

Ile Gln Asp Leu Ala Arg Met Asn Gln Arg Pro Val Ser Arg
Ala Glu
130 135 140

Gly Met Ala Val Ala Gln Lys Ile Gly Ala Gln Gly Tyr Val
Glu Cys
145 150 155
160

Ser Ala Lys Thr Gly Glu Gly Val Arg Glu Val Phe Gln Thr
Ala Thr
165 170

175
Arg His Ala Leu Gln Ser Lys Lys Ser Lys Ser Gly Arg Gly
Lys Lys
180 185 190

Gly Cys Val Val Leu
195

<210> 248

<211> 693

<212> DNA

<213> Cryptococcus neoformans var. neoformans B-3501A

<220>

<221> CDS

<222> (1)..(693)

<400> 248

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ttc ttg 48

Met Ser Val Ser Ala Gly Ile Arg Asn Thr Ser Lys Arg Ser
Phe Leu
1 5 10
15

atc gag ata act gac gcc gca cag acg tac gac agc gca cct
atg aga 96

Ile Glu Ile Thr Asp Ala Ala Gln Thr Tyr Asp Ser Ala Pro
Met Arg
20 25 30

cgg ccg gat atc aaa aag aaa ctc gtt gtg gtt ggc gat ggt
ggc tgt 144

Arg Pro Asp Ile Lys Lys Lys Leu Val Val Val Gly Asp Gly
Gly Cys
35 40 45

ggc aag act tgt cta tta acg gtc tac gcc gag aat cgt ttt

0070110

cct	gaa		192											
Gly	Lys	Thr	Cys	Leu	Leu	Thr	Val	Tyr	Ala	Glu	Asn	Arg	Phe	
Pro	Glu													
	50					55					60			
gaa	tac	gtc	cca	acc	gtt	ttt	gag	aat	ctc	atg	acc	acc	gtt	
cct	tcc		240											
Glu	Tyr	Val	Pro	Thr	Val	Phe	Glu	Asn	Leu	Met	Thr	Thr	Val	
Pro	Ser													
65					70					75				
80														
cct	acc	gac	cct	tcc	aaa	atc	att	gaa	ctg	gct	ctt	tgg	gat	
aca	gca		288											
Pro	Thr	Asp	Pro	Ser	Lys	Ile	Ile	Glu	Leu	Ala	Leu	Trp	Asp	
Thr	Ala													
			85						90					
95														
gga	cag	gag	gac	ttt	gac	aga	ctg	cga	cca	tta	agt	tat	aac	
gac	aca		336											
Gly	Gln	Glu	Asp	Phe	Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Asn	
Asp	Thr													
			100					105					110	
gat	gtg	atc	cta	ata	gta	ttc	gcc	tgc	aac	cat	cga	cca	agc	
ttg	ttg		384											
Asp	Val	Ile	Leu	Ile	Val	Phe	Ala	Cys	Asn	His	Arg	Pro	Ser	
Leu	Leu													
		115				120						125		
aac	gtg	caa	gat	aag	tgg	tat	cca	gaa	atg	gcc	cat	ttc	tgc	
gaa	aat		432											
Asn	Val	Gln	Asp	Lys	Trp	Tyr	Pro	Glu	Met	Ala	His	Phe	Cys	
Glu	Asn													
130						135					140			
gtc	ccc	ctc	atc	tta	gtt	tgc	act	aaa	acc	gat	ctt	cgc	gaa	
gac	caa		480											
Val	Pro	Leu	Ile	Leu	Val	Cys	Thr	Lys	Thr	Asp	Leu	Arg	Glu	
Asp	Gln													
145					150					155				
160														
cag	acc	gtc	tcc	ctt	atg	gct	gct	caa	ggc	aca	aca	cca	atc	
agt	gct		528											
Gln	Thr	Val	Ser	Leu	Met	Ala	Ala	Gln	Gly	Thr	Thr	Pro	Ile	
Ser	Ala													
			165							170				
175														
tca	gaa	ggc	gaa	cga	ata	gca	aag	gag	att	gga	gcc	aga	cgg	
tat	atg		576											
Ser	Glu	Gly	Glu	Arg	Ile	Ala	Lys	Glu	Ile	Gly	Ala	Arg	Arg	
Tyr	Met													

0070110

180

185

190

gag tgc tca gca aag gct ggg atg ggt gta gga gag gtg ttc
gac gcc 624
Glu Cys Ser Ala Lys Ala Gly Met Gly Val Gly Glu Val Phe
Asp Ala
195 200 205
gct att aga gaa agc atg aag aag gga ggg tta aaa aag atg
aag ggc 672
Ala Ile Arg Glu Ser Met Lys Lys Gly Gly Leu Lys Lys Met
Lys Gly
210 215 220
agg aag tgc gtg gtt ctg tag
693
Arg Lys Cys Val Val Leu
225 230

<210> 249

<211> 230

<212> PRT

<213> Cryptococcus neoformans var. neoformans B-3501A

<400> 249

Met Ser Val Ser Ala Gly Ile Arg Asn Thr Ser Lys Arg Ser
Phe Leu
1 5 10
15
Ile Glu Ile Thr Asp Ala Ala Gln Thr Tyr Asp Ser Ala Pro
Met Arg
20 25 30
Arg Pro Asp Ile Lys Lys Lys Leu Val Val Val Gly Asp Gly
Gly Cys
35 40 45
Gly Lys Thr Cys Leu Leu Thr Val Tyr Ala Glu Asn Arg Phe
Pro Glu
50 55 60
Glu Tyr Val Pro Thr Val Phe Glu Asn Leu Met Thr Thr Val
Pro Ser
65 70 75
80
Pro Thr Asp Pro Ser Lys Ile Ile Glu Leu Ala Leu Trp Asp
Thr Ala
85 90
95
Gly Gln Glu Asp Phe Asp Arg Leu Arg Pro Leu Ser Tyr Asn
Seite 390

0070110

Asp	Thr													
		100					105					110		
Asp	Val	Ile	Leu	Ile	Val	Phe	Ala	Cys	Asn	His	Arg	Pro	Ser	
Leu	Leu	115					120					125		
Asn	Val	Gln	Asp	Lys	Trp	Tyr	Pro	Glu	Met	Ala	His	Phe	Cys	
Glu	Asn	130					135					140		
Val	Pro	Leu	Ile	Leu	Val	Cys	Thr	Lys	Thr	Asp	Leu	Arg	Glu	
Asp	Gln	145					150					155		
		160												
Gln	Thr	Val	Ser	Leu	Met	Ala	Ala	Gln	Gly	Thr	Thr	Pro	Ile	
Ser	Ala	165					170							
		175												
Ser	Glu	Gly	Glu	Arg	Ile	Ala	Lys	Glu	Ile	Gly	Ala	Arg	Arg	
Tyr	Met	180					185					190		
Glu	Cys	Ser	Ala	Lys	Ala	Gly	Met	Gly	Val	Gly	Glu	Val	Phe	
Asp	Ala	195					200					205		
Ala	Ile	Arg	Glu	Ser	Met	Lys	Lys	Gly	Gly	Leu	Lys	Lys	Met	
Lys	Gly	210					215					220		
Arg	Lys	Cys	Val	Val	Leu									
225					230									

<210> 250

<211> 675

<212> DNA

<213> Cryptococcus neoformans var. neoformans B-3501A

<220>

<221> CDS

<222> (1) . . (675)

<400> 250

atg tct tca agt ccc aac aac cgt gca att agg aga aag ctc
gtc atc 48
Met Ser Ser Ser Pro Asn Asn Arg Ala Ile Arg Arg Lys Leu
val ile

0070110

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

0070110

Asp	His	Ala	Thr	Gly	Gln	Arg	Ile	Ala	Asp	Ser	Ile	Gly	Ala
Lys	Gly												
145					150					155			
160													
tac	ttt	gaa	act	tca	gct	ttg	caa	aac	cga	aat	gtc	gat	gcc
gta	ttt			528									
Tyr	Phe	Glu	Thr	Ser	Ala	Leu	Gln	Asn	Arg	Asn	Val	Asp	Ala
Val	Phe												
				165						170			
175													
gaa	gct	gct	acg	cga	gca	gca	gtc	tta	gtc	agg	gat	gcg	ggg
cat	ggc			576									
Glu	Ala	Ala	Thr	Arg	Ala	Ala	Val	Leu	Val	Arg	Asp	Ala	Gly
His	Gly												
			180					185					190
ggg	gtg	ggt	gcc	ccg	aat	ggg	agc	ttt	gat	gcg	gga	gga	cgg
aaa	gat			624									
Gly	Val	Gly	Ala	Pro	Asn	Gly	Ser	Phe	Asp	Ala	Gly	Gly	Arg
Lys	Asp												
		195				200					205		
tgg	ggg	agg	gag	aag	gag	gag	aaa	aaa	ttt	ggg	tgt	tgt	gtc
att	gct			672									
Trp	Gly	Arg	Glu	Lys	Glu	Glu	Lys	Lys	Phe	Gly	Cys	Cys	Val
Ile	Ala												
	210					215					220		
taa													
			675										

<210> 251

<211> 224

<212> PRT

<213> Cryptococcus neoformans var. neoformans B-3501A

<400> 251

Met	Ser	Ser	Ser	Pro	Asn	Asn	Arg	Ala	Ile	Arg	Arg	Lys	Leu
Val	Ile												
1				5					10				
15													
Val	Gly	Asp	Gly	Ala	Ala	Gly	Lys	Thr	Ser	Leu	Leu	Asn	Val
Phe	Ala												
			20				25					30	
Val	Gly	His	Phe	Ser	Glu	Ser	Tyr	Glu	Pro	Thr	Val	Phe	Asp
Asn	Tyr												

0070110

35

40

45

Val Thr Glu Ile Glu Leu Asp Gly Lys Pro Val Gln Leu Ala
 Leu Trp
 50 55 60

Asp Thr Ala Gly Gln Glu Glu Tyr Glu Arg Leu Arg Pro Leu
 Ser Tyr
 65 70 75
 80

Ser Lys Ala His Val Ile Leu Ile Ala Phe Ala Val Asp Thr
 Pro Asp
 85 90

95
 Ser Leu Glu Asn Val Thr Gln Lys Trp Ile Glu Glu Val Arg
 Ser Ile
 100 105 110

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

Arg Asp Lys Ala Val Ala Asn Gly Thr Tyr Ser Pro Glu Arg
 Phe Thr
 130 135 140

Asp His Ala Thr Gly Gln Arg Ile Ala Asp Ser Ile Gly Ala
 Lys Gly
 145 150 155
 160

Tyr Phe Glu Thr Ser Ala Leu Gln Asn Arg Asn Val Asp Ala
 Val Phe
 165 170

175
 Glu Ala Ala Thr Arg Ala Ala Val Leu Val Arg Asp Ala Gly
 His Gly
 180 185 190

Gly Val Gly Ala Pro Asn Gly Ser Phe Asp Ala Gly Gly Arg
 Lys Asp
 195 200 205

Trp Gly Arg Glu Lys Glu Glu Lys Lys Phe Gly Cys Cys Val
 Ile Ala
 210 215 220

<210> 252

0070110

<211> 597

<212> DNA

<213> Cryptococcus neoformans var. neoformans B-3501A

<220>

<221> CDS

<222> (1)..(597)

<400> 252

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ggt gcc          48
Met Ala Thr Thr Arg Asn Ile Lys Cys Val Val Val Gly Asp
Gly Ala
  1              5              10
15
ggt gga aag aca tgt ctt ctt atc agt tac aca acc aat gct
ttc ccg          96
Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Ala
Phe Pro
      20              25              30
gga gaa tat gtc cca aca gtt ttt gac aac tac tcg agc cag
gtg att          144
Gly Glu Tyr Val Pro Thr Val Phe Asp Asn Tyr Ser Ser Gln
Val Ile
      35              40              45
gta gat ggt atg acg gta tct ttg gga ctg tgg gat aca gcc
ggt caa          192
Val Asp Gly Met Thr Val Ser Leu Gly Leu Trp Asp Thr Ala
Gly Gln
      50              55              60
gaa gat tac gac cgt ctt cga cct tta tcc tac ccg cag act
gat gtc          240
Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr
Asp Val
  65              70              75
80
ttc ctt ctc tgc ttt tcc gtc gtc tcc cct gct tcc ttt gaa
aac gtc          288
Phe Leu Leu Cys Phe Ser Val Val Ser Pro Ala Ser Phe Glu
Asn Val
      85              90
95
cga acc aaa tgg tat cct gaa att cag cac cat tca cca gga
act cct          336
Arg Thr Lys Trp Tyr Pro Glu Ile Gln His His Ser Pro Gly
Thr Pro
      100              105              110
```

0070110

```

atc atc ctt gtc ggt acc aag ctc gat ttg aga gac gac cct
atg cag      384
ile ile Leu val Gly Thr Lys Leu Asp Leu Arg Asp Asp Pro
Met Gln
      115      120      125
att gaa aaa ctg agg gaa cga agg caa gcg ccc att gga tat
tct caa      432
ile Glu Lys Leu Arg Glu Arg Arg Gln Ala Pro ile Gly Tyr
Ser Gln
      130      135      140
ggc tca tct atg gcg aat gac atc aag gct gcc aag tac ctc
gaa tgc      480
Gly Ser Ser Met Ala Asn Asp ile Lys Ala Ala Lys Tyr Leu
Glu Cys
145      150      155
      160
tcg gct ttg acg cag aag aac ctc aag tct gtt ttt gac gag
gct atc      528
Ser Ala Leu Thr Gln Lys Asn Leu Lys Ser val Phe Asp Glu
Ala ile
      165      170
175
cgg acg gtc ctc aac cct aat cga cga gcg ggc aag gcg aag
aag agc      576
Arg Thr val Leu Asn Pro Asn Arg Arg Ala Gly Lys Ala Lys
Lys Ser
      180      185      190

agc gga tgt ctt gtc atg taa
      597
Ser Gly Cys Leu val Met
      195

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<210> 253

<211> 198

<212> PRT

<213> Cryptococcus neoformans var. neoformans B-3501A

<400> 253

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Met Ala Thr Thr Arg Asn ile Lys Cys val val val Gly Asp
Gly Ala
1      5      10
15
Val Gly Lys Thr Cys Leu Leu ile Ser Tyr Thr Thr Asn Ala
Phe Pro
      20      25      30

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0070110

Gly Glu Tyr Val Pro Thr Val Phe Asp Asn Tyr Ser Ser Gln
 Val Ile
 35 40 45

Val Asp Gly Met Thr Val Ser Leu Gly Leu Trp Asp Thr Ala
 Gly Gln
 50 55 60

Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr
 Asp Val
 65 70 75

Phe Leu Leu Cys Phe Ser Val Val Ser Pro Ala Ser Phe Glu
 Asn Val
 80 85 90

95
 Arg Thr Lys Trp Tyr Pro Glu Ile Gln His His Ser Pro Gly
 Thr Pro
 100 105 110

Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Pro
 Met Gln
 115 120 125

Ile Glu Lys Leu Arg Glu Arg Arg Gln Ala Pro Ile Gly Tyr
 Ser Gln
 130 135 140

Gly Ser Ser Met Ala Asn Asp Ile Lys Ala Ala Lys Tyr Leu
 Glu Cys
 145 150 155

160
 Ser Ala Leu Thr Gln Lys Asn Leu Lys Ser Val Phe Asp Glu
 Ala Ile
 165 170

175
 Arg Thr Val Leu Asn Pro Asn Arg Arg Ala Gly Lys Ala Lys
 Lys Ser
 180 185 190

Ser Gly Cys Leu Val Met
 195

<210> 254

<211> 585

<212> DNA

<213> Strongylocentrotus purpuratus

0070110

<220>

<221> CDS

<222> (1)..(585)

<400> 254

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atg cag gct att aaa tgt gtc gtc gtc ggg gac gga gct gtg
gga aag                               48
Met Gln Ala Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys                               10
1
15
aca tgt ctt ctc atc agt tac acc aca aat gca ttt ccc gga
gaa tac                               96
Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Ala Phe Pro Gly
Glu Tyr
20                               25                               30
att ccc act gta ttt gac aat tat tct gcc aat gtg atg gtt
gat ggc                               144
Ile Pro Thr Val Phe Asp Asn Tyr Ser Ala Asn Val Met Val
Asp Gly
35                               40                               45
cgc cca gtg aac tta gga ttg tgg gat aca gct ggt cag gaa
gat tat                               192
Arg Pro Val Asn Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu
Asp Tyr
50                               55                               60
gac aga ctg aga cca ctc tct tat cca cag aca gat gta ttt
ctg att                               240
Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
Leu Ile
65                               70                               75
80
tgc ttc tcg ttg gtg agc cct gct tcc ttt gac aac gtt cgt
gct aaa                               288
Cys Phe Ser Leu Val Ser Pro Ala Ser Phe Asp Asn Val Arg
Ala Lys
85                               90
95
tgg tat cca gaa gtg agt cat cat tgt cct aac aca ccc atc
atc ttg                               336
Trp Tyr Pro Glu Val Ser His His Cys Pro Asn Thr Pro Ile
Ile Leu
100                               105                               110
gtt gga acc aag ttg gat ctt cgg gat gat aga gag acg att
gac aag                               384
Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Arg Glu Thr Ile
Asp Lys

```

0070110

		115					120					125		
ctt	gct	cag	agg	aac	cta	tca	cca	gtc	aca	tac	cct	aag	ggt	
tta	tta		432											
Leu	Ala	Gln	Arg	Asn	Leu	Ser	Pro	Val	Thr	Tyr	Pro	Lys	Gly	
Leu	Leu													
	130					135					140			
atg	atg	aag	gag	att	agt	ggg	gtg	aag	tat	ttg	gaa	tgc	tct	
gct	ctc		480											
Met	Met	Lys	Glu	Ile	Ser	Gly	Val	Lys	Tyr	Leu	Glu	Cys	Ser	
Ala	Leu													
145					150						155			
	160													
act	cag	aaa	gga	ctc	aag	aca	gtg	ttt	gat	gaa	gct	att	cga	
gct	gta		528											
Thr	Gln	Lys	Gly	Leu	Lys	Thr	Val	Phe	Asp	Glu	Ala	Ile	Arg	
Ala	Val													
			165						170					
175														
ctc	tgc	cca	gat	cag	aac	aag	aag	aag	aag	aag	ggc	aac	aag	
tgt	aga		576											
Leu	Cys	Pro	Asp	Gln	Asn	Lys	Lys	Lys	Lys	Lys	Gly	Asn	Lys	
Cys	Arg													
			180					185					190	
tta	att	tga												
			585											
Leu	Ile													

<210> 255
 <211> 194
 <212> PRT
 <213> Strongylocentrotus purpuratus

<400> 255
 Met Gln Ala Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
 Gly Lys
 1 5 10
 15
 Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Ala Phe Pro Gly
 Glu Tyr
 20 25 30
 Ile Pro Thr Val Phe Asp Asn Tyr Ser Ala Asn Val Met Val
 Asp Gly
 35 40 45
 Arg Pro Val Asn Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu
 Seite 399

0070110

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

<210> 256
 <211> 576
 <212> DNA
 <213> Tribolium castaneum

<220>
 <221> CDS
 <222> (1)..(576)

<400> 256

0070110

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

0070110

Glu Lys
130 135 140
tta gct aaa gaa tta aaa gcg gtc aaa tat gtc gag tgt tcg
gct tta 480
Leu Ala Lys Glu Leu Lys Ala Val Lys Tyr Val Glu Cys Ser
Ala Leu
145 150 155
160
acg caa aaa ggt ctg aaa aat gtt ttc gat gaa gct att cta
gcc gcg 528
Thr Gln Lys Gly Leu Lys Asn Val Phe Asp Glu Ala Ile Leu
Ala Ala
165 170
175
ttg gaa cca cca gaa cca att aaa cgt aaa aag tgt gtt att
ttg 573
Leu Glu Pro Pro Glu Pro Ile Lys Arg Lys Lys Cys Val Ile
Leu
180 185 190
taa
576

<210> 257
<211> 191
<212> PRT
<213> Tribolium castaneum

<400> 257
Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys
1 5 10
15
Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe Pro Ser
Glu Tyr
20 25 30
Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val Met Ile
Gly Gly 35 40 45
Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu
Asp Tyr 50 55 60
Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
Seite 402

0070110

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

<210> 258
 <211> 588
 <212> DNA
 <213> Tribolium castaneum

<220>
 <221> CDS
 <222> (1)..(588)

<400> 258
 atg tca tcg ggt cgc ccc att aag tgt gta gtt gta ggt gac
 ggc act 48
 Met Ser Ser Gly Arg Pro Ile Lys Cys Val Val Val Gly Asp
 Gly Thr
 1 5 10
 15

0070110

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

0070110

160

tcg gct ttg acg caa agg ggg ctc aag cag gtg ttt gat gaa
gcg gtc
Ser Ala Leu Thr Gln Arg Gly Leu Lys Gln Val Phe Asp Glu
Ala Val

165

170

175

agg gct gtc cta aga ccc gaa ccg cag aaa agg cga caa cgc
aag tgt
Arg Ala Val Leu Arg Pro Glu Pro Gln Lys Arg Arg Gln Arg
Lys Cys

180

185

190

ctt ctt atg taa
588

Leu Leu Met
195

<210> 259

<211> 195

<212> PRT

<213> Tribolium castaneum

<400> 259

Met Ser Ser Gly Arg Pro Ile Lys Cys Val Val Val Gly Asp
Gly Thr

1 5 10

15

Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Thr Asp Ser
Phe Pro

20

25

30

Gly Glu Tyr Val Pro Thr Val Phe Asp Asn Tyr Ser Ala Pro
Met Val

35

40

45

Val Asp Gly Ile Ser Val Ser Leu Gly Leu Trp Asp Thr Ala
Gly Gln

50

55

60

Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr
Asp Val

65

70

75

80

Phe Leu Ile Cys Phe Ser Val Ala Ser Pro Ser Ser Phe Glu
Asn Val

85

90

0070110

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95
Thr Ser Lys Trp Tyr Pro Glu Ile Lys His His Cys Pro Asp
Ala Pro
100 105 110

Met Ile Leu Val Gly Thr Lys Ile Asp Leu Arg Asp Asp Arg
Glu Thr
115 120 125

Leu Thr Ala Leu Ala Asp Gln Gly Leu Ser Pro Ile Lys Arg
Glu Gln
130 135 140

Gly Gln Lys Leu Ala Asn Lys Ile Arg Ala Val Lys Tyr Met
Glu Cys
145 150 155
160
Ser Ala Leu Thr Gln Arg Gly Leu Lys Gln Val Phe Asp Glu
Ala Val
165 170

175
Arg Ala Val Leu Arg Pro Glu Pro Gln Lys Arg Arg Gln Arg
Lys Cys
180 185 190

Leu Leu Met
195

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<210> 260
<211> 579
<212> DNA
<213> Tribolium castaneum

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<220>
<221> CDS
<222> (1)..(579)

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<400> 260
atg cag gcg ata aag tgc gtg gtt gtg ggt gat ggt gct gtt
ggt aaa 48
Met Gln Ala Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys
1 5 10
15
aca tgc ctc ctc atc agt tac aca aca aac gcc ttc cca ggc
gaa tat 96
Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Ala Phe Pro Gly
Glu Tyr

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0070110

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

0070110

Ala Val
165 170
175
ctt tgc ccc gta atg caa gtc aaa cct aaa cgt aaa tgt gtg
tta ttg 576
Leu Cys Pro Val Met Gln Val Lys Pro Lys Arg Lys Cys Val
Leu Leu
180 185 190
taa
579

<210> 261
<211> 192
<212> PRT
<213> Tribolium castaneum

<400> 261
Met Gln Ala Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys
1 5 10
15
Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Ala Phe Pro Gly
Glu Tyr
20 25 30
Ile Pro Thr Val Phe Asp Asn Tyr Ser Ala Asn Val Met Val
Asp Gly
35 40 45
Lys Pro Ile Asn Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu
Asp Tyr
50 55 60
Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
Leu Ile
65 70 75
80
Cys Phe Ser Leu Val Asn Pro Ala Ser Phe Glu Asn Val Arg
Ala Lys
85 90
95
Trp Tyr Pro Glu Val Arg His His Cys Pro Asn Thr Pro Ile
Ile Leu
100 105 110

0070110

Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Arg	Gly	Thr	Ile
Glu	Lys												
		115					120					125	
Leu	Lys	Asp	Lys	Lys	Leu	Thr	Pro	Ile	Thr	Tyr	Pro	Gln	Gly
Leu	Ala												
	130					135					140		
Met	Ala	Lys	Glu	Ile	Ser	Ala	Val	Lys	Tyr	Leu	Glu	Cys	Ser
Ala	Leu												
145					150					155			
160													
Thr	Gln	Lys	Gly	Leu	Lys	Thr	Val	Phe	Asp	Glu	Ala	Ile	Arg
Ala	Val												
				165					170				
175													
Leu	Cys	Pro	Val	Met	Gln	Val	Lys	Pro	Lys	Arg	Lys	Cys	Val
Leu	Leu												
			180					185					190

<210> 262
 <211> 588
 <212> DNA
 <213> Tribolium castaneum

<220>
 <221> CDS
 <222> (1)..(588)

<400> 262
 atg acg acg cct tcg aga gaa gaa aac ggc cct ccg ggc gaa
 aac gtt 48
 Met Thr Thr Pro Ser Arg Glu Glu Asn Gly Pro Pro Gly Glu
 Asn Val 5 10
 15
 aaa gtc aca gtg gtc gga gac ggt gta gtg gga aaa acc tgt
 ctc ttg 96
 Lys Val Thr Val Val Gly Asp Gly Val Val Gly Lys Thr Cys
 Leu Leu 20 25 30
 att tca tac acg aag gac gag ttc ccc gaa gaa tat gtt ccc
 aca gta 144
 Ile Ser Tyr Thr Lys Asp Glu Phe Pro Glu Glu Tyr Val Pro
 Thr Val 35 40 45
 ttc gaa cat tac ggg caa gac atc acc gtc gac gac gtc aaa
 Seite 409

0070110

tac	aac		192											
Phe	Glu	His	Tyr	Gly	Gln	Asp	Ile	Thr	Val	Asp	Asp	Val	Lys	
Tyr	Asn													
	50					55				60				
atg	act	ctc	tgg	gac	act	gcc	ggc	caa	gaa	gac	tac	gaa	aga	
ctg	cgc		240											
Met	Thr	Leu	Trp	Asp	Thr	Ala	Gly	Gln	Glu	Asp	Tyr	Glu	Arg	
Leu	Arg													
65					70					75				
80														
ccc	ctg	gct	tac	ccc	aat	acg	aaa	tgc	ttc	ctt	gta	tgt	ttc	
tcc	gtc		288											
Pro	Leu	Ala	Tyr	Pro	Asn	Thr	Lys	Cys	Phe	Leu	Val	Cys	Phe	
Ser	Val													
				85					90					
95														
gac	gct	tct	ata	ccg	tct	tac	gag	aac	gtt	ata	att	aaa	tgg	
gtg	cca		336											
Asp	Ala	Ser	Ile	Pro	Ser	Tyr	Glu	Asn	Val	Ile	Ile	Lys	Trp	
Val	Pro													
			100				105						110	
gaa	gtc	agg	cac	cac	aat	cca	cac	acg	ccc	ata	gtt	cta	gta	
gcc	act		384											
Glu	Val	Arg	His	His	Asn	Pro	His	Thr	Pro	Ile	Val	Leu	Val	
Ala	Thr													
		115				120						125		
aaa	ata	gat	ctc	aga	gat	gat	cca	agt	gtc	cac	tgt	tac	tca	
acc	cag		432											
Lys	Ile	Asp	Leu	Arg	Asp	Asp	Pro	Ser	Val	His	Cys	Tyr	Ser	
Thr	Gln													
	130				135					140				
gac	ggc	aaa	aaa	tta	aaa	agg	aaa	gtc	aaa	gcc	gaa	gga	tac	
gtc	gaa		480											
Asp	Gly	Lys	Lys	Leu	Lys	Arg	Lys	Val	Lys	Ala	Glu	Gly	Tyr	
Val	Glu													
145					150					155				
160														
tgc	tct	gcc	aaa	acc	agg	gaa	gga	ctg	aag	gaa	gtc	ttc	gaa	
gag	gcg		528											
Cys	Ser	Ala	Lys	Thr	Arg	Glu	Gly	Leu	Lys	Glu	Val	Phe	Glu	
Glu	Ala													
				165						170				
175														
ata	cga	gcg	tac	aag	aag	acc	aaa	atc	aaa	gcg	aga	caa	gtc	
aac	tgt		576											
Ile	Arg	Ala	Tyr	Lys	Lys	Thr	Lys	Ile	Lys	Ala	Arg	Gln	Val	
Asn	Cys													

0070110

180

185

190

gct ttg tta taa
588

Ala Leu Leu
195

<210> 263

<211> 195

<212> PRT

<213> Tribolium castaneum

<400> 263

Met Thr Thr Pro Ser Arg Glu Glu Asn Gly Pro Pro Gly Glu
Asn Val

1 5 10

15

Lys Val Thr Val Val Gly Asp Gly Val Val Gly Lys Thr Cys
Leu Leu

20

25

30

Ile Ser Tyr Thr Lys Asp Glu Phe Pro Glu Glu Tyr Val Pro
Thr Val

35

40

45

Phe Glu His Tyr Gly Gln Asp Ile Thr Val Asp Asp Val Lys
Tyr Asn

50

55

60

Met Thr Leu Trp Asp Thr Ala Gly Gln Glu Asp Tyr Glu Arg
Leu Arg

65

70

75

80

Pro Leu Ala Tyr Pro Asn Thr Lys Cys Phe Leu Val Cys Phe
Ser Val

85

90

95

Asp Ala Ser Ile Pro Ser Tyr Glu Asn Val Ile Ile Lys Trp
Val Pro

100

105

110

Glu Val Arg His His Asn Pro His Thr Pro Ile Val Leu Val
Ala Thr

115

120

125

Lys Ile Asp Leu Arg Asp Asp Pro Ser Val His Cys Tyr Ser
Thr Gln

130

135

140

0070110

Asp Gly Lys Lys Leu Lys Arg Lys Val Lys Ala Glu Gly Tyr
Val Glu
145 150 155
160
Cys Ser Ala Lys Thr Arg Glu Gly Leu Lys Glu Val Phe Glu
Glu Ala
165 170
175
Ile Arg Ala Tyr Lys Lys Thr Lys Ile Lys Ala Arg Gln Val
Asn Cys
180 185 190

Ala Leu Leu
195

<210> 264
<211> 600
<212> DNA
<213> Tribolium castaneum

<220>
<221> CDS
<222> (1)..(600)

<400> 264
atg tct agc aag aaa att gtt gta att ggt gac ggt gcg tgt
ggg aaa 48
Met Ser Ser Lys Lys Ile Val Val Ile Gly Asp Gly Ala Cys
Gly Lys
1 5 10
15
acg agt ctg tca gtt gcc ttc agc caa aac gaa ttt ccg gaa
acc cac 96
Thr Ser Leu Ser Val Ala Phe Ser Gln Asn Glu Phe Pro Glu
Thr His
20 25 30
gtt ccg aca att tac gat acg tac acc aaa aca ata act gtc
gat gag 144
Val Pro Thr Ile Tyr Asp Thr Tyr Thr Lys Thr Ile Thr Val
Asp Glu
35 40 45
caa aat gtg gaa ctc aca atc tgg gat acc gcc ggt gag gaa
gat tac 192
Gln Asn Val Glu Leu Thr Ile Trp Asp Thr Ala Gly Glu Glu
Asp Tyr
50 55 60
gac aga ctt agg cct ttg tcg tac aca aag gca agt gtt ata
Seite 412

atc	gtg			240									
Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Thr	Lys	Ala	Ser	Val	Ile
Ile	Val												
65					70					75			
80													
tgc	ttt	aca	att	gac	aat	ccg	gtt	tct	ttg	aaa	aac	gtt	aag
aca	aga			288									
Cys	Phe	Thr	Ile	Asp	Asn	Pro	Val	Ser	Leu	Lys	Asn	Val	Lys
Thr	Arg												
				85					90				
95													
tgg	gcg	ccc	gaa	gtc	aaa	cat	ttc	tgc	cgg	aaa	gtc	ccc	ata
ctc	cta			336									
Trp	Ala	Pro	Glu	Val	Lys	His	Phe	Cys	Arg	Lys	Val	Pro	Ile
Leu	Leu												
			100					105					110
gtc	ggt	aat	aaa	tta	gat	ttg	cga	aat	aat	aaa	gaa	aca	gtt
gaa	gat			384									
Val	Gly	Asn	Lys	Leu	Asp	Leu	Arg	Asn	Asn	Lys	Glu	Thr	Val
Glu	Asp												
		115					120					125	
ctg	aaa	aga	aat	aac	atg	caa	ccc	gtt	aag	ttc	gaa	caa	ggt
ttg	aag			432									
Leu	Lys	Arg	Asn	Asn	Met	Gln	Pro	Val	Lys	Phe	Glu	Gln	Gly
Leu	Lys						135				140		
gtg	tcg	aag	aaa	att	ggg	gca	cgg	aag	tac	atc	gaa	tgc	tcg
gct	aaa			480									
Val	Ser	Lys	Lys	Ile	Gly	Ala	Arg	Lys	Tyr	Ile	Glu	Cys	Ser
Ala	Lys												
145					150					155			
160													
cat	atg	gtg	ggg	gtg	cag	gac	gtt	ttc	aga	aat	gct	gcc	aga
att	gcc			528									
His	Met	Val	Gly	Val	Gln	Asp	Val	Phe	Arg	Asn	Ala	Ala	Arg
Ile	Ala												
				165					170				
175													
ttg	aag	acg	cca	cag	aaa	aaa	gga	ctc	aag	cgg	tta	tgt	cga
tgt	gtc			576									
Leu	Lys	Thr	Pro	Gln	Lys	Lys	Gly	Leu	Lys	Arg	Leu	Cys	Arg
Cys	Val												
			180					185					190
cgt	gtt	ccg	tgc	aaa	act	acc	tga						
			600										
Arg	Val	Pro	Cys	Lys	Thr	Thr							

<210> 265

<211> 199

<212> PRT

<213> Tribolium castaneum

<400> 265

Met Ser Ser Lys Lys Ile Val Val Ile Gly Asp Gly Ala Cys
Gly Lys

1 5 10

15

Thr Ser Leu Ser Val Ala Phe Ser Gln Asn Glu Phe Pro Glu
Thr His

20 25 30

Val Pro Thr Ile Tyr Asp Thr Tyr Thr Lys Thr Ile Thr Val
Asp Glu

35 40 45

Gln Asn Val Glu Leu Thr Ile Trp Asp Thr Ala Gly Glu Glu
Asp Tyr

50 55 60

Asp Arg Leu Arg Pro Leu Ser Tyr Thr Lys Ala Ser Val Ile
Ile Val

65 70 75

80

Cys Phe Thr Ile Asp Asn Pro Val Ser Leu Lys Asn Val Lys
Thr Arg

85 90

95

Trp Ala Pro Glu Val Lys His Phe Cys Arg Lys Val Pro Ile
Leu Leu

100 105 110

Val Gly Asn Lys Leu Asp Leu Arg Asn Asn Lys Glu Thr Val
Glu Asp

115 120 125

Leu Lys Arg Asn Asn Met Gln Pro Val Lys Phe Glu Gln Gly
Leu Lys

130 135 140

Val Ser Lys Lys Ile Gly Ala Arg Lys Tyr Ile Glu Cys Ser
Ala Lys

145 150 155

160

0070110

His Met Val Gly Val Gln Asp Val Phe Arg Asn Ala Ala Arg
Ile Ala

165

170

175

Leu Lys Thr Pro Gln Lys Lys Gly Leu Lys Arg Leu Cys Arg
Cys Val

180

185

190

Arg Val Pro Cys Lys Thr Thr
195

<210> 266

<211> 579

<212> DNA

<213> Tribolium castaneum

<220>

<221> CDS

<222> (1)..(579)

<400> 266

atg tcc tcc gtc caa aag aag ctc atc att gtg ggc gac ggc
gcc tgc 48

Met Ser Ser Val Gln Lys Lys Leu Ile Ile Val Gly Asp Gly
Ala Cys

1

5

10

15

ggc aag acc tgc ctc ctg atc gcc ttc gcc aaa gac atc ttc
aac tcc 96

Gly Lys Thr Cys Leu Leu Ile Ala Phe Ala Lys Asp Ile Phe
Asn Ser

20

25

30

gaa tac cgc ccc aca gtt ttc gaa aac tac gtc gcc gat gtg
gag ctg 144

Glu Tyr Arg Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Val
Glu Leu

35

40

45

gac gcc ctc acc gtg gag ctc tcc ctc tgg gac acc tca ggc
cag gag 192

Asp Ala Leu Thr Val Glu Leu Ser Leu Trp Asp Thr Ser Gly
Gln Glu

50

55

60

gac tac gac cgc ctt aga ccc atc cag tac ccc gaa acg gac
gtg gtg 240

Asp Tyr Asp Arg Leu Arg Pro Ile Gln Tyr Pro Glu Thr Asp
Val Val

65

70

75

80

0070110

ctg ata tgc ttc tcg gtg atg tgg agg gac tct ctt ttg aac
 gtc tcg 288
 Leu Ile Cys Phe Ser Val Met Trp Arg Asp Ser Leu Leu Asn
 Val Ser

85

90

95

gca aag tgg tgc ccc gaa gtc agg cat ttc tgc ccc aac gtc
 cct ata 336
 Ala Lys Trp Cys Pro Glu Val Arg His Phe Cys Pro Asn Val
 Pro Ile

100

105

110

ctg ctc ata ggg acg aag aac gat ctc agg gag gac aag gag
 gag ttg 384
 Leu Leu Ile Gly Thr Lys Asn Asp Leu Arg Glu Asp Lys Glu
 Glu Leu

115

120

125

gag aag ttg aaa atg atg aag aaa tcc ccg gtt acg agg gac
 gaa gcc 432
 Glu Lys Leu Lys Met Met Lys Lys Ser Pro Val Thr Arg Asp
 Glu Ala

130

135

140

gag gcc atg gcg agg acc att ggg gcc gtt tgc tac atc gaa
 tgt tca 480
 Glu Ala Met Ala Arg Thr Ile Gly Ala Val Cys Tyr Ile Glu
 Cys Ser

145

150

155

160

gcc aag acc aaa tat aac gtg cag gag gtg ttc aag gag gcc
 gcg agg 528
 Ala Lys Thr Lys Tyr Asn Val Gln Glu Val Phe Lys Glu Ala
 Ala Arg

165

170

175

gcc aca atc gca aaa cga aag aag cgg aaa caa cgc tgt gta
 cta att 576
 Ala Thr Ile Ala Lys Arg Lys Lys Arg Lys Gln Arg Cys Val
 Leu Ile

180

185

190

tga

579

<210> 267

<211> 192

<212> PRT

0070110

<213> Tribolium castaneum

<400> 267

Met Ser Ser Val Gln Lys Lys Leu Ile Ile Val Gly Asp Gly
Ala Cys

1 5 10

15

Gly Lys Thr Cys Leu Leu Ile Ala Phe Ala Lys Asp Ile Phe
Asn Ser

20 25 30

Glu Tyr Arg Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Val
Glu Leu

35 40 45

Asp Ala Leu Thr Val Glu Leu Ser Leu Trp Asp Thr Ser Gly
Gln Glu
50 55 60

Asp Tyr Asp Arg Leu Arg Pro Ile Gln Tyr Pro Glu Thr Asp
Val Val
65 70 75

80

Leu Ile Cys Phe Ser Val Met Trp Arg Asp Ser Leu Leu Asn
Val Ser

85 90

95

Ala Lys Trp Cys Pro Glu Val Arg His Phe Cys Pro Asn Val
Pro Ile

100 105 110

Leu Leu Ile Gly Thr Lys Asn Asp Leu Arg Glu Asp Lys Glu
Glu Leu

115 120 125

Glu Lys Leu Lys Met Met Lys Lys Ser Pro Val Thr Arg Asp
Glu Ala
130 135 140

Glu Ala Met Ala Arg Thr Ile Gly Ala Val Cys Tyr Ile Glu
Cys Ser
145 150 155

160

Ala Lys Thr Lys Tyr Asn Val Gln Glu Val Phe Lys Glu Ala
Ala Arg

165 170

175

Ala Thr Ile Ala Lys Arg Lys Lys Arg Lys Gln Arg Cys Val

0070110

Leu Ile

180

185

190

<210> 268

<211> 579

<212> DNA

<213> Tribolium castaneum

<220>

<221> CDS

<222> (1)..(579)

<400> 268

atg gca gcc atc agg aag aag ctg gtg att gtg ggc gac ggc

gcc tgc 48

Met Ala Ala Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly

Ala Cys

1

5

10

15

ggc aag acc tgc ctc ctc atc gtc ttc agc aag gac cag ttc

ccc gag 96

Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Asp Gln Phe

Pro Glu

20

25

30

gtg tac gtg ccc acc gtg ttc gag aac tat gtg gcc gac atc

gag gtg 144

Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Ile

Glu Val

35

40

45

gac ggc aag cag gtg gag ctc gcg ctg tgg gac acg gcc ggc

cag gag 192

Asp Gly Lys Gln Val Glu Leu Ala Leu Trp Asp Thr Ala Gly

Gln Glu

50

55

60

gac tac gac cgg ctg cgg ccg ctg tcc tac ccc gac acc gac

gtc atc 240

Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Thr Asp

Val Ile

65

70

75

80

ctc atg tgc ttc tcg gtc gac tcg ccc gac tcg ctc gag aac

atc ccc 288

Leu Met Cys Phe Ser Val Asp Ser Pro Asp Ser Leu Glu Asn

Ile Pro

85

90

95

0070110

gag aag tgg acg ccc gag gtg aag cac ttc tgc ccc aac gtg
 ccc atc 336
 Glu Lys Trp Thr Pro Glu Val Lys His Phe Cys Pro Asn Val
 Pro Ile
 100 105 110

atc ctc gtc ggc aac aag aag gac ctg cgc aac gac ccc aac
 acc atc 384
 Ile Leu Val Gly Asn Lys Lys Asp Leu Arg Asn Asp Pro Asn
 Thr Ile
 115 120 125

aac gag ctc aag aag atg aag cag gag ccg gtc aag ccg cag
 gac ggg 432
 Asn Glu Leu Lys Lys Met Lys Gln Glu Pro Val Lys Pro Gln
 Asp Gly
 130 135 140

cgc gcc atg gcc gag aag atc aac gcc ttc gcc tac ctg gag
 tgc tcc 480
 Arg Ala Met Ala Glu Lys Ile Asn Ala Phe Ala Tyr Leu Glu
 Cys Ser
 145 150 155

160
 gcc aag agc aag gag ggc gtg agg gag gtg ttc gag aac gcc
 acg cgc 528
 Ala Lys Ser Lys Glu Gly Val Arg Glu Val Phe Glu Asn Ala
 Thr Arg
 165 170

175
 gcg gcc tta caa gtc aag aag aag aag aag cac cgc tgc gcc
 ctg ctg 576
 Ala Ala Leu Gln Val Lys Lys Lys Lys Lys His Arg Cys Ala
 Leu Leu
 180 185 190

tga
 579

<210> 269
 <211> 192
 <212> PRT
 <213> Tribolium castaneum

<400> 269
 Met Ala Ala Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly
 Ala Cys
 1 5 10

0070110

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

<210> 270
<211> 591

0070110

<212> DNA

<213> *Cryptococcus neoformans* var

<220>

<221> CDS

<222> (1)..(591)

<400> 270

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atg cag act atc aaa tgt gtc gtc gtg ggt gac ggc gct gtt
gga aag          48
Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys
1          5          10
15
aca tgt ctg ttg ata tcg tat acg aca aac aag ttt cca tcg
gaa tat          96
Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe Pro Ser
Glu Tyr
20          25          30
gtg cct acg gtg ttt gat aac tat gcg gtg act gtt atg att
ggc gat          144
Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val Met Ile
Gly Asp
35          40          45
agc cct tat acg ctc ggg cta ttc gac acc gct ggc caa gaa
gac tat          192
Ser Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu
Asp Tyr
50          55          60
gac cgc ctt cgc ccg cta tct tac ccg cag aca gac gtc ttc
ctc atc          240
Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
Leu Ile
65          70          75
80
tgc ttc tcc atc gcg tcc ccc gct tcg ttc gag aat gtc cgt
gaa aaa          288
Cys Phe Ser Ile Ala Ser Pro Ala Ser Phe Glu Asn Val Arg
Glu Lys
85          90
95
tgg ttt cac gaa atc tca cac cac tgc cct ggg gcg cct tgc
ctg ata          336
Trp Phe His Glu Ile Ser His His Cys Pro Gly Ala Pro Cys
Leu Ile
100          105          110
gtg ggg acg cag gtc gat ttg agg gat gat cca aag cag gtg
```

0070110

```

gag agg      384
Val Gly Thr Gln Val Asp Leu Arg Asp Asp Pro Lys Gln Val
Glu Arg
      115      120      125
atg atg gcg agt cag agg ggg ggc agg gcg gcg ggg ttg ata
acg caa      432
Met Met Ala Ser Gln Arg Gly Gly Arg Ala Ala Gly Leu Ile
Thr Gln
      130      135      140
gag caa ggg gag agg ttg gcg aga gaa ttg ggg ggg aga aag
tat gta      480
Glu Gln Gly Glu Arg Leu Ala Arg Glu Leu Gly Gly Arg Lys
Tyr Val
145      150      155
      160
gag tgt tcg gcg ttg acg caa aag ggg ttg aag aat gtg ttt
gat gag      528
Glu Cys Ser Ala Leu Thr Gln Lys Gly Leu Lys Asn Val Phe
Asp Glu
      165      170
175
gca atc gta gcg gct ctt gaa ccg cca gtc gtg aaa aag acc
aaa aag      576
Ala Ile Val Ala Ala Leu Glu Pro Pro Val Val Lys Lys Thr
Lys Lys
      180      185      190

tgc ttg atc ctc tag
      591
Cys Leu Ile Leu
      195

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<210> 271

<211> 196

<212> PRT

<213> *Cryptococcus neoformans* var

<400> 271

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Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys
1      5      10
15
Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe Pro Ser
Glu Tyr
      20      25      30

Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val Met Ile
Gly Asp

```

0070110
40

35

45

Ser Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu
Asp Tyr
50 55 60

Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
Leu Ile
65 70 75

80
Cys Phe Ser Ile Ala Ser Pro Ala Ser Phe Glu Asn Val Arg
Glu Lys
85 90

95
Trp Phe His Glu Ile Ser His His Cys Pro Gly Ala Pro Cys
Leu Ile
100 105 110

Val Gly Thr Gln Val Asp Leu Arg Asp Asp Pro Lys Gln Val
Glu Arg
115 120 125

Met Met Ala Ser Gln Arg Gly Gly Arg Ala Ala Gly Leu Ile
Thr Gln
130 135 140

Glu Gln Gly Glu Arg Leu Ala Arg Glu Leu Gly Gly Arg Lys
Tyr Val
145 150 155

160
Glu Cys Ser Ala Leu Thr Gln Lys Gly Leu Lys Asn Val Phe
Asp Glu
165 170

175
Ala Ile Val Ala Ala Leu Glu Pro Pro Val Val Lys Lys Thr
Lys Lys
180 185 190

Cys Leu Ile Leu
195

<210> 272
<211> 582
<212> DNA
<213> Cryptococcus neoformans var

<220>
<221> CDS

<222> (1)..(582)

<400> 272

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atg cag aca atc aag tgt gtc gta gtc gga gac ggt gcc gtt
gga aag      48
Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys
  1              5              10
15
acc tgc ttg ctc atc tcg tac act acc aac aag ttc cca tcc
gag tat      96
Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe Pro Ser
Glu Tyr
      20              25              30
gtt cca acc gtc ttt gac aac tac gcc gtc agt gta acc atc
ggt gac      144
Val Pro Thr Val Phe Asp Asn Tyr Ala Val Ser Val Thr Ile
Gly Asp
      35              40              45
gac cca tac act ctt gga ctc ttt gat act gcc ggt caa gaa
gat tat      192
Asp Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu
Asp Tyr
  50              55              60
gac cgt ctc cgt cca ctc tca tac cct caa act gat gtc ttc
ctc gtt      240
Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
Leu Val
  65              70              75
80
tgc ttc tct gta aca tct ccc gcg tca ttc gaa aac gtc cgc
gaa aag      288
Cys Phe Ser Val Thr Ser Pro Ala Ser Phe Glu Asn Val Arg
Glu Lys
      85              90
95
tgg ttt ccc gaa atc gcc cat cat tgc cca ggc gtc ccc gca
ctt att      336
Trp Phe Pro Glu Ile Ala His His Cys Pro Gly Val Pro Ala
Leu Ile
      100              105              110
gtc ggt acc caa gtg gac ttg agg gat gac ccc gcc cag atg
gag aag      384
Val Gly Thr Gln Val Asp Leu Arg Asp Asp Pro Ala Gln Met
Glu Lys
  115              120              125
ttg gga agg cag aag atg aag ccg att aca cag gat atg gga

```

0070110

gaa aga 432
 Leu Gly Arg Gln Lys Met Lys Pro Ile Thr Gln Asp Met Gly
 Glu Arg 130 135 140
 ttg gcg aga gaa ttg gga gcg gtg aaa tat gtg gag tgt tcg
 gcg ttg 480
 Leu Ala Arg Glu Leu Gly Ala Val Lys Tyr Val Glu Cys Ser
 Ala Leu 145 150 155
 160
 acg cag agg gga ttg aag aac gtt ttt gac gag gca atc gtg
 gcg gca 528
 Thr Gln Arg Gly Leu Lys Asn Val Phe Asp Glu Ala Ile Val
 Ala Ala 165 170
 175
 tta gaa ccc cct atg gcg act aag aaa aag tct aaa aag tgc
 ctc atc 576
 Leu Glu Pro Pro Met Ala Thr Lys Lys Lys Ser Lys Lys Cys
 Leu Ile 180 185 190
 ctt tga 582
 Leu

<210> 273
 <211> 193
 <212> PRT
 <213> Cryptococcus neoformans var

<400> 273
 Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
 Gly Lys 1 5 10
 15
 Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe Pro Ser
 Glu Tyr 20 25 30
 Val Pro Thr Val Phe Asp Asn Tyr Ala Val Ser Val Thr Ile
 Gly Asp 35 40 45
 Asp Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu
 Asp Tyr 50 55 60

0070110

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

<210> 274
<211> 600
<212> DNA
<213> Epichloe festucae

<220>
<221> CDS
<222> (1)..(600)

<400> 274
atg gct caa ccc ggt gtt cag tct cta aag tgt gtc gtg acc
ggc gac 48

0070110

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

0070110

tac ctg 480
 Glu Gln Ala Leu Ala Cys Ala Arg Glu Ile Lys Ala Tyr Lys
 Tyr Leu
 145 150 155

160
 gag tgc tct gcc ctc acc cag cgc aac ctg aag agc gta ttc
 gac gag 528
 Glu Cys Ser Ala Leu Thr Gln Arg Asn Leu Lys Ser Val Phe
 Asp Glu
 165 170

175
 gct att cgt gct gtg ttg aac ccc cgt cca caa ccg tcc aag
 cac aag 576
 Ala Ile Arg Ala Val Leu Asn Pro Arg Pro Gln Pro Ser Lys
 His Lys
 180 185 190

aag tcc aag tgt tca atc ctg taa
 600
 Lys Ser Lys Cys Ser Ile Leu
 195

<210> 275
 <211> 199
 <212> PRT
 <213> Epichloe festucae

<400> 275
 Met Ala Gln Pro Gly Val Gln Ser Leu Lys Cys Val Val Thr
 Gly Asp
 1 5 10
 15
 Gly Ala Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Thr
 Asn Ala
 20 25 30

Phe Pro Gly Glu Tyr Ile Pro Thr Val Phe Asp Asn Tyr Ser
 Ala Ser
 35 40 45

Val Met Val Asp Gly Lys Pro Ile Ser Leu Gly Leu Trp Asp
 Thr Ala
 50 55 60

Gly Gln Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro
 Gln Thr
 65 70 75
 80

0070110

Asp Val Phe Leu Ile Cys Phe Ser Ile Val Ser Pro Pro Ser
Phe Asp

85

90

95

Asn Val Lys Ala Lys Trp Tyr Pro Glu Ile Asp His His Ala
Pro Asn

100

105

110

Ile Pro Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Glu
Asp Ala

115

120

125

Ala Thr Leu Asp Ser Leu Arg Gln Lys Arg Met Glu Pro Val
Ser Tyr
130 135 140

Glu Gln Ala Leu Ala Cys Ala Arg Glu Ile Lys Ala Tyr Lys
Tyr Leu
145 150 155

160

Glu Cys Ser Ala Leu Thr Gln Arg Asn Leu Lys Ser Val Phe
Asp Glu

165

170

175

Ala Ile Arg Ala Val Leu Asn Pro Arg Pro Gln Pro Ser Lys
His Lys

180

185

190

Lys Ser Lys Cys Ser Ile Leu
195

<210> 276

<211> 579

<212> DNA

<213> *Maconellicoccus hirsutus*

<220>

<221> CDS

<222> (1)..(579)

<400> 276

atg gcc gcg att cgt aag aag ttg gtt atc gta gga gac ggc
gct tgc 48
Met Ala Ala Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly
Ala Cys

1

5

10

15

ggt aaa act tgc ctg ttg ata gta ttc agc aaa gat caa ttt

0070110

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ccc gaa          96
Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Asp Gln Phe
Pro Glu

          20          25          30
gtc tac gtt ccg act gtt ttc gaa aat tac gtc gcc gac atc
gaa gtt          144
Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Ile
Glu Val

          35          40          45
gac ggc aaa caa gtt gaa ttg gcc tta tgg gat acg gct ggc
caa gaa          192
Asp Gly Lys Gln Val Glu Leu Ala Leu Trp Asp Thr Ala Gly
Gln Glu

          50          55          60
gac tat gat cgt ctg cgt ccg tta tcg tat ccg gat acc gat
gtt att          240
Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Thr Asp
Val Ile

          65          70          75
          80
ctg atg tgt ttc tca atc gat tcg ccg gat tca ttg gag aac
ata ccg          288
Leu Met Cys Phe Ser Ile Asp Ser Pro Asp Ser Leu Glu Asn
Ile Pro

          85          90
95
gaa aaa tgg act cca gaa gtg aag cat ttc tgt cca aac gta
ccg att          336
Glu Lys Trp Thr Pro Glu Val Lys His Phe Cys Pro Asn Val
Pro Ile

          100          105          110
att tta gtt ggt aac aaa aaa gac ttg agg aat gat ccg gtc
act att          384
Ile Leu Val Gly Asn Lys Lys Asp Leu Arg Asn Asp Pro Val
Thr Ile

          115          120          125
aaa gag ttg gct aaa atg aaa caa gaa cca gtt aag cct gaa
gaa ggt          432
Lys Glu Leu Ala Lys Met Lys Gln Glu Pro Val Lys Pro Glu
Glu Gly

          130          135          140
cgt gcc atg gcc gaa aag atc aac gct ttt gct tat ttg gaa
tgt tcg          480
Arg Ala Met Ala Glu Lys Ile Asn Ala Phe Ala Tyr Leu Glu
Cys Ser

          145          150          155
          160

```

0070110

gct aaa agt aaa gaa ggt gtt agg gaa gtg ttt gaa aca tct
 act aga 528
 Ala Lys Ser Lys Glu Gly Val Arg Glu Val Phe Glu Thr Ser
 Thr Arg

165

170

175

gcc gct tta caa gtg aaa aag aag aag aag ggg cgt tgt cgt
 ttg tta 576
 Ala Ala Leu Gln Val Lys Lys Lys Lys Lys Gly Arg Cys Arg
 Leu Leu

180

185

190

taa

579

<210> 277

<211> 192

<212> PRT

<213> *Maconeillicoccus hirsutus*

<400> 277

Met Ala Ala Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly
 Ala Cys

1

5

10

15

Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Asp Gln Phe
 Pro Glu

20

25

30

Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Ile
 Glu Val

35

40

45

Asp Gly Lys Gln Val Glu Leu Ala Leu Trp Asp Thr Ala Gly
 Gln Glu

50

55

60

Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Thr Asp
 Val Ile

65

70

75

80

Leu Met Cys Phe Ser Ile Asp Ser Pro Asp Ser Leu Glu Asn
 Ile Pro

85

90

95

0070110

Glu	Lys	Trp	Thr	Pro	Glu	Val	Lys	His	Phe	Cys	Pro	Asn	Val
Pro	Ile												
			100					105					110
Ile	Leu	Val	Gly	Asn	Lys	Lys	Asp	Leu	Arg	Asn	Asp	Pro	Val
Thr	Ile												
		115					120					125	
Lys	Glu	Leu	Ala	Lys	Met	Lys	Gln	Glu	Pro	Val	Lys	Pro	Glu
Glu	Gly												
	130					135					140		
Arg	Ala	Met	Ala	Glu	Lys	Ile	Asn	Ala	Phe	Ala	Tyr	Leu	Glu
Cys	Ser												
145					150					155			
160													
Ala	Lys	Ser	Lys	Glu	Gly	Val	Arg	Glu	Val	Phe	Glu	Thr	Ser
Thr	Arg												
			165						170				
175													
Ala	Ala	Leu	Gln	Val	Lys	Lys	Lys	Lys	Lys	Gly	Arg	Cys	Arg
Leu	Leu												
		180						185					190

<210> 278
 <211> 693
 <212> DNA
 <213> Oryza sativa subsp

<220>
 <221> CDS
 <222> (1)..(693)

<400> 278
 atg gcg tcc agc gcc tcc cgg ttc atc aag tgc gtc acg gtg
 ggc gac 48
 Met Ala Ser Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val
 Gly Asp
 1 5 10
 15
 ggc gcc gtg ggc aag acc tgc atg ctc atc tgc tac acc agc
 aac aag 96
 Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser
 Asn Lys
 20 25 30
 ttc ccc act gac tac ata cca acg gtg ttc gac aat ttc agc
 gca aac 144

0070110

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

0070110

aag gta gta atc cag cct cca act aag cag agg gaa aag aag
 aaa aag 576
 Lys Val Val Ile Gln Pro Pro Thr Lys Gln Arg Glu Lys Lys
 Lys Lys
 180 185 190

aaa tca cga caa gga tgc tct atg atg atg tat ccc gtc tat
 ata aaa 624
 Lys Ser Arg Gln Gly Cys Ser Met Met Met Tyr Pro Val Tyr
 Ile Lys
 195 200 205

gaa cct agc ttt tgt ggt ggt gga aca tgt tcc gtg gaa gga
 aaa tgt 672
 Glu Pro Ser Phe Cys Gly Gly Gly Thr Cys Ser Val Glu Gly
 Lys Cys
 210 215 220

cat gct tca aat cct gat tga
 693
 His Ala Ser Asn Pro Asp
 225 230

<210> 279
 <211> 230
 <212> PRT
 <213> Oryza sativa subsp

<400> 279
 Met Ala Ser Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val
 Gly Asp
 1 5 10
 15
 Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser
 Asn Lys
 20 25 30

Phe Pro Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser
 Ala Asn
 35 40 45

Val Val Val Asp Ser Thr Thr Val Asn Leu Gly Leu Trp Asp
 Thr Ala
 50 55 60

Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg
 Gly Ala
 65 70 75
 80

Asp Val Phe Val Leu Ala Phe Ser Leu Val Ser Arg Ala Ser
 Seite 434

Tyr	Glu												
				85					90				
95													
Asn	Ile	Met	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Gln	His	Tyr	Ala
Pro	Gly												
			100					105					110
Val	Pro	Ile	Val	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Glu
Asp	Lys												
		115					120					125	
His	Tyr	Leu	Leu	Asp	His	Pro	Gly	Met	Ile	Pro	Val	Thr	Thr
Ala	Gln												
	130					135					140		
Gly	Glu	Glu	Leu	Arg	Lys	Gln	Ile	Gly	Ala	Ala	Tyr	Tyr	Ile
Glu	Cys												
145					150					155			
160													
Ser	Ser	Lys	Thr	Gln	Gln	Asn	Val	Lys	Gly	Val	Phe	Asp	Ala
Ala	Ile												
				165					170				
175													
Lys	Val	Val	Ile	Gln	Pro	Pro	Thr	Lys	Gln	Arg	Glu	Lys	Lys
Lys	Lys												
		180						185					190
Lys	Ser	Arg	Gln	Gly	Cys	Ser	Met	Met	Met	Tyr	Pro	Val	Tyr
Ile	Lys												
		195					200					205	
Glu	Pro	Ser	Phe	Cys	Gly	Gly	Gly	Thr	Cys	Ser	Val	Glu	Gly
Lys	Cys												
	210					215					220		
His	Ala	Ser	Asn	Pro	Asp								
225					230								

<220>
<221> CDS
<222> (1)..(582)

Seite 435

0070110

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

0070110

130	135	140
tac atc gaa tgc agc tca aag aca cag cag aat gta aaa gct		
gtg ttt	480	
Tyr Ile Glu Cys Ser Ser Lys Thr Gln Gln Asn Val Lys Ala		
Val Phe		
145	150	155
160		
gat gct gcc atc aag ctg caa ggg tgt cat gtc cag aag aag		
gct agt	528	
Asp Ala Ala Ile Lys Leu Gln Gly Cys His Val Gln Lys Lys		
Ala Ser		
	165	170
175		
atg ctt caa gtg aac aag agg ggt tct ttg atg agc aga gca		
gag gaa	576	
Met Leu Gln Val Asn Lys Arg Gly Ser Leu Met Ser Arg Ala		
Glu Glu		
	180	185
		190
ggt taa		
	582	
Gly		

<210> 281
 <211> 193
 <212> PRT
 <213> Oryza sativa subsp

<400> 281
Met Ala Ser Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val
Gly Asp
1 5 10
15
Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser
Asn Lys
20 25 30
Phe Pro Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser
Ala Asn
35 40 45
Val Val Val Asp Gly Thr Thr Val Asn Leu Gly Leu Trp Asp
Thr Ala
50 55 60
Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg
Gly Ala

0070110

```

15
ggc gcc gtg ggc aag acc tgc atg ctc atc tgc tac acc agc
aac aag
Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser
Asn Lys
20
ttc ccc act gac tac ata cca acg gtg ttc gac aat ttc agc
gca aac
Phe Pro Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser
Ala Asn
35
gtt gtt gtg gac agc acc acg gtg aat ctg ggc ctc tgg gat
act gct
Val Val Val Asp Ser Thr Thr Val Asn Leu Gly Leu Trp Asp
Thr Ala
50
ggg caa gag gat tac aac cgg ctc agg cct ctg agc tat cgt
ggt gct
Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg
Gly Ala
65
80
gat gtt ttc gtg ctt gcc ttc tct ctt gtg agc cga gct agc
tat gaa
Asp Val Phe Val Leu Ala Phe Ser Leu Val Ser Arg Ala Ser
Tyr Glu
85
90
95
aat att atg aag aag tgg ata ccg gag cta cag cat tat gca
ccc ggc
Asn Ile Met Lys Lys Trp Ile Pro Glu Leu Gln His Tyr Ala
Pro Gly
100
105
110
gtg ccc att gtg ttg gtt ggc aca aaa ttg gat ctc cgt gaa
gac aag
Val Pro Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Glu
Asp Lys
115
120
125
cac tac ttg ttg gac cat cct ggc atg ata cct gtt acc aca
gca cag
His Tyr Leu Leu Asp His Pro Gly Met Ile Pro Val Thr Thr
Ala Gln
130
135
140
ggg gaa gaa ctt cga aaa caa ata ggt gct gct tat tac att
gag tgc
Gly Glu Glu Leu Arg Lys Gln Ile Gly Ala Ala Tyr Tyr Ile
Glu Cys

```

0070110

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145                               150                               155
160
agc tca aag aca caa cag aat gtc aaa ggt gtg ttt gat gct
gct atc                               528
Ser Ser Lys Thr Gln Gln Asn Val Lys Gly Val Phe Asp Ala
Ala Ile

                               165                               170
175
aag gaa cat gtt ccg tgg aag gaa aat gtc atg ctt caa atc
ctg att                               576
Lys Glu His Val Pro Trp Lys Glu Asn Val Met Leu Gln Ile
Leu Ile

                               180                               185                               190
gat cga gat gtc cct tac atg atg caa tgt tct ggg tgc aac
ctc aag                               624
Asp Arg Asp Val Pro Tyr Met Met Gln Cys Ser Gly Cys Asn
Leu Lys

                               195                               200                               205
ctg gca acc ttt gga gtc tga
                               645
Leu Ala Thr Phe Gly Val
210

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<210> 283
 <211> 214
 <212> PRT
 <213> Oryza sativa subsp

<400> 283

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Met Ala Ser Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val
Gly Asp
1                               5                               10
15
Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser
Asn Lys

                               20                               25                               30
Phe Pro Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser
Ala Asn

                               35                               40                               45
Val Val Val Asp Ser Thr Thr Val Asn Leu Gly Leu Trp Asp
Thr Ala
                               50                               55                               60
Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg

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0070110

[illegible]

<210> 284

<211> 579

<212> DNA

<213> Paracoccidioides brasiliensis

<220>

<221> CDS

<222> (1) .. (579)

0070110

<400> 284

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atg gtt gtg gct act atc aaa tgc gtt gtg gtt gga gac ggt
gct gtc
Met Val Val Ala Thr Ile Lys Cys Val Val Val Gly Asp Gly
Ala Val
1 5 10
15
ggc aag aca tgt cta ctg att tcg tac acc acc aac aag ttc
ccc tct
Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe
Pro Ser
20 25 30
gaa tac gtc ccg acc gtc ttc gat aac tat gcg gtt aca gtg
atg atc
Glu Tyr Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val
Met Ile
35 40 45
gga gat gag cca tat acc ctg gga ctc ttc gat acc gca gga
caa gag
Gly Asp Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly
Gln Glu
50 55 60
gat tat gac cgt cta cga cca cta tca tac cct caa acc gat
gtg ttt
Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp
Val Phe
65 70 75
80
ctc gtc tgt ttc tcc gtt aca tcc cca gca tct ttc gag aac
gtc cgt
Leu Val Cys Phe Ser Val Thr Ser Pro Ala Ser Phe Glu Asn
Val Arg
85 90
95
gag aaa tgg ttt cct gag gtc cat cac cac tgc cca ggc gtt
ccc tgc
Glu Lys Trp Phe Pro Glu Val His His His Cys Pro Gly Val
Pro Cys
100 105 110
ctg att gta ggc acc caa acc gac ttg cgc gac gac ccc agc
gta cga
Leu Ile Val Gly Thr Gln Thr Asp Leu Arg Asp Asp Pro Ser
Val Arg
115 120 125
gaa aag ttg gcc aag cag aag atg cag ccc gtg cga aaa gag
gac ggt
Glu Lys Leu Ala Lys Gln Lys Met Gln Pro Val Arg Lys Glu

```

0070110

```

Asp Gly
130
gac cgt atg gca aag gat ctg ggt gct gtc aaa tac gtc gag
tgc tcc 480
Asp Arg Met Ala Lys Asp Leu Gly Ala Val Lys Tyr Val Glu
Cys Ser
145 150 155
160
gcg ttg act caa tat aaa ctt aag gac gtg ttc gat gag gca
atc gtc 528
Ala Leu Thr Gln Tyr Lys Leu Lys Asp Val Phe Asp Glu Ala
Ile Val
165 170
175
gct gcg ctg gaa cca gcc cca agt aag aag cct aag tgt gtc
atc ttt 576
Ala Ala Leu Glu Pro Ala Pro Ser Lys Lys Pro Lys Cys Val
Ile Phe
180 185 190
taa
579

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<210> 285
 <211> 192
 <212> PRT
 <213> Paracoccidioides brasiliensis

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<400> 285
Met Val Val Ala Thr Ile Lys Cys Val Val Val Gly Asp Gly
Ala Val
1 5 10
15
Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe
Pro Ser
20 25 30
Glu Tyr Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val
Met Ile
35 40 45
Gly Asp Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly
Gln Glu
50 55 60
Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp
Seite 443

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

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<210> 286
<211> 597
<212> DNA
<213> vitis vinifera
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<220>
<221> CDS
<222> (1) .. (597)

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<400> 286
atg gct tca agt gca tcg aag ttc atc aaa tgt gtg acg gta
gga gat
Met Ala Ser Ser Ala Ser Lys Phe Ile Lys Cys val Thr val
Gly Asp
1 5 10
15
```


0070110

```

ggg gct gtg ggg aag act tgc atg ctt att tgc tac acc agc
aac aag          96
Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser
Asn Lys

          20          25          30
ttt cca tct gac tat ata cca aca gtg ttt gac aac ttc agt
gca aat          144
Phe Pro Ser Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser
Ala Asn

          35          40          45
gtg gta gct gag ggc acc act gtt aac ttg ggc ctc tgg gac
aca gct          192
Val Val Ala Glu Gly Thr Thr Val Asn Leu Gly Leu Trp Asp
Thr Ala

          50          55          60
ggg caa gaa gat tac aat aga tta agg ccc ttg agc tat caa
ggg gca          240
Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Gln
Gly Ala

          65          70          75
          80
gat gtc ttc atc tta gcc ttc tca tta gtg agt cgg gca agc
tac gaa          288
Asp Val Phe Ile Leu Ala Phe Ser Leu Val Ser Arg Ala Ser
Tyr Glu

          85          90
95
aat gta ctt aaa aag tgg att cct gag ctt cag cat ttt gcc
cct gga          336
Asn Val Leu Lys Lys Trp Ile Pro Glu Leu Gln His Phe Ala
Pro Gly

          100          105          110
att cca att gta ctt gtt ggc aca aaa ttg gat ctt cgt gag
gac aaa          384
Ile Pro Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Glu
Asp Lys

          115          120          125
cac tat ttg gct gat cat cct gga ttg gtt cct gtg acc act
gca cag          432
His Tyr Leu Ala Asp His Pro Gly Leu Val Pro Val Thr Thr
Ala Gln

          130          135          140
ggg gag gaa ctc cgc aaa cag att ggt gct gca tat tat att
gaa tgc          480
Gly Glu Glu Leu Arg Lys Gln Ile Gly Ala Ala Tyr Tyr Ile
Glu Cys

          145          150          155

```

0070110

160

agc tca aaa act cag cag aat gtg aaa gct gtc ttt gat gct
gca atc 528
Ser Ser Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala
Ala Ile

165

170

175

aag gta gtt atc aag cca caa cag aaa caa aag gag aag aaa
aaa aaa 576
Lys Val Val Ile Lys Pro Gln Gln Lys Gln Lys Glu Lys Lys
Lys Lys

180

185

190

cgg cat cga gga tgg ctg taa
597
Arg His Arg Gly Trp Leu
195

<210> 287

<211> 198

<212> PRT

<213> Vitis vinifera

<400> 287

Met Ala Ser Ser Ala Ser Lys Phe Ile Lys Cys Val Thr Val
Gly Asp

1 5 10

15

Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser
Asn Lys

20

25

30

Phe Pro Ser Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser
Ala Asn

35

40

45

Val Val Ala Glu Gly Thr Thr Val Asn Leu Gly Leu Trp Asp
Thr Ala
50 55 60

Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Gln
Gly Ala
65 70 75

80

Asp Val Phe Ile Leu Ala Phe Ser Leu Val Ser Arg Ala Ser
Tyr Glu

85

90

95

0070110

Asn	Val	Leu	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Gln	His	Phe	Ala
Pro	Gly												
			100					105					110

Ile	Pro	Ile	Val	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Glu
Asp	Lys												
		115					120					125	

His	Tyr	Leu	Ala	Asp	His	Pro	Gly	Leu	Val	Pro	Val	Thr	Thr
Ala	Gln												
	130					135					140		

Gly	Glu	Glu	Leu	Arg	Lys	Gln	Ile	Gly	Ala	Ala	Tyr	Tyr	Ile
Glu	Cys												
145					150					155			
160													

Ser	Ser	Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala
Ala	Ile												
				165					170				

175													
Lys	Val	Val	Ile	Lys	Pro	Gln	Gln	Lys	Gln	Lys	Glu	Lys	Lys
Lys	Lys												
		180						185					190

Arg	His	Arg	Gly	Trp	Leu								
		195											

<210> 288
 <211> 597
 <212> DNA
 <213> Vitis vinifera

<220>
 <221> CDS
 <222> (1)..(597)

<400> 288													
atg	agt	gct	tca	agg	ttc	att	aag	tgc	gtc	act	gtc	ggg	gac
ggc	gcc			48									
Met	Ser	Ala	Ser	Arg	Phe	Ile	Lys	Cys	Val	Thr	Val	Gly	Asp
Gly	Ala												
1				5					10				
15													
gtc	ggc	aag	act	tgc	atg	ctt	atc	tcc	tac	acc	agc	aac	act
ttc	ccc		96										
Val	Gly	Lys	Thr	Cys	Met	Leu	Ile	Ser	Tyr	Thr	Ser	Asn	Thr
Phe	Pro												
		20						25					30

0070110

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

0070110

165

170

175

ggt ctc cag cca cca aag cag aag aag aga aag aag aga aag

gca cag 576

Val Leu Gln Pro Pro Lys Gln Lys Lys Arg Lys Lys Arg Lys

Ala Gln

180

185

190

aaa gct tgt tct ata ttg tga

597

Lys Ala Cys Ser Ile Leu

195

<210> 289

<211> 198

<212> PRT

<213> vitis vinifera

<400> 289

Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp

Gly Ala

1

5

10

15

Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr

Phe Pro

20

25

30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn

Val Val

35

40

45

Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala

Gly Gln

50

55

60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala

Asp Val

65

70

75

80

Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu

Asn Val

85

90

95

Ala Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Gly

Val Pro

100

105

110

Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys

0070110

Gln	Phe													
		115					120					125		
Phe	Ile	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Thr	Thr	Ala	Gln	
Gly	Glu													
		130				135					140			
Glu	Leu	Arg	Lys	Leu	Ile	Gly	Ala	Pro	Ala	Tyr	Ile	Glu	Cys	
Ser	Ser													
					150					155				
		160												
Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile	
Lys	Val													
				165						170				
		175												
Val	Leu	Gln	Pro	Pro	Lys	Gln	Lys	Lys	Arg	Lys	Lys	Arg	Lys	
Ala	Gln													
			180					185					190	
Lys	Ala	Cys	Ser	Ile	Leu									
		195												

<210> 290
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 <212> DNA
 <213> vitis vinifera

<220>
 <221> CDS
 <222> (1)..(633)

<400> 290													
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gga	gct		48										
Met	Ser	Ala	Ser	Lys	Phe	Ile	Lys	Cys	Val	Thr	Val	Gly	Asp
Gly	Ala												
1				5					10				
15													
gta	ggg	aaa	acc	tgt	atg	cta	att	tgt	tac	aca	agt	aac	aag
ttc	ccc		96										
Val	Gly	Lys	Thr	Cys	Met	Leu	Ile	Cys	Tyr	Thr	Ser	Asn	Lys
Phe	Pro												
			20					25					30
act	gac	tat	ata	cct	aca	gtg	ttt	gac	aat	ttc	agt	gct	aat
gta	gct		144										
Thr	Asp	Tyr	Ile	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn
Val	Ala												
		35					40					45	

0070110

gtg	gat	ggg	agc	att	gtc	aac	ttg	ggt	ctt	tgg	gat	act	gca
ggt	cag		192										
Val	Asp	Gly	Ser	Ile	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala
Gly	Gln												
	50					55					60		
gaa	gac	tat	agc	agg	ttg	agg	cca	ctg	agt	tat	aga	ggt	gca
gac	ata		240										
Glu	Asp	Tyr	Ser	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala
Asp	Ile												
65					70					75			
80													
ttt	ggt	tta	gct	ttt	tca	ttg	atc	agc	agg	gca	agc	tat	gaa
aat	ggt		288										
Phe	Val	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Arg	Ala	Ser	Tyr	Glu
Asn	Val												
			85						90				
95													
ctc	aag	aag	tgg	atg	cct	gaa	ctt	cgg	cga	ttt	gca	ccc	aat
ggt	cca		336										
Leu	Lys	Lys	Trp	Met	Pro	Glu	Leu	Arg	Arg	Phe	Ala	Pro	Asn
Val	Pro												
			100					105				110	
atc	ggt	ctt	ggt	gga	aca	aag	tta	gat	ctt	cgt	gaa	gac	aaa
gga	tat		384										
Ile	Val	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Glu	Asp	Lys
Gly	Tyr												
		115					120					125	
cta	gct	gat	cat	atg	gga	tcc	aat	gtc	ata	aca	tct	gcc	caa
gga	gag		432										
Leu	Ala	Asp	His	Met	Gly	Ser	Asn	Val	Ile	Thr	Ser	Ala	Gln
Gly	Glu												
	130					135					140		
gaa	ctg	agg	aag	cag	att	ggt	gca	gca	gct	tat	att	gag	tgc
agt	tct		480										
Glu	Leu	Arg	Lys	Gln	Ile	Gly	Ala	Ala	Ala	Tyr	Ile	Glu	Cys
Ser	Ser												
145					150					155			
160													
aag	act	caa	cag	aat	gtc	aaa	gcg	ggt	ttt	gat	act	gca	atc
aag	ggt		528										
Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Thr	Ala	Ile
Lys	Val												
			165						170				
175													
ggt	ctc	caa	cct	cca	agg	agg	aag	gag	gtg	gcc	agg	aag	aag
agg	cgc		576										
Val	Leu	Gln	Pro	Pro	Arg	Arg	Lys	Glu	Val	Ala	Arg	Lys	Lys

0070110

Arg Arg
180 185 190
aga agc aca ggg tgc tca att gtg agc att gta tgc gga ggc
tgt gct 624
Arg Ser Thr Gly Cys Ser Ile Val Ser Ile Val Cys Gly Gly
Cys Ala
195 200 205
gca gca taa
633
Ala Ala
210

<210> 291
<211> 210
<212> PRT
<213> vitis vinifera

<400> 291
Met Ser Ala Ser Lys Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10
15
Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser Asn Lys
Phe Pro
20 25 30
Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Ala
35 40 45
Val Asp Gly Ser Ile Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60
Glu Asp Tyr Ser Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Ile
65 70 75
80
Phe Val Leu Ala Phe Ser Leu Ile Ser Arg Ala Ser Tyr Glu
Asn Val
85 90
95
Leu Lys Lys Trp Met Pro Glu Leu Arg Arg Phe Ala Pro Asn
Val Pro
100 105 110
Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Glu Asp Lys
Seite 452

0070110

Gly Tyr
115 120 125
Leu Ala Asp His Met Gly Ser Asn Val Ile Thr Ser Ala Gln
Gly Glu
130 135 140
Glu Leu Arg Lys Gln Ile Gly Ala Ala Ala Tyr Ile Glu Cys
Ser Ser
145 150 155
160
Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Thr Ala Ile
Lys Val
165 170
175
Val Leu Gln Pro Pro Arg Arg Lys Glu Val Ala Arg Lys Lys
Arg Arg
180 185 190
Arg Ser Thr Gly Cys Ser Ile Val Ser Ile Val Cys Gly Gly
Cys Ala
195 200 205
Ala Ala
210

<210> 292
<211> 594
<212> DNA
<213> vitis vinifera

<220>
<221> CDS
<222> (1)..(594)

<220>
<221> misc_feature
<222> (234)..(234)
<223> w i s a o r t

<400> 292
atg agc gcc tct agg ttt ata aag tgc gtt acg gtc ggt gat
ggt gct 48
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10
15
gtc ggc aaa acc tgc atg ctg att tcc tac acc agc aac act

0070110

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

0070110

aaa aca cag cag aac gtg aag gct gtt ttt gat gca gct atc
aag gtg 528
Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Lys Val

165

170

175

gtg ctc cag cca cct aag cag aag aag aag aag aag aag gca
caa aag 576
Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Lys Lys Ala
Gln Lys

180

185

190

acc tgc tct ata ttg tga

594

Thr Cys Ser Ile Leu
195

<210> 293

<211> 197

<212> PRT

<213> Vitis vinifera

<400> 293

Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala

1

5

10

15

Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro

20

25

30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val

35

40

45

Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln

50

55

60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val

65

70

75

80

Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val

85

90

95

Ala Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Gly
Seite 455

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Val	Pro													
			100					105					110	
Ile	Ile	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys	
Gln	Phe													
		115					120				125			
Phe	Val	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Thr	Thr	Ala	Gln	
Gly	Glu													
	130					135					140			
Glu	Leu	Lys	Lys	Val	Ile	Gly	Ala	Pro	Ala	Tyr	Ile	Glu	Cys	
Ser	Ser													
145					150					155				
160														
Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile	
Lys	Val													
				165					170					
175														
Val	Leu	Gln	Pro	Pro	Lys	Gln	Lys	Lys	Lys	Lys	Lys	Lys	Ala	
Gln	Lys													
		180					185						190	
Thr	Cys	Ser	Ile	Leu										
		195												

<210> 294
 <211> 591
 <212> DNA
 <213> Musa acuminata

<220>
 <221> CDS
 <222> (1)..(591)

<400>	294													
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ggt	gcc			48										
Met	Ser	Ala	Ser	Arg	Phe	Ile	Lys	Cys	Val	Thr	Val	Gly	Asp	
Gly	Ala													
1				5					10					
15														
gtc	ggc	aag	act	tgc	atg	ctt	atc	tcc	tac	acc	agc	aac	act	
ttc	ccc			96										
Val	Gly	Lys	Thr	Cys	Met	Leu	Ile	Ser	Tyr	Thr	Ser	Asn	Thr	
Phe	Pro													
			20					25					30	
acg	gat	tat	gtt	cct	acc	gtt	ttt	gac	aat	ttc	agc	gca	aat	

0070110

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

0070110

175
gtg ctt cag cca ccc aag cag aag aag aaa aaa aag caa cag
aaa ggt 576
Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Lys Gln Gln
Lys Gly

180

185

190

tgc tcc ata ttg tga
591
Cys Ser Ile Leu
195

<210> 295

<211> 196

<212> PRT

<213> Musa acuminata

<400> 295

Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala

1 5 10

15

Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro

20

25

30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val

35

40

45

Val Asp Gly Asn Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln

50

55

60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val

65

70

75

80

Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val

85

90

95

Ala Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Gly
Val Pro

100

105

110

Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Glu Gln
Gln Phe

0070110
120

115

125

Phe Ile Asp His Pro Gly Ala Val Pro Ile Ser Thr Ala Gln
Gly Glu
130 135 140

Glu Leu Arg Lys Gln Ile Gly Ala Ala Ser Tyr Ile Glu Cys
Ser Ser
145 150 155
160

Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Lys Val
165 170

175
Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Lys Gln Gln
Lys Gly
180 185 190

Cys Ser Ile Leu
195

<210> 296
<211> 597
<212> DNA
<213> Vitis vinifera

<220>
<221> CDS
<222> (1)..(597)

<400> 296
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ggc gcc 48
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10
15
gtc ggc aag act tgc atg ctt atc tcc tac acc agc aac act
ttc ccc 96
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
20 25 30
acg gat tat gtg cca act gta ttt gac aat ttc agt gca aat
gtt gtg 144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
35 40 45
gtg gat ggg agc act gtt aat cta ggg ttg tgg gat act gca
Seite 459

0070110

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ggt aaa      192
Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Lys      50
gag gat tac aat agg ttg aga cct ttg agc tac cgt ggt gca
gat gtc      240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val      65
      70      75
      80
ttt ctg ctt gct ttc tcc ctc att agc aag gct agc tat gaa
aat gtt      288
Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val      85      90
95
gcc aag aaa tgg att cct gag ttg agg cat tat gca ccc ggt
ggt cca      336
Ala Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Gly
Val Pro      100      105      110

ata att ctt gtc ggg aca aag ctt gat ctt cga gat gat aag
cag ttc      384
Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe      115      120      125
ttc ata gat cac cct ggt gca gtg ccc att acc aca gct cag
gga gag      432
Phe Ile Asp His Pro Gly Ala Val Pro Ile Thr Thr Ala Gln
Gly Glu      130      135      140
gaa ctg aga aag ctg att gga gct cct gct tac att gaa tgt
agt tca      480
Glu Leu Arg Lys Leu Ile Gly Ala Pro Ala Tyr Ile Glu Cys
Ser Ser      145      150      155
      160
aaa aca cag cag aac gtg aag gct gtc ttt gat gcg gcc att
aag gtg      528
Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Lys Val      165      170
175
gtt ctc cag cca cca aag cag aag aag aga aag aag aga aag
gca cag      576
Val Leu Gln Pro Pro Lys Gln Lys Lys Arg Lys Lys Arg Lys
Ala Gln

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0070110

180

185

190

aaa gct tgt tct ata ttg tga

597

Lys Ala Cys Ser Ile Leu

195

<210> 297

<211> 198

<212> PRT

<213> vitis vinifera

<400> 297

Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp

Gly Ala

1

5

10

15

Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr

Phe Pro

20

25

30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn

Val Val

35

40

45

Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala

Gly Lys

50

55

60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala

Asp Val

65

70

75

80

Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu

Asn Val

85

90

95

Ala Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Gly

Val Pro

100

105

110

Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys

Gln Phe

115

120

125

Phe Ile Asp His Pro Gly Ala Val Pro Ile Thr Thr Ala Gln

Gly Glu

130

135

140

0070110

Glu Leu Arg Lys Leu Ile Gly Ala Pro Ala Tyr Ile Glu Cys
Ser Ser
145 150 155
160
Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Lys Val
165 170
175
Val Leu Gln Pro Pro Lys Gln Lys Lys Arg Lys Lys Arg Lys
Ala Gln
180 185 190
Lys Ala Cys Ser Ile Leu
195

<210> 298
<211> 600
<212> DNA
<213> Vitis vinifera

<220>
<221> CDS
<222> (1)..(600)

<400> 298
atg agt aca gta cca agc agg ttc att aag tgc gtg aca gtt
gga gat 48
Met Ser Thr Val Pro Ser Arg Phe Ile Lys Cys Val Thr Val
Gly Asp
1 5 10
15
gga gct gtt ggg aag act tgc ctt ctc atc tcc tac act agc
aac acc 96
Gly Ala Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser
Asn Thr
20 25 30
ttc cca act gac tat gtt cca act gtt ttt gat aat ttc agt
gcc aat 144
Phe Pro Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser
Ala Asn
35 40 45
gtt ttg gct gat ggg cag act att aat ctg ggt ctc tgg gat
act gct 192
Val Leu Ala Asp Gly Gln Thr Ile Asn Leu Gly Leu Trp Asp
Thr Ala
50 55 60

0070110

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ggt caa gaa gac tat aac agg cta agg cct ttg agt tat aga
gga gct      240
Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg
Gly Ala
65      70      75
80
gat gtt ttc ctc ctt gcc ttc tct ctt ata agt agg cct agc
ttt gaa      288
Asp Val Phe Leu Leu Ala Phe Ser Leu Ile Ser Arg Pro Ser
Phe Glu
85      90
95
aac ata tcg aaa aaa aag tgg gta cca gag ctg aga cat tat
gcc cca      336
Asn Ile Ser Lys Lys Lys Trp Val Pro Glu Leu Arg His Tyr
Ala Pro
100      105      110
tca gtg ccc att gtt ctc gtg ggg acc aaa cta gat ttg aga
gaa gat      384
Ser Val Pro Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg
Glu Asp
115      120      125
aag cag ttc cac atg gat tat cca ggg gcg tgt acc att tca
aca gaa      432
Lys Gln Phe His Met Asp Tyr Pro Gly Ala Cys Thr Ile Ser
Thr Glu
130      135      140
cag ggt gaa gaa cta aag aag caa ata gga gca ttg gca tac
ata gag      480
Gln Gly Glu Glu Leu Lys Lys Gln Ile Gly Ala Leu Ala Tyr
Ile Glu
145      150      155
160
tgc agc tcc aaa aca cag cag aac gtg aag gca gtg ttt gat
gct gca      528
Cys Ser Ser Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp
Ala Ala
165      170
175
atc aag gtg gtt ctg cag cct ccg aag ctc agt aaa cga aag
cga aaa      576
Ile Lys Val Val Leu Gln Pro Pro Lys Leu Ser Lys Arg Lys
Arg Lys
180      185      190
aag agg gca tgc cat gtt ctt taa
600

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0070110

Lys Arg Ala Cys His val Leu
195

<210> 299

<211> 199

<212> PRT

<213> vitis vinifera

<400> 299

Met Ser Thr val Pro Ser Arg Phe Ile Lys Cys val Thr val
Gly Asp

1 5 10
15

Gly Ala val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser
Asn Thr

20 25 30

Phe Pro Thr Asp Tyr val Pro Thr val Phe Asp Asn Phe Ser
Ala Asn

35 40 45

val Leu Ala Asp Gly Gln Thr Ile Asn Leu Gly Leu Trp Asp
Thr Ala
50 55 60

Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg
Gly Ala

65 70 75
80

Asp val Phe Leu Leu Ala Phe Ser Leu Ile Ser Arg Pro Ser
Phe Glu

85 90

95
Asn Ile Ser Lys Lys Lys Trp val Pro Glu Leu Arg His Tyr
Ala Pro

100 105 110

Ser val Pro Ile val Leu val Gly Thr Lys Leu Asp Leu Arg
Glu Asp

115 120 125

Lys Gln Phe His Met Asp Tyr Pro Gly Ala Cys Thr Ile Ser
Thr Glu

130 135 140

Gln Gly Glu Glu Leu Lys Lys Gln Ile Gly Ala Leu Ala Tyr
Ile Glu

145 150 155

0070110

160
 Cys Ser Ser Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp
 Ala Ala
 165 170
 175
 Ile Lys Val Val Leu Gln Pro Pro Lys Leu Ser Lys Arg Lys
 Arg Lys
 180 185 190
 Lys Arg Ala Cys His Val Leu
 195

<210> 300
 <211> 591
 <212> DNA
 <213> vitis vinifera

<220>
 <221> CDS
 <222> (1)..(591)

<400> 300
 atg agt gct tca agg ttc atc aag tgc gtc act gta ggg gat
 ggt gcc 48
 Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala
 1 5 10
 15
 gtt ggc aaa act tgt ctc ctt atc tcc tat acc agc aac act
 ttc ccc 96
 Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
 Phe Pro
 20 25 30
 acg gat tat gtg cca act gtt ttc gac aat ttc agt gca aat
 gtg gtt 144
 Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
 Val Val
 35 40 45
 gtc aat ggg gcc act gtt aac ctt ggg ttg tgg gat act gct
 ggg cag 192
 Val Asn Gly Ala Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
 Gly Gln
 50 55 60
 gag gat tac aac aga ttg aga cct ttg agt tat cgc ggg gca
 gat gtt 240
 Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
 Asp Val
 65 70 75

0070110

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      80
ttc ata ttg gca ttc tct ctc atc agc aag gcc agc tat gaa
aat gtt      288
Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val

      85                      90
95
tcc aag aag tgg att cca gaa ttg aag cat tat gca cct ggt
ggt ccg      336
Ser Lys Lys Trp Ile Pro Glu Leu Lys His Tyr Ala Pro Gly
Val Pro

      100                      105                      110

ata gtt ctt gtt ggc act aag ctt gat ctt cgg gaa gac aag
cag ttc      384
Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Glu Asp Lys
Gln Phe

      115                      120                      125
ttc ata gac cat cct ggt gct gtg ccc atc tct gca gct cag
gga gag      432
Phe Ile Asp His Pro Gly Ala Val Pro Ile Ser Ala Ala Gln
Gly Glu

      130                      135                      140
gag ctg aag agg ctg att gat gcc cct gct tac ata gaa tgc
agt gcc      480
Glu Leu Lys Arg Leu Ile Asp Ala Pro Ala Tyr Ile Glu Cys
Ser Ala

      145                      150                      155
      160
aaa aca cag cag aat atc aag gca gtg ttt gat cag gcc att
agg gtt      528
Lys Thr Gln Gln Asn Ile Lys Ala Val Phe Asp Gln Ala Ile
Arg Val

      165                      170
175
gtg ctc caa cca ccc aag cag aag aaa aag aag tca aag tct
aag gtc      576
Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Ser Lys Ser
Lys Val

      180                      185                      190

tgc tcc ata ttg tga
      591
Cys Ser Ile Leu
      195

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<210> 301

<211> 196

0070110

<212> PRT

<213> Vitis vinifera

<400> 301

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

0070110

Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Ser Lys Ser
 Lys Val
 180 185 190

Cys Ser Ile Leu
 195

<210> 302
 <211> 630
 <212> DNA
 <213> Medicago truncatula

<220>
 <221> CDS
 <222> (1)..(630)

<400> 302
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 ggt gct 48
 Met Ser Ala Ser Lys Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala
 1 5 10
 15
 gtt gga aaa act tgc atg ctc att tgt tac acc agt aac aaa
 ttc ccc 96
 Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser Asn Lys
 Phe Pro
 20 25 30
 act gat tat ata cca aca gta ttt gat aat ttt agt gca aat
 gta gct 144
 Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
 Val Ala
 35 40 45
 gtg gat gga agc att gtg aat ttg ggg cta tgg gac act gca
 ggc cag 192
 Val Asp Gly Ser Ile Val Asn Leu Gly Leu Trp Asp Thr Ala
 Gly Gln
 50 55 60
 gaa gac tat agc agg ttg agg cca ctg agc tat aga gga gct
 gat ata 240
 Glu Asp Tyr Ser Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
 Asp Ile
 65 70 75
 80
 ttt gtc tta gca ttc tca ttg att agt aga gct agc tat gaa
 aat gtt 288
 Phe Val Leu Ala Phe Ser Leu Ile Ser Arg Ala Ser Tyr Glu
 Asn Val

0070110

85

90

95
 ctt aag aag tgg atg cca gaa ttg cgc aga ttc gcc cct aat
 gta cca 336
 Leu Lys Lys Trp Met Pro Glu Leu Arg Arg Phe Ala Pro Asn
 Val Pro
 100 105 110
 att gtt ctt gtt ggc aca aag ttg gat ctt cgt gaa gat cgt
 gga tat 384
 Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Glu Asp Arg
 Gly Tyr
 115 120 125
 ttc gct gat cac acg gga tat aat gtt ata aca tct gct gag
 gga gaa 432
 Phe Ala Asp His Thr Gly Tyr Asn Val Ile Thr Ser Ala Glu
 Gly Glu
 130 135 140
 gaa ctg agg aaa caa att ggg gct gca gcg tac att gag tgc
 agc tca 480
 Glu Leu Arg Lys Gln Ile Gly Ala Ala Ala Tyr Ile Glu Cys
 Ser Ser
 145 150 155
 160
 aag act caa cag aat gtg aaa gct gtt ttt gat act gcc att
 aag gtt 528
 Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Thr Ala Ile
 Lys Val
 165 170
 175
 gtt ctc caa cct cca agg agg aaa gaa atg ccg agg aag aaa
 agg caa 576
 Val Leu Gln Pro Pro Arg Arg Lys Glu Met Pro Arg Lys Lys
 Arg Gln
 180 185 190
 aga agg tcc ggt tgc tcg ttt gcc ggt att gtg tgt gga ggt
 tgt gct 624
 Arg Arg Ser Gly Cys Ser Phe Ala Gly Ile Val Cys Gly Gly
 Cys Ala
 195 200 205
 gct taa
 630
 Ala

<210> 303

<211> 209

0070110

<212> PRT

<213> Medicago truncatula

<400> 303

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

0070110

Val Leu Gln Pro Pro Arg Arg Lys Glu Met Pro Arg Lys Lys
 Arg Gln
 180 185 190

Arg Arg Ser Gly Cys Ser Phe Ala Gly Ile Val Cys Gly Gly
 Cys Ala
 195 200 205

Ala

<210> 304
 <211> 585
 <212> DNA
 <213> Cordyceps militaris

<220>
 <221> CDS
 <222> (1)..(585)

<400> 304
 atg gct gaa atc cgc cga aag ctc gtc atc gtc ggc gac ggt
 gcc tgt 48
 Met Ala Glu Ile Arg Arg Lys Leu Val Ile Val Gly Asp Gly
 Ala Cys
 1 5 10
 15
 ggc aaa acc tgt ctg ttg att gtc ttt tcc aag gga act ttc
 cca gag 96
 Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Gly Thr Phe
 Pro Glu
 20 25 30
 gtt tac gtc ccc acc gtt ttc gaa aac tat gtt gcc gac gtc
 gag gtc 144
 Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Val
 Glu Val
 35 40 45
 gat ggc aaa cat gtt gag ctg gcc ctt tgg gat act gct ggt
 cag gag 192
 Asp Gly Lys His Val Glu Leu Ala Leu Trp Asp Thr Ala Gly
 Gln Glu
 50 55 60
 gat tac gac cgt ctt cgt cct ctg tcg tac cct gat tcg cac
 gtt att 240
 Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Ser His
 Val Ile
 65 70 75
 80

0070110

ctg att tgc ttt gcc atc gac tcc ccc gat tcc ctt gac aac
 gtc cag 288
 Leu Ile Cys Phe Ala Ile Asp Ser Pro Asp Ser Leu Asp Asn
 Val Gln

85

90

95

gag aag tgg atc tcc gag gtc ctt cac ttc tgc cag ggc ctt
 cct att 336
 Glu Lys Trp Ile Ser Glu Val Leu His Phe Cys Gln Gly Leu
 Pro Ile

100

105

110

att ctc gtt ggc tgc aag aag gat ctc cgt tac gac caa aag
 gtc aca 384
 Ile Leu Val Gly Cys Lys Lys Asp Leu Arg Tyr Asp Gln Lys
 Val Thr

115

120

125

aac gag ctg gct aag acg agc cag aag ccc gtc agc ccc gaa
 gag ggt 432
 Asn Glu Leu Ala Lys Thr Ser Gln Lys Pro Val Ser Pro Glu
 Glu Gly

130

135

140

gag gag atc cgc aag aag att ggt gct tac aag tac ctc gaa
 tgc tct 480
 Glu Glu Ile Arg Lys Lys Ile Gly Ala Tyr Lys Tyr Leu Glu
 Cys Ser

145

150

155

160

gcc aaa acc aac gag ggt gtc cac gag gtt ttc gag cac gcc
 act cgt 528
 Ala Lys Thr Asn Glu Gly Val His Glu Val Phe Glu His Ala
 Thr Arg

165

170

175

gct gcc ctg ctt tcg cgc agt agc cgc acc aag cac aag aag
 tgc cgc 576
 Ala Ala Leu Leu Ser Arg Ser Ser Arg Thr Lys His Lys Lys
 Cys Arg

180

185

190

atc ctg taa

585

Ile Leu

<210> 305

<211> 194

<212> PRT

0070110

<213> Cordyceps militaris

<400> 305

Met Ala Glu Ile Arg Arg Lys Leu Val Ile Val Gly Asp Gly
Ala Cys

1 5 10

15

Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Gly Thr Phe
Pro Glu

20 25 30

Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Val
Glu Val

35 40 45

Asp Gly Lys His Val Glu Leu Ala Leu Trp Asp Thr Ala Gly
Gln Glu
50 55 60

Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Ser His
Val Ile
65 70 75

80

Leu Ile Cys Phe Ala Ile Asp Ser Pro Asp Ser Leu Asp Asn
Val Gln

85 90

95

Glu Lys Trp Ile Ser Glu Val Leu His Phe Cys Gln Gly Leu
Pro Ile

100 105 110

Ile Leu Val Gly Cys Lys Lys Asp Leu Arg Tyr Asp Gln Lys
Val Thr

115 120 125

Asn Glu Leu Ala Lys Thr Ser Gln Lys Pro Val Ser Pro Glu
Glu Gly
130 135 140

Glu Glu Ile Arg Lys Lys Ile Gly Ala Tyr Lys Tyr Leu Glu
Cys Ser
145 150 155

160

Ala Lys Thr Asn Glu Gly Val His Glu Val Phe Glu His Ala
Thr Arg

165 170

175

Ala Ala Leu Leu Ser Arg Ser Ser Arg Thr Lys His Lys Lys

0070110

Cys Arg 180 185 190

Ile Leu

<210> 306
 <211> 603
 <212> DNA
 <213> Cordyceps militaris

<220>
 <221> CDS
 <222> (1)..(603)

<400> 306
 atg gct gcc gcg aac cct cca aat gtc atc cga aga aag ctc
 gtc att 48
 Met Ala Ala Ala Asn Pro Pro Asn Val Ile Arg Arg Lys Leu
 Val Ile 1 5 10
 15
 gtc ggt gac ggt gcc tgc ggc aag acg agt ctg ctc agc gtc
 ttt aca 96
 Val Gly Asp Gly Ala Cys Gly Lys Thr Ser Leu Leu Ser Val
 Phe Thr 20 25 30
 ctt ggc ttc ttc ccg acc aac tat atc ccg acc gtc ttt gag
 aat tac 144
 Leu Gly Phe Phe Pro Thr Asn Tyr Ile Pro Thr Val Phe Glu
 Asn Tyr 35 40 45
 gtc acc gac tgc cgc gtg gac ggc aag tct gtc cag ctc gca
 ctt tgg 192
 Val Thr Asp Cys Arg Val Asp Gly Lys Ser Val Gln Leu Ala
 Leu Trp 50 55 60
 gat acc gcc ggc caa gaa gac tac gag cga ctg cgc cct cta
 gct tac 240
 Asp Thr Ala Gly Gln Glu Asp Tyr Glu Arg Leu Arg Pro Leu
 Ala Tyr 65 70 75
 80
 gct aaa gcc cat gtt atc ctc att ggc ttt tcc gtc gat act
 ccc gat 288
 Ala Lys Ala His Val Ile Leu Ile Gly Phe Ser Val Asp Thr
 Pro Asp 85 90

0070110

95

tct ctt gac aat gtc aag aac aaa tgg att aca gaa gtt atg
gat ctc 336
Ser Leu Asp Asn Val Lys Asn Lys Trp Ile Thr Glu Val Met
Asp Leu

100

105

110

tgc ccc ggc atc ccc ata atc ctc gtc ggt ctc aaa aag gac
cta cgc 384
Cys Pro Gly Ile Pro Ile Ile Leu Val Gly Leu Lys Lys Asp
Leu Arg

115

120

125

gaa gac cct gtc gcc atc gag gag atg cgc aaa aag tcc ttg
cgc ttc 432
Glu Asp Pro Val Ala Ile Glu Glu Met Arg Lys Lys Ser Leu
Arg Phe

130

135

140

gtc acc acc cac gac ggc gag tct gtc gcc cgc gaa gtt ggc
gcc aag 480
Val Thr Thr His Asp Gly Glu Ser Val Ala Arg Glu Val Gly
Ala Lys

145

150

155

160

cga tat ctc gag tgc tcc agc ctc agt ggc gag ggt gtc gac
gac gtc 528
Arg Tyr Leu Glu Cys Ser Ser Leu Ser Gly Glu Gly Val Asp
Asp Val

165

170

175

ttc gag gcc gcc acc cgc gcc gcc ctg ctg acc ttt gaa aat
ggc gag 576
Phe Glu Ala Ala Thr Arg Ala Ala Leu Leu Thr Phe Glu Asn
Gly Glu

180

185

190

ggc agc ggc tgc tgc gtc gtc ttg taa
603
Gly Ser Gly Cys Cys Val Val Leu
195 200

<210> 307

<211> 200

<212> PRT

<213> Cordyceps militaris

<400> 307

Met Ala Ala Ala Asn Pro Pro Asn Val Ile Arg Arg Lys Leu
Val Ile

0070110

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

0070110

<210> 308
<211> 591
<212> DNA
<213> Medicago truncatula

<220>
<221> CDS
<222> (1)..(591)

<400> 308
atg agt aca gct aga ttc atc aaa tgt gtt act gtt gga gat
ggt gct 48
Met Ser Thr Ala Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10
15
gtt gga aag act tgt atg ctt atc tct tac aca agc aat aca
ttc cct 96
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
20 25 30
acg gat tat gtg cct act gtt ttt gat aat ttc agt gca aat
gtt gtg 144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
35 40 45
gtt gat ggc agc aca gtt aat ctt gga tta tgg gac act gct
gga caa 192
Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60
gag gat tat aac agg ctt agg cca ttg agc tat aga gga gca
gat gtg 240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65 70 75
80
ttt ttg ttg gcc ttt tca cta ctc agc aga gcc agc tat gag
aat ata 288
Phe Leu Leu Ala Phe Ser Leu Leu Ser Arg Ala Ser Tyr Glu
Asn Ile
85 90
95
tct aaa aag tgg att cct gaa ctc aga cat tat gct cca act
gta cca 336
Ser Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Thr
Val Pro

0070110

100

105

110

att gtg ctt gtg gga acc aaa ctt gat ttg agg gaa gat agg
 cag tat 384
 Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Glu Asp Arg
 Gln Tyr

115

120

125

ttg att gat cat cca gga gct aca gct att act act gcc cag
 ggt gaa 432
 Leu Ile Asp His Pro Gly Ala Thr Ala Ile Thr Thr Ala Gln
 Gly Glu

130

135

140

gag ctg aag agg gca att ggt gca gct gtg tac tta gaa tgc
 agc tca 480
 Glu Leu Lys Arg Ala Ile Gly Ala Ala Val Tyr Leu Glu Cys
 Ser Ser

145

150

155

160

aag act caa cag aat gtg aag gct gtg ttt gat gct gca atc
 aag gtt 528
 Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
 Lys Val

165

170

175

gtt ttg cag cct cct aag caa aag aaa aaa aga aag aag aac
 aga tca 576
 Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Arg Lys Lys Asn
 Arg Ser

180

185

190

tgt att ttc ctt taa
 591
 Cys Ile Phe Leu
 195

<210> 309

<211> 196

<212> PRT

<213> Medicago truncatula

<400> 309

Met Ser Thr Ala Arg Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala

1

5

10

15

Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
 Phe Pro

20

25

30

0070110

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

<210> 310

<211> 591

<212> DNA

<213> Picea sitchensis

0070110

<220>

<221> CDS

<222> (1)..(591)

<400> 310

atg agt act gcc aga ttt att aag tgc gtg act gtg ggg gat
ggt gct 48
Met Ser Thr Ala Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10

15
gtg gga aag act tgt atg ctt att tcc tac aca agc aac aca
ttc cca 96
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro

20 25 30
acg gac tat gta cca aca gtg ttt gat aac ttc agt gca aat
gta gtg 144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val

35 40 45
gtc gat gga agt aca gtg aat ctt ggc ctc tgg gac aca gca
ggg caa 192
Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln

50 55 60
gag gat tac aac agg ctc agg ccc ctg agt tac aga ggt gca
gat gtt 240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val

65 70 75
80
ttc ctc ttg gct ttc tcc ttg atc agc aag gcc agt tat gaa
aac att 288
Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Ile

85 90
95
tcc aaa aag tgg att cca gaa ttg aga cac tat gca cca tct
gtg cct 336
Ser Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Ser
Val Pro

100 105 110
atc att ttg gtg ggg act aaa tta gat tta cga gaa gac aaa
cag ttc 384
Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Glu Asp Lys

0070110

[illegible]

<210> 311
<211> 196
<212> PRT
<213> Picea sitchensis

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<400> 311
Met Ser Thr Ala Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1          5          10
15
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
          20          25          30
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
          35          40          45

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0070110

Val	Asp	Gly	Ser	Thr	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala
Gly	Gln												
	50					55					60		

Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala
Asp	Val												
65					70					75			

	80												
Phe	Leu	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Lys	Ala	Ser	Tyr	Glu
Asn	Ile												

				85					90				
95													
Ser	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Arg	His	Tyr	Ala	Pro	Ser
Val	Pro												

			100					105				110	
Ile	Ile	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Glu	Asp	Lys
Gln	Phe												

			115					120				125	
Phe	Ala	Asp	His	Pro	Gly	Ala	Ala	Pro	Ile	Ser	Thr	Ala	Gln
Gly	Glu												

						135					140		
Asp	Leu	Lys	Arg	Gln	Ile	Gly	Ala	Ala	Ala	Tyr	Ile	Glu	Cys
Ser	Ser												

145					150					155			
	160												

Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile
Lys	Val												
				165					170				

175													
Val	Leu	Gln	Pro	Pro	Arg	Gln	Lys	Lys	Arg	Arg	Lys	Lys	Gln
Arg	Thr												

			180					185				190	
Cys	Phe	Ile	Leu										
		195											

0070110

<400> 312

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

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0070110

Gly Glu
130 135 140
gag ctg agg aag cag att ggg gct gct gtt tat ata gaa tgc
agt tca 480
Glu Leu Arg Lys Gln Ile Gly Ala Ala Val Tyr Ile Glu Cys
Ser Ser
145 150 155
160
aaa act cag cag aat atc aaa gct gtt ttc gat gca gca atc
aag gtt 528
Lys Thr Gln Gln Asn Ile Lys Ala Val Phe Asp Ala Ala Ile
Lys Val
165 170
175
gtc att cag cca cca aag cag aag aag aag aag aaa agg aag
tct cac 576
Val Ile Gln Pro Pro Lys Gln Lys Lys Lys Lys Lys Arg Lys
Ser His
180 185 190

aag aac tgt tcc att atg taa
597
Lys Asn Cys Ser Ile Met
195

<210> 313
<211> 198
<212> PRT
<213> Picea sitchensis

<400> 313
Met Ser Thr Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10
15
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
20 25 30
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
35 40 45
Val Asp Gly Thr Ser Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Seite 484

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

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<210> 314
 <211> 594
 <212> DNA
 <213> Populus trichocarpa

<220>
 <221> CDS
 <222> (1)..(594)

<400> 314
 atg agc gcg tcc agg ttc att aag tgc gtg act gtt ggc gac
 ggc gcc 48
 Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala

0070110

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

0070110

Ser Ser

145 150 155
160
aaa aca cag cag aat gtg aag ggg gtt ttt gat gcg gcc ata
aag gtg 528
Lys Thr Gln Gln Asn Val Lys Gly Val Phe Asp Ala Ala Ile
Lys Val

165 170
175
gtg ctg cag cct cca aag caa aag aag aag aag aaa aag ggg
caa aag 576
Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Lys Lys Gly
Gln Lys
180 185 190

gct tgc tcc ata ttg taa
594
Ala Cys Ser Ile Leu
195

<210> 315
<211> 197
<212> PRT
<213> Populus trichocarpa

<400> 315
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala

1 5 10
15
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
20 25 30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
35 40 45

Val Asp Gly Asn Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln 50 55 60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65 70 75

80
Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Seite 487

0070110

```

Asn Val
      85      90
95
Ala Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Gly
Val Pro
      100      105      110

Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Glu Asp Lys
Gln Phe
      115      120      125

Phe Val Asp His Pro Gly Ala Val Pro Ile Thr Thr Ala Gln
Gly Glu
      130      135      140

Glu Leu Lys Lys Leu Ile Gly Ala Pro Phe Tyr Ile Glu Cys
Ser Ser
      145      150      155
      160
Lys Thr Gln Gln Asn Val Lys Gly Val Phe Asp Ala Ala Ile
Lys Val
      165      170
      175
Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Lys Gly
Gln Lys
      180      185      190

Ala Cys Ser Ile Leu
      195

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<210> 316
 <211> 594
 <212> DNA
 <213> Populus trichocarpa

<220>
 <221> CDS
 <222> (1)..(594)

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<400> 316
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gga gct      48
Met Ser Thr Ala Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
  1      5      10
15
gtt ggc aag aca tgc atg ctc atc tct tac act agc aac acc
ttc cct      96

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0070110

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

0070110

aag gtt 528
Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Lys Val

165

170

175

gtt ttg cag cct ccg agg cca aag aaa agg aga cag aag cgt
agg cca 576
Val Leu Gln Pro Pro Arg Pro Lys Lys Arg Arg Gln Lys Arg
Arg Pro

180

185

190

cca tgt gtg ttt ctc taa
594
Pro Cys Val Phe Leu
195

<210> 317

<211> 197

<212> PRT

<213> Populus trichocarpa

<400> 317

Met Ser Thr Ala Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10

15

Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
20 25 30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
35 40 45

Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65 70 75

80

Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Ile
85 90

95

Ala Lys Lys Trp Ile Ser Glu Leu Arg His Tyr Ala Pro Thr
Val Pro

0070110

100

105

110

Val Val Leu Val Gly Thr Lys Leu Asp Leu Arg Asn Asp Lys
Gln Tyr

115

120

125

Leu Ile Asp His Pro Gly Ala Thr Pro Ile Thr Thr Ala Gln
Gly Glu
130

135

140

Glu Leu Lys Lys Met Ile Gly Ala Ala Val Tyr Ile Glu Cys
Ser Ser
145

150

155

160

Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Lys Val

165

170

Val Leu Gln Pro Pro Arg Pro Lys Lys Arg Arg Gln Lys Arg
Arg Pro
175

180

185

190

Pro Cys Val Phe Leu
195

<210> 318

<211> 600

<212> DNA

<213> Claviceps purpurea

<220>

<221> CDS

<222> (1)..(600)

<400> 318

atg gct caa ccc ggc gtc cag tcc ctc aag tgt gtc gtg acc
ggt gac

48

Met Ala Gln Pro Gly Val Gln Ser Leu Lys Cys Val Val Thr
Gly Asp

1

5

10

15

ggt gcg gtt ggc aag aca tgt ctt ctc att tcg tac acg acc
aat gcc

96

Gly Ala Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Thr
Asn Ala

20

25

30

ttt ccc ggc gaa tac att ccg aca gtt ttc gac aac tac tcg
gca agt

144

0070110

Phe	Pro	Gly	Glu	Tyr	Ile	Pro	Thr	Val	Phe	Asp	Asn	Tyr	Ser
Ala	Ser												
		35					40					45	
gtc	atg	ggt	gat	gga	aag	ccc	atc	agc	ctg	ggt	ctg	tgg	gat
acc	gca		192										
Val	Met	Val	Asp	Gly	Lys	Pro	Ile	Ser	Leu	Gly	Leu	Trp	Asp
Thr	Ala												
	50					55					60		
ggc	cag	gaa	gat	tac	gat	cgc	ttg	cga	ccc	ttg	tca	tat	cct
caa	aca		240										
Gly	Gln	Glu	Asp	Tyr	Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Pro
Gln	Thr												
65					70					75			
80													
gat	ggt	ttc	ctc	atc	tgc	ttc	tcc	att	ggt	tca	cct	cca	tcc
ttt	gac		288										
Asp	Val	Phe	Leu	Ile	Cys	Phe	Ser	Ile	Val	Ser	Pro	Pro	Ser
Phe	Asp												
			85						90				
95													
aac	gtc	aag	gcc	aag	tgg	cac	ccc	gaa	atc	gac	cat	cat	gca
ccc	aac		336										
Asn	Val	Lys	Ala	Lys	Trp	His	Pro	Glu	Ile	Asp	His	His	Ala
Pro	Asn												
			100					105					110
att	ccc	atc	atc	ttg	gtc	ggc	acc	aag	ctc	gat	ttg	cga	gag
gac	gcc		384										
Ile	Pro	Ile	Ile	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Glu
Asp	Ala												
		115				120						125	
gcc	aca	ctg	gat	tcg	ttg	agg	caa	aag	aga	atg	gag	cct	gta
tca	tat		432										
Ala	Thr	Leu	Asp	Ser	Leu	Arg	Gln	Lys	Arg	Met	Glu	Pro	Val
Ser	Tyr												
	130					135					140		
gag	caa	gca	ctg	gct	tgc	gca	cga	gaa	atc	aaa	gct	tgc	aaa
tac	ttg		480										
Glu	Gln	Ala	Leu	Ala	Cys	Ala	Arg	Glu	Ile	Lys	Ala	Cys	Lys
Tyr	Leu												
145					150					155			
160													
gaa	tgc	tct	gct	ctc	acc	cag	cgc	aac	ttg	aag	agc	gta	ttt
gat	gaa		528										
Glu	Cys	Ser	Ala	Leu	Thr	Gln	Arg	Asn	Leu	Lys	Ser	Val	Phe
Asp	Glu												
			165						170				
175													

0070110

gcc att cgt gct gtc ttg aat cct cgt tca caa aca tcc aag
 agc aaa 576
 Ala Ile Arg Ala Val Leu Asn Pro Arg Ser Gln Thr Ser Lys
 Ser Lys 180 185 190

aag tcg aaa tgt tca atc ctg taa
 600
 Lys Ser Lys Cys Ser Ile Leu
 195

<210> 319
 <211> 199
 <212> PRT
 <213> Claviceps purpurea

<400> 319
 Met Ala Gln Pro Gly Val Gln Ser Leu Lys Cys Val Val Thr
 Gly Asp
 1 5 10
 15
 Gly Ala Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Thr
 Asn Ala 20 25 30

Phe Pro Gly Glu Tyr Ile Pro Thr Val Phe Asp Asn Tyr Ser
 Ala Ser 35 40 45

Val Met Val Asp Gly Lys Pro Ile Ser Leu Gly Leu Trp Asp
 Thr Ala 50 55 60

Gly Gln Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro
 Gln Thr 65 70 75

80
 Asp Val Phe Leu Ile Cys Phe Ser Ile Val Ser Pro Pro Ser
 Phe Asp 85 90

95
 Asn Val Lys Ala Lys Trp His Pro Glu Ile Asp His His Ala
 Pro Asn 100 105 110

Ile Pro Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Glu
 Asp Ala 115 120 125

0070110

Ala Thr Leu Asp Ser Leu Arg Gln Lys Arg Met Glu Pro Val
Ser Tyr
130 135 140

Glu Gln Ala Leu Ala Cys Ala Arg Glu Ile Lys Ala Cys Lys
Tyr Leu
145 150 155
160

Glu Cys Ser Ala Leu Thr Gln Arg Asn Leu Lys Ser Val Phe
Asp Glu
165 170

175
Ala Ile Arg Ala Val Leu Asn Pro Arg Ser Gln Thr Ser Lys
Ser Lys
180 185 190

Lys Ser Lys Cys Ser Ile Leu
195

<210> 320

<211> 600

<212> DNA

<213> Colletotrichum gloeosporioides f

<220>

<221> CDS

<222> (1)..(600)

<400> 320

atg gct cag cca gga gaa cag tcg ctg aag tgt gtg gtg acg
ggt gac 48
Met Ala Gln Pro Gly Glu Gln Ser Leu Lys Cys Val Val Thr
Gly Asp
1 5 10

15
ggt gcc gtc gga aag aca tgt ttg ctc att tcc tac aca acg
aac gcc 96
Gly Ala Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Thr
Asn Ala

20 25 30
ttc ccc ggc gag tac atc ccc act gtc ttc gac aac tac tct
gcg agt 144
Phe Pro Gly Glu Tyr Ile Pro Thr Val Phe Asp Asn Tyr Ser
Ala Ser

35 40 45
gtc atg gtc gat gga aag cca att agc ctg gga ctg tgg gat
act gcc 192

0070110

Val	Met	Val	Asp	Gly	Lys	Pro	Ile	Ser	Leu	Gly	Leu	Trp	Asp
Thr	Ala												
	50					55				60			
ggt	cag	gag	gat	tac	gac	aga	ctg	cgc	ccg	ctc	tcc	tac	ccc
cag	acc		240										
Gly	Gln	Glu	Asp	Tyr	Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Pro
Gln	Thr												
65					70					75			
80													
gac	ggt	ttc	ctc	atc	tgc	ttc	tcc	atc	gtc	agc	ccg	cca	tca
ttt	gac		288										
Asp	Val	Phe	Leu	Ile	Cys	Phe	Ser	Ile	Val	Ser	Pro	Pro	Ser
Phe	Asp												
			85						90				
95													
aac	gtc	aag	gcc	aag	tgg	tac	ccc	gag	atc	gac	cac	cac	gcg
ccc	aac		336										
Asn	Val	Lys	Ala	Lys	Trp	Tyr	Pro	Glu	Ile	Asp	His	His	Ala
Pro	Asn												
			100					105					110
atc	ccc	atc	atc	ctc	gtc	ggc	acc	aag	ctg	gat	ctg	aga	gaa
gac	ccc		384										
Ile	Pro	Ile	Ile	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Glu
Asp	Pro												
		115				120					125		
aac	acc	ctc	gag	tct	ctc	cgc	cag	aag	cgc	atg	gag	ccc	gtg
tcg	tac		432										
Asn	Thr	Leu	Glu	Ser	Leu	Arg	Gln	Lys	Arg	Met	Glu	Pro	Val
Ser	Tyr												
	130					135					140		
gat	caa	gct	ctg	atc	tgc	gcc	aag	gaa	atc	aag	gca	cat	aag
tac	ctg		480										
Asp	Gln	Ala	Leu	Ile	Cys	Ala	Lys	Glu	Ile	Lys	Ala	His	Lys
Tyr	Leu												
145					150					155			
160													
gag	tgc	tct	gcc	ctg	acg	cag	aga	aat	ctc	aag	agt	gtt	ttc
gac	gag		528										
Glu	Cys	Ser	Ala	Leu	Thr	Gln	Arg	Asn	Leu	Lys	Ser	Val	Phe
Asp	Glu												
			165						170				
175													
gct	atc	cgt	gct	gtc	ctc	aac	ccc	agg	cct	gtt	cct	cag	cag
aag	aag		576										
Ala	Ile	Arg	Ala	Val	Leu	Asn	Pro	Arg	Pro	Val	Pro	Gln	Gln
Lys	Lys												
			180					185					190

0070110

aag tcc aag tgc acg att ttg tga

600

Lys Ser Lys Cys Thr Ile Leu

195

<210> 321

<211> 199

<212> PRT

<213> Colletotrichum gloeosporioides f

<400> 321

Met Ala Gln Pro Gly Glu Gln Ser Leu Lys Cys Val Val Thr

Gly Asp

1

5

10

15

Gly Ala Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Thr

Asn Ala

20

25

30

Phe Pro Gly Glu Tyr Ile Pro Thr Val Phe Asp Asn Tyr Ser

Ala Ser

35

40

45

Val Met Val Asp Gly Lys Pro Ile Ser Leu Gly Leu Trp Asp

Thr Ala

50

55

60

Gly Gln Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro

Gln Thr

65

70

75

80

Asp Val Phe Leu Ile Cys Phe Ser Ile Val Ser Pro Pro Ser

Phe Asp

85

90

95

Asn Val Lys Ala Lys Trp Tyr Pro Glu Ile Asp His His Ala

Pro Asn

100

105

110

Ile Pro Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Glu

Asp Pro

115

120

125

Asn Thr Leu Glu Ser Leu Arg Gln Lys Arg Met Glu Pro Val

Ser Tyr

130

135

140

0070110

Asp Gln Ala Leu Ile Cys Ala Lys Glu Ile Lys Ala His Lys
 Tyr Leu
 145 150 155
 160
 Glu Cys Ser Ala Leu Thr Gln Arg Asn Leu Lys Ser Val Phe
 Asp Glu
 165 170
 175
 Ala Ile Arg Ala Val Leu Asn Pro Arg Pro Val Pro Gln Gln
 Lys Lys
 180 185 190
 Lys Ser Lys Cys Thr Ile Leu
 195

<210> 322
 <211> 594
 <212> DNA
 <213> Eucalyptus gunnii

<220>
 <221> CDS
 <222> (1)..(594)

<400> 322
 atg agc gcg tcg agg ttc atc aag tgc gtc acc gtc ggc gac
 ggt gcc 48

Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala
 1 5 10
 15
 gtc ggc aaa acc tgc ctg ttg att tct tat acc agc aac act
 ttc ccc 96
 Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
 Phe Pro
 20 25 30
 acg gac tat gtg ccc acg gtg ttt gac aat ttt agt gca aat
 gtg gtg 144
 Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
 Val Val
 35 40 45
 gtt aat gga agt act gtt aat ctg gga ttg tgg gat act gct
 gga caa 192
 Val Asn Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
 Gly Gln
 50 55 60
 gag gat tat aac aga tta aga cct cta agt tac cgt gga gca
 Seite 497

0070110

gat gtt	240													
Glu Asp Tyr	Asn Arg	Leu Arg	Pro Leu	Ser Tyr	Arg Gly	Ala								
Asp Val														
65			70						75					
80														
ttc ata ctt	gct ttc	tct ctc	ata agc	aag gcc	agt tat	gaa								
aac gtt	288													
Phe Ile Leu	Ala Phe	Ser Leu	Ile Ser	Lys Ala	Ser Tyr	Glu								
Asn Val														
		85							90					
95														
tca aag aag	tgg att	cca gaa	tta aag	cat tat	gca cct	ggt								
gtg cca	336													
Ser Lys Lys	Trp Ile	Pro Glu	Leu Lys	His Tyr	Ala Pro	Gly								
Val Pro														
		100							105					110
ata att ctc	gtg gga	aca aag	ctg gat	ttg cgg	gat gat	aag								
cag ttc	384													
Ile Ile Leu	Val Gly	Thr Lys	Leu Asp	Leu Arg	Asp Asp	Lys								
Gln Phe														
		115							120					125
ttt ata gac	cat cct	ggt gca	gtg cct	att acg	acc cag	cag								
gga gag	432													
Phe Ile Asp	His Pro	Gly Ala	Val Pro	Ile Thr	Thr Gln	Gln								
Gly Glu														
		130							135					140
gaa ttg agg	aag ctg	att gga	gct cct	gca tac	att gaa	tgc								
agt tcg	480													
Glu Leu Arg	Lys Leu	Ile Gly	Ala Pro	Ala Tyr	Ile Glu	Cys								
Ser Ser														
145														
			150											155
160														
aaa aca caa	cag aat	gtg aag	gcc gtc	ttt gac	gcg gcc	ata								
agg gtt	528													
Lys Thr Gln	Gln Asn	Val Lys	Ala Val	Phe Asp	Ala Ala	Ile								
Arg Val														
		165												170
175														
gtg ctt caa	cca cca	aaa cag	aag aaa	aag aag	agc aaa	gca								
caa aaa	576													
Val Leu Gln	Pro Pro	Lys Gln	Lys Lys	Lys Lys	Ser Lys	Ala								
Gln Lys														
		180												190
gcc tgc tca	ata ttg	tga												
	594													
Ala Cys Ser	Ile Leu													

<210> 323
 <211> 197
 <212> PRT
 <213> Eucalyptus gunnii

<400> 323
 Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala
 1 5 10
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 Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
 Phe Pro
 20 25 30
 Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
 Val Val
 35 40 45
 Val Asn Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
 Gly Gln
 50 55 60
 Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
 Asp Val
 65 70 75
 80
 Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
 Asn Val
 85 90
 95
 Ser Lys Lys Trp Ile Pro Glu Leu Lys His Tyr Ala Pro Gly
 Val Pro
 100 105 110
 Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
 Gln Phe
 115 120 125
 Phe Ile Asp His Pro Gly Ala Val Pro Ile Thr Thr Gln Gln
 Gly Glu
 130 135 140
 Glu Leu Arg Lys Leu Ile Gly Ala Pro Ala Tyr Ile Glu Cys
 Ser Ser
 145 150 155

0070110

160
Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Arg Val
165 170
175
Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Ser Lys Ala
Gln Lys
180 185 190
Ala Cys Ser Ile Leu
195

<210> 324
<211> 636
<212> DNA
<213> Medicago truncatula

<220>
<221> CDS
<222> (1)..(636)

<400> 324
atg gct tca aca gct tca aga ttc atc aag tgc gtc aca gtt
gga gac 48
Met Ala Ser Thr Ala Ser Arg Phe Ile Lys Cys Val Thr Val
Gly Asp
1 5 10
15
gga gct gta ggc aaa acc tgc atg ctc att tgc tac acc agc
aac aaa 96
Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser
Asn Lys
20 25 30
ttc ccc act gac tat att cct aca gtg ttt gat aat ttt agt
gca aat 144
Phe Pro Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser
Ala Asn
35 40 45
gtg gtt gtg gaa ggc att act gtc aat tta ggt ctc tgg gat
aca gct 192
Val Val Val Glu Gly Ile Thr Val Asn Leu Gly Leu Trp Asp
Thr Ala
50 55 60
ggg caa gag gat tac aat agg ctg agg cct ttg agc tac aga
ggg gca 240
Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg
Gly Ala
65 70 75

0070110

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      80
gat gtc ttt gtc ttg gct ttt tct tta gtt agt cgc gca agt
tac gaa      288
Asp Val Phe Val Leu Ala Phe Ser Leu Val Ser Arg Ala Ser
Tyr Glu

      85                      90
95
aat gtg ttc aag aag tgg atc cct gaa ctc cag cat ttt gcc
cct ggc      336
Asn Val Phe Lys Lys Trp Ile Pro Glu Leu Gln His Phe Ala
Pro Gly

      100                      105                      110

gtc cct gtt gta ctt gtt gga acc aaa ttg gat ctc cga gaa
gac aga      384
Val Pro Val Val Leu Val Gly Thr Lys Leu Asp Leu Arg Glu
Asp Arg

      115                      120                      125
cat tat ttg gct gat cat cct ggc atg gtg ccg gtg act act
gag caa      432
His Tyr Leu Ala Asp His Pro Gly Met Val Pro Val Thr Thr
Glu Gln

      130                      135                      140
ggg gag gaa ctc cgt aag cag att gga gct aca tat tat att
gag tgc      480
Gly Glu Glu Leu Arg Lys Gln Ile Gly Ala Thr Tyr Tyr Ile
Glu Cys

      145                      150                      155
      160
agc tca aaa act cag cag aat gtg aag gga gtt ttt gat gct
gcg att      528
Ser Ser Lys Thr Gln Gln Asn Val Lys Gly Val Phe Asp Ala
Ala Ile

      165                      170
175
agg atg gtc atc aag cct cca caa aag caa cac gag aaa agg
aaa aaa      576
Arg Met Val Ile Lys Pro Pro Gln Lys Gln His Glu Lys Arg
Lys Lys

      180                      185                      190

gct cgt cga ggc tgt ttc cta aat gtc ctc tgt gga agg agc
atc gtt      624
Ala Arg Arg Gly Cys Phe Leu Asn Val Leu Cys Gly Arg Ser
Ile Val

      195                      200                      205
cgt cat aaa tga
      636

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0070110

Arg His Lys
210

<210> 325

<211> 211

<212> PRT

<213> Medicago truncatula

<400> 325

Met Ala Ser Thr Ala Ser Arg Phe Ile Lys Cys Val Thr Val
Gly Asp

1 5 10

15

Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser
Asn Lys

20 25 30

Phe Pro Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser
Ala Asn

35 40 45

Val Val Val Glu Gly Ile Thr Val Asn Leu Gly Leu Trp Asp
Thr Ala

50 55 60

Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg
Gly Ala

65 70 75

80

Asp Val Phe Val Leu Ala Phe Ser Leu Val Ser Arg Ala Ser
Tyr Glu

85 90

95

Asn Val Phe Lys Lys Trp Ile Pro Glu Leu Gln His Phe Ala
Pro Gly

100 105 110

Val Pro Val Val Leu Val Gly Thr Lys Leu Asp Leu Arg Glu
Asp Arg

115 120 125

His Tyr Leu Ala Asp His Pro Gly Met Val Pro Val Thr Thr
Glu Gln

130 135 140

Gly Glu Glu Leu Arg Lys Gln Ile Gly Ala Thr Tyr Tyr Ile
Glu Cys

145 150 155

0070110

160
Ser Ser Lys Thr Gln Gln Asn Val Lys Gly Val Phe Asp Ala
Ala Ile
165 170
175
Arg Met Val Ile Lys Pro Pro Gln Lys Gln His Glu Lys Arg
Lys Lys
180 185 190
Ala Arg Arg Gly Cys Phe Leu Asn Val Leu Cys Gly Arg Ser
Ile Val
195 200 205
Arg His Lys
210

<210> 326
<211> 603
<212> DNA
<213> Neurospora crassa

<220>
<221> CDS
<222> (1)..(603)

<400> 326
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act ggt 48
Met Ala Ala Ile Gly Gly Val Gln Ser Ile Lys Cys Val Val
Thr Gly
1 5 10
15
gac ggt gct gta gga aag aca tgt ctt ctc atc tca tac aca
aca aat 96
Asp Gly Ala Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr
Thr Asn
20 25 30
gcc ttc ccc ggc gaa tac att ccc aca gtc ttc gat aat tac
tcg gcg 144
Ala Phe Pro Gly Glu Tyr Ile Pro Thr Val Phe Asp Asn Tyr
Ser Ala
35 40 45
agt gtt atg gtc gat ggc aag ccc gtg agc ttg ggt ctc tgg
gat act 192
Ser Val Met Val Asp Gly Lys Pro Val Ser Leu Gly Leu Trp
Asp Thr
50 55 60
gct gga cag gag gat tac gac aga ctg cgc ccg ctt tcg tac
Seite 503

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ccc cag      240
Ala Gly Gln Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr
Pro Gln
 65      70      75
    80
acc gac gtc ttc ctc atc tgc ttt tcg ctc gtc agc cct ccg
tcg ttc      288
Thr Asp Val Phe Leu Ile Cys Phe Ser Leu Val Ser Pro Pro
Ser Phe
      85      90
95
gac aac gtc aag tcc aag tgg cac ccc gag atc cag cat cac
gcc ccc      336
Asp Asn Val Lys Ser Lys Trp His Pro Glu Ile Gln His His
Ala Pro
      100      105      110

ggc atc ccc atc atc ttg gtg ggc acc aag ctc gat ttg cgc
gag gac      384
Gly Ile Pro Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg
Glu Asp
 115      120      125
ccc gat acc att cag agc ctg agc cag aaa cgc atg gct ccg
ata acg      432
Pro Asp Thr Ile Gln Ser Leu Ser Gln Lys Arg Met Ala Pro
Ile Thr
 130      135      140
ttc gag atg ggt gtc aac tgc gcc aag gag atc ggc gcg agg
aag tac      480
Phe Glu Met Gly Val Asn Cys Ala Lys Glu Ile Gly Ala Arg
Lys Tyr
145      150      155
 160
ctc gag tgc tct gcc ctt acc caa agg aat ctc aag tct gtt
ttc gac      528
Leu Glu Cys Ser Ala Leu Thr Gln Arg Asn Leu Lys Ser Val
Phe Asp
      165      170
175
gag gcc atc aga gct gtg ctc tac cgc gtc gat acg acc caa
gaa aag      576
Glu Ala Ile Arg Ala Val Leu Tyr Arg Val Asp Thr Thr Gln
Glu Lys
      180      185      190

aag aag tcc aag tgc act atc ctc taa
        603
Lys Lys Ser Lys Cys Thr Ile Leu

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0070110
200

195

<210> 327
<211> 200
<212> PRT
<213> Neurospora crassa

<400> 327
Met Ala Ala Ile Gly Gly Val Gln Ser Ile Lys Cys Val Val
Thr Gly
1 5 10
15
Asp Gly Ala Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr
Thr Asn
20 25 30
Ala Phe Pro Gly Glu Tyr Ile Pro Thr Val Phe Asp Asn Tyr
Ser Ala
35 40 45
Ser Val Met Val Asp Gly Lys Pro Val Ser Leu Gly Leu Trp
Asp Thr
50 55 60
Ala Gly Gln Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr
Pro Gln
65 70 75
80
Thr Asp Val Phe Leu Ile Cys Phe Ser Leu Val Ser Pro Pro
Ser Phe
85 90
95
Asp Asn Val Lys Ser Lys Trp His Pro Glu Ile Gln His His
Ala Pro
100 105 110
Gly Ile Pro Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg
Glu Asp
115 120 125
Pro Asp Thr Ile Gln Ser Leu Ser Gln Lys Arg Met Ala Pro
Ile Thr
130 135 140
Phe Glu Met Gly Val Asn Cys Ala Lys Glu Ile Gly Ala Arg
Lys Tyr
145 150 155
160

0070110

Leu Glu Cys Ser Ala Leu Thr Gln Arg Asn Leu Lys Ser Val
Phe Asp

165

170

175

Glu Ala Ile Arg Ala Val Leu Tyr Arg Val Asp Thr Thr Gln
Glu Lys

180

185

190

Lys Lys Ser Lys Cys Thr Ile Leu
195 200

<210> 328

<211> 603

<212> DNA

<213> Neurospora crassa

<220>

<221> CDS

<222> (1)..(603)

<400> 328

atg gca tca ggc agc cct cag aat gtc atc cgc agg aaa ctc
gtc att 48

Met Ala Ser Gly Ser Pro Gln Asn Val Ile Arg Arg Lys Leu
Val Ile

1

5

10

15

atc ggc gac ggt gct tgc gga aaa acc agt cta ctg agc gtc
ttc act 96

Ile Gly Asp Gly Ala Cys Gly Lys Thr Ser Leu Leu Ser Val
Phe Thr

20

25

30

ttg ggt ttt ttc cca gcc aca tat atc ccc acc gtg ttc gag
aat tac 144

Leu Gly Phe Phe Pro Ala Thr Tyr Ile Pro Thr Val Phe Glu
Asn Tyr

35

40

45

gtt acc gac tgc cga gta gat ggc aag tcg gtt caa cta gcg
cta tgg 192

Val Thr Asp Cys Arg Val Asp Gly Lys Ser Val Gln Leu Ala
Leu Trp

50

55

60

gac aca gcc gga caa gaa gac tat gag cga tta cga cca cta
gca tac 240

Asp Thr Ala Gly Gln Glu Asp Tyr Glu Arg Leu Arg Pro Leu
Ala Tyr

65

70

75

80

0070110

tca aag gcg cat gtc att cta ata ggg ttt tct gtc gac acg
cca gat 288
Ser Lys Ala His Val Ile Leu Ile Gly Phe Ser Val Asp Thr
Pro Asp

85

90

95

tct ttg gac aac gtt aaa cac aag tgg gtt act gag gcc aat
gaa aga 336
Ser Leu Asp Asn Val Lys His Lys Trp Val Thr Glu Ala Asn
Glu Arg

100

105

110

tgt ccc aat gtt ccc atc att ttg gtg ggt ctc aag aag gat
ctc agg 384
Cys Pro Asn Val Pro Ile Ile Leu Val Gly Leu Lys Lys Asp
Leu Arg

115

120

125

gga gat cct gtt gcc atc gaa gaa atg cga aag cga tcc caa
cga ttc 432
Gly Asp Pro Val Ala Ile Glu Glu Met Arg Lys Arg Ser Gln
Arg Phe

130

135

140

gtg atg gag gac gaa ggc cag agg ata gca aag gag att ggc
gct cga 480
Val Met Glu Asp Glu Gly Gln Arg Ile Ala Lys Glu Ile Gly
Ala Arg

145

150

155

160

aag tat ctc gaa tgt tcc agt ctt acc gga gaa ggt gtt gac
gac gta 528
Lys Tyr Leu Glu Cys Ser Ser Leu Thr Gly Glu Gly Val Asp
Asp Val

165

170

175

ttc gag gca gcc acg cga gcg gcg ctg cta acg ttt gag aag
aag gaa 576
Phe Glu Ala Ala Thr Arg Ala Ala Leu Leu Thr Phe Glu Lys
Lys Glu

180

185

190

gga agc ggg tgc tgt gtg att cta tga
Gly Ser Gly Cys Cys Val Ile Leu
195 200

<210> 329

<211> 200

0070110

<212> PRT

<213> Neurospora crassa

<400> 329

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

0070110

Phe Glu Ala Ala Thr Arg Ala Ala Leu Leu Thr Phe Glu Lys
 Lys Glu
 180 185 190

Gly Ser Gly Cys Cys Val Ile Leu
 195 200

<210> 330

<211> 810

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(810)

<400> 330

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 aag tgg 48
 Met Ala Asp Ala Asn Glu Val Val Glu Trp Ala Asn Asn Leu
 Lys Trp
 1 5 10

15
 gat aaa tat gct gga aat aaa gaa att gtt gat gga ttg gcc
 gct ttg 96
 Asp Lys Tyr Ala Gly Asn Lys Glu Ile Val Asp Gly Leu Ala
 Ala Leu

20 25 30
 aga caa aaa atc aca gct ttg gac ggc gct gaa gga ggc tct
 ggt ggc 144
 Arg Gln Lys Ile Thr Ala Leu Asp Gly Ala Glu Gly Gly Ser
 Gly Gly

35 40 45
 aat caa aga gtt aaa tta gta gtt gtc ggt gat ggt gcc gtc
 ggc aaa 192
 Asn Gln Arg Val Lys Leu Val Val Val Gly Asp Gly Ala Val
 Gly Lys

50 55 60
 aca tct ctg ttg att tca ttc gct gaa aac aaa ttc cct gag
 gat tac 240
 Thr Ser Leu Leu Ile Ser Phe Ala Glu Asn Lys Phe Pro Glu
 Asp Tyr

65 70 75
 80
 gtc cct aca gtc ttc gaa aac tac act tct aaa atc act cgc
 gac gat 288
 Val Pro Thr Val Phe Glu Asn Tyr Thr Ser Lys Ile Thr Arg
 Asp Asp

0070110

85

90

[illegible]

0070110

Ala	Glu	Arg	Arg	Ala	His	Glu	Pro	Pro	Lys	Pro	Thr	Ala	Ala
Ser	Ser												
225					230					235			
240													
acg	aac	ggc	act	aac	ggc	act	aag	act	gag	cac	act	cct	cgc
gaa	gag		768										
Thr	Asn	Gly	Thr	Asn	Gly	Thr	Lys	Thr	Glu	His	Thr	Pro	Arg
Glu	Glu												
				245					250				
255													
ccc	atc	cga	aag	aag	aag	gag	cgt	cgc	tgc	ttg	ttg	atg	taa
			810										
Pro	Ile	Arg	Lys	Lys	Lys	Glu	Arg	Arg	Cys	Leu	Leu	Met	
			260					265					

<210> 331

<211> 269

<212> PRT

<213> Arabidopsis thaliana

<400> 331

Met	Ala	Asp	Ala	Asn	Glu	Val	Val	Glu	Trp	Ala	Asn	Asn	Leu
Lys	Trp												
1				5					10				
15													
Asp	Lys	Tyr	Ala	Gly	Asn	Lys	Glu	Ile	Val	Asp	Gly	Leu	Ala
Ala	Leu												
			20					25				30	
Arg	Gln	Lys	Ile	Thr	Ala	Leu	Asp	Gly	Ala	Glu	Gly	Gly	Ser
Gly	Gly												
		35					40				45		
Asn	Gln	Arg	Val	Lys	Leu	Val	Val	Val	Gly	Asp	Gly	Ala	Val
Gly	Lys												
	50					55					60		
Thr	Ser	Leu	Leu	Ile	Ser	Phe	Ala	Glu	Asn	Lys	Phe	Pro	Glu
Asp	Tyr												
65					70					75			
80													
Val	Pro	Thr	Val	Phe	Glu	Asn	Tyr	Thr	Ser	Lys	Ile	Thr	Arg
Asp	Asp												
				85						90			
95													
Gly	Thr	Leu	Val	Leu	Leu	His	Leu	Trp	Asp	Thr	Ala	Gly	Gln
Glu	Asp												
			100					105					110

0070110

Tyr	Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Pro	Gly	Ala	Asp	Val
Ile	Leu												
		115					120					125	
Leu	Cys	Phe	Ser	Thr	Val	Thr	Ala	Ser	Ser	Phe	Ala	Ser	Ile
Lys	Glu												
	130					135					140		
Lys	Trp	Tyr	Pro	Glu	Val	Asn	His	Tyr	Val	Pro	Asp	Ala	Pro
Tyr	Ile												
145					150					155			
160													
Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Glu	Ala	Gly	Leu	Pro
Asp	Pro												
				165					170				
175													
Ser	Thr	Gly	Glu	Ser	Asp	Pro	Val	Thr	Pro	Glu	Lys	Ala	Glu
Glu	Met												
			180					185				190	
Arg	Lys	Gln	Ile	Lys	Ala	Leu	Lys	Tyr	Ile	Glu	Val	Ser	Ala
Lys	Thr												
		195					200					205	
Arg	Lys	Asn	Leu	Gln	Thr	Leu	Phe	Ser	Glu	Ala	Val	Asp	Ile
Val	Leu												
	210					215					220		
Ala	Glu	Arg	Arg	Ala	His	Glu	Pro	Pro	Lys	Pro	Thr	Ala	Ala
Ser	Ser												
225					230					235			
240													
Thr	Asn	Gly	Thr	Asn	Gly	Thr	Lys	Thr	Glu	His	Thr	Pro	Arg
Glu	Glu												
				245					250				
255													
Pro	Ile	Arg	Lys	Lys	Lys	Glu	Arg	Arg	Cys	Leu	Leu	Met	
			260					265					

<210> 332
 <211> 594
 <212> DNA
 <213> Nicotiana tabacum

<220>
 <221> CDS
 <222> (1)..(594)

0070110

<400> 332

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ggg	gcc			48									
Met	Ser	Ala	Pro	Arg	Phe	Ile	Lys	Cys	Val	Thr	Val	Gly	Asp
Gly	Ala												
1				5					10				
15													
gtt	ggg	aaa	act	tgt	ctt	ttg	att	tca	tac	acc	agc	aat	act
ttc	cct		96										
Val	Gly	Lys	Thr	Cys	Leu	Leu	Ile	Ser	Tyr	Thr	Ser	Asn	Thr
Phe	Pro												
			20					25					30
atg	gat	tat	gtg	ccc	act	gtg	ttt	gac	aat	ttc	agt	gca	aat
gtt	gtt		144										
Met	Asp	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn
Val	Val												
		35					40					45	
gtc	aat	ggg	agc	act	gtc	aac	cta	ggg	ttg	tgg	gat	act	gcc
gga	cag		192										
Val	Asn	Gly	Ser	Thr	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala
Gly	Gln												
	50					55					60		
gag	gat	tac	aat	agg	tta	aga	cct	ctg	agt	tac	cgt	gga	gcc
gat	gtc		240										
Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala
Asp	Val												
65					70					75			
80													
ttc	att	ttg	gca	ttc	tct	ctc	att	agt	aaa	gcc	agc	tat	gag
aat	gta		288										
Phe	Ile	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Lys	Ala	Ser	Tyr	Glu
Asn	Val												
			85						90				
95													
tcc	aag	aag	tgg	att	cct	gag	ttg	aag	cac	tat	gct	cct	ggg
gtc	cca		336										
Ser	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Lys	His	Tyr	Ala	Pro	Gly
Val	Pro												
			100					105					110
ata	gtt	ctt	gtt	gga	aca	aaa	ctt	gat	ctt	cgg	gat	gat	aag
caa	ttc		384										
Ile	Val	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys
Gln	Phe												
		115					120					125	
ttc	ata	gac	cac	ccc	ggg	gct	gtg	cca	att	act	act	gct	cag
ggg	gag		432										

0070110

Phe	Ile	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Thr	Thr	Ala	Gln
Gly	Glu												
	130					135					140		
gag	cta	agg	aaa	act	ata	ggg	gca	cct	gct	tac	atc	gaa	tgt
agt	tca		480										
Glu	Leu	Arg	Lys	Thr	Ile	Gly	Ala	Pro	Ala	Tyr	Ile	Glu	Cys
Ser	Ser												
145					150					155			
160													
aaa	aca	caa	cag	aat	gtg	aaa	gca	gtc	ttt	gat	gca	gcc	att
aag	gtc		528										
Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile
Lys	Val												
				165					170				
175													
gtc	ctc	cag	ccg	cct	aaa	aca	aag	aaa	aag	aag	ggg	aaa	tca
caa	aag		576										
Val	Leu	Gln	Pro	Pro	Lys	Thr	Lys	Lys	Lys	Lys	Gly	Lys	Ser
Gln	Lys												
			180					185				190	
tcc	tgc	tcg	ata	ttg	tga								
			594										
Ser	Cys	Ser	Ile	Leu									
		195											

<210> 333
 <211> 197
 <212> PRT
 <213> Nicotiana tabacum

<400> 333													
Met	Ser	Ala	Pro	Arg	Phe	Ile	Lys	Cys	Val	Thr	Val	Gly	Asp
Gly	Ala												
1				5					10				
15													
Val	Gly	Lys	Thr	Cys	Leu	Leu	Ile	Ser	Tyr	Thr	Ser	Asn	Thr
Phe	Pro												
			20					25				30	
Met	Asp	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn
Val	Val												
		35					40					45	
Val	Asn	Gly	Ser	Thr	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala
Gly	Gln												
	50					55					60		

0070110

Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala
Asp	Val												
65					70					75			
	80												
Phe	Ile	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Lys	Ala	Ser	Tyr	Glu
Asn	Val												
				85					90				
95													
Ser	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Lys	His	Tyr	Ala	Pro	Gly
Val	Pro												
			100					105					110
Ile	Val	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys
Gln	Phe												
		115					120				125		
Phe	Ile	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Thr	Thr	Ala	Gln
Gly	Glu												
	130					135					140		
Glu	Leu	Arg	Lys	Thr	Ile	Gly	Ala	Pro	Ala	Tyr	Ile	Glu	Cys
Ser	Ser												
145					150					155			
	160												
Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile
Lys	Val												
				165					170				
175													
Val	Leu	Gln	Pro	Pro	Lys	Thr	Lys	Lys	Lys	Lys	Gly	Lys	Ser
Gln	Lys												
			180					185					190
Ser	Cys	Ser	Ile	Leu									
		195											

<210> 334
 <211> 597
 <212> DNA
 <213> Brassica campestris

<220>
 <221> CDS
 <222> (1)..(597)

<400> 334
 atg agt gct tcg agg ttt atc aag tgt gtc acc gtc ggc aac
 ggc gct 48

0070110

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

0070110

agt gca 480
 Glu Leu Lys Lys Leu Ile Gly Ala Pro Ala Tyr Ile Glu Cys
 Ser Ala
 145 150 155

160
 aaa aca caa cag aat gta aaa gcg gtg ttt gat gcg gct atc
 aag gta 528
 Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
 Lys Val
 165 170

175
 gtt ctc cag cca ccc aaa aac aag aag agg aag aag aga aag
 tct cag 576
 Val Leu Gln Pro Pro Lys Asn Lys Lys Arg Lys Lys Arg Lys
 Ser Gln
 180 185 190

aaa ggt tgt tct ata ttg tga
 597
 Lys Gly Cys Ser Ile Leu
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<210> 335
 <211> 198
 <212> PRT
 <213> Brassica campestris

<400> 335
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 Gly Ala
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 15
 Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
 Phe Pro
 20 25 30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Leu Ser Ala Asn
 Val Ile
 35 40 45

Val Asp Gly Asn Thr Ile Asn Leu Gly Leu Trp Asp Thr Ala
 Gly Gln
 50 55 60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
 Asp Val
 65 70 75
 80

0070110

Phe Leu Leu Ala Phe Ser Leu Val Ser Lys Ala Ser Tyr Glu
Asn Val

85

90

95

Ser Lys Lys Trp Val Pro Glu Leu Arg His Tyr Ala Pro Gly
Val Pro

100

105

110

Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe

115

120

125

Phe Val Glu His Pro Gly Ala Val Pro Ile Ser Thr Ala Gln
Gly Glu

130

135

140

Glu Leu Lys Lys Leu Ile Gly Ala Pro Ala Tyr Ile Glu Cys
Ser Ala

145

150

155

160

Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Lys Val

165

170

175

Val Leu Gln Pro Pro Lys Asn Lys Lys Arg Lys Lys Arg Lys
Ser Gln

180

185

190

Lys Gly Cys Ser Ile Leu
195

<210> 336

<211> 576

<212> DNA

<213> Ciona savignyi

<220>

<221> CDS

<222> (1)..(576)

<400> 336

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ggt aaa 48

Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys

1

5

10

15

acc tgt ttg cta ata tcc tat acc aca aac aag ttt cca caa
Seite 518

0070110

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

0070110

act caa aaa gga tta aag aat gta ttt gat gaa gct att tta
gct gct 528
Thr Gln Lys Gly Leu Lys Asn Val Phe Asp Glu Ala Ile Leu
Ala Ala

165

170

175

tta gag cca ccg gag cct aaa aga cgt cgc cga tgt caa att
ttg 573
Leu Glu Pro Pro Glu Pro Lys Arg Arg Arg Arg Cys Gln Ile
Leu

180

185

190

tga

576

<210> 337

<211> 191

<212> PRT

<213> Ciona savignyi

<400> 337

Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys

1

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10

15

Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe Pro Gln
Glu Tyr

20

25

30

Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val Met Ile
Gly Gly

35

40

45

Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu
Asp Tyr

50

55

60

Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
Leu Val

65

70

75

80

Cys Phe Ser Val Val Ser Pro Ser Ser Tyr Glu Asn Ile Lys
Glu Lys

85

90

95

Trp Val Pro Glu Ile Thr His His Cys Pro Lys Thr Pro Phe

Leu	Leu												
			100					105					110
Val	Gly	Thr	Gln	Val	Asp	Leu	Arg	Asp	Asp	Ala	Ala	Thr	Ile
Glu	Lys												
		115					120					125	
Leu	Ser	Lys	Asn	Lys	Gln	Lys	Ala	Ile	Thr	Pro	Asp	Leu	Gly
Asp	Lys												
	130					135					140		
Leu	Ala	Arg	Glu	Leu	Lys	Ala	Val	Lys	Tyr	Val	Glu	Cys	Ser
Ala	Leu												
145					150					155			
160													
Thr	Gln	Lys	Gly	Leu	Lys	Asn	Val	Phe	Asp	Glu	Ala	Ile	Leu
Ala	Ala												
				165					170				
175													
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Leu													
			180					185					190

<220>
<221> CDS
<222> (1) .. (597)

Seite 521

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

0070110

tct	cac			576										
Val	Leu	Gln	Pro	Pro	Lys	Val	Lys	Arg	Lys	Lys	Lys	Arg	Lys	
Ser	His													
			180					185					190	

aag	act	tgt	tca	atc	ctg	tga								
			597											
Lys	Thr	Cys	Ser	Ile	Leu									
		195												

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 <213> Picea mariana

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Gly	Ala													
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15														
Val	Gly	Lys	Thr	Cys	Met	Leu	Ile	Ser	Tyr	Thr	Ser	Asn	Thr	
Phe	Pro													
			20					25					30	

Thr	Asp	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn	
Val	Val													
		35					40					45		

Val	Asp	Gly	Asn	Thr	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala	
Gly	Gln													
	50					55					60			

Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala	
Asp	Val													
65					70					75				

80														
Phe	Ile	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Lys	Ala	Ser	Tyr	Glu	
Asn	Ile													
			85						90					

95														
Met	Lys	Lys	Trp	Leu	Leu	Glu	Leu	Arg	His	Phe	Ala	Pro	Gly	
Val	Pro													
			100					105					110	

Ile	Val	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys	
Gln	Phe													
		115					120					125		

0070110

Phe Thr Asp His Pro Ser Ala Val Pro Ile Thr Thr Ala Gln
Gly Glu
130 135 140

Glu Leu Lys Lys Gln Ile Gly Ala Ala Ala Tyr Ile Glu Cys
Ser Ser
145 150 155

160
Lys Thr Gln Gln Asn Ile Lys Ala Val Phe Asp Ser Ala Ile
Arg Val
165 170

175
Val Leu Gln Pro Pro Lys Val Lys Arg Lys Lys Lys Arg Lys
Ser His
180 185 190

Lys Thr Cys Ser Ile Leu
195

<210> 340
<211> 579
<212> DNA
<213> Hemicentrotus pulcherrimus

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<222> (1)..(579)

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gct tgt 48
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Ala Cys
1 5 10

15
ggg aag acg tgt ctg ctc ata gta ttt agc aaa gac cag ttc
cct gaa 96
Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Asp Gln Phe
Pro Glu

20 25 30
gtc tat gtc cca aca gtt ttt gag aac tat gta gct gat ata
gaa gta 144
Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Ile
Glu Val

35 40 45
gac ggt aaa cag gtt gag ttg gca tta tgg gat aca gca ggt
cag gaa 192
Asp Gly Lys Gln Val Glu Leu Ala Leu Trp Asp Thr Ala Gly

0070110

Gln	Glu													
	50					55					60			
gac	tac	gac	aga	ctg	aga	ccg	ctc	tca	tat	cca	gac	aca	gac	
ggt	ata		240											
Asp	Tyr	Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Pro	Asp	Thr	Asp	
Val	Ile													
65					70					75				
80														
ctc	atg	tgc	ttt	tca	atc	gac	aac	cca	gac	agt	tta	gaa	acc	
atc	cca		288											
Leu	Met	Cys	Phe	Ser	Ile	Asp	Asn	Pro	Asp	Ser	Leu	Glu	Thr	
Ile	Pro													
				85						90				
95														
gaa	aaa	tgg	aca	cca	gag	gtg	aag	cac	ttt	tgc	cct	aat	gta	
cct	gtc		336											
Glu	Lys	Trp	Thr	Pro	Glu	Val	Lys	His	Phe	Cys	Pro	Asn	Val	
Pro	Val													
			100					105					110	
atc	ttg	gtc	ggc	aac	aag	aaa	gat	ctt	cga	aat	gac	gat	gcc	
aca	aaa		384											
Ile	Leu	Val	Gly	Asn	Lys	Lys	Asp	Leu	Arg	Asn	Asp	Asp	Ala	
Thr	Lys													
		115					120				125			
cgg	gaa	ctg	agt	aag	atg	aag	cag	gaa	ccg	gtg	aaa	tat	aat	
gat	gcc		432											
Arg	Glu	Leu	Ser	Lys	Met	Lys	Gln	Glu	Pro	Val	Lys	Tyr	Asn	
Asp	Ala													
	130					135					140			
cag	acc	atg	tca	gat	aag	atc	aac	gcc	tac	aaa	tac	cta	gaa	
tgc	tca		480											
Gln	Thr	Met	Ser	Asp	Lys	Ile	Asn	Ala	Tyr	Lys	Tyr	Leu	Glu	
Cys	Ser													
145					150						155			
160														
gcc	aag	tct	aac	gat	ggt	gtc	agg	gaa	gtg	ttt	gag	aca	gca	
acc	aga		528											
Ala	Lys	Ser	Asn	Asp	Gly	Val	Arg	Glu	Val	Phe	Glu	Thr	Ala	
Thr	Arg													
				165						170				
175														
gca	gca	cta	caa	gtt	aaa	aag	aag	aag	tca	tca	aaa	tgc	agc	
ctc	ttg		576											
Ala	Ala	Leu	Gln	Val	Lys	Lys	Lys	Lys	Ser	Ser	Lys	Cys	Ser	
Leu	Leu													
			180					185					190	

0070110

taa

579

<210> 341

<211> 192

<212> PRT

<213> *Hemicentrotus pulcherrimus*

<400> 341

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Ala Cys

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Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Asp Gln Phe
Pro Glu

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Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Ile
Glu Val

35 40 45

Asp Gly Lys Gln Val Glu Leu Ala Leu Trp Asp Thr Ala Gly
Gln Glu

50 55 60

Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Thr Asp
Val Ile

65 70 75

80

Leu Met Cys Phe Ser Ile Asp Asn Pro Asp Ser Leu Glu Thr
Ile Pro

85 90

95

Glu Lys Trp Thr Pro Glu Val Lys His Phe Cys Pro Asn Val
Pro Val

100 105 110

Ile Leu Val Gly Asn Lys Lys Asp Leu Arg Asn Asp Asp Ala
Thr Lys

115 120 125

Arg Glu Leu Ser Lys Met Lys Gln Glu Pro Val Lys Tyr Asn
Asp Ala

130 135 140

Gln Thr Met Ser Asp Lys Ile Asn Ala Tyr Lys Tyr Leu Glu

Seite 526

Cys Ser
 145 150 155
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 Ala Lys Ser Asn Asp Gly Val Arg Glu Val Phe Glu Thr Ala
 Thr Arg
 165 170
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 Leu Leu
 180 185 190

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<221> CDS
<222> (1)..(570)

Seite 527

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 tac gag 288
 Asp Ala Met Leu Leu Ala Phe Ser Cys Asp Ser Arg Glu Ser
 Tyr Glu

85 90
 95
 agc gtg gag acg aag tgg gta cag gag cta cga gcc aag tcg
 cct ggg 336
 Ser Val Glu Thr Lys Trp Val Gln Glu Leu Arg Ala Lys Ser
 Pro Gly

100 105 110
 acg ccg atc gtg ctc gtg tgc aca aag att gat ctc agg gac
 agc gcg 384
 Thr Pro Ile Val Leu Val Cys Thr Lys Ile Asp Leu Arg Asp
 Ser Ala

115 120 125
 aaa ggg gtt att gga cgg gtg gag ggg gag gct ctg agc gag
 cgc atc 432
 Lys Gly Val Ile Gly Arg Val Glu Gly Glu Ala Leu Ser Glu
 Arg Ile

130 135 140
 aag gcg acg gcg tac gtg gag tgt agt gcg tta acg cag agc
 ggc tta 480
 Lys Ala Thr Ala Tyr Val Glu Cys Ser Ala Leu Thr Gln Ser
 Gly Leu

145 150 155
 160
 cag acg gtg ttc gac acg gtt att gat gtc cgt ttg cgc ccc
 gag ctg 528
 Gln Thr Val Phe Asp Thr Val Ile Asp Val Arg Leu Arg Pro
 Glu Leu

165 170
 175
 ttc gcg aag aaa gcc cag ggt gga tgt tgt tca att cag tga
 Phe Ala Lys 570
 Lys Ala Gln Gly Gly Cys Cys Ser Ile Gln
 180 185

<210> 343
 <211> 189
 <212> PRT
 <213> Ostreococcus tauri

<400> 343
 Met Ala Ile Asp His Met Ser Val Lys Cys Val Val Val Gly
 Asp Gly

0070110

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

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 <212> DNA

0070110

<213> *Petunia integrifolia* subsp

<220>

<221> CDS

<222> (1)..(594)

<400> 344

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Gly Ala
  1              5              10
15
gtt ggc aag act tgt ctt ttg att tca tac acc agc aat acc
ttc ccc          96
Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
      20              25              30
acg gat tat gtg cca act gtg ttc gac aat ttc agt gca aat
gtg gtt          144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
      35              40              45
gtc aat ggg gca acc gtc aac cta ggg ttg tgg gat act gct
gga cag          192
Val Asn Gly Ala Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
      50              55              60
gag gat tac aat agg tta aga cct ctg agt tac cgt gga gct
gat gtt          240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
      65              70              75
80
ttc att ttg gca ttc tct ctc atc agt aaa gcc agc tat gaa
aat gtt          288
Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val
      85              90
95
tcc aag aag tgg att cct gag ttg aag cat tac gcc cct ggt
gtc cct          336
Ser Lys Lys Trp Ile Pro Glu Leu Lys His Tyr Ala Pro Gly
Val Pro
      100              105              110
att gtg ctt gtt gga aca aaa ctt gat ctt cga gat gat aag
caa ttc          384

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0070110

Ile Gln	Val Phe	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys	
		115						120						125
ttc	ata	gac	cat	cct	ggt	gcc	gtg	cca	att	act	act	gct	cag	
ggt	gaa	432												
Phe	Ile	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Thr	Thr	Ala	Gln	
Gly	Glu						135						140	
130														
gag	ctg	agg	aaa	act	att	aat	gca	cct	tcc	tac	att	gaa	tgt	
agt	tca	480												
Glu	Leu	Arg	Lys	Thr	Ile	Asn	Ala	Pro	Ser	Tyr	Ile	Glu	Cys	
Ser	Ser						150						155	
145														
160														
aaa	acc	cag	gaa	aat	gta	aaa	gca	gtg	ttt	gat	gct	gcc	ata	
aaa	gtt	528												
Lys	Thr	Gln	Glu	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile	
Lys	Val						165						170	
175														
gtg	ctc	cag	cca	ccc	aag	cag	aag	aaa	aag	aaa	gga	aaa	tct	
caa	agg	576												
Val	Leu	Gln	Pro	Pro	Lys	Gln	Lys	Lys	Lys	Lys	Gly	Lys	Ser	
Gln	Arg						180						185	190
gcc	tgc	tca	att	ttg	tga									
		594												
Ala	Cys	Ser	Ile	Leu										
		195												

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<210> 345
<211> 197
<212> PRT
<213> Petunia integrifolia subsp
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<400> 345
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1          5          10
15
Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
          20          25          30
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
          35          40          45

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0070110

Val Asn Gly Ala Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65 70 75

80
Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val
85 90

95
Ser Lys Lys Trp Ile Pro Glu Leu Lys His Tyr Ala Pro Gly
Val Pro
100 105 110

Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe
115 120 125

Phe Ile Asp His Pro Gly Ala Val Pro Ile Thr Thr Ala Gln
Gly Glu
130 135 140

Glu Leu Arg Lys Thr Ile Asn Ala Pro Ser Tyr Ile Glu Cys
Ser Ser
145 150 155

160
Lys Thr Gln Glu Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Lys Val
165 170

175
Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Gly Lys Ser
Gln Arg
180 185 190

Ala Cys Ser Ile Leu
195

<210> 346
<211> 636
<212> DNA
<213> Gossypium hirsutum

<220>
<221> CDS
<222> (1)..(636)

0070110

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<400> 346
atg gct tca agc gct tca aga ttt atc aaa tgt gta aca gtt
gga gat
Met Ala Ser Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val
Gly Asp
1 5 10
15
gga gct gtt ggc aag act tgc atg ctt att tgc tat aca agt
aac aag
Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser
Asn Lys
20 25 30
ttc ccg aca gat tac ata cca aca gtt ttt gat aac ttc agt
gcc aac
Phe Pro Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser
Ala Asn
35 40 45
gtt gta gtt gaa ggc aca act gtg aac tta ggt ctt tgg gac
acg gct
Val Val Val Glu Gly Thr Thr Val Asn Leu Gly Leu Trp Asp
Thr Ala
50 55 60
gga caa gag gat tac aac aga cta agg cca ttg agc tac aga
ggt gca
Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg
Gly Ala
65 70 75
80
gat gtc ttt gtc cta gct ttc tca tta gtt agt cga gca agc
tat gag
Asp Val Phe Val Leu Ala Phe Ser Leu Val Ser Arg Ala Ser
Tyr Glu
85 90
95
aac ata cta aaa aag tgg att cct gaa ctt cag cat tat gcc
cca ggc
Asn Ile Leu Lys Lys Trp Ile Pro Glu Leu Gln His Tyr Ala
Pro Gly
100 105 110
115 120 125
gtc cct gtg gtt ctg gtt ggc acc aaa ttg gat ctt cgt gag
gat aaa
Val Pro Val Val Leu Val Gly Thr Lys Leu Asp Leu Arg Glu
Asp Lys
130 135 140
cat tat ctg gct gat cat cct ggc ttg ctg ccg gtt agc act
gca cag
145 150 155

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0070110

His	Tyr	Leu	Ala	Asp	His	Pro	Gly	Leu	Leu	Pro	Val	Ser	Thr
Ala	Gln												
130						135					140		
ggt	gag	gag	ctc	tgc	aaa	cag	ata	ggt	gct	gct	tat	tac	att
gag	tgc			480									
Gly	Glu	Glu	Leu	Cys	Lys	Gln	Ile	Gly	Ala	Ala	Tyr	Tyr	Ile
Glu	Cys												
145					150					155			
160													
agc	tca	aaa	act	cag	cag	aac	gtg	aaa	gca	ggt	ttt	gat	gct
gca	atc			528									
Ser	Ser	Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala
Ala	Ile												
				165						170			
175													
aaa	ggt	gtg	atc	aag	cca	ccc	caa	aaa	cag	aag	gag	aag	aag
aaa	aag			576									
Lys	Val	Val	Ile	Lys	Pro	Pro	Gln	Lys	Gln	Lys	Glu	Lys	Lys
Lys	Lys												
			180					185					190
cca	agt	cga	gga	tgt	cta	ata	aat	gtc	ttc	tgc	ggg	agg	aac
ttt	gtg			624									
Pro	Ser	Arg	Gly	Cys	Leu	Ile	Asn	Val	Phe	Cys	Gly	Arg	Asn
Phe	Val												
		195					200					205	
cct	gct	aaa	tga										
			636										
Pro	Ala	Lys											
	210												

<210> 347

<211> 211

<212> PRT

<213> Gossypium hirsutum

<400> 347

Met	Ala	Ser	Ser	Ala	Ser	Arg	Phe	Ile	Lys	Cys	Val	Thr	Val
Gly	Asp												
1				5					10				
15													
Gly	Ala	Val	Gly	Lys	Thr	Cys	Met	Leu	Ile	Cys	Tyr	Thr	Ser
Asn	Lys												
			20					25					30
Phe	Pro	Thr	Asp	Tyr	Ile	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser
Ala	Asn												
		35					40					45	

0070110

Val	Val	Val	Glu	Gly	Thr	Thr	Val	Asn	Leu	Gly	Leu	Trp	Asp
Thr	Ala												
	50					55					60		

Gly	Gln	Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg
Gly	Ala												
65					70					75			

	80												
Asp	Val	Phe	Val	Leu	Ala	Phe	Ser	Leu	Val	Ser	Arg	Ala	Ser
Tyr	Glu												

			85						90				
95													
Asn	Ile	Leu	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Gln	His	Tyr	Ala
Pro	Gly												

			100					105					110
Val	Pro	Val	Val	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Glu
Asp	Lys												

			115				120					125	
His	Tyr	Leu	Ala	Asp	His	Pro	Gly	Leu	Leu	Pro	Val	Ser	Thr
Ala	Gln												

						135					140		
Gly	Glu	Glu	Leu	Cys	Lys	Gln	Ile	Gly	Ala	Ala	Tyr	Tyr	Ile
Glu	Cys												

					150					155			
145													
	160												

Ser	Ser	Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala
Ala	Ile												
				165					170				

175													
Lys	Val	Val	Ile	Lys	Pro	Pro	Gln	Lys	Gln	Lys	Glu	Lys	Lys
Lys	Lys												

			180					185					190

Pro	Ser	Arg	Gly	Cys	Leu	Ile	Asn	Val	Phe	Cys	Gly	Arg	Asn
Phe	Val												
		195					200					205	

Pro	Ala	Lys											
	210												

<210>	348												
<211>	582												
<212>	DNA												
<213>	Halocynthia roretzi												

0070110

<220>

<221> CDS

<222> (1)..(582)

<400> 348

atg gca gcg atc cgt aaa aaa ctt gtc atc gtt ggt gat ggt
gct tgc 48
Met Ala Ala Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly
Ala Cys

1 5 10

15

ggt aaa act tgc ttg ttg atc gtc ttc agc aaa gac caa ttc
cca gaa 96
Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Asp Gln Phe
Pro Glu

20 25 30
gtt tat gta cct act gtg ttt gaa aac tat gtt gcc gat atc
gaa gta 144
Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Ile
Glu Val

35 40 45
gat gga aaa acg gtt gaa cta gcc ttg tgg gac act gct ggg
cag gaa 192
Asp Gly Lys Thr Val Glu Leu Ala Leu Trp Asp Thr Ala Gly
Gln Glu

50 55 60
gac tat gat aga ttg cga cca ctc tct tat cct gac aca gat
gtc att 240
Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Thr Asp
Val Ile

65 70 75

80

ctg atg tgt ttt tca atc gac agc cca gat tcc ctg gaa aac
att cct 288
Leu Met Cys Phe Ser Ile Asp Ser Pro Asp Ser Leu Glu Asn
Ile Pro

85 90

95

gaa aaa tgg aca cca gag gtg aaa cac ttt tgt cca aac gtt
ccc att 336
Glu Lys Trp Thr Pro Glu Val Lys His Phe Cys Pro Asn Val
Pro Ile

100 105 110

att ctt gtc gga aac aaa aaa gat ctc cga gga gat gaa ggc
act ata 384

0070110

Ile	Leu	val	Gly	Asn	Lys	Lys	Asp	Leu	Arg	Gly	Asp	Glu	Gly
Thr	Ile												
		115					120					125	
aaa	gaa	ctt	tct	aag	atg	aaa	caa	gaa	ccg	ggt	aaa	cag	gag
gag	ggt		432										
Lys	Glu	Leu	Ser	Lys	Met	Lys	Gln	Glu	Pro	val	Lys	Gln	Glu
Glu	Gly												
	130					135					140		
cgt	gct	atg	gct	gag	aaa	att	gga	gct	ttt	gga	tac	ctg	gaa
tgc	tct		480										
Arg	Ala	Met	Ala	Glu	Lys	Ile	Gly	Ala	Phe	Gly	Tyr	Leu	Glu
Cys	Ser												
145					150					155			
160													
tca	aaa	aca	aag	gaa	gga	gtc	cgt	gaa	ggt	ttc	gaa	aac	gcg
act	cga		528										
Ser	Lys	Thr	Lys	Glu	Gly	val	Arg	Glu	val	Phe	Glu	Asn	Ala
Thr	Arg												
			165						170				
175													
gcc	gca	ctt	caa	act	aga	aag	cat	aag	aaa	aag	gga	gga	tgt
gat	ggt		576										
Ala	Ala	Leu	Gln	Thr	Arg	Lys	His	Lys	Lys	Lys	Gly	Gly	Cys
Asp	val												
			180					185				190	
ctt	taa												
			582										
Leu													

<210> 349
 <211> 193
 <212> PRT
 <213> Halocynthia roretzi

<400> 349													
Met	Ala	Ala	Ile	Arg	Lys	Lys	Leu	val	Ile	val	Gly	Asp	Gly
Ala	Cys												
1				5					10				
15													
Gly	Lys	Thr	Cys	Leu	Leu	Ile	val	Phe	Ser	Lys	Asp	Gln	Phe
Pro	Glu												
			20					25				30	
val	Tyr	val	Pro	Thr	val	Phe	Glu	Asn	Tyr	val	Ala	Asp	Ile
Glu	val												
		35					40					45	

0070110

Asp Gly Lys Thr Val Glu Leu Ala Leu Trp Asp Thr Ala Gly
Gln Glu
50 55 60

Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Thr Asp
Val Ile
65 70 75
80

Leu Met Cys Phe Ser Ile Asp Ser Pro Asp Ser Leu Glu Asn
Ile Pro
85 90

95
Glu Lys Trp Thr Pro Glu Val Lys His Phe Cys Pro Asn Val
Pro Ile
100 105 110

Ile Leu Val Gly Asn Lys Lys Asp Leu Arg Gly Asp Glu Gly
Thr Ile
115 120 125

Lys Glu Leu Ser Lys Met Lys Gln Glu Pro Val Lys Gln Glu
Glu Gly
130 135 140

Arg Ala Met Ala Glu Lys Ile Gly Ala Phe Gly Tyr Leu Glu
Cys Ser
145 150 155
160

Ser Lys Thr Lys Glu Gly Val Arg Glu Val Phe Glu Asn Ala
Thr Arg
165 170

175
Ala Ala Leu Gln Thr Arg Lys His Lys Lys Lys Gly Gly Cys
Asp Val
180 185 190

Leu

<210> 350
<211> 597
<212> DNA
<213> Solanum chacoense

<220>
<221> CDS
<222> (1)..(597)

0070110

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<400> 350
atg agt gct tct agg ttt ata aag tgt gtt act gtg ggc gat
gga gct          48
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
  1              5              10
15
gtg ggt aaa act tgt ctt ctc att tcg tat acc agc aac act
ttt ccc          96
Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
      20              25              30
act gat tat gtc cca act gta ttt gac aat ttt agt gca aat
gtg gtc          144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
      35              40              45
gtc gat gga agc act gtt aat ctg ggg ctc tgg gat act gca
ggg cag          192
Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
      50              55              60
gag gat tac aat aga tta aga cct ttg agc tat cgt ggg gca
gat gta          240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
      65              70              75
80
ttt ata ctg gca ttt tct ctc att agc aag gcg agc tat gaa
aat gtc          288
Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val
      85              90
95
tcc aaa aag tgg att cct gaa ttg agg cat tat gct cct gga
gtt cca          336
Ser Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Gly
Val Pro
      100              105              110
att att ctt gtt gga aca aag cta gat ctc cga gag gat aaa
caa ttc          384
Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Glu Asp Lys
Gln Phe
      115              120              125
ttt gtg gac cat cca ggt gct gtt cca ctt agc aca gct cag
ggt gag          432

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0070110

Phe	Val	Asp	His	Pro	Gly	Ala	Val	Pro	Leu	Ser	Thr	Ala	Gln
Gly	Glu												
	130					135					140		
gag	ctg	aga	aag	tcg	att	ggt	gct	gct	gct	tac	att	gaa	tgt
agt	gca		480										
Glu	Leu	Arg	Lys	Ser	Ile	Gly	Ala	Ala	Ala	Tyr	Ile	Glu	Cys
Ser	Ala												
145					150					155			
160													
aaa	aca	caa	cag	aac	att	aag	gct	ggt	ttt	gat	gct	gcc	att
aag	gtg		528										
Lys	Thr	Gln	Gln	Asn	Ile	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile
Lys	Val												
					165					170			
175													
gtc	cta	caa	cca	ccc	cag	caa	aag	aag	aag	aag	aag	aga	aag
ggt	cag		576										
Val	Leu	Gln	Pro	Pro	Gln	Gln	Lys	Lys	Lys	Lys	Lys	Arg	Lys
Gly	Gln												
			180					185				190	
aaa	gcc	tgc	tct	atc	ttg	tga							
			597										
Lys	Ala	Cys	Ser	Ile	Leu								
		195											

<210> 351
 <211> 198
 <212> PRT
 <213> Solanum chacoense

<400> 351													
Met	Ser	Ala	Ser	Arg	Phe	Ile	Lys	Cys	Val	Thr	Val	Gly	Asp
Gly	Ala												
1				5					10				
15													
Val	Gly	Lys	Thr	Cys	Leu	Leu	Ile	Ser	Tyr	Thr	Ser	Asn	Thr
Phe	Pro												
			20					25				30	
Thr	Asp	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn
Val	Val												
		35					40					45	
Val	Asp	Gly	Ser	Thr	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala
Gly	Gln												
	50					55					60		

0070110

Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala
Asp	Val												
65					70					75			
	80												
Phe	Ile	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Lys	Ala	Ser	Tyr	Glu
Asn	Val												
				85					90				
95													
Ser	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Arg	His	Tyr	Ala	Pro	Gly
Val	Pro												
			100					105					110
Ile	Ile	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Glu	Asp	Lys
Gln	Phe												
		115					120					125	
Phe	Val	Asp	His	Pro	Gly	Ala	Val	Pro	Leu	Ser	Thr	Ala	Gln
Gly	Glu												
	130					135					140		
Glu	Leu	Arg	Lys	Ser	Ile	Gly	Ala	Ala	Ala	Tyr	Ile	Glu	Cys
Ser	Ala												
145					150					155			
	160												
Lys	Thr	Gln	Gln	Asn	Ile	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile
Lys	Val												
				165					170				
175													
Val	Leu	Gln	Pro	Pro	Gln	Gln	Lys	Lys	Lys	Lys	Lys	Arg	Lys
Gly	Gln												
			180					185					190
Lys	Ala	Cys	Ser	Ile	Leu								
		195											

<210> 352

<211> 588

<212> DNA

<213> Fusarium oxysporum

<220>

<221> CDS

<222> (1)..(588)

<400> 352

atg	gct	gag	atc	cgc	cga	aag	ctc	gtc	att	gtc	ggc	gat	ggt
gct	tgt			48									
Met	Ala	Glu	Ile	Arg	Arg	Lys	Leu	Val	Ile	Val	Gly	Asp	Gly

0070110

Ala	Cys													
1				5						10				
15														
ggt	aaa	acc	tgt	ttg	ttg	att	ggt	ttc	tcc	aag	ggc	act	ttc	
cct	gag		96											
Gly	Lys	Thr	Cys	Leu	Leu	Ile	Val	Phe	Ser	Lys	Gly	Thr	Phe	
Pro	Glu													
			20					25					30	
gtc	tac	gtc	ccc	acc	ggt	ttc	gag	aac	tac	gtc	gcc	gat	gtc	
gag	ggt		144											
Val	Tyr	Val	Pro	Thr	Val	Phe	Glu	Asn	Tyr	Val	Ala	Asp	Val	
Glu	Val													
		35				40						45		
gat	ggc	aag	cac	gtc	gag	ctc	gca	cta	tgg	gat	act	gct	ggt	
cag	gag		192											
Asp	Gly	Lys	His	Val	Glu	Leu	Ala	Leu	Trp	Asp	Thr	Ala	Gly	
Gln	Glu													
		50				55					60			
gat	tac	gac	cgt	ctt	cga	ccc	ctg	tct	tac	ccc	gac	tcc	cac	
ggt	atc		240											
Asp	Tyr	Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Pro	Asp	Ser	His	
Val	Ile													
65				70						75				
80														
ctg	atc	tgc	ttc	gct	ggt	gac	tct	ccc	gac	tct	ctt	gac	aac	
gtc	cag		288											
Leu	Ile	Cys	Phe	Ala	Val	Asp	Ser	Pro	Asp	Ser	Leu	Asp	Asn	
Val	Gln													
			85							90				
95														
gag	aag	tgg	atc	tct	gag	ggt	ctg	cac	ttc	tgc	caa	ggt	ctc	
cct	atc		336											
Glu	Lys	Trp	Ile	Ser	Glu	Val	Leu	His	Phe	Cys	Gln	Gly	Leu	
Pro	Ile													
			100					105					110	
att	ctt	gtc	ggc	tgc	aag	aag	gat	ttg	cga	tac	gac	cag	aag	
acc	atc		384											
Ile	Leu	Val	Gly	Cys	Lys	Lys	Asp	Leu	Arg	Tyr	Asp	Gln	Lys	
Thr	Ile													
		115				120						125		
gag	gag	ctc	cga	aag	acc	agt	cag	aag	cct	gtc	tcc	ccc	gag	
gag	ggt		432											
Glu	Glu	Leu	Arg	Lys	Thr	Ser	Gln	Lys	Pro	Val	Ser	Pro	Glu	
Glu	Gly													
		130				135					140			
gag	gag	gtt	cgc	aag	aag	atc	gct	gcc	tac	aag	tac	ctt	gag	
tgc	tca		480											

0070110

Glu Glu val Arg Lys Lys Ile Ala Ala Tyr Lys Tyr Leu Glu
Cys Ser
145 150 155

160
gcc aag acc aac gag ggt gtc cgc gag gtg ttc gag cac gct
act cgc 528
Ala Lys Thr Asn Glu Gly val Arg Glu val Phe Glu His Ala
Thr Arg

165 170
175
gct gct ctg ctg tcg cga agc acc agt ggt agc aag cac aag
aag tgc 576
Ala Ala Leu Leu Ser Arg Ser Thr Ser Gly Ser Lys His Lys
Lys Cys
180 185 190

ctt gtt ctg taa
588
Leu val Leu
195

<210> 353
<211> 195
<212> PRT
<213> Fusarium oxysporum

<400> 353
Met Ala Glu Ile Arg Arg Lys Leu val Ile val Gly Asp Gly
Ala Cys
1 5 10
15
Gly Lys Thr Cys Leu Leu Ile val Phe Ser Lys Gly Thr Phe
Pro Glu
20 25 30

val Tyr val Pro Thr val Phe Glu Asn Tyr val Ala Asp val
Glu val
35 40 45

Asp Gly Lys His val Glu Leu Ala Leu Trp Asp Thr Ala Gly
Gln Glu
50 55 60

Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Ser His
val Ile
65 70 75

80
Leu Ile Cys Phe Ala val Asp Ser Pro Asp Ser Leu Asp Asn
Seite 543

0070110

Val Gln
85 90
95
Glu Lys Trp Ile Ser Glu Val Leu His Phe Cys Gln Gly Leu
Pro Ile
100 105 110
Ile Leu Val Gly Cys Lys Lys Asp Leu Arg Tyr Asp Gln Lys
Thr Ile
115 120 125
Glu Glu Leu Arg Lys Thr Ser Gln Lys Pro Val Ser Pro Glu
Glu Gly
130 135 140
Glu Glu Val Arg Lys Lys Ile Ala Ala Tyr Lys Tyr Leu Glu
Cys Ser
145 150 155
160
Ala Lys Thr Asn Glu Gly Val Arg Glu Val Phe Glu His Ala
Thr Arg
165 170
175
Ala Ala Leu Leu Ser Arg Ser Thr Ser Gly Ser Lys His Lys
Lys Cys
180 185 190
Leu Val Leu
195

<210> 354
<211> 579
<212> DNA
<213> Lytechinus variegatus

<220>
<221> CDS
<222> (1)..(579)

<400> 354
atg gct gct ata agg aaa aag ctg gtc atc gtt gga gat ggt
gct tgc 48
Met Ala Ala Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly
Ala Cys
1 5 10
15
gga aag aca tgt ttg ctg ata gtg ttc agc aaa gat cag ttc
cca gaa 96

0070110

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

0070110

acc agg 528
Ala Lys Ser Asn Asp Gly Val Arg Glu Val Phe Glu Thr Ala
Thr Arg

165

170

175

gca gca cta caa gtc aaa aag aag aat aaa tca aaa tgc aat
ctc ttg 576
Ala Ala Leu Gln Val Lys Lys Lys Asn Lys Ser Lys Cys Asn
Leu Leu

180

185

190

taa

579

<210> 355

<211> 192

<212> PRT

<213> Lytechinus variegatus

<400> 355

Met Ala Ala Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly
Ala Cys
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15

Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Asp Gln Phe
Pro Glu
20 25 30

Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Ile
Glu Val
35 40 45

Asp Gly Lys Gln Val Glu Leu Ala Leu Trp Asp Thr Ala Gly
Gln Glu
50 55 60

Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Thr Asp
Val Ile
65 70 75

80

Leu Met Cys Phe Ser Ile Asp Asn Pro Asp Ser Leu Glu Asn
Ile Pro
85 90

95

Glu Lys Trp Thr Pro Glu Val Lys His Phe Cys Pro Asn Val
Pro Val

0070110

	100	105	110
Ile Leu Val Gly Asn Lys Lys Asp Leu Arg Met Asp Glu Asn			
Thr Lys			
	115	120	125
Arg Glu Leu Met Lys Met Lys Gln Glu Pro Val Arg Thr Ala			
Asp Ala			
	130	135	140
Gln Ser Met Ser Asp Lys Ile Ser Ala Tyr Lys Tyr Leu Glu			
Cys Ser			
	145	150	155
	160		
Ala Lys Ser Asn Asp Gly Val Arg Glu Val Phe Glu Thr Ala			
Thr Arg			
	165	170	
	175		
Ala Ala Leu Gln Val Lys Lys Lys Asn Lys Ser Lys Cys Asn			
Leu Leu			
	180	185	190

<210> 356
 <211> 588
 <212> DNA
 <213> Claviceps purpurea

<220>
 <221> CDS
 <222> (1)..(588)

<400> 356

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Met Ala val val Ala Thr Ile Lys Cys val val val Gly Asp			
Gly Ala			
	1	5	10
	15		
gtc ggc aag acg tgc tta ctt atc agc tat acc acc aat aaa			
ttc ccc	96		
Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys			
Phe Pro			
	20	25	30
tcg gaa tac gtc ccg acc gta ttc gac aac tat gcc gtc acg			
gta atg	144		
Ser Glu Tyr Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr			
Val Met			

0070110

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

Val Ala Ala Leu Glu Pro Pro Met Pro Lys Lys Lys Ser Leu
Lys Cys
180 185 190

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<210> 357
<211> 195
<212> PRT
<213> Claviceps purpurea
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Ser Glu Tyr Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr
Val Met

35 40 45

Ile Gly Asp Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala
Gly Gln
50 55 60

Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr
Asp Val
65 70 75
80

Phe Leu Val Cys Phe Ser Val Thr Ser Pro Ala Ser Phe Glu
Asn Val 85 90

```

95 Arg Glu Lys Trp Phe Pro Glu Val His His His Cys Pro Gly
Val Pro
100
105
110

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Cys Leu Ile Val Gly Thr Gln Val Asp Leu Arg Asp Asp Pro
Ser Val
115 120 125

Arg Glu Lys Leu Ala Lys Gln Lys Met Ala Pro Val Lys Lys
Seite 549

0070110

[illegible]

<210> 358
<211> 633
<212> DNA
<213> Candida albicans

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<220>
<221> CDS
<222> (1)..(633)
<223> transl_table=12
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att	gtc		48										
Met	Pro	Leu	Cys	Gly	Gly	Gly	Gln	Lys	Thr	Ile	Gln	Arg	Lys
Ile	Val												
1			5						10				
15													
att	ctt	gga	gat	ggt	gcg	tgt	ggt	aaa	aca	tcg	ctt	ttg	aat
gtc	ttc		96										
Ile	Leu	Gly	Asp	Gly	Ala	Cys	Gly	Lys	Thr	Ser	Leu	Leu	Asn
Val	Phe												
			20					25					30
act	aga	gga	tat	ttt	ccc	caa	gtc	tat	gag	cct	aca	gtg	ttt
gaa	aat		144										
Thr	Arg	Gly	Tyr	Phe	Pro	Gln	Val	Tyr	Glu	Pro	Thr	Val	Phe
Glu	Asn												
		35					40					45	
tac	gtg	cat	gat	ata	ttt	att	gat	ggt	caa	tcc	gtt	caa	ttg
tca	tta		192										
Tyr	Val	His	Asp	Ile	Phe	Ile	Asp	Gly	Gln	Ser	Val	Gln	Leu

Seite 550

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

0070110

aaa cct aaa ggt gcc aat gac aat gaa cca caa aag aaa ggt
 tgt gta 624
 Lys Pro Lys Gly Ala Asn Asp Asn Glu Pro Gln Lys Lys Gly
 Cys Val
 195 200 205
 gtt atg taa
 633
 Val Met
 210

<210> 359
 <211> 210
 <212> PRT
 <213> Candida albicans

<400> 359
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 Ile Val
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 15
 Ile Leu Gly Asp Gly Ala Cys Gly Lys Thr Ser Leu Leu Asn
 Val Phe
 20 25 30
 Thr Arg Gly Tyr Phe Pro Gln Val Tyr Glu Pro Thr Val Phe
 Glu Asn
 35 40 45
 Tyr Val His Asp Ile Phe Ile Asp Gly Gln Ser Val Gln Leu
 Ser Leu
 50 55 60
 Trp Asp Thr Ala Gly Gln Glu Glu Phe Asp Arg Leu Arg Ser
 Leu Ser
 65 70 75
 80
 Tyr Ser Asp Thr His Cys Ile Met Leu Cys Phe Ser Val Asp
 Ser Pro
 85 90
 95
 Asp Ser Leu Glu Asn Val Gln Ser Lys Trp Val Gly Glu Ile
 Ala Asp
 100 105 110
 His Cys Glu Gly Val Lys Leu Val Leu Val Ala Leu Lys Cys
 Asp Leu
 115 120 125

0070110

Arg Asn Asn Glu Asp Ile Glu Asp Gln Gln Gln Ser Asn Pro
Tyr Ser
130 135 140

Ser Gln Lys Arg Leu Ile Thr Tyr Glu Glu Gly Leu Ala Val
Ala Lys
145 150 155

160
Lys Val Gly Ala Leu Arg Tyr Leu Glu Cys Ser Ala Lys Lys
Asn Lys
165 170

175
Gly Val Asn Glu Ala Phe Ser Glu Ala Ala Arg Cys Ala Leu
Asn Ala
180 185 190

Lys Pro Lys Gly Ala Asn Asp Asn Glu Pro Gln Lys Lys Gly
Cys Val
195 200 205

Val Met
210

<210> 360
<211> 594
<212> DNA
<213> Capsicum annuum

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<221> CDS
<222> (1)..(594)

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ggt gct 48
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
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15
gtt ggc aag act tgt tta ttg att tct tac aca agc aat act
ttc cct 96
Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
20 25 30
acg gac tat gtg ccc acc gtg ttc gac aat ttc agc gca aat
gtg gtt 144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val

0070110													
<div style="display: flex; justify-content: space-between;"> 35 40 45 </div>													
gtc	aat	gga	gcc	act	gtc	aac	cta	ggg	ttg	tgg	gat	act	gct
gga	cag		192										
Val	Asn	Gly	Ala	Thr	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala
Gly	Gln												
<div style="display: flex; justify-content: space-between;"> 50 55 60 </div>													
gag	gac	tac	aat	agg	tta	aga	ccc	ctg	agt	tac	cgt	ggg	gcc
gat	ggt		240										
Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala
Asp	Val												
<div style="display: flex; justify-content: space-between;"> 65 70 75 </div>													
<div style="display: flex; justify-content: space-between;"> 80 </div>													
ttc	att	ttg	gca	ttc	tct	ctc	att	agt	aaa	gcc	agc	tat	gag
aat	gtc		288										
Phe	Ile	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Lys	Ala	Ser	Tyr	Glu
Asn	Val												
<div style="display: flex; justify-content: space-between;"> 85 90 </div>													
<div style="display: flex; justify-content: space-between;"> 95 </div>													
tcc	aag	aag	tgg	att	cct	gag	ttg	aag	cac	tat	gct	cct	ggt
gtc	cca		336										
Ser	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Lys	His	Tyr	Ala	Pro	Gly
Val	Pro												
<div style="display: flex; justify-content: space-between;"> 100 105 110 </div>													
ata	gtt	ctt	gtt	gga	aca	aaa	ctt	gat	ctt	cgg	gat	gac	aag
caa	ttc		384										
Ile	Val	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys
Gln	Phe												
<div style="display: flex; justify-content: space-between;"> 115 120 125 </div>													
ttc	gta	gac	cat	cct	ggt	gct	gtg	cca	att	gct	act	gct	cag
ggc	gag		432										
Phe	Val	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Ala	Thr	Ala	Gln
Gly	Glu												
<div style="display: flex; justify-content: space-between;"> 130 135 140 </div>													
gag	cta	agg	aaa	aca	atc	ggt	gca	cca	tct	tac	gtt	gaa	tgt
agt	tca		480										
Glu	Leu	Arg	Lys	Thr	Ile	Gly	Ala	Pro	Ser	Tyr	Val	Glu	Cys
Ser	Ser												
<div style="display: flex; justify-content: space-between;"> 145 150 155 </div>													
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aag	ggt		528										
Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile
Lys	Gly												
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caa	aag		576										

0070110

Arg Pro Pro Ala Ser Gln Asp Glu Glu Lys Lys Gly Lys Ser
Gln Lys
180 185 190

gcc tgc tcg ata ttg tga
594
Ala Cys Ser Ile Leu
195

<210> 361
<211> 197
<212> PRT
<213> Capsicum annuum

<400> 361
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Gly Ala
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Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
20 25 30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
35 40 45

Val Asn Gly Ala Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65 70 75
80

Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val
85 90

95
Ser Lys Lys Trp Ile Pro Glu Leu Lys His Tyr Ala Pro Gly
Val Pro
100 105 110

Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe
115 120 125

Phe Val Asp His Pro Gly Ala Val Pro Ile Ala Thr Ala Gln
Seite 555

0070110

Gly Glu
130 135 140
Glu Leu Arg Lys Thr Ile Gly Ala Pro Ser Tyr Val Glu Cys
Ser Ser
145 150 155
160
Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Lys Gly
165 170
175
Arg Pro Pro Ala Ser Gln Asp Glu Glu Lys Lys Gly Lys Ser
Gln Lys
180 185 190
Ala Cys Ser Ile Leu
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<210> 362
<211> 579
<212> DNA
<213> Medicago varia

<220>
<221> CDS
<222> (1)..(579)

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ggc aag 48
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Gly Lys
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15
acc tgc ctg ctc atc gcc tac acc tcc aac tcc ttc cct cag
gag tat 96
Thr Cys Leu Leu Ile Ala Tyr Thr Ser Asn Ser Phe Pro Gln
Glu Tyr
20 25 30
gtg ccc acc gtg ttt gac aac tac tct gcc aac gtc atg gtc
gat ggt 144
Val Pro Thr Val Phe Asp Asn Tyr Ser Ala Asn Val Met Val
Asp Gly
35 40 45
cgc atg gtt tcc ctc ggt ctt tgg gac acg gcc ggc cag gag
gat tac 192

Arg Met Val Ser Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu
Seite 556

0070110

Asp	Tyr													
	50					55					60			
gac	cgt	ctc	cgc	ccc	ctg	tct	tac	cct	ggc	acc	gac	gtg	ttc	
ctc	ctc		240											
Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Pro	Gly	Thr	Asp	Val	Phe	
Leu	Leu													
65					70					75				
80														
tgc	ttc	tcc	gtg	atc	tcc	ccc	acc	tct	ttc	tcg	aac	gtg	aag	
agc	aag		288											
Cys	Phe	Ser	Val	Ile	Ser	Pro	Thr	Ser	Phe	Ser	Asn	Val	Lys	
Ser	Lys													
				85						90				
95														
tgg	tgg	cct	gag	gtc	tct	cac	cac	tgc	ccc	aac	gcc	aag	atg	
atc	ctc		336											
Trp	Trp	Pro	Glu	Val	Ser	His	His	Cys	Pro	Asn	Ala	Lys	Met	
Ile	Leu													
			100					105					110	
gtg	ggc	acc	aag	atg	gat	ctc	cgc	gac	gac	cgt	gac	acc	ctc	
gac	ggt		384											
Val	Gly	Thr	Lys	Met	Asp	Leu	Arg	Asp	Asp	Arg	Asp	Thr	Leu	
Asp	Gly													
		115				120						125		
ctc	aag	cgc	aag	ggc	ctc	tcc	ccc	atc	tct	cag	act	gat	ggt	
gag	ggc		432											
Leu	Lys	Arg	Lys	Gly	Leu	Ser	Pro	Ile	Ser	Gln	Thr	Asp	Gly	
Glu	Gly													
						135					140			
ctc	gcc	cgc	gat	atc	ggc	gcc	gtc	gcc	tac	atg	gag	tgc	tct	
gcc	ctc		480											
Leu	Ala	Arg	Asp	Ile	Gly	Ala	Val	Ala	Tyr	Met	Glu	Cys	Ser	
Ala	Leu													
145					150					155				
160														
acc	cag	gct	ggc	ctc	aag	cag	gtg	ttc	gac	gag	gcc	atc	aag	
gcc	gtg		528											
Thr	Gln	Ala	Gly	Leu	Lys	Gln	Val	Phe	Asp	Glu	Ala	Ile	Lys	
Ala	Val													
				165						170				
175														
gtc	gtc	aaa	aaa	acc	cca	tcc	ccg	caa	gaa	aaa	aat	tgc	acc	
ctc	ttc		576											
Val	Val	Lys	Lys	Thr	Pro	Ser	Pro	Gln	Glu	Lys	Asn	Cys	Thr	
Leu	Phe													
			180					185					190	

0070110

taa

579

<210> 363

<211> 192

<212> PRT

<213> Medicago varia

<400> 363

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Gly Lys

1 5 10

15

Thr Cys Leu Leu Ile Ala Tyr Thr Ser Asn Ser Phe Pro Gln
Glu Tyr

20 25 30

Val Pro Thr Val Phe Asp Asn Tyr Ser Ala Asn Val Met Val
Asp Gly

35 40 45

Arg Met Val Ser Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu
Asp Tyr

50 55 60

Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gly Thr Asp Val Phe
Leu Leu

65 70 75

80

Cys Phe Ser Val Ile Ser Pro Thr Ser Phe Ser Asn Val Lys
Ser Lys

85 90

95

Trp Trp Pro Glu Val Ser His His Cys Pro Asn Ala Lys Met
Ile Leu

100 105 110

Val Gly Thr Lys Met Asp Leu Arg Asp Asp Arg Asp Thr Leu
Asp Gly

115 120 125

Leu Lys Arg Lys Gly Leu Ser Pro Ile Ser Gln Thr Asp Gly
Glu Gly

130 135 140

Leu Ala Arg Asp Ile Gly Ala Val Ala Tyr Met Glu Cys Ser
Seite 558

0070110

Ala Leu
 145 150 155
 160
 Thr Gln Ala Gly Leu Lys Gln Val Phe Asp Glu Ala Ile Lys
 Ala Val
 165 170
 175
 Val Val Lys Lys Thr Pro Ser Pro Gln Glu Lys Asn Cys Thr
 Leu Phe
 180 185 190

<210> 364
 <211> 594
 <212> DNA
 <213> Medicago varia

<220>
 <221> CDS
 <222> (1)..(594)

<400> 364
 atg agt ggt tcc agg ttc atc aag tgt gtc act gtt ggt gat
 ggt gcc 48
 Met Ser Gly Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala
 1 5 10
 15
 gtt gga aag act tgt ttg ctt atc tct tac acc agt aac act
 ttc cct 96
 Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
 Phe Pro
 20 25 30
 acg gac tat gtg ccg act gtc ttt gac aat ttc agt gca aat
 gta gtt 144
 Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
 Val Val
 35 40 45
 gtg gat ggg agc act ata aat ctc ggg ttg tgg gat act gct
 ggc caa 192
 Val Asp Gly Ser Thr Ile Asn Leu Gly Leu Trp Asp Thr Ala
 Gly Gln
 50 55 60
 gaa gat tac aat aga tta aga ccc tta agc tat cgt gga gca
 gat gtt 240
 Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
 Asp Val

0070110

65					70							75	
80													
ttt	ctg	ctt	gct	ttt	tct	ctc	ata	agc	aag	gcc	agc	tat	gaa
aat	att		288										
Phe	Leu	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Lys	Ala	Ser	Tyr	Glu
Asn	Ile												
			85						90				
95													
gcc	aaa	aaa	tgg	att	cct	gag	ttg	agg	cat	tat	gct	cct	ggt
ggt	cca		336										
Ala	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Arg	His	Tyr	Ala	Pro	Gly
Val	Pro												
			100						105				110
att	att	ctc	ggt	gga	aca	aaa	ctt	gat	ctt	cgg	gat	gat	agc
cag	ttc		384										
Ile	Ile	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Ser
Gln	Phe												
		115					120					125	
ttt	caa	gac	cat	cct	ggt	gca	gca	cca	ata	acc	aca	gca	cag
ggt	gag		432										
Phe	Gln	Asp	His	Pro	Gly	Ala	Ala	Pro	Ile	Thr	Thr	Ala	Gln
Gly	Glu												
		130				135						140	
gaa	ctg	aaa	aaa	ctt	atc	ggt	gct	cca	att	tac	att	gaa	tgt
tat	tcc		480										
Glu	Leu	Lys	Lys	Leu	Ile	Gly	Ala	Pro	Ile	Tyr	Ile	Glu	Cys
Tyr	Ser												
145					150					155			
160													
aaa	aca	caa	aag	aat	gtg	aag	gct	ggt	ttc	gat	tcg	gcc	atc
aaa	gta		528										
Lys	Thr	Gln	Lys	Asn	Val	Lys	Ala	Val	Phe	Asp	Ser	Ala	Ile
Lys	Val												
			165						170				
175													
ggt	cta	caa	ccg	cca	aag	caa	aag	aaa	aca	aag	aga	aag	ggg
caa	aaa		576										
Val	Leu	Gln	Pro	Pro	Lys	Gln	Lys	Lys	Thr	Lys	Arg	Lys	Gly
Gln	Lys												
			180						185				190
gca	tgt	tcc	att	ttg	tga								
			594										
Ala	Cys	Ser	Ile	Leu									
		195											

<210> 365

0070110

<211> 197

<212> PRT

<213> Medicago varia

<400> 365

Met Ser Gly Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala

1 5 10

15

Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro

20

25

30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val

35

40

45

Val Asp Gly Ser Thr Ile Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln

50

55

60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val

65

70

75

80

Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Ile

85

90

95

Ala Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Gly
Val Pro

100

105

110

Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Ser
Gln Phe

115

120

125

Phe Gln Asp His Pro Gly Ala Ala Pro Ile Thr Thr Ala Gln
Gly Glu

130

135

140

Glu Leu Lys Lys Leu Ile Gly Ala Pro Ile Tyr Ile Glu Cys
Tyr Ser

145

150

155

160

Lys Thr Gln Lys Asn Val Lys Ala Val Phe Asp Ser Ala Ile
Lys Val

0070110

165

170

175
Val Leu Gln Pro Pro Lys Gln Lys Lys Thr Lys Arg Lys Gly
Gln Lys

180

185

190

Ala Cys Ser Ile Leu
195

<210> 366

<211> 594

<212> DNA

<213> Medicago varia

<220>

<221> CDS

<222> (1)..(594)

<400> 366

atg agt gct tct agg ttt att aaa tgt gtt act gtt ggt gat

gga gct 48

Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp

Gly Ala

1

5

10

15

gtt gga aaa act tgt ttg ttg att tct tac acc agc aat act

ttc ccc 96

Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr

Phe Pro

20

25

30

acg gat tat gtg ccg aca gtt ttt gac aat ttc agt gcg aat

gtg gtt 144

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn

Val Val

35

40

45

gtt aat gga agt att gtg aat ctg ggt ttg tgg gat act gct

ggg caa 192

Val Asn Gly Ser Ile Val Asn Leu Gly Leu Trp Asp Thr Ala

Gly Gln

50

55

60

gag gat tat aac aga tta aga cct ttg agt tac cgt ggt gcc

gat gtt 240

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala

Asp Val

65

70

75

80

ttc ata ttg gct ttc tct ctc ata agc aaa gcc agt tat gaa

aat gtc 288

0070110

Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val

85

90

95

tcc aaa aag tgg att cca gag ttg aag cat tat gca cct ggt
gtc ccc
Ser Lys Lys Trp Ile Pro Glu Leu Lys His Tyr Ala Pro Gly
Val Pro

100

105

110

ata att ctg gtt gga aca aag ctt gac ctt cgg gat gat cag
cag ttc
Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Gln
Gln Phe

115

120

125

tgc ata gac cat cct ggt gcc gtt ccc att acc aca gct cag
gga gaa
Cys Ile Asp His Pro Gly Ala Val Pro Ile Thr Thr Ala Gln
Gly Glu

130

135

140

gag ctg agg aag ctg att aat gca cca gct tac att gaa tgc
agt tca
Glu Leu Arg Lys Leu Ile Asn Ala Pro Ala Tyr Ile Glu Cys
Ser Ser

145

150

155

160

aaa tca cag gag aac gtg aag gcg gtg ttt gac gca gcc ata
aga gtt
Lys Ser Gln Glu Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Arg Val

165

170

175

gtc ctt caa cca cca aag cag aag aaa aag aag aat aaa gca
caa aag
Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Asn Lys Ala
Gln Lys

180

185

190

gcc tgt tca ata ttg taa
594

Ala Cys Ser Ile Leu
195

<210> 367

<211> 197

<212> PRT

<213> Medicago varia

0070110

<400> 367

Met	Ser	Ala	Ser	Arg	Phe	Ile	Lys	Cys	Val	Thr	Val	Gly	Asp
Gly	Ala												
1				5					10				
15													
Val	Gly	Lys	Thr	Cys	Leu	Leu	Ile	Ser	Tyr	Thr	Ser	Asn	Thr
Phe	Pro												
			20					25					30
Thr	Asp	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn
Val	Val												
		35					40					45	
Val	Asn	Gly	Ser	Ile	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala
Gly	Gln												
	50					55					60		
Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala
Asp	Val												
65					70					75			
	80												
Phe	Ile	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Lys	Ala	Ser	Tyr	Glu
Asn	Val												
			85						90				
95													
Ser	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Lys	His	Tyr	Ala	Pro	Gly
Val	Pro												
			100					105					110
Ile	Ile	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Gln
Gln	Phe												
		115					120					125	
Cys	Ile	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Thr	Thr	Ala	Gln
Gly	Glu												
	130					135				140			
Glu	Leu	Arg	Lys	Leu	Ile	Asn	Ala	Pro	Ala	Tyr	Ile	Glu	Cys
Ser	Ser												
145					150					155			
	160												
Lys	Ser	Gln	Glu	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile
Arg	Val												
			165						170				
175													
Val	Leu	Gln	Pro	Pro	Lys	Gln	Lys	Lys	Lys	Lys	Asn	Lys	Ala
Gln	Lys												
			180					185					190

0070110

Ala Cys Ser Ile Leu
195

<210> 368

<211> 594

<212> DNA

<213> Medicago varia

<220>

<221> CDS

<222> (1)..(594)

<400> 368

atg agc gct tct agg ttc atc aag tgt gtt act gtt ggg gat
gga gct 48
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10

15
gtt ggt aaa act tgt ttg ttg att tca tac acc agc aat acc
ttc ccc 96
Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro

20 25 30
act gat tat gtg cca act gtc ttc gac aat ttc agt gca aat
gtg gtt 144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val

35 40 45
gtg aat gga agc act gtg aat ctg ggt tta tgg gac act gca
gga caa 192
Val Asn Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln

50 55 60
gag gat tat aac aga tta aga cct ttg agt tat cgt ggt gct
gat gtt 240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val

65 70 75
80
ttc att ctc gct ttc tca ctc ata agc aag gcc agt tat gaa
aat gtt 288
Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val

85 90
95
tct aaa aag tgg att cga gag ttg aag cat tat gca cct ggt

0070110

gtt ccc 336
 Ser Lys Lys Trp Ile Arg Glu Leu Lys His Tyr Ala Pro Gly
 Val Pro 100 105 110

att att ctg gtt ggc aca aag ctt gac ctt cgg gat gac aag
 cag ttc 384
 Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
 Gln Phe 115 120 125

ttt gtc gac cat cct ggt gct gtt ccc att acc acc gct cag
 gga gaa 432
 Phe Val Asp His Pro Gly Ala Val Pro Ile Thr Thr Ala Gln
 Gly Glu 130 135 140

gag ctc agg aag ctg atc aat gca cct gct tat att gaa tgc
 agt tca 480
 Glu Leu Arg Lys Leu Ile Asn Ala Pro Ala Tyr Ile Glu Cys
 Ser Ser 145 150 155
 160

aaa tca cag cag aac gtc aaa gca gtc ttt gat gca gcc ata
 aga gtt 528
 Lys Ser Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
 Arg Val 165 170

175
 gtc ctt caa cca cca aag caa aag aaa aag aag agt aaa gct
 caa aag 576
 Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Ser Lys Ala
 Gln Lys 180 185 190

gcc tgt tcg ata ttg tga
 594
 Ala Cys Ser Ile Leu
 195

<210> 369
 <211> 197
 <212> PRT
 <213> Medicago varia

<400> 369
 Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala
 1 5 10

0070110

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

0070110

<210> 370
<211> 579
<212> DNA
<213> *Biomphalaria glabrata*

<220>
<221> CDS
<222> (1)..(579)

<400> 370
atg gca gca ata cgt aag aag ctt gtg att gtt ggt gat ggt
gca tgt 48
Met Ala Ala Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly
Ala Cys
1 5 10
15
ggg aaa aca tgt cta ctg ata gtt ttt agc aaa gac cag ttt
cct gaa 96
Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Asp Gln Phe
Pro Glu
20 25 30
gtt tat gtg cca aca gtt ttt gaa aat tat gta gca gat att
gaa gta 144
Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Ile
Glu Val
35 40 45
gat agc aaa cag gta gaa cta gcc tta tgg gac aca gct ggt
caa gag 192
Asp Ser Lys Gln Val Glu Leu Ala Leu Trp Asp Thr Ala Gly
Gln Glu
50 55 60
gat tat gat agg ctt cga cca tta tca tat cct gat act gat
gtt att 240
Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Thr Asp
Val Ile
65 70 75
80
cta atg tgc ttc tct ata gac agt cca gac agt ttg gaa aat
atc cct 288
Leu Met Cys Phe Ser Ile Asp Ser Pro Asp Ser Leu Glu Asn
Ile Pro
85 90
95
gaa aaa tgg acc cct gag gtt cgt cat ttt tgc cca aac gtt
ccg atc 336
Glu Lys Trp Thr Pro Glu Val Arg His Phe Cys Pro Asn Val
Pro Ile
100 105 110

0070110

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att ctt gtt ggc aat aag aaa gat ctt cgc aat gat gaa agc
acc aaa                               384
Ile Leu val Gly Asn Lys Lys Asp Leu Arg Asn Asp Glu Ser
Thr Lys
      115                               120                               125
cga gaa ttg atg aaa atg aaa caa gaa cct gtg cgg cca gaa
gag ggt                               432
Arg Glu Leu Met Lys Met Lys Gln Glu Pro val Arg Pro Glu
Glu Gly
      130                               135                               140
aga gcc atg gct gaa aaa atc aat gcc tac tca tac ctc gag
tgc tct                               480
Arg Ala Met Ala Glu Lys Ile Asn Ala Tyr Ser Tyr Leu Glu
Cys Ser
145                               150                               155
      160
gct aaa aca aag gaa ggt gta cgt gaa gtg ttt gaa act gct
act aga                               528
Ala Lys Thr Lys Glu Gly val Arg Glu val Phe Glu Thr Ala
Thr Arg
      165                               170
175
gct gca ctc caa gtt aaa aag aag aaa aag ggt gga tgt att
gta ttg                               576
Ala Ala Leu Gln val Lys Lys Lys Lys Lys Gly Gly Cys Ile
val Leu
      180                               185                               190

tga
      579

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<210> 371
 <211> 192
 <212> PRT
 <213> Biomphalaria glabrata

<400> 371
 Met Ala Ala Ile Arg Lys Lys Leu val Ile val Gly Asp Gly
 Ala Cys
 1 5 10
 15
 Gly Lys Thr Cys Leu Leu Ile val Phe Ser Lys Asp Gln Phe
 Pro Glu
 20 25 30

0070110

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

<210> 372

<211> 600

<212> DNA

<213> Paracoccidioides brasiliensis

<220>

0070110

<221> CDS

<222> (1)..(600)

<400> 372

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

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0070110

aag acc act gct gac aat ctt cgc gcg aag aag atg gag cca
 gtt tcc 432
 Lys Thr Thr Ala Asp Asn Leu Arg Ala Lys Lys Met Glu Pro
 Val Ser

130 135 140
 tat gaa cag gcc ctt gca gtt gct aag gag atc aag gca caa
 aag tat 480
 Tyr Glu Gln Ala Leu Ala Val Ala Lys Glu Ile Lys Ala Gln
 Lys Tyr
 145 150 155

160
 ctc gag tgc tct gct ctt aca cag cga aat ttg aag agt gtc
 ttt gac 528
 Leu Glu Cys Ser Ala Leu Thr Gln Arg Asn Leu Lys Ser Val
 Phe Asp

165 170
 175
 gaa gct atc cgt gcc gta ctg aac cca cgt ccc att gcc aaa
 cca aaa 576
 Glu Ala Ile Arg Ala Val Leu Asn Pro Arg Pro Ile Ala Lys
 Pro Lys
 180 185 190

aag tcc aaa tgc aga atc ctc taa
 600
 Lys Ser Lys Cys Arg Ile Leu
 195

<210> 373
 <211> 199
 <212> PRT
 <213> Paracoccidioides brasiliensis

<400> 373
 Met Ala Ser Gly Pro Ala Thr Gln Ser Leu Lys Cys Val Val
 Thr Gly
 1 5 10
 15
 Asp Gly Ala Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr
 Thr Asn
 20 25 30
 Ala Phe Pro Gly Glu Tyr Ile Pro Thr Val Phe Asp Asn Tyr
 Ser Ala
 35 40 45
 Ser Val Met Val Asp Gly Lys Pro Ile Ser Leu Gly Leu Trp
 Asp Thr

0070110
55

50

60

Ala Gly Gln Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr
Pro Gln
65 70 75

80
Thr Asp Val Phe Leu Ile Cys Phe Ser Ile Val Ser Pro Pro
Ser Phe
85 90

95
Asp Asn Val Lys Ala Lys Trp Tyr Pro Glu Ile Glu His His
Ala Pro
100 105 110

Asn Val Pro Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg
Asp Asp
115 120 125

Lys Thr Thr Ala Asp Asn Leu Arg Ala Lys Lys Met Glu Pro
Val Ser
130 135 140

Tyr Glu Gln Ala Leu Ala Val Ala Lys Glu Ile Lys Ala Gln
Lys Tyr
145 150 155

160
Leu Glu Cys Ser Ala Leu Thr Gln Arg Asn Leu Lys Ser Val
Phe Asp
165 170

175
Glu Ala Ile Arg Ala Val Leu Asn Pro Arg Pro Ile Ala Lys
Pro Lys
180 185 190

Lys Ser Lys Cys Arg Ile Leu
195

<210> 374
<211> 576
<212> DNA
<213> *Phallusia mammilata*

<220>
<221> CDS
<222> (1)..(576)

<400> 374
atg caa act ata aaa tgt gtt gtg gtt ggt gat ggt gcg gtt
Seite 573

0070110

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

```

0070110

ctg gca agg gag tta aaa gcc gtc aaa tat gtt gaa tgt tct
 gct tta 480
 Leu Ala Arg Glu Leu Lys Ala Val Lys Tyr Val Glu Cys Ser
 Ala Leu

145 150 155

160

aca cag aaa gga ctc aaa aat gtt ttt gat gaa gcc atc tta
 gct gca 528
 Thr Gln Lys Gly Leu Lys Asn Val Phe Asp Glu Ala Ile Leu
 Ala Ala

165 170

175

ctt gaa cct ccg gaa cct agg cgc aaa cga aag tgc aac att
 ttg 573
 Leu Glu Pro Pro Glu Pro Arg Arg Lys Arg Lys Cys Asn Ile
 Leu

180 185 190

tga

576

<210> 375

<211> 191

<212> PRT

<213> Phallusia mammilata

<400> 375

Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
 Gly Lys

1 5 10

15

Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe Pro Gln
 Glu Tyr

20 25 30

Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val Met Ile
 Gly Gly

35 40 45

Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu
 Asp Tyr

50 55 60

Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
 Leu Val

65 70 75

0070110

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

<210> 376
 <211> 636
 <212> DNA
 <213> Gossypium hirsutum

<220>
 <221> CDS
 <222> (1)..(636)

<400> 376
 atg gct tca agc gct tca aga ttt atc aaa tgt gta aca gtt
 gga gat 48
 Met Ala Ser Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val
 Gly Asp
 1 5 10
 15
 gga gct gtt ggc aag act tgc atg ctt att tgc tat aca agt
 aac aag 96

0070110

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

0070110

agc tca aaa act cag cag aac gtg aaa gca gtt ttt gat gat
 gca atc 528
 Ser Ser Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Asp
 Ala Ile

165

170

175

aaa gtt gta atc aag cca ccc cag aaa cag aag gag aag aag
 aaa aag 576
 Lys Val Val Ile Lys Pro Pro Gln Lys Gln Lys Glu Lys Lys
 Lys Lys

180

185

190

cca agt cga gga tgt cta ata aat gtc ttc tgc ggg agg aac
 ttc gtg 624
 Pro Ser Arg Gly Cys Leu Ile Asn Val Phe Cys Gly Arg Asn
 Phe Val

195

200

205

cct gct aaa tga
 636

Pro Ala Lys
 210

<210> 377

<211> 211

<212> PRT

<213> Gossypium hirsutum

<400> 377

Met Ala Ser Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val
 Gly Asp

1

5

10

15

Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser
 Asn Lys

20

25

30

Phe Pro Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser
 Ala Asn

35

40

45

Val Val Val Glu Gly Thr Thr Val Asn Leu Gly Leu Trp Asp
 Thr Ala
 50

55

60

Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg
 Gly Ala

65

70

75

80

0070110

Asp Val Phe Val Leu Ala Phe Ser Leu Val Ser Arg Ala Ser
His Glu

85

90

95

Asn Val Leu Lys Lys Trp Ile Pro Glu Leu Gln His Tyr Ala
Pro Gly

100

105

110

Val Pro Val Val Leu Val Gly Thr Lys Leu Asp Leu Arg Glu
Asp Lys

115

120

125

His Tyr Leu Ala Asp His Pro Gly Leu Leu Pro Val Ser Thr
Ala Gln

130

135

140

Gly Glu Glu Leu Arg Lys Gln Ile Gly Ala Ala Tyr Tyr Ile
Glu Cys

145

150

155

160

Ser Ser Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Asp
Ala Ile

165

170

175

Lys Val Val Ile Lys Pro Pro Gln Lys Gln Lys Glu Lys Lys
Lys Lys

180

185

190

Pro Ser Arg Gly Cys Leu Ile Asn Val Phe Cys Gly Arg Asn
Phe Val

195

200

205

Pro Ala Lys
210

<210> 378

<211> 588

<212> DNA

<213> Gossypium hirsutum

<220>

<221> CDS

<222> (1)..(588)

<400> 378

atg agc gcc tcg aga ttc ata aag tgc gtc acc gtc ggc gat
gga gcc 48

Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Seite 579

0070110

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

0070110

Glu Leu Lys Lys Gln Ile Ala Ala Pro Ala Tyr Ile Glu Cys
 Ser Ser
 145 150 155

160
 aaa aca cag cag aat gtg aag gca gtg ttt gat gca gcc att
 aag gta 528
 Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
 Lys Val
 165 170

175
 gtg ctg cag cct ccg aat aaa aat aag aag aaa aag tca ggt
 ggt tgc 576
 Val Leu Gln Pro Pro Asn Lys Asn Lys Lys Lys Lys Ser Gly
 Gly Cys
 180 185 190

tca ata tta tga
 588
 Ser Ile Leu
 195

<210> 379
 <211> 195
 <212> PRT
 <213> Gossypium hirsutum

<400> 379
 Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala
 1 5 10

15
 Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
 Phe Pro
 20 25 30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
 Val Val
 35 40 45

Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
 Gly Gln
 50 55 60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
 Asp Val
 65 70 75

80
 Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
 Seite 581

0070110

Asn Val
85 90
95
Ala Lys Lys Trp Ile Pro Glu Leu Lys His Tyr Ala Pro Gly
Val Pro 100 105 110
Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Gln
Gln Phe 115 120 125
Leu Thr Asp His Pro Asn Ala Val Pro Ile Ser Thr Ala Gln
Gly Glu 130 135 140
Glu Leu Lys Lys Gln Ile Ala Ala Pro Ala Tyr Ile Glu Cys
Ser Ser 145 150 155
160
Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Lys Val 165 170
175
Val Leu Gln Pro Pro Asn Lys Asn Lys Lys Lys Lys Ser Gly
Gly Cys 180 185 190
Ser Ile Leu
195

<210> 380
<211> 600
<212> DNA
<213> Aspergillus niger

<220>
<221> CDS
<222> (1)..(600)

<220>
<221> misc_feature
<222> (108)..(108)
<223> s i s g o r c

<400> 380
atg gcc act ggt cca gct act caa tcc ctc aag tgt gtg gtg
acg ggt 48
Met Ala Thr Gly Pro Ala Thr Gln Ser Leu Lys Cys Val Val

0070110

Thr	Gly												
1				5					10				
15													
gat	ggt	gcg	gta	gga	aag	aca	tgt	ctc	ctg	att	tcg	tac	acg
acc	aac		96										
Asp	Gly	Ala	Val	Gly	Lys	Thr	Cys	Leu	Leu	Ile	Ser	Tyr	Thr
Thr	Asn												
			20					25					30
gct	ttc	ccc	ggs	gaa	tat	atc	cct	acc	gta	ttt	gat	aac	tac
acc	gct		144										
Ala	Phe	Pro	Gly	Glu	Tyr	Ile	Pro	Thr	Val	Phe	Asp	Asn	Tyr
Thr	Ala												
		35					40					45	
agt	gtc	atg	gta	gat	ggc	cga	ccg	att	agc	ttg	gga	ctc	tgg
gat	act		192										
Ser	Val	Met	Val	Asp	Gly	Arg	Pro	Ile	Ser	Leu	Gly	Leu	Trp
Asp	Thr												
		50				55				60			
gct	gga	cag	gaa	gat	tac	gac	cgt	ctt	cgc	cca	ttg	tcc	tac
ccg	caa		240										
Ala	Gly	Gln	Glu	Asp	Tyr	Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr
Pro	Gln												
65					70					75			
80													
acc	gac	gtc	ttc	ctg	atc	tgc	ttc	tcc	atc	gtt	agc	ccg	ccg
tcc	ttt		288										
Thr	Asp	Val	Phe	Leu	Ile	Cys	Phe	Ser	Ile	Val	Ser	Pro	Pro
Ser	Phe												
			85							90			
95													
gac	aac	gtt	aaa	gcc	aag	tgg	ttc	ccg	gag	att	gaa	cac	cat
gcc	ccc		336										
Asp	Asn	Val	Lys	Ala	Lys	Trp	Phe	Pro	Glu	Ile	Glu	His	His
Ala	Pro												
			100					105				110	
aac	gtc	ccc	att	atc	ttg	gtc	ggc	acc	aag	ctc	gac	ctt	cga
gac	gac		384										
Asn	Val	Pro	Ile	Ile	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg
Asp	Asp												
		115					120				125		
cgt	ggt	acc	ata	gat	gct	ctc	cga	cag	cgg	aag	atg	gag	ccc
gtc	tcc		432										
Arg	Gly	Thr	Ile	Asp	Ala	Leu	Arg	Gln	Arg	Lys	Met	Glu	Pro
Val	Ser												
		130				135					140		
tac	gaa	caa	gct	ctg	gcc	gtg	gcc	aag	gaa	atc	cgg	gca	cac
aag	tac		480										

0070110

Tyr Glu Gln Ala Leu Ala Val Ala Lys Glu Ile Arg Ala His
 Lys Tyr
 145 150 155

160
 ctc gaa tgt tcg gcc ctg acg cag cgc aac ctg aag agt gta
 ttc gac 528
 Leu Glu Cys Ser Ala Leu Thr Gln Arg Asn Leu Lys Ser Val
 Phe Asp
 165 170

175
 gag gcg att cgc gcc gtg ctc aat ccc cgg cct gcg gcc aaa
 ccg aag 576
 Glu Ala Ile Arg Ala Val Leu Asn Pro Arg Pro Ala Ala Lys
 Pro Lys
 180 185 190

aac aag aaa tgc gtg att ctg tag
 600
 Asn Lys Lys Cys Val Ile Leu
 195

<210> 381
 <211> 199
 <212> PRT
 <213> Aspergillus niger

<400> 381
 Met Ala Thr Gly Pro Ala Thr Gln Ser Leu Lys Cys Val Val
 Thr Gly
 1 5 10
 15
 Asp Gly Ala Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr
 Thr Asn
 20 25 30

Ala Phe Pro Gly Glu Tyr Ile Pro Thr Val Phe Asp Asn Tyr
 Thr Ala
 35 40 45

Ser Val Met Val Asp Gly Arg Pro Ile Ser Leu Gly Leu Trp
 Asp Thr
 50 55 60

Ala Gly Gln Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr
 Pro Gln
 65 70 75

80
 Thr Asp Val Phe Leu Ile Cys Phe Ser Ile Val Ser Pro Pro
 Seite 584

0070110

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Ser Phe
      85          90
95
Asp Asn Val Lys Ala Lys Trp Phe Pro Glu Ile Glu His His
Ala Pro
      100          105          110
Asn Val Pro Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg
Asp Asp
      115          120          125
Arg Gly Thr Ile Asp Ala Leu Arg Gln Arg Lys Met Glu Pro
Val Ser
      130          135          140
Tyr Glu Gln Ala Leu Ala Val Ala Lys Glu Ile Arg Ala His
Lys Tyr
      145          150          155
      160
Leu Glu Cys Ser Ala Leu Thr Gln Arg Asn Leu Lys Ser Val
Phe Asp
      165          170
      175
Glu Ala Ile Arg Ala Val Leu Asn Pro Arg Pro Ala Ala Lys
Pro Lys
      180          185          190
Asn Lys Lys Cys Val Ile Leu
      195

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<210> 382
 <211> 591
 <212> DNA
 <213> Vigna radiata

<220>
 <221> CDS
 <222> (1)..(591)

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<400> 382
atg agt acg gcc agg ttt atc aag tgt gta aca gtt gga gat
ggt gct      48
Met Ser Thr Ala Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
  1          5          10
15
gtg gga aag aca tgc atg ctc ata tcc tat acc agc aac acg
ttt ccc      96

```

0070110

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

0070110

aaa aca cag cag aat gtg aag aca gtt ttt gat gct gca ata
aag gtc
Lys Thr Gln Gln Asn Val Lys Thr Val Phe Asp Ala Ala Ile
Lys Val

165

170

175

gca ttg agg cca cca aag cca aag aag aaa cca cgc aag aaa
agg acc
Ala Leu Arg Pro Pro Lys Pro Lys Lys Lys Pro Arg Lys Lys
Arg Thr

180

185

190

tgt ttt ttc ctc taa
591
Cys Phe Phe Leu
195

<210> 383

<211> 196

<212> PRT

<213> Vigna radiata

<400> 383

Met Ser Thr Ala Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala

1

5

10

15

Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro

20

25

30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Thr

35

40

45

Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val

65

70

75

80

Phe Leu Leu Cys Tyr Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Ile

85

90

95

Ser Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Asn

[illegible]

<220>
<221> CDS
<222> (1)..(585)

<400> 384													
atg	acc	aca	caa	tct	cta	aag	tgc	gtc	gtg	aca	ggc	gat	ggg
gcc	gtc			48									
Met	Thr	Thr	Gln	Ser	Leu	Lys	Cys	Val	Val	Thr	Gly	Asp	Gly
Ala	Val												
1				5					10				
15													
gga	aag	aca	tgt	ctg	ctc	atc	tcc	tac	acc	acc	aat	gct	ttc
cca	ggc			96									
Gly	Lys	Thr	Cys	Leu	Leu	Ile	Ser	Tyr	Thr	Thr	Asn	Ala	Phe
Pro	Gly												
			20					25					30
gaa	tac	atc	ccc	acc	gtc	ttc	gac	aac	tac	tcc	gct	agt	gtc

0070110

atg gtc	144												
Glu Tyr	Ile	Pro	Thr	Val	Phe	Asp	Asn	Tyr	Ser	Ala	Ser	Val	
Met Val													
	35				40						45		
gac gga	aag	cct	atc	agc	ttg	gga	ctg	tgg	gat	act	gcc	ggt	
cag gag		192											
Asp Gly	Lys	Pro	Ile	Ser	Leu	Gly	Leu	Trp	Asp	Thr	Ala	Gly	
Gln Glu													
	50				55						60		
gat tac	gac	aga	ctg	aga	cca	ttg	tcg	tac	cca	cag	acc	gat	
ggt ttc		240											
Asp Tyr	Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Pro	Gln	Thr	Asp	
Val Phe													
	65			70					75				
	80												
ctt atc	tgt	ttc	tcg	cta	gtg	tcg	ccg	cca	tca	ttc	gag	aac	
ggt aaa		288											
Leu Ile	Cys	Phe	Ser	Leu	Val	Ser	Pro	Pro	Ser	Phe	Glu	Asn	
Val Lys													
		85					90						
95													
aca aag	tgg	ttc	ccg	gaa	att	agc	cat	cac	gcg	cca	aat	ggt	
cca att		336											
Thr Lys	Trp	Phe	Pro	Glu	Ile	Ser	His	His	Ala	Pro	Asn	Val	
Pro Ile													
		100				105						110	
atc ctc	gtc	ggc	acc	aag	ctc	gat	ttg	aga	gac	gac	cca	aag	
atc cag		384											
Ile Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Pro	Lys	
Ile Gln													
	115				120						125		
cag tct	ttg	aag	gat	aag	aag	atg	gcc	cca	atc	cag	ttc	aca	
aat ggt		432											
Gln Ser	Leu	Lys	Asp	Lys	Lys	Met	Ala	Pro	Ile	Gln	Phe	Thr	
Asn Gly													
	130				135						140		
gtc gcc	atc	gca	aag	gat	att	gga	gct	gtc	aag	tat	ctc	gag	
tgc tcc		480											
Val Ala	Ile	Ala	Lys	Asp	Ile	Gly	Ala	Val	Lys	Tyr	Leu	Glu	
Cys Ser													
				150					155				
145													
	160												
gct cta	acc	cag	aag	ggt	ctg	aag	aac	ggt	ttc	gac	gaa	gcc	
atc aga		528											
Ala Leu	Thr	Gln	Lys	Gly	Leu	Lys	Asn	Val	Phe	Asp	Glu	Ala	
Ile Arg													
		165						170					

0070110

175

gca gtc ttg tcg cca cca cca aag cca acc aag agc aag aag
tgc act 576
Ala Val Leu Ser Pro Pro Pro Lys Pro Thr Lys Ser Lys Lys
Cys Thr

180

185

190

atc ctg taa

585

Ile Leu

<210> 385

<211> 194

<212> PRT

<213> Monacrosporium haptotylum

<400> 385

Met Thr Thr Gln Ser Leu Lys Cys Val Val Thr Gly Asp Gly
Ala Val

1 5 10

15

Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Ala Phe
Pro Gly

20

25

30

Glu Tyr Ile Pro Thr Val Phe Asp Asn Tyr Ser Ala Ser Val
Met Val

35

40

45

Asp Gly Lys Pro Ile Ser Leu Gly Leu Trp Asp Thr Ala Gly
Gln Glu

50

55

60

Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp
Val Phe

65

70

75

80

Leu Ile Cys Phe Ser Leu Val Ser Pro Pro Ser Phe Glu Asn
Val Lys

85

90

95

Thr Lys Trp Phe Pro Glu Ile Ser His His Ala Pro Asn Val
Pro Ile

100

105

110

Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Pro Lys
Ile Gln

0070110
120

115

125

Gln Ser Leu Lys Asp Lys Lys Met Ala Pro Ile Gln Phe Thr
Asn Gly
130 135 140

Val Ala Ile Ala Lys Asp Ile Gly Ala Val Lys Tyr Leu Glu
Cys Ser
145 150 155
160

Ala Leu Thr Gln Lys Gly Leu Lys Asn Val Phe Asp Glu Ala
Ile Arg
165 170

175
Ala Val Leu Ser Pro Pro Pro Lys Pro Thr Lys Ser Lys Lys
Cys Thr
180 185 190

Ile Leu

<210> 386
<211> 582
<212> DNA
<213> Monacrosporium haptotylum

<220>
<221> CDS
<222> (1)..(582)

<400> 386
atg gct gat atc aga cga aag ctt gtc atc gtc ggt gac ggc
gcg tgc 48
Met Ala Asp Ile Arg Arg Lys Leu Val Ile Val Gly Asp Gly
Ala Cys
1 5 10
15
ggc aaa acc tgt ctt ttg att gtc ttc tca aag ggg act ttc
cca gag 96
Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Gly Thr Phe
Pro Glu
20 25 30
gtc tat gtt cct acc gtt ttc gag aat tac gtc gcc gat gtc
gaa gtt 144
Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Val
Glu Val
35 40 45
gat ggg gag cat gtc gaa ttg gca cta tgg gat acg gca ggt
Seite 591

0070110

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

0070110

180

185

190

ttg taa

582

Leu

<210> 387

<211> 193

<212> PRT

<213> Monacrosporium haptotylum

<400> 387

Met Ala Asp Ile Arg Arg Lys Leu Val Ile Val Gly Asp Gly

Ala Cys

1

5

10

15

Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Gly Thr Phe

Pro Glu

20

25

30

Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Val

Glu Val

35

40

45

Asp Gly Glu His Val Glu Leu Ala Leu Trp Asp Thr Ala Gly

Gln Glu

50

55

60

Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Ser His

Val Ile

65

70

75

80

Leu Ile Cys Phe Ala Ile Asp Ser Pro Asp Ser Leu Asp Asn

Val Gln

85

90

95

Glu Lys Trp Ile Ser Glu Val Leu His Phe Cys Gln Gly Leu

Pro Ile

100

105

110

Ile Leu Val Gly Cys Lys Lys Asp Leu Arg Phe Asp Ser Lys

Thr Met

115

120

125

Glu Glu Leu Arg Lys Thr Ser Gln Lys Pro Val Thr Pro Glu

Glu Gly

130

135

140

0070110

Glu Gln Val Arg Gly Lys Ile Gly Ala Ala Lys Tyr Leu Glu
Cys Ser
145 150 155
160
Ala Lys Thr Asn Asp Gly Val Arg Glu Val Phe Glu His Ala
Thr Arg
165 170
175
Ala Ala Leu Thr Thr Phe Lys Lys Lys Lys Ser Ser Lys Cys
Ser Ile
180 185 190

Leu

<210> 388
<211> 648
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)..(648)

<400> 388
atg gct tca agt gct tca aag ttc atc aag tgt gtg act gtt
ggt gat 48
Met Ala Ser Ser Ala Ser Lys Phe Ile Lys Cys Val Thr Val
Gly Asp
1 5 10
15
ggt gct gtt ggt aaa acc tgt atg ctc atc tgc tac acc agc
aat aaa 96
Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser
Asn Lys
20 25 30
ttc ccc act gac tac ata cca aca gtt ttt gac aac ttt agt
gca aat 144
Phe Pro Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser
Ala Asn
35 40 45
gtt gtt gtt gaa ggc acc act gtc aat ttg ggg ctt tgg gac
act gct 192
Val Val Val Glu Gly Thr Thr Val Asn Leu Gly Leu Trp Asp
Thr Ala
50 55 60
ggg caa gaa gac tat aac aga tta agg cct tta agt tac agg
Seite 594

0070110

gga gca 240
 Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg
 Gly Ala
 65 70 75
 80
 gat gtt ttc gtc ttg tct ttc tca tta gtc agc cga gtt agc
 tac gag 288
 Asp Val Phe Val Leu Ser Phe Ser Leu Val Ser Arg Val Ser
 Tyr Glu
 85 90
 95
 aat gtt ttt aaa aag tgg atc cct gaa ctc caa cac ttt gct
 cca gga 336
 Asn Val Phe Lys Lys Trp Ile Pro Glu Leu Gln His Phe Ala
 Pro Gly
 100 105 110
 gtt ccc ctt gtc ctt gtt ggt acc aaa tta gat ctt cgt gaa
 gat aag 384
 Val Pro Leu Val Leu Val Gly Thr Lys Leu Asp Leu Arg Glu
 Asp Lys
 115 120 125
 cat tat ttg gct gat cat cct gga cta tcc cct gta act act
 gca cag 432
 His Tyr Leu Ala Asp His Pro Gly Leu Ser Pro Val Thr Thr
 Ala Gln
 130 135 140
 gga gag gag ttg cgt aag cta att ggt gcg acg tat tac att
 gag tgt 480
 Gly Glu Glu Leu Arg Lys Leu Ile Gly Ala Thr Tyr Tyr Ile
 Glu Cys
 145 150 155
 160
 agt tca aaa act caa cag aat gtg aaa gca gtt ttt gat tct
 gcg ata 528
 Ser Ser Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ser
 Ala Ile
 165 170
 175
 aag gaa gtg atc aaa cct ctg gtt aaa caa aag gag aag act
 aag aag 576
 Lys Glu Val Ile Lys Pro Leu Val Lys Gln Lys Glu Lys Thr
 Lys Lys
 180 185 190
 aag aag aag caa aag tcg aat cac ggc tgt tta tca aat gtt
 ctg tgt 624

0070110

Lys Lys Lys Gln Lys Ser Asn His Gly Cys Leu Ser Asn Val
 Leu Cys
 195 200 205
 ggg agg ata gtg act cgg cat tga
 648
 Gly Arg Ile Val Thr Arg His
 210 215

<210> 389
 <211> 215
 <212> PRT
 <213> Arabidopsis thaliana

<400> 389
 Met Ala Ser Ser Ala Ser Lys Phe Ile Lys Cys Val Thr Val
 Gly Asp
 1 5 10
 15
 Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser
 Asn Lys
 20 25 30

Phe Pro Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser
 Ala Asn
 35 40 45

Val Val Val Glu Gly Thr Thr Val Asn Leu Gly Leu Trp Asp
 Thr Ala
 50 55 60

Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg
 Gly Ala
 65 70 75

80
 Asp Val Phe Val Leu Ser Phe Ser Leu Val Ser Arg Val Ser
 Tyr Glu
 85 90

95
 Asn Val Phe Lys Lys Trp Ile Pro Glu Leu Gln His Phe Ala
 Pro Gly
 100 105 110

Val Pro Leu Val Leu Val Gly Thr Lys Leu Asp Leu Arg Glu
 Asp Lys
 115 120 125

His Tyr Leu Ala Asp His Pro Gly Leu Ser Pro Val Thr Thr
 Ala Gln

0070110

130

135

140

Gly Glu Glu Leu Arg Lys Leu Ile Gly Ala Thr Tyr Tyr Ile
Glu Cys

145

150

155

160

Ser Ser Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ser
Ala Ile

165

170

175

Lys Glu Val Ile Lys Pro Leu Val Lys Gln Lys Glu Lys Thr
Lys Lys

180

185

190

Lys Lys Lys Gln Lys Ser Asn His Gly Cys Leu Ser Asn Val
Leu Cys

195

200

205

Gly Arg Ile Val Thr Arg His
210 215

<210> 390

<211> 594

<212> DNA

<213> Medicago sativa

<220>

<221> CDS

<222> (1)..(594)

<400> 390

atg agt ggt tcc agg ttc atc aag tgt gtc act gtt ggt gat
ggt gcc 48

Met Ser Gly Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala

1

5

10

15

gtt gga aag act tgt ttg ctt atc tct tac acc agc aac act
ttc cct 96

Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro

20

25

30

acg gac tat gtg ccg act gtc ttt gac aat ttc agt gca aat
gta gtt 144

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val

35

40

45

gtg gat ggg agc act ata aat ctc ggg ttg tgg gat act gct
Seite 597

0070110

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ggc caa      192
Val Asp Gly Ser Thr Ile Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln      50
gaa gat tac aat aga tta aga ccc tta agc tat cgt gga gca
gat gtt      240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val      65
      70      75
      80
ttt ctg ctt gct ttt tct ctc ata agc aag gcc agc tat gaa
aat att      288
Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Ile
      85      90
95
gcc aaa aaa tgg att cct gag ttg agg cat tat gct cct ggt
ggt cca      336
Ala Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Gly
Val Pro
      100      105      110

att att ctc gtt gga aca aaa ctt gat ctt cgg gat gat agc
cag ttc      384
Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Ser
Gln Phe
      115      120      125
ttt caa gac cat cct ggt gca gca cca ata acc aca gca cag
ggt gag      432
Phe Gln Asp His Pro Gly Ala Ala Pro Ile Thr Thr Ala Gln
Gly Glu
      130      135      140
gaa ctg aga aaa ctt atc ggt gct cca gtt tac att gaa tgt
agt tcc      480
Glu Leu Arg Lys Leu Ile Gly Ala Pro Val Tyr Ile Glu Cys
Ser Ser
      145      150      155
      160
aaa aca caa aag aat gtg aag gca gtt ttc gat tcg gcc atc
aaa gta      528
Lys Thr Gln Lys Asn Val Lys Ala Val Phe Asp Ser Ala Ile
Lys Val
      165      170
175
gtt cta caa ccg cca aag caa aag aaa aca aag aga aag ggg
caa aaa      576
Val Leu Gln Pro Pro Lys Gln Lys Lys Thr Lys Arg Lys Gly
Gln Lys

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0070110

180

185

190

gca tgt tcc att atg tga

594

Ala Cys Ser Ile Met

195

<210> 391

<211> 197

<212> PRT

<213> Medicago sativa

<400> 391

Met Ser Gly Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp

Gly Ala

1

5

10

15

Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr

Phe Pro

20

25

30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn

Val Val

35

40

45

Val Asp Gly Ser Thr Ile Asn Leu Gly Leu Trp Asp Thr Ala

Gly Gln

50

55

60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala

Asp Val

65

70

75

80

Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu

Asn Ile

85

90

95

Ala Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Gly

Val Pro

100

105

110

Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Ser

Gln Phe

115

120

125

Phe Gln Asp His Pro Gly Ala Ala Pro Ile Thr Thr Ala Gln

Gly Glu

130

135

140

0070110

Glu Leu Arg Lys Leu Ile Gly Ala Pro Val Tyr Ile Glu Cys
Ser Ser
145 150 155
160
Lys Thr Gln Lys Asn Val Lys Ala Val Phe Asp Ser Ala Ile
Lys Val
165 170
175
Val Leu Gln Pro Pro Lys Gln Lys Lys Thr Lys Arg Lys Gly
Gln Lys
180 185 190
Ala Cys Ser Ile Met
195

<210> 392
<211> 576
<212> DNA
<213> Sitobion avenae

<220>
<221> CDS
<222> (1)..(576)

<400> 392
atg cag acc atc aag tgc gtg gtt gtt ggt gat gga gct gtt
ggt aag 48
Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys
1 5 10
15
act tgt ctg ctc ata tcg tac acg aca aac aag ttt cct tca
gaa tat 96
Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe Pro Ser
Glu Tyr
20 25 30
gta ccg act gtt ttt gac aat tat gca gtg acc gtt atg att
ggc ggg 144
Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val Met Ile
Gly Gly
35 40 45
gag cca tat aca ttg ggt tta ttt gat aca gca ggt cag gaa
gat tat 192
Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu
Asp Tyr
50 55 60
gat cgc ctc aga cct ttg agt tat cca caa act gat gtg ttt
Seite 600

0070110

```

ctt gtt      240
Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
Leu Val
 65      70      75
 80
tgt ttc tcc gtg gtt tca cca tct tca ttt gaa aat gtc aaa
gaa aaa      288
Cys Phe Ser Val Val Ser Pro Ser Ser Phe Glu Asn Val Lys
Glu Lys
      85      90
95
tgg gtt cca gag ata aca cgt cac tgt caa aaa aca cca ttc
ctg ttg      336
Trp Val Pro Glu Ile Thr Arg His Cys Gln Lys Thr Pro Phe
Leu Leu
      100      105      110
gtt ggc aca caa ata gac ctt aga gaa gat gcc acg act gta
gag aaa      384
Val Gly Thr Gln Ile Asp Leu Arg Glu Asp Ala Thr Thr Val
Glu Lys
      115      120      125
cta gcc aaa aat aaa caa aaa tca ata tca tct gaa caa gga
gag aag      432
Leu Ala Lys Asn Lys Gln Lys Ser Ile Ser Ser Glu Gln Gly
Glu Lys
 130      135      140
cta gct aaa gaa ctt aaa gct gta aaa tat gtt gaa tgc tca
gca ctt      480
Leu Ala Lys Glu Leu Lys Ala Val Lys Tyr Val Glu Cys Ser
Ala Leu
145      150      155
 160
aca caa aaa gga cta aaa aat gta ttt gat gaa gct att ctt
gca gct      528
Thr Gln Lys Gly Leu Lys Asn Val Phe Asp Glu Ala Ile Leu
Ala Ala
      165      170
175
tta gag cct cct gaa cca gtt aag aag agg aag tgt gtt ata
ttg      573
Leu Glu Pro Pro Glu Pro Val Lys Lys Arg Lys Cys Val Ile
Leu
      180      185      190
taa
      576

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0070110

<210> 393
<211> 191
<212> PRT
<213> Sitobion avenae

<400> 393
Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys
1 5 10
15
Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe Pro Ser
Glu Tyr
20 25 30
Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val Met Ile
Gly Gly
35 40 45
Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu
Asp Tyr
50 55 60
Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
Leu Val
65 70 75
80
Cys Phe Ser Val Val Ser Pro Ser Ser Phe Glu Asn Val Lys
Glu Lys
85 90
95
Trp Val Pro Glu Ile Thr Arg His Cys Gln Lys Thr Pro Phe
Leu Leu
100 105 110
Val Gly Thr Gln Ile Asp Leu Arg Glu Asp Ala Thr Thr Val
Glu Lys
115 120 125
Leu Ala Lys Asn Lys Gln Lys Ser Ile Ser Ser Glu Gln Gly
Glu Lys
130 135 140
Leu Ala Lys Glu Leu Lys Ala Val Lys Tyr Val Glu Cys Ser
Ala Leu
145 150 155

0070110

160
Thr Gln Lys Gly Leu Lys Asn Val Phe Asp Glu Ala Ile Leu
Ala Ala
165 170
175
Leu Glu Pro Pro Glu Pro Val Lys Lys Arg Lys Cys Val Ile
Leu
180 185 190

<210> 394
<211> 576
<212> DNA
<213> Rhopalosiphum padi

<220>
<221> CDS
<222> (1)..(576)

<400> 394
atg cag acc atc aag tgc gtt gtt gtt ggt gat gga gct gtc
ggt aag 48
Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys
1 5 10
15
act tgt ctg ctc ata tcg tac aca aca aac aaa ttt cct tca
gaa tat 96
Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe Pro Ser
Glu Tyr
20 25 30
gta ccg act gtt ttc gac aat tat gca gtg aca gtt atg att
ggt ggg 144
Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val Met Ile
Gly Gly
35 40 45
gaa cca tac aca tta ggt tta ttt gat aca gca ggt cag gaa
gat tat 192
Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu
Asp Tyr
50 55 60
gat cgc ctc aga cct ttg agt tat cca caa act gat gtg ttt
ctt gtt 240
Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
Leu Val
65 70 75
80
tgt ttc tct gtg gtt tta cca tct tca ttt gaa aat gtc aaa

0070110

gaa	aaa			288										
Cys	Phe	Ser	Val	Val	Leu	Pro	Ser	Ser	Phe	Glu	Asn	Val	Lys	
Glu	Lys													
				85					90					
95														
tgg	gtt	ccg	gag	ata	acg	cat	cac	tgt	caa	aaa	aca	cca	ttc	
ctg	ttg			336										
Trp	Val	Pro	Glu	Ile	Thr	His	His	Cys	Gln	Lys	Thr	Pro	Phe	
Leu	Leu													
				100				105					110	
gtt	ggc	aca	caa	ata	gac	ctt	aga	gaa	gat	gcc	aca	act	gtg	
gag	aaa			384										
Val	Gly	Thr	Gln	Ile	Asp	Leu	Arg	Glu	Asp	Ala	Thr	Thr	Val	
Glu	Lys													
		115					120					125		
cta	gcc	aaa	aat	aaa	caa	aaa	tca	ata	tca	ttt	gaa	caa	gga	
gag	aag			432										
Leu	Ala	Lys	Asn	Lys	Gln	Lys	Ser	Ile	Ser	Phe	Glu	Gln	Gly	
Glu	Lys													
		130				135					140			
cta	gct	aaa	gaa	ctt	aaa	gct	gtg	aaa	tat	gtc	gaa	tgc	tca	
gca	ctt			480										
Leu	Ala	Lys	Glu	Leu	Lys	Ala	Val	Lys	Tyr	Val	Glu	Cys	Ser	
Ala	Leu													
145					150						155			
160														
aca	caa	aaa	gga	cta	aaa	aat	gta	ttt	gat	gaa	gct	att	ctt	
gca	gct			528										
Thr	Gln	Lys	Gly	Leu	Lys	Asn	Val	Phe	Asp	Glu	Ala	Ile	Leu	
Ala	Ala													
				165							170			
175														
tta	gag	cct	cct	gaa	cca	gtt	aag	aag	agg	aag	tgt	gtt	ata	
ttg				573										
Leu	Glu	Pro	Pro	Glu	Pro	Val	Lys	Lys	Arg	Lys	Cys	Val	Ile	
Leu														
				180				185					190	
taa														
				576										

<210> 395
 <211> 191
 <212> PRT
 <213> Rhopalosiphum padi

0070110

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<400> 395
Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys
1          5          10
15
Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe Pro Ser
Glu Tyr
          20          25          30

Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val Met Ile
Gly Gly
          35          40          45

Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu
Asp Tyr
          50          55          60

Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
Leu Val
          65          70          75
80
Cys Phe Ser Val Val Leu Pro Ser Ser Phe Glu Asn Val Lys
Glu Lys
          85          90

95
Trp Val Pro Glu Ile Thr His His Cys Gln Lys Thr Pro Phe
Leu Leu
          100          105          110

Val Gly Thr Gln Ile Asp Leu Arg Glu Asp Ala Thr Thr Val
Glu Lys
          115          120          125

Leu Ala Lys Asn Lys Gln Lys Ser Ile Ser Phe Glu Gln Gly
Glu Lys
          130          135          140

Leu Ala Lys Glu Leu Lys Ala Val Lys Tyr Val Glu Cys Ser
Ala Leu
          145          150          155
160
Thr Gln Lys Gly Leu Lys Asn Val Phe Asp Glu Ala Ile Leu
Ala Ala
          165          170

175
Leu Glu Pro Pro Glu Pro Val Lys Lys Arg Lys Cys Val Ile
Leu

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<210> 396
 <211> 576
 <212> DNA
 <213> *Pneumocystis carinii*

<220>
 <221> CDS
 <222> (1)..(576)

<400> 396

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atg caa act att aaa tgt gtc gtt gtt ggg gat ggc gcg gtt
ggg aaa          48
Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys
  1              5              10
15
acg tgt ctt tta ata tcc tat acg aca aac aaa ttt cct tca
gaa tat          96
Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe Pro Ser
Glu Tyr
      20              25              30
gtt cct act gta ttt gat aat tat gcg gtt acc gta atg att
gga gaa          144
Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val Met Ile
Gly Glu
      35              40              45
gaa cct tat act tta gga ctt ttt gat aca gca ggt caa gaa
gat tat          192
Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu
Asp Tyr
      50              55              60
gac aga ttg cgt ccc tta tca tat cca caa acg gat gtt ttt
ctt att          240
Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
Leu Ile
      65              70              75
80
tgc ttt tct gtt act agt cca gca agt ttt gaa aat gta aga
gaa aag          288
Cys Phe Ser Val Thr Ser Pro Ala Ser Phe Glu Asn Val Arg
Glu Lys
      85              90
95
tgg cat cca gag gtt cgt cat cat tgt cca gga aca ccc tgt
ctt att          336

```

0070110

Trp	His	Pro	Glu	Val	Arg	His	His	Cys	Pro	Gly	Thr	Pro	Cys
Leu	Ile												
			100					105					110

ggt	ggt	aca	caa	atc	gat	tta	cga	gat	gat	cct	atg	att	gta
gag	aaa		384										
Val	Gly	Thr	Gln	Ile	Asp	Leu	Arg	Asp	Asp	Pro	Met	Ile	Val
Glu	Lys												

		115					120					125	
ctc	agt	cga	caa	aga	caa	acc	ccc	att	aca	aaa	gaa	tta	ggt
gaa	aaa		432										
Leu	Ser	Arg	Gln	Arg	Gln	Thr	Pro	Ile	Thr	Lys	Glu	Leu	Gly
Glu	Lys												

		130				135					140		
ctt	tca	aaa	gaa	ttg	ggt	gct	gta	aaa	tat	ggt	gag	tgc	tca
gct	ttg		480										
Leu	Ser	Lys	Glu	Leu	Gly	Ala	Val	Lys	Tyr	Val	Glu	Cys	Ser
Ala	Leu												

		145			150					155			
		160											
act	caa	aaa	gga	tta	aaa	aac	ggt	ttt	gat	gaa	gct	ata	ggt
tgc	gca		528										
Thr	Gln	Lys	Gly	Leu	Lys	Asn	Val	Phe	Asp	Glu	Ala	Ile	Val
Cys	Ala												

		165							170				
175													
ctt	gaa	cca	ccc	ggt	acg	aag	aag	aaa	act	aaa	tgt	ctt	att
tta			573										
Leu	Glu	Pro	Pro	Val	Thr	Lys	Lys	Lys	Thr	Lys	Cys	Leu	Ile
Leu													

		180						185				190	
--	--	-----	--	--	--	--	--	-----	--	--	--	-----	--

taa
576

<210> 397
 <211> 191
 <212> PRT
 <213> Pneumocystis carinii

<400> 397
 Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
 Gly Lys
 1 5 10
 15

0070110

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

<210> 398

<211> 615

0070110

<212> DNA

<213> Paracoccidioides brasiliensis

<220>

<221> CDS

<222> (1)..(615)

<400> 398

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atg gca caa caa cag ctg cag cag ctg cag acg gag aat gtc
atg aga          48
Met Ala Gln Gln Gln Leu Gln Gln Leu Gln Thr Glu Asn Val
Met Arg
  1              5              10
15
agg aag ctg gtg ata ata gga gat ggt gct tgc ggc aag aca
agt ttg          96
Arg Lys Leu Val Ile Ile Gly Asp Gly Ala Cys Gly Lys Thr
Ser Leu
      20              25              30
ttg agt gtg ttt act ctt ggc tat ttc ccg act cat tat gtt
cct aca          144
Leu Ser Val Phe Thr Leu Gly Tyr Phe Pro Thr His Tyr Val
Pro Thr
      35              40              45
gtt ttc gaa aac tac gta aca gat tgt cgc gtt gac ggt cga
tca gtc          192
Val Phe Glu Asn Tyr Val Thr Asp Cys Arg Val Asp Gly Arg
Ser Val
      50              55              60
caa ctc gct ctg tgg gat act gct ggg cag gaa gat tac gaa
cgt tta          240
Gln Leu Ala Leu Trp Asp Thr Ala Gly Gln Glu Asp Tyr Glu
Arg Leu
      65              70              75
80
cga cca ctt gca tat tca aag gcc cat gtt ctc cta att gcg
ttc gcg          288
Arg Pro Leu Ala Tyr Ser Lys Ala His Val Leu Leu Ile Ala
Phe Ala
      85              90
95
gta gat act cca gat tct ctt gag aac gtt cgg aat aag tgg
att gaa          336
Val Asp Thr Pro Asp Ser Leu Glu Asn Val Arg Asn Lys Trp
Ile Glu
      100              105              110
gaa gca aat gaa cgc tgc ccc gat gtc cca atc ata ctg gtg
```

0070110

```

ggc ttg      384
Glu Ala Asn Glu Arg Cys Pro Asp Val Pro Ile Ile Leu Val
Gly Leu
      115      120      125
aag aaa gat ctg cgc gag gac ccc ctt gca att gaa gaa atg
aga aag      432
Lys Lys Asp Leu Arg Glu Asp Pro Leu Ala Ile Glu Glu Met
Arg Lys
      130      135      140
aag tct ctg cgc ttt gtt tcc tcg aag gaa ggc cac gac aca
gca gcc      480
Lys Ser Leu Arg Phe Val Ser Ser Lys Glu Gly His Asp Thr
Ala Ala
145      150      155
      160
cag gtc ggg gca aga aaa tac tta gaa tgc tca tcc ctc acc
ggc gaa      528
Gln Val Gly Ala Arg Lys Tyr Leu Glu Cys Ser Ser Leu Thr
Gly Glu
      165      170
175
ggt gtc gat gac gtt ttc gaa gct gca acc cgc gca gct ctt
tta act      576
Gly Val Asp Asp Val Phe Glu Ala Ala Thr Arg Ala Ala Leu
Leu Thr
      180      185      190
ttc gaa aag gac aga gga tct tgc tgc gtt atc cta tga
Phe Glu Lys      615
      195      200

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<210> 399

<211> 204

<212> PRT

<213> Paracoccidioides brasiliensis

<400> 399

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Met Ala Gln Gln Gln Leu Gln Gln Leu Gln Thr Glu Asn Val
Met Arg
1      5      10
15
Arg Lys Leu Val Ile Ile Gly Asp Gly Ala Cys Gly Lys Thr
Ser Leu
      20      25      30
Leu Ser Val Phe Thr Leu Gly Tyr Phe Pro Thr His Tyr Val
Pro Thr

```

0070110
40

35

45

Val Phe Glu Asn Tyr Val Thr Asp Cys Arg Val Asp Gly Arg
Ser Val
50 55 60

Gln Leu Ala Leu Trp Asp Thr Ala Gly Gln Glu Asp Tyr Glu
Arg Leu
65 70 75

80
Arg Pro Leu Ala Tyr Ser Lys Ala His Val Leu Leu Ile Ala
Phe Ala
85 90

95
Val Asp Thr Pro Asp Ser Leu Glu Asn Val Arg Asn Lys Trp
Ile Glu
100 105 110

Glu Ala Asn Glu Arg Cys Pro Asp Val Pro Ile Ile Leu Val
Gly Leu
115 120 125

Lys Lys Asp Leu Arg Glu Asp Pro Leu Ala Ile Glu Glu Met
Arg Lys
130 135 140

Lys Ser Leu Arg Phe Val Ser Ser Lys Glu Gly His Asp Thr
Ala Ala
145 150 155

160
Gln Val Gly Ala Arg Lys Tyr Leu Glu Cys Ser Ser Leu Thr
Gly Glu
165 170

175
Gly Val Asp Asp Val Phe Glu Ala Ala Thr Arg Ala Ala Leu
Leu Thr
180 185 190

Phe Glu Lys Asp Arg Gly Ser Cys Cys Val Ile Leu
195 200

<210> 400

<211> 579

<212> DNA

<213> Tigriopus japonicus

<220>

<221> CDS

<222> (1)..(579)

<400> 400

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atg gcg gct att cgc aag aaa tta gtg att gtg ggc gat ggc
gcc tgc          48
Met Ala Ala Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly
Ala Cys
  1              5              10
15
ggc aag acc tgc ctc ttg atc gtg ttc tcc aag gat caa ttc
ccc gag          96
Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Asp Gln Phe
Pro Glu
          20              25              30
gtg tat gtg ccc aca gtg ttc gaa aac tac gtg gct gac atc
gaa gtg          144
Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Ile
Glu Val
          35              40              45
gac ggc aag caa gtg gaa ctg gcc ttg tgg gat acg gcc ggt
cag gag          192
Asp Gly Lys Gln Val Glu Leu Ala Leu Trp Asp Thr Ala Gly
Gln Glu
          50              55              60
gac tac gat cga ctc cga ccc ctg tcc tat ccg gat acg gat
gtg atc          240
Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Thr Asp
Val Ile
  65              70              75
80
ctg atg tgt ttc tcg atc gac tcg ccc gat tcg ctc gag aac
atc cct          288
Leu Met Cys Phe Ser Ile Asp Ser Pro Asp Ser Leu Glu Asn
Ile Pro
          85              90
95
gag aag tgg acg ccc gaa gtc aaa cac ttc tgc cct aat gtg
ccc att          336
Glu Lys Trp Thr Pro Glu Val Lys His Phe Cys Pro Asn Val
Pro Ile
          100              105              110
atc ctc gtg gga aac aaa aaa gac ttg cgc aat gat ccc aat
acc atc          384
Ile Leu Val Gly Asn Lys Lys Asp Leu Arg Asn Asp Pro Asn
Thr Ile
  115              120              125
aag gag ttg ggc aag atg aaa caa gaa ccg gtc aag ccg gaa

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0070110

gag ggt 432
 Lys Glu Leu Gly Lys Met Lys Gln Glu Pro Val Lys Pro Glu
 Glu Gly 130
 cgc aca atg gcc gaa aag 135 140
 tgt tcg 480
 Arg Thr Met Ala Glu Lys Ile Asn Ala Phe Ala Tyr Leu Glu
 Cys Ser

145 150 155
 160
 gcc aag agc aag gaa ggc gtc aga gaa gtc ttt gag aca gcc
 acc cga 528
 Ala Lys Ser Lys Glu Gly Val Arg Glu Val Phe Glu Thr Ala
 Thr Arg

165 170
 175
 gcg gca tta cag gtc aag aag aaa aag aag aag cct tgc gtt
 ctc ttt 576
 Ala Ala Leu Gln Val Lys Lys Lys Lys Lys Lys Pro Cys Val
 Leu Phe

180 185 190
 taa
 579

<210> 401
 <211> 192
 <212> PRT
 <213> Tigriopus japonicus

<400> 401
 Met Ala Ala Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly
 Ala Cys
 1 5 10
 15
 Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Asp Gln Phe
 Pro Glu
 20 25 30
 Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Ile
 Glu Val
 35 40 45
 Asp Gly Lys Gln Val Glu Leu Ala Leu Trp Asp Thr Ala Gly
 Gln Glu

0070110

50

55

60

Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Thr Asp
Val Ile
65 70 75

80
Leu Met Cys Phe Ser Ile Asp Ser Pro Asp Ser Leu Glu Asn
Ile Pro
85 90

95
Glu Lys Trp Thr Pro Glu Val Lys His Phe Cys Pro Asn Val
Pro Ile
100 105 110

Ile Leu Val Gly Asn Lys Lys Asp Leu Arg Asn Asp Pro Asn
Thr Ile
115 120 125

Lys Glu Leu Gly Lys Met Lys Gln Glu Pro Val Lys Pro Glu
Glu Gly
130 135 140

Arg Thr Met Ala Glu Lys Ile Asn Ala Phe Ala Tyr Leu Glu
Cys Ser
145 150 155

160
Ala Lys Ser Lys Glu Gly Val Arg Glu Val Phe Glu Thr Ala
Thr Arg
165 170

175
Ala Ala Leu Gln Val Lys Lys Lys Lys Lys Lys Pro Cys Val
Leu Phe
180 185 190

<210> 402

<211> 576

<212> DNA

<213> Paracoccidioides brasiliensis

<220>

<221> CDS

<222> (1)..(576)

<400> 402

atg gct gag att cgt cgt aaa ctt gtc att gtt ggt gat ggt
gcc tgt 48
Met Ala Glu Ile Arg Arg Lys Leu Val Ile Val Gly Asp Gly

0070110

Ala	Cys												
1				5					10				
15													
ggt	aaa	act	tgt	ctc	ttg	att	gtc	ttt	tcc	aag	ggt	acc	ttc
cct	gag		96										
Gly	Lys	Thr	Cys	Leu	Leu	Ile	Val	Phe	Ser	Lys	Gly	Thr	Phe
Pro	Glu												
			20					25					30
gtc	tac	gtc	cca	acc	gtc	ttc	gag	aac	tat	gtg	gcc	gac	gtt
gag	gtc		144										
Val	Tyr	Val	Pro	Thr	Val	Phe	Glu	Asn	Tyr	Val	Ala	Asp	Val
Glu	Val												
		35				40						45	
gat	gga	aag	cat	gtc	gag	ctc	gca	ctt	tgg	gat	acg	gct	ggc
cag	gaa		192										
Asp	Gly	Lys	His	Val	Glu	Leu	Ala	Leu	Trp	Asp	Thr	Ala	Gly
Gln	Glu												
		50				55					60		
gat	tac	gat	cga	ctc	aga	cct	ctt	tcc	tac	cct	gat	tca	cat
gtt	att		240										
Asp	Tyr	Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Pro	Asp	Ser	His
Val	Ile												
65					70					75			
80													
ctg	atc	tgt	ttc	gct	atc	gat	tcc	ccc	gac	tct	ctc	gac	aac
gtc	cag		288										
Leu	Ile	Cys	Phe	Ala	Ile	Asp	Ser	Pro	Asp	Ser	Leu	Asp	Asn
Val	Gln												
			85							90			
95													
gag	aag	tgg	att	tct	gaa	gtc	ctt	cat	ttc	tgc	cag	ggt	cat
ccc	att		336										
Glu	Lys	Trp	Ile	Ser	Glu	Val	Leu	His	Phe	Cys	Gln	Gly	His
Pro	Ile												
			100						105				110
atc	ctc	gtt	ggg	tgc	aag	aaa	gat	ctt	cgt	gac	gac	ccc	aga
acg	att		384										
Ile	Leu	Val	Gly	Cys	Lys	Lys	Asp	Leu	Arg	Asp	Asp	Pro	Arg
Thr	Ile												
		115					120					125	
gag	gag	ctg	cgc	aag	acg	tct	cag	aag	ccc	gtg	acc	acc	gaa
cag	ggt		432										
Glu	Glu	Leu	Arg	Lys	Thr	Ser	Gln	Lys	Pro	Val	Thr	Thr	Glu
Gln	Gly												
		130				135					140		
gag	gag	gtc	cgc	aag	aag	att	ggc	gct	tac	aag	tat	ctg	gaa
tgc	tcc		480										

0070110

Glu Glu val Arg Lys Lys Ile Gly Ala Tyr Lys Tyr Leu Glu
 Cys Ser
 145 150 155
 160
 gcc cga aca aac gac gga gtt cgt gag gtg ttc gag tca gct
 act cga 528
 Ala Arg Thr Asn Asp Gly val Arg Glu val Phe Glu Ser Ala
 Thr Arg
 165 170
 175
 gct gca ctg ctg gcg aag aag gag aaa aag aaa tgc aag atc
 ttg 573
 Ala Ala Leu Leu Ala Lys Lys Glu Lys Lys Lys Cys Lys Ile
 Leu
 180 185 190
 taa
 576

<210> 403
 <211> 191
 <212> PRT
 <213> Paracoccidioides brasiliensis

<400> 403
 Met Ala Glu Ile Arg Arg Lys Leu val Ile val Gly Asp Gly
 Ala Cys
 1 5 10
 15
 Gly Lys Thr Cys Leu Leu Ile val Phe Ser Lys Gly Thr Phe
 Pro Glu
 20 25 30
 val Tyr val Pro Thr val Phe Glu Asn Tyr val Ala Asp val
 Glu val
 35 40 45
 Asp Gly Lys His val Glu Leu Ala Leu Trp Asp Thr Ala Gly
 Gln Glu
 50 55 60
 Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Ser His
 val Ile
 65 70 75
 80
 Leu Ile Cys Phe Ala Ile Asp Ser Pro Asp Ser Leu Asp Asn
 Seite 616

0070110

Val	Gln													
				85						90				
95														
Glu	Lys	Trp	Ile	Ser	Glu	Val	Leu	His	Phe	Cys	Gln	Gly	His	
Pro	Ile													
				100				105					110	
Ile	Leu	Val	Gly	Cys	Lys	Lys	Asp	Leu	Arg	Asp	Asp	Pro	Arg	
Thr	Ile													
				115				120					125	
Glu	Glu	Leu	Arg	Lys	Thr	Ser	Gln	Lys	Pro	Val	Thr	Thr	Glu	
Gln	Gly													
	130						135					140		
Glu	Glu	Val	Arg	Lys	Lys	Ile	Gly	Ala	Tyr	Lys	Tyr	Leu	Glu	
Cys	Ser													
145						150				155				
160														
Ala	Arg	Thr	Asn	Asp	Gly	Val	Arg	Glu	Val	Phe	Glu	Ser	Ala	
Thr	Arg													
				165						170				
175														
Ala	Ala	Leu	Leu	Ala	Lys	Lys	Glu	Lys	Lys	Lys	Cys	Lys	Ile	
Leu														
				180				185					190	

<210> 404
 <211> 591
 <212> DNA
 <213> Schizophyllum commune

<220>
 <221> CDS
 <222> (1)..(591)

<400> 404
 atg cag gcc atc aag tgt gtt gtc gta gga gat ggt gcg gtc
 gga aag 48
 Met Gln Ala Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
 Gly Lys
 1 5 10
 15
 acc tgc ctg cta atc tcg tat acc acg aac gcg ttc ccg gga
 gaa tat 96
 Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Ala Phe Pro Gly
 Glu Tyr

0070110

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

0070110

val val
 165 170
 175
 ttg tac ccg tcc gcg cgg tcc gac aac aaa cgc agc aag ggc
 cgc tca 576
 Leu Tyr Pro Ser Ala Arg Ser Asp Asn Lys Arg Ser Lys Gly
 Arg Ser
 180 185 190

tgc att gtc gca taa
 591
 Cys Ile val Ala
 195

<210> 405
 <211> 196
 <212> PRT
 <213> Schizophyllum commune

<400> 405
 Met Gln Ala Ile Lys Cys val val val Gly Asp Gly Ala val
 Gly Lys
 1 5 10
 15
 Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Ala Phe Pro Gly
 Glu Tyr
 20 25 30
 Ile Pro Thr val Phe Asp Asn Tyr Ser Ala Asn val Met val
 Asp Gly
 35 40 45
 Lys Thr Ile Ser Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu
 Asp Tyr
 50 55 60
 Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp val Phe
 Leu Ile
 65 70 75
 80
 Cys Phe Ser Leu val Ser Pro Pro Ser Phe Glu Asn val Arg
 Thr Lys
 85 90
 95
 Trp Tyr Pro Glu Ile Ser His His Ala Pro Gln Thr Pro val
 val Leu
 100 105 110

0070110

Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Glu	Asp	Pro	Ala	Thr	Ile
Glu	Lys												
		115					120					125	

Leu	Arg	Asp	Arg	Arg	Met	Ser	Pro	Ile	Gln	Tyr	Ser	Gln	Gly
Val	Ala												
	130					135					140		

Met	Met	Lys	Asp	Ile	Gly	Ala	Val	Lys	Tyr	Leu	Glu	Cys	Ser
Ala	Leu												
145					150					155			

Thr	Gln	Lys	Gly	Leu	Lys	Thr	Val	Phe	Asp	Glu	Ala	Ile	Arg
Val	Val												
				165					170				

175													
Leu	Tyr	Pro	Ser	Ala	Arg	Ser	Asp	Asn	Lys	Arg	Ser	Lys	Gly
Arg	Ser												

		180					185					190	
--	--	-----	--	--	--	--	-----	--	--	--	--	-----	--

Cys	Ile	Val	Ala										
		195											

<210> 406
 <211> 657
 <212> DNA
 <213> Hordeum vulgare var

<220>
 <221> CDS
 <222> (1)..(657)

<400> 406													
atg	agc	ggc	gga	gcg	ggg	gcg	gcg	acg	gcg	gtg	agc	agg	ttc
atc	aag			48									
Met	Ser	Gly	Gly	Ala	Gly	Ala	Ala	Thr	Ala	Val	Ser	Arg	Phe
Ile	Lys												
1				5					10				
15													
tgc	gtg	gcc	gtg	ggc	gac	ggc	gcc	gtg	ggc	aag	acc	tgc	atg
ctc	atc			96									
Cys	Val	Ala	Val	Gly	Asp	Gly	Ala	Val	Gly	Lys	Thr	Cys	Met
Leu	Ile												
		20					25					30	
tgc	tac	acc	tgc	aac	aag	ttc	ccc	acc	gac	tac	atc	ccc	acc
gtg	ttc			144									
Cys	Tyr	Thr	Cys	Asn	Lys	Phe	Pro	Thr	Asp	Tyr	Ile	Pro	Thr

0070110

Val	Phe												
		35				40					45		
gac	aac	ttc	agc	gcc	aat	gtc	tcc	gtg	gac	ggg	agc	atc	gtc
aac	ctc		192										
Asp	Asn	Phe	Ser	Ala	Asn	Val	Ser	Val	Asp	Gly	Ser	Ile	Val
Asn	Leu												
	50					55					60		
ggc	ctc	tgg	gac	acc	gca	ggc	cag	gag	gat	tac	agc	agg	ctg
agg	cct		240										
Gly	Leu	Trp	Asp	Thr	Ala	Gly	Gln	Glu	Asp	Tyr	Ser	Arg	Leu
Arg	Pro												
65					70					75			
80													
ctg	agc	tac	agg	gga	gcc	gat	gtc	ttc	atc	ctc	tcc	ttc	tcc
ctc	acc		288										
Leu	Ser	Tyr	Arg	Gly	Ala	Asp	Val	Phe	Ile	Leu	Ser	Phe	Ser
Leu	Thr												
				85					90				
95													
agc	aga	gca	agc	tat	gag	aat	gtg	cac	aag	aag	tgg	atg	ccg
gag	ctt		336										
Ser	Arg	Ala	Ser	Tyr	Glu	Asn	Val	His	Lys	Lys	Trp	Met	Pro
Glu	Leu												
			100					105				110	
cgc	cgg	tac	gcc	ccc	ggc	att	cct	gta	ctg	ctt	ggt	gga	acc
aag	ttg		384										
Arg	Arg	Tyr	Ala	Pro	Gly	Ile	Pro	Val	Leu	Leu	Val	Gly	Thr
Lys	Leu												
		115					120					125	
gat	ctc	cgg	gag	gat	aga	gct	tat	ctt	gct	gat	cat	gca	gct
gat	tcc		432										
Asp	Leu	Arg	Glu	Asp	Arg	Ala	Tyr	Leu	Ala	Asp	His	Ala	Ala
Asp	Ser												
	130					135					140		
atc	ata	aca	act	gag	cag	ggc	gag	gat	ctt	agg	aga	caa	ata
ggc	gct		480										
Ile	Ile	Thr	Thr	Glu	Gln	Gly	Glu	Asp	Leu	Arg	Arg	Gln	Ile
Gly	Ala												
145					150					155			
160													
gtg	gca	tac	ata	gaa	tgc	agc	tcc	aag	aca	caa	agg	aac	att
aag	gct		528										
Val	Ala	Tyr	Ile	Glu	Cys	Ser	Ser	Lys	Thr	Gln	Arg	Asn	Ile
Lys	Ala												
				165						170			
175													
ggt	ttc	gac	acc	gca	atc	aag	gcg	ggt	ctt	caa	cct	caa	agg

0070110

cac aag 576
 Val Phe Asp Thr Ala Ile Lys Ala Val Leu Gln Pro Gln Arg
 His Lys 180 185 190

gag gta gcc aga aag gaa act cgg aca cgc tct agt cgg tca
 gta agg 624
 Glu Val Ala Arg Lys Glu Thr Arg Thr Arg Ser Ser Arg Ser
 Val Arg 195 200 205

cag tac ttc tgt ggg agt tct tgt ttc gcg tag
 Gln Tyr Phe Cys Gly Ser Ser Cys Phe Ala
 210 215

<210> 407
 <211> 218
 <212> PRT
 <213> Hordeum vulgare var

<400> 407
 Met Ser Gly Gly Ala Gly Ala Ala Thr Ala Val Ser Arg Phe
 Ile Lys 1 5 10
 15
 Cys Val Ala Val Gly Asp Gly Ala Val Gly Lys Thr Cys Met
 Leu Ile 20 25 30

Cys Tyr Thr Cys Asn Lys Phe Pro Thr Asp Tyr Ile Pro Thr
 Val Phe 35 40 45

Asp Asn Phe Ser Ala Asn Val Ser Val Asp Gly Ser Ile Val
 Asn Leu 50 55 60

Gly Leu Trp Asp Thr Ala Gly Gln Glu Asp Tyr Ser Arg Leu
 Arg Pro 65 70 75

80
 Leu Ser Tyr Arg Gly Ala Asp Val Phe Ile Leu Ser Phe Ser
 Leu Thr 85 90

95
 Ser Arg Ala Ser Tyr Glu Asn Val His Lys Lys Trp Met Pro
 Glu Leu

0070110

	100	105	110
Arg Arg Tyr Ala Pro Gly Ile Pro Val Leu Leu Val Gly Thr			
Lys Leu			
	115	120	125
Asp Leu Arg Glu Asp Arg Ala Tyr Leu Ala Asp His Ala Ala			
Asp Ser			
	130	135	140
Ile Ile Thr Thr Glu Gln Gly Glu Asp Leu Arg Arg Gln Ile			
Gly Ala			
	145	150	155
	160		
Val Ala Tyr Ile Glu Cys Ser Ser Lys Thr Gln Arg Asn Ile			
Lys Ala			
	165	170	
	175		
Val Phe Asp Thr Ala Ile Lys Ala Val Leu Gln Pro Gln Arg			
His Lys			
	180	185	190
Glu Val Ala Arg Lys Glu Thr Arg Thr Arg Ser Ser Arg Ser			
Val Arg			
	195	200	205
Gln Tyr Phe Cys Gly Ser Ser Cys Phe Ala			
	210	215	

<210> 408
 <211> 642
 <212> DNA
 <213> Hordeum vulgare var

<220>
 <221> CDS
 <222> (1)..(642)

<400> 408
 atg gcg tcc agc gcc tcc cgg ttc atc aag tgc gtc acg gtg
 ggc gac 48
 Met Ala Ser Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val
 Gly Asp
 1 5 10
 15
 ggc gcc gtc ggc aag acc tgc atg ctc atc tgc tac acc agc
 aac aag 96

0070110

Gly	Ala	Val	Gly	Lys	Thr	Cys	Met	Leu	Ile	Cys	Tyr	Thr	Ser
Asn	Lys												
			20					25					30
ttc	ccc	acc	gac	tac	ata	ccc	acg	gtg	ttc	gac	aat	ttc	agc
gcg	aac		144										
Phe	Pro	Thr	Asp	Tyr	Ile	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser
Ala	Asn												
		35					40					45	
gtg	gtg	gcg	gac	ggc	acc	acg	gtg	aat	ttg	ggc	ctt	tgg	gac
acc	gcc		192										
Val	Val	Ala	Asp	Gly	Thr	Thr	Val	Asn	Leu	Gly	Leu	Trp	Asp
Thr	Ala												
	50					55				60			
ggg	cag	gag	gat	tac	aac	cgg	ctg	agg	cct	cta	agc	tac	cgc
ggc	gcc		240										
Gly	Gln	Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg
Gly	Ala												
65					70					75			
80													
gac	ggt	ttc	gtg	ctt	gcc	ttc	tcc	ctt	gtg	agc	cga	gct	agc
tat	gag		288										
Asp	Val	Phe	Val	Leu	Ala	Phe	Ser	Leu	Val	Ser	Arg	Ala	Ser
Tyr	Glu												
			85						90				
95													
aat	atc	atg	aag	aag	tgg	ata	ccg	gag	ctt	cag	cat	tac	gcg
ccc	ggc		336										
Asn	Ile	Met	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Gln	His	Tyr	Ala
Pro	Gly												
			100					105					110
gta	cct	gtt	gtg	ctg	gta	ggc	aca	aaa	ctg	gat	ctt	cgt	gaa
gat	aag		384										
Val	Pro	Val	Val	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Glu
Asp	Lys												
		115					120				125		
cac	tat	ttg	ctg	gac	cac	cct	ggg	atg	ata	ccc	ggt	acc	aca
gca	cag		432										
His	Tyr	Leu	Leu	Asp	His	Pro	Gly	Met	Ile	Pro	Val	Thr	Thr
Ala	Gln												
	130					135					140		
ggg	gag	gaa	ctt	cgt	aag	caa	ggt	ggt	gct	tta	tat	tac	ata
gag	tgc		480										
Gly	Glu	Glu	Leu	Arg	Lys	Gln	Val	Gly	Ala	Leu	Tyr	Tyr	Ile
Glu	Cys												
145					150					155			
160													

0070110

agc tca aag aca caa cag aat gtc aaa gct gtg ttt gat gct
gct atc 528
Ser Ser Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala
Ala Ile

165

170

175

aag gta gta atc cag ccc cca act aaa caa aga gaa aag aag
aaa aag 576
Lys Val Val Ile Gln Pro Pro Thr Lys Gln Arg Glu Lys Lys
Lys Lys

180

185

190

aaa cag cgt cgg gga tgt tct atg atg aac ttc agc gga agg
aaa atg 624
Lys Gln Arg Arg Gly Cys Ser Met Met Asn Phe Ser Gly Arg
Lys Met

195

200

205

cta tgc ttc aaa tcc tga
642

Leu Cys Phe Lys Ser
210

<210> 409

<211> 213

<212> PRT

<213> Hordeum vulgare var

<400> 409

Met Ala Ser Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val
Gly Asp

1

5

10

15

Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser
Asn Lys

20

25

30

Phe Pro Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser
Ala Asn

35

40

45

Val Val Ala Asp Gly Thr Thr Val Asn Leu Gly Leu Trp Asp
Thr Ala
50 55 60

Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg
Gly Ala

65

70

75

80

0070110

Asp Val Phe Val Leu Ala Phe Ser Leu Val Ser Arg Ala Ser
Tyr Glu

85

90

95

Asn Ile Met Lys Lys Trp Ile Pro Glu Leu Gln His Tyr Ala
Pro Gly

100

105

110

Val Pro Val Val Leu Val Gly Thr Lys Leu Asp Leu Arg Glu
Asp Lys

115

120

125

His Tyr Leu Leu Asp His Pro Gly Met Ile Pro Val Thr Thr
Ala Gln

130

135

140

Gly Glu Glu Leu Arg Lys Gln Val Gly Ala Leu Tyr Tyr Ile
Glu Cys

145

150

155

160

Ser Ser Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala
Ala Ile

165

170

175

Lys Val Val Ile Gln Pro Pro Thr Lys Gln Arg Glu Lys Lys
Lys Lys

180

185

190

Lys Gln Arg Arg Gly Cys Ser Met Met Asn Phe Ser Gly Arg
Lys Met

195

200

205

Leu Cys Phe Lys Ser
210

<210> 410

<211> 642

<212> DNA

<213> Hordeum vulgare

<220>

<221> CDS

<222> (1)..(642)

<400> 410

atg gcg tcc agc gcc tcc cgg ttc atc aag tgc gtc acc gtc
ggg gac 48

Met Ala Ser Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val
Seite 626

0070110

Gly	Asp												
1				5					10				
15													
ggc	gcc	gtc	ggc	aag	acc	tgc	atg	ctc	atc	tgc	tac	acc	agc
aac	aag		96										
Gly	Ala	Val	Gly	Lys	Thr	Cys	Met	Leu	Ile	Cys	Tyr	Thr	Ser
Asn	Lys												
			20					25					30
ttc	ccc	acc	gac	tac	gtg	ccc	acc	gtg	ttc	gac	aat	ttc	agc
gcg	aac		144										
Phe	Pro	Thr	Asp	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser
Ala	Asn												
		35				40						45	
gtg	gtg	gtg	gac	ggc	acc	acc	gtg	aac	ctg	ggc	ctc	tgg	gac
act	gca		192										
Val	Val	Val	Asp	Gly	Thr	Thr	Val	Asn	Leu	Gly	Leu	Trp	Asp
Thr	Ala												
		50				55					60		
ggg	cag	gag	gac	tac	aac	aga	ttg	aga	ccg	ctg	agc	tac	cgg
gga	gcc		240										
Gly	Gln	Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg
Gly	Ala												
65					70					75			
80													
gac	gtc	ttc	gtg	ctc	tcc	ttc	tcg	ctc	gtc	agc	cga	gcc	agc
tac	gag		288										
Asp	Val	Phe	Val	Leu	Ser	Phe	Ser	Leu	Val	Ser	Arg	Ala	Ser
Tyr	Glu												
			85						90				
95													
aat	gtc	atg	aag	aag	tgg	cta	ccg	gag	ctt	cag	cac	cat	gca
ccc	ggc		336										
Asn	Val	Met	Lys	Lys	Trp	Leu	Pro	Glu	Leu	Gln	His	His	Ala
Pro	Gly												
			100					105					110
gtg	cca	aca	gtg	ctg	gtt	ggc	aca	aag	cta	gat	cta	cgt	gaa
gac	aag		384										
Val	Pro	Thr	Val	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Glu
Asp	Lys												
		115				120						125	
caa	tac	tta	ctt	gac	cac	ccc	ggc	gtg	gtg	cct	gtt	act	aca
gct	cag		432										
Gln	Tyr	Leu	Leu	Asp	His	Pro	Gly	Val	Val	Pro	Val	Thr	Thr
Ala	Gln												
		130				135					140		
ggg	gag	gaa	ctc	cgc	aag	cac	atc	ggc	gca	act	tgt	tat	gtc
gaa	tgc		480										

0070110

Gly Glu Glu Leu Arg Lys His Ile Gly Ala Thr Cys Tyr Val
 Glu Cys
 145 150 155

160
 agc tca aag aca cag cag aat gtc aaa gct gtg ttt gat gct
 gcc atc 528
 Ser Ser Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala
 Ala Ile

165 170
 175
 aag gta gtg atc aaa cct cca aca aag cag agg gaa agg agg
 aag aag 576
 Lys Val Val Ile Lys Pro Pro Thr Lys Gln Arg Glu Arg Arg
 Lys Lys
 180 185 190

aaa gca cgg caa gga tgt gca tca ttg ggt acc ctg tca aga
 agg aag 624
 Lys Ala Arg Gln Gly Cys Ala Ser Leu Gly Thr Leu Ser Arg
 Arg Lys
 195 200 205

ctg gca tgc ttc aag tga
 642
 Leu Ala Cys Phe Lys
 210

<210> 411
 <211> 213
 <212> PRT
 <213> Hordeum vulgare

<400> 411
 Met Ala Ser Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val
 Gly Asp
 1 5 10

15
 Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser
 Asn Lys
 20 25 30

Phe Pro Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser
 Ala Asn
 35 40 45

Val Val Val Asp Gly Thr Thr Val Asn Leu Gly Leu Trp Asp
 Thr Ala
 50 55 60

0070110

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

<210> 412
 <211> 594
 <212> DNA
 <213> Hordeum vulgare

<220>
 <221> CDS
 <222> (1)..(594)

0070110

<400> 412

atg agc gca tct cgg ttc atc aag tgc gtg acg gtg ggg gac
ggc gcc 48
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala

1 5 10
15

gtg gga aag aca tgc ctc ctc atc tca tac aca tcc aac acc
ttc ccc 96
Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro

20 25 30
aca gac tat gtc cca aca gtt ttc gac aac ttc agc gct aac
gtc gtg 144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val

35 40 45
gtt gac ggc agc acc gtc aac ctc gga tta tgg gat act gca
gga caa 192
Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln

50 55 60
gaa gac tat aat cga cta cgc cca cta agc tac cgt ggt gcc
gat gtc 240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65 70 75

80
ttc ctg ctc gcc ttt tct ctc atc agc aaa gca agc tac gag
aat gtc 288
Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val

85 90
95
act aag aag tgg att cca gag tta cgg cac tat gct cct ggc
gtg ccc 336
Thr Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Gly
Val Pro
100 105 110

ata att ctt gtt gga aca aag ctt gat ctg cgg gat gac aag
cag ttt 384
Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe

115 120 125
ttt gtg gat cac cct ggg gcg gtt cct att tcc act gct cag
ggg gaa 432
Phe Val Asp His Pro Gly Ala Val Pro Ile Ser Thr Ala Gln

0070110

Gly Glu
130 135 140
gag ctg aag aag gtg att ggc gcg act gcc tac atc gag tgc
agc tca 480
Glu Leu Lys Lys Val Ile Gly Ala Thr Ala Tyr Ile Glu Cys
Ser Ser
145 150 155
160
aaa aca cag cag aac atc aag gcg gtg ttt gat gcg gcg atc
aag gtg 528
Lys Thr Gln Gln Asn Ile Lys Ala Val Phe Asp Ala Ala Ile
Lys Val
165 170
175
gtc ctc cag cct ccg aag cag aag cgg aag aag agg aag tca
cag aaa 576
Val Leu Gln Pro Pro Lys Gln Lys Arg Lys Lys Arg Lys Ser
Gln Lys
180 185 190
gga tgc agc atc ttg taa
594
Gly Cys Ser Ile Leu
195

<210> 413
<211> 197
<212> PRT
<213> Hordeum vulgare

<400> 413
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10
15
Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
20 25 30
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
35 40 45
Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Seite 631

[illegible]

<220>
<221> CDS
<222> (1) .. (639)

Seite 632

0070110

1	5												10		
15															
gtc	ggc	aag	acc	tgc	atg	ctc	atc	tgc	tac	acc	agc	aac	agg		
ttc	ccc		96												
Val	Gly	Lys	Thr	Cys	Met	Leu	Ile	Cys	Tyr	Thr	Ser	Asn	Arg		
Phe	Pro														
	20												25		30
agt	gat	tac	atc	ccc	acg	gtg	ttc	gac	aac	ttc	agc	gcc	aac		
gtc	tcc		144												
Ser	Asp	Tyr	Ile	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn		
Val	Ser														
	35												40		45
gtc	gac	ggc	aac	atc	gtc	aac	ctc	ggc	cta	tgg	gac	acc	gcc		
ggg	caa		192												
Val	Asp	Gly	Asn	Ile	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala		
Gly	Gln														
	50												55		60
gaa	gac	tac	agc	cgg	ctg	agg	ccg	ctg	agc	tac	aga	ggc	gcc		
gac	gtg		240												
Glu	Asp	Tyr	Ser	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala		
Asp	Val														
65	70												75		
80															
ttc	gtg	ctc	gcc	ttc	tcc	ctc	atc	agc	agc	gcc	agc	tac	gag		
aat	gtt		288												
Phe	Val	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Ser	Ala	Ser	Tyr	Glu		
Asn	Val														
	85												90		
95															
ctt	aag	aag	tgg	atg	cca	gag	ctc	cgc	cgg	ttc	gcg	ccg	aat		
gtc	ccc		336												
Leu	Lys	Lys	Trp	Met	Pro	Glu	Leu	Arg	Arg	Phe	Ala	Pro	Asn		
Val	Pro														
	100												105		110
att	gtt	ctt	gtt	ggg	acc	aag	cta	gat	ctg	cgt	gac	cac	aga		
gcc	tac		384												
Ile	Val	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	His	Arg		
Ala	Tyr														
	115												120		125
ctc	gcc	gac	cac	ccc	ggg	gct	tca	gca	atc	aca	act	gca	cag		
ggg	gaa		432												
Leu	Ala	Asp	His	Pro	Gly	Ala	Ser	Ala	Ile	Thr	Thr	Ala	Gln		
Gly	Glu														
	130												135		140
gaa	ctt	agg	aag	cag	atc	ggc	gcc	gcg	gct	tac	atc	gag	tgc		
agc	tcc		480												
Glu	Leu	Arg	Lys	Gln	Ile	Gly	Ala	Ala	Ala	Tyr	Ile	Glu	Cys		

0070110

Ser Ser
145 150 155
160
aag aca cag cag aac gtc aag gct gtg ttt gac acc gcc ata
aag gtg 528
Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Thr Ala Ile
Lys Val
165 170
175
gtc ctc cag ccg ccg agg aga agg gag gtg atg tcc gcc agg
aag aaa 576
Val Leu Gln Pro Pro Arg Arg Arg Glu Val Met Ser Ala Arg
Lys Lys
180 185 190
acc agg cga agc tct gga tgc tcc atc aag cac ttg atc tgc
ggg agt 624
Thr Arg Arg Ser Ser Gly Cys Ser Ile Lys His Leu Ile Cys
Gly Ser
195 200 205
acg tgc gct gct tga
639
Thr Cys Ala Ala
210

<210> 415
<211> 212
<212> PRT
<213> Hordeum vulgare

<400> 415
Met Ser Val Thr Lys Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10
15
Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser Asn Arg
Phe Pro
20 25 30
Ser Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Ser
35 40 45
Val Asp Gly Asn Ile Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60
Glu Asp Tyr Ser Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Seite 634

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

<210> 416
 <211> 576
 <212> DNA
 <213> Ciona intestinalis

<220>
 <221> CDS
 <222> (1)..(576)

<400> 416

0070110

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

0070110

130 135 140
 ctt gca agg gaa tta aaa gct gta aaa tat gtt gaa tgt tca
 gct ctg 480
 Leu Ala Arg Glu Leu Lys Ala Val Lys Tyr Val Glu Cys Ser
 Ala Leu
 145 150 155
 160
 act cag cgt ggt tta aaa aat gtc ttt gat gaa gca att ctt
 gct gca 528
 Thr Gln Arg Gly Leu Lys Asn Val Phe Asp Glu Ala Ile Leu
 Ala Ala
 165 170
 175
 ttg gaa cca ccc cag gaa aag aaa aag ggt gct tgc cgt gtg
 ata 573
 Leu Glu Pro Pro Gln Glu Lys Lys Lys Gly Ala Cys Arg Val
 Ile
 180 185 190
 taa
 576

<210> 417
 <211> 191
 <212> PRT
 <213> Ciona intestinalis

<400> 417
 Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
 Gly Lys
 1 5 10
 15
 Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe Pro Gln
 Glu Tyr
 20 25 30
 Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val Met Ile
 Gly Gly
 35 40 45
 Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu
 Asp Tyr
 50 55 60
 Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
 Leu Val

0070110

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

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<210> 418
<211> 600
<212> DNA
<213> Colletotrichum trifolii
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$\langle 220 \rangle$
 $\langle 221 \rangle$ CDS
 $\langle 222 \rangle$ (1) .. (600)

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<400> 418
atg gct caa cca gga gta cag tcg ctg aag tgt gtg gtg acg
ggg gac          48
Met Ala Gln Pro Gly Val Gln Ser Leu Lys Cys Val Val Thr
Gly Asp
      1          5          10
15
ggg gct gtc gga aag aca tgt ttg ctg att tcc tac aca acg
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0070110

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

0070110

gag tgt tct gcc ctg aca cag agg aat ctg aag agc gtt ttt
gac gag 528
Glu Cys Ser Ala Leu Thr Gln Arg Asn Leu Lys Ser Val Phe
Asp Glu

165

170

175

gcc att cgt gct gtc ctg aac ccc agg ccc gtc gcg cag cag
aag aag 576
Ala Ile Arg Ala Val Leu Asn Pro Arg Pro Val Ala Gln Gln
Lys Lys

180

185

190

aag tcg aag tgt acg att ttg tga
600
Lys Ser Lys Cys Thr Ile Leu
195

<210> 419

<211> 199

<212> PRT

<213> Colletotrichum trifolii

<400> 419

Met Ala Gln Pro Gly Val Gln Ser Leu Lys Cys Val Val Thr
Gly Asp

1

5

10

15

Gly Ala Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Thr
Asn Ala

20

25

30

Phe Pro Gly Glu Tyr Ile Pro Thr Val Phe Asp Asn Tyr Ser
Ala Ser

35

40

45

Val Met Val Asp Gly Lys Pro Ile Ser Leu Gly Leu Trp Asp
Thr Ala
50 55 60

Gly Gln Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro
Gln Thr
65 70 75

80

Asp Val Phe Leu Ile Cys Phe Ser Ile Val Ser Pro Pro Ser
Phe Asp

85

90

95

Asn Val Lys Ala Lys Trp Tyr Pro Glu Ile Asp His His Ala
Seite 640

0070110

Pro	Asn													
				100				105					110	
Ile	Pro	Ile	Ile	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Glu	
Asp	Pro													
			115					120				125		
Asn	Thr	Leu	Glu	Ser	Leu	Arg	Gln	Lys	Arg	Met	Glu	Pro	Val	
Ser	Tyr													
						135					140			
Asp	Gln	Ala	Leu	Ile	Cys	Ala	Lys	Glu	Ile	Lys	Ala	His	Lys	
Tyr	Leu													
145					150					155				
160														
Glu	Cys	Ser	Ala	Leu	Thr	Gln	Arg	Asn	Leu	Lys	Ser	Val	Phe	
Asp	Glu													
				165						170				
175														
Ala	Ile	Arg	Ala	Val	Leu	Asn	Pro	Arg	Pro	Val	Ala	Gln	Gln	
Lys	Lys													
			180					185					190	
Lys	Ser	Lys	Cys	Thr	Ile	Leu								
			195											

<210> 420
 <211> 576
 <212> DNA
 <213> Aplysia californica

<220>
 <221> CDS
 <222> (1)..(576)

<400>	420													
atg	caa	acc	ata	aag	tgt	gtg	ggt	gtg	ggg	gat	ggg	gca	gtc	
gga	aaa			48										
Met	Gln	Thr	Ile	Lys	Cys	Val	Val	Val	Gly	Asp	Gly	Ala	Val	
Gly	Lys													
1				5					10					
15														
acc	tgc	ctt	ctc	att	tca	tac	acc	aca	aat	aaa	ttt	cct	tca	
gaa	tat			96										
Thr	Cys	Leu	Leu	Ile	Ser	Tyr	Thr	Thr	Asn	Lys	Phe	Pro	Ser	
Glu	Tyr													
			20					25					30	
gtg	cca	aca	gtg	ttt	gac	aac	tat	gcg	gtg	acc	gtg	atg	atc	

Seite 641

0070110

[illegible]

165

170

0070110

175
cta gaa ccc cca gag cca ccc aag aaa aag aaa tgt gtg ctc
ttg 573
Leu Glu Pro Pro Glu Pro Pro Lys Lys Lys Lys Cys Val Leu
Leu
180 185 190
taa
576

<210> 421
<211> 191
<212> PRT
<213> *Aplysia californica*

<400> 421
Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys
1 5 10
15
Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe Pro Ser
Glu Tyr
20 25 30
Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val Met Ile
Gly Gly
35 40 45
Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu
Asp Tyr
50 55 60
Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
Leu Val
65 70 75
80
Cys Phe Ser Val Val Thr Pro Ser Ser Phe Glu Asn Val Arg
Glu Lys
85 90
95
Trp Val Pro Glu Ile Thr His His Cys Gln Arg Thr Pro Phe
Leu Leu
100 105 110
Val Gly Thr Gln Ile Asp Leu Arg Asp Asp Thr Pro Thr Val
Glu Lys

0070110
120

115

125

Leu Ala Lys Asn Lys Gln Lys Pro Ile Thr Ala Asp His Gly
Glu Arg
130 135 140

Leu Ala Arg Glu Leu Arg Ala Val Lys Tyr Val Glu Cys Ser
Ala Leu
145 150 155
160

Asn Gln Arg Gly Leu Lys Asn Val Phe Asp Glu Ala Ile Leu
Ala Ala
165 170

175
Leu Glu Pro Pro Glu Pro Pro Lys Lys Lys Lys Cys Val Leu
Leu
180 185 190

<210> 422
<211> 579
<212> DNA
<213> *Aplysia californica*

<220>
<221> CDS
<222> (1)..(579)

<400> 422
atg cag gct atc aag tgt gtg gta gtc ggg gac ggt gct gtg
ggt aag 48
Met Gln Ala Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys 1 5 10
15
aca tgt ctt ctt atc agc tac act acc aat gcc ttc ccc gga
gaa tac 96
Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Ala Phe Pro Gly
Glu Tyr 20 25 30
att cca act gtc ttt gac aac tac tct gca aat gtt atg gta
gat ggc 144
Ile Pro Thr Val Phe Asp Asn Tyr Ser Ala Asn Val Met Val
Asp Gly 35 40 45
aag cca atc aat ctt gga cta tgg gat act gct gga caa gag
gac tat 192
Lys Pro Ile Asn Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu
Seite 644

0070110

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

0070110

tga

579

<210> 423

<211> 192

<212> PRT

<213> *Aplysia californica*

<400> 423

Met Gln Ala Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys

1 5 10

15

Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Ala Phe Pro Gly
Glu Tyr

20 25 30

Ile Pro Thr Val Phe Asp Asn Tyr Ser Ala Asn Val Met Val
Asp Gly

35 40 45

Lys Pro Ile Asn Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu
Asp Tyr

50 55 60

Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
Leu Ile

65 70 75

80

Cys Phe Ser Leu Ile Ser Pro Thr Ser Phe Glu Asn Val Arg
Ala Lys

85 90

95

Trp Phe Pro Glu Val Ser His His Cys Pro His Thr Pro Ile
Ile Leu

100 105 110

Val Gly Thr Lys Leu Asp Leu Arg Glu Asp Lys Glu Thr Ile
Glu Lys

115 120 125

Leu Arg Asp Lys Lys Leu Ser Pro Ile Thr Tyr Pro Gln Gly
Leu Ala

130 135 140

0070110

Met	Ala	Arg	Glu	Ile	Ser	Ala	Val	Lys	Tyr	Leu	Glu	Cys	Ser
Ala	Leu												
145					150					155			
160													
Thr	Gln	Lys	Gly	Leu	Lys	Asn	Val	Phe	Asp	Glu	Ala	Ile	Arg
Ala	Val												
				165						170			
175													
Leu	Cys	Pro	Lys	Pro	Lys	Pro	Lys	Lys	Lys	Lys	Gly	Cys	Glu
Ile	Leu												
			180					185					190

<210> 424
 <211> 633
 <212> DNA
 <213> Nicotiana tabacum

<220>
 <221> CDS
 <222> (1)..(633)

<400> 424													
atg	gcc	tca	agt	gct	tca	aga	ttc	atc	aaa	tgt	gtc	acg	gtt
ggt	gat			48									
Met	Ala	Ser	Ser	Ala	Ser	Arg	Phe	Ile	Lys	Cys	Val	Thr	Val
Gly	Asp												
1				5					10				
15													
ggt	gcc	gtt	gga	aag	act	tgt	atg	ctt	att	tgc	tat	acc	agt
aac	aag			96									
Gly	Ala	Val	Gly	Lys	Thr	Cys	Met	Leu	Ile	Cys	Tyr	Thr	Ser
Asn	Lys												
			20					25					30
ttc	ccc	act	gat	tat	gtt	ccc	aca	gtg	ttt	gac	aac	ttc	agt
gcc	aat			144									
Phe	Pro	Thr	Asp	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser
Ala	Asn												
		35						40				45	
gtg	gtt	gtc	gaa	ggg	acc	aca	gta	aat	tta	ggt	ctt	tgg	gat
act	gca			192									
Val	Val	Val	Glu	Gly	Thr	Thr	Val	Asn	Leu	Gly	Leu	Trp	Asp
Thr	Ala												
		50				55				60			
ggc	caa	gaa	gat	tat	aac	aga	tta	agg	cca	ctg	agc	tac	cga
gga	gca			240									
Gly	Gln	Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg
Gly	Ala												

0070110

65					70						75			
80														
gat	ggt	ttt	gtc	cta	gcg	ttc	tcc	ttg	ggt	agt	cgc	gca	agc	
tac	gag		288											
Asp	Val	Phe	Val	Leu	Ala	Phe	Ser	Leu	Val	Ser	Arg	Ala	Ser	
Tyr	Glu													
			85						90					
95														
aac	ata	ctt	aaa	aag	tgg	att	cct	gaa	ctt	cag	cat	tat	gct	
cct	gga		336											
Asn	Ile	Leu	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Gln	His	Tyr	Ala	
Pro	Gly													
		100						105					110	
ata	ccg	gtg	gta	tta	gct	ggc	acc	aaa	ctt	gat	ctt	cgt	gag	
gat	aag		384											
Ile	Pro	Val	Val	Leu	Ala	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Glu	
Asp	Lys													
		115						120					125	
cac	ttc	ttg	gct	gat	cat	cct	gga	tta	ggt	cct	gtc	acc	acc	
gcg	cag		432											
His	Phe	Leu	Ala	Asp	His	Pro	Gly	Leu	Val	Pro	Val	Thr	Thr	
Ala	Gln													
		130						135					140	
gga	gag	gag	cta	cgg	aaa	caa	att	ggt	gct	gcc	tat	tac	atc	
gaa	tgt		480											
Gly	Glu	Glu	Leu	Arg	Lys	Gln	Ile	Gly	Ala	Ala	Tyr	Tyr	Ile	
Glu	Cys													
145					150						155			
160														
agc	tct	aaa	aca	caa	cag	aat	gtg	aaa	gct	gtc	ttt	gat	gct	
gca	atc		528											
Ser	Ser	Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	
Ala	Ile													
			165										170	
175														
aag	gtc	gtc	atc	aag	cca	ccg	cag	aag	caa	aag	gag	aag	aag	
aaa	caa		576											
Lys	Val	Val	Ile	Lys	Pro	Pro	Gln	Lys	Gln	Lys	Glu	Lys	Lys	
Lys	Gln													
			180										185	
														190
cgt	cga	gga	tgt	ctc	atg	aat	gtg	atg	tgc	gga	agg	aag	ctc	
ggt	tgt		624											
Arg	Arg	Gly	Cys	Leu	Met	Asn	Val	Met	Cys	Gly	Arg	Lys	Leu	
Val	Cys													
		195						200					205	
ttg	aag	tga												

Leu Lys
210

<210> 425
<211> 210
<212> PRT
<213> Nicotiana tabacum

<400> 425
Met Ala Ser Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val
Gly Asp
1 5 10
15
Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser
Asn Lys
20 25 30

Phe Pro Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser
Ala Asn
35 40 45

Val Val Val Glu Gly Thr Thr Val Asn Leu Gly Leu Trp Asp
Thr Ala
50 55 60

Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg
Gly Ala
65 70 75

80
Asp Val Phe Val Leu Ala Phe Ser Leu Val Ser Arg Ala Ser
Tyr Glu
85 90

95
Asn Ile Leu Lys Lys Trp Ile Pro Glu Leu Gln His Tyr Ala
Pro Gly
100 105 110

Ile Pro Val Val Leu Ala Gly Thr Lys Leu Asp Leu Arg Glu
Asp Lys
115 120 125

His Phe Leu Ala Asp His Pro Gly Leu Val Pro Val Thr Thr
Ala Gln
130 135 140

Gly Glu Glu Leu Arg Lys Gln Ile Gly Ala Ala Tyr Tyr Ile
Glu Cys

0070110

145					150						155			
160	Ser	Ser	Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala
	Ala	Ile												
					165						170			
175	Lys	Val	Val	Ile	Lys	Pro	Pro	Gln	Lys	Gln	Lys	Glu	Lys	Lys
	Lys	Gln												
				180					185					190
Arg	Arg	Gly	Cys	Leu	Met	Asn	Val	Met	Cys	Gly	Arg	Lys	Leu	
Val	Cys													
		195					200					205		
Leu	Lys													
	210													

<210> 426
 <211> 594
 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (1)..(594)

<400> 426														
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gga	gct		48											
Met	Ser	Ala	Ser	Arg	Phe	Ala	Lys	Cys	Val	Thr	Val	Gly	Asp	
Gly	Ala													
1				5					10					
15														
gtc	gga	aaa	aca	tgt	ttg	ttg	att	tct	tac	aca	agc	aac	act	
ttc	cct		96											
Val	Gly	Lys	Thr	Cys	Leu	Leu	Ile	Ser	Tyr	Thr	Ser	Asn	Thr	
Phe	Pro													
			20					25					30	
acg	gat	tat	gtg	cca	act	ggt	ttc	gat	aat	ttc	agt	gca	aat	
ggt	gtg		144											
Thr	Asp	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn	
Val	Val													
		35					40					45		
ggt	aat	gga	gcc	acc	ggt	aat	ctt	gga	ttg	tgg	gat	act	gca	
ggg	caa		192											
Val	Asn	Gly	Ala	Thr	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala	
Gly	Gln													
	50						55				60			

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gag	gat	tac	aac	aga	tta	aga	cca	cta	agc	tac	cgt	gga	gct
gat	gtt			240									
Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala
Asp	Val												
65					70					75			
80													
ttc	ata	ttg	gcc	ttc	tct	ctt	atc	agt	aaa	gcc	agt	tat	gaa
aac	gtc			288									
Phe	Ile	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Lys	Ala	Ser	Tyr	Glu
Asn	Val												
				85						90			
95													
tcc	aaa	aag	tgg	atc	ccg	gag	ttg	aag	cat	tac	gcg	cct	ggt
gtc	ccc			336									
Ser	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Lys	His	Tyr	Ala	Pro	Gly
Val	Pro												
				100					105				110
atc	atc	ctt	gtt	gga	tca	aag	ctt	gat	ctt	cga	gat	gat	aag
caa	ttc			384									
Ile	Ile	Leu	Val	Gly	Ser	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys
Gln	Phe												
		115						120				125	
ttc	gtc	gac	cat	cct	ggc	gct	gtc	ccg	att	aca	act	gct	cag
gga	gag			432									
Phe	Val	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Thr	Thr	Ala	Gln
Gly	Glu												
		130				135				140			
gag	ctg	agg	aag	cta	ata	gat	gca	cct	act	tac	atc	gaa	tgc
agt	tcc			480									
Glu	Leu	Arg	Lys	Leu	Ile	Asp	Ala	Pro	Thr	Tyr	Ile	Glu	Cys
Ser	Ser												
145					150					155			
160													
aaa	tct	caa	gag	aat	gtg	aaa	gct	gtc	ttt	gac	gca	gcc	ata
cga	gtg			528									
Lys	Ser	Gln	Glu	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile
Arg	Val												
				165						170			
175													
gtg	ttg	caa	ccg	cct	aag	cag	aag	aag	aaa	aag	agc	aaa	acg
cag	aag			576									
Val	Leu	Gln	Pro	Pro	Lys	Gln	Lys	Lys	Lys	Lys	Ser	Lys	Thr
Gln	Lys												
				180						185			190
gca	tgc	tcc	atc	caa	tga								
			594										

0070110

Ala Cys Ser Ile Gln
195

<210> 427
<211> 197
<212> PRT
<213> Brassica napus

<400> 427
Met Ser Ala Ser Arg Phe Ala Lys Cys Val Thr Val Gly Asp
Gly Ala

1 5 10
15

Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro 20 25 30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val 35 40 45

Val Asn Gly Ala Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln 50 55 60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val 65 70 75

80
Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val 85 90

95
Ser Lys Lys Trp Ile Pro Glu Leu Lys His Tyr Ala Pro Gly
Val Pro 100 105 110

Ile Ile Leu Val Gly Ser Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe 115 120 125

Phe Val Asp His Pro Gly Ala Val Pro Ile Thr Thr Ala Gln
Gly Glu 130 135 140

Glu Leu Arg Lys Leu Ile Asp Ala Pro Thr Tyr Ile Glu Cys
Ser Ser 145 150 155

0070110

160

Lys Ser Gln Glu Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Arg Val

165

170

175

Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Ser Lys Thr
Gln Lys

180

185

190

Ala Cys Ser Ile Gln
195

<210> 428

<211> 594

<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (1)..(594)

<400> 428

atg agc gca tct cgg ttc ata aag tgc gtg acg gtt ggg gac
gga gca 48
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10

15

gtg ggc aaa aca tgt ctc ctc atc tct tac acc agc aac act
ttc cct 96
Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro

20

25

30

acg gat tat gtt cca act gtt ttc gat aac ttc agc gct aat
gtt gtt 144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val

35

40

45

gtt aac gga gcc act gtc aac tta gga ctc tgg gat acc gca
ggg cag 192
Val Asn Gly Ala Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln

50

55

60

gag gat tat aac aga ttg aga ccc ttg agt tac cgc ggt gct
gac gtt 240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val

0070110

65					70								75
80													
ttc	atc	ttg	gcc	ttc	tct	ctc	atc	agt	aag	gct	agt	tat	gag
aat	gtc		288										
Phe	Ile	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Lys	Ala	Ser	Tyr	Glu
Asn	Val												
				85									90
95													
tcc	aag	aag	tgg	atc	cct	gag	ctg	acc	cac	tat	gcc	cct	ggt
gtc	cct		336										
Ser	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Thr	His	Tyr	Ala	Pro	Gly
Val	Pro												
			100					105					110
atc	gtt	ctt	gtt	ggt	acc	aaa	cta	gat	ctt	agg	gat	gac	aaa
cag	ttc		384										
Ile	Val	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys
Gln	Phe												
		115					120					125	
ttc	gtt	gac	cac	cct	ggt	gct	gta	cct	att	acc	act	tct	cag
gga	gag		432										
Phe	Val	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Thr	Thr	Ser	Gln
Gly	Glu												
		130				135					140		
gaa	cta	atg	aag	cta	att	gga	gct	cct	tcg	tac	atc	gag	tgc
agt	tca		480										
Glu	Leu	Met	Lys	Leu	Ile	Gly	Ala	Pro	Ser	Tyr	Ile	Glu	Cys
Ser	Ser												
145					150						155		
160													
aaa	tct	caa	gag	aac	gtg	aaa	ggg	gtg	ttt	gat	gca	gcg	atc
aga	gtg		528										
Lys	Ser	Gln	Glu	Asn	Val	Lys	Gly	Val	Phe	Asp	Ala	Ala	Ile
Arg	Val												
				165							170		
175													
gta	ctt	caa	cct	cca	aag	cag	aag	aaa	aag	aag	agc	aag	gca
caa	aag		576										
Val	Leu	Gln	Pro	Pro	Lys	Gln	Lys	Lys	Lys	Lys	Ser	Lys	Ala
Gln	Lys												
			180					185					190
gcc	tgc	tcc	att	ttg	taa								
			594										
Ala	Cys	Ser	Ile	Leu									
		195											

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<210> 429

<211> 197

<212> PRT

<213> Brassica napus

<400> 429

Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala

1 5 10

15

Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro

20 25 30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val

35 40 45

Val Asn Gly Ala Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln

50 55 60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val

65 70 75

80

Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val

85 90

95

Ser Lys Lys Trp Ile Pro Glu Leu Thr His Tyr Ala Pro Gly
Val Pro

100 105 110

Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe

115 120 125

Phe Val Asp His Pro Gly Ala Val Pro Ile Thr Thr Ser Gln
Gly Glu

130 135 140

Glu Leu Met Lys Leu Ile Gly Ala Pro Ser Tyr Ile Glu Cys
Ser Ser

145 150 155

160

Lys Ser Gln Glu Asn Val Lys Gly Val Phe Asp Ala Ala Ile
Arg Val

0070110

165

170

175
Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Ser Lys Ala
Gln Lys

180

185

190

Ala Cys Ser Ile Leu
195

<210> 430

<211> 594

<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (1)..(594)

<400> 430

atg agc gca tcg aga ttc gta aag tgt gtg acg gtt ggt gat
gga gct 48
Met Ser Ala Ser Arg Phe Val Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10

15
gtc gga aaa aca tgt ttg ctg att tct tac aca agc aac act
ttc cct 96
Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro

20 25 30
acg gat tat gtg cca acc gtt ttc gat aat ttc agt gca aat
gtt gtg 144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val

35 40 45
gtt aat gga gcc acc gtt aat ctt gga ttg tgg gat act gca
ggg caa 192
Val Asn Gly Ala Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln

50 55 60
gag gat tac aac aga tta aga cca cta agc tac cgt gga gca
gat gtt 240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val

65 70 75
80
ttc ata ttg gcc ttc tct ctt att agt aaa gcc agt tat gaa
aac gtc 288

0070110

Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val

85

90

95

tcc aaa aag tgg atc ccg gag ttg aaa cat tac gcg cct ggt
gtc cca
Ser Lys Lys Trp Ile Pro Glu Leu Lys His Tyr Ala Pro Gly
Val Pro

100

105

110

atc att ctt gtt gga tca aag ctt gat ctt cga gat gat aag
caa ttc
Ile Ile Leu Val Gly Ser Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe

115

120

125

ttc gtc gac cat cct ggc gct gtc gcg att aca act gct cag
gga gag
Phe Val Asp His Pro Gly Ala Val Ala Ile Thr Thr Ala Gln
Gly Glu

130

135

140

gag ctg agg aag cta ata gat gca cct act tac atc gaa tgc
agt tcc
Glu Leu Arg Lys Leu Ile Asp Ala Pro Thr Tyr Ile Glu Cys
Ser Ser

145

150

155

160

aaa tct caa gag aat gtg aaa gcc gtc ttt gat gca gcc ata
cga gtg
Lys Ser Gln Glu Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Arg Val

165

170

175

gtg ttg caa ccg cct aag cag aag aag aaa aag agc aaa gcg
caa aag
Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Ser Lys Ala
Gln Lys

180

185

190

gca tgc tcc atc caa tga
Ala Cys Ser Ile Gln

195

<210> 431

<211> 197

<212> PRT

<213> Brassica napus

0070110

<400> 431

Met Ser Ala Ser Arg Phe Val Lys Cys Val Thr Val Gly Asp
Gly Ala

1 5 10

15

Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro

20 25 30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val

35 40 45

Val Asn Gly Ala Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln

50 55 60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val

65 70 75

80

Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val

85 90

95

Ser Lys Lys Trp Ile Pro Glu Leu Lys His Tyr Ala Pro Gly
Val Pro

100 105 110

Ile Ile Leu Val Gly Ser Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe

115 120 125

Phe Val Asp His Pro Gly Ala Val Ala Ile Thr Thr Ala Gln
Gly Glu

130 135 140

Glu Leu Arg Lys Leu Ile Asp Ala Pro Thr Tyr Ile Glu Cys
Ser Ser

145 150 155

160

Lys Ser Gln Glu Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Arg Val

165 170

175

Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Ser Lys Ala
Gln Lys

0070110

180

185

190

Ala Cys Ser Ile Gln
195

<210> 432
<211> 594
<212> DNA
<213> Brassica napus

<220>
<221> CDS
<222> (1)..(594)

<400> 432
atg agc ggc ttc aga ttc gta aag tgt gtg aca gtt ggt gat
gga gct 48
Met Ser Gly Phe Arg Phe Val Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10
15
gtc gga aaa aca tgt ttg ttg att tct tac aca agc aac act
ttc cct 96
Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
20 25 30
acg gat tat gtg cca act gtt ttc gat aat ttc agt gca aat
gtt gtg 144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
35 40 45
gtt aat gga gcc acc gtt aat ctt gga ttg tgg gat act gca
ggg caa 192
Val Asn Gly Ala Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60
gag gat tac aac aga tta aga cca cta agc tac cgt gga gct
gat gtt 240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65 70 75
80
ttc ata ttg gcc ttc tct ctt atc agt aaa gcc agt tat gaa
aac gtc 288
Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val
85 90
95

0070110

tcc aaa aag tgg atc ccg gag ttg aag cat tac gcg cct ggt
 gtc ccc 336
 Ser Lys Lys Trp Ile Pro Glu Leu Lys His Tyr Ala Pro Gly
 Val Pro 100 105 110

atc atc ctt gtt gga tca aag ctt gat ctt cga gat gat aag
 caa ttc 384
 Ile Ile Leu Val Gly Ser Lys Leu Asp Leu Arg Asp Asp Lys
 Gln Phe 115 120 125

ttc gtc gac cat cct ggc gct gtc ccg att aca act gct cag
 gga gag 432
 Phe Val Asp His Pro Gly Ala Val Pro Ile Thr Thr Ala Gln
 Gly Glu 130 135 140

gag ctg agg aag cta ata gat gca cct act tac atc gaa tgc
 agt tcc 480
 Glu Leu Arg Lys Leu Ile Asp Ala Pro Thr Tyr Ile Glu Cys
 Ser Ser 145 150 155
 160

aaa tct caa gag aat gtg aaa gct gtc ttt gac gca gcc ata
 cga gtg 528
 Lys Ser Gln Glu Asn Val Lys Ala Val Phe Asp Ala Ala Ile
 Arg Val 165 170

175
 gtg ttg caa ccg cct aag cag aag aag aaa aag agc aaa gcg
 cag aag 576
 Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Ser Lys Ala
 Gln Lys 180 185 190

gca tgc tcc atc cag tga
 594
 Ala Cys Ser Ile Gln
 195

<210> 433
 <211> 197
 <212> PRT
 <213> Brassica napus

<400> 433
 Met Ser Gly Phe Arg Phe Val Lys Cys Val Thr Val Gly Asp
 Gly Ala
 1 5 10

0070110

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

0070110

<210> 434
<211> 594
<212> DNA
<213> Brassica napus

<220>
<221> CDS
<222> (1)..(594)

<400> 434
atg agc gca tct cgg ttc ata aag tgt gta acg gtt ggt gat
gga gct 48
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10
15
gtc gga aaa aca tgt ttg ttg att tct tac aca agc aac act
ttc cct 96
Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
20 25 30
acg gac tat gtg ccc acc gtt ttc gat aat ttc agt gct aat
gtg gtg 144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
35 40 45
gtt aac gga gcc acc gtt aat ctt gga ttg tgg gat act gca
ggg caa 192
Val Asn Gly Ala Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60
gag gat tac aac aga tta aga cca cta agc tac cgt gga gct
gat gtt 240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65 70 75
80
ttc ata ttg gcc ttc tct ctt atc agt aaa gcc agt tat gaa
aac gtc 288
Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val
85 90
95
tcc aaa aag tgg atc ccg gag ttg aag cat tac gcg cct ggt
gtc ccc 336
Ser Lys Lys Trp Ile Pro Glu Leu Lys His Tyr Ala Pro Gly
Val Pro
100 105 110

0070110

```

gtc atc ctt gtt gga tca aag ctt gat ctt cga gat gat aag
caa ttc          384
Val Ile Leu Val Gly Ser Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe
          115          120          125
ttc gtc gac cat cct ggc gct gtc ccg att aca act gct cag
gga gag          432
Phe Val Asp His Pro Gly Ala Val Pro Ile Thr Thr Ala Gln
Gly Glu
          130          135          140
gag ctg agg aag cta ata gat gca cct act tac atc gaa tgc
agt tcc          480
Glu Leu Arg Lys Leu Ile Asp Ala Pro Thr Tyr Ile Glu Cys
Ser Ser
145          150          155
          160
aaa tct caa gag aat gtg aaa gct gtc ttt gac gca gcc ata
cga gtg          528
Lys Ser Gln Glu Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Arg Val
          165          170
175
gtg ttg caa ccg cct aag cag aag aag aaa aag agc aaa gcg
cag aag          576
Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Ser Lys Ala
Gln Lys
          180          185          190

gca tgc tcc atc cag tga
          594
Ala Cys Ser Ile Gln
          195

```

<210> 435
 <211> 197
 <212> PRT
 <213> Brassica napus

<400> 435
 Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala
 1 5 10
 15
 Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
 Phe Pro
 20 25 30

0070110

Thr	Asp	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn
Val	Val												
		35					40					45	

Val	Asn	Gly	Ala	Thr	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala
Gly	Gln												
	50					55					60		

Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala
Asp	Val												
65					70					75			

	80												
Phe	Ile	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Lys	Ala	Ser	Tyr	Glu
Asn	Val												
				85					90				

95													
Ser	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Lys	His	Tyr	Ala	Pro	Gly
Val	Pro												
			100					105				110	

Val	Ile	Leu	Val	Gly	Ser	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys
Gln	Phe												
		115					120				125		

Phe	Val	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Thr	Thr	Ala	Gln
Gly	Glu												
	130					135					140		

Glu	Leu	Arg	Lys	Leu	Ile	Asp	Ala	Pro	Thr	Tyr	Ile	Glu	Cys
Ser	Ser												
145					150					155			

	160												
Lys	Ser	Gln	Glu	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile
Arg	Val												
				165					170				

175													
Val	Leu	Gln	Pro	Pro	Lys	Gln	Lys	Lys	Lys	Lys	Ser	Lys	Ala
Gln	Lys												
			180					185				190	

Ala	Cys	Ser	Ile	Gln
		195		

<210> 436
 <211> 594
 <212> DNA
 <213> Zinnia elegans

0070110

<220>

<221> CDS

<222> (1)..(594)

<400> 436

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atg agt gca tca aga ttt ata aag tgt gtt act gtt ggt gat
ggg gct          48
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
  1                    5                    10
15
gtt gga aag act tgt ttg ttg att tct tac acc agt aat acc
ttc cct          96
Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
      20                    25                    30
acg gat tac gtc cca acg gta ttt gat aat ttc agt gct aat
gta gtt          144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
      35                    40                    45
gtc aat gga agc aca gtt aat cta ggc ttg tgg gac act gct
gga cag          192
Val Asn Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
      50                    55                    60
gag gac tat aac aga tta aga ccg ttg agt tat cgt gga gct
gat gtt          240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
      65                    70                    75
80
ttc att ttg gcg ttc tca ctc att agc aag gct agc tat gag
aac gtt          288
Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val
      85                    90
95
tcc aag aag tgg att cca gaa ttg aag cat tat gct cct ggt
gtt cca          336
Ser Lys Lys Trp Ile Pro Glu Leu Lys His Tyr Ala Pro Gly
Val Pro
      100                    105                    110
atc gtt ctt gtt ggg acg aaa cta gat ctc cga gat gat aag
cag ttt          384
Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe

```

0070110

		115					120					125	
ttt	gta	gat	cac	cct	ggt	gca	act	cct	att	acc	act	gca	cag
gga	gag		432										
Phe	Val	Asp	His	Pro	Gly	Ala	Thr	Pro	Ile	Thr	Thr	Ala	Gln
Gly	Glu												
	130					135					140		
gaa	tta	aag	aag	aca	atc	ggt	gct	cct	gag	tac	att	gaa	tgt
agt	tca		480										
Glu	Leu	Lys	Lys	Thr	Ile	Gly	Ala	Pro	Glu	Tyr	Ile	Glu	Cys
Ser	Ser												
145					150						155		
160													
aaa	aca	caa	ttg	aat	gtg	aag	caa	gtt	ttc	gat	gct	gcc	att
aaa	gtc		528										
Lys	Thr	Gln	Leu	Asn	Val	Lys	Gln	Val	Phe	Asp	Ala	Ala	Ile
Lys	Val												
			165						170				
175													
gtt	ctg	gcg	cct	cca	aag	gcg	aag	aaa	aag	aag	gga	aaa	gct
caa	aag		576										
Val	Leu	Ala	Pro	Pro	Lys	Ala	Lys	Lys	Lys	Lys	Gly	Lys	Ala
Gln	Lys												
			180						185				190

gca tgc tca ata ttg tga
 594
 Ala Cys Ser Ile Leu
 195

<210> 437
 <211> 197
 <212> PRT
 <213> Zinnia elegans

<400> 437
 Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala
 1 5 10
 15
 Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
 Phe Pro
 20 25 30
 Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
 Val Val
 35 40 45
 Val Asn Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
 Seite 666

0070110

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

<210> 438
 <211> 597
 <212> DNA
 <213> Zinnia elegans

<220>
 <221> CDS
 <222> (1)..(597)

0070110

<400> 438

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atg gca gca gca gcc acc aga ttc atc aag tgc gtc acc gtt
ggc gac
Met Ala Ala Ala Ala Thr Arg Phe Ile Lys Cys Val Thr Val
Gly Asp
1 5 10
15
ggg gcg gtc gga aaa acc tgc atg ctc atc tcc tac acc agc
aat act
Gly Ala Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser
Asn Thr
20 25 30
ttc ccc acc gat tat gtg ccg aca gtg ttt gat aac ttc agt
gcg aat
Phe Pro Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser
Ala Asn
35 40 45
gtt gtg gtc gga gac agc act gtc aat ctt ggc ctt tgg gat
act gcc
Val Val Val Gly Asp Ser Thr Val Asn Leu Gly Leu Trp Asp
Thr Ala
50 55 60
ggg cag gag gat tat aac aga ctg agg cca ctg agt tat aga
ggg gca
Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg
Gly Ala
65 70 75
80
gat gtg ttt tta ttg gca ttt tct ctc att agc aga ccc agt
tat gaa
Asp Val Phe Leu Leu Ala Phe Ser Leu Ile Ser Arg Pro Ser
Tyr Glu
85 90
95
aac atc tcc aag aag tgg atc tca gaa cta agg cat tat gcc
cca gat
Asn Ile Ser Lys Lys Trp Ile Ser Glu Leu Arg His Tyr Ala
Pro Asp
100 105 110
115 120 125
gtc ccc att gtg ctg gtg gga acc aaa tta gat tta cgt gaa
gac aaa
Val Pro Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Glu
Asp Lys
130 135 140
caa tat ttg agt gat cat cca aat gtt aca gcc atc aca act
tct cag
Gln Tyr Leu Ser Asp His Pro Asn Val Thr Ala Ile Thr Thr

```


0070110

Ser Gln
130 135 140
ggt gaa gaa ctg aag aaa agt att ggt gca gca gtg tac att
gag tgt 480
Gly Glu Glu Leu Lys Lys Ser Ile Gly Ala Ala Val Tyr Ile
Glu Cys
145 150 155
160
agc tcc aaa act caa cag aat gtg aag gct gtt ttt gat gct
gcg att 528
Ser Ser Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala
Ala Ile
165 170
175
aga gtt gtt tta caa cca cca aag ctg aag aaa aag cga agc
aag caa 576
Arg Val Val Leu Gln Pro Pro Lys Leu Lys Lys Lys Arg Ser
Lys Gln
180 185 190

cga cta tgt gtc tat cta tag
597
Arg Leu Cys Val Tyr Leu
195

<210> 439
<211> 198
<212> PRT
<213> Zinnia elegans

<400> 439
Met Ala Ala Ala Ala Thr Arg Phe Ile Lys Cys Val Thr Val
Gly Asp
1 5 10
15
Gly Ala Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser
Asn Thr
20 25 30
Phe Pro Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser
Ala Asn
35 40 45
Val Val Val Gly Asp Ser Thr Val Asn Leu Gly Leu Trp Asp
Thr Ala
50 55 60
Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg
Seite 669

0070110

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

Val Pro Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Glu
Asp Lys
115 120 125

Gln Tyr Leu Ser Asp His Pro Asn Val Thr Ala Ile Thr Thr
Ser Gln
130 135 140

Gly Glu Glu Leu Lys Lys Ser Ile Gly Ala Ala Val Tyr Ile
Glu Cys
145 150 155
160

Ser Ser Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala
Ala Ile
165 170

175
Arg Val Val Leu Gln Pro Pro Lys Leu Lys Lys Lys Arg Ser
Lys Gln
180 185 190

Arg Leu Cys Val Tyr Leu
195

<210> 440
<211> 600
<212> DNA
<213> *Penicillium marneffe*

<220>
<221> CDS
<222> (1)..(600)

<400> 440
atg gcg tct ggg cct gcg act caa tcg ttg aag tgt gtg gtg
acc ggt 48
Met Ala Ser Gly Pro Ala Thr Gln Ser Leu Lys Cys Val Val

0070110

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

0070110

Tyr Glu Gln Ala Leu Ala Val Ala Lys Glu Ile Arg Ala His
 Lys Tyr
 145 150 155

160
 ctg gag tgt tcg gcc ttg acc cag agg aat ttg aag agc gtg
 ttt gat 528
 Leu Glu Cys Ser Ala Leu Thr Gln Arg Asn Leu Lys Ser Val
 Phe Asp
 165 170

175
 gaa gct att cgg gcc gtc ctc aat cct cgc cct caa ccc aag
 aac aag 576
 Glu Ala Ile Arg Ala Val Leu Asn Pro Arg Pro Gln Pro Lys
 Asn Lys
 180 185 190

gca aaa cga tgc act att ctg taa
 600
 Ala Lys Arg Cys Thr Ile Leu
 195

<210> 441
 <211> 199
 <212> PRT
 <213> Penicillium marneffeii

<400> 441
 Met Ala Ser Gly Pro Ala Thr Gln Ser Leu Lys Cys Val Val
 Thr Gly
 1 5 10
 15
 Asp Gly Ala Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr
 Thr Asn
 20 25 30

Ala Phe Pro Gly Glu Tyr Ile Pro Thr Val Phe Asp Asn Tyr
 Ser Ala
 35 40 45

Ser Val Met Val Asp Gly Arg Pro Ile Ser Leu Gly Leu Trp
 Asp Thr
 50 55 60

Ala Gly Gln Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr
 Pro Gln
 65 70 75

80
 Thr Asp Val Phe Leu Ile Cys Phe Ser Ile Val Ser Pro Pro
 Seite 672

0070110

```

Ser Phe
      85                      90
95
Asp Asn Val Lys Ala Lys Trp Phe Pro Glu Ile Glu His His
Ala Pro
      100                      105                      110

Gly Val Pro Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg
Glu Asp
      115                      120                      125

Arg Ala Thr Ala Glu Ala Leu Arg Ala Lys Lys Met Glu Pro
Val Ser
      130                      135                      140

Tyr Glu Gln Ala Leu Ala Val Ala Lys Glu Ile Arg Ala His
Lys Tyr
      145                      150                      155
      160
Leu Glu Cys Ser Ala Leu Thr Gln Arg Asn Leu Lys Ser Val
Phe Asp
      165                      170
      175
Glu Ala Ile Arg Ala Val Leu Asn Pro Arg Pro Gln Pro Lys
Asn Lys
      180                      185                      190

Ala Lys Arg Cys Thr Ile Leu
      195

```

<210> 442
 <211> 582
 <212> DNA
 <213> Ustilago maydis

<220>
 <221> CDS
 <222> (1)..(582)

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<400> 442
atg cag acc atc aag tgt gta gtc gtc gga gac ggt gcc gtc
gga aag
Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys
      1                      5                      10
      15
acg tgt ctt ctt atc tcg tat aca acc aac gcc ttc ccg ggc
gaa tac
      96

```

0070110

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

0070110

agc gtt 528
Thr Gln Lys Gly Leu Lys Gly Val Phe Asp Glu Ala Ile Arg
Ser Val

165

170

175

ttg gct cct gca cca gtc cag agt aag aag aaa aac aac tgt
ttg att 576
Leu Ala Pro Ala Pro Val Gln Ser Lys Lys Lys Asn Asn Cys
Leu Ile

180

185

190

ctt taa

582

Leu

<210> 443

<211> 193

<212> PRT

<213> Ustilago maydis

<400> 443

Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys

1

5

10

15

Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Ala Phe Pro Gly
Glu Tyr

20

25

30

Ile Pro Thr Val Phe Asp Asn Tyr Ser Ala Asn Val Met Val
Asp Gly

35

40

45

Lys Pro Val Ser Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu
Asp Tyr

50

55

60

Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
Leu Val

65

70

75

80

Cys Phe Ser Leu Val Ser Pro Pro Ser Phe Glu Asn Val Arg
Thr Lys

85

90

95

Trp Trp Pro Glu Val Ser His His Ala Pro Asn Ile Pro Thr
Ile Leu

0070110

	100	105	110
Val Gly Thr Lys Leu Asp Leu Arg Glu Asp Pro Glu Thr Ile			
Ala Lys	115	120	125
Leu Arg Asp Arg Arg Met Gln Pro Ile Thr Tyr Ala Gln Gly			
Asn Gln	130	135	140
Met Ala Arg Asp Ile His Ala Thr Lys Tyr Leu Glu Cys Ser			
Ala Leu	145	150	155
160			
Thr Gln Lys Gly Leu Lys Gly Val Phe Asp Glu Ala Ile Arg			
Ser Val	165	170	
175			
Leu Ala Pro Ala Pro Val Gln Ser Lys Lys Lys Asn Asn Cys			
Leu Ile	180	185	190

Leu

<210> 444
 <211> 645
 <212> DNA
 <213> Ustilago maydis

<220>
 <221> CDS
 <222> (1)..(645)

<400> 444

atg gca ccg gca gca att tgt agg aag ctt gta att gtc ggc			
gac ggt	48		
Met Ala Pro Ala Ala Ile Cys Arg Lys Leu Val Ile Val Gly			
Asp Gly	5	10	
1			
15			
gct tgc ggc aag acg agt ttg ctt tgc gtt ttt gcc att ggc			
gag ttc	96		
Ala Cys Gly Lys Thr Ser Leu Leu Cys Val Phe Ala Ile Gly			
Glu Phe	20	25	30
ccg caa gag tat gaa ccc acc att ttc gaa aac tac gtc gcc			
gag atc	144		

0070110

Pro	Gln	Glu	Tyr	Glu	Pro	Thr	Ile	Phe	Glu	Asn	Tyr	Val	Ala
Glu	Ile												
		35					40					45	
cgc	ctt	gat	ggc	aag	cct	gtc	cag	ctg	gcg	cta	tgg	gac	acc
gcg	ggt		192										
Arg	Leu	Asp	Gly	Lys	Pro	Val	Gln	Leu	Ala	Leu	Trp	Asp	Thr
Ala	Gly												
	50					55					60		
cag	gaa	gaa	tac	gag	cgt	ctt	cgt	cca	ctc	tcc	tac	tca	caa
gca	cac		240										
Gln	Glu	Glu	Tyr	Glu	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Ser	Gln
Ala	His												
65					70					75			
80													
gtc	atc	ttg	atc	gcc	ttt	gcc	atc	gat	aca	ccc	gac	tcg	ctc
gaa	aac		288										
Val	Ile	Leu	Ile	Ala	Phe	Ala	Ile	Asp	Thr	Pro	Asp	Ser	Leu
Glu	Asn												
				85					90				
95													
gtg	caa	gtc	aag	tgg	atg	gag	gag	gta	cgt	caa	ata	tgc	ggc
ccc	tca		336										
Val	Gln	Val	Lys	Trp	Met	Glu	Glu	Val	Arg	Gln	Ile	Cys	Gly
Pro	Ser												
			100					105				110	
gtg	cct	gtg	ctc	ctg	gta	ggc	tgc	aag	aag	gat	ctt	cgc	gaa
aat	gcc		384										
Val	Pro	Val	Leu	Leu	Val	Gly	Cys	Lys	Lys	Asp	Leu	Arg	Glu
Asn	Ala												
		115				120					125		
atc	gct	aag	ggc	aag	ccg	gtt	cag	ggt	cac	tat	gta	aag	aga
caa	cag		432										
Ile	Ala	Lys	Gly	Lys	Pro	Val	Gln	Gly	His	Tyr	Val	Lys	Arg
Gln	Gln												
	130					135					140		
gct	aaa	ctg	gta	gca	gca	cag	atc	ggc	gct	cga	tcg	tat	cac
gaa	tgc		480										
Ala	Lys	Leu	Val	Ala	Ala	Gln	Ile	Gly	Ala	Arg	Ser	Tyr	His
Glu	Cys												
145					150					155			
160													
tca	tca	ctc	aac	aac	caa	ggc	gtc	gac	gcc	gtg	ttc	gaa	gcc
gcg	acg		528										
Ser	Ser	Leu	Asn	Asn	Gln	Gly	Val	Asp	Ala	Val	Phe	Glu	Ala
Ala	Thr												
				165					170				
175													

0070110

cgc gcg gcc atg ctt gtg cgc aat tcc ggt gct tct tca gga
 ggc gcc 576
 Arg Ala Ala Met Leu Val Arg Asn Ser Gly Ala Ser Ser Gly
 Gly Ala 180 185 190

atc tcg cag agc aag acc aag gag gca tta cac aac gat gct
 ggc tct 624
 Ile Ser Gln Ser Lys Thr Lys Glu Ala Leu His Asn Asp Ala
 Gly Ser 195 200 205
 tgc aaa tgt atc gtc ctc tag
 Cys Lys Cys Ile Val Leu 645
 210

<210> 445
 <211> 214
 <212> PRT
 <213> Ustilago maydis

<400> 445
 Met Ala Pro Ala Ala Ile Cys Arg Lys Leu Val Ile Val Gly
 Asp Gly 1 5 10
 15
 Ala Cys Gly Lys Thr Ser Leu Leu Cys Val Phe Ala Ile Gly
 Glu Phe 20 25 30

Pro Gln Glu Tyr Glu Pro Thr Ile Phe Glu Asn Tyr Val Ala
 Glu Ile 35 40 45

Arg Leu Asp Gly Lys Pro Val Gln Leu Ala Leu Trp Asp Thr
 Ala Gly 50 55 60

Gln Glu Glu Tyr Glu Arg Leu Arg Pro Leu Ser Tyr Ser Gln
 Ala His 65 70 75

80
 Val Ile Leu Ile Ala Phe Ala Ile Asp Thr Pro Asp Ser Leu
 Glu Asn 85 90

95
 Val Gln Val Lys Trp Met Glu Glu Val Arg Gln Ile Cys Gly
 Pro Ser

0070110

100

105

110

Val Pro Val Leu Leu Val Gly Cys Lys Lys Asp Leu Arg Glu
Asn Ala

115

120

125

Ile Ala Lys Gly Lys Pro Val Gln Gly His Tyr Val Lys Arg
Gln Gln

130

135

140

Ala Lys Leu Val Ala Ala Gln Ile Gly Ala Arg Ser Tyr His
Glu Cys

145

150

155

160

Ser Ser Leu Asn Asn Gln Gly Val Asp Ala Val Phe Glu Ala
Ala Thr

165

170

175

Arg Ala Ala Met Leu Val Arg Asn Ser Gly Ala Ser Ser Gly
Gly Ala

180

185

190

Ile Ser Gln Ser Lys Thr Lys Glu Ala Leu His Asn Asp Ala
Gly Ser

195

200

205

Cys Lys Cys Ile Val Leu
210

<210> 446

<211> 594

<212> DNA

<213> Hordeum vulgare

<220>

<221> CDS

<222> (1)..(594)

<400> 446

atg agc gcg tcc agg ttc ata aag tgc gtc acc gtg ggg gac
ggc gcc 48

Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala

1

5

10

15

gtc ggc aag acc tgc atg ctc atc tcc tac acc tcc aac acc
ttc ccc 96

Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Seite 679

0070110

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

0070110

Lys Thr Gln Leu Asn Val Lys Gly Val Phe Asp Ala Ala Ile
Lys Val

165

170

175

gta ctg cag cca cca aag gca aag aag aag aaa aag gcg cag

agg ggg

576

Val Leu Gln Pro Pro Lys Ala Lys Lys Lys Lys Lys Ala Gln

Arg Gly

180

185

190

gct tgc tcc atc ttg tga

594

Ala Cys Ser Ile Leu

195

<210> 447

<211> 197

<212> PRT

<213> Hordeum vulgare

<400> 447

Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp

Gly Ala

1

5

10

15

Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr

Phe Pro

20

25

30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn

Val Val

35

40

45

Val Asp Gly Asn Thr Val Asn Leu Gly Leu Trp Asp Thr Ala

Gly Gln

50

55

60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala

Asp Val

65

70

75

80

Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu

Asn Val

85

90

95

Ser Lys Lys Trp Ile Pro Glu Leu Lys His Tyr Ala Pro Gly

Val Pro

100

105

110

0070110

Ile	Ile	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys
Gln	Phe												
		115					120					125	

Phe	Val	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Thr	Thr	Ala	Gln
Gly	Glu												
	130					135					140		

Glu	Leu	Lys	Lys	Leu	Ile	Gly	Ala	Pro	Tyr	Tyr	Ile	Glu	Cys
Ser	Ser												
145					150					155			
	160												

Lys	Thr	Gln	Leu	Asn	Val	Lys	Gly	Val	Phe	Asp	Ala	Ala	Ile
Lys	Val												
				165					170				

175													
Val	Leu	Gln	Pro	Pro	Lys	Ala	Lys	Lys	Lys	Lys	Lys	Ala	Gln
Arg	Gly												
			180					185					190

Ala	Cys	Ser	Ile	Leu
		195		

<210> 448
<211> 594
<212> DNA
<213> Medicago truncatula

<220>
<221> CDS
<222> (1)..(594)

<400>	448												
atg	agt	gct	tct	agg	ttt	att	aaa	tgt	gtt	act	gtt	ggt	gat
gga	gct		48										
Met	Ser	Ala	Ser	Arg	Phe	Ile	Lys	Cys	Val	Thr	Val	Gly	Asp
Gly	Ala												
1				5					10				
15													
gtt	ggc	aaa	act	tgt	ttg	ttg	att	tct	tac	acc	agc	aat	act
ttc	ccc		96										
Val	Gly	Lys	Thr	Cys	Leu	Leu	Ile	Ser	Tyr	Thr	Ser	Asn	Thr
Phe	Pro												
			20					25					30
acg	gat	tat	gtg	ccg	aca	gtt	ttt	gac	aat	ttc	agt	gcg	aat
gtg	gtt		144										
Thr	Asp	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn

0070110

Val	Val												
		35				40					45		
ggt	aat	gga	agt	att	gtg	aat	ctg	ggt	ttg	tgg	gat	act	gct
gga	caa		192										
Val	Asn	Gly	Ser	Ile	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala
Gly	Gln												
	50					55					60		
gag	gat	tat	aac	aga	tta	aga	cct	ttg	agt	tac	cgt	ggt	gcc
gat	ggt		240										
Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala
Asp	Val												
65					70					75			
80													
ttc	ata	ttg	gct	ttc	tct	ctc	ata	agc	aaa	gcc	agt	tat	gaa
aat	gtc		288										
Phe	Ile	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Lys	Ala	Ser	Tyr	Glu
Asn	Val												
			85						90				
95													
tcc	aaa	aag	tgg	att	cca	gag	ttg	aag	cat	tat	gca	cct	ggt
gtc	ccc		336										
Ser	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Lys	His	Tyr	Ala	Pro	Gly
Val	Pro												
			100					105				110	
ata	att	ctg	ggt	gga	aca	aag	ctt	gat	ctt	cgg	gat	gat	aag
cag	ttc		384										
Ile	Ile	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys
Gln	Phe												
		115					120				125		
tgc	ata	gac	cat	cct	ggt	gcc	ggt	ccc	att	acc	aca	gct	cag
gga	gaa		432										
Cys	Ile	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Thr	Thr	Ala	Gln
Gly	Glu												
	130					135					140		
gag	ctg	agg	aag	ctg	att	aat	gca	cca	gct	tac	att	gaa	tgc
agt	tca		480										
Glu	Leu	Arg	Lys	Leu	Ile	Asn	Ala	Pro	Ala	Tyr	Ile	Glu	Cys
Ser	Ser												
145					150					155			
160													
aaa	tca	cag	gag	aac	gtg	aag	gcg	gtg	ttt	gat	gca	gcc	ata
aga	ggt		528										
Lys	Ser	Gln	Glu	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile
Arg	Val												
			165						170				
175													
gtc	ctt	caa	cca	cca	aag	cag	aag	aaa	aag	aag	aat	aaa	gca

0070110

caa aag 576
 Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Asn Lys Ala
 Gln Lys
 180 185 190

gcc tgt tca ata ttg taa
 594
 Ala Cys Ser Ile Leu
 195

<210> 449
 <211> 197
 <212> PRT
 <213> Medicago truncatula

<400> 449
 Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala
 1 5 10
 15

Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
 Phe Pro
 20 25 30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
 Val Val
 35 40 45

Val Asn Gly Ser Ile Val Asn Leu Gly Leu Trp Asp Thr Ala
 Gly Gln
 50 55 60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
 Asp Val
 65 70 75

80
 Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
 Asn Val
 85 90

95
 Ser Lys Lys Trp Ile Pro Glu Leu Lys His Tyr Ala Pro Gly
 Val Pro
 100 105 110

Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
 Gln Phe
 115 120 125

0070110

Cys	Ile	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Thr	Thr	Ala	Gln
Gly	Glu												
	130					135						140	

Glu	Leu	Arg	Lys	Leu	Ile	Asn	Ala	Pro	Ala	Tyr	Ile	Glu	Cys
Ser	Ser												
145					150					155			

	160												
Lys	Ser	Gln	Glu	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile
Arg	Val												
				165					170				

175													
Val	Leu	Gln	Pro	Pro	Lys	Gln	Lys	Lys	Lys	Lys	Asn	Lys	Ala
Gln	Lys												
			180					185					190

Ala	Cys	Ser	Ile	Leu
		195		

<210> 450
<211> 594

<212> DNA
<213> Medicago truncatula

<220>
<221> CDS
<222> (1)..(594)

<400> 450													
atg	agc	gct	tct	agg	ttc	atc	aag	tgt	gtt	act	gtt	ggg	gat
gga	gct			48									
Met	Ser	Ala	Ser	Arg	Phe	Ile	Lys	Cys	Val	Thr	Val	Gly	Asp
Gly	Ala												
1				5					10				
15													
gtt	ggt	aaa	act	tgt	ttg	tta	att	tca	tac	acc	agc	aat	acc
ttc	ccc			96									
Val	Gly	Lys	Thr	Cys	Leu	Leu	Ile	Ser	Tyr	Thr	Ser	Asn	Thr
Phe	Pro												
			20					25					30
act	gac	tat	gtg	cca	act	gtc	ttc	gac	aat	ttc	agt	gca	aat
gtg	ggt			144									
Thr	Asp	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn
Val	Val												
		35					40					45	
gtg	aat	gga	agc	act	gtg	aat	ctg	ggt	ttg	tgg	gac	act	gca
gga	caa			192									

0070110

Val	Asn	Gly	Ser	Thr	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala
Gly	Gln												
	50					55					60		
gag	gat	tat	aac	aga	tta	aga	cct	ttg	agt	tat	cgt	ggt	gcc
gat	ggt		240										
Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala
Asp	Val												
65					70					75			
80													
ttc	att	ctc	gct	ttc	tcc	ctc	ata	agc	aag	gcc	agt	tat	gaa
aat	ggt		288										
Phe	Ile	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Lys	Ala	Ser	Tyr	Glu
Asn	Val												
				85					90				
95													
tcc	aaa	aag	tgg	att	cca	gag	ttg	aag	cat	tat	gca	cct	ggt
ggt	ccc		336										
Ser	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Lys	His	Tyr	Ala	Pro	Gly
Val	Pro												
			100					105					110
att	att	ctg	ggt	ggc	aca	aag	ctt	gac	ctt	cgg	gat	gac	aag
cag	ttc		384										
Ile	Ile	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys
Gln	Phe												
		115					120				125		
ttc	gtc	gac	cat	cct	ggt	gct	ggt	cct	att	acc	act	gct	cag
gga	gaa		432										
Phe	Val	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Thr	Thr	Ala	Gln
Gly	Glu												
	130					135					140		
gag	ctt	agg	aag	ctg	atc	aat	gca	cct	gct	tat	atc	gaa	tgc
agt	tcg		480										
Glu	Leu	Arg	Lys	Leu	Ile	Asn	Ala	Pro	Ala	Tyr	Ile	Glu	Cys
Ser	Ser												
145					150					155			
160													
aaa	tca	cag	cag	aat	gtg	aaa	gca	gtc	ttt	gat	gca	gcc	ata
aga	ggt		528										
Lys	Ser	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile
Arg	Val												
			165						170				
175													
gtc	ctt	caa	cca	cca	aag	caa	aag	aaa	aag	aag	agt	aaa	gca
cca	aag		576										
Val	Leu	Gln	Pro	Pro	Lys	Gln	Lys	Lys	Lys	Lys	Ser	Lys	Ala
Pro	Lys												
			180					185					190

0070110

gct tgt tcg ata ttg tga
594
Ala Cys Ser Ile Leu
195

<210> 451
<211> 197
<212> PRT
<213> Medicago truncatula

<400> 451
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10
15
Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro 20 25 30
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val 35 40 45
Val Asn Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln 50 55 60
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val 65 70 75
80
Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val 85 90
95
Ser Lys Lys Trp Ile Pro Glu Leu Lys His Tyr Ala Pro Gly
Val Pro 100 105 110
Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe 115 120 125
Phe Val Asp His Pro Gly Ala Val Pro Ile Thr Thr Ala Gln
Gly Glu 130 135 140

0070110

Glu Leu Arg Lys Leu Ile Asn Ala Pro Ala Tyr Ile Glu Cys
 Ser Ser
 145 150 155
 160
 Lys Ser Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
 Arg Val
 165 170
 175
 Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Ser Lys Ala
 Pro Lys
 180 185 190
 Ala Cys Ser Ile Leu
 195

<210> 452
 <211> 594
 <212> DNA
 <213> Medicago truncatula

<220>
 <221> CDS
 <222> (1)..(594)

<400> 452
 atg agt ggt tcc agg ttc atc aag tgt gtc aca gtt ggt gat
 ggt gcc 48
 Met Ser Gly Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala
 1 5 10
 15
 gtt gga aag act tgt ttg ctt atc tcc tac acc agc aac act
 ttc cct 96
 Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
 Phe Pro
 20 25 30
 acg gac tat gtg ccg act gtc ttt gac aat ttc agt gca aat
 gta gtt 144
 Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
 Val Val
 35 40 45
 gtg gat ggg agc act ata aat ctc ggg ttg tgg gat act gct
 ggc caa 192
 Val Asp Gly Ser Thr Ile Asn Leu Gly Leu Trp Asp Thr Ala
 Gly Gln
 50 55 60
 gaa gat tac aat aga tta aga ccc tta agc tat cgt gga gca
 gat gtt 240

0070110

Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala
Asp	Val												
65					70					75			
80													
ttc	ctg	ctt	gct	ttt	tct	ctc	ata	agc	aag	gct	agc	tat	gaa
aat	att		288										
Phe	Leu	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Lys	Ala	Ser	Tyr	Glu
Asn	Ile												
				85					90				
95													
gcc	aaa	aaa	tgg	att	cct	gag	ttg	agg	cat	tat	gct	cct	ggt
ggt	cca		336										
Ala	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Arg	His	Tyr	Ala	Pro	Gly
Val	Pro												
			100					105					110
att	att	ctc	ggt	gga	aca	aaa	ctt	gat	ctt	cgg	gat	gat	agc
cag	ttc		384										
Ile	Ile	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Ser
Gln	Phe												
		115					120					125	
ttt	caa	gac	cat	cct	ggt	gcg	gcg	cca	atc	acc	aca	gca	cag
ggt	gag		432										
Phe	Gln	Asp	His	Pro	Gly	Ala	Ala	Pro	Ile	Thr	Thr	Ala	Gln
Gly	Glu												
		130				135				140			
gaa	ctg	aga	aaa	ctt	atc	ggt	gct	cca	ggt	tac	att	gaa	tgt
agt	tcc		480										
Glu	Leu	Arg	Lys	Leu	Ile	Gly	Ala	Pro	Val	Tyr	Ile	Glu	Cys
Ser	Ser												
145					150					155			
160													
aaa	aca	cag	aag	aat	gtg	aag	gct	ggt	ttt	gat	tcg	gcc	atc
aaa	gta		528										
Lys	Thr	Gln	Lys	Asn	Val	Lys	Ala	Val	Phe	Asp	Ser	Ala	Ile
Lys	Val												
				165					170				
175													
ggt	cta	cag	cca	cca	aag	caa	aag	aaa	aca	aag	aga	aag	ggg
caa	aaa		576										
Val	Leu	Gln	Pro	Pro	Lys	Gln	Lys	Lys	Thr	Lys	Arg	Lys	Gly
Gln	Lys												
			180					185					190
gcc	tgt	tcc	att	ttg	tga								
			594										
Ala	Cys	Ser	Ile	Leu									
		195											

0070110

<210> 453
<211> 197
<212> PRT
<213> Medicago truncatula

<400> 453
Met Ser Gly Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10
15
Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
20 25 30
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
35 40 45
Val Asp Gly Ser Thr Ile Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65 70 75
80
Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Ile
85 90
95
Ala Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Gly
Val Pro
100 105 110
Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Ser
Gln Phe
115 120 125
Phe Gln Asp His Pro Gly Ala Ala Pro Ile Thr Thr Ala Gln
Gly Glu
130 135 140
Glu Leu Arg Lys Leu Ile Gly Ala Pro Val Tyr Ile Glu Cys
Ser Ser
145 150 155
160
Lys Thr Gln Lys Asn Val Lys Ala Val Phe Asp Ser Ala Ile
Seite 690

0070110

Lys Val
 165 170
 175
 Val Leu Gln Pro Pro Lys Gln Lys Lys Thr Lys Arg Lys Gly
 Gln Lys
 180 185 190
 Ala Cys Ser Ile Leu
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<210> 454
 <211> 573
 <212> DNA
 <213> Anopheles gambiae

<220>
 <221> CDS
 <222> (1)..(573)

<400> 454
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 ggc acg 48
 Met Ser Ser Gly Arg Pro Ile Lys Cys Val Val Val Gly Asp
 Gly Thr
 1 5 10
 15
 gtg ggg aag acg tgc atg ttg atc agc tac acg acc gac agc
 ttt ccc 96
 Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Thr Asp Ser
 Phe Pro
 20 25 30
 ggc gaa tac gta ccc acg agc ttc gac aac tac tcc gcc ccg
 atg gtg 144
 Gly Glu Tyr Val Pro Thr Ser Phe Asp Asn Tyr Ser Ala Pro
 Met Val
 35 40 45
 gtg gac ggt gtg caa gtg tcg ctc ggg ctg tgg gat acg gcc
 ggg cag 192
 Val Asp Gly Val Gln Val Ser Leu Gly Leu Trp Asp Thr Ala
 Gly Gln
 50 55 60
 gaa gac tac gat cgg cta agg ccc ctg tcc tac cca cag acg
 gac gtg 240
 Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr
 Asp Val
 65 70 75
 80
 ttc ctc ata tgc tac agt gtg gcc agc ccg tcg tcg ttc gaa
 Seite 691

0070110

aac gtt 288
Phe Leu Ile Cys Tyr Ser Val Ala Ser Pro Ser Ser Phe Glu
Asn Val

85

90

95

acc tcc aaa tgg tat ccc gag atc aag cac cac tgc ccg gat
gcg ccc 336
Thr Ser Lys Trp Tyr Pro Glu Ile Lys His His Cys Pro Asp
Ala Pro

100

105

110

atc att tta gtc gga acc aaa atc gat ctg cgc gag gat cgg
gaa acg 384
Ile Ile Leu Val Gly Thr Lys Ile Asp Leu Arg Glu Asp Arg
Glu Thr

115

120

125

ata agc ttg ctg gcg gac cag ggc ctt tcc gcg ctg aag cgc
gaa cag 432
Ile Ser Leu Leu Ala Asp Gln Gly Leu Ser Ala Leu Lys Arg
Glu Gln

130

135

140

ggc caa aag cta gcg aac aag ata cgg gcg gta aag tat atg
gaa tgt 480
Gly Gln Lys Leu Ala Asn Lys Ile Arg Ala Val Lys Tyr Met
Glu Cys

145

150

155

160

tcg gca cta acc cag cgg ggc cta aag cag gtg ttt gac gaa
gcg ctt 528
Ser Ala Leu Thr Gln Arg Gly Leu Lys Gln Val Phe Asp Glu
Ala Leu

165

170

175

tgc gcc acg gaa gag aaa gag cga atg ccg gta gaa gag gag
tag 573
Cys Ala Thr Glu Glu Lys Glu Arg Met Pro Val Glu Glu Glu

180

185

190

<210> 455

<211> 190

<212> PRT

<213> Anopheles gambiae

<400> 455

Met Ser Ser Gly Arg Pro Ile Lys Cys Val Val Val Gly Asp
Gly Thr

0070110

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15														
Val	Gly	Lys	Thr	Cys	Met	Leu	Ile	Ser	Tyr	Thr	Thr	Asp	Ser	
Phe	Pro													
			20					25					30	
Gly	Glu	Tyr	Val	Pro	Thr	Ser	Phe	Asp	Asn	Tyr	Ser	Ala	Pro	
Met	Val													
		35					40					45		
Val	Asp	Gly	Val	Gln	Val	Ser	Leu	Gly	Leu	Trp	Asp	Thr	Ala	
Gly	Gln													
	50					55					60			
Glu	Asp	Tyr	Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Pro	Gln	Thr	
Asp	Val													
65					70					75				
	80													
Phe	Leu	Ile	Cys	Tyr	Ser	Val	Ala	Ser	Pro	Ser	Ser	Phe	Glu	
Asn	Val													
				85					90					
95														
Thr	Ser	Lys	Trp	Tyr	Pro	Glu	Ile	Lys	His	His	Cys	Pro	Asp	
Ala	Pro													
		100						105					110	
Ile	Ile	Leu	Val	Gly	Thr	Lys	Ile	Asp	Leu	Arg	Glu	Asp	Arg	
Glu	Thr													
		115					120					125		
Ile	Ser	Leu	Leu	Ala	Asp	Gln	Gly	Leu	Ser	Ala	Leu	Lys	Arg	
Glu	Gln													
	130					135					140			
Gly	Gln	Lys	Leu	Ala	Asn	Lys	Ile	Arg	Ala	Val	Lys	Tyr	Met	
Glu	Cys													
145					150					155				
	160													
Ser	Ala	Leu	Thr	Gln	Arg	Gly	Leu	Lys	Gln	Val	Phe	Asp	Glu	
Ala	Leu													
				165					170					
175														
Cys	Ala	Thr	Glu	Glu	Lys	Glu	Arg	Met	Pro	Val	Glu	Glu	Glu	
			180					185					190	

<210> 456
 <211> 579
 <212> DNA

0070110

<213> Saccharomyces cerevisiae

<220>

<221> CDS

<222> (1)..(579)

<400> 456

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gat ggt 48

Met Ser Glu Lys Ala Val Arg Arg Lys Leu Val Ile Ile Gly

Asp Gly

1 5 10

15

gct tgt ggc aag acc tct tta cta tat gta ttt aca tta gga

aaa ttc 96

Ala Cys Gly Lys Thr Ser Leu Leu Tyr Val Phe Thr Leu Gly

Lys Phe

20 25 30

cct gaa caa tat cat ccg aca gtg ttc gag aat tat gtc act

gat tgc 144

Pro Glu Gln Tyr His Pro Thr Val Phe Glu Asn Tyr Val Thr

Asp Cys

35 40 45

aga gtt gac gga ata aaa gtg tcc tta acg ctc tgg gat aca

gcg gga 192

Arg Val Asp Gly Ile Lys Val Ser Leu Thr Leu Trp Asp Thr

Ala Gly

50 55 60

caa gag gaa tat gaa cgt tta cgt cca ttc tca tat tca aaa

gca gat 240

Gln Glu Glu Tyr Glu Arg Leu Arg Pro Phe Ser Tyr Ser Lys

Ala Asp

65 70 75

80

ata ata tta att ggg ttt gct gta gac aat ttt gaa tca cta

att aac 288

Ile Ile Leu Ile Gly Phe Ala Val Asp Asn Phe Glu Ser Leu

Ile Asn

85 90

95

gca agg acg aaa tgg gcg gat gag gca tta cga tat tgt cct

gac gca 336

Ala Arg Thr Lys Trp Ala Asp Glu Ala Leu Arg Tyr Cys Pro

Asp Ala

100 105 110

cca atc gtt ctt gta ggc ttg aaa aaa gat ttg agg caa gaa

0070110

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gcc cat      384
Pro Ile Val Leu Val Gly Leu Lys Lys Asp Leu Arg Gln Glu
Ala His
      115      120      125
ttt aaa gag aat gct acc gat gaa atg gtt ccc att gaa gat
gca aaa      432
Phe Lys Glu Asn Ala Thr Asp Glu Met Val Pro Ile Glu Asp
Ala Lys
      130      135      140
caa gtt gca agg gcc gtt ggg gcc aag aaa tac atg gaa tgt
agt gca      480
Gln Val Ala Arg Ala Val Gly Ala Lys Lys Tyr Met Glu Cys
Ser Ala
145      150      155
      160
ctg act ggt gag ggt gtg gat gat gtc ttt gaa gta gct aca
aga acc      528
Leu Thr Gly Glu Gly Val Asp Asp Val Phe Glu Val Ala Thr
Arg Thr
      165      170
175
agt ttg ctt atg aag aag gaa cca ggg gct aac tgt tgc ata
att tta      576
Ser Leu Leu Met Lys Lys Glu Pro Gly Ala Asn Cys Cys Ile
Ile Leu
      180      185      190

taa
      579

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<210> 457
 <211> 192
 <212> PRT
 <213> Saccharomyces cerevisiae

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<400> 457
Met Ser Glu Lys Ala Val Arg Arg Lys Leu Val Ile Ile Gly
Asp Gly
1      5      10
15
Ala Cys Gly Lys Thr Ser Leu Leu Tyr Val Phe Thr Leu Gly
Lys Phe
      20      25      30

Pro Glu Gln Tyr His Pro Thr Val Phe Glu Asn Tyr Val Thr
Asp Cys

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0070110
40

35

45

Arg Val Asp Gly Ile Lys Val Ser Leu Thr Leu Trp Asp Thr
Ala Gly
50 55 60

Gln Glu Glu Tyr Glu Arg Leu Arg Pro Phe Ser Tyr Ser Lys
Ala Asp
65 70 75

80
Ile Ile Leu Ile Gly Phe Ala Val Asp Asn Phe Glu Ser Leu
Ile Asn
85 90

95
Ala Arg Thr Lys Trp Ala Asp Glu Ala Leu Arg Tyr Cys Pro
Asp Ala
100 105 110

Pro Ile Val Leu Val Gly Leu Lys Lys Asp Leu Arg Gln Glu
Ala His
115 120 125

Phe Lys Glu Asn Ala Thr Asp Glu Met Val Pro Ile Glu Asp
Ala Lys
130 135 140

Gln Val Ala Arg Ala Val Gly Ala Lys Lys Tyr Met Glu Cys
Ser Ala
145 150 155

160
Leu Thr Gly Glu Gly Val Asp Asp Val Phe Glu Val Ala Thr
Arg Thr
165 170

175
Ser Leu Leu Met Lys Lys Glu Pro Gly Ala Asn Cys Cys Ile
Ile Leu
180 185 190

<210> 458

<211> 588

<212> DNA

<213> Mucor rouxii

<220>

<221> CDS

<222> (1)..(588)

0070110

<400> 458

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gct tgt      48
Met Ala Glu Ile Arg Arg Lys Leu Val Ile Val Gly Asp Gly
Ala Cys
  1              5              10
15
ggg aaa acc tgt ttg ttg att gtc ttt tca aag ggt act ttt
cct gag      96
Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Gly Thr Phe
Pro Glu
      20              25              30
ttc tat gtt ccc acc gtt ttt gaa aat tac gta gct gat gtc
gaa gtc      144
Phe Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Val
Glu Val
      35              40              45
gat gga aaa cac gtg gaa tta gct tta tgg gat aca gca ggc
caa gaa      192
Asp Gly Lys His Val Glu Leu Ala Leu Trp Asp Thr Ala Gly
Gln Glu
      50              55              60
gat tat gat cgt ctc cgt ccc ttg tct tac cct gat tct cat
gtt atc      240
Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Ser His
Val Ile
      65              70              75
80
ttg att tgt ttt gct gtt gat tca ccc gat tca ttg gaa aac
gtt caa      288
Leu Ile Cys Phe Ala Val Asp Ser Pro Asp Ser Leu Glu Asn
Val Gln
      85              90
95
gag aag tgg atc tct gaa gta ctc cac ttc tgt caa ggt tta
cct att      336
Glu Lys Trp Ile Ser Glu Val Leu His Phe Cys Gln Gly Leu
Pro Ile
      100              105              110
gtt tta gtt ggt tgt aag aaa gat tta aga aat gat cct gga
aca att      384
Val Leu Val Gly Cys Lys Lys Asp Leu Arg Asn Asp Pro Gly
Thr Ile
      115              120              125
gaa gaa ctt aga aga aac tct caa aaa cct gtc agt tca gaa
gag ggt      432

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0070110

Glu	Glu	Leu	Arg	Arg	Asn	Ser	Gln	Lys	Pro	Val	Ser	Ser	Glu
Glu	Gly												
	130					135				140			
gct	tct	att	gct	caa	aga	att	agt	gct	tac	aag	tac	ctt	gaa
tgt	tct			480									
Ala	Ser	Ile	Ala	Gln	Arg	Ile	Ser	Ala	Tyr	Lys	Tyr	Leu	Glu
Cys	Ser												
145					150					155			
160													
gcc	aag	act	ggt	gaa	ggt	gta	cgt	gaa	gta	ttt	gaa	cac	gca
aca	aga			528									
Ala	Lys	Thr	Gly	Glu	Gly	Val	Arg	Glu	Val	Phe	Glu	His	Ala
Thr	Arg												
				165					170				
175													
gct	gca	tta	atg	gtt	tct	aag	aag	aaa	aag	tca	aag	agt	ggt
gtc	tg			576									
Ala	Ala	Leu	Met	Val	Ser	Lys	Lys	Lys	Lys	Ser	Lys	Ser	Gly
Val	Cys												
			180				185					190	

aac ctt ttg taa
 588
 Asn Leu Leu
 195

<210> 459
 <211> 195
 <212> PRT
 <213> Mucor rouxii

<400>	459												
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Ala	Cys												
1				5				10					
15													
Gly	Lys	Thr	Cys	Leu	Leu	Ile	Val	Phe	Ser	Lys	Gly	Thr	Phe
Pro	Glu												
			20				25					30	
Phe	Tyr	Val	Pro	Thr	Val	Phe	Glu	Asn	Tyr	Val	Ala	Asp	Val
Glu	Val												
		35				40					45		
Asp	Gly	Lys	His	Val	Glu	Leu	Ala	Leu	Trp	Asp	Thr	Ala	Gly
Gln	Glu												
	50					55					60		

0070110

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

<210> 460
 <211> 756
 <212> DNA
 <213> Neurospora crassa

<220>
 <221> CDS
 <222> (1)..(756)

<400> 460
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 ggc gat 48
 Met Thr Glu Gly Pro Ala Tyr Ser Lys Lys Val Val Val Val
 Seite 699

0070110

Gly	Asp												
1				5					10				
15													
ggc	ggt	tgc	gga	aag	aca	tgt	ctc	ctg	atc	agt	tat	agt	cag
gga	tac		96										
Gly	Gly	cys	Gly	Lys	Thr	Cys	Leu	Leu	Ile	Ser	Tyr	Ser	Gln
Gly	Tyr												
			20					25					30
ttc	cca	gag	aaa	tat	gtc	cca	acc	gtc	ttt	gag	aac	tac	atc
acc	tac		144										
Phe	Pro	Glu	Lys	Tyr	Val	Pro	Thr	Val	Phe	Glu	Asn	Tyr	Ile
Thr	Tyr												
		35					40					45	
cca	acg	cat	cca	ccg	acc	ggt	aag	acc	gtc	gag	ctc	gcc	ctg
tgg	gat		192										
Pro	Thr	His	Pro	Pro	Thr	Gly	Lys	Thr	Val	Glu	Leu	Ala	Leu
Trp	Asp												
	50					55				60			
acc	gcc	ggc	caa	gag	gaa	tac	gac	cgc	ttg	cga	ccg	ctt	tca
tac	cca		240										
Thr	Ala	Gly	Gln	Glu	Glu	Tyr	Asp	Arg	Leu	Arg	Pro	Leu	Ser
Tyr	Pro												
65					70					75			
80													
gaa	acc	gac	ctt	att	ttt	gtc	tgc	ttc	gcc	att	gac	tgc	ccc
aac	tcc		288										
Glu	Thr	Asp	Leu	Ile	Phe	Val	Cys	Phe	Ala	Ile	Asp	Cys	Pro
Asn	Ser												
			85						90				
95													
ctc	gag	aat	gtc	atg	gac	aag	tgg	tac	ccc	gaa	gtc	ctc	cac
ttc	tgt		336										
Leu	Glu	Asn	Val	Met	Asp	Lys	Trp	Tyr	Pro	Glu	Val	Leu	His
Phe	Cys												
			100						105				110
ccg	tat	aca	ccc	ctt	atc	ctc	gtc	ggc	ctc	aag	tcc	gac	ctc
cgc	aat		384										
Pro	Tyr	Thr	Pro	Leu	Ile	Leu	Val	Gly	Leu	Lys	Ser	Asp	Leu
Arg	Asn												
		115					120					125	
aag	aag	acg	tgc	atc	gac	atg	ctc	aag	aca	caa	ggt	ctc	acc
ccc	gtc		432										
Lys	Lys	Thr	Cys	Ile	Asp	Met	Leu	Lys	Thr	Gln	Gly	Leu	Thr
Pro	Val												
	130					135				140			
acc	acc	gaa	caa	gga	ctc	gcc	gtc	gct	aag	aag	atg	ggc	gct
cag	tac		480										

0070110

Thr	Thr	Glu	Gln	Gly	Leu	Ala	Val	Ala	Lys	Lys	Met	Gly	Ala
Gln	Tyr												
145					150					155			
160													
atg	gag	tgc	tca	tca	aag	gag	atg	aag	ggt	gta	gag	gag	att
ttt	gag			528									
Met	Glu	Cys	Ser	Ser	Lys	Glu	Met	Lys	Gly	Val	Glu	Glu	Ile
Phe	Glu												
				165					170				
175													
cag	gcc	atc	ctc	aca	gta	gtc	gcc	aac	gac	agg	aaa	aca	ctg
gaa	cag			576									
Gln	Ala	Ile	Leu	Thr	Val	Val	Ala	Asn	Asp	Arg	Lys	Thr	Leu
Glu	Gln												
			180					185					190
gaa	gcc	gcg	aac	ggc	atg	ctg	ggt	gtt	ggc	gcg	ggc	tcg	gga
agc	gga			624									
Glu	Ala	Ala	Asn	Gly	Met	Leu	Gly	Val	Gly	Ala	Gly	Ser	Gly
Ser	Gly												
		195					200					205	
aag	ggc	agc	gga	atc	tcg	ttc	agc	agt	ggt	gac	aag	gcc	ggt
tcc	ggg			672									
Lys	Gly	Ser	Gly	Ile	Ser	Phe	Ser	Ser	Gly	Asp	Lys	Ala	Gly
Ser	Gly												
		210				215					220		
ata	ggg	ccc	gtc	aag	gcg	gcc	ggt	gtg	ggt	ggc	acg	att	gtc
ccg	aaa			720									
Ile	Gly	Pro	Val	Lys	Ala	Ala	Gly	Val	Gly	Gly	Thr	Ile	Val
Pro	Lys												
225					230						235		
240													
acg	agg	aag	aag	aag	aga	aag	tgt	ggt	atg	atg	tga		
			756										
Thr	Arg	Lys	Lys	Lys	Arg	Lys	Cys	Gly	Met	Met			
				245					250				

<210> 461

<211> 251

<212> PRT

<213> Neurospora crassa

<400> 461

Met	Thr	Glu	Gly	Pro	Ala	Tyr	Ser	Lys	Lys	Val	Val	Val	Val
Gly	Asp												

1

5

10

15

Gly	Gly	Cys	Gly	Lys	Thr	Cys	Leu	Leu	Ile	Ser	Tyr	Ser	Gln
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

0070110

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

0070110

Ser	Gly													
210						215					220			
Ile	Gly	Pro	Val	Lys	Ala	Ala	Gly	Val	Gly	Gly	Thr	Ile	Val	
Pro	Lys													
225					230					235				
240														
Thr	Arg	Lys	Lys	Lys	Arg	Lys	Cys	Gly	Met	Met				
				245					250					

<210> 462
 <211> 594
 <212> DNA
 <213> Nicotiana tabacum

<220>
 <221> CDS
 <222> (1)..(594)

<400> 462														
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ggg	gcc		48											
Met	Ser	Ala	Ser	Arg	Phe	Ile	Lys	Cys	Val	Thr	Val	Gly	Asp	
Gly	Ala													
1			5						10					
15														
gtt	gga	aaa	acg	tgt	ctc	ttg	att	tct	tac	acc	agc	aac	acc	
ttt	cct		96											
Val	Gly	Lys	Thr	Cys	Leu	Leu	Ile	Ser	Tyr	Thr	Ser	Asn	Thr	
Phe	Pro													
			20					25					30	
acg	gat	tat	gtg	cct	act	gtg	ttc	gat	aat	ttc	agt	gca	aat	
gtg	gtc		144											
Thr	Asp	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn	
Val	Val													
		35					40					45		
gtc	aat	ggg	agt	act	gtc	aac	cta	ggg	ttg	tgg	gat	aca	gct	
gga	cag		192											
Val	Asn	Gly	Ser	Thr	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala	
Gly	Gln													
50						55					60			
gag	gat	tac	aat	agg	tta	aga	cct	ctg	agt	tac	cgt	gga	gct	
gat	gtt		240											
Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala	
Asp	Val													
65					70						75			
80														
ttc	atc	ttg	gca	ttc	tct	ctc	att	agt	aaa	gcc	agc	tat	gaa	

0070110

aat gtt 288
Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val

85

90

95

tcc aag aag tgg att cct gag ttg aag cat tat gct ccc ggt
ggt cca 336
Ser Lys Lys Trp Ile Pro Glu Leu Lys His Tyr Ala Pro Gly
Val Pro

100

105

110

ata gtg ctt gtt gga aca aaa ctt gat ctt cgg gat gat aag
cag ttc 384
Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe

115

120

125

ttc ata gac cat cct ggt gct gtg cca att act act gct cag
ggc gag 432
Phe Ile Asp His Pro Gly Ala Val Pro Ile Thr Thr Ala Gln
Gly Glu

130

135

140

gag ctg agg aaa acg att ggg gcc cct gct tac att gaa tgt
agt tca 480
Glu Leu Arg Lys Thr Ile Gly Ala Pro Ala Tyr Ile Glu Cys
Ser Ser

145

150

155

160

aaa aca caa cag aat gtg aaa gca gtc ttt gat gct gct att
aag gtc 528
Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Lys Val

165

170

175

gtg ctc cag cca ccc aag cag aaa aaa aag aag ggg aag gcc
caa aag 576
Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Gly Lys Ala
Gln Lys

180

185

190

gca tgt tcg att ttg tga
594
Ala Cys Ser Ile Leu
195

<210> 463

<211> 197

<212> PRT

<213> Nicotiana tabacum

0070110

<400> 463

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

0070110

180

185

190

Ala Cys Ser Ile Leu
195

<210> 464
<211> 579
<212> DNA
<213> Blumeria graminis

<220>
<221> CDS
<222> (1)..(579)

<400> 464
atg gct gaa att cgc aga aaa cta gtt atc gtt ggt gat gga
gct tgt 48
Met Ala Glu Ile Arg Arg Lys Leu Val Ile Val Gly Asp Gly
Ala Cys
1 5 10
15
gga aag act tgt tta ctg att gtc ttc tcc aag ggc aca ttt
cca gag 96
Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Gly Thr Phe
Pro Glu
20 25 30
gtc tat gtg cca act gtc ttc gaa aac tac gtc gca gat gtc
gag gtg 144
Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Val
Glu Val
35 40 45
gac gga aaa cac gtc gaa ctt gcg ctt tgg gat acg gct ggt
caa gag 192
Asp Gly Lys His Val Glu Leu Ala Leu Trp Asp Thr Ala Gly
Gln Glu
50 55 60
gat tat gac cgc ctg aga cca ctt tca tat cca gac tcc cat
gtc atc 240
Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Ser His
Val Ile
65 70 75
80
ctt att tgt ttt gcc gtt gat tcc ccg gat tct ctc gat aac
gtt cag 288
Leu Ile Cys Phe Ala Val Asp Ser Pro Asp Ser Leu Asp Asn
Val Gln
85 90
95

0070110

gag aag tgg atc tca gaa gta ttg cat ttc tgt tgt ggt ctc
ccc ata 336
Glu Lys Trp Ile Ser Glu Val Leu His Phe Cys Cys Gly Leu
Pro Ile
100 105 110

att ctt gtc ggc tgc aag aaa gac ttg cgt cat gaa caa aag
aca ctt 384
Ile Leu Val Gly Cys Lys Lys Asp Leu Arg His Glu Gln Lys
Thr Leu
115 120 125

gag gag ctt cac aaa acc agt caa aag cca gtg acc cca gaa
caa ggc 432
Glu Glu Leu His Lys Thr Ser Gln Lys Pro Val Thr Pro Glu
Gln Gly
130 135 140

gaa gaa gtc cga aag aaa ata gga gct tac aag tat ctt gag
tgt tcc 480
Glu Glu Val Arg Lys Lys Ile Gly Ala Tyr Lys Tyr Leu Glu
Cys Ser
145 150 155
160

gcc aaa acc aat gaa ggt gtc cgt gag gta ttc gaa cat gcc
acg cgc 528
Ala Lys Thr Asn Glu Gly Val Arg Glu Val Phe Glu His Ala
Thr Arg
165 170

175
gca gca ctc tta acc aag aaa aag aag gag aag aga tgc att
atc ttg 576
Ala Ala Leu Leu Thr Lys Lys Lys Lys Glu Lys Arg Cys Ile
Ile Leu
180 185 190

taa
579

<210> 465
<211> 192
<212> PRT
<213> Blumeria graminis

<400> 465
Met Ala Glu Ile Arg Arg Lys Leu Val Ile Val Gly Asp Gly
Ala Cys
1 5 10

0070110

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

<210> 466

<211> 579

0070110

<212> DNA

<213> *Penicillium marneffe*i

<220>

<221> CDS

<222> (1)..(579)

<400> 466

atg gtt gtg gct aca att aaa tgt gtc gtc gtt ggt gac ggt
gcg gtc 48
Met Val Val Ala Thr Ile Lys Cys Val Val Val Gly Asp Gly
Ala Val
1 5 10

15
gga aag act tgc tta ttg att tcg tat acg aca aat aaa ttt
cca tcg 96
Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe
Pro Ser

20 25 30
gaa tat gtt cct act gtt ttc gat aat tat gcc gtg act gtc
atg atc 144
Glu Tyr Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val
Met Ile

35 40 45
ggc gat gag cct tat acc ctc ggc ctc ttc gat acc gcc gga
caa gaa 192
Gly Asp Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly
Gln Glu

50 55 60
gat tac gac cgc ctg cgc cct ctc tcc tac cct caa acc gat
gtc ttc 240
Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp
Val Phe

65 70 75
80
ctt gtc tgc ttc tcc gtc act tcc cca gcc tca ttt gag aac
gtg cga 288
Leu Val Cys Phe Ser Val Thr Ser Pro Ala Ser Phe Glu Asn
Val Arg

85 90
95
gag aaa tgg ttt cca gaa gtc cat cat cac tgt ccc ggt gtt
ccc tgc 336
Glu Lys Trp Phe Pro Glu Val His His His Cys Pro Gly Val
Pro Cys

100 105 110
ctg att gtc ggc acc cag acc gat ttg cga gat gat cct gcg

0070110

```

gtg cgc          384
Leu Ile Val Gly Thr Gln Thr Asp Leu Arg Asp Asp Pro Ala
Val Arg
      115          120          125
gag aag ctg gcg aaa cag aag atg cag ccc gtg cgt aag gag
gat ggt          432
Glu Lys Leu Ala Lys Gln Lys Met Gln Pro Val Arg Lys Glu
Asp Gly
      130          135          140
gat cgg atg gca aag gag ttg ggt gcc gtc aag tac gtg gaa
tgt tca          480
Asp Arg Met Ala Lys Glu Leu Gly Ala Val Lys Tyr Val Glu
Cys Ser
145          150          155
      160
gct ttg acg cag tat aag ctg aag gat gtt ttt gat gag gct
atc gtt          528
Ala Leu Thr Gln Tyr Lys Leu Lys Asp Val Phe Asp Glu Ala
Ile Val
      165          170
175
gct gct ctc gaa ccc gcc cca aag aag aga ccc aag tgc gtt
ggt cta          576
Ala Ala Leu Glu Pro Ala Pro Lys Lys Arg Pro Lys Cys Val
Val Leu
      180          185          190

taa
      579

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<210> 467
 <211> 192
 <212> PRT
 <213> Penicillium marneffeii

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<400> 467
Met Val Val Ala Thr Ile Lys Cys Val Val Val Gly Asp Gly
Ala Val
1          5          10
15
Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe
Pro Ser
      20          25          30

Glu Tyr Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val
Met Ile

```

0070110
40

35

45

Gly Asp Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly
Gln Glu
50 55 60

Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp
Val Phe
65 70 75
80

Leu Val Cys Phe Ser Val Thr Ser Pro Ala Ser Phe Glu Asn
Val Arg
85 90

95
Glu Lys Trp Phe Pro Glu Val His His His Cys Pro Gly Val
Pro Cys
100 105 110

Leu Ile Val Gly Thr Gln Thr Asp Leu Arg Asp Asp Pro Ala
Val Arg
115 120 125

Glu Lys Leu Ala Lys Gln Lys Met Gln Pro Val Arg Lys Glu
Asp Gly
130 135 140

Asp Arg Met Ala Lys Glu Leu Gly Ala Val Lys Tyr Val Glu
Cys Ser
145 150 155
160

Ala Leu Thr Gln Tyr Lys Leu Lys Asp Val Phe Asp Glu Ala
Ile Val
165 170

175
Ala Ala Leu Glu Pro Ala Pro Lys Lys Arg Pro Lys Cys Val
Val Leu
180 185 190

<210> 468
<211> 624
<212> DNA
<213> Trichoderma reesei

<220>
<221> CDS
<222> (1)..(624)

0070110

<400> 468

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atg cct ctc tgc ggc ggc tcc aag acg gtg cag cgc aag ctg
ggt ctt      48
Met Pro Leu Cys Gly Gly Ser Lys Thr Val Gln Arg Lys Leu
Val Leu
1      5      10
15
ctg ggc gat ggt gcc agc gga aag acg tcg ctg ctc aac gtc
ttc aca      96
Leu Gly Asp Gly Ala Ser Gly Lys Thr Ser Leu Leu Asn Val
Phe Thr
20      25      30
aga ggt tac ttt ccc acc gtc tac gaa cct acc gtc ttt gaa
aat tac      144
Arg Gly Tyr Phe Pro Thr Val Tyr Glu Pro Thr Val Phe Glu
Asn Tyr
35      40      45
gtc cac gac atc ttt gtc gac aac gtc cac atc gag ctc tcc
ctc tgg      192
Val His Asp Ile Phe Val Asp Asn Val His Ile Glu Leu Ser
Leu Trp
50      55      60
gat acg gcg gga cag gag gaa ttc gat cgg ctg cga tcg ctc
tcc tac      240
Asp Thr Ala Gly Gln Glu Glu Phe Asp Arg Leu Arg Ser Leu
Ser Tyr
65      70      75
80
gat gac acc gat ttg atc gtg ctc tgt tac tcg gtc gat agc
aaa gac      288
Asp Asp Thr Asp Leu Ile Val Leu Cys Tyr Ser Val Asp Ser
Lys Asp
85      90
95
tcg cta gaa aac gtc gaa tcc aaa tgg gtc gga gag att gcc
gac aac      336
Ser Leu Glu Asn Val Glu Ser Lys Trp Val Gly Glu Ile Ala
Asp Asn
100      105      110
115      120      125
tgc ccc ggc gtc aag ctg gtc ctc gtc gcc ctc aag tgc gac
ctg cgc      384
Cys Pro Gly Val Lys Leu Val Leu Val Ala Leu Lys Cys Asp
Leu Arg
130      135      140
cag caa gag gac gac gag ccc gag gac cag gca gcg gcc gac
ggc aac      432
Gln Gln Glu Asp Asp Glu Pro Glu Asp Gln Ala Ala Ala Asp

```

[illegible]

<210> 469
<211> 207
<212> PRT
<213> Trichoderma reesei

```

<400> 469
Met  Pro  Leu  Cys  Gly  Gly  Ser  Lys  Thr  Val  Gln  Arg  Lys  Leu
Val  Leu
1          5          10
15
Leu  Gly  Asp  Gly  Ala  Ser  Gly  Lys  Thr  Ser  Leu  Leu  Asn  Val
Phe  Thr
20          25          30
Arg  Gly  Tyr  Phe  Pro  Thr  Val  Tyr  Glu  Pro  Thr  Val  Phe  Glu
Asn  Tyr
35          40          45

```

0070110

Val His Asp Ile Phe Val Asp Asn Val His Ile Glu Leu Ser
Leu Trp
50 55 60

Asp Thr Ala Gly Gln Glu Glu Phe Asp Arg Leu Arg Ser Leu
Ser Tyr
65 70 75

80
Asp Asp Thr Asp Leu Ile Val Leu Cys Tyr Ser Val Asp Ser
Lys Asp
85 90

95
Ser Leu Glu Asn Val Glu Ser Lys Trp Val Gly Glu Ile Ala
Asp Asn
100 105 110

Cys Pro Gly Val Lys Leu Val Leu Val Ala Leu Lys Cys Asp
Leu Arg
115 120 125

Gln Gln Glu Asp Asp Glu Pro Glu Asp Gln Ala Ala Ala Asp
Gly Asn
130 135 140

Ala Gln Arg Glu Lys Pro Pro Thr Ile Ser Tyr Asp Glu Gly
Leu Glu
145 150 155

160
Val Ala Lys Arg Ile Gly Ala Ser Arg Tyr Leu Glu Cys Ser
Ala Met
165 170

175
Lys Asn Arg Gly Val Asn Glu Ala Phe Thr Glu Ala Ala Arg
Val Ala
180 185 190

Leu Ser Val Lys Lys Glu Arg Glu Asp Asn Lys Cys Thr Ile
Met
195 200 205

<210> 470

<211> 615

<212> DNA

<213> Yarrowia lipolytica

<220>

<221> CDS

<222> (1)..(615)

<400> 470

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atg ccc caa cca acg gat ctg cga aga aaa ctc gtc att gtc
ggc gac
Met Pro Gln Pro Thr Asp Leu Arg Arg Lys Leu Val Ile Val
Gly Asp
1 5 10
15
gga gcc tgc ggc aag acc tgt ctg ctg att gtc ttc gcg aag
ggc acc
Gly Ala Cys Gly Lys Thr Cys Leu Leu Ile Val Phe Ala Lys
Gly Thr
20 25 30
ttc ccg gag gtg tac gtg ccc acc gtg ttt gag aac tac gtg
gcc gac
Phe Pro Glu Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val
Ala Asp
35 40 45
gtg gag att gac ggc cga cga gtg gag ctg gcc ctg tgg gat
acc gcc
Val Glu Ile Asp Gly Arg Arg Val Glu Leu Ala Leu Trp Asp
Thr Ala
50 55 60
ggc cag gag gat tac gac cga ctg cga ccc ctg tcc tac ccc
gac gcc
Gly Gln Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro
Asp Ala
65 70 75
80
aac gtc atc atc atc tgc ttc gcc atc gac agc ccc gac tcg
ctc gac
Asn Val Ile Ile Ile Cys Phe Ala Ile Asp Ser Pro Asp Ser
Leu Asp
85 90
95
aac gtg cag gag aag tgg atc tcc gag gtg ctg cac ttt tgc
cag ggc
Asn Val Gln Glu Lys Trp Ile Ser Glu Val Leu His Phe Cys
Gln Gly
100 105 110
gtg cct att ctg ctg gtc ggt tgc aag gtc gac ctg cga aac
gac ccc
Val Pro Ile Leu Leu Val Gly Cys Lys Val Asp Leu Arg Asn
Asp Pro
115 120 125
aag acc atc gag gag ctg aga aga acg tcc cag cga ccc gtc

```

0070110

```

acg acc      432
Lys Thr Ile Glu Glu Leu Arg Arg Thr Ser Gln Arg Pro Val
Thr Thr
130
gag gag gga aat gcc gtg gcc cag aag att ggc gcc ggc aag
tac ctg      480
Glu Glu Gly Asn Ala val Ala Gln Lys Ile Gly Ala Gly Lys
Tyr Leu
145      150      155
160
gag tgc tct gcc cga acc cac gac gga gtg aga gag gtc ttc
gag cat      528
Glu Cys Ser Ala Arg Thr His Asp Gly val Arg Glu val Phe
Glu His
165      170
175
gcc acc cga gct gcc ctg act gcc cac ggc cag aag ggc tcc
aag agc      576
Ala Thr Arg Ala Ala Leu Thr Ala His Gly Gln Lys Gly Ser
Lys Ser
180      185      190

tcc agc aga gag ggc aag aaa aag tgt ttg att ttg taa
Ser Ser Arg Glu Gly Lys Lys Lys Cys Leu Ile Leu
195      200

```

<210> 471
 <211> 204
 <212> PRT
 <213> Yarrowia lipolytica

```

<400> 471
Met Pro Gln Pro Thr Asp Leu Arg Arg Lys Leu Val Ile Val
Gly Asp
1      5      10
15
Gly Ala Cys Gly Lys Thr Cys Leu Leu Ile Val Phe Ala Lys
Gly Thr
20      25      30

Phe Pro Glu Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val
Ala Asp
35      40      45

val Glu Ile Asp Gly Arg Arg Val Glu Leu Ala Leu Trp Asp
Thr Ala
50      55      60

```


0070110

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

<210> 472
 <211> 639
 <212> DNA
 <213> Tradescantia virginiana

<220>
 <221> CDS
 <222> (1)..(639)

<400> 472
 atg tct tca agt gtt tca agg ttc atc aaa tgt gtt aca gtt
 ggg gat 48

0070110

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

0070110

gag tgt 480
Gly Glu Glu Leu Arg Lys Gln Ile Gly Ala Ala Tyr Tyr Val
Glu Cys
145 150 155

160
agt tca aaa act cag cag aat gtt aag gca gtg ttt gat gct
gcc att 528
Ser Ser Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala
Ala Ile
165 170
175

aag gta gtt atc cag cct ccg aag cat aaa gat aag aag aag
aaa agg 576
Lys Val Val Ile Gln Pro Pro Lys His Lys Asp Lys Lys Lys
Lys Arg
180 185 190

cca cga cat gga tgt tca ata ttg aat atc ttc tgc ggg aga
aag ctc 624
Pro Arg His Gly Cys Ser Ile Leu Asn Ile Phe Cys Gly Arg
Lys Leu
195 200 205

gtc tgt ttt aaa tga
639
Val Cys Phe Lys
210

<210> 473
<211> 212
<212> PRT
<213> Tradescantia virginiana

<400> 473
Met Ser Ser Ser Val Ser Arg Phe Ile Lys Cys Val Thr Val
Gly Asp
1 5 10
15
Gly Ala Val Gly Glu Thr Cys Met Leu Ile Cys Tyr Thr Ser
Asn Lys
20 25 30

Phe Pro Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser
Ala Asn
35 40 45

Val Ile Val Glu Asn Thr Thr Val Asn Leu Gly Leu Trp Asp
Thr Ala

0070110
55

50

60

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

Val Cys Phe Lys
210

<210> 474
<211> 585
<212> DNA
<213> Suillus bovinus

<220>

0070110

<221> CDS

<222> (1)..(585)

<400> 474

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atg cac aac atc aaa tgt gtt gta gtc ggc gat ggt gct gtt
ggc aag                               48
Met His Asn Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys                               10
1
15
acg tgt ctt ctc atc tct tat acc aca aat gcc ttt cca gga
gaa tac                               96
Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Ala Phe Pro Gly
Glu Tyr
20
25
30
gtg cca aca gta ttc gac aac tac tct gca aat gtg atg gtc
gac ggg                               144
Val Pro Thr Val Phe Asp Asn Tyr Ser Ala Asn Val Met Val
Asp Gly
35
40
45
aaa act atc tct ctc ggt cta tgg gat acc gct gga caa gaa
gat tac                               192
Lys Thr Ile Ser Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu
Asp Tyr
50
55
60
gat cgt ctc cgg cca ctc tcc tac cct caa aca gat gtc ttt
ttg atc                               240
Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
Leu Ile
65
70
75
80
tgt ttc tcg ctc gtc agt cca cct agc tac gag aac gtt aga
acc aag                               288
Cys Phe Ser Leu Val Ser Pro Pro Ser Tyr Glu Asn Val Arg
Thr Lys
85
90
95
tgg tgg cct gag att tca cat cat gcg cca tct act tcg gtg
gtc ttg                               336
Trp Trp Pro Glu Ile Ser His His Ala Pro Ser Thr Ser Val
Val Leu
100
105
110
gtt ggc act aaa ctg gat ttg cgt gaa gat cct gct acc atc
gag aaa                               384
Val Gly Thr Lys Leu Asp Leu Arg Glu Asp Pro Ala Thr Ile
Glu Lys
115
120
125

```

0070110

```

ctc cgt gac cgg cgt atg cag cct atc cag tac acg caa ggg
gtc tcg      432
Leu Arg Asp Arg Arg Met Gln Pro Ile Gln Tyr Thr Gln Gly
Val Ser
      130      135      140
atg gcg agg gat att ggc gcc gtc aag tat ctt gaa tgt tct
gcg cta      480
Met Ala Arg Asp Ile Gly Ala Val Lys Tyr Leu Glu Cys Ser
Ala Leu
145      150      155
      160
tcg caa aag ggc cta aag acc gtg ttt gat gag gtt atc cgt
gct gtt      528
Ser Gln Lys Gly Leu Lys Thr Val Phe Asp Glu Val Ile Arg
Ala Val
      165      170
175
ttg aac cct ccc ccg aag gaa aag aag cgc agt ggt cgt ggt
tgt gtt      576
Leu Asn Pro Pro Pro Lys Glu Lys Lys Arg Ser Gly Arg Gly
Cys Val
      180      185      190

atc gta tga
ile val      585

```

<210> 475
 <211> 194
 <212> PRT
 <213> Suillus bovinus

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<400> 475
Met His Asn Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
Gly Lys
1      5      10
15
Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Ala Phe Pro Gly
Glu Tyr
      20      25      30

Val Pro Thr Val Phe Asp Asn Tyr Ser Ala Asn Val Met Val
Asp Gly
      35      40      45

Lys Thr Ile Ser Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu
Asp Tyr

```

0070110
55

50

60

```

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

```

<210> 476
 <211> 576
 <212> DNA
 <213> Yarrowia lipolytica

<220>
 <221> CDS
 <222> (1)..(576)

<400> 476
 atg cag acc ata aaa tgt gtt gtt gtc ggc gat ggt gcc gtc
 Seite 723

0070110

gga	aag		48											
Met	Gln	Thr	Ile	Lys	Cys	Val	Val	Val	Gly	Asp	Gly	Ala	Val	
Gly	Lys													
1				5					10					
15														
act	tgt	ctc	ctc	atc	tca	tac	aca	aca	aac	aag	ttc	ccc	tct	
gaa	tac		96											
Thr	Cys	Leu	Leu	Ile	Ser	Tyr	Thr	Thr	Asn	Lys	Phe	Pro	Ser	
Glu	Tyr													
			20					25					30	
gtt	ccc	acc	gtt	ttt	gac	aac	tat	gcc	gtg	act	gtc	atg	att	
gga	gac		144											
Val	Pro	Thr	Val	Phe	Asp	Asn	Tyr	Ala	Val	Thr	Val	Met	Ile	
Gly	Asp													
		35				40						45		
gag	ccc	tac	aca	ctc	gga	ctg	ttc	gac	acc	gcc	ggg	cag	gag	
gat	tac		192											
Glu	Pro	Tyr	Thr	Leu	Gly	Leu	Phe	Asp	Thr	Ala	Gly	Gln	Glu	
Asp	Tyr													
	50				55					60				
gac	cga	ctg	cga	cct	ctt	tgt	tac	cct	cag	acc	gat	gtt	ttc	
ctc	gtc		240											
Asp	Arg	Leu	Arg	Pro	Leu	Cys	Tyr	Pro	Gln	Thr	Asp	Val	Phe	
Leu	Val													
	65				70					75				
	80													
tgc	ttt	tcc	gtc	acc	tct	ccc	gcc	tcc	ttt	gag	aac	gtc	aag	
gag	aag		288											
Cys	Phe	Ser	Val	Thr	Ser	Pro	Ala	Ser	Phe	Glu	Asn	Val	Lys	
Glu	Lys													
			85							90				
95														
tgg	ttc	cct	gag	gtc	cac	cac	cac	tgc	ccc	ggc	gtg	cct	tgc	
ctc	att		336											
Trp	Phe	Pro	Glu	Val	His	His	His	Cys	Pro	Gly	Val	Pro	Cys	
Leu	Ile													
			100					105					110	
gtt	ggg	acc	cag	gtt	gat	ccg	cga	agt	gac	agg	atg	att	ctt	
gac	aag		384											
Val	Gly	Thr	Gln	Val	Asp	Pro	Arg	Ser	Asp	Arg	Met	Ile	Leu	
Asp	Lys													
		115				120						125		
ctt	tcc	cga	cac	aag	ctg	cga	ccc	atg	acc	act	gag	caa	ggc	
tac	cag		432											
Leu	Ser	Arg	His	Lys	Leu	Arg	Pro	Met	Thr	Thr	Glu	Gln	Gly	
Tyr	Gln													

0070110

130		135		140
ctc gcc cga gaa ctc ggt gcc gtc aag tac gtc gag tgt tct				
gcc ctt	480			
Leu Ala Arg Glu Leu Gly Ala Val Lys Tyr Val Glu Cys Ser				
Ala Leu				
145		150		155
160				
act cag aag ggt ctc aag gac gtt ttc gac gag gcc atc gtg				
gca gct	528			
Thr Gln Lys Gly Leu Lys Asp Val Phe Asp Glu Ala Ile Val				
Ala Ala				
	165		170	
175				
ctt gag cct cca gtg gtc aag aag aac aaa aag tgc att gtg				
ctc	573			
Leu Glu Pro Pro Val Val Lys Lys Asn Lys Lys Cys Ile Val				
Leu				
	180		185	190
tag				
	576			

<210> 477
 <211> 191
 <212> PRT
 <213> Yarrowia lipolytica

<400> 477
 Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
 Gly Lys

1		5		10
15				
Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe Pro Ser				
Glu Tyr				
	20		25	30
Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val Met Ile				
Gly Asp				
	35		40	45
Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu				
Asp Tyr				
50		55		60
Asp Arg Leu Arg Pro Leu Cys Tyr Pro Gln Thr Asp Val Phe				
Leu Val				

0070110

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

<210> 478
 <211> 594
 <212> DNA
 <213> Nicotiana tabacum

<220>
 <221> CDS
 <222> (1)..(594)

<400> 478
 atg agt gct tca agg ttt atc aag tgt gtt acg gtg ggt gat
 ggt gct 48
 Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala
 1 5 10
 15
 gtt ggc aaa act tgt ctt ttg att tca tac acc agc aat act

0070110

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

0070110

aaa acc caa cag aat gtg aaa gca gtc ttt gat gca gcc att
aag gtc
Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Lys Val

165

170

175

gtc ctc cag ccg cct aaa aca aag aaa aag aag ggg aaa tca
caa aag
Val Leu Gln Pro Pro Lys Thr Lys Lys Lys Lys Gly Lys Ser
Gln Lys

180

185

190

tcc tgc tcg ata ttg tga
Ser Cys Ser Ile Leu
195

<210> 479

<211> 197

<212> PRT

<213> Nicotiana tabacum

<400> 479

Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala

1

5

10

15

Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro

20

25

30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val

35

40

45

Val Asn Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln

50

55

60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val

65

70

75

80

Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val

85

90

95

Ser Lys Lys Trp Ile Pro Glu Leu Lys His Tyr Ala Pro Gly
Seite 728

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Val Pro
100 105 110
Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe
115 120 125
Phe Ile Asp His Pro Gly Ala Val Pro Ile Thr Thr Ala Gln
Gly Glu
130 135 140
Glu Leu Arg Lys Thr Ile Gly Ala Pro Ala Tyr Ile Glu Cys
Ser Ser
145 150 155
160
Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Lys Val
165 170
175
Val Leu Gln Pro Pro Lys Thr Lys Lys Lys Lys Gly Lys Ser
Gln Lys
180 185 190
Ser Cys Ser Ile Leu
195

<210> 480
<211> 594
<212> DNA
<213> Medicago sativa

<220>
<221> CDS
<222> (1)..(594)

<220>
<221> misc_feature
<222> (232)..(232)
<223> k i s g o r t

<220>
<221> misc_feature
<222> (328)..(328)
<223> n i s a , g , c o r t

<400> 480
atg agt gct tct agg ttt att aaa tgt gtt act gtt ggt gat
gga gct 48

0070110

Met	Ser	Ala	Ser	Arg	Phe	Ile	Lys	Cys	Val	Thr	Val	Gly	Asp
Gly	Ala												
1				5					10				
15													
ggt	gga	aaa	act	tgt	ttg	ttg	att	tct	tac	acc	agc	aat	act
ttc	ccc		96										
Val	Gly	Lys	Thr	Cys	Leu	Leu	Ile	Ser	Tyr	Thr	Ser	Asn	Thr
Phe	Pro												
		20						25				30	
acg	gat	tat	gtg	ccg	aca	ggt	ttt	gac	aat	ttc	agt	gcg	aat
gtg	ggt		144										
Thr	Asp	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn
Val	Val												
		35					40					45	
ggt	aat	gga	agt	att	gtg	aat	ctg	ggt	ttg	tgg	gat	act	gct
ggg	caa		192										
Val	Asn	Gly	Ser	Ile	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala
Gly	Gln												
		50				55					60		
gag	gat	tat	aac	aga	tta	aga	cct	ttg	agt	tac	cgt	ggt	kcc
gat	ggt		240										
Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Xaa
Asp	Val												
65					70					75			
80													
ttc	ata	ttg	gct	ttc	tct	ctc	ata	agc	aaa	gcc	agt	tat	gaa
aat	gtc		288										
Phe	Ile	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Lys	Ala	Ser	Tyr	Glu
Asn	Val												
				85						90			
95													
tcc	aaa	aag	tgg	att	cca	gag	ttg	aag	cat	tat	gca	cct	ngt
gtc	ccc		336										
Ser	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Lys	His	Tyr	Ala	Pro	Xaa
Val	Pro												
			100					105				110	
ata	att	ctg	ggt	gga	aca	aag	ctt	gac	ctt	cgg	gat	gat	aag
cag	ttc		384										
Ile	Ile	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys
Gln	Phe												
		115					120					125	
tgc	ata	gac	cat	cct	ggt	gcc	ggt	ccc	att	acc	aca	gct	cag
gga	gaa		432										
Cys	Ile	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Thr	Thr	Ala	Gln
Gly	Glu												
		130				135				140			
gag	ctg	agg	aag	ctg	att	aat	gca	cca	gct	tac	att	gaa	tgc

0070110

agt tca 480
Glu Leu Arg Lys Leu Ile Asn Ala Pro Ala Tyr Ile Glu Cys
Ser Ser
145 150 155

160
aaa tca cag gag aac gtg aag gcg gtg ttt gac gca gcc ata
aga gtt 528
Lys Ser Gln Glu Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Arg Val
165 170

175
gtc ctt caa cca cca aag cag aag aaa aag aag aat aaa gca
caa aag 576
Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Asn Lys Ala
Gln Lys
180 185 190

gcc tgt tca ata ttg taa
594
Ala Cys Ser Ile Leu
195

<210> 481
<211> 197
<212> PRT
<213> Medicago sativa

<220>
<221> misc_feature
<222> (78)..(78)
<223> The xaa at location 78 stands for Ala, or Ser.

<220>
<221> misc_feature
<222> (110)..(110)
<223> The xaa at location 110 stands for Arg, Cys, Gly,
or Ser.

<400> 481
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10
15
Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
20 25 30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Seite 731

0070110

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

<210> 482

<211> 597

<212> DNA

<213> Gossypium hirsutum

<220>

0070110

<221> CDS

<222> (1)..(597)

<400> 482

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atg agt gct tcc agg ttc ata aaa tgc gtc acg gtc ggt gac
ggt gcc          48
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
  1              5              10
15
gtc ggc aag act tgt ctg ctc att tcc tac act agc aat act
ttc cct          96
Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
      20              25              30
acc gat tat gtg cca act gtc ttt gac aac ttt agt gct aat
gtg gtt          144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
      35              40              45
gtg gat ggg aac act gtt aat ctg gga ttg tgg gat act gct
gga cag          192
Val Asp Gly Asn Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
      50              55              60
gaa gat tac aat aga tta aga cca ttg agc tat cgt gga gca
gat gtc          240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
      65              70              75
      80
ttc ttg ctg gca ttt tct ctc att agc aaa gct agc tat gaa
aat gtt          288
Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val
      85              90
95
gct aag aaa tgg att cca gaa ttg aga cat tat gca ccc ggt
ggt cca          336
Ala Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Gly
Val Pro
      100              105              110
att att ctt gtt ggg act aag ctt gat ctt cga gaa gat aag
cag ttc          384
Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Glu Asp Lys
Gln Phe
      115              120              125

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0070110

ttc ata gat cac cct ggt gcg gtg ccc att acc aca gca cag
 ggt gag 432
 Phe Ile Asp His Pro Gly Ala Val Pro Ile Thr Thr Ala Gln
 Gly Glu

130 135 140
 gaa ttg aga aag cta att gga gcg cat ttt tac att gag tgt
 agt tca 480
 Glu Leu Arg Lys Leu Ile Gly Ala His Phe Tyr Ile Glu Cys
 Ser Ser
 145 150 155

160
 aaa aca caa cag aat gtg aaa gcg gtc ttt gat gcg gcc atc
 aaa gta 528
 Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
 Lys Val

165 170
 175
 gtt ctc cag cct cca aag aag aag aag aaa aag aag aga aag
 gca caa 576
 Val Leu Gln Pro Pro Lys Lys Lys Lys Lys Lys Lys Arg Lys
 Ala Gln
 180 185 190

aaa gct tgc tca ata ttg tga
 597
 Lys Ala Cys Ser Ile Leu
 195

<210> 483
 <211> 198
 <212> PRT
 <213> Gossypium hirsutum

<400> 483
 Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala
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 15
 Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
 Phe Pro
 20 25 30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
 Val Val
 35 40 45

Val Asp Gly Asn Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
 Gly Gln

0070110
55

50

60

Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala
Asp	Val												
65					70					75			
	80												
Phe	Leu	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Lys	Ala	Ser	Tyr	Glu
Asn	Val												
				85					90				
95													
Ala	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Arg	His	Tyr	Ala	Pro	Gly
Val	Pro												
			100					105				110	
Ile	Ile	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Glu	Asp	Lys
Gln	Phe												
		115					120				125		
Phe	Ile	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Thr	Thr	Ala	Gln
Gly	Glu												
	130					135					140		
Glu	Leu	Arg	Lys	Leu	Ile	Gly	Ala	His	Phe	Tyr	Ile	Glu	Cys
Ser	Ser												
145					150					155			
	160												
Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile
Lys	Val												
				165					170				
175													
Val	Leu	Gln	Pro	Pro	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Arg	Lys
Ala	Gln												
			180					185				190	
Lys	Ala	Cys	Ser	Ile	Leu								
		195											

<210> 484

<211> 594

<212> DNA

<213> Cicer arietinum

<220>

<221> CDS

<222> (1)..(594)

<400> 484

atg agt ggg tcc agg ttc att aag tgt gtt acc gta ggt gac

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0070110

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

0070110

gaa ctg aga aag ctt att ggt gct cca gtt tac att gaa tgt
 agt tcc 480
 Glu Leu Arg Lys Leu Ile Gly Ala Pro Val Tyr Ile Glu Cys
 Ser Ser
 145 150 155

160
 aaa aca caa aag aat gtg aag gct gtt ttt gat gcg gcc atc
 aaa gta 528
 Lys Thr Gln Lys Asn Val Lys Ala Val Phe Asp Ala Ala Ile
 Lys Val
 165 170

175
 gtt cta cag ccg cca aag caa aag aaa act aag aga aag ggg
 caa aaa 576
 Val Leu Gln Pro Pro Lys Gln Lys Lys Thr Lys Arg Lys Gly
 Gln Lys
 180 185 190

gcc tgt tcc att ttg tga
 594
 Ala Cys Ser Ile Leu
 195

<210> 485
 <211> 197
 <212> PRT
 <213> Cicer arietinum

<400> 485
 Met Ser Gly Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala
 1 5 10
 15
 Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
 Phe Pro
 20 25 30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
 Val Val
 35 40 45

Val Asp Gly Ser Thr Ile Asn Leu Gly Leu Trp Asp Thr Ala
 Gly Gln
 50 55 60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
 Asp Val
 65 70 75

0070110

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      80
Phe Leu Leu Ala Phe Ser Leu Ile Ser Arg Ala Ser Tyr Glu
Asn Ile
      85
95
Ala Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Gly
Val Pro
      100
      105
      110
Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe
      115
      120
      125
Phe Gln Asp His Pro Gly Ala Val Pro Ile Thr Thr Ala Gln
Gly Glu
      130
      135
      140
Glu Leu Arg Lys Leu Ile Gly Ala Pro Val Tyr Ile Glu Cys
Ser Ser
      145
      150
      155
      160
Lys Thr Gln Lys Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Lys Val
      165
      170
      175
Val Leu Gln Pro Pro Lys Gln Lys Lys Thr Lys Arg Lys Gly
Gln Lys
      180
      185
      190
Ala Cys Ser Ile Leu
      195

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<210> 486
 <211> 573
 <212> DNA
 <213> Drosophila melanogaster

<220>
 <221> CDS
 <222> (1)..(573)

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acc atc
Met Thr Ala Asn Ile Thr Lys Ser Pro Arg Pro Leu Lys Ile
Thr Ile
      1
      5
      10
      15

```

0070110

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

0070110

160

aag cag aac ctg cag cag gtc ttc gag gag gcg gtt aga gcc
gtg gag 528
Lys Gln Asn Leu Gln Gln Val Phe Glu Glu Ala Val Arg Ala
Val Glu

165

170

175

agg aaa cca aag acg acg tcc aag caa tcg tgc aaa ata ctg
tga 573
Arg Lys Pro Lys Thr Thr Ser Lys Gln Ser Cys Lys Ile Leu

180

185

190

<210> 487

<211> 190

<212> PRT

<213> *Drosophila melanogaster*

<400> 487

Met Thr Ala Asn Ile Thr Lys Ser Pro Arg Pro Leu Lys Ile
Thr Ile

1 5 10

15

Val Gly Asp Gly Met Val Gly Lys Thr Cys Met Leu Ile Thr
Tyr Thr

20

25

30

Arg Asn Glu Phe Pro Glu Glu Tyr Ile Pro Thr Val Phe Asp
Asn His

35

40

45

Ala Cys Asn Ile Ala Val Asp Asp Arg Asp Tyr Asn Leu Thr
Leu Trp

50

55

60

Asp Thr Ala Gly Gln Glu Asp Tyr Glu Arg Leu Arg Pro Leu
Ser Tyr

65

70

75

80

Pro Ser Thr Asn Cys Phe Leu Leu Cys Tyr Ser Ile Ser Ser
Arg Thr

85

90

95

Ser Phe Glu Asn Val Lys Ser Lys Trp Trp Pro Glu Ile Arg
His Phe

100

105

110

0070110

Ser Ala His Val Pro Val Val Leu Val Gly Thr Lys Leu Asp
 Leu Arg
 115 120 125

Ile Pro Ser Ser Glu Lys Phe Val Thr Thr Gln Glu Gly Lys
 Lys Met
 130 135 140

Arg Lys Glu Ile His Ala Phe Asn Leu Val Glu Cys Ser Ala
 Lys Lys
 145 150 155

160
 Lys Gln Asn Leu Gln Gln Val Phe Glu Glu Ala Val Arg Ala
 Val Glu
 165 170

175
 Arg Lys Pro Lys Thr Thr Ser Lys Gln Ser Cys Lys Ile Leu
 180 185 190

<210> 488

<211> 582

<212> DNA

<213> Exophiala dermatitidis

<220>

<221> CDS

<222> (1)..(582)

<400> 488

atg gtt gtc gca acg atc aag tgt gtg gtt gtc ggt gac ggc
 gcg gtc 48
 Met Val Val Ala Thr Ile Lys Cys Val Val Val Gly Asp Gly
 Ala Val
 1 5 10

15
 ggc aag aca tgc ttg ctt atc tcg tac acc acc aac aag ttc
 cct tcg 96
 Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe
 Pro Ser

20 25 30
 gaa tat gtc ccg acc gtc ttt gac aat tac gcc gtc acg gtg
 atg atc 144
 Glu Tyr Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val
 Met Ile

35 40 45
 gga gat gag cca tac act ctt ggt cta ttt gat aca gca gga
 caa gag 192
 Gly Asp Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly

0070110

Gln	Glu													
	50					55					60			
gat	tac	gac	cgg	ctt	cga	cct	ttg	tca	tac	ccg	cag	acc	gat	
gtc	ttt		240											
Asp	Tyr	Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Pro	Gln	Thr	Asp	
Val	Phe													
65					70					75				
80														
ctc	gtc	tgt	ttc	tcc	gtc	act	tcg	cca	gca	tcg	ttt	gag	aac	
gtg	cga		288											
Leu	Val	Cys	Phe	Ser	Val	Thr	Ser	Pro	Ala	Ser	Phe	Glu	Asn	
Val	Arg													
				85						90				
95														
gag	aaa	tgg	ttt	ccc	gag	gtc	cac	cac	cac	tgt	ccc	ggt	gtg	
cca	tgt		336											
Glu	Lys	Trp	Phe	Pro	Glu	Val	His	His	His	Cys	Pro	Gly	Val	
Pro	Cys													
			100					105					110	
ctg	atc	gtc	gga	act	cag	acc	gat	cta	cgt	gac	gac	cca	caa	
gtc	cgt		384											
Leu	Ile	Val	Gly	Thr	Gln	Thr	Asp	Leu	Arg	Asp	Asp	Pro	Gln	
Val	Arg													
		115					120				125			
gag	aaa	ctc	gcc	aaa	cag	aag	atg	caa	ccc	ggt	cgt	aag	gag	
gat	ggt		432											
Glu	Lys	Leu	Ala	Lys	Gln	Lys	Met	Gln	Pro	Val	Arg	Lys	Glu	
Asp	Gly													
	130					135					140			
gaa	aga	atg	gcc	aag	gag	ttg	ggc	gcg	gtc	aaa	tac	gtc	gaa	
tgc	agt		480											
Glu	Arg	Met	Ala	Lys	Glu	Leu	Gly	Ala	Val	Lys	Tyr	Val	Glu	
Cys	Ser													
145					150					155				
160														
gct	ctc	acc	cag	tac	aaa	ctc	aag	gac	gtc	ttt	gat	gag	gca	
atc	gtt		528											
Ala	Leu	Thr	Gln	Tyr	Lys	Leu	Lys	Asp	Val	Phe	Asp	Glu	Ala	
Ile	Val													
				165						170				
175														
gct	gct	ctc	gag	cct	cca	cca	aag	aag	agt	agt	aag	aaa	tgc	
acg	att		576											
Ala	Ala	Leu	Glu	Pro	Pro	Pro	Lys	Lys	Ser	Ser	Lys	Lys	Cys	
Thr	Ile													
			180					185					190	

0070110

ctt tga

582

Leu

<210> 489

<211> 193

<212> PRT

<213> Exophiala dermatitidis

<400> 489

Met Val Val Ala Thr Ile Lys Cys Val Val Val Gly Asp Gly
Ala Val

1 5 10

15

Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe
Pro Ser

20 25 30

Glu Tyr Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val
Met Ile

35 40 45

Gly Asp Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly
Gln Glu

50 55 60

Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp
Val Phe

65 70 75

80

Leu Val Cys Phe Ser Val Thr Ser Pro Ala Ser Phe Glu Asn
Val Arg

85 90

95

Glu Lys Trp Phe Pro Glu Val His His His Cys Pro Gly Val
Pro Cys

100 105 110

Leu Ile Val Gly Thr Gln Thr Asp Leu Arg Asp Asp Pro Gln
Val Arg

115 120 125

Glu Lys Leu Ala Lys Gln Lys Met Gln Pro Val Arg Lys Glu
Asp Gly

130 135 140

Glu Arg Met Ala Lys Glu Leu Gly Ala Val Lys Tyr Val Glu

Seite 743

0070110

Cys Ser
145 150 155
160
Ala Leu Thr Gln Tyr Lys Leu Lys Asp Val Phe Asp Glu Ala
Ile Val
165 170
175
Ala Ala Leu Glu Pro Pro Pro Lys Lys Ser Ser Lys Lys Cys
Thr Ile
180 185 190

Leu

<210> 490
<211> 597
<212> DNA
<213> Nicotiana tabacum

<220>
<221> CDS
<222> (1)..(597)

<400> 490
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gga gct 48
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10
15
gtg ggt aaa act tgt ctt ctc att tcc tat acc agc aac aca
ttt ccc 96
Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
20 25 30
act gat tac gtc cca act gta ttc gac aat ttt agt gca aat
gtg gtt 144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
35 40 45
gtc gat ggg agc act gtc aat ctg ggg ctg tgg gat act gca
ggc cag 192
Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60
gag gat tac aat aga tta aga ccg ttg agc tac cgg ggg gca
gat gta 240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Seite 744

0070110

Asp Val													
65					70					75			
80													
ttt ata	ctg gca	ttt tct	ctc att	agc aaa	gcg agc	tat gaa							
aat gtc		288											
Phe Ile	Leu Ala	Phe Ser	Leu Ile	Ser Lys	Ala Ser	Tyr Glu							
Asn Val													
		85								90			
95													
tcc aaa	aag tgg	att cct	gaa ttg	agg cat	tat gct	cct gga							
ggt cca		336											
Ser Lys	Lys Trp	Ile Pro	Glu Leu	Arg His	Tyr Ala	Pro Gly							
Val Pro													
		100								105			110
att att	ctt gtt	gga aca	aag cta	gat ctc	cga gag	gat aag							
caa ttc		384											
Ile Ile	Leu Val	Gly Thr	Lys Leu	Asp Leu	Arg Glu	Asp Lys							
Gln Phe													
	115						120					125	
ttc ctg	gac cat	cca ggt	gct gtt	cca ctt	acc aca	gct cag							
ggt gaa		432											
Phe Leu	Asp His	Pro Gly	Ala Val	Pro Leu	Thr Thr	Ala Gln							
Gly Glu													
	130						135					140	
gag ctg	aga aag	tcg att	ggt gct	tcc gct	tac att	gaa tgt							
agt gca		480											
Glu Leu	Arg Lys	Ser Ile	Gly Ala	Ser Ala	Tyr Ile	Glu Cys							
Ser Ala													
145							150					155	
160													
aaa aca	caa cag	aat gtg	aag gct	gtt ttt	gat gct	gcc att							
aag gtg		528											
Lys Thr	Gln Gln	Asn Val	Lys Ala	Val Phe	Asp Ala	Ala Ile							
Lys Val													
		165								170			
175													
gtt cta	caa cca	ccc aaa	caa aag	aag aaa	aag aag	aga aag							
ggt caa		576											
Val Leu	Gln Pro	Pro Lys	Gln Lys	Lys Lys	Lys Lys	Arg Lys							
Gly Gln													
		180								185			190
aaa gcc	tgc tct	atc ttg	tga										
		597											
Lys Ala	Cys Ser	Ile Leu											
	195												

0070110

<210> 491
 <211> 198
 <212> PRT
 <213> Nicotiana tabacum

<400> 491
 Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala
 1 5 10
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 Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
 Phe Pro
 20 25 30
 Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
 Val Val
 35 40 45
 Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
 Gly Gln
 50 55 60
 Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
 Asp Val
 65 70 75
 80
 Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
 Asn Val
 85 90
 95
 Ser Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Gly
 Val Pro
 100 105 110
 Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Glu Asp Lys
 Gln Phe
 115 120 125
 Phe Leu Asp His Pro Gly Ala Val Pro Leu Thr Thr Ala Gln
 Gly Glu
 130 135 140
 Glu Leu Arg Lys Ser Ile Gly Ala Ser Ala Tyr Ile Glu Cys
 Ser Ala
 145 150 155
 160
 Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
 Lys Val

0070110

165

170

175

Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Lys Arg Lys
Gly Gln

180

185

190

Lys Ala Cys Ser Ile Leu
195

<210> 492

<211> 576

<212> DNA

<213> Aedes aegypti

<220>

<221> CDS

<222> (1)..(576)

<400> 492

atg caa acg ata aag tgc gtc gtg gtg ggc gac ggt gcc gtc

ggg aag 48

Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val

Gly Lys

1

5

10

15

acc tgc ctg ctc atc tcc tac acg acc aac aaa ttt ccc tcg

gag tac 96

Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe Pro Ser

Glu Tyr

20

25

30

gtg ccg acc gtc ttc gac aac tat gcc gtc acg gtc atg atc

ggc gga 144

Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val Met Ile

Gly Gly

35

40

45

gag cca tac acg ctg gga ctg ttc gat act gcc ggt cag gag

gat tac 192

Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu

Asp Tyr

50

55

60

gat cgg ttg agg cca ctg tcc tat ccg cag aca gac gtg ttc

ctg gtg 240

Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe

Leu Val

65

70

75

80

tgc ttc tcc gtc gtc agt ccc agt tcg ttt gag aac gtc aaa

gaa aag 288

0070110

Cys Phe Ser Val Val Ser Pro Ser Ser Phe Glu Asn Val Lys
Glu Lys

85

90

95

tgg gta ccg gag ata acg cac cac tgt cag aag acg ccg ttc
ctg ctc
Trp Val Pro Glu Ile Thr His His Cys Gln Lys Thr Pro Phe
Leu Leu

100

105

110

gtc ggg acg cag atc gat ctg cgc gac gag cag agc acg ctg
gag aag
Val Gly Thr Gln Ile Asp Leu Arg Asp Glu Gln Ser Thr Leu
Glu Lys

115

120

125

ctg gcc aag aac aaa cag aaa ccg atc acg ctg gag cag ggc
gag aag
Leu Ala Lys Asn Lys Gln Lys Pro Ile Thr Leu Glu Gln Gly
Glu Lys

130

135

140

ctg gcc aag gaa ctg aag gcg gtc aag tac gtc gag tgc tcg
gcg ctg
Leu Ala Lys Glu Leu Lys Ala Val Lys Tyr Val Glu Cys Ser
Ala Leu

145

150

155

160

acg cag aaa ggg ctc aag aac gtg ttc gac gag gcg atc ctg
gcc gcg
Thr Gln Lys Gly Leu Lys Asn Val Phe Asp Glu Ala Ile Leu
Ala Ala

165

170

175

ctg gaa ccc cca gag cca acc aaa aag cga aag tgc aag ttt
ctg
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Leu

180

185

190

taa

576

<210> 493

<211> 191

<212> PRT

<213> Aedes aegypti

0070110

<400> 493

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Gly Lys

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Glu Tyr

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Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val Met Ile
Gly Gly

35 40 45

Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu
Asp Tyr

50 55 60

Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
Leu Val

65 70 75

80

Cys Phe Ser Val Val Ser Pro Ser Ser Phe Glu Asn Val Lys
Glu Lys

85 90

95

Trp Val Pro Glu Ile Thr His His Cys Gln Lys Thr Pro Phe
Leu Leu

100 105 110

Val Gly Thr Gln Ile Asp Leu Arg Asp Glu Gln Ser Thr Leu
Glu Lys

115 120 125

Leu Ala Lys Asn Lys Gln Lys Pro Ile Thr Leu Glu Gln Gly
Glu Lys

130 135 140

Leu Ala Lys Glu Leu Lys Ala Val Lys Tyr Val Glu Cys Ser
Ala Leu

145 150 155

160

Thr Gln Lys Gly Leu Lys Asn Val Phe Asp Glu Ala Ile Leu
Ala Ala

165 170

175

Leu Glu Pro Pro Glu Pro Thr Lys Lys Arg Lys Cys Lys Phe
Leu

180 185 190

0070110

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<211> 620
<212> DNA
<213> *Anopheles gambiae*

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<221> CDS
<222> (45)..(620)

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aca ata 56 Met Gln

Thr Ile

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ctg ctc 104
Lys Cys val val val Gly Asp Gly Ala val Gly Lys Thr Cys
Leu Leu 5 10 15

20
att tcc tac acg acc aac aaa ttt cca tcc gag tac gta ccg
acc gtg 152
Ile Ser Tyr Thr Thr Asn Lys Phe Pro Ser Glu Tyr val Pro
Thr val 25 30

35
ttc gac aac tac gcc gtc acg gtc atg atc ggt ggc gaa ccc
tac acg 200
Phe Asp Asn Tyr Ala val Thr val Met Ile Gly Gly Glu Pro
Tyr Thr 40 45 50

ctc ggt ttg ttt gac aca gct ggc cag gaa gat tac gat cga
cta cga 248
Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu Asp Tyr Asp Arg
Leu Arg 55 60 65

cca ctg tcg tat cca cag acc gat gta ttt tta gtg tgc ttt
tcc gtc 296
Pro Leu Ser Tyr Pro Gln Thr Asp val Phe Leu val Cys Phe
Ser val 70 75 80

gtg agt ccc agt tcg ttc gaa aac gtt aaa gaa aag tgg gta
cca gaa 344
val Ser Pro Ser Ser Phe Glu Asn val Lys Glu Lys Trp val
Pro Glu

0070110

85					90					95				
100														
ata	acg	cac	cat	tgc	cag	aaa	acg	ccg	ttc	ctg	ctg	gtg	ggc	
acg	cag			392										
Ile	Thr	His	His	Cys	Gln	Lys	Thr	Pro	Phe	Leu	Leu	Val	Gly	
Thr	Gln													
					105					110				
115														
atc	gat	ctg	cgc	gac	gaa	aac	agc	aca	ctg	gag	aag	ctg	gct	
aag	aac		440											
Ile	Asp	Leu	Arg	Asp	Glu	Asn	Ser	Thr	Leu	Glu	Lys	Leu	Ala	
Lys	Asn													
					120				125				130	
aaa	caa	aaa	ccc	atc	acc	ctc	gag	cag	ggc	gag	aag	ctg	gcg	
aag	gaa		488											
Lys	Gln	Lys	Pro	Ile	Thr	Leu	Glu	Gln	Gly	Glu	Lys	Leu	Ala	
Lys	Glu													
		135				140						145		
ctg	aag	gag	gtg	aag	tat	gtc	gag	tgt	tcg	gag	ttg	acc	cag	
aaa	ggg		536											
Leu	Lys	Ala	Val	Lys	Tyr	Val	Glu	Cys	Ser	Ala	Leu	Thr	Gln	
Lys	Gly													
		150				155						160		
ctg	aag	aac	gtg	ttc	gac	gag	gca	atc	ctg	gag	gag	ctg	gaa	
ccc	cca		584											
Leu	Lys	Asn	Val	Phe	Asp	Glu	Ala	Ile	Leu	Ala	Ala	Leu	Glu	
Pro	Pro													
165					170					175				
180														
gag	ccg	acg	aaa	aag	agg	aag	tgc	cga	ttt	ttg	taa			
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<212> PRT

<213> Anopheles gambiae

<400> 495

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Thr	Cys	Leu	Leu	Ile	Ser	Tyr	Thr	Thr	Asn	Lys	Phe	Pro	Ser
Glu	Tyr												
					20				25				30

0070110

Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val Met Ile
Gly Gly 35 40 45

Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu
Asp Tyr 50 55 60

Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
Leu Val 65 70 75
80

Cys Phe Ser Val Val Ser Pro Ser Ser Phe Glu Asn Val Lys
Glu Lys 85 90

95
Trp Val Pro Glu Ile Thr His His Cys Gln Lys Thr Pro Phe
Leu Leu 100 105 110

Val Gly Thr Gln Ile Asp Leu Arg Asp Glu Asn Ser Thr Leu
Glu Lys 115 120 125

Leu Ala Lys Asn Lys Gln Lys Pro Ile Thr Leu Glu Gln Gly
Glu Lys 130 135 140

Leu Ala Lys Glu Leu Lys Ala Val Lys Tyr Val Glu Cys Ser
Ala Leu 145 150 155
160

Thr Gln Lys Gly Leu Lys Asn Val Phe Asp Glu Ala Ile Leu
Ala Ala 165 170

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Leu Glu Pro Pro Glu Pro Thr Lys Lys Arg Lys Cys Arg Phe
Leu 180 185 190

<210> 496

<211> 576

<212> DNA

<213> Drosophila melanogaster

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<221> CDS

<222> (1)..(576)

<400> 496

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Gly Lys                               10
1
15
aca tgc ctg ctc atc tcg tat aca acc aac aag ttc ccg tcg
gag tac                               96
Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe Pro Ser
Glu Tyr
20                               25                               30
gtg ccc acg gtg ttc gac aac tat gcg gtc act gtg atg atc
ggc ggt                               144
Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val Met Ile
Gly Gly
35                               40                               45
gag ccc tac aca ctg ggc ctg ttc gat acg gcc gga cag gag
gat tac                               192
Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu
Asp Tyr
50                               55                               60
gat cgg ctg cgt ccg ctc tcc tat ccg cag acg gat gtc ttc
ctt gtc                               240
Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
Leu Val
65                               70                               75
80
tgc ttt tcg gtg gtc agt ccc agt tcc ttc gag aac gtc aag
gag aag                               288
Cys Phe Ser Val Val Ser Pro Ser Ser Phe Glu Asn Val Lys
Glu Lys
85                               90
95
tgg gtg ccc gag att aca cac cat tgc caa aag acg ccg ttc
ctg ctg                               336
Trp Val Pro Glu Ile Thr His His Cys Gln Lys Thr Pro Phe
Leu Leu
100                               105                               110
gtg ggc aca cag att gat ttg cgc gac gag aac agc acg ctg
gag aag                               384
Val Gly Thr Gln Ile Asp Leu Arg Asp Glu Asn Ser Thr Leu
Glu Lys

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0070110

		115					120					125	
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gag	aag		432										
Leu	Ala	Lys	Asn	Lys	Gln	Lys	Pro	Ile	Thr	Met	Glu	Gln	Gly
Glu	Lys												
	130					135					140		
ctg	gcc	aag	gag	ctg	aag	gcc	gtc	aag	tac	gtg	gag	tgc	tcg
gcc	ttg		480										
Leu	Ala	Lys	Glu	Leu	Lys	Ala	Val	Lys	Tyr	Val	Glu	Cys	Ser
Ala	Leu												
145					150						155		
160													
aca	cag	aag	ggc	ctg	aaa	aat	gta	ttc	gac	gag	gcc	atc	ctg
gcc	gcc		528										
Thr	Gln	Lys	Gly	Leu	Lys	Asn	Val	Phe	Asp	Glu	Ala	Ile	Leu
Ala	Ala												
			165						170				
175													
ctc	gag	cca	cca	gag	ccc	aca	aag	aaa	agg	aag	tgc	aaa	ttc
tta			573										
Leu	Glu	Pro	Pro	Glu	Pro	Thr	Lys	Lys	Arg	Lys	Cys	Lys	Phe
Leu													
			180						185				190
taa													
			576										

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 <213> *Drosophila melanogaster*

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 Glu Tyr
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 Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val Met Ile
 Gly Gly
 35 40 45
 Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu
 Seite 754

Asp	Tyr												
	50												
						55					60		
Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Pro	Gln	Thr	Asp	Val	Phe
Leu	Val												
65					70					75			
	80												
Cys	Phe	Ser	Val	Val	Ser	Pro	Ser	Ser	Phe	Glu	Asn	Val	Lys
Glu	Lys												
				85					90				
95													
Trp	Val	Pro	Glu	Ile	Thr	His	His	Cys	Gln	Lys	Thr	Pro	Phe
Leu	Leu												
			100					105					110
Val	Gly	Thr	Gln	Ile	Asp	Leu	Arg	Asp	Glu	Asn	Ser	Thr	Leu
Glu	Lys												
		115					120					125	
Leu	Ala	Lys	Asn	Lys	Gln	Lys	Pro	Ile	Thr	Met	Glu	Gln	Gly
Glu	Lys												
	130					135					140		
Leu	Ala	Lys	Glu	Leu	Lys	Ala	Val	Lys	Tyr	Val	Glu	Cys	Ser
Ala	Leu												
145					150					155			
	160												
Thr	Gln	Lys	Gly	Leu	Lys	Asn	Val	Phe	Asp	Glu	Ala	Ile	Leu
Ala	Ala												
				165					170				
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Leu													
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<222> (1)..(579)

Seite 755

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

0070110

gct ttg 480
Leu Ala Arg Glu Leu Gly Ala Val Lys Tyr Val Glu Cys Ser
Ala Leu
145 150 155
160
acc caa aaa ggg tta aag aat gtt ttt gat gaa gct att gta
gcc gct 528
Thr Gln Lys Gly Leu Lys Asn Val Phe Asp Glu Ala Ile Val
Ala Ala
165 170
175
ctt gat cct cct gtt cct cac aag aaa aag tca aag tgt ttg
gta ctg 576
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Val Leu
180 185 190
taa
579

<210> 499
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<213> Schizosaccharomyces pombe

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Gly Lys
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Asp Tyr
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Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val Met Ile
Gly Asp
35 40 45
Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu
Asp Tyr
50 55 60
Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
Leu Val
65 70 75
80

0070110

Cys	Phe	Ser	Val	Thr	Ser	Pro	Ala	Ser	Phe	Glu	Asn	Val	Lys
Glu	Lys												
				85					90				
95													
Trp	Phe	Pro	Glu	Val	His	His	His	Cys	Pro	Gly	Val	Pro	Cys
Leu	Ile												
			100					105					110
Val	Gly	Thr	Gln	Ile	Asp	Leu	Arg	Asp	Asp	Pro	Ser	Val	Gln
Gln	Lys												
			115				120					125	
Leu	Ala	Arg	Gln	His	Gln	His	Pro	Leu	Thr	His	Glu	Gln	Gly
Glu	Arg												
	130					135					140		
Leu	Ala	Arg	Glu	Leu	Gly	Ala	Val	Lys	Tyr	Val	Glu	Cys	Ser
Ala	Leu												
145					150					155			
160													
Thr	Gln	Lys	Gly	Leu	Lys	Asn	Val	Phe	Asp	Glu	Ala	Ile	Val
Ala	Ala												
				165					170				
175													
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Val	Leu												
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Gly	Asp												
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15													
ggt	gct	gtt	ggt	aaa	acc	tgt	atg	ctc	atc	tgc	tac	acc	agc
aat	aaa			96									
Gly	Ala	Val	Gly	Lys	Thr	Cys	Met	Leu	Ile	Cys	Tyr	Thr	Ser

0070110

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

0070110

gcg ata 528
Ser Ser Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ser
Ala Ile

165

170

175

aag gaa gtg atc aaa cct ctg gtt aaa caa aag gag aag act
aag aag 576
Lys Glu Val Ile Lys Pro Leu Val Lys Gln Lys Glu Lys Thr
Lys Lys

180

185

190

aag aag aag caa aag tcg aat cac ggc tgt tta tca aat gtt
ctg tgt 624
Lys Lys Lys Gln Lys Ser Asn His Gly Cys Leu Ser Asn Val
Leu Cys

195

200

205

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210 215

<210> 501

<211> 215

<212> PRT

<213> Arabidopsis thaliana

<400> 501

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Gly Asp
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Asn Lys

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25

30

Phe Pro Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser
Ala Asn

35

40

45

Val Val Val Glu Gly Thr Thr Val Asn Leu Gly Leu Trp Asp
Thr Ala
50 55 60

Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg
Gly Ala
65 70 75

80

0070110

Asp Val Phe Val Leu Ser Phe Ser Leu Val Ser Arg Ala Ser
Tyr Glu

85

90

95

Asn Val Phe Lys Lys Trp Ile Pro Glu Leu Gln His Phe Ala
Pro Gly

100

105

110

Val Pro Leu Val Leu Val Gly Thr Lys Leu Asp Leu Arg Glu
Asp Lys

115

120

125

His Tyr Leu Ala Asp His Pro Gly Leu Ser Pro Val Thr Thr
Ala Gln

130

135

140

Gly Glu Glu Leu Arg Lys Leu Ile Gly Ala Thr Tyr Tyr Ile
Glu Cys

145

150

155

160

Ser Ser Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ser
Ala Ile

165

170

175

Lys Glu Val Ile Lys Pro Leu Val Lys Gln Lys Glu Lys Thr
Lys Lys

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Lys Lys Lys Gln Lys Ser Asn His Gly Cys Leu Ser Asn Val
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200

205

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<211> 594

<212> DNA

<213> Arabidopsis thaliana

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<221> CDS

<222> (1)..(594)

<400> 502

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gga gct 48

Met Ser Ala Ser Arg Phe Val Lys Cys Val Thr Val Gly Asp
Seite 761

0070110

Gly	Ala												
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15													
gtc	gga	aaa	act	tgt	ttg	ttg	att	tct	tac	aca	agc	aac	act
ttc	cct		96										
Val	Gly	Lys	Thr	Cys	Leu	Leu	Ile	Ser	Tyr	Thr	Ser	Asn	Thr
Phe	Pro												
			20					25					30
acg	gat	tat	gtg	cct	acc	ggt	ttc	gat	aat	ttc	agt	gcc	aat
ggt	gtg		144										
Thr	Asp	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn
Val	Val												
		35					40					45	
ggt	aat	gga	agc	act	gtg	aat	ctt	gga	ttg	tgg	gac	act	gca
ggg	caa		192										
Val	Asn	Gly	Ser	Thr	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala
Gly	Gln												
		50				55					60		
gag	gat	tac	aat	aga	tta	aga	cca	ctg	agt	tac	cgt	gga	gca
gat	ggt		240										
Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala
Asp	Val												
65					70					75			
80													
ttc	att	ttg	gcc	ttc	tct	ctt	atc	agt	aaa	gcc	agt	tat	gaa
aac	gtc		288										
Phe	Ile	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Lys	Ala	Ser	Tyr	Glu
Asn	Val												
			85							90			
95													
tcc	aaa	aag	tgg	atc	ccg	gag	ttg	aaa	cat	tac	gcg	cct	ggt
gtc	ccc		336										
Ser	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Lys	His	Tyr	Ala	Pro	Gly
Val	Pro												
			100					105					110
atc	gtc	ctt	gtt	gga	aca	aag	ctt	gat	ctt	cga	gat	gat	aaa
cag	ttc		384										
Ile	Val	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys
Gln	Phe												
		115					120					125	
ttt	atc	gac	cat	cct	ggt	gct	gtt	ccg	att	act	act	gct	cag
gga	gag		432										
Phe	Ile	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Thr	Thr	Ala	Gln
Gly	Glu												
		130				135					140		
gag	ctg	agg	aag	caa	ata	gga	gca	cct	act	tac	atc	gaa	tgc
agt	tcc		480										

0070110

Glu Leu Arg Lys Gln Ile Gly Ala Pro Thr Tyr Ile Glu Cys
 Ser Ser
 145 150 155

160
 aaa act caa gag aat gtg aag gcg gtg ttt gac gca gcc atc
 cga gtg 528
 Lys Thr Gln Glu Asn Val Lys Ala Val Phe Asp Ala Ala Ile
 Arg Val
 165 170

175
 gtg ttg caa ccg cca aag cag aag aag aag aag agc aaa gcg
 cag aag 576
 Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Ser Lys Ala
 Gln Lys
 180 185 190

gca tgc tcc att cta tga
 594
 Ala Cys Ser Ile Leu
 195

<210> 503
 <211> 197
 <212> PRT
 <213> Arabidopsis thaliana

<400> 503
 Met Ser Ala Ser Arg Phe Val Lys Cys Val Thr Val Gly Asp
 Gly Ala
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15
 Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
 Phe Pro
 20 25 30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
 Val Val
 35 40 45

Val Asn Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
 Gly Gln 50 55 60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
 Asp Val
 65 70 75

80
 Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
 Seite 763

0070110

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Asn Val
      85      90
95
Ser Lys Lys Trp Ile Pro Glu Leu Lys His Tyr Ala Pro Gly
Val Pro
      100      105      110

Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe
      115      120      125

Phe Ile Asp His Pro Gly Ala Val Pro Ile Thr Thr Ala Gln
Gly Glu
      130      135      140

Glu Leu Arg Lys Gln Ile Gly Ala Pro Thr Tyr Ile Glu Cys
Ser Ser
      145      150      155
      160
Lys Thr Gln Glu Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Arg Val
      165      170
      175
Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Ser Lys Ala
Gln Lys
      180      185      190

Ala Cys Ser Ile Leu
      195

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<210> 504
 <211> 591
 <212> DNA
 <213> Gossypium hirsutum

<220>
 <221> CDS
 <222> (1)..(591)

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<400> 504
atg agc act gca aga ttt atc aag tgt gtc acg gtc ggt gat
gga gct      48
Met Ser Thr Ala Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
      1      5      10
      15
gtg ggg aaa act tgt atg ctc att tca tat acc agc aat act
ttc cca      96

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0070110

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

0070110

aaa gta 528
Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Lys Val

165

170

175

gct ttg agg cca cca aaa cca aag aga aag cct tgc aaa agg
aga aca 576
Ala Leu Arg Pro Pro Lys Pro Lys Arg Lys Pro Cys Lys Arg
Arg Thr

180

185

190

tgt gct ttc ctt tga
591
Cys Ala Phe Leu
195

<210> 505

<211> 196

<212> PRT

<213> Gossypium hirsutum

<400> 505

Met Ser Thr Ala Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala

1

5

10

15

Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro

20

25

30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val

35

40

45

Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val

65

70

75

80

Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Ile

85

90

95

Tyr Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala His Asn
Seite 766

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Val	Pro													
			100					105					110	
Val	Val	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys	
Gln	Phe		115					120				125		
Leu	Ile	Asp	His	Pro	Gly	Ala	Thr	Pro	Ile	Ser	Thr	Ser	Gln	
Gly	Glu					135					140			
Glu	Leu	Lys	Lys	Met	Ile	Gly	Ala	Val	Thr	Tyr	Ile	Glu	Cys	
Ser	Ser					150				155				
145														
160														
Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile	
Lys	Val					165				170				
175														
Ala	Leu	Arg	Pro	Pro	Lys	Pro	Lys	Arg	Lys	Pro	Cys	Lys	Arg	
Arg	Thr													
			180					185					190	
Cys	Ala	Phe	Leu											
		195												

<210> 506
 <211> 594
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (1)..(594)

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gga	gct		48											
Met	Ser	Ala	Ser	Arg	Phe	Ile	Lys	Cys	Val	Thr	Val	Gly	Asp	
Gly	Ala													
1				5					10					
15														
gtt	ggt	aaa	acc	tgt	ttg	ctg	att	tct	tac	acc	agc	aac	act	
ttt	cct		96											
Val	Gly	Lys	Thr	Cys	Leu	Leu	Ile	Ser	Tyr	Thr	Ser	Asn	Thr	
Phe	Pro													
			20					25					30	
acg	gat	tat	gta	ccg	act	gtt	ttc	gat	aac	ttt	agc	gca	aat	

0070110

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

0070110

175

gtt ctt caa cct cca aag cag aag aaa aag aaa agc aaa gca
caa aaa 576
Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Ser Lys Ala
Gln Lys

180

185

190

gcc tgc tcc att ttg taa
594
Ala Cys Ser Ile Leu
195

<210> 507

<211> 197

<212> PRT

<213> Arabidopsis thaliana

<400> 507

Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala

1 5 10

15

Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro

20

25

30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val

35

40

45

Val Asn Gly Ala Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65 70 75

80

Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val

85

90

95

Ser Lys Lys Trp Ile Pro Glu Leu Lys His Tyr Ala Pro Gly
Val Pro

100

105

110

Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe

0070110
120

115

125

Phe Ile Asp His Pro Gly Ala Val Pro Ile Thr Thr Ala Gln
Gly Glu
130 135 140

Glu Leu Lys Lys Leu Ile Gly Ala Pro Ala Tyr Ile Glu Cys
Ser Ser
145 150 155
160

Lys Thr Gln Glu Asn Val Lys Gly Val Phe Asp Ala Ala Ile
Arg Val
165 170

175
Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Ser Lys Ala
Gln Lys
180 185 190

Ala Cys Ser Ile Leu
195

<210> 508
<211> 594
<212> DNA
<213> Beta vulgaris

<220>
<221> CDS
<222> (1)..(594)

<400> 508
atg agt gct tcg agg ttc ata aaa tgt gtt aca gtt ggt gat
ggt gcc 48
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10
15
gtt ggt aaa act tgc ttg ttg att tct tac acc agc aac acc
ttt cct 96
Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
20 25 30
acg gac tac gtg ccc act gtt ttt gac aat ttc agt gcc aat
gtc gtc 144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
35 40 45
gtt aac ggg gcc aca gtt aat ctg gga tta tgg gat act gca
Seite 770

0070110

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

0070110

Gln Lys 180 185 190

gct tgc tcc ata ttg taa
594
Ala Cys Ser Ile Leu
195

<210> 509

<211> 197

<212> PRT

<213> Beta vulgaris

<400> 509

Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala

1 5 10
15

Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro

20 25 30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val

35 40 45

Val Asn Gly Ala Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln

50 55 60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val

65 70 75
80

Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val

85 90

95

Ser Lys Lys Trp Ile Pro Glu Leu Lys His Tyr Ala Pro Gly
Val Pro

100 105 110

Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe

115 120 125

Phe Ile Asp His Pro Gly Ala Val Pro Ile Thr Thr Ala Gln
Seite 772

0070110

Gly	Glu													
130						135					140			
Glu	Leu	Arg	Lys	Leu	Ile	Gly	Ala	Pro	Ala	Tyr	Ile	Glu	Cys	
Ser	Ser													
145					150					155				
160														
Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile	
Lys	Val													
				165					170					
175														
Val	Leu	Gln	Pro	Pro	Lys	Thr	Lys	Lys	Lys	Lys	Ser	Lys	Ala	
Gln	Lys													
			180					185					190	
Ala	Cys	Ser	Ile	Leu										
		195												

<210> 510
 <211> 579
 <212> DNA
 <213> Drosophila melanogaster

<220>
 <221> CDS
 <222> (1)..(579)

<400> 510														
atg	cag	gcg	atc	aag	tgc	gtc	gtc	gtg	ggc	gac	gga	gcc	gtg	
gga	aag			48										
Met	Gln	Ala	Ile	Lys	Cys	Val	Val	Val	Gly	Asp	Gly	Ala	Val	
Gly	Lys													
1				5					10					
15														
acc	tgc	ctg	ctg	atc	agc	tac	acg	acc	aat	gcc	ttt	ccc	ggc	
gag	tac			96										
Thr	Cys	Leu	Leu	Ile	Ser	Tyr	Thr	Thr	Asn	Ala	Phe	Pro	Gly	
Glu	Tyr													
			20					25					30	
ata	ccc	acc	gtg	ttc	gac	aac	tac	tcg	gcc	aac	gtg	atg	gtg	
gac	gcc			144										
Ile	Pro	Thr	Val	Phe	Asp	Asn	Tyr	Ser	Ala	Asn	Val	Met	Val	
Asp	Ala													
		35				40						45		
aag	ccc	atc	aac	ctg	ggc	ctg	tgg	gat	acg	gcc	ggg	cag	gag	
gac	tac			192										
Lys	Pro	Ile	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala	Gly	Gln	Glu	
Asp	Tyr													

<210> 511
 <211> 192
 <212> PRT
 <213> *Drosophila melanogaster*

<400> 511
 Met Gln Ala Ile Lys Cys Val Val Val Gly Asp Gly Ala Val
 Gly Lys
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 Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Ala Phe Pro Gly
 Glu Tyr
 20 25 30
 Ile Pro Thr Val Phe Asp Asn Tyr Ser Ala Asn Val Met Val
 Asp Ala
 35 40 45
 Lys Pro Ile Asn Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu
 Asp Tyr
 50 55 60
 Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
 Leu Ile
 65 70 75
 80
 Cys Phe Ser Leu Val Asn Pro Ala Ser Phe Glu Asn Val Arg
 Ala Lys
 85 90
 95
 Trp Tyr Pro Glu Val Arg His His Cys Pro Ser Thr Pro Ile
 Ile Leu
 100 105 110
 Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys Asn Thr Ile
 Glu Lys
 115 120 125
 Leu Arg Asp Lys Lys Leu Ala Pro Ile Thr Tyr Pro Gln Gly
 Leu Ala
 130 135 140
 Met Ala Lys Glu Ile Gly Ala Val Lys Tyr Leu Glu Cys Ser
 Ala Leu

0070110

145		150		155
160				
Thr	Gln	Lys	Gly	Leu
Ser	Val	Lys	Thr	Val
			Phe	Asp
			Glu	Ala
			Ile	Arg
		165		170
175				
Leu	Cys	Pro	Val	Leu
Leu	Leu	Gln	Pro	Lys
			Ser	Lys
			Arg	Lys
			Cys	Ala
		180		185
				190

<210> 512
 <211> 594
 <212> DNA
 <213> Lotus japonicus

<220>
 <221> CDS
 <222> (1)..(594)

<400> 512	
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ggc gct	48
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp	
Gly Ala	
1	5
15	10
gtg ggc aaa acc tgc ttg ttg att tcc tac acc agc aac act	
ttt ccc	96
Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr	
Phe Pro	
	20
acg gac tac gtg ccc acc gtt ttt gac aat ttc agt gct aat	
gtt gtt	144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn	
Val Val	
	35
gtg gat gga agc act gta aac cta ggt tta tgg gat act gct	
ggt cag	192
Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala	
Gly Gln	
	50
gag gat tac aat aga tta aga ccc ttg agc tac cga gga gct	
gat gtc	240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala	
Asp Val	
65	70
	75
80	

0070110

ttt ata ctg gca ttt tct ctt atc agc aag gcc agc tat gaa
aat att 288
Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Ile

85

90

95

gca aag aag tgg atc cct gaa ctg agg cat tac gca ccc ggt
gtt cca 336
Ala Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Gly
Val Pro

100

105

110

ata att cta gtt gga acg aag tta gat ctt cgg gat gat aaa
cac ttt 384
Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
His Phe

115

120

125

ttg gca gac cac cct ggt gca gta cca att act aca gca cag
gga gaa 432
Leu Ala Asp His Pro Gly Ala Val Pro Ile Thr Thr Ala Gln
Gly Glu

130

135

140

gaa ttg aga aag ctg att gga gct cct gcc tac atc gag tgt
agt tcg 480
Glu Leu Arg Lys Leu Ile Gly Ala Pro Ala Tyr Ile Glu Cys
Ser Ser

145

150

155

160

aaa aca cag cag aat gtg aaa gcc gtc ttt gac gct gcc atc
aaa gtg 528
Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Lys Val

165

170

175

gtt ctg caa ccg cca aag caa aag aaa aag aag agg gag gca
cag aag 576
Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Arg Glu Ala
Gln Lys

180

185

190

tcc tgc tca ata ttg tga
594
Ser Cys Ser Ile Leu
195

<210> 513

<211> 197

<212> PRT

0070110

<213> Lotus japonicus

<400> 513

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

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Gln Lys 180 185 190

Ser Cys Ser Ile Leu
195

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<213> Arabidopsis thaliana

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Gly Ala
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15
gtg gga aag act tgt atg ctc att tca tat acc agc aat acg
ttt cct 96
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
20 25 30
acg gat tat gtt cca aca gtt ttc gac aac ttc agc gca aat
gtg gtg 144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
35 40 45
gtc gac ggg agt acc gtg aac ctt ggc ctg tgg gat act gcc
ggc cag 192
Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60
gaa gat tat aat agg ctt agg cct ttg agt tac aga gga gca
gat gtc 240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65 70 75
80
ttc tta tta gca ttt tcc ctt ata agc aag gcc agt tac gag
aat att 288
Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Ile
85 90

0070110

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95
cac aaa aag tgg ctt ccg gag ctg aaa cat tat gct cct ggc
atc ccc
His Lys Lys Trp Leu Pro Glu Leu Lys His Tyr Ala Pro Gly
Ile Pro
100 105 110

att gtg ctc gtc gga aca aaa tta gat ttg agg gat gac aag
cag ttc
Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe
115 120 125

ttg aag gat cat cca gga gca gct tct ata aca act gct cag
gga gaa
Leu Lys Asp His Pro Gly Ala Ala Ser Ile Thr Thr Ala Gln
Gly Glu
130 135 140
gaa tta agg aaa atg att gga gct gtt agg tac tta gag tgc
agc tcc
Glu Leu Arg Lys Met Ile Gly Ala Val Arg Tyr Leu Glu Cys
Ser Ser
145 150 155
160
aaa acc caa cag aat gtg aag gca gtg ttt gat aca gcg ata
agg gta
Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Thr Ala Ile
Arg Val
165 170

175
gct ttg agg cca cca aag gca aag aaa aag ata aaa cca ttg
aag act
Ala Leu Arg Pro Pro Lys Ala Lys Lys Lys Ile Lys Pro Leu
Lys Thr
180 185 190

aag aga tca aga ata tgc ttt ttc cta taa
606
Lys Arg Ser Arg Ile Cys Phe Phe Leu
195 200

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<211> 201

<212> PRT

<213> Arabidopsis thaliana

<400> 515

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

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<213> *Drosophila melanogaster*

<220>
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Gly Lys                               10
1                               5
15                               10
acc tgt ctg ctg atc agc tat acg acc aac gcc ttc ccc ggc
gag tac                               96
Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Ala Phe Pro Gly
Glu Tyr                               20
20                               25
ata ccc acg gtg ttc gac aac tat tcg gcg aat gtg atg gtg
gat gcc                               144
Ile Pro Thr Val Phe Asp Asn Tyr Ser Ala Asn Val Met Val
Asp Ala                               35
35                               40
aag ccc atc aat ctg ggc ctc tgg gat acg gct gga cag gag
gac tac                               192
Lys Pro Ile Asn Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu
Asp Tyr                               50
50                               55
gat cgc ctg agg ccg cta tcc tat ccg caa acg gat gtc ttt
ctc atc                               240
Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe
Leu Ile                               65
65                               70
70                               75
80                               75
tgt ttc tca ctg gtg aat ccg gca tcg ttt gag aat gtg cga
gcc aaa                               288
Cys Phe Ser Leu Val Asn Pro Ala Ser Phe Glu Asn Val Arg
Ala Lys                               85
85                               90
95                               90
tgg ttt ccc gag gtg cgt cat cat tgc ccg agt gtg ccg ata
atc ctg                               336
Trp Phe Pro Glu Val Arg His His Cys Pro Ser Val Pro Ile

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0070110

Ile	Leu												
			100					105				110	
gtc	ggc	acc	aaa	ctg	gat	ctg	cgc	gac	gat	aag	cag	acg	atc
gag	aag		384										
Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys	Gln	Thr	Ile
Glu	Lys												
		115					120				125		
ctg	aag	gac	aag	aag	cta	aca	ccg	atc	acc	tat	ccc	caa	gga
ctg	gcg		432										
Leu	Lys	Asp	Lys	Lys	Leu	Thr	Pro	Ile	Thr	Tyr	Pro	Gln	Gly
Leu	Ala												
	130					135					140		
atg	gcc	aag	gaa	ata	gct	gcg	gtc	aag	tat	ctg	gag	tgc	tcg
gcc	ctg		480										
Met	Ala	Lys	Glu	Ile	Ala	Ala	Val	Lys	Tyr	Leu	Glu	Cys	Ser
Ala	Leu												
145					150					155			
160													
acc	caa	aag	ggc	ctg	aag	acg	gtc	ttc	gac	gag	gcc	ata	cga
tcc	gtg		528										
Thr	Gln	Lys	Gly	Leu	Lys	Thr	Val	Phe	Asp	Glu	Ala	Ile	Arg
Ser	Val												
			165						170				
175													
cta	tgt	cct	gtc	gtt	cga	gga	ccc	aag	cgg	cac	aag	tgc	gcc
ctg	ctc		576										
Leu	Cys	Pro	Val	Val	Arg	Gly	Pro	Lys	Arg	His	Lys	Cys	Ala
Leu	Leu												
			180					185				190	
taa													
			579										

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 <212> PRT
 <213> Drosophila melanogaster

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 Gly Lys
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 Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Ala Phe Pro Gly
 Glu Tyr

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

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 <213> Lotus japonicus

0070110

<220>

<221> CDS

<222> (1)..(591)

<400> 518

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Gly Ala
  1              5              10
15
gtg gga aag acc tgt atg ctt atc tct tac acc agc aac aca
ttc cca      96
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
      20              25              30
acg gat tat gtg cct act gtt ttt gat aac ttc agt gca aat
gtg gtg      144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
      35              40              45
gtt gat ggc agc aca gtt aac ctg gga tta tgg gac act gct
gga cag      192
Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
      50              55              60
gag gat tac aat agg ctt agg cct ttg agc tac aga gga gca
gat gtg      240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
      65              70              75
80
ttc ttg ctg gct ttt tcc ctc ctt agc aga gcc agc tat gaa
aat atc      288
Phe Leu Leu Ala Phe Ser Leu Leu Ser Arg Ala Ser Tyr Glu
Asn Ile
      85              90
95
tcc aaa aag tgg att cct gaa ctg aga cac tat gcc cca act
gtg cca      336
Ser Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Thr
Val Pro
      100              105              110
att gtt ctt gtg gga acc aaa ctt gat ttg agg gaa gac agg
cag tat      384
Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Glu Asp Arg
Gln Tyr

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		115					120					125		
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gga	gaa			432										
Leu	Ile	Asp	His	Pro	Gly	Ala	Thr	Pro	Ile	Thr	Thr	Ala	Gln	
Gly	Glu													
	130					135						140		
gag	ctg	aag	aag	gca	att	ggg	gct	gct	gtg	tac	cta	gaa	tgc	
agc	tca		480											
Glu	Leu	Lys	Lys	Ala	Ile	Gly	Ala	Ala	Val	Tyr	Leu	Glu	Cys	
Ser	Ser													
145					150					155				
160														
aag	act	caa	cag	aat	gtg	aag	gct	gtg	ttt	gat	gct	gct	atc	
aag	ggt		528											
Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile	
Lys	Val													
			165						170					
175														
ggt	ttg	cag	cca	cct	aaa	cca	aag	aaa	aaa	cga	aag	aag	acc	
aga	cca		576											
Val	Leu	Gln	Pro	Pro	Lys	Pro	Lys	Lys	Lys	Arg	Lys	Lys	Thr	
Arg	Pro													
			180						185				190	

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 Cys Val Phe Leu
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<210> 519
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 <212> PRT
 <213> Lotus japonicus

<400> 519
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 Gly Ala
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 Phe Pro
 20 25 30
 Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
 Val Val
 35 40 45
 Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
 Seite 786

0070110

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

0070110

130						135						140	
gaa	cta	aag	aag	ctg	att	ggg	gcg	cct	gct	tat	atc	gaa	tgc
agt	gca			480									
Glu	Leu	Lys	Lys	Leu	Ile	Gly	Ala	Pro	Ala	Tyr	Ile	Glu	Cys
Ser	Ala												
145					150						155		
160													
aaa	act	caa	cag	aat	gtg	aaa	gca	gtg	ttt	gat	gcg	gct	atc
aag	gtc			528									
Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile
Lys	Val												
					165						170		
175													
ggt	ctc	cag	cca	cca	aaa	aac	aag	aag	aag	aag	aag	aga	aaa
tct	cag			576									
Val	Leu	Gln	Pro	Pro	Lys	Asn	Lys	Lys	Lys	Lys	Lys	Arg	Lys
Ser	Gln												
			180						185				190
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			597										
Lys	Gly	Cys	Ser	Ile	Leu								
		195											

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 <212> PRT
 <213> Arabidopsis thaliana

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Phe	Pro												
			20						25				30
Thr	Asp	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn
Val	Ile												
		35					40					45	
Val	Asp	Gly	Asn	Thr	Ile	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala
Gly	Gln												
	50					55					60		
Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala
Asp	Val												

0070110

65					70					75			
	80												
Phe	Leu	Leu	Ala	Phe	Ser	Leu	Val	Ser	Lys	Ala	Ser	Tyr	Glu
Asn	Val												
				85					90				
95													
Ser	Lys	Lys	Trp	Val	Pro	Glu	Leu	Arg	His	Tyr	Ala	Pro	Gly
Val	Pro												
			100					105				110	
Ile	Ile	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys
Gln	Phe												
		115					120				125		
Phe	Ala	Glu	His	Pro	Gly	Ala	Val	Pro	Ile	Ser	Thr	Ala	Gln
Gly	Glu												
	130					135				140			
Glu	Leu	Lys	Lys	Leu	Ile	Gly	Ala	Pro	Ala	Tyr	Ile	Glu	Cys
Ser	Ala												
145					150					155			
	160												
Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile
Lys	Val												
				165					170				
175													
Val	Leu	Gln	Pro	Pro	Lys	Asn	Lys	Lys	Lys	Lys	Lys	Arg	Lys
Ser	Gln												
			180					185				190	
Lys	Gly	Cys	Ser	Ile	Leu								
		195											

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 <213> Arabidopsis thaliana

<220>
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 Ala Val

0070110

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

0070110

Ser Lys
145 150 155
160
aca cag cag aac gtg aag gca gtg ttt gat gca gct ata aaa
gtg gtg 528
Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile Lys
Val Val
165 170
175
ctt cag cca cca aag cag aag aag aag aaa aag aat aag aac
cgt tgc 576
Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Lys Asn Lys Asn
Arg Cys
180 185 190

gcg ttc ttg tga
588
Ala Phe Leu
195

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

0070110

85

90

95
Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Gly Val
Pro Ile

100

105

110

Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys Gln
Phe Phe

115

120

125

Ile Asp His Pro Gly Ala Val Pro Ile Thr Thr Asn Gln Gly
Glu Glu

130

135

140

Leu Lys Lys Leu Ile Gly Ser Ala Val Tyr Ile Glu Cys Ser
Ser Lys

145

150

155

Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile Lys
Val Val

160

165

170

175
Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Lys Asn Lys Asn
Arg Cys

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185

190

Ala Phe Leu
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Gly Ala

1

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10

15

gtc gga aaa act tgt atg ctg att tct tac aca agc aac act
ttc cct 96

Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Seite 793

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

0070110

Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Lys Val

165

170

175

gtg ctt cag cca ccg aaa cag aag aag aag aaa aag aac aag

aac cgc 576

Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Lys Asn Lys

Asn Arg

180

185

190

tgc gtg ttc ttg tga

591

Cys Val Phe Leu

195

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<213> Arabidopsis thaliana

<400> 525

Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp

Gly Ala

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Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr

Phe Pro

20

25

30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn

Val Val

35

40

45

Val Asp Gly Asn Thr Val Asn Leu Gly Leu Trp Asp Thr Ala

Gly Gln

50

55

60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala

Asp Val

65

70

75

80

Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu

Asn Val

85

90

95

Ala Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Gly

Val Pro

100

105

110

0070110

Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe
115 120 125

Phe Ile Asp His Pro Gly Ala Val Pro Ile Thr Thr Asn Gln
Gly Glu
130 135 140

Glu Leu Lys Lys Leu Ile Gly Ser Pro Ile Tyr Ile Glu Cys
Ser Ser
145 150 155
160

Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Lys Val
165 170

175
Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Lys Asn Lys
Asn Arg
180 185 190

Cys Val Phe Leu
195

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Gly Ala
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15
gtt ggt aaa acc tgt ttg ctg att tct tat acc agc aac acc
ttt ccc 96
Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
20 25 30
acg gat tat gtt ccg act gtt ttc gat aac ttt agt gca aat
gtg gtt 144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Seite 796

0070110

val	val													
		35					40					45		
gtt	aat	gga	gcc	acg	gtg	aat	ctt	gga	ttg	tgg	gat	act	gca	
ggg	caa		192											
val	asn	gly	ala	thr	val	asn	leu	gly	leu	trp	asp	thr	ala	
gly	gln													
	50					55					60			
gag	gac	tat	aac	aga	tta	aga	cct	ttg	agt	tac	cgt	ggt	gct	
gat	ggt		240											
glu	asp	tyr	asn	arg	leu	arg	pro	leu	ser	tyr	arg	gly	ala	
asp	val													
65					70					75				
80														
ttc	att	ctt	gcc	ttc	tct	ctc	att	agt	aag	gct	agt	tat	gag	
aat	ggt		288											
phe	ile	leu	ala	phe	ser	leu	ile	ser	lys	ala	ser	tyr	glu	
asn	val													
			85						90					
95														
tcc	aag	aag	tgg	att	cct	gag	ttg	aag	cac	tat	gct	cct	ggt	
gtc	cca		336											
ser	lys	lys	trp	ile	pro	glu	leu	lys	his	tyr	ala	pro	gly	
val	pro													
			100					105					110	
att	gtc	ctt	gtt	gga	acc	aaa	cta	gat	ctt	cga	gat	gac	aaa	
cag	ttt		384											
ile	val	leu	val	gly	thr	lys	leu	asp	leu	arg	asp	asp	lys	
gln	phe													
		115					120					125		
ttc	atc	gac	cat	cct	ggt	gct	gtc	cct	att	acc	act	ggt	cag	
gga	gag		432											
phe	ile	asp	his	pro	gly	ala	val	pro	ile	thr	thr	val	gln	
gly	glu													
	130					135					140			
gag	ctg	aag	aag	cta	att	gga	gcg	cca	gct	tac	atc	gag	tgc	
agt	tca		480											
glu	leu	lys	lys	leu	ile	gly	ala	pro	ala	tyr	ile	glu	cys	
ser	ser													
145					150					155				
160														
aaa	tca	caa	gag	aac	gtg	aag	ggc	gtg	ttt	gat	gca	gcg	atc	
aga	gtg		528											
lys	ser	gln	glu	asn	val	lys	gly	val	phe	asp	ala	ala	ile	
arg	val													
			165						170					
175														

0070110

gtc ctt caa cct cca aag cag aag aaa aag aag aac aaa gca
 caa aag 576
 Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Asn Lys Ala
 Gln Lys
 180 185 190

gcc tgc tcc atc ttg taa
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 Ala Cys Ser Ile Leu
 195

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 <212> PRT
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 Gly Ala
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 Phe Pro
 20 25 30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
 Val Val
 35 40 45

Val Asn Gly Ala Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
 Gly Gln
 50 55 60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
 Asp Val
 65 70 75

80
 Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
 Asn Val
 85 90

95
 Ser Lys Lys Trp Ile Pro Glu Leu Lys His Tyr Ala Pro Gly
 Val Pro
 100 105 110

Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
 Gln Phe
 115 120 125

0070110

Phe Ile Asp His Pro Gly Ala Val Pro Ile Thr Thr Val Gln
Gly Glu
130 135 140

Glu Leu Lys Lys Leu Ile Gly Ala Pro Ala Tyr Ile Glu Cys
Ser Ser
145 150 155
160

Lys Ser Gln Glu Asn Val Lys Gly Val Phe Asp Ala Ala Ile
Arg Val
165 170

175
Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Asn Lys Ala
Gln Lys
180 185 190

Ala Cys Ser Ile Leu
195

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Gly Ala
1 5 10
15
gtt ggg aag aca tgt atg ctt atc tgt tac act agc aac aag
ttt cct 96
Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser Asn Lys
Phe Pro
20 25 30
act gat tat ata ccg act gtg ttc gac aat ttc agt gcc aat
gta gct 144
Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Ala
35 40 45
gtg gat gga caa atc gtt aat tta ggg cta tgg gac act gcc
ggt caa 192

0070110

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

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aga tcc ggt tgc tcc att gcg agt att gtc tgt gga ggt tgc
acc gct 624
Arg Ser Gly Cys Ser Ile Ala Ser Ile Val Cys Gly Gly Cys
Thr Ala
195 200 205
gct taa
630
Ala

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Gly Ala
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Phe Pro
20 25 30
Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Ala
35 40 45
Val Asp Gly Gln Ile Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60
Glu Asp Tyr Ser Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Ile
65 70 75
80
Phe Val Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val
85 90
95
Leu Lys Lys Trp Met Pro Glu Leu Arg Arg Phe Ala Pro Asn
Val Pro
100 105 110
Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gly Tyr
115 120 125

0070110

Leu Ala Asp His Thr Asn Val Ile Thr Ser Thr Gln Gly Glu
Glu Leu
130 135 140

Arg Lys Gln Ile Gly Ala Ala Ala Tyr Ile Glu Cys Ser Ser
Lys Thr
145 150 155

160
Gln Gln Asn Val Lys Ala Val Phe Asp Thr Ala Ile Lys Val
Val Leu
165 170

175
Gln Pro Pro Arg Arg Lys Glu Val Pro Arg Arg Arg Lys Asn
His Arg
180 185 190

Arg Ser Gly Cys Ser Ile Ala Ser Ile Val Cys Gly Gly Cys
Thr Ala
195 200 205

Ala

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gga gat 48
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Gly Asp
1 5 10
15
ggt gcc gtt gga aaa act tgt atg ctc atc tgc tac act agc
aac aaa 96
Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser
Asn Lys
20 25 30
ttc cct act gac tac ata cca aca gtt ttt gac aac ttt agt
gtt aat 144
Phe Pro Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser
Seite 802

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

0070110

aag aag 576
 Lys Val Val Ile Lys Pro Ala Val Lys Gln Lys Glu Lys Lys
 Lys Lys
 180 185 190

cag aag cct cgc agc gga tgt ctc tca aac att ctg tgt ggg
 aag aat 624
 Gln Lys Pro Arg Ser Gly Cys Leu Ser Asn Ile Leu Cys Gly
 Lys Asn
 195 200 205
 tga
 627

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 <212> PRT
 <213> Arabidopsis thaliana

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 Gly Asp
 1 5 10
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 Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser
 Asn Lys
 20 25 30

Phe Pro Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser
 Val Asn
 35 40 45

Val Val Val Glu Gly Ile Thr Val Asn Leu Gly Leu Trp Asp
 Thr Ala
 50 55 60

Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg
 Gly Ala
 65 70 75

80
 Asp Val Phe Val Leu Ala Phe Ser Leu Ile Ser Arg Ala Ser
 Tyr Glu
 85 90

95
 Asn Val Phe Lys Lys Trp Ile Pro Glu Leu Gln His Phe Ala
 Pro Gly
 100 105 110

0070110

Val	Pro	Ile	Val	Leu	Val	Gly	Thr	Lys	Met	Asp	Leu	Arg	Glu
Asp	Arg												
		115					120					125	
His	Tyr	Leu	Ser	Asp	His	Pro	Gly	Leu	Ser	Pro	Val	Thr	Thr
Ser	Gln												
	130					135					140		
Gly	Glu	Glu	Leu	Arg	Lys	His	Ile	Gly	Ala	Thr	Tyr	Tyr	Ile
Glu	Cys												
145					150					155			
160													
Ser	Ser	Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala
Ala	Ile												
				165					170				
175													
Lys	Val	Val	Ile	Lys	Pro	Ala	Val	Lys	Gln	Lys	Glu	Lys	Lys
Lys	Lys												
			180					185					190
Gln	Lys	Pro	Arg	Ser	Gly	Cys	Leu	Ser	Asn	Ile	Leu	Cys	Gly
Lys	Asn												
		195					200					205	

<210> 532
 <211> 630
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (1)..(630)

<400> 532													
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gct	aca				48								
Met	Ser	Ala	Ser	Met	Ala	Ala	Thr	Ser	Thr	Ser	Ser	Ala	Thr
Ala	Thr												
1				5					10				
15													
acg	ttt	ata	aag	tgt	gtc	act	gtt	ggc	gat	gga	gct	gtg	ggc
aaa	act				96								
Thr	Phe	Ile	Lys	Cys	Val	Thr	Val	Gly	Asp	Gly	Ala	Val	Gly
Lys	Thr												
			20					25					30
tgt	ctt	ctt	att	tcc	tac	acc	agc	aac	acg	ttc	ccc	act	gat

0070110

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

0070110

175

aac gta aaa gcc gtg ttt gat gaa gcg atc aaa gta gtt tta
cat cct
Asn Val Lys Ala Val Phe Asp Glu Ala Ile Lys Val Val Leu
His Pro

180

185

190

cct tca aag act aag aag cga aag aga aag atc ggt tta tgc
cat gtt
Pro Ser Lys Thr Lys Lys Arg Lys Arg Lys Ile Gly Leu Cys
His Val

195

200

205

ctt tga

630

Leu

<210> 533

<211> 209

<212> PRT

<213> Arabidopsis thaliana

<400> 533

Met Ser Ala Ser Met Ala Ala Thr Ser Thr Ser Ser Ala Thr
Ala Thr

1

5

10

15

Thr Phe Ile Lys Cys Val Thr Val Gly Asp Gly Ala Val Gly
Lys Thr

20

25

30

Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr Phe Pro Thr Asp
Tyr Val

35

40

45

Pro Thr Val Phe Asp Asn Phe Asn Ala Asn Val Leu Val Asp
Gly Lys
50

55

60

Thr Val Asn Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu Asp
Tyr Asn
65

70

75

80

Arg Val Arg Pro Leu Ser Tyr Arg Gly Ala Asp Val Phe Ile
Leu Ala

85

90

95

Phe Ser Leu Ile Ser Arg Pro Ser Phe Glu Asn Ile Ala Lys

Seite 807

0070110

Lys	Trp													
			100					105					110	
Val	Pro	Glu	Leu	Arg	His	Tyr	Ala	Pro	Thr	Val	Pro	Ile	Val	
Leu	Val													
			115					120				125		
Gly	Thr	Lys	Ser	Asp	Leu	Arg	Asp	Asn	Met	Gln	Phe	Pro	Lys	
Asn	Tyr													
							135				140			
Pro	Gly	Ala	Cys	Thr	Ile	Phe	Pro	Glu	Gln	Gly	Gln	Glu	Leu	
Arg	Lys													
145						150				155				
160														
Glu	Ile	Gly	Ala	Leu	Ala	Tyr	Ile	Glu	Cys	Ser	Ser	Lys	Ala	
Gln	Met													
				165						170				
175														
Asn	Val	Lys	Ala	Val	Phe	Asp	Glu	Ala	Ile	Lys	Val	Val	Leu	
His	Pro													
			180					185					190	
Pro	Ser	Lys	Thr	Lys	Lys	Arg	Lys	Arg	Lys	Ile	Gly	Leu	Cys	
His	Val													
			195					200				205		
Leu														

<210> 534
 <211> 591
 <212> DNA
 <213> Gossypium hirsutum

<220>
 <221> CDS
 <222> (1)..(591)

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 gga gca 48
 Met Asn Thr Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala
 1 5 10
 15
 gtg ggg aag act tgc atg ctt att tcg tat act agc aat acg
 ttc cca 96

0070110

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

0070110

aag ata 528
Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Val Ala Ile
Lys Ile

165

170

175

gca ttg agg cca cca aaa cca aag aga aaa cct ata aaa aga
aga tca 576
Ala Leu Arg Pro Pro Lys Pro Lys Arg Lys Pro Ile Lys Arg
Arg Ser

180

185

190

tgt gct ttc ctt tga
591
Cys Ala Phe Leu
195

<210> 535

<211> 196

<212> PRT

<213> Gossypium hirsutum

<400> 535

Met Asn Thr Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10

15

Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
20 25 30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
35 40 45

Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65 70 75

80

Phe Leu Leu Ala Phe Ser Leu Ile Ser Arg Ala Ser Tyr Glu
Asn Val
85 90

95

His Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Asn
Val Pro

0070110

100

105

110

Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe

115

120

125

Leu Ser Asp Asn Pro Gly Ala Ile Ser Ile Thr Thr Ser Gln
Gly Glu
130

135

140

Glu Leu Lys Lys Met Ile Gly Ala Val Thr Tyr Ile Glu Cys
Ser Ser
145

150

155

160

Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Val Ala Ile
Lys Ile

165

170

175

Ala Leu Arg Pro Pro Lys Pro Lys Arg Lys Pro Ile Lys Arg
Arg Ser

180

185

190

Cys Ala Phe Leu
195

<210> 536

<211> 624

<212> DNA

<213> Ashbya gossypii

<220>

<221> CDS

<222> (1)..(624)

<400> 536

atg tct cag caa atg cat aac ccc agt atc agg aga aaa ttg
gtg atc

48

Met Ser Gln Gln Met His Asn Pro Ser Ile Arg Arg Lys Leu
Val Ile

1

5

10

15

gtc gga gat ggt gca tgc ggg aaa aca tgt ctt ttg att gtg
ttt gcc

96

Val Gly Asp Gly Ala Cys Gly Lys Thr Cys Leu Leu Ile Val
Phe Ala

20

25

30

aag gga aag ttc cca cag gtg tat gtt cct acg gtt ttc gac
aac tac

144

0070110

Lys	Gly	Lys	Phe	Pro	Gln	Val	Tyr	Val	Pro	Thr	Val	Phe	Asp
Asn	Tyr												
		35					40					45	
gtt	gca	gat	gtg	gag	gta	gac	ggc	aga	cgg	gtg	gag	ctt	gcg
ctt	tgg		192										
Val	Ala	Asp	Val	Glu	Val	Asp	Gly	Arg	Arg	Val	Glu	Leu	Ala
Leu	Trp												
	50					55					60		
gat	acg	gct	ggg	cag	gag	gat	tac	gac	agg	cta	cgg	ccg	tta
tcg	tac		240										
Asp	Thr	Ala	Gly	Gln	Glu	Asp	Tyr	Asp	Arg	Leu	Arg	Pro	Leu
Ser	Tyr												
65					70					75			
80													
cca	gac	tcc	aat	gtt	gtg	ttg	atc	tgc	tac	tcg	att	gac	cta
cca	gac		288										
Pro	Asp	Ser	Asn	Val	Val	Leu	Ile	Cys	Tyr	Ser	Ile	Asp	Leu
Pro	Asp												
			85						90				
95													
tcg	ttg	gag	aac	gtg	atg	gag	aag	tgg	atc	agc	gag	gtg	cta
tac	ttc		336										
Ser	Leu	Glu	Asn	Val	Met	Glu	Lys	Trp	Ile	Ser	Glu	Val	Leu
Tyr	Phe												
			100					105				110	
tgc	cag	ggc	gtt	ccg	atc	atc	ttg	gtg	ggg	tgc	aag	gct	gac
ttg	cgg		384										
Cys	Gln	Gly	Val	Pro	Ile	Ile	Leu	Val	Gly	Cys	Lys	Ala	Asp
Leu	Arg												
		115					120					125	
aac	gat	ccg	caa	gtg	atc	gag	cag	ttg	aga	cag	cag	gga	cag
cag	cct		432										
Asn	Asp	Pro	Gln	Val	Ile	Glu	Gln	Leu	Arg	Gln	Gln	Gly	Gln
Gln	Pro												
	130					135					140		
gtc	tcg	cag	gct	cag	gcg	cag	gag	gta	gcg	gac	cag	atc	ggc
gcg	gta		480										
Val	Ser	Gln	Ala	Gln	Ala	Gln	Glu	Val	Ala	Asp	Gln	Ile	Gly
Ala	Val												
145					150					155			
160													
gag	tac	att	gag	tgc	tct	gca	aag	acc	ggc	ttt	ggt	gtg	cgc
gag	gtg		528										
Glu	Tyr	Ile	Glu	Cys	Ser	Ala	Lys	Thr	Gly	Phe	Gly	Val	Arg
Glu	Val												
			165						170				
175													

0070110

ttt gag gcg gcc acg cgt gct tcc ttg atg ggg aaa caa ggc
aag tct 576
Phe Glu Ala Ala Thr Arg Ala Ser Leu Met Gly Lys Gln Gly
Lys Ser
180 185 190

aag gcg aag tct gac aag aag aag aag aaa aag tgt gtg gtc
ttg 621
Lys Ala Lys Ser Asp Lys Lys Lys Lys Lys Lys Cys Val Val
Leu
195 200 205

tag

624

<210> 537

<211> 207

<212> PRT

<213> Ashbya gossypii

<400> 537

Met Ser Gln Gln Met His Asn Pro Ser Ile Arg Arg Lys Leu
Val Ile
1 5 10

15
Val Gly Asp Gly Ala Cys Gly Lys Thr Cys Leu Leu Ile Val
Phe Ala
20 25 30

Lys Gly Lys Phe Pro Gln Val Tyr Val Pro Thr Val Phe Asp
Asn Tyr
35 40 45

Val Ala Asp Val Glu Val Asp Gly Arg Arg Val Glu Leu Ala
Leu Trp
50 55 60

Asp Thr Ala Gly Gln Glu Asp Tyr Asp Arg Leu Arg Pro Leu
Ser Tyr
65 70 75

80
Pro Asp Ser Asn Val Val Leu Ile Cys Tyr Ser Ile Asp Leu
Pro Asp
85 90

95
Ser Leu Glu Asn Val Met Glu Lys Trp Ile Ser Glu Val Leu
Tyr Phe

0070110

			100					105					110
Cys	Gln	Gly	Val	Pro	Ile	Ile	Leu	Val	Gly	Cys	Lys	Ala	Asp
Leu	Arg												
		115					120					125	
Asn	Asp	Pro	Gln	Val	Ile	Glu	Gln	Leu	Arg	Gln	Gln	Gly	Gln
Gln	Pro												
	130					135					140		
Val	Ser	Gln	Ala	Gln	Ala	Gln	Glu	Val	Ala	Asp	Gln	Ile	Gly
Ala	Val												
145						150					155		
160													
Glu	Tyr	Ile	Glu	Cys	Ser	Ala	Lys	Thr	Gly	Phe	Gly	Val	Arg
Glu	Val												
				165					170				
175													
Phe	Glu	Ala	Ala	Thr	Arg	Ala	Ser	Leu	Met	Gly	Lys	Gln	Gly
Lys	Ser												
			180					185				190	
Lys	Ala	Lys	Ser	Asp	Lys	Lys	Lys	Lys	Lys	Lys	Cys	Val	Val
Leu													
		195					200					205	

<210> 538
 <211> 597
 <212> DNA
 <213> Candida albicans

<220>
 <221> CDS
 <222> (1)..(597)
 <223> transl_table=12

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 gtc ggt 48
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 Val Gly
 1 5 10
 15
 gat ggt gct tgt ggt aag act tgt tta tta att gtt ttt tca
 aaa ggt 96
 Asp Gly Ala Cys Gly Lys Thr Cys Leu Leu Ile Val Phe Ser
 Lys Gly

0070110

			20					25					30
act	ttc	cca	gaa	ggt	tat	gtc	cca	aca	ggt	ttt	gaa	aat	tac
ggt	gct		144										
Thr	Phe	Pro	Glu	Val	Tyr	Val	Pro	Thr	Val	Phe	Glu	Asn	Tyr
Val	Ala												
		35					40					45	
gat	ggt	gaa	ggt	gat	ggt	aga	aaa	ggt	gaa	ttg	gca	tta	tgg
gat	act		192										
Asp	Val	Glu	Val	Asp	Gly	Arg	Lys	Val	Glu	Leu	Ala	Leu	Trp
Asp	Thr												
	50					55					60		
gct	ggt	caa	gaa	gat	tat	gat	aga	tta	aga	cca	tta	tct	tat
cca	gat		240										
Ala	Gly	Gln	Glu	Asp	Tyr	Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr
Pro	Asp												
65					70					75			
	80												
tct	aat	ggt	att	ttg	att	tgt	ttt	tca	ggt	gat	tca	cca	gat
tct	tta		288										
Ser	Asn	Val	Ile	Leu	Ile	Cys	Phe	Ser	Val	Asp	Ser	Pro	Asp
Ser	Leu												
			85							90			
95													
gat	aac	ggt	tta	gaa	aaa	tgg	att	tct	gaa	ggt	tta	cat	ttc
tgt	caa		336										
Asp	Asn	Val	Leu	Glu	Lys	Trp	Ile	Ser	Glu	Val	Leu	His	Phe
Cys	Gln												
		100						105				110	
ggt	ggt	cca	atc	att	tta	ggt	tgt	aaa	tct	gat	tta	aga	
gat	gat		384										
Gly	Val	Pro	Ile	Ile	Leu	Val	Gly	Cys	Lys	Ser	Asp	Leu	Arg
Asp	Asp												
		115					120					125	
cct	cat	act	att	gaa	gcc	ttg	aga	caa	caa	caa	caa	caa	cca
gtc	tca		432										
Pro	His	Thr	Ile	Glu	Ala	Leu	Arg	Gln	Gln	Gln	Gln	Gln	Pro
Val	Ser												
	130					135					140		
act	tct	gaa	ggt	caa	caa	ggt	gct	caa	aga	att	ggt	gct	gct
gat	tac		480										
Thr	Ser	Glu	Gly	Gln	Gln	Val	Ala	Gln	Arg	Ile	Gly	Ala	Ala
Asp	Tyr												
145					150					155			
	160												
ttg	gaa	tgt	tct	gct	aaa	acc	ggt	aga	ggt	ggt	aga	gaa	gtg
ttt	gaa		528										
Leu	Glu	Cys	Ser	Ala	Lys	Thr	Gly	Arg	Gly	Val	Arg	Glu	Val

0070110

Phe Glu
 165 170
 175
 gct gct act aga gct tct tta aga gtt aaa gaa aag aag gaa
 aag aag 576
 Ala Ala Thr Arg Ala Ser Leu Arg Val Lys Glu Lys Lys Glu
 Lys Lys
 180 185 190

aag aaa tgt gtt gtc ttg taa
 597
 Lys Lys Cys Val Val Leu
 195

<210> 539
 <211> 198
 <212> PRT
 <213> Candida albicans

<400> 539
 Met Val Asn Gly Pro Ala Glu Leu Arg Arg Lys Leu Val Ile
 Val Gly
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 Asp Gly Ala Cys Gly Lys Thr Cys Leu Leu Ile Val Phe Ser
 Lys Gly
 20 25 30

Thr Phe Pro Glu Val Tyr Val Pro Thr Val Phe Glu Asn Tyr
 Val Ala
 35 40 45

Asp Val Glu Val Asp Gly Arg Lys Val Glu Leu Ala Leu Trp
 Asp Thr
 50 55 60

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

0070110

Gly	Val	Pro	Ile	Ile	Leu	Val	Gly	Cys	Lys	Ser	Asp	Leu	Arg
Asp	Asp												
		115					120					125	
Pro	His	Thr	Ile	Glu	Ala	Leu	Arg	Gln	Gln	Gln	Gln	Gln	Pro
Val	Ser												
	130					135					140		
Thr	Ser	Glu	Gly	Gln	Gln	Val	Ala	Gln	Arg	Ile	Gly	Ala	Ala
Asp	Tyr												
145					150					155			
160													
Leu	Glu	Cys	Ser	Ala	Lys	Thr	Gly	Arg	Gly	Val	Arg	Glu	Val
Phe	Glu												
				165					170				
175													
Ala	Ala	Thr	Arg	Ala	Ser	Leu	Arg	Val	Lys	Glu	Lys	Lys	Glu
Lys	Lys												
			180				185					190	
Lys	Lys	Cys	Val	Val	Leu								
		195											

<210> 540
<211> 579
<212> DNA
<213> Drosophila melanogaster

<220>
<221> CDS
<222> (1)..(579)

<400> 540													
atg	acg	acg	att	cgc	aag	aaa	ttg	gta	att	gtc	ggc	gac	ggt
gcc	tgc			48									
Met	Thr	Thr	Ile	Arg	Lys	Lys	Leu	Val	Ile	Val	Gly	Asp	Gly
Ala	Cys												
1				5					10				
15													
ggt	aaa	act	tgc	ctt	ctg	att	gtc	ttc	agc	aaa	gat	cag	ttc
ccc	gag			96									
Gly	Lys	Thr	Cys	Leu	Leu	Ile	Val	Phe	Ser	Lys	Asp	Gln	Phe
Pro	Glu												
			20				25					30	
gtc	tat	gtg	ccc	acc	gta	ttc	gag	aat	tat	gtg	gcc	gac	atc
gag	gtg		144										
Val	Tyr	Val	Pro	Thr	Val	Phe	Glu	Asn	Tyr	Val	Ala	Asp	Ile

0070110

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

0070110

ttg ctc 576
 Ala Ala Leu Gln Val Lys Lys Arg Lys Lys Thr Arg Cys Leu
 Leu Leu 180 185 190

taa 579

<210> 541
 <211> 192
 <212> PRT
 <213> Drosophila melanogaster

<400> 541
 Met Thr Thr Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly
 Ala Cys 5 10
 15
 Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Asp Gln Phe
 Pro Glu 20 25 30
 Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Ile
 Glu Val 35 40 45
 Asp Gly Lys Gln Val Glu Leu Ala Leu Trp Asp Thr Ala Gly
 Gln Glu 50 55 60
 Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Thr Asp
 Val Ile 65 70 75
 80
 Leu Met Cys Phe Ser Val Asp Ser Pro Asp Ser Leu Glu Asn
 Ile Pro 85 90
 95
 Glu Lys Trp Thr Pro Glu Val Lys His Phe Cys Pro Asn Val
 Pro Ile 100 105 110
 Ile Leu Val Gly Asn Lys Lys Asp Leu Arg Asn Asp Pro Asn
 Thr Ile 115 120 125

0070110

Arg	Asp	Leu	Ala	Lys	Met	Lys	Gln	Glu	Pro	Val	Lys	Pro	Gln
Glu	Gly												
	130					135					140		

Arg	Ala	Met	Ala	Glu	Lys	Ile	Asn	Ala	Phe	Ala	Tyr	Leu	Glu
Cys	Ser												
145					150					155			

	160												
Ala	Lys	Ser	Lys	Glu	Gly	Val	Arg	Asp	Val	Phe	Glu	Thr	Ala
Thr	Arg												
				165					170				

175													
Ala	Ala	Leu	Gln	Val	Lys	Lys	Arg	Lys	Lys	Thr	Arg	Cys	Leu
Leu	Leu												
			180					185				190	

<210> 542
 <211> 627
 <212> DNA
 <213> Kluyveromyces lactis

<220>
 <221> CDS
 <222> (1)..(627)

<400> 542													
atg	tct	caa	gct	ggt	ggt	aat	ggt	gcc	agc	att	aga	aga	aag
cta	ggt			48									
Met	Ser	Gln	Ala	Val	Gly	Asn	Val	Ala	Ser	Ile	Arg	Arg	Lys
Leu	Val												
1				5				10					
15													
att	gtc	ggt	gat	ggt	gcg	tgt	ggt	aag	act	tgt	tta	ttg	att
ggt	ttc			96									
Ile	Val	Gly	Asp	Gly	Ala	Cys	Gly	Lys	Thr	Cys	Leu	Leu	Ile
Val	Phe												
			20					25				30	
gcc	aag	ggt	aag	ttc	cct	cag	ggt	tac	gtg	ccc	act	ggt	ttc
gat	aat			144									
Ala	Lys	Gly	Lys	Phe	Pro	Gln	Val	Tyr	Val	Pro	Thr	Val	Phe
Asp	Asn												
		35					40					45	
tac	ggt	gct	gat	gtc	gaa	ggt	gac	ggt	cgt	cgc	gta	gaa	ttg
gcg	ttg			192									
Tyr	Val	Ala	Asp	Val	Glu	Val	Asp	Gly	Arg	Arg	Val	Glu	Leu
Ala	Leu												
	50						55				60		

0070110

tgg gat act gct ggc caa gaa gat tat gat aga ttg aga cca
 ctt tcg 240
 Trp Asp Thr Ala Gly Gln Glu Asp Tyr Asp Arg Leu Arg Pro
 Leu Ser 65 70 75

80
 tac cca gat tcc aac gtt gtg tta atc tgt tac tca att gat
 ttg cca 288
 Tyr Pro Asp Ser Asn Val Val Leu Ile Cys Tyr Ser Ile Asp
 Leu Pro 85 90

95
 gat tcc tta gaa aac gtg atg gaa aaa tgg atc tct gaa gtt
 tta cac 336
 Asp Ser Leu Glu Asn Val Met Glu Lys Trp Ile Ser Glu Val
 Leu His 100 105 110

115
 ttt tgt caa ggt gtt cca atc atc ttg gtt ggt tgt aaa gca
 gat ttg 384
 Phe Cys Gln Gly Val Pro Ile Ile Leu Val Gly Cys Lys Ala
 Asp Leu 120 125

aga aat gat cct caa gtt gtt gaa gaa cta aga gct caa gga
 tta caa 432
 Arg Asn Asp Pro Gln Val Val Glu Glu Leu Arg Ala Gln Gly
 Leu Gln 130 135 140

cct gtg tct cag gct caa gca caa gaa gtc gct gac caa atc
 ggt gct 480
 Pro Val Ser Gln Ala Gln Ala Gln Glu Val Ala Asp Gln Ile
 Gly Ala 145 150 155

160
 gtt gac tac atc gaa tgt tct gcc aag acc ggt tac ggt gtc
 aga gaa 528
 Val Asp Tyr Ile Glu Cys Ser Ala Lys Thr Gly Tyr Gly Val
 Arg Glu 165 170

175
 gtc ttc gag gct gct aca aga gct tct ttg gtc ggt aaa caa
 ggt aag 576
 Val Phe Glu Ala Ala Thr Arg Ala Ser Leu Val Gly Lys Gln
 Gly Lys 180 185 190

agc aaa cct aag act aag tct agc aaa aaa aag aag tgt gtc
 Seite 821

0070110

gtc ttg 624
Ser Lys Pro Lys Thr Lys Ser Ser Lys Lys Lys Lys Cys Val
Val Leu
195 200 205
taa
627

<210> 543
<211> 208
<212> PRT
<213> Kluyveromyces lactis

<400> 543
Met Ser Gln Ala Val Gly Asn Val Ala Ser Ile Arg Arg Lys
Leu Val
1 5 10
15
Ile Val Gly Asp Gly Ala Cys Gly Lys Thr Cys Leu Leu Ile
Val Phe
20 25 30

Ala Lys Gly Lys Phe Pro Gln Val Tyr Val Pro Thr Val Phe
Asp Asn
35 40 45

Tyr Val Ala Asp Val Glu Val Asp Gly Arg Arg Val Glu Leu
Ala Leu
50 55 60

Trp Asp Thr Ala Gly Gln Glu Asp Tyr Asp Arg Leu Arg Pro
Leu Ser
65 70 75

80
Tyr Pro Asp Ser Asn Val Val Leu Ile Cys Tyr Ser Ile Asp
Leu Pro
85 90

95
Asp Ser Leu Glu Asn Val Met Glu Lys Trp Ile Ser Glu Val
Leu His
100 105 110

Phe Cys Gln Gly Val Pro Ile Ile Leu Val Gly Cys Lys Ala
Asp Leu
115 120 125

Arg Asn Asp Pro Gln Val Val Glu Glu Leu Arg Ala Gln Gly
Seite 822

Leu	Gln												
	130					135					140		
Pro	Val	Ser	Gln	Ala	Gln	Ala	Gln	Glu	Val	Ala	Asp	Gln	Ile
Gly	Ala												
145					150					155			
	160												
Val	Asp	Tyr	Ile	Glu	Cys	Ser	Ala	Lys	Thr	Gly	Tyr	Gly	Val
Arg	Glu												
				165					170				
175													
Val	Phe	Glu	Ala	Ala	Thr	Arg	Ala	Ser	Leu	Val	Gly	Lys	Gln
Gly	Lys												
			180					185					190
Ser	Lys	Pro	Lys	Thr	Lys	Ser	Ser	Lys	Lys	Lys	Lys	Cys	Val
Val	Leu												
		195					200					205	

<220>
<221> CDS
<222> (1)..(594)

[illegible]

0070110

Val	Asn	Gly	Ser	Thr	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala
Gly	Gln												
	50					55					60		
gag	gat	tat	aac	aga	tta	aga	cct	ttg	agt	tat	cgt	ggt	gcc
gat	ggt		240										
Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala
Asp	Val												
65					70					75			
80													
ttc	att	ctg	gct	ttc	tcc	ctc	att	agc	aag	gcc	agt	tat	gaa
aat	ggt		288										
Phe	Ile	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Lys	Ala	Ser	Tyr	Glu
Asn	Val												
				85						90			
95													
tcc	aaa	aag	tgg	att	cca	gag	tta	aag	cat	tat	gca	cct	ggt
ggt	ccc		336										
Ser	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Lys	His	Tyr	Ala	Pro	Gly
Val	Pro												
				100				105					110
att	ata	ctg	ggt	ggc	act	aag	ctt	gat	ctt	cgg	gat	gac	aag
cag	ttc		384										
Ile	Ile	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys
Gln	Phe												
		115					120				125		
ttt	ggt	gac	cat	cct	ggt	gct	gtg	ccc	att	acc	act	gct	cag
gga	gaa		432										
Phe	Val	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Thr	Thr	Ala	Gln
Gly	Glu												
		130				135					140		
gag	ctt	agg	aag	ctg	atc	aat	gca	cct	gct	tat	att	gaa	tgc
agt	tcg		480										
Glu	Leu	Arg	Lys	Leu	Ile	Asn	Ala	Pro	Ala	Tyr	Ile	Glu	Cys
Ser	Ser												
145					150					155			
160													
aaa	tca	cag	cag	aat	gtg	aaa	gca	gtg	ttt	gat	gca	gcc	ata
aga	ggt		528										
Lys	Ser	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile
Arg	Val												
				165						170			
175													
gtc	ctt	caa	cca	cct	aag	caa	aag	aaa	aag	aag	agt	aaa	gca
caa	aag		576										
Val	Leu	Gln	Pro	Pro	Lys	Gln	Lys	Lys	Lys	Lys	Ser	Lys	Ala
Gln	Lys												
				180						185			190

0070110

gcc tgt tcg ata ttg tga
594
Ala Cys Ser Ile Leu
195

<210> 545
<211> 197
<212> PRT
<213> Pisum sativum

<400> 545
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10
15
Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro 20 25 30
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val 35 40 45
Val Asn Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln 50 55 60
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val 65 70 75
80
Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val 85 90
95
Ser Lys Lys Trp Ile Pro Glu Leu Lys His Tyr Ala Pro Gly
Val Pro 100 105 110
Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe 115 120 125
Phe Val Asp His Pro Gly Ala Val Pro Ile Thr Thr Ala Gln
Gly Glu 130 135 140

0070110

Glu Leu Arg Lys Leu Ile Asn Ala Pro Ala Tyr Ile Glu Cys
 Ser Ser
 145 150 155
 160
 Lys Ser Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
 Arg Val
 165 170
 175
 Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Ser Lys Ala
 Gln Lys
 180 185 190
 Ala Cys Ser Ile Leu
 195

<210> 546
 <211> 609
 <212> DNA
 <213> Schizosaccharomyces pombe

<220>
 <221> CDS
 <222> (1)..(609)

<400> 546
 atg gcg aca gaa ctt cgc aga aag ctc gtt att gtg gga gat
 ggt gca 48
 Met Ala Thr Glu Leu Arg Arg Lys Leu Val Ile Val Gly Asp
 Gly Ala
 1 5 10
 15
 tgt ggt aaa aca tgc tta tta att gta ttt tct aaa gga acc
 ttt ccc 96
 Cys Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Gly Thr
 Phe Pro
 20 25 30
 gag gtc tat gtt ccc act gtt ttt gaa aat tat gta gct gat
 gtt gag 144
 Glu Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp
 Val Glu
 35 40 45
 gtt gat gga cgc cac gtt gag ttg gct ctt tgg gat acg gct
 gga caa 192
 Val Asp Gly Arg His Val Glu Leu Ala Leu Trp Asp Thr Ala
 Gly Gln
 50 55 60
 gaa gat tac gac cgt cta cgt ccc ttg tca tat cct gac tca
 cat gtt 240

0070110

Glu	Asp	Tyr	Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Pro	Asp	Ser
His	Val												
65					70					75			
80													
atc	ctt	att	tgc	ttt	gct	ggt	gat	tct	ccc	gat	tct	ctt	gac
aat	ggt			288									
Ile	Leu	Ile	Cys	Phe	Ala	Val	Asp	Ser	Pro	Asp	Ser	Leu	Asp
Asn	Val												
				85					90				
95													
caa	gaa	aaa	tgg	att	tcc	gag	ggt	ctc	cat	ttc	tgt	tcc	agt
ctt	cct		336										
Gln	Glu	Lys	Trp	Ile	Ser	Glu	Val	Leu	His	Phe	Cys	Ser	Ser
Leu	Pro												
			100					105					110
att	ttg	ctt	gtc	gct	tgc	aag	gct	gat	ctc	cgt	aac	gac	cca
aaa	att		384										
Ile	Leu	Leu	Val	Ala	Cys	Lys	Ala	Asp	Leu	Arg	Asn	Asp	Pro
Lys	Ile												
		115						120				125	
att	gag	gag	tta	tcc	aag	act	aat	cag	cat	ccc	gtc	acc	aca
gaa	gaa		432										
Ile	Glu	Glu	Leu	Ser	Lys	Thr	Asn	Gln	His	Pro	Val	Thr	Thr
Glu	Glu												
		130					135				140		
ggt	caa	gca	gta	gct	cag	aag	att	ggt	gct	tac	aaa	tac	ctt
gag	tgt		480										
Gly	Gln	Ala	Val	Ala	Gln	Lys	Ile	Gly	Ala	Tyr	Lys	Tyr	Leu
Glu	Cys												
145					150					155			
160													
tct	gcc	aag	acg	aat	gaa	ggt	ggt	cgt	gag	ggt	ttt	gaa	tca
gcc	act		528										
Ser	Ala	Lys	Thr	Asn	Glu	Gly	Val	Arg	Glu	Val	Phe	Glu	Ser
Ala	Thr												
				165						170			
175													
cgt	gct	gct	atg	ctc	aaa	cac	aag	ccc	aaa	gtg	aag	ccc	tct
agt	gga		576										
Arg	Ala	Ala	Met	Leu	Lys	His	Lys	Pro	Lys	Val	Lys	Pro	Ser
Ser	Gly												
			180					185					190
act	aag	aag	aag	aag	cgt	tgt	atc	ttg	ttg	taa			
			609										
Thr	Lys	Lys	Lys	Lys	Arg	Cys	Ile	Leu	Leu				
		195					200						

0070110

<210> 547
<211> 202
<212> PRT
<213> Schizosaccharomyces pombe

<400> 547
Met Ala Thr Glu Leu Arg Arg Lys Leu Val Ile Val Gly Asp
Gly Ala
1 5 10
15
Cys Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Gly Thr
Phe Pro
20 25 30
Glu Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp
Val Glu
35 40 45
Val Asp Gly Arg His Val Glu Leu Ala Leu Trp Asp Thr Ala
Gly Gln
50 55 60
Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Ser
His Val
65 70 75
80
Ile Leu Ile Cys Phe Ala Val Asp Ser Pro Asp Ser Leu Asp
Asn Val
85 90
95
Gln Glu Lys Trp Ile Ser Glu Val Leu His Phe Cys Ser Ser
Leu Pro
100 105 110
Ile Leu Leu Val Ala Cys Lys Ala Asp Leu Arg Asn Asp Pro
Lys Ile
115 120 125
Ile Glu Glu Leu Ser Lys Thr Asn Gln His Pro Val Thr Thr
Glu Glu
130 135 140
Gly Gln Ala Val Ala Gln Lys Ile Gly Ala Tyr Lys Tyr Leu
Glu Cys
145 150 155
160
Ser Ala Lys Thr Asn Glu Gly Val Arg Glu Val Phe Glu Ser
Seite 828

0070110

Ala Thr
 165 170
 175
 Arg Ala Ala Met Leu Lys His Lys Pro Lys Val Lys Pro Ser
 Ser Gly
 180 185 190
 Thr Lys Lys Lys Lys Arg Cys Ile Leu Leu
 195 200

<210> 548
 <211> 630
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(630)

<400> 548
 atg tca caa caa gtt ggt aac agt atc aga aga aag ctg gta
 atc gtt 48
 Met Ser Gln Gln Val Gly Asn Ser Ile Arg Arg Lys Leu Val
 Ile Val
 1 5 10
 15
 ggt gat ggt gcc tgt ggt aag aca tgt tta tta atc gtc ttt
 tcc aag 96
 Gly Asp Gly Ala Cys Gly Lys Thr Cys Leu Leu Ile Val Phe
 Ser Lys
 20 25 30
 ggc caa ttt cca gaa gtc tac gta cca act gtc ttt gaa aac
 tat gta 144
 Gly Gln Phe Pro Glu Val Tyr Val Pro Thr Val Phe Glu Asn
 Tyr Val
 35 40 45
 gca gat gtt gaa gtt gat ggg cgt cgt gta gag cta gcg cta
 tgg gat 192
 Ala Asp Val Glu Val Asp Gly Arg Arg Val Glu Leu Ala Leu
 Trp Asp
 50 55 60
 acc gct ggt caa gaa gat tat gat aga cta aga cca ttg tca
 tac cca 240
 Thr Ala Gly Gln Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser
 Tyr Pro
 65 70 75
 80
 gac tcc aat gtc gta tta att tgt ttc tct atc gat ctt cca

0070110

gat tct	288													
Asp Ser	Val	Val	Leu	Ile	Cys	Phe	Ser	Ile	Asp	Leu	Pro			
Asp Ser														
	85						90							
95														
tta gag	aat	gta	caa	gaa	aaa	tgg	att	gcc	gaa	gta	tta	cat		
ttc tgt		336												
Leu Glu	Asn	Val	Gln	Glu	Lys	Trp	Ile	Ala	Glu	Val	Leu	His		
Phe Cys														
	100						105					110		
caa ggt	gtg	cca	att	att	ctt	gtt	ggt	tgt	aaa	gtg	gat	ttg		
aga aac		384												
Gln Gly	Val	Pro	Ile	Ile	Leu	Val	Gly	Cys	Lys	Val	Asp	Leu		
Arg Asn														
	115						120					125		
gac cca	caa	acc	att	gaa	caa	tta	aga	caa	gaa	ggt	caa	caa		
ccc gtt		432												
Asp Pro	Gln	Thr	Ile	Glu	Gln	Leu	Arg	Gln	Glu	Gly	Gln	Gln		
Pro Val														
	130						135					140		
aca tca	cag	gag	gga	caa	tct	gta	gca	gac	cag	att	ggc	gca		
acc gga		480												
Thr Ser	Gln	Glu	Gly	Gln	Ser	Val	Ala	Asp	Gln	Ile	Gly	Ala		
Thr Gly														
145														
	150													
160														
tac tac	gaa	tgt	tcg	gcc	aag	act	ggt	tat	ggt	gtc	aga	gaa		
gtg ttt		528												
Tyr Tyr	Glu	Cys	Ser	Ala	Lys	Thr	Gly	Tyr	Gly	Val	Arg	Glu		
Val Phe														
	165													
175														
gag gcc	gcc	act	aga	gct	tca	ttg	atg	ggt	aaa	tct	aaa	acg		
aat ggt		576												
Glu Ala	Ala	Thr	Arg	Ala	Ser	Leu	Met	Gly	Lys	Ser	Lys	Thr		
Asn Gly														
	180													
aaa gct	aag	aag	aac	act	act	gaa	aag	aag	aag	aag	aag	tgt		
gtc ttg		624												
Lys Ala	Lys	Lys	Asn	Thr	Thr	Glu	Lys	Lys	Lys	Lys	Lys	Cys		
Val Leu														
	195													
tta tag														
Leu	630													

0070110

<210> 549
<211> 209
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 549
Met Ser Gln Gln Val Gly Asn Ser Ile Arg Arg Lys Leu Val
Ile Val
1 5 10
15
Gly Asp Gly Ala Cys Gly Lys Thr Cys Leu Leu Ile Val Phe
Ser Lys
20 25 30
Gly Gln Phe Pro Glu Val Tyr Val Pro Thr Val Phe Glu Asn
Tyr Val
35 40 45
Ala Asp Val Glu Val Asp Gly Arg Arg Val Glu Leu Ala Leu
Trp Asp
50 55 60
Thr Ala Gly Gln Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser
Tyr Pro
65 70 75
80
Asp Ser Asn Val Val Leu Ile Cys Phe Ser Ile Asp Leu Pro
Asp Ser
85 90
95
Leu Glu Asn Val Gln Glu Lys Trp Ile Ala Glu Val Leu His
Phe Cys
100 105 110
Gln Gly Val Pro Ile Ile Leu Val Gly Cys Lys Val Asp Leu
Arg Asn
115 120 125
Asp Pro Gln Thr Ile Glu Gln Leu Arg Gln Glu Gly Gln Gln
Pro Val
130 135 140
Thr Ser Gln Glu Gly Gln Ser Val Ala Asp Gln Ile Gly Ala
Thr Gly
145 150 155
160
Tyr Tyr Glu Cys Ser Ala Lys Thr Gly Tyr Gly Val Arg Glu
Seite 831

0070110

Val Phe
165 170
175
Glu Ala Ala Thr Arg Ala Ser Leu Met Gly Lys Ser Lys Thr
Asn Gly
180 185 190
Lys Ala Lys Lys Asn Thr Thr Glu Lys Lys Lys Lys Lys Cys
Val Leu
195 200 205

Leu

<210> 550
<211> 603
<212> DNA
<213> Schizosaccharomyces pombe

<220>
<221> CDS
<222> (1)..(603)

<400> 550
atg ttg caa tct caa ccg att aga agg aaa cta gta gtt gta
ggc gat 48
Met Leu Gln Ser Gln Pro Ile Arg Arg Lys Leu Val Val Val
Gly Asp
1 5 10
15
ggt gcc tgc ggg aag acg tct ttg tta tcc gtt ttc act ttg
gga tat 96
Gly Ala Cys Gly Lys Thr Ser Leu Leu Ser Val Phe Thr Leu
Gly Tyr
20 25 30
ttt cct act gaa tat gtt ccg act gtg ttt gaa aac tat gtt
tca gat 144
Phe Pro Thr Glu Tyr Val Pro Thr Val Phe Glu Asn Tyr Val
Ser Asp
35 40 45
tgt cga gtt gat gga aaa tca gtt caa ctg gca ttg tgg gat
acc gca 192
Cys Arg Val Asp Gly Lys Ser Val Gln Leu Ala Leu Trp Asp
Thr Ala
50 55 60
ggt caa gag gaa tat gag aga tta aga cca atg tct tac gct
aaa gca 240
Gly Gln Glu Glu Tyr Glu Arg Leu Arg Pro Met Ser Tyr Ala
Seite 832

0070110

Lys	Ala												
65		70						75					
80													
cac	att	att	ttg	ggt	ggg	ttt	gcg	ata	gac	tct	cct	gat	tca
ctt	gaa		288										
His	Ile	Ile	Leu	Val	Gly	Phe	Ala	Ile	Asp	Ser	Pro	Asp	Ser
Leu	Glu	85						90					
95													
aat	ggt	tct	acg	aag	tgg	att	gag	gaa	att	aat	aca	ctt	tgc
cca	aat		336										
Asn	Val	Ser	Thr	Lys	Trp	Ile	Glu	Glu	Ile	Asn	Thr	Leu	Cys
Pro	Asn	100						105					
		110											
ggt	ccg	ttt	att	tta	gtg	ggc	atg	aaa	gcc	gac	tta	agg	tca
gat	ccc		384										
Val	Pro	Phe	Ile	Leu	Val	Gly	Met	Lys	Ala	Asp	Leu	Arg	Ser
Asp	Pro	115						120					
		125											
ggt	gct	att	gaa	gaa	atg	cga	cgt	cga	aat	caa	aat	ttt	gta
aaa	tca		432										
Val	Ala	Ile	Glu	Glu	Met	Arg	Arg	Arg	Asn	Gln	Asn	Phe	Val
Lys	Ser	130						135					
		140											
caa	cag	gct	gaa	tta	gta	gct	cag	cgg	att	ggt	gcg	aga	aag
tat	atg		480										
Gln	Gln	Ala	Glu	Leu	Val	Ala	Gln	Arg	Ile	Gly	Ala	Arg	Lys
Tyr	Met	145						150					
		155											
160													
gaa	tgt	tct	tca	ttg	act	ggt	gac	ggc	gtg	gac	gat	gta	ttt
gaa	gct		528										
Glu	Cys	Ser	Ser	Leu	Thr	Gly	Asp	Gly	Val	Asp	Asp	Val	Phe
Glu	Ala	165						170					
175													
gct	act	agg	gca	gca	cta	aca	ggt	cgg	gat	tcg	gaa	aat	gac
aag	agt		576										
Ala	Thr	Arg	Ala	Ala	Leu	Thr	Val	Arg	Asp	Ser	Glu	Asn	Asp
Lys	Ser	180						185					
		190											
tct	aca	aaa	tgc	tgc	atc	att	tca	taa					
			603										
Ser	Thr	Lys	Cys	Cys	Ile	Ile	Ser						
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<210> 551

<211> 200

<212> PRT

<213> Schizosaccharomyces pombe

<400> 551

Met Leu Gln Ser Gln Pro Ile Arg Arg Lys Leu Val Val Val
Gly Asp

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Gly Ala Cys Gly Lys Thr Ser Leu Leu Ser Val Phe Thr Leu
Gly Tyr

20 25 30

Phe Pro Thr Glu Tyr Val Pro Thr Val Phe Glu Asn Tyr Val
Ser Asp

35 40 45

Cys Arg Val Asp Gly Lys Ser Val Gln Leu Ala Leu Trp Asp
Thr Ala

50 55 60

Gly Gln Glu Glu Tyr Glu Arg Leu Arg Pro Met Ser Tyr Ala
Lys Ala

65 70 75

80

His Ile Ile Leu Val Gly Phe Ala Ile Asp Ser Pro Asp Ser
Leu Glu

85 90

95

Asn Val Ser Thr Lys Trp Ile Glu Glu Ile Asn Thr Leu Cys
Pro Asn

100 105 110

Val Pro Phe Ile Leu Val Gly Met Lys Ala Asp Leu Arg Ser
Asp Pro

115 120 125

Val Ala Ile Glu Glu Met Arg Arg Arg Asn Gln Asn Phe Val
Lys Ser

130 135 140

Gln Gln Ala Glu Leu Val Ala Gln Arg Ile Gly Ala Arg Lys
Tyr Met

145 150 155

160

Glu Cys Ser Ser Leu Thr Gly Asp Gly Val Asp Asp Val Phe
Glu Ala

0070110

165

170

175

Ala Thr Arg Ala Ala Leu Thr Val Arg Asp Ser Glu Asn Asp
Lys Ser

180

185

190

Ser Thr Lys Cys Cys Ile Ile Ser
195 200

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<212> DNA

<213> *Ashbya gossypii*

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<400> 552

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gag cgc 48

Met Pro Leu Cys Gly Ser Ser Ser Ser Ser Lys His Pro Ile
Glu Arg

1

5

10

15

aag atc gtc atc ctc gga gac ggt gct tgc ggg aag acg tcg
ctg ttg 96

Lys Ile Val Ile Leu Gly Asp Gly Ala Cys Gly Lys Thr Ser
Leu Leu

20

25

30

aac gtg ttc acg cga ggg tac ttt ccg aag gtg tac gag ccc
acg gta 144

Asn Val Phe Thr Arg Gly Tyr Phe Pro Lys Val Tyr Glu Pro
Thr Val

35

40

45

ttc gaa aac tac atc cat gac atc ttc gtg gac aac cag cac
atc acg 192

Phe Glu Asn Tyr Ile His Asp Ile Phe Val Asp Asn Gln His
Ile Thr

50

55

60

ctg agc ctg tgg gac act gct ggg cag gag gag ttt gac cgg
ttg cga 240

Leu Ser Leu Trp Asp Thr Ala Gly Gln Glu Glu Phe Asp Arg
Leu Arg

65

70

75

80

tcg ctg tcg tac tcg gac aca cac acg att atg ctg tgt ttc

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tcg	gtg		288											
Ser	Leu	Ser	Tyr	Ser	Asp	Thr	His	Thr	Ile	Met	Leu	Cys	Phe	
Ser	Val													
			85						90					
95														
gac	tcg	cgg	gac	tcg	ctg	gag	aac	gtc	aag	aac	aag	tgg	gtg	
agc	gaa		336											
Asp	Ser	Arg	Asp	Ser	Leu	Glu	Asn	Val	Lys	Asn	Lys	Trp	Val	
Ser	Glu													
			100						105				110	
att	gcg	gac	cac	tgc	gag	ggc	gtg	aag	ctg	gtg	cta	gtg	gcg	
ctg	aag		384											
Ile	Ala	Asp	His	Cys	Glu	Gly	Val	Lys	Leu	Val	Leu	Val	Ala	
Leu	Lys													
		115						120					125	
tgc	gac	ttg	cgc	agc	agc	gac	gag	tac	ggc	aac	gag	agc	gcc	
atc	acg		432											
Cys	Asp	Leu	Arg	Ser	Ser	Asp	Glu	Tyr	Gly	Asn	Glu	Ser	Ala	
Ile	Thr													
		130						135					140	
ccg	ggg	tcc	atc	cag	aac	cag	aag	tac	aac	ggc	ggc	ggc	ggc	
aac	ggg		480											
Pro	Gly	Ser	Ile	Gln	Asn	Gln	Lys	Tyr	Asn	Gly	Gly	Gly	Gly	
Asn	Gly													
145					150					155				
160														
ctg	atc	ccc	tac	gac	gag	ggg	ctg	gcg	atg	gcc	aag	cag	att	
ggg	gcg		528											
Leu	Ile	Pro	Tyr	Asp	Glu	Gly	Leu	Ala	Met	Ala	Lys	Gln	Ile	
Gly	Ala													
			165							170				
175														
ctg	cgc	tat	ctg	gag	tgc	agc	gcc	aag	atg	aac	cgt	ggc	gtg	
aac	gag		576											
Leu	Arg	Tyr	Leu	Glu	Cys	Ser	Ala	Lys	Met	Asn	Arg	Gly	Val	
Asn	Glu													
			180						185				190	
gcg	ttc	acc	gag	gct	gcg	cgc	tgc	gcg	ctg	act	gcg	aca	ccg	
aag	ggg		624											
Ala	Phe	Thr	Glu	Ala	Ala	Arg	Cys	Ala	Leu	Thr	Ala	Thr	Pro	
Lys	Gly													
		195						200					205	
gcc	cgg	gac	tct	gcg	ccc	gag	gcc	gaa	agc	agc	agt	tgt	act	
atc	atg		672											
Ala	Arg	Asp	Ser	Ala	Pro	Glu	Ala	Glu	Ser	Ser	Ser	Cys	Thr	
Ile	Met													

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 tga 675

 <210> 553
 <211> 224
 <212> PRT
 <213> Ashbya gossypii

 <400> 553
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 Glu Arg
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 Lys Ile Val Ile Leu Gly Asp Gly Ala Cys Gly Lys Thr Ser
 Leu Leu
 20 25 30

 Asn Val Phe Thr Arg Gly Tyr Phe Pro Lys Val Tyr Glu Pro
 Thr Val
 35 40 45

 Phe Glu Asn Tyr Ile His Asp Ile Phe Val Asp Asn Gln His
 Ile Thr
 50 55 60

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

 Ile Ala Asp His Cys Glu Gly Val Lys Leu Val Leu Val Ala
 Leu Lys
 115 120 125

 Cys Asp Leu Arg Ser Ser Asp Glu Tyr Gly Asn Glu Ser Ala
 Ile Thr
 130 135 140

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Pro	Gly	Ser	Ile	Gln	Asn	Gln	Lys	Tyr	Asn	Gly	Gly	Gly	Gly
Asn	Gly												
145					150					155			
160													
Leu	Ile	Pro	Tyr	Asp	Glu	Gly	Leu	Ala	Met	Ala	Lys	Gln	Ile
Gly	Ala												
				165					170				
175													
Leu	Arg	Tyr	Leu	Glu	Cys	Ser	Ala	Lys	Met	Asn	Arg	Gly	Val
Asn	Glu												
			180					185					190
Ala	Phe	Thr	Glu	Ala	Ala	Arg	Cys	Ala	Leu	Thr	Ala	Thr	Pro
Lys	Gly												
		195					200					205	
Ala	Arg	Asp	Ser	Ala	Pro	Glu	Ala	Glu	Ser	Ser	Ser	Cys	Thr
Ile	Met												
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ccg	atc			48									
Met	Ala	Leu	Cys	Gly	Ser	Ser	Lys	Gly	Arg	Gly	Arg	Gly	Arg
Pro	Ile												
1				5					10				
15													
cag	cgc	aag	gtc	gtc	gta	tgc	ggc	gac	ggc	gcg	tgc	ggg	aag
acg	agt			96									
Gln	Arg	Lys	Val	Val	Val	Cys	Gly	Asp	Gly	Ala	Cys	Gly	Lys
Thr	Ser												
			20					25					30
ctg	ctg	aac	gtc	ttc	acg	agg	ggg	ttc	ttc	acg	cag	gtt	tat
gaa	ccg		144										
Leu	Leu	Asn	Val	Phe	Thr	Arg	Gly	Phe	Phe	Thr	Gln	Val	Tyr
Glu	Pro												
		35					40					45	
acg	gtg	ttc	gag	aac	tac	gtg	cac	gat	ctg	tat	atc	gac	gac

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

0070110

180

185

190

cac tcg atc agg cag ggg agc gcc ggg tcg tgt tgt gtc atg
tag
His Ser Ile Arg Gln Gly Ser Ala Gly Ser Cys Cys Val Met

195

200

205

<210> 555

<211> 206

<212> PRT

<213> Schizophyllum commune

<400> 555

Met Ala Leu Cys Gly Ser Ser Lys Gly Arg Gly Arg Gly Arg
Pro Ile

1 5 10

15

Gln Arg Lys Val Val Val Cys Gly Asp Gly Ala Cys Gly Lys
Thr Ser

20

25

30

Leu Leu Asn Val Phe Thr Arg Gly Phe Phe Thr Gln Val Tyr
Glu Pro

35

40

45

Thr Val Phe Glu Asn Tyr Val His Asp Leu Tyr Ile Asp Asp
Gln Leu

50

55

60

Val Glu Leu Ser Leu Trp Asp Thr Ala Gly Gln Glu Glu Phe
Asp Arg

65

70

75

80

Leu Arg Ser Leu Ser Tyr Ala Glu Thr His Val Ile Met Ile
Cys Phe

85

90

95

Ser Val Asp Asn Pro Thr Ser Leu Glu Asn Val Glu Ser Lys
Trp Leu

100

105

110

Asp Glu Ile Leu Glu Tyr Cys Pro Gly Val Lys Leu Val Leu
Val Asp

115

120

125

Ser Lys Cys Asp Leu Arg Asp Asp Pro Ala Val Leu Asp Arg

Seite 840

0070110

Leu	Gln												
	130					135					140		
Arg	Tyr	Gly	Thr	His	Thr	Asp	Gln	Tyr	Glu	Glu	Gly	Leu	Gly
Val	Ala												
	145				150					155			
	160												
Arg	Arg	Ile	Arg	Ala	Ser	Arg	Tyr	Leu	Glu	Cys	Ser	Ser	Lys
His	Asn												
				165					170				
	175												
Arg	Gly	Val	Asn	Glu	Val	Phe	Leu	Arg	Gly	Arg	Ala	Arg	Val
Thr	Val												
			180					185					190
His	Ser	Ile	Arg	Gln	Gly	Ser	Ala	Gly	Ser	Cys	Cys	Val	Met
		195					200					205	

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<212> DNA
<213> Schizosaccharomyces pombe
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<222> (1) .. (618)

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

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Gly Ala Asp⁶¹⁸ Glu Ser His Gly Thr Gly Cys Ile Ile Ala
 195 200 205

<210> 557

<211> 205

<212> PRT

<213> Schizosaccharomyces pombe

<400> 557

Met Ser Ser Cys Phe Gly Ser Lys Lys Lys Pro Ile Tyr Arg
 Lys Ile

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Val Ile Leu Gly Asp Gly Ala Ala Gly Lys Thr Ser Leu Leu
 Asn Val

20 25 30

Phe Thr Lys Gly Tyr Phe Pro Gln Val Tyr Glu Pro Thr Ile
 Phe Glu

35 40 45

Asn Tyr Ile His Asp Ile Phe Val Asp Gly Asn Ser Ile Glu
 Leu Ser
 50 55 60

Leu Trp Asp Thr Ala Gly Gln Glu Glu Tyr Asp Gln Leu Arg
 Ser Leu

65 70 75

80

Ser Tyr Ser Asp Thr His Val Ile Met Ile Cys Phe Ala Val
 Asp Ser

85 90

95

Arg Asp Ser Leu Glu Asn Val Ile Thr Lys Trp Leu Pro Glu
 Val Ser

100 105 110

Ser Asn Cys Pro Gly Val Lys Leu Val Leu Val Ala Leu Lys
 Cys Asp

115 120 125

Leu Arg Gly Ala Asp Glu Glu Gln Val Asp His Ser Lys Ile
 Ile Asp

130 135 140

Tyr Glu Glu Gly Leu Ala Ala Ala Lys Lys Ile Asn Ala Val
 Arg Tyr

0070110

145		150		155									
160													
Leu	Glu	Cys	Ser	Ala	Lys	Leu	Asn	Arg	Gly	Val	Asn	Glu	Ala
Phe	Thr												
		165		170									
175													
Glu	Ala	Ala	Arg	Val	Ala	Leu	Ala	Ala	Gln	Pro	Arg	Gly	Thr
Lys	Asp												
		180		185								190	
Gly	Ala	Asp	Glu	Ser	His	Gly	Thr	Gly	Cys	Ile	Ile	Ala	
		195					200					205	

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 <213> Saccharomyces cerevisiae

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atc gaa 48
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Ile Glu
1 5 10
15
aga aag atc gtt att ttg ggc gac ggt gcc tgt ggt aaa act
tcg ttg 96
Arg Lys Ile Val Ile Leu Gly Asp Gly Ala Cys Gly Lys Thr
Ser Leu
20 25 30
ctg aat gtt ttc acc aga ggt tat ttt ccc gaa gtt tat gag
cct act 144
Leu Asn Val Phe Thr Arg Gly Tyr Phe Pro Glu Val Tyr Glu
Pro Thr
35 40 45
gtt ttt gaa aac tat atc cat gat att ttc gtt gac agt aaa
cat atc 192
Val Phe Glu Asn Tyr Ile His Asp Ile Phe Val Asp Ser Lys
His Ile
50 55 60
acg cta tcg ttg tgg gat act gcg ggc caa gag gaa ttt gac
agg tta 240
Thr Leu Ser Leu Trp Asp Thr Ala Gly Gln Glu Glu Phe Asp
Arg Leu

0070110

65					70					75			
80													
cga	tcc	ttg	tct	tat	tca	gat	acg	caa	tgt	ata	atg	tta	tgt
ttc	agt		288										
Arg	Ser	Leu	Ser	Tyr	Ser	Asp	Thr	Gln	Cys	Ile	Met	Leu	Cys
Phe	Ser												
			85						90				
95													
att	gat	tca	cgc	gat	tct	tta	gaa	aat	gtc	caa	aat	aaa	tgg
gtg	ggt		336										
Ile	Asp	Ser	Arg	Asp	Ser	Leu	Glu	Asn	Val	Gln	Asn	Lys	Trp
Val	Gly												
			100						105				110
gaa	atc	act	gat	cat	tgt	gaa	ggc	gtc	aag	tta	gtc	tta	gtt
gca	cta		384										
Glu	Ile	Thr	Asp	His	Cys	Glu	Gly	Val	Lys	Leu	Val	Leu	Val
Ala	Leu												
		115						120				125	
aag	tgt	gac	tta	aga	aac	aat	gaa	aat	gaa	tct	aac	gca	atc
aca	ccg		432										
Lys	Cys	Asp	Leu	Arg	Asn	Asn	Glu	Asn	Glu	Ser	Asn	Ala	Ile
Thr	Pro												
		130				135					140		
aac	aat	atc	caa	cag	gat	aac	agc	gtt	tct	aac	gac	aac	gga
aat	aac		480										
Asn	Asn	Ile	Gln	Gln	Asp	Asn	Ser	Val	Ser	Asn	Asp	Asn	Gly
Asn	Asn												
145					150					155			
160													
ata	aat	agc	acc	tca	aac	ggc	aaa	aac	ctg	ata	agt	tat	gaa
gaa	ggt		528										
Ile	Asn	Ser	Thr	Ser	Asn	Gly	Lys	Asn	Leu	Ile	Ser	Tyr	Glu
Glu	Gly												
			165						170				
175													
cta	gct	atg	gct	aaa	aag	atc	ggt	gcg	cta	cgt	tat	ttg	gaa
tgt	agc		576										
Leu	Ala	Met	Ala	Lys	Lys	Ile	Gly	Ala	Leu	Arg	Tyr	Leu	Glu
Cys	Ser												
			180						185				190
gct	aag	ctg	aat	aaa	ggt	gtc	aac	gaa	gct	ttc	aca	gaa	gcc
gca	aga		624										
Ala	Lys	Leu	Asn	Lys	Gly	Val	Asn	Glu	Ala	Phe	Thr	Glu	Ala
Ala	Arg												
		195				200						205	
ggt	gct	tta	acc	gcg	ggc	cca	gta	gca	acc	gaa	gtg	aaa	agt

0070110

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Val Ala Leu Thr Ala Gly Pro Val Ala Thr Glu Val Lys Ser
Asp Ser 210 215 220
gga tcc agc tgt acc att atg taa
Gly Ser Ser Cys Thr Ile Met
225 230

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<212> PRT
<213> Saccharomyces cerevisiae

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

<210> 560
 <211> 780
 <212> DNA
 <213> Ashbya gossypii

<220>
 <221> CDS
 <222> (1)..(780)

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gga	gca		48											
Met	Ser	Ala	Gly	Pro	Leu	Gln	Ala	Ala	Pro	Lys	Lys	Asn	Tyr	
Gly	Ala													
1				5					10					
15														
ctg	ata	ggc	gcg	ggg	ccg	gcg	gtg	ggc	ggg	gcg	gca	ttc	aac	
cgg	acg		96											
Leu	Ile	Gly	Ala	Gly	Pro	Ala	Val	Gly	Gly	Ala	Ala	Phe	Asn	
Arg	Thr													
			20					25					30	

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ctg	agc	gag	gtt	gcg	agc	tac	gag	cgc	agc	cgg	cgc	gac	cac
gcg	acg		144										
Leu	Ser	Glu	Val	Ala	Ser	Tyr	Glu	Arg	Ser	Arg	Arg	Asp	His
Ala	Thr												
		35				40						45	
ccg	gac	tac	cgg	atc	aag	atc	gtg	gtg	gtg	ggg	gac	ggc	gcg
acg	ggg		192										
Pro	Asp	Tyr	Arg	Ile	Lys	Ile	Val	Val	Val	Gly	Asp	Gly	Ala
Thr	Gly												
	50					55					60		
aag	acg	tct	ctg	ctg	atg	tcg	tac	aca	cag	ggc	cag	ttc	cca
gag	gac		240										
Lys	Thr	Ser	Leu	Leu	Met	Ser	Tyr	Thr	Gln	Gly	Gln	Phe	Pro
Glu	Asp												
65					70					75			
80													
tac	gtg	ccg	acc	atc	ttc	gag	aac	tac	gtg	acg	aac	att	gag
ggc	cca		288										
Tyr	Val	Pro	Thr	Ile	Phe	Glu	Asn	Tyr	Val	Thr	Asn	Ile	Glu
Gly	Pro												
			85						90				
95													
cgc	ggg	aag	gtg	atc	gag	ctg	gcg	ctg	tgg	gac	act	gct	ggg
cag	gag		336										
Arg	Gly	Lys	Val	Ile	Glu	Leu	Ala	Leu	Trp	Asp	Thr	Ala	Gly
Gln	Glu												
			100					105				110	
gag	tac	agc	cgg	ctg	cgg	ccg	ctg	tct	tac	ggg	gac	gtg	gac
atc	gtg		384										
Glu	Tyr	Ser	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Gly	Asp	Val	Asp
Ile	Val												
		115				120					125		
atg	gtg	tgc	tac	gcg	gca	gac	aac	cgc	acg	tcg	ctg	acg	aac
gcg	gaa		432										
Met	Val	Cys	Tyr	Ala	Ala	Asp	Asn	Arg	Thr	Ser	Leu	Thr	Asn
Ala	Glu												
	130					135					140		
gag	ctg	tgg	ttc	ccg	gag	gtg	cgc	cac	ttc	tgc	ccg	cac	gcg
ccg	atg		480										
Glu	Leu	Trp	Phe	Pro	Glu	Val	Arg	His	Phe	Cys	Pro	His	Ala
Pro	Met												
145					150					155			
160													
atg	ctg	gtg	ggg	ctc	aag	agc	gac	ctg	tac	tcg	ctt	gat	gcg
ctg	gac		528										
Met	Leu	Val	Gly	Leu	Lys	Ser	Asp	Leu	Tyr	Ser	Leu	Asp	Ala
Leu	Asp												

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175
cgg ctc gtg gac ccg acg gac gcg gaa ctg gtg gcg cgc aag
atg ggc
Arg Leu Val Asp Pro Thr Asp Ala Glu Leu Val Ala Arg Lys
Met Gly
180
gcc ttc gtg cac ctg cag tgc tcg gcc aag acg cga cag tgc
ctg gag
Ala Phe Val His Leu Gln Cys Ser Ala Lys Thr Arg Gln Cys
Leu Glu
195
gac gtg ttc aac acg gcg ata cac acg gcg ctg tac gac gag
ctg cgc
Asp Val Phe Asn Thr Ala Ile His Thr Ala Leu Tyr Asp Glu
Leu Arg
210
gcg ccc ccg cag cgc ggg gtg aag ggc atg ttc aag aag aag
cag cag
Ala Pro Pro Gln Arg Gly Val Lys Gly Met Phe Lys Lys Lys
Gln Gln
225
230
235
240
cgg gac ccg cag gcg cag tct tac aag cgg gtg cgc aag cac
cgc tgt
Arg Asp Pro Gln Ala Gln Ser Tyr Lys Arg Val Arg Lys His
Arg Cys
245
250
255
gtg gtc cta tag
val val Leu
780

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<210> 561
 <211> 259
 <212> PRT
 <213> Ashbya gossypii

<400> 561
 Met Ser Ala Gly Pro Leu Gln Ala Ala Pro Lys Lys Asn Tyr
 Gly Ala
 1 5 10
 15
 Leu Ile Gly Ala Gly Pro Ala Val Gly Gly Ala Ala Phe Asn
 Arg Thr
 20 25 30

0070110

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

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Ala Pro Pro Gln Arg Gly Val Lys Gly Met Phe Lys Lys Lys
Gln Gln
225 230 235
240
Arg Asp Pro Gln Ala Gln Ser Tyr Lys Arg Val Arg Lys His
Arg Cys
245 250
255
Val Val Leu

<210> 562
<211> 612
<212> DNA
<213> Schizosaccharomyces pombe

<220>
<221> CDS
<222> (1)..(612)

<400> 562
atg tct gct ttc aaa aag agt gga tcc aag tca gag act tca
aag aaa 48
Met Ser Ala Phe Lys Lys Ser Gly Ser Lys Ser Glu Thr Ser
Lys Lys
1 5 10
15
ctt gtg gtc gta gga gat ggc ggt tgt gga aag aca tgt ctt
tta att 96
Leu Val Val Val Gly Asp Gly Gly Cys Gly Lys Thr Cys Leu
Leu Ile
20 25 30
gta ttc tca agc gga act ttt ccc gag aga tat gtg cct aca
gtg ttt 144
Val Phe Ser Ser Gly Thr Phe Pro Glu Arg Tyr Val Pro Thr
Val Phe
35 40 45
gaa aat tat atc acc gat ata aca tat gga ccg aac agc aaa
gtt att 192
Glu Asn Tyr Ile Thr Asp Ile Thr Tyr Gly Pro Asn Ser Lys
Val Ile
50 55 60
gaa ctt gct ttg tgg gat act gct ggt cag gag gaa tat gat
cgt tta 240
Glu Leu Ala Leu Trp Asp Thr Ala Gly Gln Glu Glu Tyr Asp
Arg Leu
65 70 75

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      80
cgt cct cta agt tac ccg aat agc aac gtt att ttg ttg tgt
ttc tca      288
Arg Pro Leu Ser Tyr Pro Asn Ser Asn Val Ile Leu Leu Cys
Phe Ser

      85                      90
95
att gat tgt ccg gct tct ctg aat aac gtt acg gag aag tgg
tat cct      336
Ile Asp Cys Pro Ala Ser Leu Asn Asn Val Thr Glu Lys Trp
Tyr Pro

      100                      105                      110

gaa gtt caa cac ttt tgc cct aga act ccc atc gtt ctc gtc
ggg cta      384
Glu Val Gln His Phe Cys Pro Arg Thr Pro Ile Val Leu Val
Gly Leu

      115                      120                      125
aaa gcg gat tta cgc aaa gat agg aat gct act gaa gta cta
aga acc      432
Lys Ala Asp Leu Arg Lys Asp Arg Asn Ala Thr Glu Val Leu
Arg Thr

      130                      135                      140
cag ggt tta aca cca gta acc tac caa caa gct caa tcc gtt
gct tta      480
Gln Gly Leu Thr Pro Val Thr Tyr Gln Gln Ala Gln Ser Val
Ala Leu

      145                      150                      155
      160
tca atg aac gct cca tat gtc gaa tgc tct gcc aaa gaa aac
act ggt      528
Ser Met Asn Ala Pro Tyr Val Glu Cys Ser Ala Lys Glu Asn
Thr Gly

      165                      170
175
gta aat gaa gtt ttt caa ctt gct gtt ggc ctc act ata aaa
aaa tca      576
Val Asn Glu Val Phe Gln Leu Ala Val Gly Leu Thr Ile Lys
Lys Ser

      180                      185                      190

ttt tcg ttt tct aaa aag tct tgc gtg att tta taa
      612
Phe Ser Phe Ser Lys Lys Ser Cys Val Ile Leu
      195                      200

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<210> 563

0070110

<211> 203

<212> PRT

<213> Schizosaccharomyces pombe

<400> 563

Met Ser Ala Phe Lys Lys Ser Gly Ser Lys Ser Glu Thr Ser
Lys Lys

1 5 10

15

Leu Val Val Val Gly Asp Gly Gly Cys Gly Lys Thr Cys Leu
Leu Ile

20 25 30

Val Phe Ser Ser Gly Thr Phe Pro Glu Arg Tyr Val Pro Thr
Val Phe

35 40 45

Glu Asn Tyr Ile Thr Asp Ile Thr Tyr Gly Pro Asn Ser Lys
Val Ile

50 55 60

Glu Leu Ala Leu Trp Asp Thr Ala Gly Gln Glu Glu Tyr Asp
Arg Leu

65 70 75

80

Arg Pro Leu Ser Tyr Pro Asn Ser Asn Val Ile Leu Leu Cys
Phe Ser

85 90

95

Ile Asp Cys Pro Ala Ser Leu Asn Asn Val Thr Glu Lys Trp
Tyr Pro

100 105 110

Glu Val Gln His Phe Cys Pro Arg Thr Pro Ile Val Leu Val
Gly Leu

115 120 125

Lys Ala Asp Leu Arg Lys Asp Arg Asn Ala Thr Glu Val Leu
Arg Thr

130 135 140

Gln Gly Leu Thr Pro Val Thr Tyr Gln Gln Ala Gln Ser Val
Ala Leu

145 150 155

160

Ser Met Asn Ala Pro Tyr Val Glu Cys Ser Ala Lys Glu Asn
Thr Gly

165 170

0070110

175
Val Asn Glu Val Phe Gln Leu Ala Val Gly Leu Thr Ile Lys
Lys Ser
180 185 190

Phe Ser Phe Ser Lys Lys Ser Cys Val Ile Leu
195 200

<210> 564
<211> 603
<212> DNA
<213> Schizosaccharomyces pombe

<220>
<221> CDS
<222> (1)..(603)

<400> 564
atg act act gag ctc cgt cgt aaa ttg gtt att gtt ggc gat
ggt gct 48
Met Thr Thr Glu Leu Arg Arg Lys Leu Val Ile Val Gly Asp
Gly Ala
1 5 10
15
tgt ggt aaa aca tgc ttg ttg att gtt ttt tcc aaa gga act
ttt cct 96
Cys Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Gly Thr
Phe Pro
20 25 30
gaa gtt tac gtc cct act gtt ttc gaa aat tat gtt gcc gat
gtc gag 144
Glu Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp
Val Glu
35 40 45
gtt gat gga agg cat att gaa ttg gca cta tgg gat aca gct
ggt cag 192
Val Asp Gly Arg His Ile Glu Leu Ala Leu Trp Asp Thr Ala
Gly Gln
50 55 60
gag gat tac gat cgt tta cgc cct ctt tcc tat cca gac tct
cac gtc 240
Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Ser
His Val
65 70 75
80
gtt ttg att tgt ttt tca gtt gat gct cca gag agt ttg gac
aat gtt 288
Val Leu Ile Cys Phe Ser Val Asp Ala Pro Glu Ser Leu Asp
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Asn Val

85

90

95

caa gaa aaa tgg att tct gaa gtt ctt cac ttc tgc tcc aat
tta ccc
Gln Glu Lys Trp Ile Ser Glu Val Leu His Phe Cys Ser Asn
Leu Pro
100 105 110

att ttg cta gtt ggg tgt aaa gtg gat tta cga aac gat cca
aaa aca
Ile Leu Leu Val Gly Cys Lys Val Asp Leu Arg Asn Asp Pro
Lys Thr
115 120 125

atc gaa gag ctc tcc aaa acc tca cag aag cct atc aca ttt
gaa gaa
Ile Glu Glu Leu Ser Lys Thr Ser Gln Lys Pro Ile Thr Phe
Glu Glu
130 135 140

gga cag gta gta gct caa aag att ggc gcc tat aag tat ctc
gaa tgt
Gly Gln Val Val Ala Gln Lys Ile Gly Ala Tyr Lys Tyr Leu
Glu Cys
145 150 155
160

tca gcg aaa ttg aac gaa ggg gtc aat gag gtt ttt gag act
gca gct
Ser Ala Lys Leu Asn Glu Gly Val Asn Glu Val Phe Glu Thr
Ala Ala
165 170

175
cgt gct tcc atg ctt aaa ttt aag cct gct agt gta ccg aag
aca aaa
Arg Ala Ser Met Leu Lys Phe Lys Pro Ala Ser Val Pro Lys
Thr Lys
180 185 190

aag aag aag cac tgt atc tta ctc tga
Lys Lys Lys His Cys Ile Leu Leu
195 200

<210> 565

<211> 200

<212> PRT

<213> Schizosaccharomyces pombe

0070110

<400> 565

Met	Thr	Thr	Glu	Leu	Arg	Arg	Lys	Leu	Val	Ile	Val	Gly	Asp
Gly	Ala												
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15													
Cys	Gly	Lys	Thr	Cys	Leu	Leu	Ile	Val	Phe	Ser	Lys	Gly	Thr
Phe	Pro												
			20					25					30
Glu	Val	Tyr	Val	Pro	Thr	Val	Phe	Glu	Asn	Tyr	Val	Ala	Asp
Val	Glu												
		35					40					45	
Val	Asp	Gly	Arg	His	Ile	Glu	Leu	Ala	Leu	Trp	Asp	Thr	Ala
Gly	Gln												
	50					55					60		
Glu	Asp	Tyr	Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Pro	Asp	Ser
His	Val												
65					70					75			
	80												
Val	Leu	Ile	Cys	Phe	Ser	Val	Asp	Ala	Pro	Glu	Ser	Leu	Asp
Asn	Val												
				85					90				
95													
Gln	Glu	Lys	Trp	Ile	Ser	Glu	Val	Leu	His	Phe	Cys	Ser	Asn
Leu	Pro												
					100			105					110
Ile	Leu	Leu	Val	Gly	Cys	Lys	Val	Asp	Leu	Arg	Asn	Asp	Pro
Lys	Thr												
		115					120					125	
Ile	Glu	Glu	Leu	Ser	Lys	Thr	Ser	Gln	Lys	Pro	Ile	Thr	Phe
Glu	Glu												
	130					135					140		
Gly	Gln	Val	Val	Ala	Gln	Lys	Ile	Gly	Ala	Tyr	Lys	Tyr	Leu
Glu	Cys												
145					150					155			
	160												
Ser	Ala	Lys	Leu	Asn	Glu	Gly	Val	Asn	Glu	Val	Phe	Glu	Thr
Ala	Ala												
				165					170				
175													
Arg	Ala	Ser	Met	Leu	Lys	Phe	Lys	Pro	Ala	Ser	Val	Pro	Lys
Thr	Lys												
			180					185				190	

0070110

Lys Lys Lys His Cys Ile Leu Leu
195 200

<210> 566
<211> 582
<212> DNA
<213> *Emericella nidulans*

<220>
<221> CDS
<222> (1)..(582)

<400> 566
atg gct gag atc cgc cgc aag ctt gtt atc gtt ggt gat ggt
gcc tgc 48
Met Ala Glu Ile Arg Arg Lys Leu Val Ile Val Gly Asp Gly
Ala Cys
1 5 10
15

ggt aag acc tgt ctg ttg atc gtc ttc tca aag ggc act ttc
cct gag 96
Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Gly Thr Phe
Pro Glu

20 25 30
gtc tac gtc ccc acc gtc ttt gag aac tac gtt gcc gat gtt
gag gtt 144
Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Val
Glu Val

35 40 45
gat ggc aag cac gtc gag ctc gct ctc tgg gat acg gct ggt
caa gaa 192
Asp Gly Lys His Val Glu Leu Ala Leu Trp Asp Thr Ala Gly
Gln Glu

50 55 60
gat tac gac cgt ctc cgc cct ctc tcc tac cct gac tcg cat
gtc atc 240
Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Ser His
Val Ile
65 70 75

80
ctg att tgc ttc gct gtc gac tca ccg gat tcc ctt gac aac
gtt caa 288
Leu Ile Cys Phe Ala Val Asp Ser Pro Asp Ser Leu Asp Asn
Val Gln

85 90

95

0070110

gag aag tgg atc tct gaa gtc cta cac ttc tgc cag ggt ctc
 ccc atc 336
 Glu Lys Trp Ile Ser Glu Val Leu His Phe Cys Gln Gly Leu
 Pro Ile
 100 105 110

atc ctc gtc gga tgc aag aag gat ctt cgc cat gac ccc aag
 acg atc 384
 Ile Leu Val Gly Cys Lys Lys Asp Leu Arg His Asp Pro Lys
 Thr Ile
 115 120 125

gag gag ctg aac aag acc tct cag aag cct gtc acc ccc gaa
 cag ggt 432
 Glu Glu Leu Asn Lys Thr Ser Gln Lys Pro Val Thr Pro Glu
 Gln Gly
 130 135 140

gag gaa gtc cgc aag aag att ggc gcc tac aag tac ctc gag
 tgc tct 480
 Glu Glu Val Arg Lys Lys Ile Gly Ala Tyr Lys Tyr Leu Glu
 Cys Ser
 145 150 155
 160

gct cga acc aac gag ggt gtc cgt gag gtc ttt gag gct gcc
 acg cgt 528
 Ala Arg Thr Asn Glu Gly Val Arg Glu Val Phe Glu Ala Ala
 Thr Arg
 165 170

175
 gct gcc ctc ttg acc aag acc cac aag agc aag aag aag tgc
 agc atc 576
 Ala Ala Leu Leu Thr Lys Thr His Lys Ser Lys Lys Lys Cys
 Ser Ile
 180 185 190

ctg taa
 582
 Leu

<210> 567
 <211> 193
 <212> PRT
 <213> Emericella nidulans

<400> 567
 Met Ala Glu Ile Arg Arg Lys Leu Val Ile Val Gly Asp Gly
 Ala Cys
 1 5 10

0070110

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

0070110

<210> 568
<211> 693
<212> DNA
<213> *Emericella nidulans*

<220>
<221> CDS
<222> (1)..(693)

<400> 568
atg tcc agt ggg agg gta tcg gaa gcg aca aat atc acc cag
ccg cca 48
Met Ser Ser Gly Arg Val Ser Glu Ala Thr Asn Ile Thr Gln
Pro Pro 1 5 10
15
gcc tat tcc aag aag ttc gtg gtg gtg gga gac gga ggt tgt
ggg aag 96
Ala Tyr Ser Lys Lys Phe Val Val Val Gly Asp Gly Gly Cys
Gly Lys 20 25 30
acc tgt ctg ttg att agt tat tcg cag ggt tac ttt cca gaa
aaa tat 144
Thr Cys Leu Leu Ile Ser Tyr Ser Gln Gly Tyr Phe Pro Glu
Lys Tyr 35 40 45
gtc ccg acg gta ttt gaa aac tat atc aca caa acg ctt cat
aga agg 192
Val Pro Thr Val Phe Glu Asn Tyr Ile Thr Gln Thr Leu His
Arg Arg 50 55 60
tct ggg aaa act gtg gag ttg gcg ctc tgg gat act gct ggc
cag gag 240
Ser Gly Lys Thr Val Glu Leu Ala Leu Trp Asp Thr Ala Gly
Gln Glu 65 70 75
80
gaa tac gac cga ttg cgc cct ctc tca tat ccc gag acc gac
ctt ctc 288
Glu Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Glu Thr Asp
Leu Leu 85 90
95
ttt gtt tgt ttt gct att gat tgt cct gca tct ctt gag aac
gtt atg 336
Phe Val Cys Phe Ala Ile Asp Cys Pro Ala Ser Leu Glu Asn
Val Met 100 105 110

0070110

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gat aag tgg tat ccc gag gtg ttg cat ttc tgc cct acg acc
cca att          384
Asp Lys Trp Tyr Pro Glu Val Leu His Phe Cys Pro Thr Thr
Pro Ile
      115          120          125
atc ctc gtt ggg ctg aaa tca gac ctg cgc aac aag cga acg
tgt atc          432
Ile Leu Val Gly Leu Lys Ser Asp Leu Arg Asn Lys Arg Thr
Cys Ile
      130          135          140
gag ctc cta aag aca caa ggc ttg acg ccc gtc acg ccg gag
caa ggt          480
Glu Leu Leu Lys Thr Gln Gly Leu Thr Pro Val Thr Pro Glu
Gln Gly
145          150          155
      160
cag gcg gtg gcc ggc cgg atg aat gca tgc tat gta gag tgc
agc agt          528
Gln Ala Val Ala Gly Arg Met Asn Ala Ser Tyr Val Glu Cys
Ser Ser
      165          170
175
aag gag atg cga ggt gtc gac tct gtt ttt caa ctg gca gtg
gac act          576
Lys Glu Met Arg Gly Val Asp Ser Val Phe Gln Leu Ala Val
Asp Thr
      180          185          190
gtc gtg tcc ctc gag gag caa aac tgg gac act cgc cta ccg
tca tcc          624
Val Val Ser Leu Glu Glu Gln Asn Trp Asp Thr Arg Leu Pro
Ser Ser
      195          200          205
tcc gga aaa cct ggt ggc aag ccc atc ggt ggt aag aag atc
aag aag          672
Ser Gly Lys Pro Gly Gly Lys Pro Ile Gly Gly Lys Lys Ile
Lys Lys
      210          215          220
cgc agc tgc aag att ctg tga
          693
Arg Ser Cys Lys Ile Leu
225          230

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<210> 569

<211> 230

<212> PRT

<213> Emericella nidulans

0070110

<400> 569

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

0070110

180

185

190

Val Val Ser Leu Glu Glu Gln Asn Trp Asp Thr Arg Leu Pro
Ser Ser

195

200

205

Ser Gly Lys Pro Gly Gly Lys Pro Ile Gly Gly Lys Lys Ile
Lys Lys
210 215 220

Arg Ser Cys Lys Ile Leu
225 230

<210> 570

<211> 573

<212> DNA

<213> Drosophila melanogaster

<220>

<221> CDS

<222> (1)..(573)

<400> 570

atg acg gcg aac ata acg aag agt ccg cgc ccg ctg aaa ata
acc atc 48

Met Thr Ala Asn Ile Thr Lys Ser Pro Arg Pro Leu Lys Ile
Thr Ile

1

5

10

15

gtg ggc gat ggc atg gtg ggc aaa acc tgc atg ctg ata acc
tac aca 96

Val Gly Asp Gly Met Val Gly Lys Thr Cys Met Leu Ile Thr
Tyr Thr

20

25

30

cgg aac gag ttc ccc gag gag tac ata ccc aca gtg ttc gac
aat cac 144

Arg Asn Glu Phe Pro Glu Glu Tyr Ile Pro Thr Val Phe Asp
Asn His

35

40

45

gcc tgc aac ata gcc gta gat gat cgg gac tac aat ctg acc
ctc tgg 192

Ala Cys Asn Ile Ala Val Asp Asp Arg Asp Tyr Asn Leu Thr
Leu Trp

50

55

60

gac act gcc ggc cag gag gat tac gaa agg ctg cgc ccc ctg
agc tat 240

Asp Thr Ala Gly Gln Glu Asp Tyr Glu Arg Leu Arg Pro Leu
Ser Tyr

0070110

```

65      70      75
  80
ccc agt acc aac tgc ttc ctg ttg tgc tat tcg atc agc agt
agg acc      288
Pro Ser Thr Asn Cys Phe Leu Leu Cys Tyr Ser Ile Ser Ser
Arg Thr

      85      90
95
tca ttc gaa aac gtg aaa agc aag tgg tgg ccg gag atc cgt
cac ttc      336
Ser Phe Glu Asn Val Lys Ser Lys Trp Trp Pro Glu Ile Arg
His Phe

      100      105      110
tcc gcc cac gtt ccc gtg gtt ctc gtg ggc acc aaa ctg gac
ttg cgc      384
Ser Ala His Val Pro Val Val Leu Val Gly Thr Lys Leu Asp
Leu Arg

      115      120      125
att ccc aac tcg gag aag ttc gtg acc aca cag gag gga aaa
aag atg      432
Ile Pro Asn Ser Glu Lys Phe Val Thr Thr Gln Glu Gly Lys
Lys Met

      130      135      140
cgc aaa gag ata cac gca ttc aac ttg gtc gag tgc tcc gcc
aag aag      480
Arg Lys Glu Ile His Ala Phe Asn Leu Val Glu Cys Ser Ala
Lys Lys

      145      150      155
      160
aag cag aac ctg cag cag gtc ttc gag gag gcg gtt aga gcc
gtg gag      528
Lys Gln Asn Leu Gln Gln Val Phe Glu Glu Ala Val Arg Ala
Val Glu

      165      170
175
agg aaa cca aag acg acg tcc aag caa tcg tgc aaa ata ctg
tga      573
Arg Lys Pro Lys Thr Thr Ser Lys Gln Ser Cys Lys Ile Leu

      180      185      190

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<210> 571
 <211> 190
 <212> PRT
 <213> Drosophila melanogaster

0070110

<400> 571

Met	Thr	Ala	Asn	Ile	Thr	Lys	Ser	Pro	Arg	Pro	Leu	Lys	Ile
Thr	Ile												
1				5					10				
15													
Val	Gly	Asp	Gly	Met	Val	Gly	Lys	Thr	Cys	Met	Leu	Ile	Thr
Tyr	Thr												
			20					25					30
Arg	Asn	Glu	Phe	Pro	Glu	Glu	Tyr	Ile	Pro	Thr	Val	Phe	Asp
Asn	His												
		35					40					45	
Ala	Cys	Asn	Ile	Ala	Val	Asp	Asp	Arg	Asp	Tyr	Asn	Leu	Thr
Leu	Trp												
	50					55					60		
Asp	Thr	Ala	Gly	Gln	Glu	Asp	Tyr	Glu	Arg	Leu	Arg	Pro	Leu
Ser	Tyr												
65					70					75			
	80												
Pro	Ser	Thr	Asn	Cys	Phe	Leu	Leu	Cys	Tyr	Ser	Ile	Ser	Ser
Arg	Thr												
			85						90				
95													
Ser	Phe	Glu	Asn	Val	Lys	Ser	Lys	Trp	Trp	Pro	Glu	Ile	Arg
His	Phe												
			100					105				110	
Ser	Ala	His	Val	Pro	Val	Val	Leu	Val	Gly	Thr	Lys	Leu	Asp
Leu	Arg												
		115					120					125	
Ile	Pro	Asn	Ser	Glu	Lys	Phe	Val	Thr	Thr	Gln	Glu	Gly	Lys
Lys	Met												
	130					135					140		
Arg	Lys	Glu	Ile	His	Ala	Phe	Asn	Leu	Val	Glu	Cys	Ser	Ala
Lys	Lys												
145					150					155			
	160												
Lys	Gln	Asn	Leu	Gln	Gln	Val	Phe	Glu	Glu	Ala	Val	Arg	Ala
Val	Glu												
				165					170				
175													
Arg	Lys	Pro	Lys	Thr	Thr	Ser	Lys	Gln	Ser	Cys	Lys	Ile	Leu
			180					185					190

0070110

<210> 572
<211> 579
<212> DNA
<213> *Aplysia californica*

<220>
<221> CDS
<222> (1)..(579)

<400> 572
atg gca gcg ata cga aag aag ctt gtt ata gtc gga gat ggt
gcg tgt 48
Met Ala Ala Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly
Ala Cys
1 5 10
15
ggg aaa aca tgt cta ctt att gtc ttc agc aaa gac cag ttc
cct gaa 96
Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Asp Gln Phe
Pro Glu
20 25 30
gtt tac gtg cca aca gtt ttt gaa aat tat gta gca gac att
gaa gtt 144
Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Ile
Glu Val
35 40 45
gat ggc aaa cag gtt gag cta gct ctg tgg gac aca gcg gga
caa gag 192
Asp Gly Lys Gln Val Glu Leu Ala Leu Trp Asp Thr Ala Gly
Gln Glu
50 55 60
gac tat gac aga ctg agg ccg ctg tct tac cct gac aca gat
gtc atc 240
Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Thr Asp
Val Ile
65 70 75
80
ctc atg tgt ttc tct ata gac agt cca gac agt ctg gag aac
ata ccg 288
Leu Met Cys Phe Ser Ile Asp Ser Pro Asp Ser Leu Glu Asn
Ile Pro
85 90
95
gag aag tgg acg cct gag gtt cgt cac ttt tgt cca aat gtt
cct ata 336
Glu Lys Trp Thr Pro Glu Val Arg His Phe Cys Pro Asn Val
Pro Ile
100 105 110

0070110

```

ata ctt gtg ggt aac aaa aag gat ctt cgc aac gat gaa agt
acc aaa                               384
Ile Leu val Gly Asn Lys Lys Asp Leu Arg Asn Asp Glu Ser
Thr Lys                               115                               120                               125
cgt gag ctc atg aaa atg aaa cag gaa cca gtg aga cca gag
gat ggg                               432
Arg Glu Leu Met Lys Met Lys Gln Glu Pro val Arg Pro Glu
Asp Gly                               130                               135                               140
cgc gcc atg gct gag aaa atc aac gcc tac tct tat ctt gag
tgc tct                               480
Arg Ala Met Ala Glu Lys Ile Asn Ala Tyr Ser Tyr Leu Glu
Cys Ser                               145                               150                               155
                               160
gct aaa acc aag gag ggc gtg agg gat gtg ttt gag aca gct
acc aga                               528
Ala Lys Thr Lys Glu Gly val Arg Asp val Phe Glu Thr Ala
Thr Arg                               165                               170
175
gct gcg ctg caa gtg aaa aag aag aag aag ggt gga tgt gtt
gta ttg                               576
Ala Ala Leu Gln val Lys Lys Lys Lys Lys Gly Gly Cys val
val Leu                               180                               185                               190

tga                               579

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<210> 573
 <211> 192
 <212> PRT
 <213> *Aplysia californica*

<400> 573
 Met Ala Ala Ile Arg Lys Lys Leu val Ile val Gly Asp Gly
 Ala Cys
 1 5 10
 15
 Gly Lys Thr Cys Leu Leu Ile val Phe Ser Lys Asp Gln Phe
 Pro Glu
 20 25 30

0070110

Val	Tyr	Val	Pro	Thr	Val	Phe	Glu	Asn	Tyr	Val	Ala	Asp	Ile
Glu	Val												
		35					40					45	

Asp	Gly	Lys	Gln	Val	Glu	Leu	Ala	Leu	Trp	Asp	Thr	Ala	Gly
Gln	Glu												
	50					55					60		

Asp	Tyr	Asp	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Pro	Asp	Thr	Asp
Val	Ile												
65					70					75			

	80												
Leu	Met	Cys	Phe	Ser	Ile	Asp	Ser	Pro	Asp	Ser	Leu	Glu	Asn
Ile	Pro												
				85					90				

95													
Glu	Lys	Trp	Thr	Pro	Glu	Val	Arg	His	Phe	Cys	Pro	Asn	Val
Pro	Ile												
			100				105					110	

Ile	Leu	Val	Gly	Asn	Lys	Lys	Asp	Leu	Arg	Asn	Asp	Glu	Ser
Thr	Lys												
		115					120					125	

Arg	Glu	Leu	Met	Lys	Met	Lys	Gln	Glu	Pro	Val	Arg	Pro	Glu
Asp	Gly												
	130					135					140		

Arg	Ala	Met	Ala	Glu	Lys	Ile	Asn	Ala	Tyr	Ser	Tyr	Leu	Glu
Cys	Ser												
145					150					155			

	160												
Ala	Lys	Thr	Lys	Glu	Gly	Val	Arg	Asp	Val	Phe	Glu	Thr	Ala
Thr	Arg												
			165						170				

175													
Ala	Ala	Leu	Gln	Val	Lys	Lys	Lys	Lys	Lys	Gly	Gly	Cys	Val
Val	Leu												

	180						185					190	
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<210> 574
 <211> 645
 <212> DNA
 <213> Oryza sativa

<220>

0070110

<221> CDS

<222> (1)..(645)

<400> 574

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atg agc tcg gcg gcg gcg gcg acg agg ttc atc aag tgc gtc
acc gtg          48
Met Ser Ser Ala Ala Ala Ala Thr Arg Phe Ile Lys Cys Val
Thr Val
1          5          10
15
ggg gac ggc gcg gtg ggg aag acg tgc atg ctc atc tgc tac
acc tgc          96
Gly Asp Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr
Thr Cys
20          25          30
aac aag ttc ccc acc gat tac atc ccc acc gtg ttc gac aac
ttc agc          144
Asn Lys Phe Pro Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn
Phe Ser
35          40          45
gcc aat gtc tcc gtg gac ggg agc gtc gtc aac ctc ggc ctc
tgg gac          192
Ala Asn Val Ser Val Asp Gly Ser Val Val Asn Leu Gly Leu
Trp Asp
50          55          60
act gca ggt cag gag gat tac agc agg ttg agg cct ctg agc
tac agg          240
Thr Ala Gly Gln Glu Asp Tyr Ser Arg Leu Arg Pro Leu Ser
Tyr Arg
65          70          75
80
gga gcc gat gtg ttc atc ctg tcc ttc tcc ctg ata agc agg
gcg agc          288
Gly Ala Asp Val Phe Ile Leu Ser Phe Ser Leu Ile Ser Arg
Ala Ser
85          90
95
tat gag aat gtt cag aag aag tgg atg cca gag ctt cgc cgg
ttt gcg          336
Tyr Glu Asn Val Gln Lys Lys Trp Met Pro Glu Leu Arg Arg
Phe Ala
100          105          110
cct ggt gtt cct gta gtt ctt gtt gga acc aag ttg gat ctc
cgt gaa          384
Pro Gly Val Pro Val Val Leu Val Gly Thr Lys Leu Asp Leu
Arg Glu
115          120          125

```

0070110

```

gat agg gcc tat ctt gct gat cat cca gct tct tcc ata ata
aca acg          432
Asp Arg Ala Tyr Leu Ala Asp His Pro Ala Ser Ser Ile Ile
Thr Thr
      130          135          140
gag cag gga gaa gaa ctg agg aag cta ata gga gcg gtc gcc
tac atc          480
Glu Gln Gly Glu Glu Leu Arg Lys Leu Ile Gly Ala Val Ala
Tyr Ile
145          150          155
      160
gaa tgc agc tcc aag aca cag aga aac att aaa gct gtt ttc
gac act          528
Glu Cys Ser Ser Lys Thr Gln Arg Asn Ile Lys Ala Val Phe
Asp Thr
      165          170
175
gcc atc aaa gtg gtg ctt caa cct cca aga cat aag gat gta
acc aga          576
Ala Ile Lys Val Val Leu Gln Pro Pro Arg His Lys Asp Val
Thr Arg
      180          185          190

aag aaa ctc caa tca agc tcc aat cgg cca gta agg cgg tac
ttt tgc          624
Lys Lys Leu Gln Ser Ser Ser Asn Arg Pro Val Arg Arg Tyr
Phe Cys
      195          200          205
gga agc gct tgt ttc gcg tag
      645
Gly Ser Ala Cys Phe Ala
      210

```

<210> 575

<211> 214

<212> PRT

<213> Oryza sativa

<400> 575

```

Met Ser Ser Ala Ala Ala Ala Thr Arg Phe Ile Lys Cys Val
Thr Val
1          5          10
15
Gly Asp Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr
Thr Cys
      20          25          30

Asn Lys Phe Pro Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn

```

0070110

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

<210> 576

<211> 594

0070110

<212> DNA

<213> Oryza sativa

<220>

<221> CDS

<222> (1)..(594)

<400> 576

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atg agc gcg tcc agg ttc ata aag tgc gtc acc gtc ggg gac
ggc gcc          48
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1              5              10
15
gtc ggc aag acc tgc atg ctc atc tcc tac acc tcc aac acc
ttc ccc          96
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
20              25              30
act gat tat gtt ccg acg gtg ttt gac aac ttc agt gcc aac
gtc gtg          144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
35              40              45
gtt gat ggt aac acc gtc aac ctc ggg cta tgg gac act gca
ggt cag          192
Val Asp Gly Asn Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50              55              60
gag gat tac aac aga ctg aga cca ctg agt tat cgt gga gct
gat gtt          240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65              70              75
80
ttc ctt ctg gcc ttc tcg cta atc agc aag gcc agc tat gag
aat gtt          288
Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val
85              90
95
tca aag aag tgg ata cct gag ctg aag cat tat gca cct ggt
gtg cct          336
Ser Lys Lys Trp Ile Pro Glu Leu Lys His Tyr Ala Pro Gly
Val Pro
100              105              110
atc atc ctt gtg gga aca aag ctt gat ctt cga gat gac aag
```

0070110

```

cag ttt      384
Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe
      115      120      125
ttt gtg gac cat cct ggt gct gtt cct atc acc act gct cag
gga gag      432
Phe Val Asp His Pro Gly Ala Val Pro Ile Thr Thr Ala Gln
Gly Glu
      130      135      140
gaa cta aga aag caa ata ggc gcc cca tac tac atc gaa tgc
agc tca      480
Glu Leu Arg Lys Gln Ile Gly Ala Pro Tyr Tyr Ile Glu Cys
Ser Ser
145      150      155
      160
aag acc caa cta aac gtc aag ggc gtt ttc gat gcg gca ata
aag gtg      528
Lys Thr Gln Leu Asn Val Lys Gly Val Phe Asp Ala Ala Ile
Lys Val
      165      170
175
gtg ctg cag cca ccc aag gcg aag aag aag aaa aag gcg caa
agg ggg      576
Val Leu Gln Pro Pro Lys Ala Lys Lys Lys Lys Lys Ala Gln
Arg Gly
      180      185      190

gcg tgc tcc att ttg tga
      594
Ala Cys Ser Ile Leu
      195

```

<210> 577
 <211> 197
 <212> PRT
 <213> Oryza sativa

```

<400> 577
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1      5      10
15
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
      20      25      30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val

```

0070110
40

35

45

Val Asp Gly Asn Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65 70 75
80

Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val
85 90

95
Ser Lys Lys Trp Ile Pro Glu Leu Lys His Tyr Ala Pro Gly
Val Pro
100 105 110

Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe
115 120 125

Phe Val Asp His Pro Gly Ala Val Pro Ile Thr Thr Ala Gln
Gly Glu
130 135 140

Glu Leu Arg Lys Gln Ile Gly Ala Pro Tyr Tyr Ile Glu Cys
Ser Ser
145 150 155
160

Lys Thr Gln Leu Asn Val Lys Gly Val Phe Asp Ala Ala Ile
Lys Val
165 170

175
Val Leu Gln Pro Pro Lys Ala Lys Lys Lys Lys Lys Ala Gln
Arg Gly
180 185 190

Ala Cys Ser Ile Leu
195

<210> 578
<211> 594
<212> DNA
<213> Oryza sativa

<220>
<221> CDS

<222> (1)..(594)

<400> 578

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atg agc acg gcg agg ttc atc aag tgc gtc acc gtc ggc gac
ggc gcc
Met Ser Thr Ala Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10
15
gtc ggc aag aca tgc atg ctc atc tcc tac acc agc aac act
ttc ccc
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
20 25 30
acg gat tat gtg ccg acg gtt ttc gac aac ttc agc gcc aac
gtg gtc
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
35 40 45
gtc gac ggc aac acg gtg aac ctt ggg ctc tgg gat act gct
gga caa
Val Asp Gly Asn Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60
gag gat tac aat agg ctg agg cct ctc agc tac aga gga gct
gat gtc
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65 70 75
80
ttt tta cta gca ttt tcc ctc atc agc aaa gcg agc tat gag
aat att
Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Ile
85 90
95
cac aag aag tgg ata cca gag ctg agg cat tat gct cct aat
gtg cca
His Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Asn
Val Pro
100 105 110
atc gta tta gtt gga acc aag ctt gac ttg cgt gag gac aag
cag ttc
Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Glu Asp Lys
Gln Phe
115 120 125
ttc ctg gac cac cct ggt cta gca cct att tcc act gca cag

```

0070110

```

ggg gag      432
Phe Leu Asp His Pro Gly Leu Ala Pro Ile Ser Thr Ala Gln
Gly Glu
130
gag ctg aag agg atg ata ggt gct gcg gcg tac atc gaa tgc
agc tcc      480
Glu Leu Lys Arg Met Ile Gly Ala Ala Ala Tyr Ile Glu Cys
Ser Ser
145      150      155
160
aag acg cag cag aat gtg aaa tca gta ttc gac tcg gcg atc
aaa gtt      528
Lys Thr Gln Gln Asn Val Lys Ser Val Phe Asp Ser Ala Ile
Lys Val
165      170
175
gta ctt tgc ccg cca aag ccg aag aag aag aac acc agg aag
cag agg      576
Val Leu Cys Pro Pro Lys Pro Lys Lys Lys Asn Thr Arg Lys
Gln Arg
180      185      190

agt tgc tgg atc cta tga
594
Ser Cys Trp Ile Leu
195

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<210> 579
 <211> 197
 <212> PRT
 <213> Oryza sativa

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<400> 579
Met Ser Thr Ala Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1      5      10
15
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
20      25      30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
35      40      45

Val Asp Gly Asn Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50      55      60

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0070110

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

<210> 580

<211> 645

<212> DNA

<213> Oryza sativa

<220>

<221> CDS

<222> (1)..(645)

<400> 580

atg gcg tcc agc gcc tcc cgg ttc atc aag tgc gtc acg gtg

0070110

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

0070110

ggt gaa gaa ctt cga aaa caa ata ggt gct gct tat tac att
 gag tgc 480
 Gly Glu Glu Leu Arg Lys Gln Ile Gly Ala Ala Tyr Tyr Ile
 Glu Cys
 145 150 155

160
 agc tca aag aca caa cag aat gtc aaa ggt gtg ttt gat gct
 gct atc 528
 Ser Ser Lys Thr Gln Gln Asn Val Lys Gly Val Phe Asp Ala
 Ala Ile
 165 170

175
 aag gta gta atc cag cct cca act aag cag agg gaa aag aag
 aaa aag 576
 Lys Val Val Ile Gln Pro Pro Thr Lys Gln Arg Glu Lys Lys
 Lys Lys
 180 185 190

aaa tca cga caa gga tgc tct atg atg aac atg ttc cgt gga
 agg aaa 624
 Lys Ser Arg Gln Gly Cys Ser Met Met Asn Met Phe Arg Gly
 Arg Lys
 195 200 205

atg tca tgc ttc aaa tcc tga
 645
 Met Ser Cys Phe Lys Ser
 210

<210> 581
 <211> 214
 <212> PRT
 <213> Oryza sativa

<400> 581
 Met Ala Ser Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val
 Gly Asp
 1 5 10
 15
 Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser
 Asn Lys
 20 25 30

Phe Pro Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser
 Ala Asn
 35 40 45

Val Val Val Asp Ser Thr Thr Val Asn Leu Gly Leu Trp Asp
 Thr Ala

0070110
55

50

60

Gly	Gln	Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg
Gly	Ala												
65					70					75			
	80												
Asp	Val	Phe	Val	Leu	Ala	Phe	Ser	Leu	Val	Ser	Arg	Ala	Ser
Tyr	Glu												
				85					90				
95													
Asn	Ile	Met	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Gln	His	Tyr	Ala
Pro	Gly												
			100					105					110
Val	Pro	Ile	Val	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Glu
Asp	Lys												
		115				120					125		
His	Tyr	Leu	Leu	Asp	His	Pro	Gly	Met	Ile	Pro	Val	Thr	Thr
Ala	Gln												
	130					135					140		
Gly	Glu	Glu	Leu	Arg	Lys	Gln	Ile	Gly	Ala	Ala	Tyr	Tyr	Ile
Glu	Cys												
145					150					155			
	160												
Ser	Ser	Lys	Thr	Gln	Gln	Asn	Val	Lys	Gly	Val	Phe	Asp	Ala
Ala	Ile												
				165					170				
175													
Lys	Val	Val	Ile	Gln	Pro	Pro	Thr	Lys	Gln	Arg	Glu	Lys	Lys
Lys	Lys												
			180					185					190
Lys	Ser	Arg	Gln	Gly	Cys	Ser	Met	Met	Asn	Met	Phe	Arg	Gly
Arg	Lys												
		195					200				205		
Met	Ser	Cys	Phe	Lys	Ser								
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<210> 582
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 <212> DNA
 <213> Oryza sativa

<220>
 <221> CDS

<222> (1)..(594)

<400> 582

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atg agc gcg tct cgg ttc atc aag tgc gtc acc gtg ggg gac
ggc gcc          48
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
  1              5              10
15
gtg ggc aag acc tgc atg ctc atc tcc tac acc tcc aac acc
ttc ccc          96
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
      20              25              30
acg gac tat gtt cca act gtt ttt gat aac ttc agt gca aat
ggt gtg          144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
      35              40              45
gtc gat ggg agc act gtg aac ttg ggg ttg tgg gat aca gca
gga caa          192
Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
      50              55              60
gag gac tac aat agg cta cgc ccg ttg agc tat cgt ggc gct
gat gtt          240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
      65              70              75
80
ttc ctg ctg gcc ttt tct ctg atc agc aaa gca agc tat gag
aat gtt          288
Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val
      85              90
95
tct aaa aag tgg ata cct gaa tta agg cat tat gct cct ggt
gtg cca          336
Ser Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Gly
Val Pro
      100              105              110
ata att ctc gtt gga aca aag ctt gat ctg cgg gat gat aag
caa ttt          384
Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe
      115              120              125

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0070110

ttc gta gat cac cct ggt gct gta cct att tcc act gct cag
 ggc gaa 432
 Phe Val Asp His Pro Gly Ala Val Pro Ile Ser Thr Ala Gln
 Gly Glu

130 135 140
 gag ctg agg aaa ctc att ggt gca gcg gca tac att gaa tgc
 agt tca 480
 Glu Leu Arg Lys Leu Ile Gly Ala Ala Ala Tyr Ile Glu Cys
 Ser Ser
 145 150 155

160
 aaa aca cag caa aac atc aag gca gtt ttc gat gct gcg att
 aag gtg 528
 Lys Thr Gln Gln Asn Ile Lys Ala Val Phe Asp Ala Ala Ile
 Lys Val

165 170
 175
 gtt ctc cag cct cca aag caa aag aag aag aag aaa aag gcg
 cag aaa 576
 Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Lys Lys Ala
 Gln Lys
 180 185 190

gga tgt gcc atc ttg taa
 594
 Gly Cys Ala Ile Leu
 195

<210> 583
 <211> 197
 <212> PRT
 <213> Oryza sativa

<400> 583
 Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala
 1 5 10
 15
 Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
 Phe Pro
 20 25 30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
 Val Val
 35 40 45

Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
 Gly Gln

0070110
55

50

60

Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala
Asp	Val												
65					70					75			
	80												
Phe	Leu	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Lys	Ala	Ser	Tyr	Glu
Asn	Val												
				85					90				
95													
Ser	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Arg	His	Tyr	Ala	Pro	Gly
Val	Pro												
			100					105					110
Ile	Ile	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys
Gln	Phe												
		115					120				125		
Phe	Val	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Ser	Thr	Ala	Gln
Gly	Glu												
	130					135					140		
Glu	Leu	Arg	Lys	Leu	Ile	Gly	Ala	Ala	Ala	Tyr	Ile	Glu	Cys
Ser	Ser												
145					150					155			
	160												
Lys	Thr	Gln	Gln	Asn	Ile	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile
Lys	Val												
				165					170				
175													
Val	Leu	Gln	Pro	Pro	Lys	Gln	Lys	Lys	Lys	Lys	Lys	Lys	Ala
Gln	Lys												
			180					185					190
Gly	Cys	Ala	Ile	Leu									
		195											

<210> 584

<211> 588

<212> DNA

<213> Oryza sativa

<220>

<221> CDS

<222> (1)..(588)

<400> 584

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0070110

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

0070110

agg aaa ctc att ggt gca gcg gca tac att gaa tgc agt tca
 aaa aca 480
 Arg Lys Leu Ile Gly Ala Ala Ala Tyr Ile Glu Cys Ser Ser
 Lys Thr
 145 150 155

160
 cag caa aac atc aag gca gtt ttc gat gct gcg att aag gtg
 gtt ctc 528
 Gln Gln Asn Ile Lys Ala Val Phe Asp Ala Ala Ile Lys Val
 Val Leu
 165 170

175
 cag cct cca aag caa aag aag aag aag aaa aag gcg cag aaa
 gga tgt 576
 Gln Pro Pro Lys Gln Lys Lys Lys Lys Lys Lys Ala Gln Lys
 Gly Cys
 180 185 190

gcc atc ttg taa
 588
 Ala Ile Leu
 195

<210> 585
 <211> 195
 <212> PRT
 <213> Oryza sativa

<400> 585
 Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala
 1 5 10
 15
 Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
 Phe Pro
 20 25 30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
 Val Val
 35 40 45

Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
 Glu Asp
 50 55 60

Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala Asp Val
 Phe Leu
 65 70 75

0070110

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      80
Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu Asn Val
Ser Lys
      85
      90
95
Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Gly Val Pro
Ile Ile
      100
      105
      110
Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys Gln Phe
Phe Val
      115
      120
      125
Asp His Pro Gly Ala Val Pro Ile Ser Thr Ala Gln Gly Glu
Glu Leu
      130
      135
      140
Arg Lys Leu Ile Gly Ala Ala Ala Tyr Ile Glu Cys Ser Ser
Lys Thr
      145
      150
      155
      160
Gln Gln Asn Ile Lys Ala Val Phe Asp Ala Ala Ile Lys Val
Val Leu
      165
      170
      175
Gln Pro Pro Lys Gln Lys Lys Lys Lys Lys Lys Ala Gln Lys
Gly Cys
      180
      185
      190
Ala Ile Leu
      195

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<210> 586
 <211> 645
 <212> DNA
 <213> Oryza sativa

<220>
 <221> CDS
 <222> (1)..(645)

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<400> 586
atg agc ggc gcc acc aag ttc atc aag tgc gtc acc gtc ggc
gac ggc
Met Ser Gly Ala Thr Lys Phe Ile Lys Cys Val Thr Val Gly
Asp Gly
      1
      5
      10
      15

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0070110

```

gcc gtc ggc aag acc tgc atg ctc atc tgc tac acc agc aac
aag ttc          96

Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser Asn
Lys Phe

          20          25          30
ccc acc gat tac atc ccc acc gtg ttc gac aac ttc agt gct
aat gtt          144
Pro Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser Ala
Asn Val

          35          40          45
tca gtg gat ggg aac atc gtc aac ttg gga tta tgg gac act
gct gga          192
Ser Val Asp Gly Asn Ile Val Asn Leu Gly Leu Trp Asp Thr
Ala Gly
          50          55          60
caa gag gat tac agc agg ctg agg cca ctg agc tac agg gga
gcg gat          240
Gln Glu Asp Tyr Ser Arg Leu Arg Pro Leu Ser Tyr Arg Gly
Ala Asp
          65          70          75
          80
ata ttt gtg ctg gca ttc tca ctg atc agc aga gca agc tat
gag aat          288
Ile Phe Val Leu Ala Phe Ser Leu Ile Ser Arg Ala Ser Tyr
Glu Asn

          85          90
95
gtt ctc aag aag tgg atg ccg gag ctt cgc cgg ttc gca ccg
aat gtt          336
Val Leu Lys Lys Trp Met Pro Glu Leu Arg Arg Phe Ala Pro
Asn Val

          100          105          110

cca att gtt ctt gtt ggg acc aag tta gat cta cgt gac cac
aga tct          384
Pro Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Asp His
Arg Ser

          115          120          125
tac ctt gcg gac cat cct gct gct tcc gca att acg act gca
cag ggt          432
Tyr Leu Ala Asp His Pro Ala Ala Ser Ala Ile Thr Thr Ala
Gln Gly
          130          135          140
gaa gaa ctt aga aag cag ata ggc gcc gcg gct tac atc gaa
tgc agt          480
Glu Glu Leu Arg Lys Gln Ile Gly Ala Ala Ala Tyr Ile Glu
Cys Ser

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0070110

145					150					155			
160													
tcg	aaa	aca	caa	cag	aac	atc	aag	gcc	gtg	ttt	gat	act	gcc
atc	aag			528									
Ser	Lys	Thr	Gln	Gln	Asn	Ile	Lys	Ala	Val	Phe	Asp	Thr	Ala
Ile	Lys												
					165					170			
175													
gtg	gtc	ctt	cag	cct	cct	cgg	aga	agg	ggg	gag	acg	acg	atg
gca	agg		576										
Val	Val	Leu	Gln	Pro	Pro	Arg	Arg	Arg	Gly	Glu	Thr	Thr	Met
Ala	Arg												
					180					185			190
aag	aag	aca	agg	cga	agc	acc	ggc	tgc	tcg	tta	aag	aac	ttg
atg	tgt		624										
Lys	Lys	Thr	Arg	Arg	Ser	Thr	Gly	Cys	Ser	Leu	Lys	Asn	Leu
Met	Cys												
		195					200					205	
ggc	agt	gca	tgt	ggt	ggt	tag							
			645										
Gly	Ser	Ala	Cys	Val	Val								
	210												
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<212>	PRT												
<213>	Oryza sativa												
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Met	Ser	Gly	Ala	Thr	Lys	Phe	Ile	Lys	Cys	Val	Thr	Val	Gly
Asp	Gly												
1				5					10				
15													
Ala	Val	Gly	Lys	Thr	Cys	Met	Leu	Ile	Cys	Tyr	Thr	Ser	Asn
Lys	Phe												
			20					25				30	
Pro	Thr	Asp	Tyr	Ile	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala
Asn	Val												
		35					40				45		
Ser	Val	Asp	Gly	Asn	Ile	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr
Ala	Gly												
	50					55				60			
Gln	Glu	Asp	Tyr	Ser	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly
Ala	Asp												

0070110

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

<210> 588
 <211> 648
 <212> DNA
 <213> Oryza sativa

 <220>
 <221> CDS
 <222> (1)..(648)

 <400> 588

0070110

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

0070110

130	135	140
gga gag gaa ctc cgc aag	cac att ggc gca acg	tgt tac atc
gaa tgc	480	
Gly Glu Glu	Leu Arg Lys	His Ile Gly Ala Thr Cys Tyr Ile
Glu Cys		
145	150	155
160		
agc tca aag aca cag	cag aat gta aaa gct gtg	ttt gat gct
gcc atc	528	
Ser Ser Lys	Thr Gln Gln Asn Val Lys	Ala Val Phe Asp Ala
Ala Ile		
	165	170
175		
aag gta gta atc aag	cct cca aca aag	cag agg gac agg aag
aag aag	576	
Lys Val Val	Ile Lys Pro Pro Thr	Lys Gln Arg Asp Arg Lys
Lys Lys		
	180	185
		190
aaa aca cgg cgc gga	tgt tct ttc ttc tgc	aag ggt gtc atg
tcc aga	624	
Lys Thr Arg	Arg Gly Cys Ser Phe Phe	Cys Lys Gly Val Met
Ser Arg		
	195	200
		205
aga agg cta gta tgc ttc	aag tga	
	648	
Arg Arg Leu	Val Cys Phe Lys	
210	215	

<210> 589
 <211> 215
 <212> PRT
 <213> Oryza sativa

<400> 589
 Met Ala Ser Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val
 Gly Asp
 1 5 10
 15
 Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser
 Asn Lys
 20 25 30
 Phe Pro Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser
 Ala Asn
 35 40 45
 Val Val Val Asp Gly Thr Thr Val Asn Leu Gly Leu Trp Asp
 Seite 891

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

<210> 590
 <211> 639
 <212> DNA
 <213> Zea mays

<220>

0070110

<221> CDS

<222> (1)..(639)

<400> 590

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ggc gcg          48
Met Ser Val Thr Lys Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
  1              5              10
15
gtg ggc aag acc tgc atg ctc atc tgc tac acc agc aac aag
ttc ccc          96
Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser Asn Lys
Phe Pro
      20              25              30
acg gac tac atc ccc acg gtg ttc gac aac ttc agc gcc aac
gtc tcc          144
Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Ser
      35              40              45
gtg gac ggc agc atc gtc aac ctg ggc ctc tgg gac acc gcg
ggg caa          192
Val Asp Gly Ser Ile Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
      50              55              60
gag gac tac agc agg ctg cgg ccg ctg agc tac agg ggc gcg
gac gtg          240
Glu Asp Tyr Ser Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
      65              70              75
80
ttc gtg ctg gcc ttc tcc ctg atc agc agg gcg agc tac gag
aac gtt          288
Phe Val Leu Ala Phe Ser Leu Ile Ser Arg Ala Ser Tyr Glu
Asn Val
      85              90
95
ctt aag aag tgg gtg cca gag ctt cgc aga ttc gcg ccc aac
gtc ccg          336
Leu Lys Lys Trp Val Pro Glu Leu Arg Arg Phe Ala Pro Asn
Val Pro
      100              105              110
gtc gtt ctt gtt ggg acc aag tta gat ctc cgc gac cac aga
gcc tac          384
Val Val Leu Val Gly Thr Lys Leu Asp Leu Arg Asp His Arg
Ala Tyr
      115              120              125

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0070110

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ctc gcc gac cat cct gga gct tca gca gtc acc acg gcg cag
ggg gag          432
Leu Ala Asp His Pro Gly Ala Ser Ala Val Thr Thr Ala Gln
Gly Glu
130          135          140
gaa ctg agg aag cag atc ggc gct gcg gcc tac atc gag tgc
agt tcc          480
Glu Leu Arg Lys Gln Ile Gly Ala Ala Ala Tyr Ile Glu Cys
Ser Ser
145          150          155
160
aaa acc cag cag aac gtc aag tct gtc ttc gat acg gcc atc
aaa gtg          528
Lys Thr Gln Gln Asn Val Lys Ser Val Phe Asp Thr Ala Ile
Lys Val
165          170
175
gtc ctt cag ccc cca cgg agg agg gag gca gtg cct gcc agg
aag aag          576
Val Leu Gln Pro Pro Arg Arg Arg Glu Ala Val Pro Ala Arg
Lys Lys
180          185          190
aac agg cgt ggc tcc gga tgc tct ata atg aac ctt gtg tgt
ggc agc          624
Asn Arg Arg Gly Ser Gly Cys Ser Ile Met Asn Leu Val Cys
Gly Ser
195          200          205
aca tgt gct gct tag
          639
Thr Cys Ala Ala
210

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<210> 591
 <211> 212
 <212> PRT
 <213> Zea mays

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<400> 591
Met Ser Val Thr Lys Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1          5          10
15
Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser Asn Lys
Phe Pro
20          25          30

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Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
 Seite 894

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

Seite 895

0070110

<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (1)..(630)

<400> 592

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gga gct          48
Met Ser Ala Ser Lys Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1          5          10
15
gtc ggg aag aca tgt atg ctt atc tgt tac act agc aac aag
ttt ccc          96
Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser Asn Lys
Phe Pro
20          25          30
act gat tat ata ccc act gtg ttc gac aac ttc agt gcc aat
gtc tcc          144
Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Ser
35          40          45
gtg gat gga caa atc gtg aat ctg ggg ctt tgg gac act gcc
ggt caa          192
Val Asp Gly Gln Ile Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50          55          60
gaa gat tac agt agg ttg agg cca ttg agt tac aga gga gct
gat atc          240
Glu Asp Tyr Ser Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Ile
65          70          75
80
ttc gtc tta gcc ttt tct ctt atc agc aag gct agt tac gag
aat gta          288
Phe Val Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val
85          90
95
ctt aag aag tgg atg cct gaa ctt cgt cgg ttt gcg cct aat
gtt ccc          336
Leu Lys Lys Trp Met Pro Glu Leu Arg Arg Phe Ala Pro Asn
Val Pro
100          105          110
att gtc ctt gtt ggt aca aag cta gat ctc cgt gat gac aag
```

0070110

```

gga tac          384
Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gly Tyr
      115          120          125
ctc gcg gat cac acc aat gtc att acc tct gct cag gga gag
gaa ttg          432
Leu Ala Asp His Thr Asn Val Ile Thr Ser Ala Gln Gly Glu
Glu Leu
      130          135          140
agg aag caa atc ggt gca gct gct tac atc gag tgc agt tcc
aag act          480
Arg Lys Gln Ile Gly Ala Ala Ala Tyr Ile Glu Cys Ser Ser
Lys Thr
145          150          155
      160
caa cag aat gtg aaa gga gtg ttt gac aca gct atc aaa gtg
gtt ctc          528
Gln Gln Asn Val Lys Gly Val Phe Asp Thr Ala Ile Lys Val
Val Leu
      165          170
175
cag cca cca cgg agg aaa gag gtc act ggg aat aag aag aaa
cac aga          576
Gln Pro Pro Arg Arg Lys Glu Val Thr Gly Asn Lys Lys Lys
His Arg
      180          185          190
aga tca ggc tgc tcc ttt gcg agc att gtc tgc gga ggc tgc
gcc aca          624
Arg Ser Gly Cys Ser Phe Ala Ser Ile Val Cys Gly Gly Cys
Ala Thr
      195          200          205
gct tag
      630
Ala

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<210> 593
 <211> 209
 <212> PRT
 <213> Brassica napus

<400> 593
 Met Ser Ala Ser Lys Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala
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 15
 Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser Asn Lys

0070110

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

0070110

<210> 594
<211> 606
<212> DNA
<213> Brassica napus

<220>
<221> CDS
<222> (1)..(606)

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gga gct 48
Met Ser Thr Ala Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10
15
gtg ggg aag act tgt atg ctg att tca tat acc agc aat act
ttt cct 96
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
20 25 30
acg gat tac gtt ccg aca gtt ttt gac aat ttc agt gcg aat
gtg gtg 144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
35 40 45
gtc gat gga agt act gtc aac ctc ggc ctg tgg gat act gct
ggg cag 192
Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60
gaa gat tat aac agg ctt cgg cct ttg agt tac aga gga gca
gat gtg 240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65 70 75
80
ttt tta ttg gca ttt tcc cta att agc aag gcc agt tac gag
aac att 288
Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Ile
85 90
95
tac aaa aag tgg ctt ccg gag ctg aaa cat tat gcg cct agc
atc ccc 336
Tyr Lys Lys Trp Leu Pro Glu Leu Lys His Tyr Ala Pro Ser
Seite 899

0070110

Ile	Pro												
			100				105					110	
att	gta	ctc	gtc	gga	acc	aag	tta	gat	ttg	agg	gat	gac	aaa
cag	ttc		384										
Ile	Val	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys
Gln	Phe												
		115					120					125	
ttg	aaa	gat	cat	cca	gga	gca	gct	tca	ata	aca	act	gcc	cag
gga	gag		432										
Leu	Lys	Asp	His	Pro	Gly	Ala	Ala	Ser	Ile	Thr	Thr	Ala	Gln
Gly	Glu												
		130				135						140	
gaa	tta	aga	aag	atg	att	gga	gcc	atc	aag	tac	tta	gaa	tgc
agc	tcc		480										
Glu	Leu	Arg	Lys	Met	Ile	Gly	Ala	Ile	Lys	Tyr	Leu	Glu	Cys
Ser	Ser												
145					150					155			
	160												
aaa	acc	cag	cag	aat	gtg	aag	gca	gtg	ttt	gat	aca	gcg	atc
cgg	gta		528										
Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Thr	Ala	Ile
Arg	Val												
			165						170				
175													
gcg	ttg	agg	cct	cca	aag	gca	aag	aag	aag	ata	aag	cca	ttg
agg	acc		576										
Ala	Leu	Arg	Pro	Pro	Lys	Ala	Lys	Lys	Lys	Ile	Lys	Pro	Leu
Arg	Thr												
			180						185				190
aaa	aga	tca	aga	aca	tgc	ttt	ttc	ttc	taa				
			606										
Lys	Arg	Ser	Arg	Thr	Cys	Phe	Phe	Phe					
		195					200						

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 <212> PRT
 <213> Brassica napus

<400> 595
 Met Ser Thr Ala Arg Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala
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 Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
 Phe Pro

0070110

20

25

30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
35 40 45

Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65 70 75

80
Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Ile
85 90

95
Tyr Lys Lys Trp Leu Pro Glu Leu Lys His Tyr Ala Pro Ser
Ile Pro
100 105 110

Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe
115 120 125

Leu Lys Asp His Pro Gly Ala Ala Ser Ile Thr Thr Ala Gln
Gly Glu
130 135 140

Glu Leu Arg Lys Met Ile Gly Ala Ile Lys Tyr Leu Glu Cys
Ser Ser
145 150 155

160
Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Thr Ala Ile
Arg Val
165 170

175
Ala Leu Arg Pro Pro Lys Ala Lys Lys Lys Ile Lys Pro Leu
Arg Thr
180 185 190

Lys Arg Ser Arg Thr Cys Phe Phe Phe
195 200

<210> 596
<211> 651
<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (1)..(651)

<400> 596

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ggt gat          48
Met Ala Ser Ser Ala Ser Lys Phe Ile Lys Cys Val Thr Val
Gly Asp
  1              5              10
15
ggt gcc gtt ggt aaa acc tgt atg ctc atc tgc tat acc agc
aac aag          96
Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser
Asn Lys
      20              25              30
ttc cct act gac tat gta cca acg gtt ttt gac aac ttt agt
gca aac          144
Phe Pro Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser
Ala Asn
      35              40              45
gtt gta gtt gaa gga act act gtg aac tta ggg cta tgg gat
act gct          192
Val Val Val Glu Gly Thr Thr Val Asn Leu Gly Leu Trp Asp
Thr Ala
      50              55              60
gga caa gaa gac tat aac aga tta agg cct tta agc tac aga
gga gca          240
Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg
Gly Ala
      65              70              75
80
gat gtc ttc gtc ttg tct ttc tca ttg gtt agc cga gct agc
tac gag          288
Asp Val Phe Val Leu Ser Phe Ser Leu Val Ser Arg Ala Ser
Tyr Glu
      85              90
95
aat gtt ttt aaa aag tgg atc cct gaa ctc caa cac ttt gct
cca gga          336
Asn Val Phe Lys Lys Trp Ile Pro Glu Leu Gln His Phe Ala
Pro Gly
      100              105              110
gtt cca tta gtt ctt gtc ggt acc aaa tta gat ctc cgt gag
gat aag          384

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0070110

Val	Pro	Leu	Val	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Glu
Asp	Lys												
		115					120					125	
cat	tat	ctg	gct	gac	cat	cct	gga	cta	tcc	cct	gta	act	act
gca	cag		432										
His	Tyr	Leu	Ala	Asp	His	Pro	Gly	Leu	Ser	Pro	Val	Thr	Thr
Ala	Gln												
	130					135					140		
gga	gag	gag	ttg	cgt	aag	ctc	att	ggt	gca	aca	tat	tac	att
gaa	tgt		480										
Gly	Glu	Glu	Leu	Arg	Lys	Leu	Ile	Gly	Ala	Thr	Tyr	Tyr	Ile
Glu	Cys												
145					150					155			
160													
agc	tca	aaa	act	caa	cag	aat	gtc	aaa	gca	ggt	ttt	gat	tcg
gca	atc		528										
Ser	Ser	Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ser
Ala	Ile												
			165						170				
175													
aag	gaa	gtg	atc	aaa	ccg	gtg	ctt	aaa	cag	aag	ggc	aag	acc
aag	aaa		576										
Lys	Glu	Val	Ile	Lys	Pro	Val	Leu	Lys	Gln	Lys	Gly	Lys	Thr
Lys	Lys												
			180					185				190	
aag	aag	aag	caa	cag	tcg	aat	cac	cac	ggg	tgt	tta	tca	aac
ggt	ttg		624										
Lys	Lys	Lys	Gln	Gln	Ser	Asn	His	His	Gly	Cys	Leu	Ser	Asn
Val	Leu												
		195						200				205	
tgt	ggg	agg	ata	gtg	acc	cgg	cat	tga					
			651										
Cys	Gly	Arg	Ile	Val	Thr	Arg	His						
	210					215							

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<211> 216

<212> PRT

<213> Brassica napus

<400> 597

Met	Ala	Ser	Ser	Ala	Ser	Lys	Phe	Ile	Lys	Cys	Val	Thr	Val
Gly	Asp												

1

5

10

15

Gly	Ala	Val	Gly	Lys	Thr	Cys	Met	Leu	Ile	Cys	Tyr	Thr	Ser
Asn	Lys												

0070110

20

25

30

Phe Pro Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser
Ala Asn

35

40

45

Val Val Val Glu Gly Thr Thr Val Asn Leu Gly Leu Trp Asp
Thr Ala
50 55 60

Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg
Gly Ala
65 70 75

80

Asp Val Phe Val Leu Ser Phe Ser Leu Val Ser Arg Ala Ser
Tyr Glu
85 90

95

Asn Val Phe Lys Lys Trp Ile Pro Glu Leu Gln His Phe Ala
Pro Gly
100 105 110

Val Pro Leu Val Leu Val Gly Thr Lys Leu Asp Leu Arg Glu
Asp Lys
115 120 125

His Tyr Leu Ala Asp His Pro Gly Leu Ser Pro Val Thr Thr
Ala Gln
130 135 140

Gly Glu Glu Leu Arg Lys Leu Ile Gly Ala Thr Tyr Tyr Ile
Glu Cys
145 150 155

160

Ser Ser Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ser
Ala Ile
165 170

175

Lys Glu Val Ile Lys Pro Val Leu Lys Gln Lys Gly Lys Thr
Lys Lys
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Val Leu
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Cys Gly Arg Ile Val Thr Arg His
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0070110

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<213> Brassica napus

<220>
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ggt gcc 48
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Gly Ala

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gtc gga aaa acc tgt atg ctg atc tct tac acg agc aac acc
ttc cct 96
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro

20 25 30
acg gac tat gta cca act gtt ttc gat aac ttc agt gct aat
gtg gtt 144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val

35 40 45
gtt gat ggg aac act gtg aat ctt ggc ttg tgg gat aca gct
ggt caa 192
Val Asp Gly Asn Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln

50 55 60
gaa gac tat aac agg tta aga cca ttg agt tac cgt ggt gcg
gat gtc 240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val

65 70 75
80
ttc att ctt gct ttc tct ctt atc agc aaa gct agc tac gag
aat ata 288
Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Ile

85 90
95
gct aag aag tgg att cct gag ctc agg cac tat gcc cct ggt
gtt cct 336
Ala Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Gly

0070110

Val	Pro												
			100				105					110	
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cag	ttc			384									
Ile	Ile	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys
Gln	Phe												
		115					120					125	
ttc	ata	gac	cac	cct	ggt	gca	gtg	ccg	att	agt	act	aac	cag
gga	gag		432										
Phe	Ile	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Ser	Thr	Asn	Gln
Gly	Glu												
	130					135					140		
gaa	cta	aag	aaa	ctg	ata	ggg	tct	ccg	gct	tac	att	gaa	tgc
agt	tca		480										
Glu	Leu	Lys	Lys	Leu	Ile	Gly	Ser	Pro	Ala	Tyr	Ile	Glu	Cys
Ser	Ser												
145					150					155			
160													
aag	acg	cag	cag	aac	gtg	aag	gca	gtc	ttt	gac	gca	gcc	ata
aaa	gta		528										
Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile
Lys	Val												
			165						170				
175													
gtg	ctt	cag	cca	cca	aag	caa	aag	aag	aag	aaa	aag	aag	aat
ggt	tgt		576										
Val	Leu	Gln	Pro	Pro	Lys	Gln	Lys	Lys	Lys	Lys	Lys	Lys	Asn
Gly	Cys												
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gtt	ttc	ttg	tga										
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Val	Phe	Leu											
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 <212> PRT
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 Gly Ala
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 Phe Pro

0070110

20

25

30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val 35 40 45

Val Asp Gly Asn Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln 50 55 60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val 65 70 75

80
Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Ile 85 90

95
Ala Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Gly
Val Pro 100 105 110

Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe 115 120 125

Phe Ile Asp His Pro Gly Ala Val Pro Ile Ser Thr Asn Gln
Gly Glu 130 135 140

Glu Leu Lys Lys Leu Ile Gly Ser Pro Ala Tyr Ile Glu Cys
Ser Ser 145 150 155

160
Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Lys Val 165 170

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Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Lys Lys Asn
Gly Cys 180 185 190

Val Phe Leu
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  1              5              10
15
gga gct gta ggc aaa act tgc atg ctc att tgc tat aca agc
aac aaa          96
Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser
Asn Lys
      20              25              30
ttc ccc acg gac tat att cca acg gtg ttt gat aat ttc agt
gca aat          144
Phe Pro Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser
Ala Asn
      35              40              45
gtg gtt gtt gaa aac aca act gtc aat tta ggc ctc tgg gac
act gct          192
Val Val Val Glu Asn Thr Thr Val Asn Leu Gly Leu Trp Asp
Thr Ala
      50              55              60
ggg caa gag gat tac aac agg ctg agg cca ttg agc tac agg
ggg gca          240
Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg
Gly Ala
      65              70              75
80
gat gtc ttt gtc ttg gct ttc tct tta gtt agc cat gca agc
tac gaa          288
Asp Val Phe Val Leu Ala Phe Ser Leu Val Ser His Ala Ser
Tyr Glu
      85              90
95
aat gtg ttg aag aag tgg gtt cct gaa ctg cag cat ttt gct
cct ggt          336
Asn Val Leu Lys Lys Trp Val Pro Glu Leu Gln His Phe Ala
Pro Gly
      100              105              110

gtc cca gtg gtg cta gtt ggc acc aaa ttg gat ctt cga gaa
gac aag          384

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0070110

Val	Pro	Val	Val	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Glu
Asp	Lys												
		115					120					125	
cac	tat	ttg	gct	gat	cat	cct	ggg	ctg	gcg	cct	gtg	act	tct
gag	caa		432										
His	Tyr	Leu	Ala	Asp	His	Pro	Gly	Leu	Ala	Pro	Val	Thr	Ser
Glu	Gln												
	130					135					140		
ggg	gag	gaa	ttg	cgt	aaa	ctg	gtc	gga	gct	acg	tat	tat	ata
gag	tg		480										
Gly	Glu	Glu	Leu	Arg	Lys	Leu	Val	Gly	Ala	Thr	Tyr	Tyr	Ile
Glu	Cys												
145					150					155			
160													
agc	tca	aag	act	cag	cag	aat	gtg	aag	tca	gtt	ttt	gat	gct
gct	atc		528										
Ser	Ser	Lys	Thr	Gln	Gln	Asn	Val	Lys	Ser	Val	Phe	Asp	Ala
Ala	Ile												
			165						170				
175													
aag	gtg	gtc	atc	gag	cct	cca	caa	aaa	cat	gag	aag	aag	aaa
aaa	cca		576										
Lys	Val	Val	Ile	Glu	Pro	Pro	Gln	Lys	His	Glu	Lys	Lys	Lys
Lys	Pro												
			180					185				190	
cgt	cga	ggg	tgt	cta	ctg	tca	gta	cac	ttt	ttt	cat	atc	ata
aca	act		624										
Arg	Arg	Gly	Cys	Leu	Leu	Ser	Val	His	Phe	Phe	His	Ile	Ile
Thr	Thr												
		195				200					205		
cct	gca	cgt	gaa	act	ttc	tta	ctt	gtg	aaa	agg	gat	aga	tca
tta	agt		672										
Pro	Ala	Arg	Glu	Thr	Phe	Leu	Leu	Val	Lys	Arg	Asp	Arg	Ser
Leu	Ser												
	210					215					220		
gtt	cat	tga											
			681										
Val	His												
225													

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<213> Glycine max

<400> 601

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

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Thr Thr
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 Pro Ala Arg Glu Thr Phe Leu Leu Val Lys Arg Asp Arg Ser
 Leu Ser
 210 215 220
 Val His
 225

<210> 602
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 <222> (1)..(588)

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 Ala Val
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 ccc acc 96
 Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Arg Asn Thr Phe
 Pro Thr
 20 25 30
 ggt gat gtg tca aat gtt ttt gat aat gtc tgc gcc cat gtg
 att gtc 144
 Gly Asp Val Ser Asn Val Phe Asp Asn Val Cys Ala His Val
 Ile Val
 35 40 45
 gat ggg agc acc atc aac ttg gaa ttg ttt gac act gca gga
 caa gat 192
 Asp Gly Ser Thr Ile Asn Leu Glu Leu Phe Asp Thr Ala Gly
 Gln Asp
 50 55 60
 gac tac aac aga cta aga cca tta agc tat cca tgt act gat
 gtc ttc 240
 Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Pro Cys Thr Asp
 Val Phe
 65 70 75
 80
 ttg ctc gca ttc tct ctt gtt aac aaa gcg agc tat gaa aat

0070110

ggt gct 288
 Leu Leu Ala Phe Ser Leu Val Asn Lys Ala Ser Tyr Glu Asn
 Val Ala

85

90

95

aaa aag tgg gtt cct gaa ctc aga cat cat gct cct gat gtt
 ccc atc 336
 Lys Lys Trp Val Pro Glu Leu Arg His His Ala Pro Asp Val
 Pro Ile

100

105

110

gta ctt gtt gga aca aag ctc gat gct cga gat gat aag cag
 tac ttt 384
 Val Leu Val Gly Thr Lys Leu Asp Ala Arg Asp Asp Lys Gln
 Tyr Phe

115

120

125

ctt gag cac cct gaa gct gtt cct ata tct act gct cag ggt
 gaa gaa 432
 Leu Glu His Pro Glu Ala Val Pro Ile Ser Thr Ala Gln Gly
 Glu Glu

130

135

140

cta aag agg ctt gtt gga gct tct gct tat ata gaa tgc agt
 tca aag 480
 Leu Lys Arg Leu Val Gly Ala Ser Ala Tyr Ile Glu Cys Ser
 Ser Lys

145

150

155

160

aca caa ctg aat gtt aaa gct gtc ttt gac gag gcc atc aaa
 gta gtt 528
 Thr Gln Leu Asn Val Lys Ala Val Phe Asp Glu Ala Ile Lys
 Val Val

165

170

175

ctc gag cca ccc aat aac aac aac att agt aca tct cag aaa
 ggc tgt 576
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 Gly Cys

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185

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tcc ata ttg tga
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Ser Ile Leu
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Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Arg Asn Thr Phe
Pro Thr

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Gly Asp Val Ser Asn Val Phe Asp Asn Val Cys Ala His Val
Ile Val

35 40 45

Asp Gly Ser Thr Ile Asn Leu Glu Leu Phe Asp Thr Ala Gly
Gln Asp

50 55 60

Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Pro Cys Thr Asp
Val Phe

65 70 75

80

Leu Leu Ala Phe Ser Leu Val Asn Lys Ala Ser Tyr Glu Asn
Val Ala

85 90

95

Lys Lys Trp Val Pro Glu Leu Arg His His Ala Pro Asp Val
Pro Ile

100 105 110

Val Leu Val Gly Thr Lys Leu Asp Ala Arg Asp Asp Lys Gln
Tyr Phe

115 120 125

Leu Glu His Pro Glu Ala Val Pro Ile Ser Thr Ala Gln Gly
Glu Glu

130 135 140

Leu Lys Arg Leu Val Gly Ala Ser Ala Tyr Ile Glu Cys Ser
Ser Lys

145 150 155

160

Thr Gln Leu Asn Val Lys Ala Val Phe Asp Glu Ala Ile Lys
Val Val

165 170

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Gly Cys

0070110

180

185

190

Ser Ile Leu
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<213> Triticum aestivum

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<222> (1)..(624)

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ggc gac 48
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agc ggg gtc ggg aag acg tcg ctg atg aac cag tac gtc aac
aac aag 96
Ser Gly Val Gly Lys Thr Ser Leu Met Asn Gln Tyr Val Asn
Asn Lys 20 25 30
ttc agc aac cag tac aag gcc acc atc ggc gcc gat ttc ctc
acc aag 144
Phe Ser Asn Gln Tyr Lys Ala Thr Ile Gly Ala Asp Phe Leu
Thr Lys 35 40 45
gag gtc aag atc gac gac cgc ctc ttc act cta cag ata tgg
gac acg 192
Glu Val Lys Ile Asp Asp Arg Leu Phe Thr Leu Gln Ile Trp
Asp Thr 50 55 60
gca gga cag gaa cgt ttt cag agt ctt ggt gtg gcg ttt tat
cgg gga 240
Ala Gly Gln Glu Arg Phe Gln Ser Leu Gly Val Ala Phe Tyr
Arg Gly 65 70 75
80
gct gac tgt tgt gtt ctt gta tat gat gtc aat gtt acc aag
tca ttt 288
Ala Asp Cys Cys Val Leu Val Tyr Asp Val Asn Val Thr Lys
Ser Phe 85 90
95

0070110

gaa	aaa	ctc	aac	aac	tgg	cgt	gag	gaa	ttt	cta	att	caa	gct
agc	ccg			336									
Glu	Lys	Leu	Asn	Asn	Trp	Arg	Glu	Glu	Phe	Leu	Ile	Gln	Ala
Ser	Pro												
			100					105					110

tca	gat	cca	gag	aat	ttt	cct	ttt	gtt	tta	ctt	gga	aac	aag
att	gat		384										
Ser	Asp	Pro	Glu	Asn	Phe	Pro	Phe	Val	Leu	Leu	Gly	Asn	Lys
Ile	Asp												

gtt	gat	ggt	ggt	aac	agc	agg	act	gtt	tct	gag	aaa	aaa	gct
aaa	gcc		432										
Val	Asp	Gly	Gly	Asn	Ser	Arg	Thr	Val	Ser	Glu	Lys	Lys	Ala
Lys	Ala												
						135					140		

tgg	tgt	gct	tcc	aag	gga	aac	atc	cct	tat	ttt	gag	acg	tct
gct	aaa		480										
Trp	Cys	Ala	Ser	Lys	Gly	Asn	Ile	Pro	Tyr	Phe	Glu	Thr	Ser
Ala	Lys												
145					150					155			

gaa	ggc	ttc	aat	gtg	gaa	gca	gct	ttc	gag	tgt	ata	gca	agg
aat	gcc		528										
Glu	Gly	Phe	Asn	Val	Glu	Ala	Ala	Phe	Glu	Cys	Ile	Ala	Arg
Asn	Ala												

			165					170					
175													
atc	aag	aat	gaa	cct	gaa	gaa	gat	ata	tat	ctc	cct	gat	aca
atc	gac		576										
Ile	Lys	Asn	Glu	Pro	Glu	Glu	Asp	Ile	Tyr	Leu	Pro	Asp	Thr
Ile	Asp												

			180					185					190
atg	ggc	ggt	gct	gga	agg	caa	caa	cgc	tcg	tca	ggt	tgt	gaa
tgc	tag		624										
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Cys													
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 <213> Triticum aestivum

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 Met Ala Ser Arg Arg Arg Met Leu Leu Lys Val Ile Ile Leu
 Seite 915

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

0070110

Cys

195

200

205

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<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (1)..(612)

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Val Leu
1 5 10
15
ctt gga gat gtg ggc gct ggc aaa tct agc ttg gtt ctt cgg
ttt gtt 96
Leu Gly Asp Val Gly Ala Gly Lys Ser Ser Leu Val Leu Arg
Phe Val
20 25 30
aag gga cag ttt gtt gaa ttc cag gaa tca aca att gga gca
gcc ttc 144
Lys Gly Gln Phe Val Glu Phe Gln Glu Ser Thr Ile Gly Ala
Ala Phe
35 40 45
ttt tcc cag acc tta gcg gtc aat gat gag act gtt aag ttc
gaa atc 192
Phe Ser Gln Thr Leu Ala Val Asn Asp Glu Thr Val Lys Phe
Glu Ile
50 55 60
tgg gat act gcc ggg cag gag agg tat cat agc ttg gct ccc
atg tac 240
Trp Asp Thr Ala Gly Gln Glu Arg Tyr His Ser Leu Ala Pro
Met Tyr
65 70 75
80
tat agg ggt gca gct gct gcc att gtt gtc tat gac atc aca
aat ccg 288
Tyr Arg Gly Ala Ala Ala Ala Ile Val Val Tyr Asp Ile Thr
Asn Pro
85 90
95
gcc tcc ttc acc cgt gcc aag aaa tgg gtt caa gaa ctt caa

0070110

gct caa 336
Ala Ser Phe Thr Arg Ala Lys Lys Trp Val Gln Glu Leu Gln
Ala Gln
100 105 110

gga aat cag aat acc ata gtg gct ctt gct gga aac aag gct
gat atg 384
Gly Asn Gln Asn Thr Ile Val Ala Leu Ala Gly Asn Lys Ala
Asp Met
115 120 125

cta gat gcg agg cag gtg cca gca gag gaa gca aag gcg tat
gct cag 432
Leu Asp Ala Arg Gln Val Pro Ala Glu Glu Ala Lys Ala Tyr
Ala Gln
130 135 140

gag aat ggg ctc ttc ttc atg gag aca tct gct aaa act gca
atc aat 480
Glu Asn Gly Leu Phe Phe Met Glu Thr Ser Ala Lys Thr Ala
Ile Asn
145 150 155

160
gtg aat gac ata ttt tat gag att gca aag aaa ttg ctt caa
ggg caa 528
Val Asn Asp Ile Phe Tyr Glu Ile Ala Lys Lys Leu Leu Gln
Gly Gln
165 170

175
caa gct cca agc cca cag gct gga atg gtt ctg aat cag aga
cca aat 576
Gln Ala Pro Ser Pro Gln Ala Gly Met Val Leu Asn Gln Arg
Pro Asn
180 185 190

gag agg acg gtc agc agt tct tca tgc tgc tct tga
612
Glu Arg Thr Val Ser Ser Ser Ser Cys Cys Ser
195 200

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<212> PRT
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Val Leu
1 5 10
15

0070110

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

0070110

<210> 608
<211> 648
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (1)..(648)

<400> 608
atg gat tcc tcc tcg tcc agc ctc agc cag cag ccc gag ttc
gac tac 48
Met Asp Ser Ser Ser Ser Ser Leu Ser Gln Gln Pro Glu Phe
Asp Tyr
1 5 10
15
ctc ttc aag cta ctc ctt atc ggc gac tcc ggc gtc ggc aag
agc agc 96
Leu Phe Lys Leu Leu Leu Ile Gly Asp Ser Gly Val Gly Lys
Ser Ser
20 25 30
ctc ctc ctc cgc ttc acc gcc gac tcc ttc gat gac ctc tcc
cct acc 144
Leu Leu Leu Arg Phe Thr Ala Asp Ser Phe Asp Asp Leu Ser
Pro Thr
35 40 45
ata ggt gtt gac ttc aag gtg aag atg gtt agc att ggt ggc
aaa aaa 192
Ile Gly Val Asp Phe Lys Val Lys Met Val Ser Ile Gly Gly
Lys Lys
50 55 60
ctc aag ctt gcc atc tgg gac aca gct gga caa gag agg ttt
agg acc 240
Leu Lys Leu Ala Ile Trp Asp Thr Ala Gly Gln Glu Arg Phe
Arg Thr
65 70 75
80
ttg acc agc tct tac tac aga ggg gca cag ggg atc att atg
gtg tat 288
Leu Thr Ser Ser Tyr Tyr Arg Gly Ala Gln Gly Ile Ile Met
Val Tyr
85 90
95
gat gtc agt cga cga gag acg ttc acc aat ctt tct gat ata
tgg gcc 336
Asp Val Ser Arg Arg Glu Thr Phe Thr Asn Leu Ser Asp Ile
Trp Ala

0070110

100

105

110

aag gaa att gac ctg tat tca acc aac cag gac tgt gta aag
 atg ctt 384
 Lys Glu Ile Asp Leu Tyr Ser Thr Asn Gln Asp Cys Val Lys
 Met Leu

115 120 125
 gtt gga aat aaa gta gac aag gaa agt gag agg gct gtc acg
 aaa aag 432
 Val Gly Asn Lys Val Asp Lys Glu Ser Glu Arg Ala Val Thr
 Lys Lys

130 135 140
 gag gga att gaa ttt gcc agg gaa tac ggt tgt ttg ttt cta
 gaa tgc 480
 Glu Gly Ile Glu Phe Ala Arg Glu Tyr Gly Cys Leu Phe Leu
 Glu Cys

145 150 155
 160
 agt gcg aaa aca aaa gta aac gta gaa cag tgt ttt gag gaa
 ctg gtt 528
 Ser Ala Lys Thr Lys Val Asn Val Glu Gln Cys Phe Glu Glu
 Leu Val

165 170
 175
 cta aag atc tta gac acg cca agc ctc ctg gcg gat gct tcc
 tca gca 576
 Leu Lys Ile Leu Asp Thr Pro Ser Leu Leu Ala Asp Ala Ser
 Ser Ala

180 185 190
 ggg gtc agc aag aag aac atc ttc aag cag aag gct cca gaa
 gct gac 624
 Gly Val Ser Lys Lys Asn Ile Phe Lys Gln Lys Ala Pro Glu
 Ala Asp

195 200 205
 gcc gcc aca ggc agc tgc tgt taa
 648
 Ala Ala Thr Gly Ser Cys Cys
 210 215

<210> 609
 <211> 215
 <212> PRT
 <213> Zea mays

<400> 609
 Met Asp Ser Ser Ser Ser Ser Leu Ser Gln Gln Pro Glu Phe
 Asp Tyr

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1				5				10						
15														
Leu	Phe	Lys	Leu	Leu	Leu	Ile	Gly	Asp	Ser	Gly	Val	Gly	Lys	
Ser	Ser													
			20					25					30	
Leu	Leu	Leu	Arg	Phe	Thr	Ala	Asp	Ser	Phe	Asp	Asp	Leu	Ser	
Pro	Thr													
		35					40					45		
Ile	Gly	Val	Asp	Phe	Lys	Val	Lys	Met	Val	Ser	Ile	Gly	Gly	
Lys	Lys													
	50					55					60			
Leu	Lys	Leu	Ala	Ile	Trp	Asp	Thr	Ala	Gly	Gln	Glu	Arg	Phe	
Arg	Thr													
65					70					75				
	80													
Leu	Thr	Ser	Ser	Tyr	Tyr	Arg	Gly	Ala	Gln	Gly	Ile	Ile	Met	
Val	Tyr													
				85					90					
95														
Asp	Val	Ser	Arg	Arg	Glu	Thr	Phe	Thr	Asn	Leu	Ser	Asp	Ile	
Trp	Ala													
			100					105				110		
Lys	Glu	Ile	Asp	Leu	Tyr	Ser	Thr	Asn	Gln	Asp	Cys	Val	Lys	
Met	Leu													
		115					120					125		
Val	Gly	Asn	Lys	Val	Asp	Lys	Glu	Ser	Glu	Arg	Ala	Val	Thr	
Lys	Lys													
	130					135					140			
Glu	Gly	Ile	Glu	Phe	Ala	Arg	Glu	Tyr	Gly	Cys	Leu	Phe	Leu	
Glu	Cys													
145					150					155				
	160													
Ser	Ala	Lys	Thr	Lys	Val	Asn	Val	Glu	Gln	Cys	Phe	Glu	Glu	
Leu	Val													
				165					170					
175														
Leu	Lys	Ile	Leu	Asp	Thr	Pro	Ser	Leu	Leu	Ala	Asp	Ala	Ser	
Ser	Ala													
			180					185					190	
Gly	Val	Ser	Lys	Lys	Asn	Ile	Phe	Lys	Gln	Lys	Ala	Pro	Glu	
Ala	Asp													

0070110
200

195

205

Ala Ala Thr Gly Ser Cys Cys
210 215

<210> 610
<211> 603
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (1)..(603)

<400> 610
atg gct acg atc gga cac aac aat ctc aat gcc aaa ttg gtt
ctt ctc 48
Met Ala Thr Ile Gly His Asn Asn Leu Asn Ala Lys Leu Val
Leu Leu 1 5 10
15
ggg gac atg ggt gct ggg aaa tcc agc ctc gtt ttg cgc ttt
gtc aag 96
Gly Asp Met Gly Ala Gly Lys Ser Ser Leu Val Leu Arg Phe
Val Lys 20 25 30
ggg gca gca gca gca gca gca gca gca gca gca gca gca gca gca
ttc ttt 144
Gly Gln Phe Leu Glu Phe Gln Glu Ser Thr Ile Gly Ala Ala
Phe Phe 35 40 45
tca cag acg ctg gca gta aat gac gcg acg gta aag ttt gag
ata tgg 192
Ser Gln Thr Leu Ala Val Asn Asp Ala Thr Val Lys Phe Glu
Ile Trp 50 55 60
gac aca gca gga caa gag agg tac cat agc ttg gct ccc atg
tat tac 240
Asp Thr Ala Gly Gln Glu Arg Tyr His Ser Leu Ala Pro Met
Tyr Tyr 65 70 75
80
aga ggt gct gct gct gct atc att gtc tat gac atc act agc
tcg gac 288
Arg Gly Ala Ala Ala Ala Ile Ile Val Tyr Asp Ile Thr Ser
Ser Asp 85 90
95

0070110

tcc	ttt	acc	cga	act	aag	aag	tgg	gtc	caa	gag	ctt	caa	aag
caa	ggg			336									
Ser	Phe	Thr	Arg	Thr	Lys	Lys	Trp	Val	Gln	Glu	Leu	Gln	Lys
Gln	Gly												
			100					105					110

aat	cct	aat	atg	gtc	atg	gct	ctt	gct	ggt	aac	aaa	gct	gat
ttg	gaa		384										
Asn	Pro	Asn	Met	Val	Met	Ala	Leu	Ala	Gly	Asn	Lys	Ala	Asp
Leu	Glu												
		115					120					125	

gat	aag	agg	aaa	gtg	aca	gct	gaa	gaa	gca	cgt	gta	tat	gct
gaa	gaa		432										
Asp	Lys	Arg	Lys	Val	Thr	Ala	Glu	Glu	Ala	Arg	Val	Tyr	Ala
Glu	Glu												
		130				135					140		

aat	ggt	ttg	ttt	ttc	atg	gag	acc	tct	gcc	aaa	act	gca	tcc
aac	ggt		480										
Asn	Gly	Leu	Phe	Phe	Met	Glu	Thr	Ser	Ala	Lys	Thr	Ala	Ser
Asn	Val												
145					150					155			
160													

aat	gat	ata	ttc	tat	gaa	ata	gcc	aag	agg	tta	cca	agg	gct
cag	cca		528										
Asn	Asp	Ile	Phe	Tyr	Glu	Ile	Ala	Lys	Arg	Leu	Pro	Arg	Ala
Gln	Pro												
			165						170				

gct	cag	aac	cca	gct	ggg	atg	gta	ctt	ggt	gat	aga	ccc	gcc
gaa	gga		576										
Ala	Gln	Asn	Pro	Ala	Gly	Met	Val	Leu	Val	Asp	Arg	Pro	Ala
Glu	Gly												
		180						185				190	

act	agg	gct	gca	tca	tgt	tgt	tca	taa
			603					
Thr	Arg	Ala	Ala	Ser	Cys	Cys	Ser	
		195					200	

<210> 611
 <211> 200
 <212> PRT
 <213> Glycine max

<400> 611
 Met Ala Thr Ile Gly His Asn Asn Leu Asn Ala Lys Leu Val
 Leu Leu
 1 5 10

0070110

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

0070110

<210> 612
<211> 618
<212> DNA
<213> Triticum aestivum

<220>
<221> CDS
<222> (1)..(618)

<400> 612
atg gcg gcc agc gcc ggc agc aag atc cgc aac gcc aaa ctg
ggt ctt 48
Met Ala Ala Ser Ala Gly Ser Lys Ile Arg Asn Ala Lys Leu
Val Leu 1 5 10
15
ctt ggc gat gtg ggt gct ggg aaa tcc agc ctg gtg ctt cgg
ttt gta 96
Leu Gly Asp Val Gly Ala Gly Lys Ser Ser Leu Val Leu Arg
Phe Val 20 25 30
aaa gga caa ttt gtt gaa ttc cag gaa tcg aca att gga gcg
gct ttc 144
Lys Gly Gln Phe Val Glu Phe Gln Glu Ser Thr Ile Gly Ala
Ala Phe 35 40 45
ttc tct caa aca ttg gct gtt aat gac gag act gtg aag ttt
gaa att 192
Phe Ser Gln Thr Leu Ala Val Asn Asp Glu Thr Val Lys Phe
Glu Ile 50 55 60
tgg gat act gct ggg cag gag agg tat cac agc ttg gcc ccc
atg tac 240
Trp Asp Thr Ala Gly Gln Glu Arg Tyr His Ser Leu Ala Pro
Met Tyr 65 70 75
80
tac agg ggt gct gcc gca gcc ata gtt gtc tat gac atc tcg
aac cag 288
Tyr Arg Gly Ala Ala Ala Ala Ile Val Val Tyr Asp Ile Ser
Asn Gln 85 90
95
gca tcc ttc acc cga gca aag aaa tgg gtt caa gaa ctt caa
gct caa 336
Ala Ser Phe Thr Arg Ala Lys Lys Trp Val Gln Glu Leu Gln
Ala Gln

0070110

100

105

110

```

gga aac cag aat aca gta gtg gct ctt gct ggc aac aaa gct
gat ttg          384
Gly Asn Gln Asn Thr Val Val Ala Leu Ala Gly Asn Lys Ala
Asp Leu
          115          120          125
ctt gag gcg agg gag gtt caa ata gag gaa gcc aag acg tat
gcg cag          432
Leu Glu Ala Arg Glu Val Gln Ile Glu Glu Ala Lys Thr Tyr
Ala Gln
          130          135          140
gag aat ggc ctc ttc ttc atg gaa aca tct gct aaa act gca
acc aat          480
Glu Asn Gly Leu Phe Phe Met Glu Thr Ser Ala Lys Thr Ala
Thr Asn
145          150          155
          160
gtg aat gac ata ttt tat gag att gcg aag aga ttg ctg caa
ggg cag          528
Val Asn Asp Ile Phe Tyr Glu Ile Ala Lys Arg Leu Leu Gln
Gly Gln
          165          170
175
gca gcg cag aac cca cag gcg gcg ggg atg gtt ctc tcc cag
aga ccc          576
Ala Ala Gln Asn Pro Gln Ala Ala Gly Met Val Leu Ser Gln
Arg Pro
          180          185          190
aat gag aga gtg gtc agc gcg gct tcg tgc tgc tcc tcc tga
          618
Asn Glu Arg Val Val Ser Ala Ala Ser Cys Cys Ser Ser
          195          200          205

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<210> 613

<211> 205

<212> PRT

<213> Triticum aestivum

<400> 613

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Met Ala Ala Ser Ala Gly Ser Lys Ile Arg Asn Ala Lys Leu
Val Leu
          5          10
1
15
Leu Gly Asp Val Gly Ala Gly Lys Ser Ser Leu Val Leu Arg
Phe Val
          20          25          30

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0070110

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

<210> 614
 <211> 612
 <212> DNA
 <213> Zea mays

0070110

<220>

<221> CDS

<222> (1)..(612)

<400> 614

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atg aat ccc gag tac gac tac ctt ttc aaa ctt ctg ctt att
ggt gat          48
Met Asn Pro Glu Tyr Asp Tyr Leu Phe Lys Leu Leu Leu Ile
Gly Asp
1          5          10
15
tct ggt gtt ggg aaa tca tgc ttg ctt ctc aga ttt gca gac
gat tct          96
Ser Gly Val Gly Lys Ser Cys Leu Leu Leu Arg Phe Ala Asp
Asp Ser
20          25          30
tat ttg gac agc tat atc agc aca att ggg gtt gat ttc aaa
att cgc          144
Tyr Leu Asp Ser Tyr Ile Ser Thr Ile Gly Val Asp Phe Lys
Ile Arg
35          40          45
aca gtg gag caa gat ggg aag acc ata aaa ctt caa att tgg
gat act          192
Thr Val Glu Gln Asp Gly Lys Thr Ile Lys Leu Gln Ile Trp
Asp Thr
50          55          60
gct ggg caa gag cgc ttc agg aca atc act agc agc tac tac
cgc gga          240
Ala Gly Gln Glu Arg Phe Arg Thr Ile Thr Ser Ser Tyr Tyr
Arg Gly
65          70          75
80
gct cat gga atc att att gta tat gac gtg aca gac caa gaa
agc ttc          288
Ala His Gly Ile Ile Ile Val Tyr Asp Val Thr Asp Gln Glu
Ser Phe
85          90
95
aat aat gtg aag caa tgg ttg aac gag ata gac cgt tat gca
agt gat          336
Asn Asn Val Lys Gln Trp Leu Asn Glu Ile Asp Arg Tyr Ala
Ser Asp
100          105          110
aat gtt aac aag ctc ctt gtt ggg aac aag agt gac ctt act
gcc aac          384
Asn Val Asn Lys Leu Leu Val Gly Asn Lys Ser Asp Leu Thr
```

0070110

Ala	Asn																					
		115												120				125				
aaa	ggt	gtg	gca	act	gag	aca	gca	aag	gcg	ttt	gct	gat	gag									
atg	ggc													432								
Lys	Val	Val	Ala	Thr	Glu	Thr	Ala	Lys	Ala	Phe	Ala	Asp	Glu									
Met	Gly													130				135				140
atc	cca	ttc	atg	gag	acg	agt	gcc	aaa	aac	gcc	atc	aac	gtg									
gag	cag													480								
Ile	Pro	Phe	Met	Glu	Thr	Ser	Ala	Lys	Asn	Ala	Ile	Asn	Val									
Glu	Gln													145				150				155
	160																					
gcc	ttc	atg	gct	atg	gct	gca	tcc	atc	aag	gat	agg	atg	gcc									
agc	caa													528								
Ala	Phe	Met	Ala	Met	Ala	Ala	Ser	Ile	Lys	Asp	Arg	Met	Ala									
Ser	Gln													165				170				
	175																					
cca	gcc	gcg	gcc	aac	gca	agg	cca	gcg	acc	gtg	cag	atc	cgc									
ggg	caa													576								
Pro	Ala	Ala	Ala	Asn	Ala	Arg	Pro	Ala	Thr	Val	Gln	Ile	Arg									
Gly	Gln													180				185				190
ccc	gtc	aac	cag	aag	acg	tct	tgc	tgc	tcg	tcc	taa											
														612								
Pro	Val	Asn	Gln	Lys	Thr	Ser	Cys	Cys	Ser	Ser												
		195													200							

<210>	615
<211>	203
<212>	PRT
<213>	Zea mays

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<400> 615
Met Asn Pro Glu Tyr Asp Tyr Leu Phe Lys Leu Leu Leu Ile
Gly Asp
1          5          10
15
Ser Gly Val Gly Lys Ser Cys Leu Leu Leu Arg Phe Ala Asp
Asp Ser
          20          25          30
Tyr Leu Asp Ser Tyr Ile Ser Thr Ile Gly Val Asp Phe Lys
Ile Arg
          35          40          45

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0070110

Thr Val Glu Gln Asp Gly Lys Thr Ile Lys Leu Gln Ile Trp
 Asp Thr
 50 55 60

Ala Gly Gln Glu Arg Phe Arg Thr Ile Thr Ser Ser Tyr Tyr
 Arg Gly
 65 70 75

80
 Ala His Gly Ile Ile Ile Val Tyr Asp Val Thr Asp Gln Glu
 Ser Phe
 85 90

95
 Asn Asn Val Lys Gln Trp Leu Asn Glu Ile Asp Arg Tyr Ala
 Ser Asp
 100 105 110

Asn Val Asn Lys Leu Leu Val Gly Asn Lys Ser Asp Leu Thr
 Ala Asn
 115 120 125

Lys Val Val Ala Thr Glu Thr Ala Lys Ala Phe Ala Asp Glu
 Met Gly
 130 135 140

Ile Pro Phe Met Glu Thr Ser Ala Lys Asn Ala Ile Asn Val
 Glu Gln
 145 150 155

160
 Ala Phe Met Ala Met Ala Ala Ser Ile Lys Asp Arg Met Ala
 Ser Gln
 165 170

175
 Pro Ala Ala Ala Asn Ala Arg Pro Ala Thr Val Gln Ile Arg
 Gly Gln
 180 185 190

Pro Val Asn Gln Lys Thr Ser Cys Cys Ser Ser
 195 200

<210> 616
 <211> 594
 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (1)..(594)

0070110

<400> 616

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

```


0070110

Gly Glu
 130 135 140
 gag ctg aag aag cta ata gaa gca cct ttt tac atc gaa tgc
 agt tcc 480
 Glu Leu Lys Lys Leu Ile Glu Ala Pro Phe Tyr Ile Glu Cys
 Ser Ser
 145 150 155
 160
 aaa tct caa gag aat gtg aaa gca gtg ttt gac gca gcc ata
 cga gtg 528
 Lys Ser Gln Glu Asn Val Lys Ala Val Phe Asp Ala Ala Ile
 Arg Val
 165 170
 175
 gtc ttg caa cct ccg aag cag aag aag aaa aag agc aaa gcg
 cag aag 576
 Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Ser Lys Ala
 Gln Lys
 180 185 190
 gca tgc tcc atc cta tga
 594
 Ala Cys Ser Ile Leu
 195

<210> 617
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 <212> PRT
 <213> Brassica napus

<400> 617
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 Gly Ala
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 Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
 Phe Pro
 20 25 30
 Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
 Val Val
 35 40 45
 Val Asp Gly Asn Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
 Gly Gln
 50 55 60
 Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
 Seite 933

0070110

Asp Val													
65					70					75			
80													
Phe Ile	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Lys	Ala	Ser	Tyr	Glu	
Asn Ile													
					85				90				
95													
Ala Lys	Lys	Trp	Ile	Pro	Glu	Leu	Arg	His	Tyr	Ala	Pro	Gly	
Val Pro													
					100				105			110	
Ile Ile	Leu	Val	Gly	Ser	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys	
Gln Phe													
					115				120			125	
Phe Ile	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Thr	Thr	Ala	Gln	
Gly Glu													
					130				135			140	
Glu Leu	Lys	Lys	Leu	Ile	Glu	Ala	Pro	Phe	Tyr	Ile	Glu	Cys	
Ser Ser													
					145				150			155	
160													
Lys Ser	Gln	Glu	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile	
Arg Val													
					165				170				
175													
Val Leu	Gln	Pro	Pro	Lys	Gln	Lys	Lys	Lys	Lys	Ser	Lys	Ala	
Gln Lys													
					180				185			190	
Ala Cys	Ser	Ile	Leu										
					195								

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<220>
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 gga gct 48
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 Gly Ala

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

0070110

Lys Thr
 145 150 155
 160
 caa cag aat gtg aaa gca gtg ttt gac aca gcg atc aaa gtg
 gtt ctc 528
 Gln Gln Asn Val Lys Ala Val Phe Asp Thr Ala Ile Lys Val
 Val Leu
 165 170
 175
 cag cca cca cgg agg aaa gag gtc act ggg aat aag aag aaa
 cac aga 576
 Gln Pro Pro Arg Arg Lys Glu Val Thr Gly Asn Lys Lys Lys
 His Arg
 180 185 190
 aga tcc ggc tgc tcc ttt gcg agc att gtc tgc gga ggc tgg
 cca cag 624
 Arg Ser Gly Cys Ser Phe Ala Ser Ile Val Cys Gly Gly Trp
 Pro Gln
 195 200 205
 cgt agg aca taa
 636
 Arg Arg Thr
 210
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 <212> PRT
 <213> Brassica napus
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 Gly Ala
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 Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser Asn Lys
 Phe Pro
 20 25 30
 Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
 Val Ser
 35 40 45
 Val Asp Gly Gln Ile Val Asn Leu Gly Leu Trp Asp Thr Ala
 Gly Gln
 50 55 60
 Glu Asp Tyr Ser Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
 Seite 936

0070110

Asp Ile													
65					70					75			
	80												
Phe Val	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Lys	Ala	Ser	Tyr	Glu	
Asn Val													
			85					90					
95													
Leu Lys	Lys	Trp	Met	Pro	Glu	Leu	Arg	Arg	Phe	Ala	Pro	Asn	
Val Pro													
		100					105					110	
Ile val	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys	
Gly Tyr													
	115					120					125		
Leu Ala	Asp	His	Thr	Asn	Val	Ile	Thr	Ser	Thr	Gln	Gly	Glu	
Glu Leu													
	130					135				140			
Arg Lys	Gln	Ile	Gly	Ala	Ala	Ala	Tyr	Ile	Glu	Cys	Ser	Ser	
Lys Thr													
145					150				155				
	160												
Gln Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Thr	Ala	Ile	Lys	Val	
Val Leu													
			165					170					
175													
Gln Pro	Pro	Arg	Arg	Lys	Glu	Val	Thr	Gly	Asn	Lys	Lys	Lys	
His Arg													
		180					185					190	
Arg Ser	Gly	Cys	Ser	Phe	Ala	Ser	Ile	Val	Cys	Gly	Gly	Trp	
Pro Gln													
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Arg Arg	Thr												
	210												

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 <213> Brassica napus

 <220>
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 <222> (1)..(597)

 <400> 620

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Gly	Ala			5					10				
1													
15													
gtc	gga	aag	act	tgt	ctg	ctc	atc	tcc	tac	act	agc	aac	act
ttc	ccc		96										
Val	Gly	Lys	Thr	Cys	Leu	Leu	Ile	Ser	Tyr	Thr	Ser	Asn	Thr
Phe	Pro												
			20					25					30
acg	gac	tat	gtg	cca	act	gtg	ttt	gat	aat	ttc	agc	gcg	aat
gtg	att		144										
Thr	Asp	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn
Val	Ile												
		35				40						45	
gtg	gat	ggg	aac	act	atc	aac	ttg	gga	ttg	tgg	gat	act	gca
ggg	caa		192										
Val	Asp	Gly	Asn	Thr	Ile	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala
Gly	Gln												
50						55					60		
gag	gac	tac	aat	aga	cta	aga	cca	ttg	agc	tat	cgc	ggc	gca
gat	gtc		240										
Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala
Asp	Val												
65					70					75			
80													
ttc	tta	ctc	gct	ttc	tcc	ctt	gtc	agc	aaa	gct	agc	tat	gaa
aat	gtt		288										
Phe	Leu	Leu	Ala	Phe	Ser	Leu	Val	Ser	Lys	Ala	Ser	Tyr	Glu
Asn	Val												
			85						90				
95													
tct	aaa	aag	tgg	gta	cct	gaa	ctg	aga	cat	tat	gct	cct	ggt
ggt	cca		336										
Ser	Lys	Lys	Trp	Val	Pro	Glu	Leu	Arg	His	Tyr	Ala	Pro	Gly
Val	Pro												
			100					105				110	
atc	atc	ctc	gtc	gga	acc	aag	ctt	gat	ctt	cga	gat	gac	aag
caa	ttc		384										
Ile	Ile	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys
Gln	Phe												
		115				120						125	
ttt	ggt	gag	cac	cct	ggt	gct	ggt	cct	atc	tct	act	gct	cag
ggt	gaa		432										
Phe	Val	Glu	His	Pro	Gly	Ala	Val	Pro	Ile	Ser	Thr	Ala	Gln
Gly	Glu												

0070110

130						135						140	
gaa	ctg	aag	aag	gtg	att	ggg	gca	cct	gct	tat	att	gaa	tgc
agt	gca			480									
Glu	Leu	Lys	Lys	Val	Ile	Gly	Ala	Pro	Ala	Tyr	Ile	Glu	Cys
Ser	Ala												
145					150					155			
160													
aaa	aca	caa	cag	aat	gta	aaa	gcg	gtg	ttt	gat	gcg	gct	atc
aag	gta		528										
Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile
Lys	Val												
					165					170			
175													
gtt	ctc	caa	cca	ccc	aaa	aac	aag	aag	agg	aag	aag	aga	aag
tct	cag		576										
Val	Leu	Gln	Pro	Pro	Lys	Asn	Lys	Lys	Arg	Lys	Lys	Arg	Lys
Ser	Gln												
			180						185				190
aaa	gct	tgt	tct	ata	ttg	tga							
			597										
Lys	Ala	Cys	Ser	Ile	Leu								
		195											

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 <212> PRT
 <213> Brassica napus

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Val	Gly	Lys	Thr	Cys	Leu	Leu	Ile	Ser	Tyr	Thr	Ser	Asn	Thr
Phe	Pro												
			20					25				30	
Thr	Asp	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn
Val	Ile												
		35					40					45	
Val	Asp	Gly	Asn	Thr	Ile	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala
Gly	Gln												
	50					55					60		
Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala
Asp	Val												

0070110

65					70					75			
	80												
Phe	Leu	Leu	Ala	Phe	Ser	Leu	Val	Ser	Lys	Ala	Ser	Tyr	Glu
Asn	Val												
				85					90				
95													
Ser	Lys	Lys	Trp	Val	Pro	Glu	Leu	Arg	His	Tyr	Ala	Pro	Gly
Val	Pro												
			100					105				110	
Ile	Ile	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys
Gln	Phe												
		115					120				125		
Phe	Val	Glu	His	Pro	Gly	Ala	Val	Pro	Ile	Ser	Thr	Ala	Gln
Gly	Glu												
	130					135				140			
Glu	Leu	Lys	Lys	Val	Ile	Gly	Ala	Pro	Ala	Tyr	Ile	Glu	Cys
Ser	Ala												
145					150					155			
	160												
Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile
Lys	Val												
				165					170				
175													
Val	Leu	Gln	Pro	Pro	Lys	Asn	Lys	Lys	Arg	Lys	Lys	Arg	Lys
Ser	Gln												
			180					185				190	
Lys	Ala	Cys	Ser	Ile	Leu								
		195											

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 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (1)..(597)

<400> 622
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 ggc gcc 48
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 Gly Ala
 1 5 10

0070110

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15
gtc ggc aag act tgt cta ctc atc tcc tac aca agc aac act
ttc ccc
Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro

20
act gat tat gtg cca act gtc ttt gat aat ttc agt gct aat
gtg att
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Ile

35
gtt gat ggg aac acc atc aac ttg gga ttg tgg gac act gca
gga caa
Val Asp Gly Asn Thr Ile Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln

50
gag gac tat aat aga cta aga cca ttg agc tat cgt ggt gct
gat gtc
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val

65
70
75
80
ttc ttg ctc gca ttc tct cta gtc agc aaa gct agc tat gaa
aat gtt
Phe Leu Leu Ala Phe Ser Leu Val Ser Lys Ala Ser Tyr Glu
Asn Val

85
90
95
gct aaa aag tgg gtt cct gaa ctc aga cat tac gct cct ggt
gtt cca
Ala Lys Lys Trp Val Pro Glu Leu Arg His Tyr Ala Pro Gly
Val Pro

100
105
110
atc atc ctt gtt gga aca aag ctt gat ctt cga gat gat aag
cag tac
Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Tyr

115
120
125
ttt gtt gag cac cct gga gct gtg cct ata tct act gct cag
ggt gaa
Phe Val Glu His Pro Gly Ala Val Pro Ile Ser Thr Ala Gln
Gly Glu

130
135
140
gaa ctg aag aag ctt gtt gga act tct gct tat ata gaa tcc
agt gca
Glu Leu Lys Lys Leu Val Gly Thr Ser Ala Tyr Ile Glu Ser
Ser Ala

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						150								
						155								
160														
aag	acc	caa	cag	aat	gta	aaa	gct	gtc	ttt	gat	gcg	gct	att	
aaa	gta	528												
Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile	
Lys	Val													
						165								
170														
gtt	ctc	cag	cca	cct	aaa	aac	aag	aag	aaa	aag	aag	aga	aag	
tct	cag	576												
Val	Leu	Gln	Pro	Pro	Lys	Asn	Lys	Lys	Lys	Lys	Lys	Arg	Lys	
Ser	Gln													
						180								
						185								
						190								
195														
aaa	ggc	tgt	tct	ata	ttg	tga								
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Lys	Gly	Cys	Ser	Ile	Leu									
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<210> 623
<211> 198
<212> PRT
<213> Brassica napus
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Gly Ala
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Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
          20          25          30
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Ile
          35          40          45
Val Asp Gly Asn Thr Ile Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
          50          55          60
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65          70          75
80
Phe Leu Leu Ala Phe Ser Leu Val Ser Lys Ala Ser Tyr Glu
Asn Val
          85          90

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95
Ala Lys Lys Trp Val Pro Glu Leu Arg His Tyr Ala Pro Gly
Val Pro
100 105 110
Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Tyr
115 120 125
Phe Val Glu His Pro Gly Ala Val Pro Ile Ser Thr Ala Gln
Gly Glu
130 135 140
Glu Leu Lys Lys Leu Val Gly Thr Ser Ala Tyr Ile Glu Ser
Ser Ala
145 150 155
160
Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Lys Val
165 170
175
Val Leu Gln Pro Pro Lys Asn Lys Lys Lys Lys Arg Lys
Ser Gln
180 185 190
Lys Gly Cys Ser Ile Leu
195

<210> 624
<211> 606
<212> DNA
<213> Brassica napus

<220>
<221> CDS
<222> (1)..(606)

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gga gct 48
Met Ser Thr Ala Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10
15
gtg ggg aag act tgt atg ctg att tca tat acc agc aat act
ttt cct 96
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro

0070110

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

0070110

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Arg Val
                                165                                170
175
gcg ttg agg cct cca aag gca aag aag aag ata aag cca ttg
agg acc
Ala Leu Arg Pro Pro Lys Ala Lys Lys Lys Ile Lys Pro Leu
Arg Thr
                                180                                185                                190

aaa aga tca aga aca tgc ttt ttc ctc taa
                                606
Lys Arg Ser Arg Thr Cys Phe Phe Leu
                                195                                200

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<212> PRT
<213> Brassica napus

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

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
                                35                                40                                45

Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
                                50                                55                                60

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

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0070110

Ile Val	Leu Val	Gly Thr	Lys Leu	Asp Leu	Arg Asp	Asp Lys
Gln Phe						
	115		120			125

Leu Lys	Asp His	Pro Gly	Ala Ala	Ser Ile	Thr Thr	Ala Gln
Gly Glu						
	130		135			140

Glu Leu	Arg Lys	Met Ile	Gly Ala	Ile Lys	Tyr Leu	Glu Cys
Ser Ser						
	145		150			155

Lys Thr	Gln Gln	Asn Val	Lys Ala	Val Phe	Asp Thr	Ala Ile
Arg Val						
		165			170	

Ala Leu	Arg Pro	Pro Lys	Ala Lys	Lys Lys	Ile Lys	Pro Leu
Arg Thr						
	180			185		190

Lys Arg	Ser Arg	Thr Cys	Phe Phe	Leu
	195		200	

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 <213> Brassica napus

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ggt gat			48										
Met Ala Ser Ser Ala Ser Lys Phe Ile Lys Cys Val Thr Val													
Gly Asp													
1			5					10					
15													
ggc gcc gtt ggt aaa acc tgt atg ctc atc tgc tac acc agc													
aac aaa			96										
Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser													
Asn Lys													
		20				25						30	
ttc cct act gac tac ata cca aca gtt ttt gac aac ttt agt													
gca aac			144										
Phe Pro Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser													
Ala Asn													

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

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Lys	Glu	Val	Ile	Lys	Pro	Val	Val	Lys	Gln	Lys	Glu	Lys	Thr
Lys	Lys												
			180					185					190

aag	aag	aag	caa	aag	tca	aaa	cat	ggg	tgt	tta	tca	aac	att
ctg	tgt		624										
Lys	Lys	Lys	Gln	Lys	Ser	Lys	His	Gly	Cys	Leu	Ser	Asn	Ile
Leu	Cys												
		195						200					205

ggg	agg	ata	gtg	act	cgg	cat	tga						
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Gly	Arg	Ile	Val	Thr	Arg	His							
	210					215							

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 <213> Brassica napus

<400> 627													
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Gly	Asp												
1				5					10				
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Gly	Ala	Val	Gly	Lys	Thr	Cys	Met	Leu	Ile	Cys	Tyr	Thr	Ser
Asn	Lys												
			20					25					30

Phe	Pro	Thr	Asp	Tyr	Ile	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser
Ala	Asn												
		35					40					45	

Val	Val	Val	Glu	Gly	Thr	Thr	Val	Asn	Leu	Gly	Leu	Trp	Asp
Thr	Ala												
	50					55					60		

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

0070110

Val	Pro	Leu	Val	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Glu
Asp	Lys												
		115					120					125	

His	Tyr	Leu	Ala	Asp	His	Pro	Gly	Leu	Ser	Pro	Val	Thr	Thr
Ala	Gln												
	130					135					140		

Gly	Glu	Glu	Leu	Arg	Lys	Leu	Ile	Gly	Ala	Thr	Tyr	Tyr	Ile
Glu	Cys												
145					150					155			

		160											
Ser	Ser	Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ser
Ala	Ile												
				165					170				

		175											
Lys	Glu	Val	Ile	Lys	Pro	Val	Val	Lys	Gln	Lys	Glu	Lys	Thr
Lys	Lys												
			180					185					190

Lys	Lys	Lys	Gln	Lys	Ser	Lys	His	Gly	Cys	Leu	Ser	Asn	Ile
Leu	Cys												
		195					200					205	

Gly	Arg	Ile	Val	Thr	Arg	His
210						215

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 <213> Brassica napus

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<400> 628													
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gga	gct		48										
Met	Ser	Thr	Ala	Arg	Phe	Ile	Lys	Cys	Val	Thr	Val	Gly	Asp
Gly	Ala												
1				5					10				
15													
gtg	ggg	aag	act	tgt	atg	ctg	att	tca	tat	acc	agc	aat	act
ttt	cct		96										
Val	Gly	Lys	Thr	Cys	Met	Leu	Ile	Ser	Tyr	Thr	Ser	Asn	Thr
Phe	Pro												
			20					25					30

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

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0070110

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Arg Val
                                165                                170
175
gcg ttg agg cct cca aag gca aag aag aag ata aag cca ttg
agg acc
Ala Leu Arg Pro Pro Lys Ala Lys Lys Lys Ile Lys Pro Leu
Arg Thr
                                180                                185                                190

aaa aga tca aga aca tgc ttt ttc ttc taa
                                606
Lys Arg Ser Arg Thr Cys Phe Phe Phe
                                195                                200

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<212> PRT
<213> Brassica napus

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Met Ser Thr Ala Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1                                5                                10
15
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
                                20                                25                                30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
                                35                                40                                45

Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
                                50                                55                                60

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

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0070110

Ile Val	Leu Val	Gly Thr	Lys Leu	Asp Leu	Arg Asp	Asp Lys
Gln Phe						
	115		120			125

Leu Lys	Asp His	Pro Gly	Ala Ala	Ser Ile	Thr Thr	Ala Gln
Gly Glu						
	130		135			140

Glu Leu	Arg Lys	Met Val	Gly Ala	Ile Lys	Tyr Leu	Glu Cys
Ser Ser						
145			150			155

Lys Thr	Gln Gln	Asn Val	Lys Ala	Val Phe	Asp Thr	Ala Ile
Arg Val						
		165			170	

Ala Leu	Arg Pro	Pro Lys	Ala Lys	Lys Lys	Ile Lys	Pro Leu
Arg Thr						
	180			185		190

Lys Arg	Ser Arg	Thr Cys	Phe Phe	Phe
	195		200	

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 <213> Brassica napus

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ggt gcc		48											
Met Ser	Ala Ser	Arg Phe	Ile Lys	Cys Val	Thr Val	Gly Asp							
Gly Ala													
1		5			10								
15													
gtc gga	aaa aca	tgt atg	ctg atc	tct tac	acc agc	aac act							
ttc cct		96											
Val Gly	Lys Thr	Cys Met	Leu Ile	Ser Tyr	Thr Ser	Asn Thr							
Phe Pro													
		20			25					30			
acg gac	tat gtt	cca act	ggt ttc	gac aac	ttc agt	gct aac							
gtg gtt		144											
Thr Asp	Tyr Val	Pro Thr	Val Phe	Asp Asn	Phe Ser	Ala Asn							
Val Val													

0070110

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

Val	Leu	Gln	Pro	Pro	Lys	Gln	Lys	Lys	Lys	Lys	Lys	Lys	Asn
Gly	Cys												
			180					185					190

<210> 631
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<212> PRT
<213> Brassica napus

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
35 40 45

Val Asp Gly Asn Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65 70 75
80

Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Ile
85 90

95
Ala Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Gly
Val Pro
100 105 110

Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe
115 120 125

Phe Ile Asp His Pro Gly Ala Val Pro Ile Thr Thr Asn Gln
Seite 954

[illegible]

<220>
<221> CDS
<222> (1)..(597)

Seite 955

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

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Lys Gly Cys Ser Ile Leu
195

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<211> 198

<212> PRT

<213> Brassica napus

<400> 633

Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala

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15

Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro

20 25 30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Ile

35 40 45

Val Asp Gly Asn Thr Ile Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln

50 55 60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val

65 70 75

80

Phe Leu Leu Ala Phe Ser Leu Val Ser Lys Ala Ser Tyr Glu
Asn Val

85 90

95

Ser Lys Lys Trp Val Pro Glu Leu Arg His Tyr Ala Pro Gly
Val Pro

100 105 110

Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe

115 120 125

Phe Val Glu His Pro Gly Ala Val Pro Ile Ser Thr Ala Gln
Gly Glu

130 135 140

Glu Leu Lys Lys Leu Ile Gly Ala Pro Ala Tyr Ile Glu Cys
Ser Ala

0070110

145 150 155
 160
 Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
 Lys Val
 165 170
 175
 Val Leu Gln Pro Pro Lys Asn Lys Lys Arg Lys Lys Arg Lys
 Ser Gln
 180 185 190
 Lys Gly Cys Ser Ile Leu
 195

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 <212> DNA
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 <222> (1)..(603)

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 ttg ctt 48
 Met Ala Thr Ala Gly Asn Lys Asn Ile Asn Ala Lys Leu Val
 Leu Leu
 1 5 10
 15
 gga gat gtt ggg gct gga aaa tca agt ctt gtg ctt cgg ttt
 gtc aaa 96
 Gly Asp Val Gly Ala Gly Lys Ser Ser Leu Val Leu Arg Phe
 Val Lys
 20 25 30
 gat cag ttt gtt gag ttc cag gaa tca acc ata ggt gca gct
 ttt ttc 144
 Asp Gln Phe Val Glu Phe Gln Glu Ser Thr Ile Gly Ala Ala
 Phe Phe
 35 40 45
 tct caa aca ctg gct gtg aat gac gca act gtc aag ttt gag
 ata tgg 192
 Ser Gln Thr Leu Ala Val Asn Asp Ala Thr Val Lys Phe Glu
 Ile Trp
 50 55 60
 gat aca gct ggt cag gaa cgt tac cat agc ttg gct cca atg
 tac tac 240
 Asp Thr Ala Gly Gln Glu Arg Tyr His Ser Leu Ala Pro Met
 Tyr Tyr

0070110

65					70					75				
80														
agg	ggt	gca	gct	gct	gcc	att	att	gtc	ttt	gac	att	act	aat	
caa	gcg			288										
Arg	Gly	Ala	Ala	Ala	Ala	Ile	Ile	Val	Phe	Asp	Ile	Thr	Asn	
Gln	Ala													
				85					90					
95														
tca	ttt	gag	aga	gcg	aag	aaa	tgg	gtt	caa	gaa	ctg	cag	gca	
caa	ggt			336										
Ser	Phe	Glu	Arg	Ala	Lys	Lys	Trp	Val	Gln	Glu	Leu	Gln	Ala	
Gln	Gly													
				100					105					
aac	cct	aat	atg	gtg	atg	gct	ctt	gct	gga	aac	aaa	gct	gat	
tta	ttg			384										
Asn	Pro	Asn	Met	Val	Met	Ala	Leu	Ala	Gly	Asn	Lys	Ala	Asp	
Leu	Leu													
		115					120					125		
gat	gca	agg	aaa	gtg	tct	cca	gag	gag	gca	gag	aca	tat	gcg	
caa	gag			432										
Asp	Ala	Arg	Lys	Val	Ser	Pro	Glu	Glu	Ala	Glu	Thr	Tyr	Ala	
Gln	Glu													
		130					135					140		
aac	agc	ctt	ttc	ttc	atg	gaa	acc	tca	gcg	aag	act	gca	aca	
aat	gtc			480										
Asn	Ser	Leu	Phe	Phe	Met	Glu	Thr	Ser	Ala	Lys	Thr	Ala	Thr	
Asn	Val													
				145					150					
				155					160					
aaa	gac	atc	ttc	tac	gaa	atc	gca	aaa	agg	cta	ccg	cgc	gtg	
cag	cca			528										
Lys	Asp	Ile	Phe	Tyr	Glu	Ile	Ala	Lys	Arg	Leu	Pro	Arg	Val	
Gln	Pro													
				165					170					
175														
gca	gaa	aac	cca	aca	ggg	atg	ggt	ctc	cca	aac	ggg	cca	gga	
gct	acg			576										
Ala	Glu	Asn	Pro	Thr	Gly	Met	Val	Leu	Pro	Asn	Gly	Pro	Gly	
Ala	Thr													
				180					185					
gca	gca	agc	gca	tca	tgt	tgt	gct	taa						
			603											
Ala	Ala	Ser	Ala	Ser	Cys	Cys	Ala							
		195					200							

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0070110

<211> 200

<212> PRT

<213> Brassica napus

<400> 635

Met Ala Thr Ala Gly Asn Lys Asn Ile Asn Ala Lys Leu Val
Leu Leu

1 5 10

15

Gly Asp Val Gly Ala Gly Lys Ser Ser Leu Val Leu Arg Phe
Val Lys

20 25 30

Asp Gln Phe Val Glu Phe Gln Glu Ser Thr Ile Gly Ala Ala
Phe Phe

35 40 45

Ser Gln Thr Leu Ala Val Asn Asp Ala Thr Val Lys Phe Glu
Ile Trp

50 55 60

Asp Thr Ala Gly Gln Glu Arg Tyr His Ser Leu Ala Pro Met
Tyr Tyr

65 70 75

80

Arg Gly Ala Ala Ala Ala Ile Ile Val Phe Asp Ile Thr Asn
Gln Ala

85 90

95

Ser Phe Glu Arg Ala Lys Lys Trp Val Gln Glu Leu Gln Ala
Gln Gly

100 105 110

Asn Pro Asn Met Val Met Ala Leu Ala Gly Asn Lys Ala Asp
Leu Leu

115 120 125

Asp Ala Arg Lys Val Ser Pro Glu Glu Ala Glu Thr Tyr Ala
Gln Glu

130 135 140

Asn Ser Leu Phe Phe Met Glu Thr Ser Ala Lys Thr Ala Thr
Asn Val

145 150 155

160

Lys Asp Ile Phe Tyr Glu Ile Ala Lys Arg Leu Pro Arg Val
Gln Pro

165 170

0070110

175
Ala Glu Asn Pro Thr Gly Met Val Leu Pro Asn Gly Pro Gly
Ala Thr
180 185 190

Ala Ala Ser Ala Ser Cys Cys Ala
195 200

<210> 636
<211> 594
<212> DNA
<213> Brassica napus

<220>
<221> CDS
<222> (1)..(594)

<400> 636
atg agc gct tcg agg ttc ata aag tgt gtc aca gtc ggc gat
ggt gcc 48
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10
15
gtc gga aaa aca tgt atg ctg atc tct tac acc agc aac act
ttc cct 96
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
20 25 30
acg gac tat gta cca act gtt ttc gac aac ttc agt gct aat
ggt gtt 144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
35 40 45
gta gat ggg aac aca gtt aat ctt ggc ttg tgg gat aca gcc
ggt caa 192
Val Asp Gly Asn Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60
gaa gac tat aac agg tta aga cca ttg agt tac cgt ggt gca
gat gtc 240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65 70 75
80
ttc att ctt gct ttc tcg ctt att agc aaa gct agc tac gag
aac ata 288
Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Seite 961

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Asn Ile
      85                      90
95
gcc aaa aag tgg att cct gag ctc agg cat tat gca cct ggt
gtc ccc
Ala Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Gly
Val Pro
      100                      105                      110

att atc ctc gtt gga tca aag ctt gat ctt cga gat gat aag
cag ttc
Ile Ile Leu Val Gly Ser Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe
      115                      120                      125
ttc atc gac cat cct ggt gct gtc ccc att act act gct cag
gga gag
Phe Ile Asp His Pro Gly Ala Val Pro Ile Thr Thr Ala Gln
Gly Glu
      130                      135                      140
gag ctg agg aag cta ata gat gca cct ttt tac gtc gaa tgc
agt tcc
Glu Leu Arg Lys Leu Ile Asp Ala Pro Phe Tyr Val Glu Cys
Ser Ser
      145                      150                      155
      160
aaa tct caa gag aat gtg aaa gcg gtg ttt gac gca gcc ata
cga gtg
Lys Ser Gln Glu Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Arg Val
      165                      170
      175
gtc ttg caa cct ccg aag cag aag aag aag aag agc aaa gcg
cag aag
Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Ser Lys Ala
Gln Lys
      180                      185                      190

gca tgc tcc atc cta tga
Ala Cys Ser Ile Leu
      195

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<210> 637

<211> 197

<212> PRT

<213> Brassica napus

<400> 637

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Met	Ser	Ala	Ser	Arg	Phe	Ile	Lys	Cys	Val	Thr	Val	Gly	Asp
Gly	Ala												
1				5					10				
15													
Val	Gly	Lys	Thr	Cys	Met	Leu	Ile	Ser	Tyr	Thr	Ser	Asn	Thr
Phe	Pro												
			20					25					30
Thr	Asp	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn
Val	Val												
		35					40					45	
Val	Asp	Gly	Asn	Thr	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala
Gly	Gln												
	50					55					60		
Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala
Asp	Val												
65					70					75			
80													
Phe	Ile	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Lys	Ala	Ser	Tyr	Glu
Asn	Ile												
				85					90				
95													
Ala	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Arg	His	Tyr	Ala	Pro	Gly
Val	Pro												
			100					105					110
Ile	Ile	Leu	Val	Gly	Ser	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys
Gln	Phe												
		115					120					125	
Phe	Ile	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Thr	Thr	Ala	Gln
Gly	Glu												
	130					135						140	
Glu	Leu	Arg	Lys	Leu	Ile	Asp	Ala	Pro	Phe	Tyr	Val	Glu	Cys
Ser	Ser												
145					150					155			
160													
Lys	Ser	Gln	Glu	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile
Arg	Val												
				165					170				
175													
Val	Leu	Gln	Pro	Pro	Lys	Gln	Lys	Lys	Lys	Lys	Ser	Lys	Ala
Gln	Lys												
			180					185					190

0070110

Ala Cys Ser Ile Leu
195

<210> 638
<211> 597
<212> DNA
<213> Brassica napus

<220>
<221> CDS
<222> (1)..(597)

<400> 638
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ggc gcc 48
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10
15
gtc ggc aag act tgt cta ctc atc tcc tac aca agc aac act
ttc ccc 96
Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
20 25 30
act gat tat gtt cca act gtc ttt gat aat ttc agt gct aat
gtg att 144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Ile
35 40 45
gtt gat ggg aac acc atc aac ttg gga ttg tgg gac act gca
gga caa 192
Val Asp Gly Asn Thr Ile Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60
gag gac tat aat aga cta aga cca ttg agc tat cgt ggt gct
gat gtc 240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65 70 75
80
ttc ttg ctc gca ttc tct cta gtc agc aaa gct agc tat gaa
aat gtt 288
Phe Leu Leu Ala Phe Ser Leu Val Ser Lys Ala Ser Tyr Glu
Asn Val
85 90
95
gct aaa aag tgg gtt cct gaa ctc aga cat tac gct cct ggt
gtt cca 336

0070110

Ala	Lys	Lys	Trp	Val	Pro	Glu	Leu	Arg	His	Tyr	Ala	Pro	Gly
Val	Pro												
			100					105					110

atc	atc	ctt	ggt	gga	aca	aag	ctt	gat	ctt	cga	gat	gat	aag
cag	tac			384									
Ile	Ile	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys
Gln	Tyr												

		115					120					125	
ttt	ggt	gag	cac	cct	gga	gct	gtg	cct	ata	tct	act	gct	cag
ggt	gaa		432										
Phe	Val	Glu	His	Pro	Gly	Ala	Val	Pro	Ile	Ser	Thr	Ala	Gln
Gly	Glu												

						135					140		
gaa	ctg	aag	aag	ctt	ggt	gga	gct	tct	gct	tat	ata	gaa	tcc
agt	gca		480										
Glu	Leu	Lys	Lys	Leu	Val	Gly	Ala	Ser	Ala	Tyr	Ile	Glu	Ser
Ser	Ala												

					150					155			
160													
aag	acc	caa	cag	aat	gta	aaa	gct	gtc	ttt	gat	gcg	gct	att
aaa	gta		528										
Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile
Lys	Val												

					165					170			
175													
ggt	ctc	cag	ccc	cct	aaa	aac	aag	aag	aaa	aag	aag	aga	aag
tct	cag		576										
Val	Leu	Gln	Pro	Pro	Lys	Asn	Lys	Lys	Lys	Lys	Lys	Arg	Lys
Ser	Gln												

					180					185			190
aaa	ggc	tgt	tct	ata	ttg	tga							
			597										
Lys	Gly	Cys	Ser	Ile	Leu								
		195											

<210> 639
 <211> 198
 <212> PRT
 <213> Brassica napus

<400> 639
 Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala
 1 5 10
 15
 Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
 Seite 965

0070110

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

<210> 640

<211> 630

0070110

<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (1)..(630)

<400> 640

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gga gct          48
Met Ser Ala Ser Lys Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1          5          10
15
gtc ggg aag aca tgt atg ctt atc tgt tac act agc aac aag
ttt ccc          96
Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser Asn Lys
Phe Pro
20          25          30
act gat tat ata ccg act gtg ttc gac aac ttc agt gcc aat
gtc tcc          144
Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Ser
35          40          45
gtg gat gga cag atc gtg aat cta ggg cta tgg gac act gct
ggt caa          192
Val Asp Gly Gln Ile Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50          55          60
gaa gat tac agt agg ttg agg cca ttg agt tac aga gga gct
gat atc          240
Glu Asp Tyr Ser Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Ile
65          70          75
80
ttc gtc tta gcc ttt tct ctt atc agc aag gcc agt tac gag
aat gta          288
Phe Val Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val
85          90
95
cta aag aag tgg atg cct gaa ctt cgt cgg ttt gcg cct aat
gtt ccc          336
Leu Lys Lys Trp Met Pro Glu Leu Arg Arg Phe Ala Pro Asn
Val Pro
100          105          110
att gtc ctt gtt ggt aca aag cta gat ctc cgt gat gac aag
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Seite 967

0070110

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gga tac      384
Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gly Tyr
      115      120      125
ctc gcg gat cac acc aat gtc att acc tct act cag gga gag
gaa ttg      432
Leu Ala Asp His Thr Asn Val Ile Thr Ser Thr Gln Gly Glu
Glu Leu
      130      135      140
agg aag caa atc ggt gca gct gct tac atc gag tgc agt tcc
aag act      480
Arg Lys Gln Ile Gly Ala Ala Ala Tyr Ile Glu Cys Ser Ser
Lys Thr
145      150      155
      160
caa cag aat gtg aaa gga gtg ttt gac aca gcg atc aaa gtg
gtt ctc      528
Gln Gln Asn Val Lys Gly Val Phe Asp Thr Ala Ile Lys Val
Val Leu
      165      170
175
cag cca cca cgg agg aaa gag gtc act ggg aat aag aag aaa
cac aga      576
Gln Pro Pro Arg Arg Lys Glu Val Thr Gly Asn Lys Lys Lys
His Arg
      180      185      190
aga tcc ggc tgc tcc ttt gcg agc att gtc tgc gga ggc tgc
gcc aca      624
Arg Ser Gly Cys Ser Phe Ala Ser Ile Val Cys Gly Gly Cys
Ala Thr
      195      200      205
gct tag
      630
Ala

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<210> 641
 <211> 209
 <212> PRT
 <213> Brassica napus

<400> 641
 Met Ser Ala Ser Lys Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala
 1 5 10
 15
 Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser Asn Lys

0070110

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

0070110

<210> 642
<211> 594
<212> DNA
<213> Brassica napus

<220>
<221> CDS
<222> (1)..(594)

<400> 642
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gga gct 48
Met Ser Ala Ser Arg Phe Val Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10
15
gtc gga aaa aca tgt ttg ttg att tct tac aca agc aac act
ttc cct 96
Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
20 25 30
acg gac tat gtg ccc acc gtt ttc gat aat ttc agt gct aat
gtg gtg 144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
35 40 45
gtt aac gga gcc acc gtt aat ctt gga ttg tgg gat act gca
ggg caa 192
Val Asn Gly Ala Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60
gag gat tac aac aga tta aga cca cta agc tac cgt gga gca
gat gtt 240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65 70 75
80
ttc ata ttg gcc ttc tct ctt atc agt aaa gcc agt tat gaa
aac gtc 288
Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val
85 90
95
tcc aaa aag tgg atc ccg gag ttg aaa cat tac gcg cct ggt
gtc ccc 336

0070110

Ser	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Lys	His	Tyr	Ala	Pro	Gly
Val	Pro												
			100					105					110

atc	atc	ctt	ggt	gga	tca	aag	ctt	gat	ctt	cga	gat	gat	aag
cag	ttc		384										
Ile	Ile	Leu	Val	Gly	Ser	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys
Gln	Phe												

		115					120					125	
ttc	atc	gac	cat	cct	ggt	gct	gtc	cca	att	act	act	gct	cag
gga	gag		432										
Phe	Ile	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Thr	Thr	Ala	Gln
Gly	Glu												

		130				135					140		
gag	ctg	agg	aag	cta	ata	gat	gca	cct	act	tac	atc	gaa	tgc
agt	tcc		480										
Glu	Leu	Arg	Lys	Leu	Ile	Asp	Ala	Pro	Thr	Tyr	Ile	Glu	Cys
Ser	Ser												
145					150					155			

		160											
aaa	tct	caa	gag	aat	gtg	aaa	gct	gtc	ttt	gac	gca	gcc	ata
cga	gtg		528										
Lys	Ser	Gln	Glu	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile
Arg	Val												
					165					170			

		175											
gtg	ttg	caa	ccg	cct	aag	cag	aag	aag	aaa	aag	agc	aaa	gcg
cag	aag		576										
Val	Leu	Gln	Pro	Pro	Lys	Gln	Lys	Lys	Lys	Lys	Ser	Lys	Ala
Gln	Lys												
			180							185			190

gca	tgc	tcc	atc	caa	tga
			594		
Ala	Cys	Ser	Ile	Gln	
		195			

<210> 643
 <211> 197
 <212> PRT
 <213> Brassica napus

		400											
Met	Ser	Ala	Ser	Arg	Phe	Val	Lys	Cys	Val	Thr	Val	Gly	Asp
Gly	Ala												
1				5						10			
15													
Val	Gly	Lys	Thr	Cys	Leu	Leu	Ile	Ser	Tyr	Thr	Ser	Asn	Thr

0070110

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

<210> 644

<211> 636

0070110

<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (1)..(636)

<400> 644

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atg tca gct tca gtg gct gct gca tca gta tca aca aca aca
aca gca          48
Met Ser Ala Ser Val Ala Ala Ala Ser Val Ser Thr Thr Thr
Thr Ala
  1              5              10
15
gct aca acg ttt atc aag tgc gtc act gtt ggc gat gga gct
gtg ggc          96
Ala Thr Thr Phe Ile Lys Cys Val Thr Val Gly Asp Gly Ala
Val Gly
      20              25              30
aaa act tgt ctt ctt atc tcc tac acc agc aac acc ttt cct
act gat          144
Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr Phe Pro
Thr Asp
      35              40              45
tat gtt cct aca gtg ttc gac aac ttc agt gca aat gtt cta
gtc gat          192
Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn Val Leu
Val Asp
      50              55              60
ggc aaa acc gtc aat ctt ggt ctt tgg gat act gct ggt caa
gaa gat          240
Gly Lys Thr Val Asn Leu Gly Leu Trp Asp Thr Ala Gly Gln
Glu Asp
      65              70              75
80
tac aat agg ctt aga cca ttg agt tac aga gga gca gat gtt
ttc att          288
Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala Asp Val
Phe Ile
      85              90
95
ctt gcc ttt tct ctt atc agc agg cct agc ttt gag aac att
gct aaa          336
Leu Ala Phe Ser Leu Ile Ser Arg Pro Ser Phe Glu Asn Ile
Ala Lys
      100              105              110
aag tgg gtc cct gag ctg cga cat tat gcc cct aac gtg cct
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0070110

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att gtt      384
Lys Trp Val Pro Glu Leu Arg His Tyr Ala Pro Asn Val Pro
Ile Val
      115      120      125
cta gtg gga act aaa tta gat cta aga gag gat aag aag ttc
cca atg      432
Leu Val Gly Thr Lys Leu Asp Leu Arg Glu Asp Lys Lys Phe
Pro Met
      130      135      140
aac tat cca ggt gct tgc aca atc tca aca gaa caa ggt caa
gag cta      480
Asn Tyr Pro Gly Ala Cys Thr Ile Ser Thr Glu Gln Gly Gln
Glu Leu
145      150      155
      160
aga aaa gag ata gga gca tta gca tat ata gag tgc agc tca
aaa aca      528
Arg Lys Glu Ile Gly Ala Leu Ala Tyr Ile Glu Cys Ser Ser
Lys Thr
      165      170
175
caa cag aac gtg aaa gcg gtg ttt gat gca gcg ata aaa gta
gtt cta      576
Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile Lys Val
Val Leu
      180      185      190
cag cct cct aca aaa att aag aaa caa aag aga aga ttt cgt
ttc tgc      624
Gln Pro Pro Thr Lys Ile Lys Lys Gln Lys Arg Arg Phe Arg
Phe Cys
      195      200      205
cat gct ctc tga
      636
His Ala Leu
      210

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<210> 645
 <211> 211
 <212> PRT
 <213> Brassica napus

<400> 645
 Met Ser Ala Ser Val Ala Ala Ala Ser Val Ser Thr Thr Thr
 Thr Ala
 1 5 10
 15
 Ala Thr Thr Phe Ile Lys Cys Val Thr Val Gly Asp Gly Ala

0070110

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

210

<210> 646
 <211> 591
 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (1)..(591)

<400> 646
 atg agt gct tca agg ttc ata aag tgc gtc acc gtc ggt gac
 ggc gcc 48
 Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala
 1 5 10
 15
 gtc ggc aag act tgt cta ctc atc tcc tac aca agc aac act
 ttc ccc 96
 Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
 Phe Pro
 20 25 30
 act gat tat gtt cca act gtc ttt gat aat ttc agt gct aat
 gtg att 144
 Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
 Val Ile
 35 40 45
 gtt gat ggg aac acc atc aac ttg gga ttg tgg gac act gca
 gga caa 192
 Val Asp Gly Asn Thr Ile Asn Leu Gly Leu Trp Asp Thr Ala
 Gly Gln
 50 55 60
 gag gac tat aat aga cta aga cca ttg agc tat cgt ggt gct
 gat gtc 240
 Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
 Asp Val
 65 70 75
 80
 ttc ttg ctc gca ttc tct cta gtc agc aaa gct agc tat gaa
 aat gtt 288
 Phe Leu Leu Ala Phe Ser Leu Val Ser Lys Ala Ser Tyr Glu
 Asn Val
 85 90
 95
 gct aaa aag tgg gtt cct gaa ctc aga cat tac gct cct ggt
 gtt cca 336
 Ala Lys Lys Trp Val Pro Glu Leu Arg His Tyr Ala Pro Gly
 Seite 976

0070110

Val Pro

			100				105				110	
atc	atc	ctt	ggt	gga	aca	aag	ctt	gat	ctt	cga	gat	aag
cag	tac		384									
Ile	Ile	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Lys
Gln	Tyr											
		115					120				125	
ttt	ggt	gag	cac	cct	gga	gct	gtg	cct	ata	tct	act	cag
ggt	gaa		432									
Phe	Val	Glu	His	Pro	Gly	Ala	Val	Pro	Ile	Ser	Thr	Gln
Gly	Glu											
		130					135				140	
gaa	ctg	aag	aag	ctt	ggt	gga	gct	tct	gct	tat	ata	tcc
agt	gca		480									
Glu	Leu	Lys	Lys	Leu	Val	Gly	Ala	Ser	Ala	Tyr	Ile	Ser
Ser	Ala											
145					150					155		
	160											
aag	acc	caa	cag	aat	gta	aaa	gct	gtc	ttt	gat	gcg	att
aaa	gta		528									
Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ile
Lys	Val											
				165					170			
175												
ggt	ctc	cag	cca	cct	aaa	aac	aaa	aac	aag	aga	aaa	tct
aaa	gga		576									
Val	Leu	Gln	Pro	Pro	Lys	Asn	Lys	Asn	Lys	Arg	Lys	Gln
Lys	Gly											
			180						185			190
tgt	tcc	ata	ttg	tga								
			591									
Cys	Ser	Ile	Leu									
		195										

<210> 647
 <211> 196
 <212> PRT
 <213> Brassica napus

<400> 647
 Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala
 1 5 10
 15
 Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr

0070110

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

<210> 648

<211> 594

0070110

<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (1)..(594)

<400> 648

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atg agc gcg tca agg ttc ata aag tgt gtt act gtc gga gat
ggt gct          48
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1          5          10
15
gtc gga aaa acc tgc atg ctg atc tct tac acc agc aac act
ttc ccc          96
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
20          25          30
act gac tat gtg cca act gtg ttc gac aac ttc agt gct aat
gtg gtt          144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
35          40          45
gta gat ggg aac acc gtc aat ctt ggc ttg tgg gac aca gct
gga caa          192
Val Asp Gly Asn Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50          55          60
gaa gac tac aac agg tta cga cct ctg agt tac cgt ggc gct
gat gtt          240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65          70          75
80
ttc att ctt gcc ttc tct ctc atc agc aag gct agc tat gag
aat atc          288
Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Ile
85          90
95
gcc aaa aag tgg att cct gag ctg agg cac tat gct cct ggt
gtt ccc          336
Ala Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Gly
Val Pro
100          105          110
atc atc ctc gtt ggc aca aaa ctt gac ctt cga gat gac aaa
```

0070110

```

caa ttc          384
Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe
          115          120          125
ttc ata gat cat cct ggt gct gta ccc atc act aca aac cag
gga gag          432
Phe Ile Asp His Pro Gly Ala Val Pro Ile Thr Thr Asn Gln
Gly Glu
          130          135          140
gag ctg aag aaa ctg att ggg tct gcg gtc tac att gaa tgt
agt tca          480
Glu Leu Lys Lys Leu Ile Gly Ser Ala Val Tyr Ile Glu Cys
Ser Ser
145          150          155
          160
aag aca cag caa aat gtg aag gca gtg ttt gat gca gcc atc
aaa gtg          528
Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Lys Val
          165          170
175
gtg ctt cag cca cca aag cag aaa aag aag aag aaa aag aac
aag aac          576
Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Lys Lys Asn
Lys Asn
          180          185          190

cgt tgc gcc ttc ttg tga
          594
Arg Cys Ala Phe Leu
          195

```

<210> 649
 <211> 197
 <212> PRT
 <213> Brassica napus

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<400> 649
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1          5          10
15
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
          20          25          30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val

```


0070110
40

35

45

Val Asp Gly Asn Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65 70 75
80

Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Ile
85 90

95
Ala Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Gly
Val Pro
100 105 110

Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe
115 120 125

Phe Ile Asp His Pro Gly Ala Val Pro Ile Thr Thr Asn Gln
Gly Glu
130 135 140

Glu Leu Lys Lys Leu Ile Gly Ser Ala Val Tyr Ile Glu Cys
Ser Ser
145 150 155
160

Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Lys Val
165 170

175
Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Lys Asn
Lys Asn
180 185 190

Arg Cys Ala Phe Leu
195

<210> 650
<211> 648
<212> DNA
<213> Brassica napus

<220>
<221> CDS

<222> (1)..(648)

<400> 650

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atg gct tca agt gct tca aag ttc ata aaa tgt gtg act gtt
ggt gat          48
Met Ala Ser Ser Ala Ser Lys Phe Ile Lys Cys Val Thr Val
Gly Asp
  1              5              10
15
ggc gcc gtt ggt aaa acc tgt atg ctc atc tgc tac acc agc
aac aaa          96
Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser
Asn Lys
      20              25              30
ttc cct act gac tac ata cca aca gtt ttt gac aac ttt agt
gca aac          144
Phe Pro Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser
Ala Asn
      35              40              45
gtt gta gtt gaa ggc acc act gtg aac cta ggc cta tgg gac
act gct          192
Val Val Val Glu Gly Thr Thr Val Asn Leu Gly Leu Trp Asp
Thr Ala
      50              55              60
ggg caa gaa gac tat aac aga tta agg cct tta agt tac aga
gga gca          240
Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg
Gly Ala
      65              70              75
80
gat gtt ttc gtc ttg tct ttc tca ttg gtc agc cga gct agc
tac gag          288
Asp Val Phe Val Leu Ser Phe Ser Leu Val Ser Arg Ala Ser
Tyr Glu
      85              90
95
aat gtt ttt aaa aag tgg atc cct gaa ctc caa cac ttt gcc
cca gga          336
Asn Val Phe Lys Lys Trp Ile Pro Glu Leu Gln His Phe Ala
Pro Gly
      100              105              110
gtt cca tta gtc ctt gtt ggt acc aaa tta gat ctc cgt gaa
gat aag          384
Val Pro Leu Val Leu Val Gly Thr Lys Leu Asp Leu Arg Glu
Asp Lys
      115              120              125
cat tat ttg gct gac cat cct gga cta tcc cct gta act act

```

0070110

```

gca cag      432
His Tyr Leu Ala Asp His Pro Gly Leu Ser Pro Val Thr Thr
Ala Gln
130
gga gag gaa ttg cgt aag cta att ggt gca aca tat tac att
gaa tgc      480
Gly Glu Glu Leu Arg Lys Leu Ile Gly Ala Thr Tyr Tyr Ile
Glu Cys
145      150      155
160
agc tca aaa act caa cag aat gtg aaa gca gtt ttt gat tca
gca atc      528
Ser Ser Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ser
Ala Ile
165      170
175
aag gaa gtg atc aaa ccg gtg gtt aaa caa aag gag aag acg
aag aaa      576
Lys Glu Val Ile Lys Pro Val Val Lys Gln Lys Glu Lys Thr
Lys Lys
180      185      190
aag aag aag caa aag tca aat cat ggg tgt tta tca aac gtt
ctg tgt      624
Lys Lys Lys Gln Lys Ser Asn His Gly Cys Leu Ser Asn Val
Leu Cys
195      200      205
ggg agg ata gtg act cgg cat tga
Gly Arg Ile Val Thr Arg His
210      215

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<210> 651

<211> 215

<212> PRT

<213> Brassica napus

<400> 651

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Met Ala Ser Ser Ala Ser Lys Phe Ile Lys Cys Val Thr Val
Gly Asp
1      5      10
15
Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser
Asn Lys
20      25      30
Phe Pro Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser
Ala Asn

```

0070110
40

35

45

Val Val Val Glu Gly Thr Thr Val Asn Leu Gly Leu Trp Asp
Thr Ala
50 55 60

Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg
Gly Ala
65 70 75
80

Asp Val Phe Val Leu Ser Phe Ser Leu Val Ser Arg Ala Ser
Tyr Glu
85 90

95
Asn Val Phe Lys Lys Trp Ile Pro Glu Leu Gln His Phe Ala
Pro Gly
100 105 110

Val Pro Leu Val Leu Val Gly Thr Lys Leu Asp Leu Arg Glu
Asp Lys
115 120 125

His Tyr Leu Ala Asp His Pro Gly Leu Ser Pro Val Thr Thr
Ala Gln
130 135 140

Gly Glu Glu Leu Arg Lys Leu Ile Gly Ala Thr Tyr Tyr Ile
Glu Cys
145 150 155
160

Ser Ser Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ser
Ala Ile
165 170

175
Lys Glu Val Ile Lys Pro Val Val Lys Gln Lys Glu Lys Thr
Lys Lys
180 185 190

Lys Lys Lys Gln Lys Ser Asn His Gly Cys Leu Ser Asn Val
Leu Cys
195 200 205

Gly Arg Ile Val Thr Arg His
210 215

<210> 652
<211> 594
<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (1)..(594)

<400> 652

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atg agc gca tct cgg ttc ata aag tgc gtg acg gtt ggt gac
gga gca          48
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
  1              5              10
15
gtg ggc aaa aca tgt ctc ctc atc tct tac acc agc aac act
ttc cct          96
Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
      20              25              30
acg gat tat gtt ccc act gtt ttc gat aac ttt agc gct aat
ggt gtt          144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
      35              40              45
gtt aac gga gcc act gtc aac tta gga ctc tgg gat acc gca
ggg cag          192
Val Asn Gly Ala Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
      50              55              60
gag gat tat aac aga ttg aga ccc ttg agt tac cgc ggt gct
gac gtt          240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
      65              70              75
80
ttc atc tta gcc ttc tct ctc atc agt aag gct agt tat gag
aat gtc          288
Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val
      85              90
95
tcc aag aag tgg atc cct gag ctg acc cac tat gcc cct ggt
gtc cct          336
Ser Lys Lys Trp Ile Pro Glu Leu Thr His Tyr Ala Pro Gly
Val Pro
      100              105              110
att gtt ctt gtt ggt acc aaa cta gat ctt agg gat gac aaa
cag ttc          384

```

Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe

gga gag 432
Phe Val Asp His Pro Gly Ala Val Pro Ile Thr Thr Ala Gln
Gly Glu

agt tca 480
Glu Leu Met Lys Leu Ile Gly Ala Pro Ser Tyr Ile Glu Cys
Ser Ser

aaa tca cag gag aac gtg aag ggg gtg ttt gat gca gcg atc
aga gtg 528

175	165	170
-----	-----	-----

Val⁵ Leu⁶ Gln⁷ Pro⁸ Pro⁹ Lys¹⁰ Gln¹¹ Lys¹² Lys¹³ Lys¹⁴ Lys¹⁵ Ser¹⁶ Lys¹⁷ Ala¹⁸
Gln¹⁹ Lys²⁰

gcc tgc tcc att ttg tga
594

<210> 653

<213> Brassica napus

Gly	Ala	5	10	15	20	25	30	35	40	45	50	55	60	65	70	75	80	85	90	95	100
1		5		10		15		20		25		30		35		40		45		50	

Phe Pro 20 25 30

[illegible]

0070110

Val Asn Gly Ala Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln

50

55

60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65 70 75

80

Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val

85

90

95

Ser Lys Lys Trp Ile Pro Glu Leu Thr His Tyr Ala Pro Gly
Val Pro

100

105

110

Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe

115

120

125

Phe Val Asp His Pro Gly Ala Val Pro Ile Thr Thr Ala Gln
Gly Glu
130 135 140

Glu Leu Met Lys Leu Ile Gly Ala Pro Ser Tyr Ile Glu Cys
Ser Ser
145 150 155

160

Lys Ser Gln Glu Asn Val Lys Gly Val Phe Asp Ala Ala Ile
Arg Val

165

170

175

Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Ser Lys Ala
Gln Lys

180

185

190

Ala Cys Ser Ile Leu
195

<210> 654

<211> 630

<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (1)..(630)

<400> 654

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atg agt gct tca aag ttc att aaa tgt gta act gtc gga gac
gga gct          48
Met Ser Ala Ser Lys Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
  1              5              10
15
gtc ggg aag aca tgt atg ctt atc tgt tac acc agc aac aag
ttt ccc          96
Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser Asn Lys
Phe Pro
      20              25              30
act gat tat ata ccg act gtg ttc gac aac ttc agt gcc aat
gtc tcc          144
Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Ser
      35              40              45
gtg gat gga cag atc gtg aat ctg ggg cta tgg gac act gct
ggt caa          192
Val Asp Gly Gln Ile Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
      50              55              60
gaa gat tac agt agg ttg agg ccg ttg agt tac aga gga gct
gat atc          240
Glu Asp Tyr Ser Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Ile
  65              70              75
80
ttc gtc tta gcc ttt tct ctt atc agc aag gcc agt tac gag
aat gta          288
Phe Val Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val
      85              90
95
ctt aag aag tgg atg cct gaa ctt cgt agg ttt gct cca aat
ggt ccc          336
Leu Lys Lys Trp Met Pro Glu Leu Arg Arg Phe Ala Pro Asn
Val Pro
      100              105              110
ata gtt ctt gtt ggt aca aag cta gat ctt cgt gat gat aag
gga tac          384
Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gly Tyr
      115              120              125
ctc gct gat cat acc aat gtc att acc tct act cag gga gag

```


0070110

```

gaa ttg      432
Leu Ala Asp His Thr Asn Val Ile Thr Ser Thr Gln Gly Glu
Glu Leu
130
agg aag caa atc ggt gca gct gct tac atc gag tgc agt tcc
aag act      480
Arg Lys Gln Ile Gly Ala Ala Ala Tyr Ile Glu Cys Ser Ser
Lys Thr
145      150      155
160
caa cag aat gtg aaa gca gtg ttt gac aca gcg atc aaa gtg
ggt ctc      528
Gln Gln Asn Val Lys Ala Val Phe Asp Thr Ala Ile Lys Val
Val Leu
165      170
175
cag cca ccg tgg agg aaa gag gtc act ggg aat aag aag aaa
cac aga      576
Gln Pro Pro Trp Arg Lys Glu Val Thr Gly Asn Lys Lys Lys
His Arg
180      185      190
aga tcc ggt tgc tcc ttt gcg agc att gtc tgt gga ggc tgc
gcc aca      624
Arg Ser Gly Cys Ser Phe Ala Ser Ile Val Cys Gly Gly Cys
Ala Thr
195      200      205
gct tag
Ala      630

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<210> 655
 <211> 209
 <212> PRT
 <213> Brassica napus

```

<400> 655
Met Ser Ala Ser Lys Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1      5      10
15
Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser Asn Lys
Phe Pro
20      25      30
Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Ser

```

0070110
40

35

45

Val Asp Gly Gln Ile Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60

Glu Asp Tyr Ser Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Ile
65 70 75
80

Phe Val Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val
85 90

95
Leu Lys Lys Trp Met Pro Glu Leu Arg Arg Phe Ala Pro Asn
Val Pro
100 105 110

Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gly Tyr
115 120 125

Leu Ala Asp His Thr Asn Val Ile Thr Ser Thr Gln Gly Glu
Glu Leu
130 135 140

Arg Lys Gln Ile Gly Ala Ala Ala Tyr Ile Glu Cys Ser Ser
Lys Thr
145 150 155
160

Gln Gln Asn Val Lys Ala Val Phe Asp Thr Ala Ile Lys Val
Val Leu
165 170

175
Gln Pro Pro Trp Arg Lys Glu Val Thr Gly Asn Lys Lys Lys
His Arg
180 185 190

Arg Ser Gly Cys Ser Phe Ala Ser Ile Val Cys Gly Gly Cys
Ala Thr
195 200 205

Ala

<210> 656
<211> 594
<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (1)..(594)

<400> 656

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atg agc gct tcg aga ttc gta aag tgt gta acg gtt ggt gat
gga gct          48
Met Ser Ala Ser Arg Phe Val Lys Cys Val Thr Val Gly Asp
Gly Ala
  1              5              10
15
gtc gga aaa aca tgt ttg ttg att tct tac aca agc aac act
ttc cct          96
Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
      20              25              30
acg gac tat gtg ccc acc gtt ttc gat aat ttc agt gct aat
gtg gtg          144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
      35              40              45
gtt aac gga gcc acc gtt aat ctt gga ttg tgg gat act gca
ggg caa          192
Val Asn Gly Ala Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
      50              55              60
gag gat tac aac aga cta aga cca ctg agc tat cgt gga gca
gat gtt          240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
      65              70              75
80
ttc atc ttg gcc ttc tct ctt atc agt aaa gcc agt tat gaa
aac gtc          288
Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val
      85              90
95
tcc aaa aag tgg atc cct gag ctg aaa cat tac gct cct ggt
gtc ccc          336
Ser Lys Lys Trp Ile Pro Glu Leu Lys His Tyr Ala Pro Gly
Val Pro
      100              105              110
atc att ctc gtt gga tca aag ctt gat ctt cga gat gat aag
cag ttc          384

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0070110

Ile	Ile	Leu	Val	Gly	Ser	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys
Gln	Phe												
		115					120					125	
ttc	atc	gac	cat	cct	ggt	gct	gtc	ccc	att	act	act	gct	cag
gga	gag		432										
Phe	Ile	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Thr	Thr	Ala	Gln
Gly	Glu												
	130					135					140		
gag	ctg	agg	aag	ctt	ata	gat	gca	cct	act	tac	gtc	gaa	tgc
agt	tcc		480										
Glu	Leu	Arg	Lys	Leu	Ile	Asp	Ala	Pro	Thr	Tyr	Val	Glu	Cys
Ser	Ser												
145					150					155			
160													
aaa	tct	caa	gag	aat	gtg	aaa	gcg	gtg	ttt	gac	gca	gcc	ata
cga	gtg		528										
Lys	Ser	Gln	Glu	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile
Arg	Val												
				165					170				
175													
gtc	ttg	caa	cct	ccg	aag	cag	aag	aag	aag	aag	agc	aaa	gcg
cag	aag		576										
Val	Leu	Gln	Pro	Pro	Lys	Gln	Lys	Lys	Lys	Lys	Ser	Lys	Ala
Gln	Lys												
			180					185				190	
gca	tgc	tcc	atc	cta	tga								
			594										
Ala	Cys	Ser	Ile	Leu									
		195											

<210> 657
 <211> 197
 <212> PRT
 <213> Brassica napus

<400> 657													
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Gly	Ala												
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15													
Val	Gly	Lys	Thr	Cys	Leu	Leu	Ile	Ser	Tyr	Thr	Ser	Asn	Thr
Phe	Pro												
			20					25				30	
Thr	Asp	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn
Val	Val												
		35					40					45	

0070110

Val Asn Gly Ala Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65 70 75

80
Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val
85 90

95
Ser Lys Lys Trp Ile Pro Glu Leu Lys His Tyr Ala Pro Gly
Val Pro
100 105 110

Ile Ile Leu Val Gly Ser Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe
115 120 125

Phe Ile Asp His Pro Gly Ala Val Pro Ile Thr Thr Ala Gln
Gly Glu
130 135 140

Glu Leu Arg Lys Leu Ile Asp Ala Pro Thr Tyr Val Glu Cys
Ser Ser
145 150 155

160
Lys Ser Gln Glu Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Arg Val
165 170

175
Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Ser Lys Ala
Gln Lys
180 185 190

Ala Cys Ser Ile Leu
195

<210> 658
<211> 594
<212> DNA
<213> Brassica napus

<220>
<221> CDS
<222> (1)..(594)

0070110

<400> 658

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gga	gct			48									
Met	Ser	Ala	Ser	Arg	Phe	Ile	Lys	Cys	Val	Thr	Val	Gly	Asp
Gly	Ala												
1				5					10				
15													
gtg	ggc	aaa	aca	tgt	ctc	ctc	att	tct	tac	acc	agc	aac	act
ttc	cct			96									
Val	Gly	Lys	Thr	Cys	Leu	Leu	Ile	Ser	Tyr	Thr	Ser	Asn	Thr
Phe	Pro												
			20					25					30
acg	gat	tat	ggt	ccg	act	ggt	ttt	gat	aac	ttt	agc	gct	aat
gtg	ggt			144									
Thr	Asp	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn
Val	Val												
		35					40					45	
ggt	aac	gga	gcc	act	gtc	aac	ctt	ggc	ttg	tgg	gat	acc	gct
ggg	cag			192									
Val	Asn	Gly	Ala	Thr	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala
Gly	Gln												
		50				55					60		
gag	gat	tat	aac	agg	tta	aga	cca	ttg	agt	tac	cgc	ggc	gct
gat	ggt			240									
Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala
Asp	Val												
65					70					75			
80													
ttc	atc	tta	gcc	ttc	tcc	ctc	atc	agt	aag	gct	agt	tat	gag
aat	gtc			288									
Phe	Ile	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Lys	Ala	Ser	Tyr	Glu
Asn	Val												
				85					90				
95													
tcc	aag	aag	tgg	atc	cct	gag	ctg	act	cac	tat	gcc	cct	ggc
gtc	cca			336									
Ser	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Thr	His	Tyr	Ala	Pro	Gly
Val	Pro												
			100					105					110
att	ggt	ctt	ggt	ggc	acc	aaa	cta	gat	ctt	agg	gat	gac	aaa
cag	ttc			384									
Ile	Val	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys
Gln	Phe												
		115					120					125	
ttc	ggt	gac	cac	cct	ggc	gct	gta	cct	att	acc	act	gct	cag
gga	gag			432									

0070110

Phe	Val	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Thr	Thr	Ala	Gln
Gly	Glu												
	130					135					140		
gaa	ctg	atg	aag	cta	att	gga	gct	cct	tcg	tac	atc	gag	tgc
agt	tca		480										
Glu	Leu	Met	Lys	Leu	Ile	Gly	Ala	Pro	Ser	Tyr	Ile	Glu	Cys
Ser	Ser												
145					150					155			
160													
aaa	tca	cag	gag	aac	gtg	aag	ggg	gtg	ttt	gat	gca	gcg	att
aga	gtg		528										
Lys	Ser	Gln	Glu	Asn	Val	Lys	Gly	Val	Phe	Asp	Ala	Ala	Ile
Arg	Val												
				165					170				
175													
gta	ctt	caa	cct	cca	aag	cag	aag	aaa	aag	aag	ggc	aaa	gta
caa	aag		576										
Val	Leu	Gln	Pro	Pro	Lys	Gln	Lys	Lys	Lys	Lys	Gly	Lys	Val
Gln	Lys												
			180					185					190
gcc	tgc	tcc	att	ttg	taa								
			594										
Ala	Cys	Ser	Ile	Leu									
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 <213> Brassica napus

<400> 659													
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Gly	Ala												
1				5					10				
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Val	Gly	Lys	Thr	Cys	Leu	Leu	Ile	Ser	Tyr	Thr	Ser	Asn	Thr
Phe	Pro												
			20					25				30	
Thr	Asp	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn
Val	Val												
		35					40					45	
Val	Asn	Gly	Ala	Thr	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala
Gly	Gln												
	50					55					60		

0070110

Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala
Asp	Val												
65					70					75			
	80												
Phe	Ile	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Lys	Ala	Ser	Tyr	Glu
Asn	Val												
				85					90				
95													
Ser	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Thr	His	Tyr	Ala	Pro	Gly
Val	Pro												
			100					105					110
Ile	Val	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys
Gln	Phe												
		115					120				125		
Phe	Val	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Thr	Thr	Ala	Gln
Gly	Glu												
	130					135					140		
Glu	Leu	Met	Lys	Leu	Ile	Gly	Ala	Pro	Ser	Tyr	Ile	Glu	Cys
Ser	Ser												
145					150					155			
	160												
Lys	Ser	Gln	Glu	Asn	Val	Lys	Gly	Val	Phe	Asp	Ala	Ala	Ile
Arg	Val												
				165					170				
175													
Val	Leu	Gln	Pro	Pro	Lys	Gln	Lys	Lys	Lys	Lys	Gly	Lys	Val
Gln	Lys												
			180					185					190
Ala	Cys	Ser	Ile	Leu									
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 <213> Brassica napus

<220>
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 <222> (1)..(591)

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 Seite 996

0070110

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

0070110

Glu Leu Lys Lys Leu Ile Gly Ser Pro Val Tyr Ile Glu Cys
 Ser Ser
 145 150 155

160
 aag acg cag cag aat gtc aaa gca gtc ttt gac gca gct att
 aaa gtg 528
 Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
 Lys Val

165 170
 175
 gtg ctt cag cca cca aaa tca aag aag aag aaa aag aac aag
 aat cgt 576
 Val Leu Gln Pro Pro Lys Ser Lys Lys Lys Lys Lys Asn Lys
 Asn Arg
 180 185 190

tgc gtt ttc ttg tga
 591
 Cys Val Phe Leu
 195

<210> 661
 <211> 196
 <212> PRT
 <213> Brassica napus

<400> 661
 Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala
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 Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
 Phe Pro
 20 25 30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
 Val Val
 35 40 45

Val Asp Gly Asn Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
 Gly Gln
 50 55 60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
 Asp Val
 65 70 75
 80

0070110

Phe Ile Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Ile

85

90

95

Ala Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Gly
Val Pro

100

105

110

Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe

115

120

125

Phe Ile Asp His Pro Gly Ala Val Pro Ile Thr Thr Asn Gln
Gly Glu

130

135

140

Glu Leu Lys Lys Leu Ile Gly Ser Pro Val Tyr Ile Glu Cys
Ser Ser

145

150

155

160

Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Lys Val

165

170

175

Val Leu Gln Pro Pro Lys Ser Lys Lys Lys Lys Lys Asn Lys
Asn Arg

180

185

190

Cys Val Phe Leu
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<210> 662

<211> 651

<212> DNA

<213> Brassica napus

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<221> CDS

<222> (1)..(651)

<400> 662

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ggt gat 48

Met Ala Ser Thr Ala Ser Lys Phe Ile Lys Cys Val Thr Val
Gly Asp

1

5

10

15

ggc gcc gta ggt aaa acc tgt atg ctc atc tgc tac acc agc
Seite 999

0070110

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

0070110

tgt agc tcg aaa act caa cag aat gtg aaa gca gtt ttt gat
 tca gcg 528
 Cys Ser Ser Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp
 Ser Ala

165

170

175

atc aag gaa gtg atc aaa ccg gtg gtt aaa caa aag gag aag
 acg cag 576
 Ile Lys Glu Val Ile Lys Pro Val Val Lys Gln Lys Glu Lys
 Thr Gln

180

185

190

aaa acg aag aag caa aag tct aat cat ggc tgt tta tca aac
 gtt ctg 624
 Lys Thr Lys Lys Gln Lys Ser Asn His Gly Cys Leu Ser Asn
 Val Leu

195

200

205

tgt ggg agg ata gtg act cgg cat tga
 651
 Cys Gly Arg Ile Val Thr Arg His
 210 215

<210> 663

<211> 216

<212> PRT

<213> Brassica napus

<400> 663

Met Ala Ser Thr Ala Ser Lys Phe Ile Lys Cys Val Thr Val
 Gly Asp
 1 5 10

15

Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser
 Asn Lys
 20 25 30

Phe Pro Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser
 Ala Asn
 35 40 45

Val Val Val Glu Gly Thr Thr Val Asn Leu Gly Leu Trp Asp
 Thr Ala
 50 55 60

Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg
 Gly Ala
 65 70 75
 80

0070110

Asp Val Phe Val Leu Ser Phe Ser Leu Val Ser Arg Ala Ser
Tyr Glu

85

90

95

Asn Val Tyr Lys Lys Trp Ile Pro Glu Leu Gln His Phe Ala
Pro Gly

100

105

110

Val Pro Leu Val Leu Val Gly Thr Lys Leu Asp Leu Arg Glu
Asp Asn

115

120

125

Lys His Tyr Leu Ala Asp His Pro Gly Leu Ser Pro Val Thr
Thr Ala

130

135

140

Gln Gly Glu Glu Leu Arg Lys Leu Ile Gly Ala Thr Tyr Tyr
Ile Glu

145

150

155

160

Cys Ser Ser Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp
Ser Ala

165

170

175

Ile Lys Glu Val Ile Lys Pro Val Val Lys Gln Lys Glu Lys
Thr Gln

180

185

190

Lys Thr Lys Lys Gln Lys Ser Asn His Gly Cys Leu Ser Asn
Val Leu

195

200

205

Cys Gly Arg Ile Val Thr Arg His
210 215

<210> 664

<211> 594

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (1)..(594)

<400> 664

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ggg gcc 48

Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Seite 1002

0070110

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

0070110

Glu Leu Arg Lys Leu Ile Gly Ala Ala Ala Tyr Ile Glu Cys
 Ser Ser
 145 150 155

160
 aaa acc cag cag aac ata aaa gca gtg ttt gac gca gca att
 aag gtg 528
 Lys Thr Gln Gln Asn Ile Lys Ala Val Phe Asp Ala Ala Ile
 Lys Val
 165 170

175
 gtt ctc cag cca cca aag caa aag aag agg aag aag aag gtg
 cag aag 576
 Val Leu Gln Pro Pro Lys Gln Lys Lys Arg Lys Lys Lys Val
 Gln Lys
 180 185 190

gga tgc acc att ttg taa
 594
 Gly Cys Thr Ile Leu
 195

<210> 665
 <211> 197
 <212> PRT
 <213> Zea mays

<400> 665
 Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala
 1 5 10

15
 Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
 Phe Pro
 20 25 30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
 Val Val
 35 40 45

Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
 Gly Gln
 50 55 60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
 Asp Val
 65 70 75

80
 Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
 Seite 1004

0070110

```

Asn Val
      85      90
95
Ser Lys Lys Trp Val Pro Glu Leu Arg His Tyr Ala Pro Gly
Val Pro
      100      105      110
Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe
      115      120      125
Phe Val Asp His Pro Gly Ala Val Pro Ile Ser Thr Ala Gln
Gly Glu
      130      135      140
Glu Leu Arg Lys Leu Ile Gly Ala Ala Ala Tyr Ile Glu Cys
Ser Ser
      145      150      155
      160
Lys Thr Gln Gln Asn Ile Lys Ala Val Phe Asp Ala Ala Ile
Lys Val
      165      170
      175
Val Leu Gln Pro Pro Lys Gln Lys Lys Arg Lys Lys Lys Val
Gln Lys
      180      185      190
Gly Cys Thr Ile Leu
      195

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 <213> Glycine max

<220>
 <221> CDS
 <222> (1)..(591)

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ggt gct      48
Met Ser Thr Ala Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
  1      5      10
15
gtg gga aag aca tgc atg ctt ata tcc tat acc agc aat acc
ttt ccc      96

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0070110

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

0070110

aag gtt 528
Lys Thr Gln Gln Asn Val Lys Thr Val Phe Asp Ala Ala Ile
Lys Val

165

170

175

gca ttg agg cca cca aag cca aag aag aaa cca cgc aag aaa
aag acc 576
Ala Leu Arg Pro Pro Lys Pro Lys Lys Lys Pro Arg Lys Lys
Lys Thr

180

185

190

tgt cct ttc ctc tga
591
Cys Pro Phe Leu
195

<210> 667

<211> 196

<212> PRT

<213> Glycine max

<400> 667

Met Ser Thr Ala Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10

15

Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
20 25 30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Thr
35 40 45

Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65 70 75

80

Phe Leu Leu Cys Tyr Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Ile
85 90

95

Ser Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Asn
Val Pro

0070110

100

105

110

Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe

115

120

125

Leu Ile Asp His Pro Gly Ser Ala Arg Ile Thr Thr Ala Gln
Gly Glu
130

135

140

Glu Leu Lys Lys Met Ile Gly Ala Val Thr Tyr Ile Glu Cys
Ser Ser
145

150

155

160

Lys Thr Gln Gln Asn Val Lys Thr Val Phe Asp Ala Ala Ile
Lys Val

165

170

175

Ala Leu Arg Pro Pro Lys Pro Lys Lys Lys Pro Arg Lys Lys
Lys Thr

180

185

190

Cys Pro Phe Leu
195

<210> 668

<211> 639

<212> DNA

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<220>

<221> CDS

<222> (1)..(639)

<400> 668

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gtt ggt 48

Met Ala Ser Ala Thr Ala Pro Arg Phe Ile Lys Cys Val Thr
Val Gly

1

5

10

15

gat gga gct gta ggg aag acc tgc atg ctc att tgc tat acc
agc aac 96

Asp Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr
Ser Asn

20

25

30

aaa ttc ccc acg gac tat atc ccc act gtg ttt gat aat ttc
agt gca 144

0070110

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

0070110

atc aga atg gtc atc aag cct cca caa aag caa aac gag aaa
 agg aag 576
 Ile Arg Met Val Ile Lys Pro Pro Gln Lys Gln Asn Glu Lys
 Arg Lys
 180 185 190

aaa aaa cca cgt ggc tgt ttc cta aat gtc ctc tgt gga agg
 aac att 624
 Lys Lys Pro Arg Gly Cys Phe Leu Asn Val Leu Cys Gly Arg
 Asn Ile
 195 200 205

gtt cgt ctt aag tga
 639
 Val Arg Leu Lys
 210

<210> 669
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 <212> PRT
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<400> 669
 Met Ala Ser Ala Thr Ala Pro Arg Phe Ile Lys Cys Val Thr
 Val Gly
 1 5 10
 15
 Asp Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr
 Ser Asn
 20 25 30

Lys Phe Pro Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe
 Ser Ala
 35 40 45

Asn Val Val Val Glu Gly Ile Thr Val Asn Leu Gly Leu Trp
 Asp Thr
 50 55 60

Ala Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr
 Arg Gly
 65 70 75
 80

Ala Asp Val Phe Val Leu Ala Phe Ser Leu Val Ser Arg Ala
 Ser Tyr
 85 90

95
 Glu Asn Val Leu Lys Lys Trp Ile Pro Glu Leu Gln His Phe
 Ala Pro

0070110

100

105

110

Gly Ile Pro Leu Val Leu Val Gly Thr Lys Leu Asp Leu Arg
Glu Asp

115

120

125

Arg His Tyr Met Ala Asp His Pro Gly Leu Val Pro Val Thr
Thr Glu

130

135

140

Gln Gly Glu Glu Leu Arg Lys His Ile Gly Ala Thr Tyr Tyr
Ile Glu

145

150

155

160

Cys Ser Ser Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp
Ala Ala

165

170

175

Ile Arg Met Val Ile Lys Pro Pro Gln Lys Gln Asn Glu Lys
Arg Lys

180

185

190

Lys Lys Pro Arg Gly Cys Phe Leu Asn Val Leu Cys Gly Arg
Asn Ile

195

200

205

Val Arg Leu Lys
210

<210> 670

<211> 639

<212> DNA

<213> Glycine max

<220>

<221> CDS

<222> (1)..(639)

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gat gga 48
Met Met Asn Ala Ser Lys Phe Ile Lys Cys Val Thr Val Gly
Asp Gly

1

5

10

15

gct gtt ggg aaa acc tgc atg ctc att tgc tac acc agc aac
aag ttc 96
Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser Asn

0070110

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

0070110

Ser Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Thr Ala
Ile Lys

165

170

175

gtt gtt ctc caa cct caa cct cca agg agg aaa gaa atg gca
agg aag
Val Val Leu Gln Pro Gln Pro Pro Arg Arg Lys Glu Met Ala
Arg Lys

180

185

190

aaa agg cat aga agg tct ggt tgc tca ttt gta agt att atg
tgc gga
Lys Arg His Arg Arg Ser Gly Cys Ser Phe Val Ser Ile Met
Cys Gly

195

200

205

ggc tgt gct gct taa
Gly Cys Ala Ala
210

<210> 671

<211> 212

<212> PRT

<213> Glycine max

<400> 671

Met Met Asn Ala Ser Lys Phe Ile Lys Cys Val Thr Val Gly
Asp Gly

1

5

10

15

Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser Asn
Lys Phe

20

25

30

Pro Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser Ala
Asn Val

35

40

45

Ala Val Asp Gly Ser Ile Val Asn Leu Gly Leu Trp Asp Thr
Ala Gly
50 55 60

Gln Glu Asp Tyr Ser Arg Leu Arg Pro Leu Ser Tyr Arg Gly
Ala Asp
65 70 75

80

Ile Phe Val Leu Ala Phe Ser Leu Ile Ser Arg Ala Ser Tyr
Glu Asn

0070110

85

90

95
Val Leu Lys Lys Trp Met Pro Glu Leu Arg Arg Phe Ala Pro
Asn Val
100 105 110

Pro Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Glu Asp
Arg Gly
115 120 125

Tyr Val Ala Asp His Met Gly Ser Ser Val Ile Thr Ser Ala
Glu Gly
130 135 140

Glu Glu Leu Arg Lys Gln Ile Gly Ala Ala Ala Tyr Ile Glu
Cys Ser

145 150 155
160
Ser Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Thr Ala
Ile Lys
165 170

175
Val Val Leu Gln Pro Gln Pro Pro Arg Arg Lys Glu Met Ala
Arg Lys
180 185 190

Lys Arg His Arg Arg Ser Gly Cys Ser Phe Val Ser Ile Met
Cys Gly
195 200 205

Gly Cys Ala Ala
210

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<211> 591
<212> DNA
<213> Glycine max

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<222> (1)..(591)

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gga gcc 48
Met Ser Thr Ala Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala

0070110

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

0070110

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Ser Ser
145                               150                               155
    160
aag act cag cag aat gtg aag gct gtg ttt gac gct gca atc
aag gtt                               528
Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Lys Val
                                165                                170
175
gtt ctg cag cca tca aag cca aag aaa aaa cga aag aag aac
aga aca                               576
Val Leu Gln Pro Ser Lys Pro Lys Lys Lys Arg Lys Lys Asn
Arg Thr
                                180                                185                                190

tgc gtt ttc ctt taa
                               591
Cys Val Phe Leu
                               195

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<211> 196
<212> PRT
<213> Glycine max

<400> 673
Met Ser Thr Ala Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1                               5                               10
15
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
                                20                                25                                30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
                                35                                40                                45

Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
                                50                                55                                60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65                                70                                75
    80
Phe Phe Leu Ala Phe Ser Leu Leu Ser Arg Ala Ser Tyr Glu
Asn Ile

```

0070110

85

90

95
Ser Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Ile
Val Pro
100 105 110
Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Glu Asp Arg
Gln Tyr
115 120 125
Leu Ile Asp His Pro Ala Ala Thr Pro Ile Thr Thr Ala Gln
Gly Glu
130 135 140
Glu Leu Lys Lys Glu Ile Gly Ala Ala Val Tyr Ile Glu Cys
Ser Ser
145 150 155
160
Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
Lys Val
165 170
175
Val Leu Gln Pro Ser Lys Pro Lys Lys Lys Arg Lys Lys Asn
Arg Thr
180 185 190
Cys Val Phe Leu
195

<210> 674
<211> 603
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (1)..(603)

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ctt ctc 48
Met Ala Thr Ile Gly His Asn Asn Leu Asn Ala Lys Leu Val
Leu Leu
1 5 10
15
ggg gac atg ggt gct ggg aaa tcc agc ctc gtt ttg cgc ttt
gtc aag 96
Gly Asp Met Gly Ala Gly Lys Ser Ser Leu Val Leu Arg Phe

0070110

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

0070110

Asn Asp Ile Phe Tyr Glu Ile Ala Lys Arg Leu Pro Arg Ala
Gln Pro

165

170

175

gct cag aac cca gct ggg atg gta ctt gtt gat aga ccc gcc

gaa gga

576

Ala Gln Asn Pro Ala Gly Met Val Leu Val Asp Arg Pro Ala

Glu Gly

180

185

190

act agg gct gca tca tgt tgt tca taa

603

Thr Arg Ala Ala Ser Cys Cys Ser

195

200

<210> 675

<211> 200

<212> PRT

<213> Glycine max

<400> 675

Met Ala Thr Ile Gly His Asn Asn Leu Asn Ala Lys Leu Val

Leu Leu

1

5

10

15

Gly Asp Met Gly Ala Gly Lys Ser Ser Leu Val Leu Arg Phe

Val Lys

20

25

30

Gly Gln Phe Leu Glu Phe Gln Glu Ser Thr Ile Gly Ala Ala

Phe Phe

35

40

45

Ser Gln Thr Leu Ala Val Asn Asp Ala Thr Val Lys Phe Glu

Ile Trp

50

55

60

Asp Thr Ala Gly Gln Glu Arg Tyr His Ser Leu Ala Pro Met

Tyr Tyr

65

70

75

80

Arg Gly Ala Ala Ala Ala Ile Ile Val Tyr Asp Ile Thr Ser

Ser Asp

85

90

95

Ser Phe Thr Arg Ala Lys Lys Trp Val Gln Glu Leu Gln Lys

Gln Gly

100

105

110

0070110

Asn Pro Asn Met Val Met Ala Leu Ala Gly Asn Lys Ala Asp
Leu Glu
115 120 125

Asp Lys Arg Lys Val Thr Ala Glu Glu Ala Arg Val Tyr Ala
Glu Glu
130 135 140

Asn Gly Leu Phe Phe Met Glu Thr Ser Ala Lys Thr Ala Ser
Asn Val
145 150 155
160

Asn Asp Ile Phe Tyr Glu Ile Ala Lys Arg Leu Pro Arg Ala
Gln Pro
165 170

175
Ala Gln Asn Pro Ala Gly Met Val Leu Val Asp Arg Pro Ala
Glu Gly
180 185 190

Thr Arg Ala Ala Ser Cys Cys Ser
195 200

<210> 676
<211> 609
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (1)..(609)

<400> 676
atg aat ccc gag tat gat tat ctg ttc aag ctc ctt ctt att
gga gac 48
Met Asn Pro Glu Tyr Asp Tyr Leu Phe Lys Leu Leu Leu Ile
Gly Asp
1 5 10
15
tct ggt gtt ggt aaa tca tgc ctt ctt ctg aga ttt tct gat
gat tcg 96
Ser Gly Val Gly Lys Ser Cys Leu Leu Leu Arg Phe Ser Asp
Asp Ser
20 25 30
tac atc gaa agc tac ata agc acc att gga gtt gat ttt aaa
ata cgt 144
Tyr Ile Glu Ser Tyr Ile Ser Thr Ile Gly Val Asp Phe Lys
Seite 1020

0070110

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

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cag cca 576
Pro Ala Asn Asn Ala Arg Pro Pro Thr Val Gln Ile Arg Gly
Gln Pro 180 185 190

gtt gca cag aaa ggt ggg tgc tgc tct tcc taa
Val Ala Gln Lys Gly Gly Cys Cys Ser Ser
195 200

<210> 677
<211> 202
<212> PRT
<213> Glycine max

<400> 677
Met Asn Pro Glu Tyr Asp Tyr Leu Phe Lys Leu Leu Leu Ile
Gly Asp 1 5 10
15
Ser Gly Val Gly Lys Ser Cys Leu Leu Leu Arg Phe Ser Asp
Asp Ser 20 25 30

Tyr Ile Glu Ser Tyr Ile Ser Thr Ile Gly Val Asp Phe Lys
Ile Arg 35 40 45

Thr Val Glu Gln Asp Gly Lys Thr Ile Lys Leu Gln Ile Trp
Asp Thr 50 55 60

Ala Gly Gln Glu Arg Phe Arg Thr Ile Thr Ser Ser Tyr Tyr
Arg Gly 65 70 75

80
Ala His Gly Ile Ile Ile Val Tyr Asp Val Thr Asp Glu Glu
Ser Phe 85 90

95
Asn Asn Val Lys Gln Trp Leu Ser Glu Ile Asp Arg Tyr Ala
Ser Asp 100 105 110

Asn Val Asn Lys Leu Leu Val Gly Asn Lys Cys Asp Leu Glu
Ala Asn 115 120 125

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Arg Ala Val Ser Tyr Glu Thr Ala Lys Ala Phe Ala Asp Glu
Ile Gly
130 135 140

Ile Pro Phe Met Glu Thr Ser Ala Lys Asp Ala Thr Asn Val
Glu Gln
145 150 155

160
Ala Phe Met Ala Met Ala Ala Ser Ile Lys Asp Arg Met Ala
Ser Gln
165 170

175
Pro Ala Asn Asn Ala Arg Pro Pro Thr Val Gln Ile Arg Gly
Gln Pro
180 185 190

Val Ala Gln Lys Gly Gly Cys Cys Ser Ser
195 200

<210> 678
<211> 594
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (1)..(594)

<400> 678
atg agt gcg tcc agg ttc atc aag tgt gtc act gag ggt gac
ggt gcc 48
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Glu Gly Asp
Gly Ala
1 5 10
15
gtt ggc aag act tgc atg ctc atc tcc tac acc agc aac act
ttt cct 96
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
20 25 30
acg gac tac gtg cca act gtc ttt gac aat ttc agt gca aat
gta gtt 144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
35 40 45
gtg gat gga agc act gtg aat ctt ggg ttg tgg gat act gct
ggc caa 192
Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Seite 1023

0070110

gcc tgt tcc att ttg tga
594
Ala Cys Ser Ile Leu
195

<210> 679
<211> 197
<212> PRT
<213> Glycine max

<400> 679
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Glu Gly Asp
Gly Ala
1 5 10
15
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro 20 25 30
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val 35 40 45
Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln 50 55 60
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val 65 70 75
80
Phe Leu Leu Ala Phe Ser Leu Ile Ser Arg Ala Ser Tyr Glu
Asn Val 85 90
95
Ala Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Gly
Val Pro 100 105 110
Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe 115 120 125
Phe Gln Asp His Pro Gly Ala Val Pro Ile Thr Thr Ala Gln
Gly Glu 130 135 140
Glu Leu Arg Lys Leu Ile Gly Ala Pro Val Tyr Ile Glu Cys
Seite 1025

0070110

Ser Ser
 145 150 155
 160
 Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
 Lys Val
 165 170
 175
 Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Arg Lys Gly
 Gln Lys
 180 185 190
 Ala Cys Ser Ile Leu
 195

<210> 680
 <211> 627
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (1)..(627)

<400> 680
 atg gat tcg agt tca acc cag gaa ttc gaa tat ttg ttt aag
 ttg ttg 48
 Met Asp Ser Ser Ser Thr Gln Glu Phe Glu Tyr Leu Phe Lys
 Leu Leu
 1 5 10
 15
 atg att ggg gac tca ggt gtt ggc aag agt agt ctc ctc ctc
 tgt ttc 96
 Met Ile Gly Asp Ser Gly Val Gly Lys Ser Ser Leu Leu Leu
 Cys Phe
 20 25 30
 aca tct gat tcc ttt gaa gat ctt tct ccc aca att ggt gtt
 gat ttt 144
 Thr Ser Asp Ser Phe Glu Asp Leu Ser Pro Thr Ile Gly Val
 Asp Phe
 35 40 45
 aaa gtc aag tat ttg aca atg gaa ggt aaa aag ctg aag ctt
 gcc att 192
 Lys Val Lys Tyr Leu Thr Met Glu Gly Lys Lys Leu Lys Leu
 Ala Ile
 50 55 60
 tgg gat aca gct ggt caa gag aga ttc aga aca ttg aca agt
 tct tac 240
 Trp Asp Thr Ala Gly Gln Glu Arg Phe Arg Thr Leu Thr Ser
 Seite 1026

0070110

Ser	Tyr												
65					70					75			
80													
tac	cga	ggt	gct	caa	ggg	atc	att	atg	gct	tat	gat	gta	act
cgg	cgg			288									
Tyr	Arg	Gly	Ala	Gln	Gly	Ile	Ile	Met	Ala	Tyr	Asp	Val	Thr
Arg	Arg												
				85						90			
95													
gaa	acg	ttt	aca	aat	ctc	tct	gaa	ata	tgg	gca	aag	gaa	ata
gac	ctt			336									
Glu	Thr	Phe	Thr	Asn	Leu	Ser	Glu	Ile	Trp	Ala	Lys	Glu	Ile
Asp	Leu												
				100					105				110
tat	tca	act	aat	caa	gat	tgc	atc	aag	atg	ctt	ggt	gga	aac
aaa	cta			384									
Tyr	Ser	Thr	Asn	Gln	Asp	Cys	Ile	Lys	Met	Leu	Val	Gly	Asn
Lys	Leu												
		115					120					125	
gat	aag	gag	ggt	gat	aga	ggt	gtg	aca	aag	aaa	gag	gga	ata
gac	ttt			432									
Asp	Lys	Glu	Gly	Asp	Arg	Val	Val	Thr	Lys	Lys	Glu	Gly	Ile
Asp	Phe												
		130				135					140		
gcc	agg	gaa	tac	ggt	tgc	cta	ttt	att	gaa	tgc	agt	gct	aaa
act	cga			480									
Ala	Arg	Glu	Tyr	Gly	Cys	Leu	Phe	Ile	Glu	Cys	Ser	Ala	Lys
Thr	Arg												
145					150						155		
160													
ggt	aat	ggt	cag	caa	tgc	ttt	gaa	gag	ctt	ggt	ttg	aag	att
ctg	gat			528									
Val	Asn	Val	Gln	Gln	Cys	Phe	Glu	Glu	Leu	Val	Leu	Lys	Ile
Leu	Asp												
				165							170		
175													
aca	cct	agc	ctc	ata	gcc	gag	ggc	tca	aag	ggt	ggt	aaa	aag
aac	att			576									
Thr	Pro	Ser	Leu	Ile	Ala	Glu	Gly	Ser	Lys	Gly	Val	Lys	Lys
Asn	Ile												
				180									190
ttc	aag	gac	agg	cca	ccc	cag	tct	gat	gca	tcc	gca	agt	agt
tgt	tgc			624									
Phe	Lys	Asp	Arg	Pro	Pro	Gln	Ser	Asp	Ala	Ser	Ala	Ser	Ser
Cys	Cys												
				195					200				205

0070110

tga

627

<210> 681
<211> 208
<212> PRT
<213> Glycine max

<400> 681
Met Asp Ser Ser Ser Thr Gln Glu Phe Glu Tyr Leu Phe Lys
Leu Leu
1 5 10
15
Met Ile Gly Asp Ser Gly Val Gly Lys Ser Ser Leu Leu Leu
Cys Phe
20 25 30
Thr Ser Asp Ser Phe Glu Asp Leu Ser Pro Thr Ile Gly Val
Asp Phe
35 40 45
Lys Val Lys Tyr Leu Thr Met Glu Gly Lys Lys Leu Lys Leu
Ala Ile
50 55 60
Trp Asp Thr Ala Gly Gln Glu Arg Phe Arg Thr Leu Thr Ser
Ser Tyr
65 70 75
80
Tyr Arg Gly Ala Gln Gly Ile Ile Met Ala Tyr Asp Val Thr
Arg Arg
85 90
95
Glu Thr Phe Thr Asn Leu Ser Glu Ile Trp Ala Lys Glu Ile
Asp Leu
100 105 110
Tyr Ser Thr Asn Gln Asp Cys Ile Lys Met Leu Val Gly Asn
Lys Leu
115 120 125
Asp Lys Glu Gly Asp Arg Val Val Thr Lys Lys Glu Gly Ile
Asp Phe
130 135 140
Ala Arg Glu Tyr Gly Cys Leu Phe Ile Glu Cys Ser Ala Lys
Seite 1028

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Thr	Arg													
145					150					155				
160														
Val	Asn	Val	Gln	Gln	Cys	Phe	Glu	Glu	Leu	Val	Leu	Lys	Ile	
Leu	Asp													
				165						170				
175														
Thr	Pro	Ser	Leu	Ile	Ala	Glu	Gly	Ser	Lys	Gly	Val	Lys	Lys	
Asn	Ile													
			180					185					190	
Phe	Lys	Asp	Arg	Pro	Pro	Gln	Ser	Asp	Ala	Ser	Ala	Ser	Ser	
Cys	Cys													
		195					200					205		

<210> 682
 <211> 630
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (1)..(630)

<400> 682														
atg	aat	gct	tca	aag	ttc	att	aaa	tgt	gtt	act	gtt	gga	gat	
gga	gct			48										
Met	Asn	Ala	Ser	Lys	Phe	Ile	Lys	Cys	Val	Thr	Val	Gly	Asp	
Gly	Ala													
1				5					10					
15														
gtt	ggg	aaa	acc	tgc	atg	ctc	att	tgc	tac	acc	agc	aac	aag	
ttc	ccc			96										
Val	Gly	Lys	Thr	Cys	Met	Leu	Ile	Cys	Tyr	Thr	Ser	Asn	Lys	
Phe	Pro													
			20					25					30	
act	gat	tac	ata	cca	aca	gta	ttt	gac	aat	ttc	agt	gcc	aat	
gta	gct			144										
Thr	Asp	Tyr	Ile	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn	
Val	Ala													
		35					40					45		
gtg	gat	gga	agc	att	gtc	aat	ttg	ggg	cta	tgg	gac	aca	gca	
ggc	cag			192										
Val	Asp	Gly	Ser	Ile	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala	
Gly	Gln													
	50					55				60				
gaa	gac	tat	agc	agg	ttg	agg	cca	ctg	agc	tat	aga	gga	gca	

0070110

gac att	240													
Glu Asp Tyr	Ser Arg	Leu Arg	Pro Leu	Ser Tyr	Arg Gly	Ala								
Asp Ile														
65		70							75					
80														
ttt gtc tta	gca ttc	tca ctg	att agc	aga gct	agc tat	gaa								
aat gtt	288													
Phe Val	Leu Ala	Phe Ser	Leu Ile	Ser Arg	Ala Ser	Tyr Glu								
Asn Val														
		85							90					
95														
ctc aag aag	tgg atg	ccg gaa	ttg cgt	aga ttt	gca cct	aat								
ggt cca	336													
Leu Lys	Lys Trp	Met Pro	Glu Leu	Arg Arg	Phe Ala	Pro Asn								
Val Pro														
		100							105					110
att gtt ctt	ggt ggt	aca aag	tta gat	ctt cgt	gaa gac	cgg								
ggt tat	384													
Ile Val	Leu Val	Gly Thr	Lys Leu	Asp Leu	Arg Glu	Asp Arg								
Gly Tyr														
	115								120					125
gta gct gat	cac atg	gga tct	agc gtc	ata aca	tct gct	gag								
ggg gaa	432													
Val Ala	Asp His	Met Gly	Ser Ser	Val Ile	Thr Ser	Ala Glu								
Gly Glu														
	130								135					140
gaa ctg agg	aaa caa	att ggt	gca gca	gct tac	ata gag	tgc								
agt tca	480													
Glu Leu	Arg Lys	Gln Ile	Gly Ala	Ala Ala	Tyr Ile	Glu Cys								
Ser Ser														
145									150					155
160														
aag act caa	cag aat	gtc aaa	gca gtg	ttt gac	act gca	att								
aag gtt	528													
Lys Thr	Gln Gln	Asn Val	Lys Ala	Val Phe	Asp Thr	Ala Ile								
Lys Val														
		165							170					
175														
gtt ctc caa	cct cca	agg agg	aaa gaa	atg gca	agg aag	aaa								
agg cat	576													
Val Leu	Gln Pro	Pro Arg	Arg Arg	Lys Glu	Met Ala	Arg Lys	Lys							
Arg His														
		180							185					190
aga agg tct	ggg tgc	tca ttt	gta agt	atc atg	tgc gga	ggc								
tgt gct	624													
Arg Arg	Ser Gly	Cys Ser	Phe Val	Ser Ile	Met Cys	Gly Gly								

0070110

Cys Ala
gct taa 195 200 205
Ala 630

<210> 683
<211> 209
<212> PRT
<213> Glycine max

<400> 683

Met Asn Ala Ser Lys Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala

1 5 10

15 Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser Asn Lys

Phe Pro 20 25 30

Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Ala

35 40 45

Val Asp Gly Ser Ile Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln

50 55 60

Glu Asp Tyr Ser Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Ile

65 70 75

80 Phe Val Leu Ala Phe Ser Leu Ile Ser Arg Ala Ser Tyr Glu
Asn Val

85 90

95 Leu Lys Lys Trp Met Pro Glu Leu Arg Arg Phe Ala Pro Asn
Val Pro

100 105 110

Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Glu Asp Arg
Gly Tyr

115 120 125

Val Ala Asp His Met Gly Ser Ser Val Ile Thr Ser Ala Glu
Gly Glu

130 135 140

0070110

Glu Leu Arg Lys Gln Ile Gly Ala Ala Ala Tyr Ile Glu Cys
Ser Ser
145 150 155

160
Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Thr Ala Ile
Lys Val
165 170
175

Val Leu Gln Pro Pro Arg Arg Lys Glu Met Ala Arg Lys Lys
Arg His
180 185 190

Arg Arg Ser Gly Cys Ser Phe Val Ser Ile Met Cys Gly Gly
Cys Ala
195 200 205

Ala

<210> 684
<211> 609
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (1)..(609)

<400> 684
atg aat ccc gag tat gat aat ctg ttc aag ctc ctt ctt att
gga gac 48
Met Asn Pro Glu Tyr Asp Asn Leu Phe Lys Leu Leu Leu Ile
Gly Asp
1 5 10
15
tct ggt gtt ggt aaa tca tgc ctt ctt ctg aga ttt gct gat
gat tcg 96
Ser Gly Val Gly Lys Ser Cys Leu Leu Leu Arg Phe Ala Asp
Asp Ser
20 25 30
tac atc gag agc tac ata agc acc att gga gtt gat ttt aaa
ata cgt 144
Tyr Ile Glu Ser Tyr Ile Ser Thr Ile Gly Val Asp Phe Lys
Ile Arg
35 40 45
act gtt gag cag gat gga aag acc att aaa cta cag atc tgg
Seite 1032

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gac	aca		192											
Thr	Val	Glu	Gln	Asp	Gly	Lys	Thr	Ile	Lys	Leu	Gln	Ile	Trp	
Asp	Thr													
	50					55					60			
gcc	ggg	caa	gaa	cga	ttt	agg	aca	atc	acc	agt	agc	tac	tat	
cgt	ggg		240											
Ala	Gly	Gln	Glu	Arg	Phe	Arg	Thr	Ile	Thr	Ser	Ser	Tyr	Tyr	
Arg	Gly													
65					70					75				
80														
gcc	cat	ggg	atc	att	att	gtt	tat	gat	gtg	aca	gat	gaa	gag	
agc	ttc		288											
Ala	His	Gly	Ile	Ile	Ile	Val	Tyr	Asp	Val	Thr	Asp	Glu	Glu	
Ser	Phe													
			85						90					
95														
aat	aat	gtg	aag	cag	tgg	ctc	agt	gaa	att	gat	cgc	tat	gca	
agt	gat		336											
Asn	Asn	Val	Lys	Gln	Trp	Leu	Ser	Glu	Ile	Asp	Arg	Tyr	Ala	
Ser	Asp													
			100					105					110	
aat	gtt	aac	aag	ctt	ttg	gtt	gga	aac	aag	tgt	gat	ctg	gaa	
gca	aat		384											
Asn	Val	Asn	Lys	Leu	Leu	Val	Gly	Asn	Lys	Cys	Asp	Leu	Glu	
Ala	Asn													
		115					120					125		
aga	gct	gtg	tca	tat	gaa	aca	gct	aaa	gca	ttc	gca	gat	gaa	
ata	ggc		432											
Arg	Ala	Val	Ser	Tyr	Glu	Thr	Ala	Lys	Ala	Phe	Ala	Asp	Glu	
Ile	Gly													
	130					135					140			
ata	cct	ttt	atg	gaa	aca	agt	gca	aaa	gat	gct	aca	aat	gtt	
gaa	cag		480											
Ile	Pro	Phe	Met	Glu	Thr	Ser	Ala	Lys	Asp	Ala	Thr	Asn	Val	
Glu	Gln													
145					150					155				
160														
gct	ttc	atg	gca	atg	gct	gct	tca	atc	aag	gat	aga	atg	gca	
agc	caa		528											
Ala	Phe	Met	Ala	Met	Ala	Ala	Ser	Ile	Lys	Asp	Arg	Met	Ala	
Ser	Gln													
			165							170				
175														
cct	gca	aac	aat	gca	agg	cct	cca	aca	gtg	cag	atc	agg	gga	
cag	cca		576											
Pro	Ala	Asn	Asn	Ala	Arg	Pro	Pro	Thr	Val	Gln	Ile	Arg	Gly	
Gln	Pro													

0070110

180

185

190

ggt gca cag aaa ggt ggg tgc tgc tct tcc taa

val Ala Gln Lys Gly Gly Cys Cys Ser Ser
609
195 200

<210> 685

<211> 202

<212> PRT

<213> Glycine max

<400> 685

Met Asn Pro Glu Tyr Asp Asn Leu Phe Lys Leu Leu Ile
Gly Asp

1 5 10

15

Ser Gly val Gly Lys Ser Cys Leu Leu Leu Arg Phe Ala Asp
Asp Ser

20

25

30

Tyr Ile Glu Ser Tyr Ile Ser Thr Ile Gly val Asp Phe Lys
Ile Arg

35

40

45

Thr val Glu Gln Asp Gly Lys Thr Ile Lys Leu Gln Ile Trp
Asp Thr

50

55

60

Ala Gly Gln Glu Arg Phe Arg Thr Ile Thr Ser Ser Tyr Tyr
Arg Gly

65

70

75

80

Ala His Gly Ile Ile Ile val Tyr Asp val Thr Asp Glu Glu
Ser Phe

85

90

95

Asn Asn val Lys Gln Trp Leu Ser Glu Ile Asp Arg Tyr Ala
Ser Asp

100

105

110

Asn val Asn Lys Leu Leu val Gly Asn Lys Cys Asp Leu Glu
Ala Asn

115

120

125

Arg Ala val Ser Tyr Glu Thr Ala Lys Ala Phe Ala Asp Glu
Ile Gly

130

135

140

0070110

Ile Pro Phe Met Glu Thr Ser Ala Lys Asp Ala Thr Asn Val
Glu Gln
145 150 155
160
Ala Phe Met Ala Met Ala Ala Ser Ile Lys Asp Arg Met Ala
Ser Gln
165 170
175
Pro Ala Asn Asn Ala Arg Pro Pro Thr Val Gln Ile Arg Gly
Gln Pro
180 185 190

Val Ala Gln Lys Gly Gly Cys Cys Ser Ser
195 200

<210> 686
<211> 594
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (1)..(594)

<400> 686
atg agc aca aca cgg ttt att aag tgt gtc aca gtt ggt gat
ggg gct 48
Met Ser Thr Thr Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10
15
gtg gga aag act tgc atg ctt atc tct tac act agc aac act
ttc ccc 96
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
20 25 30
acg gat tat gtt cct aca gtt ttc gac aat ttc agt gca aat
gtt gtg 144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
35 40 45
gtt gat ggc agc aca gtt aac ctg gga ttg tgg gac act gct
gga cag 192
Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60

0070110

gaa	gat	tac	aac	agg	ctt	agg	cca	ttg	agt	tac	aga	gga	gca
gat	gtg			240									
Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala
Asp	Val												
65					70					75			
80													
ttc	ttg	ctg	gcc	ttt	tcc	ctc	atc	agc	aaa	gcc	agc	tat	gaa
aat	ata		288										
Phe	Leu	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Lys	Ala	Ser	Tyr	Glu
Asn	Ile												
			85						90				
95													
tct	aaa	aag	tgg	att	cct	gaa	ttg	aga	cat	tat	gcc	cca	act
gtg	cct		336										
Ser	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Arg	His	Tyr	Ala	Pro	Thr
Val	Pro												
			100					105					110
att	gta	ctt	gtt	gga	act	aaa	ctt	gat	ttg	agg	gaa	gac	agg
caa	tat		384										
Ile	Val	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Glu	Asp	Arg
Gln	Tyr												
		115					120					125	
ttg	att	gat	cat	cct	gga	acc	aca	cct	ata	gct	act	gcc	cag
gga	gaa		432										
Leu	Ile	Asp	His	Pro	Gly	Thr	Thr	Pro	Ile	Ala	Thr	Ala	Gln
Gly	Glu												
		130				135				140			
gaa	ctg	aag	aag	gca	att	ggc	gct	gct	gtg	tac	ata	gag	tgc
agc	tca		480										
Glu	Leu	Lys	Lys	Ala	Ile	Gly	Ala	Ala	Val	Tyr	Ile	Glu	Cys
Ser	Ser												
145					150					155			
160													
aag	act	cag	cag	aat	gtg	aag	gcc	gtg	ttt	gat	gct	gca	atc
aag	gtt		528										
Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile
Lys	Val												
			165						170				
175													
gtt	ttg	caa	cca	cct	aag	tcc	aag	aaa	aaa	gga	aag	aag	aag
aac	acg		576										
Val	Leu	Gln	Pro	Pro	Lys	Ser	Lys	Lys	Lys	Gly	Lys	Lys	Lys
Asn	Thr												
			180					185					190
cct	tgt	gtt	ttc	ctc	tga								
			594										

0070110

Pro Cys Val Phe Leu
195

<210> 687

<211> 197

<212> PRT

<213> Glycine max

<400> 687

Met Ser Thr Thr Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala

1 5 10
15

Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro

20 25 30

Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val

35 40 45

Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln

50 55 60

Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val

65 70 75
80

Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Ile

85 90

95

Ser Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Thr
Val Pro

100 105 110

Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Glu Asp Arg
Gln Tyr

115 120 125

Leu Ile Asp His Pro Gly Thr Thr Pro Ile Ala Thr Ala Gln
Gly Glu

130 135 140

Glu Leu Lys Lys Ala Ile Gly Ala Ala Val Tyr Ile Glu Cys
Ser Ser

145 150 155

0070110

160
 Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
 Lys Val
 165 170
 175
 Val Leu Gln Pro Pro Lys Ser Lys Lys Lys Gly Lys Lys Lys
 Asn Thr
 180 185 190
 Pro Cys Val Phe Leu
 195

<210> 688
 <211> 609
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (1)..(609)

<400> 688
 atg aat ccc gag tat gat tat ctg ttc aag ctc ctt ctt att
 gga gac 48
 Met Asn Pro Glu Tyr Asp Tyr Leu Phe Lys Leu Leu Leu Ile
 Gly Asp
 1 5 10
 15
 tct ggt gtt ggt aaa tca tgc ctt ctt ctg aga ttt gct gat
 gat tcg 96
 Ser Gly Val Gly Lys Ser Cys Leu Leu Leu Arg Phe Ala Asp
 Asp Ser
 20 25 30
 tac atc gag agc tac ata agc acc att gga gtt gat ttt aaa
 ata cgt 144
 Tyr Ile Glu Ser Tyr Ile Ser Thr Ile Gly Val Asp Phe Lys
 Ile Arg
 35 40 45
 act gtt gag cag gat gga aag acc att aaa cta cag atc tgg
 gac aca 192
 Thr Val Glu Gln Asp Gly Lys Thr Ile Lys Leu Gln Ile Trp
 Asp Thr
 50 55 60
 gcc ggg caa gaa cga ttt agg aca atc acc agt agc tac tat
 cgt ggg 240
 Ala Gly Gln Glu Arg Phe Arg Thr Ile Thr Ser Ser Tyr Tyr
 Arg Gly

0070110

```

65      70      75
80
gcc cat ggg atc att att gtt tat gat gtg aca gat gaa gag
agc ttc      288
Ala His Gly Ile Ile Ile Val Tyr Asp Val Thr Asp Glu Glu
Ser Phe

85      90
95
aat aat gtg aag cag tgg ctc agt gaa att gat cgc tat gca
agt gat      336
Asn Asn Val Lys Gln Trp Leu Ser Glu Ile Asp Arg Tyr Ala
Ser Asp

100      105      110
aat gtt aac aag ctt ttg gtt gga aac aag tgt gat ctg gaa
gca aat      384
Asn Val Asn Lys Leu Leu Val Gly Asn Lys Cys Asp Leu Glu
Ala Asn

115      120      125
aga gct gtg tca tat gaa aca gct aaa gca ttc gca gat gaa
ata ggc      432
Arg Ala Val Ser Tyr Glu Thr Ala Lys Ala Phe Ala Asp Glu
Ile Gly

130      135      140
ata cct ttt atg gaa aca agt gca aaa gat gct aca aat gtt
gaa cag      480
Ile Pro Phe Met Glu Thr Ser Ala Lys Asp Ala Thr Asn Val
Glu Gln

145      150      155
160
gct ttc atg gca atg gct gct tca atc aag gat aga atg gca
agc caa      528
Ala Phe Met Ala Met Ala Ala Ser Ile Lys Asp Arg Met Ala
Ser Gln

165      170
175
cct gca aat aat gca agg cct cca aca gtg cag atc agg ggt
cag cca      576
Pro Ala Asn Asn Ala Arg Pro Pro Thr Val Gln Ile Arg Gly
Gln Pro

180      185      190
gtt gca cag aaa ggt ggg tgc tgc tct tcc tga
val Ala Gln Lys Gly Gly Cys Cys Ser Ser
195      200

```

<210> 689

0070110

<211> 202

<212> PRT

<213> Glycine max

<400> 689

Met Asn Pro Glu Tyr Asp Tyr Leu Phe Lys Leu Leu Leu Ile
Gly Asp

1 5 10

15

Ser Gly Val Gly Lys Ser Cys Leu Leu Leu Arg Phe Ala Asp
Asp Ser

20 25 30

Tyr Ile Glu Ser Tyr Ile Ser Thr Ile Gly Val Asp Phe Lys
Ile Arg

35 40 45

Thr Val Glu Gln Asp Gly Lys Thr Ile Lys Leu Gln Ile Trp
Asp Thr

50 55 60

Ala Gly Gln Glu Arg Phe Arg Thr Ile Thr Ser Ser Tyr Tyr
Arg Gly

65 70 75

80

Ala His Gly Ile Ile Ile Val Tyr Asp Val Thr Asp Glu Glu
Ser Phe

85 90

95

Asn Asn Val Lys Gln Trp Leu Ser Glu Ile Asp Arg Tyr Ala
Ser Asp

100 105 110

Asn Val Asn Lys Leu Leu Val Gly Asn Lys Cys Asp Leu Glu
Ala Asn

115 120 125

Arg Ala Val Ser Tyr Glu Thr Ala Lys Ala Phe Ala Asp Glu
Ile Gly

130 135 140

Ile Pro Phe Met Glu Thr Ser Ala Lys Asp Ala Thr Asn Val
Glu Gln

145 150 155

160

Ala Phe Met Ala Met Ala Ala Ser Ile Lys Asp Arg Met Ala
Ser Gln

165 170

0070110

175
Pro Ala Asn Asn Ala Arg Pro Pro Thr Val Gln Ile Arg Gly
Gln Pro
180 185 190

Val Ala Gln Lys Gly Gly Cys Cys Ser Ser
195 200

<210> 690
<211> 591
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (1)..(591)

<400> 690
atg agt acg gca agg ttt atc aag tgt gta aca gtt gga gat
ggt gct 48
Met Ser Thr Ala Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10
15
gtg gga aag aca tgc atg ctt ata tcc tat acc agc aat acc
ttt ccc 96
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
20 25 30
acg gat tat gtt cca aca gtg ttt gac aat ttc agt gct aat
gta acg 144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Thr
35 40 45
gtg gat ggt agt act gtt aat ctt ggt tta tgg gac act gca
ggg caa 192
Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60
gaa gat tac aac agg cta agg cct tta agc tat aga gga gct
gat gtg 240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65 70 75
80
ttt ttg ttg tgc tat tct ctc atc agc aaa gcc agt tat gag
aac atc 288

0070110

Phe Leu Leu Cys Tyr Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Ile

85

90

95

tcc aaa aag tgg ata cct gag ctg aga cat tat gct cca aat
gtg cct
Ser Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Asn
Val Pro

100

105

110

ata gtg ctg gtg gga aca aaa cta gat ttg cga gat gac aag
caa ttt
Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe

115

120

125

ctg att gat cat ccg gga tcc gca cga ata aca act gct cag
ggt gaa
Leu Ile Asp His Pro Gly Ser Ala Arg Ile Thr Thr Ala Gln
Gly Glu

130

135

140

gaa ttg aag aaa atg att ggt gca gtc act tat att gag tgc
agc tcc
Glu Leu Lys Lys Met Ile Gly Ala Val Thr Tyr Ile Glu Cys
Ser Ser

145

150

155

160

aaa aca cag ctg aat gtg aag aca gtt ttt gat gct gca ata
aag gtt
Lys Thr Gln Leu Asn Val Lys Thr Val Phe Asp Ala Ala Ile
Lys Val

165

170

175

gca ttg aag cca cca aag cca aag aag aaa cca cgc aag aaa
agg acc
Ala Leu Lys Pro Pro Lys Pro Lys Lys Lys Pro Arg Lys Lys
Arg Thr

180

185

190

tgt act ttc ctc tga
Cys Thr Phe Leu
195

<210> 691

<211> 196

<212> PRT

<213> Glycine max

0070110

<400> 691

Met	Ser	Thr	Ala	Arg	Phe	Ile	Lys	Cys	Val	Thr	Val	Gly	Asp
Gly	Ala												
1				5					10				
15													
Val	Gly	Lys	Thr	Cys	Met	Leu	Ile	Ser	Tyr	Thr	Ser	Asn	Thr
Phe	Pro												
			20					25					30
Thr	Asp	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn
Val	Thr												
		35					40					45	
Val	Asp	Gly	Ser	Thr	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala
Gly	Gln												
	50					55					60		
Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala
Asp	Val												
65					70					75			
	80												
Phe	Leu	Leu	Cys	Tyr	Ser	Leu	Ile	Ser	Lys	Ala	Ser	Tyr	Glu
Asn	Ile												
				85					90				
95													
Ser	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Arg	His	Tyr	Ala	Pro	Asn
Val	Pro												
			100					105					110
Ile	Val	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys
Gln	Phe												
		115					120					125	
Leu	Ile	Asp	His	Pro	Gly	Ser	Ala	Arg	Ile	Thr	Thr	Ala	Gln
Gly	Glu												
	130					135					140		
Glu	Leu	Lys	Lys	Met	Ile	Gly	Ala	Val	Thr	Tyr	Ile	Glu	Cys
Ser	Ser												
145					150					155			
	160												
Lys	Thr	Gln	Leu	Asn	Val	Lys	Thr	Val	Phe	Asp	Ala	Ala	Ile
Lys	Val												
				165					170				
175													
Ala	Leu	Lys	Pro	Pro	Lys	Pro	Lys	Lys	Lys	Pro	Arg	Lys	Lys
Arg	Thr												
			180					185					190

0070110

Cys Thr Phe Leu
195

<210> 692
<211> 609
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (1)..(609)

<400> 692
atg aat ccc gag tat gat tat ctg ttc aag ctc ctt ctt att
gga gac 48
Met Asn Pro Glu Tyr Asp Tyr Leu Phe Lys Leu Leu Leu Ile
Gly Asp
1 5 10
15
tct ggt gtt ggt aaa tca tgc ctt ctt ctg aga ttt tct gat
gat tcg 96
Ser Gly Val Gly Lys Ser Cys Leu Leu Leu Arg Phe Ser Asp
Asp Ser
20 25 30
tac atc gaa agc tac ata agc acc att gga gtt gat ttt aaa
ata cgt 144
Tyr Ile Glu Ser Tyr Ile Ser Thr Ile Gly Val Asp Phe Lys
Ile Arg
35 40 45
acc gtt gag caa gat gga aag acc att aaa cta cag atc tgg
gac aca 192
Thr Val Glu Gln Asp Gly Lys Thr Ile Lys Leu Gln Ile Trp
Asp Thr
50 55 60
gct ggg caa gaa cga ttt agg aca atc acc agt agc tac tac
cgt ggt 240
Ala Gly Gln Glu Arg Phe Arg Thr Ile Thr Ser Ser Tyr Tyr
Arg Gly
65 70 75
80
gcc cat ggg atc att att gtt tat gat gtg aca gat gaa gag
agc ttc 288
Ala His Gly Ile Ile Ile Val Tyr Asp Val Thr Asp Glu Glu
Ser Phe
85 90
95
aat aat gtg aag cag tgg ctc agt gaa att gat cgc tat gca

0070110

agt gat 336
 Asn Asn Val Lys Gln Trp Leu Ser Glu Ile Asp Arg Tyr Ala
 Ser Asp 100 105 110

aat gtt aac aag ctt ttg gtt ggc aac aag tgt gat ctg gaa
 gca aat 384
 Asn Val Asn Lys Leu Leu Val Gly Asn Lys Cys Asp Leu Glu
 Ala Asn 115 120 125

aga gca gtg tca tat gaa aca gct aag gca ttt gca gat gga
 ata ggc 432
 Arg Ala Val Ser Tyr Glu Thr Ala Lys Ala Phe Ala Asp Gly
 Ile Gly 130 135 140

ata cct ttt atg gaa aca agt gca aaa gat gct aca aat gtc
 gaa cag 480
 Ile Pro Phe Met Glu Thr Ser Ala Lys Asp Ala Thr Asn Val
 Glu Gln 145 150 155
 160

gct ttc atg gca atg act gct tca atc aag gat aga atg gca
 agc caa 528
 Ala Phe Met Ala Met Thr Ala Ser Ile Lys Asp Arg Met Ala
 Ser Gln 165 170

175
 cct gca aat aat gca agg cct cca aca gtg cag atc agg ggt
 cag cca 576
 Pro Ala Asn Asn Ala Arg Pro Pro Thr Val Gln Ile Arg Gly
 Gln Pro 180 185 190

gtt gca cag aaa ggt ggg tgc tgc tct ttc tga
 609
 Val Ala Gln Lys Gly Gly Cys Cys Ser Phe
 195 200

<210> 693
 <211> 202
 <212> PRT

<213> Glycine max

<400> 693
 Met Asn Pro Glu Tyr Asp Tyr Leu Phe Lys Leu Leu Leu Ile
 Gly Asp
 1 5 10

0070110

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

0070110

<210> 694
<211> 591
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (1)..(591)

<400> 694
atg agt aca gca aga ttc atc aag tgt gtt act gtg gga gat
gga gcc 48
Met Ser Thr Ala Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10
15
gtg gga aag aca tgt atg ctc atc tct tac acc agc aac aca
ttc ccc 96
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
20 25 30
acg gac tat gtg cct aca gtt ttt gac aac ttc agt gca aat
gtg gtg 144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
35 40 45
att gat gga agc aca gtt aat cta gga tta tgg gac act gct
gga cag 192
Ile Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60
gag gat tac aac agg ctt agg cct ttg agc tac aga gga gca
gat gtg 240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65 70 75
80
ttt ttg ctg gca ttt tcc ctc ctc agc aga gcc agc tat gaa
aat atc 288
Phe Leu Leu Ala Phe Ser Leu Leu Ser Arg Ala Ser Tyr Glu
Asn Ile
85 90
95
tct aag aag tgg atc cct gaa ctg aga cat tat gcc cca att
gtg cca 336
Ser Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Ile
Val Pro

0070110

100

105

110

att gta ctt gtg gga acc aaa ctt gat ttg agg gaa gat agg
 caa tat
 Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Glu Asp Arg
 Gln Tyr

115

120

125

ttg att gat cat cct gcg gcc aca cct ata act act gct cag
 gga gaa
 Leu Ile Asp His Pro Ala Ala Thr Pro Ile Thr Thr Ala Gln
 Gly Glu

130

135

140

gag ctg aag aag gaa att ggt gct gct gtg tat ata gaa tgc
 agc tca
 Glu Leu Lys Lys Glu Ile Gly Ala Ala Val Tyr Ile Glu Cys
 Ser Ser

145

150

155

160

aag act cag cag aat gtg aag gct gtg ttt gac gct gca atc
 aag gtt
 Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
 Lys Val

165

170

175

gtt ctg cag cca tca aag cca aag aaa aaa cga aag aag aac
 aga aca
 Val Leu Gln Pro Ser Lys Pro Lys Lys Lys Arg Lys Lys Asn
 Arg Thr

180

185

190

tgc gtt ttc ctt taa
 591
 Cys Val Phe Leu
 195

<210> 695

<211> 196

<212> PRT

<213> Glycine max

<400> 695

Met Ser Thr Ala Arg Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala

1

5

10

15

Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
 Phe Pro

20

25

30

0070110

Thr	Asp	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn
Val	Val												
		35					40					45	

Ile	Asp	Gly	Ser	Thr	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala
Gly	Gln												
	50					55					60		

Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala
Asp	Val												
65					70					75			

	80												
Phe	Leu	Leu	Ala	Phe	Ser	Leu	Leu	Ser	Arg	Ala	Ser	Tyr	Glu
Asn	Ile												
				85					90				

95													
Ser	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Arg	His	Tyr	Ala	Pro	Ile
Val	Pro												
			100					105				110	

Ile	Val	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Glu	Asp	Arg
Gln	Tyr												
		115					120				125		

Leu	Ile	Asp	His	Pro	Ala	Ala	Thr	Pro	Ile	Thr	Thr	Ala	Gln
Gly	Glu												
	130					135					140		

Glu	Leu	Lys	Lys	Glu	Ile	Gly	Ala	Ala	Val	Tyr	Ile	Glu	Cys
Ser	Ser												
145					150					155			

	160												
Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile
Lys	Val												
				165					170				

175													
Val	Leu	Gln	Pro	Ser	Lys	Pro	Lys	Lys	Lys	Arg	Lys	Lys	Asn
Arg	Thr												
			180					185				190	

Cys	Val	Phe	Leu
		195	

<210> 696
 <211> 612
 <212> DNA

0070110

<213> Helianthus annuus

<220>

<221> CDS

<222> (1)..(612)

<400> 696

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atg aat cac gaa tat gat tac ttg ttc aag ctt ttg ctg att
ggg gat          48
Met Asn His Glu Tyr Asp Tyr Leu Phe Lys Leu Leu Leu Ile
Gly Asp
  1              5              10
15
tcg gga gtc ggc aaa tct tgt ctc cta ctt aga ttt gct gat
gac tca          96
Ser Gly Val Gly Lys Ser Cys Leu Leu Leu Arg Phe Ala Asp
Asp Ser
      20              25              30
tat att gac agc tac atc agc aca att ggt gtg gac ttt aaa
atc cgc          144
Tyr Ile Asp Ser Tyr Ile Ser Thr Ile Gly Val Asp Phe Lys
Ile Arg
      35              40              45
acc gtt gag cag gat gga aaa acc att aag ctt caa att tgg
gac aca          192
Thr Val Glu Gln Asp Gly Lys Thr Ile Lys Leu Gln Ile Trp
Asp Thr
      50              55              60
gct gga caa gaa agg ttc agg aca att acc agt agc tac tac
cgt ggg          240
Ala Gly Gln Glu Arg Phe Arg Thr Ile Thr Ser Ser Tyr Tyr
Arg Gly
      65              70              75
80
gcc cat ggc att atc ata gtt tac gat gtt act gac cta gac
agt ttc          288
Ala His Gly Ile Ile Ile Val Tyr Asp Val Thr Asp Leu Asp
Ser Phe
      85              90
95
aac aac gtt aag caa tgg ttg agt gaa att gac cgt tat gca
agt gaa          336
Asn Asn Val Lys Gln Trp Leu Ser Glu Ile Asp Arg Tyr Ala
Ser Glu
      100              105              110

aat gtg aat aaa ctt ctt gtt gga aac aaa tgt gac ctt aca
gaa agt          384

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0070110

Asn	Val	Asn	Lys	Leu	Leu	Val	Gly	Asn	Lys	Cys	Asp	Leu	Thr
Glu	Ser												
		115					120					125	
aga	gcc	gtg	tcc	tat	gat	act	gct	aag	gaa	ttt	gcg	gat	aac
att	ggc		432										
Arg	Ala	Val	Ser	Tyr	Asp	Thr	Ala	Lys	Glu	Phe	Ala	Asp	Asn
Ile	Gly												
	130					135					140		
att	ccg	ttt	atg	gaa	act	agt	gcc	aaa	gat	gct	acc	aat	gtt
gag	cag		480										
Ile	Pro	Phe	Met	Glu	Thr	Ser	Ala	Lys	Asp	Ala	Thr	Asn	Val
Glu	Gln												
145					150					155			
160													
gct	ttc	atg	gcc	atg	tcc	tct	gac	atc	aaa	aac	agg	atg	gca
agt	cag		528										
Ala	Phe	Met	Ala	Met	Ser	Ser	Asp	Ile	Lys	Asn	Arg	Met	Ala
Ser	Gln												
			165						170				
175													
cct	ggg	gca	aac	aac	acg	agg	cca	cct	tct	gtg	cag	ctc	aag
ggt	caa		576										
Pro	Gly	Ala	Asn	Asn	Thr	Arg	Pro	Pro	Ser	Val	Gln	Leu	Lys
Gly	Gln												
			180					185				190	
cct	gtt	ggt	caa	aag	ggc	ggt	tgc	tgc	tca	tct	tag		
			612										
Pro	Val	Gly	Gln	Lys	Gly	Gly	Cys	Cys	Ser	Ser			
		195					200						

<210> 697

<211> 203

<212> PRT

<213> Helianthus annuus

<400> 697

Met	Asn	His	Glu	Tyr	Asp	Tyr	Leu	Phe	Lys	Leu	Leu	Leu	Ile
Gly	Asp												
1				5					10				
15													
Ser	Gly	Val	Gly	Lys	Ser	Cys	Leu	Leu	Leu	Arg	Phe	Ala	Asp
Asp	Ser												
			20					25				30	
Tyr	Ile	Asp	Ser	Tyr	Ile	Ser	Thr	Ile	Gly	Val	Asp	Phe	Lys
Ile	Arg												
		35					40					45	

0070110

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

<210> 698
 <211> 615
 <212> DNA
 <213> Hordeum vulgare

<220>
 <221> CDS
 <222> (1)..(615)

0070110

<400> 698

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atg agc gcc tcc gag tac gac tac ctc ttc aag ctg ctc ctc
atc ggc          48
Met Ser Ala Ser Glu Tyr Asp Tyr Leu Phe Lys Leu Leu Leu
Ile Gly
  1              5              10
15
gac tcc tcc gtc ggc aag tcc tgc ctc ctc ctc cgc ttc gcc
gac gat          96
Asp Ser Ser Val Gly Lys Ser Cys Leu Leu Leu Arg Phe Ala
Asp Asp
      20              25              30
gcg tac gtc gac acc tac atc agc acc atc gga gtt gat ttc
aaa ata          144
Ala Tyr Val Asp Thr Tyr Ile Ser Thr Ile Gly Val Asp Phe
Lys Ile
      35              40              45
cgg aca gtc gag ctc gac ggc aag tcg gtg aag ctg cag att
tgg gac          192
Arg Thr Val Glu Leu Asp Gly Lys Ser Val Lys Leu Gln Ile
Trp Asp
      50              55              60
aca gca ggc cag gaa agg ttc agg aca ata acg agc agt tac
tac cg          240
Thr Ala Gly Gln Glu Arg Phe Arg Thr Ile Thr Ser Ser Tyr
Tyr Arg
      65              70              75
80
gga gcg cat gga atc att atc gta tat gac gtg aca gat agg
gaa agc          288
Gly Ala His Gly Ile Ile Ile Val Tyr Asp Val Thr Asp Arg
Glu Ser
      85              90
95
ttc aac aat gtc aag cag tgg ttg agt gag att gat agg tat
gcc agt          336
Phe Asn Asn Val Lys Gln Trp Leu Ser Glu Ile Asp Arg Tyr
Ala Ser
      100              105              110
gac agt gtg tgc aag ctt cta gtc ggg aac aaa tgt gat ttg
gtt gac          384
Asp Ser Val Cys Lys Leu Leu Val Gly Asn Lys Cys Asp Leu
Val Asp
      115              120              125
agt aag gtc gtc gat aca gag gag gcc aag gct ttt gca gaa
tca tta          432

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0070110

Ser Lys Val Val Asp Thr Glu Glu Ala Lys Ala Phe Ala Glu
 Ser Leu
 130 135 140
 gga atg aat ttc ctg gag aca agt gca aag gag tcc atc aat
 gtg gag 480
 Gly Met Asn Phe Leu Glu Thr Ser Ala Lys Glu Ser Ile Asn
 Val Glu
 145 150 155
 160
 aca gct ttc tta acc atg tca tca gaa atc aag aac aag atg
 gcg agc 528
 Thr Ala Phe Leu Thr Met Ser Ser Glu Ile Lys Asn Lys Met
 Ala Ser
 165 170
 175
 caa cct gca gcg gag cgg aaa tcg acg gtc cat gtt cac atg
 aaa ggg 576
 Gln Pro Ala Ala Glu Arg Lys Ser Thr Val His Val His Met
 Lys Gly
 180 185 190
 cag ccc ata cag cag cag cag agc agc tgc tgc tcc tga
 615
 Gln Pro Ile Gln Gln Gln Gln Ser Ser Cys Cys Ser
 195 200

<210> 699
 <211> 204
 <212> PRT
 <213> Hordeum vulgare

<400> 699
 Met Ser Ala Ser Glu Tyr Asp Tyr Leu Phe Lys Leu Leu Leu
 Ile Gly
 1 5 10
 15
 Asp Ser Ser Val Gly Lys Ser Cys Leu Leu Leu Arg Phe Ala
 Asp Asp
 20 25 30
 Ala Tyr Val Asp Thr Tyr Ile Ser Thr Ile Gly Val Asp Phe
 Lys Ile
 35 40 45
 Arg Thr Val Glu Leu Asp Gly Lys Ser Val Lys Leu Gln Ile
 Trp Asp
 50 55 60

0070110

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

<210> 700
 <211> 642
 <212> DNA
 <213> Hordeum vulgare

<220>
 <221> CDS
 <222> (1)..(642)

<400> 700
 atg gcg tcc agc gcc tcc cgg ttc atc aag tgc gtc acc gtc
 ggg gac 48
 Met Ala Ser Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val
 Seite 1055

0070110

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

0070110

gaa tgc 480
 Gly Glu Glu Leu Arg Lys His Ile Gly Ala Thr Cys Tyr Val
 Glu Cys
 145 150 155

160
 agc tca aag aca cag cag aat gtc aaa gct gtg ttt gat gct
 gcc atc 528
 Ser Ser Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala
 Ala Ile
 165 170

175
 aag gta gtg atc aaa cct cca aca aag cag agg gaa agg agg
 aag aag 576
 Lys Val Val Ile Lys Pro Pro Thr Lys Gln Arg Glu Arg Arg
 Lys Lys
 180 185 190

aaa gca cgg caa gga tgt gca tca ttg ggt acc ctg tca aga
 agg aag 624
 Lys Ala Arg Gln Gly Cys Ala Ser Leu Gly Thr Leu Ser Arg
 Arg Lys
 195 200 205

ctg gca tgc ttc aag tga
 642
 Leu Ala Cys Phe Lys
 210

<210> 701
 <211> 213
 <212> PRT
 <213> Hordeum vulgare

<400> 701
 Met Ala Ser Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val
 Gly Asp
 1 5 10
 15
 Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser
 Asn Lys
 20 25 30

Phe Pro Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Arg
 Ala Asn
 35 40 45

Val Val Val Asp Gly Thr Thr Val Asn Leu Gly Leu Trp Asp
 Thr Ala
 50 55 60

0070110

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

<210> 702
<211> 615
<212> DNA
<213> Hordeum vulgare

<220>
<221> CDS
<222> (1)..(615)

<400> 702

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ggt ctt
Met Ala Ala Ser Ala Gly Ser Lys Ile Arg Asn Ala Lys Leu
Val Leu
1 5 10
15
ctc ggc gat gtg ggt gct ggg aaa tcc agc ctg gtg ctt cgg
ttc gta
Leu Gly Asp Val Gly Ala Gly Lys Ser Ser Leu Val Leu Arg
Phe Val
20 25 30
aaa gga caa ttt gtt gag ttc cag gaa tcg aca att gga gcg
gct ttc
Lys Gly Gln Phe Val Glu Phe Gln Glu Ser Thr Ile Gly Ala
Ala Phe
35 40 45
ttc tct caa aca ctg gct gtt aat gac gag act gtg aag ttt
gaa atc
Phe Ser Gln Thr Leu Ala Val Asn Asp Glu Thr Val Lys Phe
Glu Ile
50 55 60
tgg gat act gct ggg cag gag agg tat cat agc ttg gcc ccc
atg tac
Trp Asp Thr Ala Gly Gln Glu Arg Tyr His Ser Leu Ala Pro
Met Tyr
65 70 75
80
tat agg ggt gct gcc gca gcc ata gtt gtc tat gac atc tcg
aac cag
Tyr Arg Gly Ala Ala Ala Ala Ile Val Val Tyr Asp Ile Ser
Asn Gln
85 90
95
gca tcc ttc acc cga gca aag aaa tgg gtt caa gaa ctt caa
gct caa
Ala Ser Phe Thr Arg Ala Lys Lys Trp Val Gln Glu Leu Gln
Ala Gln
100 105 110
gga aac cag aat aca gta gtg gct ctt gct ggc aac aaa gct
gat ttg
Gly Asn Gln Asn Thr Val Val Ala Leu Ala Gly Asn Lys Ala
Asp Leu
115 120 125
cta gag gcg agg gag gtt caa ata gag gaa gcc aag aca tat
gcg cag
432

```

0070110

Leu Glu Ala Arg Glu Val Gln Ile Glu Glu Ala Lys Thr Tyr
 Ala Gln
 130 135 140
 gag aat ggc ctc ttc ttc atg gaa acg tct gcc aag act gca
 acc aat 480
 Glu Asn Gly Leu Phe Phe Met Glu Thr Ser Ala Lys Thr Ala
 Thr Asn
 145 150 155
 160
 gtg aat gac ata ttt tat gag att gcg aag aga ctg ctg caa
 ggg cag 528
 Val Asn Asp Ile Phe Tyr Glu Ile Ala Lys Arg Leu Leu Gln
 Gly Gln
 165 170
 175
 gcg gcg cag aac cca cag gcg gcg ggg atg gtt ctc tcc cag
 aga ccc 576
 Ala Ala Gln Asn Pro Gln Ala Ala Gly Met Val Leu Ser Gln
 Arg Pro
 180 185 190
 aac gag aga gtg gtc agc gcg gct tcg tgc tgc tcc tga
 615
 Asn Glu Arg Val Val Ser Ala Ala Ser Cys Cys Ser
 195 200

<210> 703
 <211> 204
 <212> PRT
 <213> Hordeum vulgare

<400> 703
 Met Ala Ala Ser Ala Gly Ser Lys Ile Arg Asn Ala Lys Leu
 Val Leu
 1 5 10
 15
 Leu Gly Asp Val Gly Ala Gly Lys Ser Ser Leu Val Leu Arg
 Phe Val
 20 25 30
 Lys Gly Gln Phe Val Glu Phe Gln Glu Ser Thr Ile Gly Ala
 Ala Phe
 35 40 45
 Phe Ser Gln Thr Leu Ala Val Asn Asp Glu Thr Val Lys Phe
 Glu Ile
 50 55 60

0070110

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

<210> 704

<211> 639

<212> DNA

<213> Linum usitatissimum

<220>

<221> CDS

<222> (1)..(639)

<400> 704

atg gga tct tct tca ggt agt agt ggg tat gat ctg tcg ttc
aag ttg 48

0070110

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

0070110

agt gcc 480
Met Glu Leu Ala Lys Gln His Gly Cys Leu Phe Leu Glu Cys
Ser Ala
145 150 155

160
aaa act cgt gaa aac gtg gag caa tgc ttc gag gag ctc gcg
caa aag 528
Lys Thr Arg Glu Asn Val Glu Gln Cys Phe Glu Glu Leu Ala
Gln Lys
165 170

175
ata aag gat gtt cca agt ctc ttg gaa gaa gga tct aca gcc
ggg aag 576
Ile Lys Asp Val Pro Ser Leu Leu Glu Glu Gly Ser Thr Ala
Gly Lys
180 185 190

agg aac att cta aag caa aac cca gat cga caa atg tct caa
agc aac 624
Arg Asn Ile Leu Lys Gln Asn Pro Asp Arg Gln Met Ser Gln
Ser Asn
195 200 205

ggc tgt tgc tct taa
639
Gly Cys Cys Ser
210

<210> 705
<211> 212
<212> PRT
<213> Linum usitatissimum

<400> 705
Met Gly Ser Ser Ser Gly Ser Ser Gly Tyr Asp Leu Ser Phe
Lys Leu
1 5 10
15
Leu Leu Ile Gly Asp Ser Ser Val Gly Lys Ser Ser Leu Leu
Val Ser
20 25 30

Phe Ile Ser Thr Thr Ser Ala Glu Glu Asp Leu Ala Pro Thr
Ile Gly
35 40 45

Val Asp Phe Lys Ile Lys Gln Leu Thr Val Ala Gly Lys Arg
Leu Lys
50 55 60

0070110

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

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 <211> 651
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 <222> (1)..(651)

0070110

<400> 706

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aag ctc
Met Ala Gly Tyr Arg Pro Glu Glu Asp Tyr Asp Tyr Leu Leu
Lys Leu
1 5 10
15
gtt ctg atc ggc gat tcc ggt gtc ggc aaa tcc aac ttg ctc
tcc agg
Val Leu Ile Gly Asp Ser Gly Val Gly Lys Ser Asn Leu Leu
Ser Arg
20 25 30
ttc acc aag aac gag ttc aat ctc gag tcc aag tcc act atc
ggg gtc
Phe Thr Lys Asn Glu Phe Asn Leu Glu Ser Lys Ser Thr Ile
Gly Val
35 40 45
gag ttc gcc acc aag agc atg aac ctc gat ggc aag gtc atc
aag gct
Glu Phe Ala Thr Lys Ser Met Asn Leu Asp Gly Lys Val Ile
Lys Ala
50 55 60
cag att tgg gac acc gct ggc caa gaa agg tac cgc gcc ata
aca agc
Gln Ile Trp Asp Thr Ala Gly Gln Glu Arg Tyr Arg Ala Ile
Thr Ser
65 70 75
80
gca tac tac aga gga gcg gtc ggt gct tta ctc gtc tac gac
gtg act
Ala Tyr Tyr Arg Gly Ala Val Gly Ala Leu Leu Val Tyr Asp
Val Thr
85 90
95
cgc cgc tca ata ttc gaa aac gtg gcg agg tgg ctg aaa gag
ttg agg
Arg Arg Ser Ile Phe Glu Asn Val Ala Arg Trp Leu Lys Glu
Leu Arg
100 105 110
gag cac acc gac ccc aac atc gtc gtc atg ctc ata ggc aac
aaa tca
Glu His Thr Asp Pro Asn Ile Val Val Met Leu Ile Gly Asn
Lys Ser
115 120 125
gat ctc agg cac ctg gta gct gtc cag acc gag gat gcg aaa
gca tat
432

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0070110

Asp	Leu	Arg	His	Leu	Val	Ala	Val	Gln	Thr	Glu	Asp	Ala	Lys
Ala	Tyr												
130						135				140			
gca	gag	agg	gag	tcc	atg	tac	ttc	atg	gag	aca	tca	gct	ctc
acc	gca			480									
Ala	Glu	Arg	Glu	Ser	Met	Tyr	Phe	Met	Glu	Thr	Ser	Ala	Leu
Thr	Ala												
145					150					155			
160													
aca	aac	gtg	gag	agt	gcc	ttc	acc	gaa	gtc	atg	acg	cag	ata
tac	aag			528									
Thr	Asn	Val	Glu	Ser	Ala	Phe	Thr	Glu	Val	Met	Thr	Gln	Ile
Tyr	Lys												
				165						170			
175													
atc	gtg	agc	aag	agg	gct	gtc	gat	gga	acc	aat	gac	ggc	acg
aca	gga			576									
Ile	Val	Ser	Lys	Arg	Ala	Val	Asp	Gly	Thr	Asn	Asp	Gly	Thr
Thr	Gly												
				180				185					190
gta	cct	ctg	aag	gga	gag	acc	atc	aac	gtg	aag	cag	gaa	ggc
tct	gtt			624									
Val	Pro	Leu	Lys	Gly	Glu	Thr	Ile	Asn	Val	Lys	Gln	Glu	Gly
Ser	Val												
		195				200						205	
ctc	aag	aga	atg	ggg	tgc	tgt	tct	tag					
			651										
Leu	Lys	Arg	Met	Gly	Cys	Cys	Ser						
	210					215							

<210> 707

<211> 216

<212> PRT

<213> Linum usitatissimum

<400> 707

Met	Ala	Gly	Tyr	Arg	Pro	Glu	Glu	Asp	Tyr	Asp	Tyr	Leu	Leu
Lys	Leu												
1					5				10				
15													
Val	Leu	Ile	Gly	Asp	Ser	Gly	Val	Gly	Lys	Ser	Asn	Leu	Leu
Ser	Arg												
			20					25				30	
Phe	Thr	Lys	Asn	Glu	Phe	Asn	Leu	Glu	Ser	Lys	Ser	Thr	Ile
Gly	Val												
		35				40						45	

0070110

Glu Phe Ala Thr Lys Ser Met Asn Leu Asp Gly Lys Val Ile
Lys Ala
50 55 60

Gln Ile Trp Asp Thr Ala Gly Gln Glu Arg Tyr Arg Ala Ile
Thr Ser
65 70 75
80

Ala Tyr Tyr Arg Gly Ala Val Gly Ala Leu Leu Val Tyr Asp
Val Thr
85 90

95
Arg Arg Ser Ile Phe Glu Asn Val Ala Arg Trp Leu Lys Glu
Leu Arg
100 105 110

Glu His Thr Asp Pro Asn Ile Val Val Met Leu Ile Gly Asn
Lys Ser
115 120 125

Asp Leu Arg His Leu Val Ala Val Gln Thr Glu Asp Ala Lys
Ala Tyr
130 135 140

Ala Glu Arg Glu Ser Met Tyr Phe Met Glu Thr Ser Ala Leu
Thr Ala
145 150 155
160

Thr Asn Val Glu Ser Ala Phe Thr Glu Val Met Thr Gln Ile
Tyr Lys
165 170

175
Ile Val Ser Lys Arg Ala Val Asp Gly Thr Asn Asp Gly Thr
Thr Gly
180 185 190

Val Pro Leu Lys Gly Glu Thr Ile Asn Val Lys Gln Glu Gly
Ser Val
195 200 205

Leu Lys Arg Met Gly Cys Cys Ser
210 215

<210> 708

<211> 597

<212> DNA

<213> Linum usitatissimum

0070110

<220>

<221> CDS

<222> (1)..(597)

<400> 708

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ggc	gcc		48										
Met	Ser	Ala	Ser	Arg	Phe	Ile	Lys	Cys	Val	Thr	Val	Gly	Asp
Gly	Ala												
1				5					10				

15

gtc	ggc	aag	acc	tgc	ttg	ctc	att	tcc	tat	acc	agc	aac	acc
ttc	ccc		96										
Val	Gly	Lys	Thr	Cys	Leu	Leu	Ile	Ser	Tyr	Thr	Ser	Asn	Thr
Phe	Pro												

acg	gac	tat	gta	ccg	act	gta	ttc	gac	aat	ttc	agc	gcg	aat
ggt	gtc		144										
Thr	Asp	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn
Val	Val												

gtg	gat	gga	agc	act	ggt	aac	ttg	gga	tta	tgg	gat	act	gct
ggt	cag		192										
Val	Asp	Gly	Ser	Thr	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala
Gly	Gln												

gag	gat	tac	aac	agg	ctg	agg	cca	ttg	agt	tat	cga	gga	gca
gat	gtc		240										
Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala
Asp	Val												

65

ttt	att	ctt	gca	ttt	tct	ctg	att	agc	aag	gcc	agc	tat	gaa
aac	att		288										
Phe	Ile	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Lys	Ala	Ser	Tyr	Glu
Asn	Ile												

gcc	aaa	aag	tgg	atc	cct	gaa	ttg	agg	cat	tat	gca	cct	ggg
ggt	cca		336										
Ala	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Arg	His	Tyr	Ala	Pro	Gly
Val	Pro												

95

att	atc	atc	gta	gga	aca	aag	ctt	gat	ctt	cgc	gag	gat	aag
caa	ttc		384										
Ile	Ile	Ile	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Glu	Asp	Lys

0070110

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<213> Linum usitatissimum
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Gly Ala
1          5          10
15
Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
          20          25          30
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
          35          40          45

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0070110

Val	Asp	Gly	Ser	Thr	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala
Gly	Gln												
	50					55					60		

Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala
Asp	Val												
65					70					75			

	80												
Phe	Ile	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Lys	Ala	Ser	Tyr	Glu
Asn	Ile												

				85					90				
95													
Ala	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Arg	His	Tyr	Ala	Pro	Gly
Val	Pro												

			100					105				110	
Ile	Ile	Ile	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Glu	Asp	Lys
Gln	Phe												

			115					120				125	
Phe	Asp	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Thr	Thr	Ala	Gln
Gly	Glu												

						135					140		
Glu	Leu	Lys	Lys	Leu	Ile	Gly	Ala	Gln	Ala	Tyr	Val	Glu	Cys
Ser	Ser												

					150					155			
160													
Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile
Lys	Val												

				165				170					
175													
Val	Leu	Gln	Pro	Pro	Lys	Gln	Lys	Lys	Lys	Lys	Arg	Lys	Gly
Lys	Gln												

			180					185				190	

0070110

<400> 710

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atg aac tct gag tac gat tac ttg ttc aag ctt ttg ctt atc
gga gat          48
Met Asn Ser Glu Tyr Asp Tyr Leu Phe Lys Leu Leu Leu Ile
Gly Asp
  1              5              10
15
tcc gga gtc ggc aag tca tgt cta ctt ttg cga ttc gct gat
gat tcg          96
Ser Gly Val Gly Lys Ser Cys Leu Leu Leu Arg Phe Ala Asp
Asp Ser
      20              25              30
tac ttg gac agt tac atc agt acc atc gga gtg gac ttc aaa
att cgc          144
Tyr Leu Asp Ser Tyr Ile Ser Thr Ile Gly Val Asp Phe Lys
Ile Arg
      35              40              45
acc gtg gag cag gat ggc aaa acc att aag ctc caa atc tgg
gat acg          192
Thr Val Glu Gln Asp Gly Lys Thr Ile Lys Leu Gln Ile Trp
Asp Thr
      50              55              60
gca ggg caa gaa cga ttc agg acc att aca agt agt tac tat
cgt ggt          240
Ala Gly Gln Glu Arg Phe Arg Thr Ile Thr Ser Ser Tyr Tyr
Arg Gly
      65              70              75
80
gct cat ggg att att gtg gtc tat gat gtc aca gac caa gag
agt ttc          288
Ala His Gly Ile Ile Val Val Tyr Asp Val Thr Asp Gln Glu
Ser Phe
      85              90
95
aac aat gtc aaa cag tgg ttg agt gaa att gat cgc tac gca
agt gag          336
Asn Asn Val Lys Gln Trp Leu Ser Glu Ile Asp Arg Tyr Ala
Ser Glu
      100              105              110
aac gtg aac aaa ctt cta gtt ggg aac aag agt gac ctc act
gcc aac          384
Asn Val Asn Lys Leu Leu Val Gly Asn Lys Ser Asp Leu Thr
Ala Asn
      115              120              125
aaa gtt gtt tca tat gaa act gct aag gca ttt gcc gat gaa
att ggg          432
Lys Val Val Ser Tyr Glu Thr Ala Lys Ala Phe Ala Asp Glu

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0070110

Ile Gly
130
att ccc ttc atg gag acg agt gcc aag aac gct tcc aat gtc
gaa gat 480
Ile Pro Phe Met Glu Thr Ser Ala Lys Asn Ala Ser Asn Val
Glu Asp
145 150 155
160
gct ttt atg gca atg tca gct gca atc aag acc agg atg gct
agc caa 528
Ala Phe Met Ala Met Ser Ala Ala Ile Lys Thr Arg Met Ala
Ser Gln
165 170
175
cct gtg tca ggc act gcc aga cct cca acg gtg caa atc cgc
gga gaa 576
Pro Val Ser Gly Thr Ala Arg Pro Pro Thr Val Gln Ile Arg
Gly Glu
180 185 190
cca gtg aac cag aag tca ggt tgc tgc tct tct tga
612
Pro Val Asn Gln Lys Ser Gly Cys Cys Ser Ser
195 200

<210> 711
<211> 203
<212> PRT
<213> Linum usitatissimum

<400> 711
Met Asn Ser Glu Tyr Asp Tyr Leu Phe Lys Leu Leu Leu Ile
Gly Asp
1 5 10
15
Ser Gly Val Gly Lys Ser Cys Leu Leu Leu Arg Phe Ala Asp
Asp Ser
20 25 30
Tyr Leu Asp Ser Tyr Ile Ser Thr Ile Gly Val Asp Phe Lys
Ile Arg
35 40 45
Thr Val Glu Gln Asp Gly Lys Thr Ile Lys Leu Gln Ile Trp
Asp Thr
50 55 60
Ala Gly Gln Glu Arg Phe Arg Thr Ile Thr Ser Ser Tyr Tyr
Seite 1072

0070110

Arg Gly													
65					70					75			
80													
Ala His Gly Ile Ile Val Val Tyr Asp Val Thr Asp Gln Glu													
Ser Phe					85				90				
95													
Asn Asn Val Lys Gln Trp Leu Ser Glu Ile Asp Arg Tyr Ala													
Ser Glu					100				105				110
Asn Val Asn Lys Leu Leu Val Gly Asn Lys Ser Asp Leu Thr													
Ala Asn					115				120				125
Lys Val Val Ser Tyr Glu Thr Ala Lys Ala Phe Ala Asp Glu													
Ile Gly													
130									135				140
Ile Pro Phe Met Glu Thr Ser Ala Lys Asn Ala Ser Asn Val													
Glu Asp													
145													
160													
Ala Phe Met Ala Met Ser Ala Ala Ile Lys Thr Arg Met Ala													
Ser Gln													
					165				170				
175													
Pro Val Ser Gly Thr Ala Arg Pro Pro Thr Val Gln Ile Arg													
Gly Glu													
					180				185				190
Pro Val Asn Gln Lys Ser Gly Cys Cys Ser Ser													
					195				200				

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 <212> DNA
 <213> Linum usitatissimum

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 aag ttg 48
 Met Gly Ser Ser Ser Gly Ser Ser Gly Tyr Asp Leu Ser Phe
 Lys Leu

0070110

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

0070110

Ser Ala
 145 150 155
 160
 aaa act cgt gaa aac gtg gag caa tgc ttc gag gag ctt gcg
 caa aag 528
 Lys Thr Arg Glu Asn Val Glu Gln Cys Phe Glu Glu Leu Ala
 Gln Lys
 165 170
 175
 ata aag gat gtt cca agt ctc ttg gaa gaa gga tct acg gcc
 ggg aag 576
 Ile Lys Asp Val Pro Ser Leu Leu Glu Glu Gly Ser Thr Ala
 Gly Lys
 180 185 190
 agg aac att cta aag caa aac cca gat cgc caa atg tct caa
 agc aac 624
 Arg Asn Ile Leu Lys Gln Asn Pro Asp Arg Gln Met Ser Gln
 Ser Asn
 195 200 205
 ggc tgt tgc tct taa
 639
 Gly Cys Cys Ser
 210

<210> 713
 <211> 212
 <212> PRT
 <213> Linum usitatissimum

<400> 713
 Met Gly Ser Ser Ser Gly Ser Ser Gly Tyr Asp Leu Ser Phe
 Lys Leu
 1 5 10
 15
 Leu Leu Ile Gly Asp Ser Ser Val Gly Lys Ser Ser Leu Leu
 Val Ser
 20 25 30
 Phe Ile Ser Thr Thr Ser Ala Glu Glu Asp Leu Ala Pro Thr
 Ile Gly
 35 40 45
 Val Asp Phe Lys Ile Lys Gln Leu Thr Val Ala Gly Lys Arg
 Leu Lys
 50 55 60
 Leu Thr Ile Trp Asp Thr Ala Gly Gln Glu Arg Phe Arg Thr
 Seite 1075

0070110

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

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 <212> DNA
 <213> Glycine max

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 <222> (1)..(684)

 <400> 714

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gtc	ggg		48										
Met	Ala	Ala	Ala	Thr	Ala	Pro	Arg	Phe	Ile	Lys	Cys	Val	Thr
Val	Gly												
1				5					10				
15													
gat	gga	gct	gta	ggc	aaa	act	tgc	atg	ctc	att	tgc	tat	aca
agc	aac		96										
Asp	Gly	Ala	Val	Gly	Lys	Thr	Cys	Met	Leu	Ile	Cys	Tyr	Thr
Ser	Asn												
			20					25					30
aaa	ttc	ccc	acg	gac	tat	att	cca	acg	gtg	ttt	gat	aat	ttc
agt	gca		144										
Lys	Phe	Pro	Thr	Asp	Tyr	Ile	Pro	Thr	Val	Phe	Asp	Asn	Phe
Ser	Ala												
		35					40					45	
aat	gtg	ggt	ggt	gaa	aac	aca	act	gtc	aat	tta	ggc	ctc	tgg
gac	act		192										
Asn	Val	Val	Val	Glu	Asn	Thr	Thr	Val	Asn	Leu	Gly	Leu	Trp
Asp	Thr												
		50				55				60			
gct	ggg	caa	gag	gat	tac	aac	agg	ctg	agg	cca	ttg	agc	tac
agg	ggg		240										
Ala	Gly	Gln	Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr
Arg	Gly												
65					70					75			
80													
gca	gat	gtc	ttt	gtc	ttg	gct	ttc	tct	tta	ggt	agc	cat	gca
agc	tac		288										
Ala	Asp	Val	Phe	Val	Leu	Ala	Phe	Ser	Leu	Val	Ser	His	Ala
Ser	Tyr												
			85						90				
95													
gaa	aat	gtg	ttg	aag	aag	tgg	ggt	cct	gaa	ctg	cag	cat	ttt
gct	cct		336										
Glu	Asn	Val	Leu	Lys	Lys	Trp	Val	Pro	Glu	Leu	Gln	His	Phe
Ala	Pro												
			100					105				110	
ggt	gtc	cca	gtg	gtg	cta	ggt	ggc	acc	aaa	ttg	gat	ctt	cga
gaa	gac		384										
Gly	Val	Pro	Val	Val	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg
Glu	Asp												
		115				120					125		
aag	cac	tat	ttg	gct	gat	cat	cct	ggt	ctg	gcg	cct	gtg	act
tct	gag		432										
Lys	His	Tyr	Leu	Ala	Asp	His	Pro	Gly	Leu	Ala	Pro	Val	Thr
Ser	Glu												

0070110

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      130      135      140
caa ggt gag gaa ttg cgt aaa ctg gtc gga gct acg tat tat
ata gag      480
Gln Gly Glu Glu Leu Arg Lys Leu Val Gly Ala Thr Tyr Tyr
Ile Glu
145      150      155
      160
tgc agc tca aag act cag cag aat gtg aag tca gtt ttt gat
gct gct      528
Cys Ser Ser Lys Thr Gln Gln Asn Val Lys Ser Val Phe Asp
Ala Ala
      165      170
175
atc aag gtg gtc atc gag cct cca caa aaa cat gag aag aag
aaa aaa      576
Ile Lys Val Val Ile Glu Pro Pro Gln Lys His Glu Lys Lys
Lys Lys
      180      185      190

cca cgt cga ggg tgt cta ctg tca gta cac ttt ttt cat atc
ata aca      624
Pro Arg Arg Gly Cys Leu Leu Ser Val His Phe Phe His Ile
Ile Thr
      195      200      205
act cct gca cgt gaa act ttc tta ctt gtg aaa agg gat aga
tca tta      672
Thr Pro Ala Arg Glu Thr Phe Leu Leu Val Lys Arg Asp Arg
Ser Leu
      210      215      220
agt gtt cat tga
      684
Ser Val His
225

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 <211> 227
 <212> PRT
 <213> Glycine max

<400> 715
 Met Ala Ala Ala Thr Ala Pro Arg Phe Ile Lys Cys Val Thr
 Val Gly
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 Asp Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr
 Ser Asn
 20 25 30

0070110

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

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Ser Val His
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<210> 716
<211> 654
<212> DNA
<213> Oryza sativa

<220>
<221> CDS
<222> (1)..(654)

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cag ccg 48
Met Asp Ser Ser Ser Ser Ser Ser Ser Thr Gln Ala Gln Ser
Gln Pro 1 5 10
15
gat ttt gat tac ctc ttt aag ctg ctc ctc atc ggc gac tcg
ggc gtc 96
Asp Phe Asp Tyr Leu Phe Lys Leu Leu Leu Ile Gly Asp Ser
Gly Val 20 25 30
ggc aag agc agt ctc ctc ctc cgc ttc acc tcc gac tct ttc
gag gat 144
Gly Lys Ser Ser Leu Leu Leu Arg Phe Thr Ser Asp Ser Phe
Glu Asp 35 40 45
ctc tcg ccc acc ata ggt gtc gac ttc aag gtc aag atg gtt
aac acc 192
Leu Ser Pro Thr Ile Gly Val Asp Phe Lys Val Lys Met Val
Asn Thr 50 55 60
ggc ggc aaa aaa ctc aag ctt gcc atc tgg gac aca gct gga
cag gag 240
Gly Gly Lys Lys Leu Lys Leu Ala Ile Trp Asp Thr Ala Gly
Gln Glu 65 70 75
80
cga ttt aga acc ttg acc agc tca tac tac aga ggt gca cag
ggc att 288
Arg Phe Arg Thr Leu Thr Ser Ser Tyr Tyr Arg Gly Ala Gln
Gly Ile 85 90
95
att atg gtg tac gat gtc act cga cgg gaa aca ttc acc aat
ctt tct 336

0070110

Ile	Met	Val	Tyr	Asp	Val	Thr	Arg	Arg	Glu	Thr	Phe	Thr	Asn
Leu	Ser												
			100					105					110

gac	ata	tgg	gct	aag	gaa	att	gac	ctc	tat	tct	aca	aac	cag
gat	tgt		384										
Asp	Ile	Trp	Ala	Lys	Glu	Ile	Asp	Leu	Tyr	Ser	Thr	Asn	Gln
Asp	Cys												

		115					120					125	
att	aag	atg	ctt	gtc	gga	aac	aaa	ggt	gac	aag	gaa	agt	gag
aga	gct		432										
Ile	Lys	Met	Leu	Val	Gly	Asn	Lys	Val	Asp	Lys	Glu	Ser	Glu
Arg	Ala												

		130				135					140		
gtg	aca	aaa	aaa	gag	ggc	att	gaa	ttt	gcc	agg	gaa	tac	ggg
tgt	tta		480										
Val	Thr	Lys	Lys	Glu	Gly	Ile	Glu	Phe	Ala	Arg	Glu	Tyr	Gly
Cys	Leu												

		145			150					155			
160													
ttt	cta	gaa	tgc	agt	gct	aaa	acc	aaa	gtg	aat	ggt	gaa	caa
tgc	ttt		528										
Phe	Leu	Glu	Cys	Ser	Ala	Lys	Thr	Lys	Val	Asn	Val	Glu	Gln
Cys	Phe												

		165								170			
175													
gag	gaa	ctc	gtc	ctg	aag	ata	ttg	gac	aca	cca	agc	ctc	ttg
gct	gat		576										
Glu	Glu	Leu	Val	Leu	Lys	Ile	Leu	Asp	Thr	Pro	Ser	Leu	Leu
Ala	Asp												

		180								185			190
--	--	-----	--	--	--	--	--	--	--	-----	--	--	-----

gct	tcc	tca	ggc	gca	aag	aag	aac	atc	ttc	aag	cag	aag	ccg
cca	gaa		624										
Ala	Ser	Ser	Gly	Ala	Lys	Lys	Asn	Ile	Phe	Lys	Gln	Lys	Pro
Pro	Glu												

		195					200					205	
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gcc	gat	gct	gcc	gct	agc	agc	tgc	tgt	taa				
			654										
Ala	Asp	Ala	Ala	Ala	Ser	Ser	Cys	Cys					
	210					215							

<210> 717

<211> 217

<212> PRT

<213> Oryza sativa

<400> 717

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1				5					10				
15													
Asp	Phe	Asp	Tyr	Leu	Phe	Lys	Leu	Leu	Leu	Ile	Gly	Asp	Ser
Gly	Val			20				25					30
Gly	Lys	Ser	Ser	Leu	Leu	Leu	Arg	Phe	Thr	Ser	Asp	Ser	Phe
Glu	Asp												
		35					40					45	
Leu	Ser	Pro	Thr	Ile	Gly	Val	Asp	Phe	Lys	Val	Lys	Met	Val
Asn	Thr												
	50						55					60	
Gly	Gly	Lys	Lys	Leu	Lys	Leu	Ala	Ile	Trp	Asp	Thr	Ala	Gly
Gln	Glu												
65					70					75			
	80												
Arg	Phe	Arg	Thr	Leu	Thr	Ser	Ser	Tyr	Tyr	Arg	Gly	Ala	Gln
Gly	Ile												
				85					90				
95													
Ile	Met	Val	Tyr	Asp	Val	Thr	Arg	Arg	Glu	Thr	Phe	Thr	Asn
Leu	Ser												
			100					105					110
Asp	Ile	Trp	Ala	Lys	Glu	Ile	Asp	Leu	Tyr	Ser	Thr	Asn	Gln
Asp	Cys												
		115					120					125	
Ile	Lys	Met	Leu	Val	Gly	Asn	Lys	Val	Asp	Lys	Glu	Ser	Glu
Arg	Ala												
	130					135					140		
Val	Thr	Lys	Lys	Glu	Gly	Ile	Glu	Phe	Ala	Arg	Glu	Tyr	Gly
Cys	Leu												
145					150					155			
	160												
Phe	Leu	Glu	Cys	Ser	Ala	Lys	Thr	Lys	Val	Asn	Val	Glu	Gln
Cys	Phe												
				165					170				
175													
Glu	Glu	Leu	Val	Leu	Lys	Ile	Leu	Asp	Thr	Pro	Ser	Leu	Leu
Ala	Asp												
			180					185					190

0070110

Ala Ser Ser Gly Ala Lys Lys Asn Ile Phe Lys Gln Lys Pro
 Pro Glu
 195 200 205

Ala Asp Ala Ala Ala Ser Ser Cys Cys
 210 215

<210> 718
 <211> 612
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (1)..(612)

<400> 718
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 ggt gat 48
 Met Asn Pro Glu Tyr Asp Tyr Leu Phe Lys Leu Leu Leu Ile
 Gly Asp 1 5 10
 15
 tct ggt gtt ggg aaa tca tgc ttg ctt ctc aga ttt gcg gat
 gat tca 96
 Ser Gly val Gly Lys Ser Cys Leu Leu Leu Arg Phe Ala Asp
 Asp Ser 20 25 30
 tat ttg gac agc tac atc agc aca att ggg gtt gat ttt aaa
 att cg 144
 Tyr Leu Asp Ser Tyr Ile Ser Thr Ile Gly val Asp Phe Lys
 Ile Arg 35 40 45
 aca gta gag caa gat ggg aag acc ata aaa ctt caa att tgg
 gat act 192
 Thr val Glu Gln Asp Gly Lys Thr Ile Lys Leu Gln Ile Trp
 Asp Thr 50 55 60
 gct ggg caa gag cgc ttc agg acc atc act agc agc tac tac
 cgt gga 240
 Ala Gly Gln Glu Arg Phe Arg Thr Ile Thr Ser Ser Tyr Tyr
 Arg Gly 65 70 75
 80
 gct cat gga atc att att gta tat gac gtg aca gac caa gaa
 agc ttc 288
 Ala His Gly Ile Ile Ile val Tyr Asp val Thr Asp Gln Glu
 Ser Phe

0070110

85

90

95

aat aat gtg aag caa tgg tta aat gaa att gat cgt tat gca
 agt gac 336
 Asn Asn Val Lys Gln Trp Leu Asn Glu Ile Asp Arg Tyr Ala
 Ser Asp
 100 105 110

aat gtt aac aag ctc ctt gtt ggg aac aag agc gac cta act
 gcc aac 384
 Asn Val Asn Lys Leu Leu Val Gly Asn Lys Ser Asp Leu Thr
 Ala Asn
 115 120 125

aaa gtt gtg gca act gag aca gca aag gca ttt gct gat gag
 atg ggc 432
 Lys Val Val Ala Thr Glu Thr Ala Lys Ala Phe Ala Asp Glu
 Met Gly
 130 135 140

atc ccg ttc atg gag acg agt gcc aaa aac gcc acc aac gtg
 gag cag 480
 Ile Pro Phe Met Glu Thr Ser Ala Lys Asn Ala Thr Asn Val
 Glu Gln
 145 150 155

160
 gcc ttc atg gct atg gct gca tcc atc aag gac agg atg gcc
 agc caa 528
 Ala Phe Met Ala Met Ala Ala Ser Ile Lys Asp Arg Met Ala
 Ser Gln
 165 170

175
 cca gcc gcg gcc aac gca agg cca gcg acg gtg cag atc cgc
 ggg caa 576
 Pro Ala Ala Ala Asn Ala Arg Pro Ala Thr Val Gln Ile Arg
 Gly Gln
 180 185 190

ccc gtc aac cag aag acg tct tgc tgc tcg tct taa
 612
 Pro Val Asn Gln Lys Thr Ser Cys Cys Ser Ser
 195 200

<210> 719
 <211> 203
 <212> PRT
 <213> Zea mays

<400> 719
 Met Asn Pro Glu Tyr Asp Tyr Leu Phe Lys Leu Leu Leu Ile
 Seite 1084

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Gly	Asp													
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15														
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Asp	Ser													
			20					25					30	
Tyr	Leu	Asp	Ser	Tyr	Ile	Ser	Thr	Ile	Gly	Val	Asp	Phe	Lys	
Ile	Arg													
		35					40					45		
Thr	Val	Glu	Gln	Asp	Gly	Lys	Thr	Ile	Lys	Leu	Gln	Ile	Trp	
Asp	Thr													
	50					55					60			
Ala	Gly	Gln	Glu	Arg	Phe	Arg	Thr	Ile	Thr	Ser	Ser	Tyr	Tyr	
Arg	Gly													
65					70					75				
	80													
Ala	His	Gly	Ile	Ile	Ile	Val	Tyr	Asp	Val	Thr	Asp	Gln	Glu	
Ser	Phe													
				85						90				
95														
Asn	Asn	Val	Lys	Gln	Trp	Leu	Asn	Glu	Ile	Asp	Arg	Tyr	Ala	
Ser	Asp													
			100					105					110	
Asn	Val	Asn	Lys	Leu	Leu	Val	Gly	Asn	Lys	Ser	Asp	Leu	Thr	
Ala	Asn													
		115					120					125		
Lys	Val	Val	Ala	Thr	Glu	Thr	Ala	Lys	Ala	Phe	Ala	Asp	Glu	
Met	Gly													
	130					135					140			
Ile	Pro	Phe	Met	Glu	Thr	Ser	Ala	Lys	Asn	Ala	Thr	Asn	Val	
Glu	Gln													
145					150					155				
	160													
Ala	Phe	Met	Ala	Met	Ala	Ala	Ser	Ile	Lys	Asp	Arg	Met	Ala	
Ser	Gln													
			165						170					
175														
Pro	Ala	Ala	Ala	Asn	Ala	Arg	Pro	Ala	Thr	Val	Gln	Ile	Arg	
Gly	Gln													
			180					185					190	
Pro	Val	Asn	Gln	Lys	Thr	Ser	Cys	Cys	Ser	Ser				

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200

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<210> 720
<211> 642
<212> DNA
<213> Triticum aestivum

<220>
<221> CDS
<222> (1)..(642)

<400> 720
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ggc gac 48
Met Ala Ser Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val
Gly Asp 1 5 10
15
ggc gcc gtc ggc aag acc tgc atg ctc atc tgc tac acc agc
aac aag 96
Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser
Asn Lys 20 25 30
ttc ccc acc gac tac ata ccc acg gtg ttc gac aat ttc agc
tca aac 144
Phe Pro Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser
Ser Asn 35 40 45
gtg gtg gcg gac ggc acc acc gtg aat ttg ggc ctt tgg gac
acc gcc 192
Val Val Ala Asp Gly Thr Thr Val Asn Leu Gly Leu Trp Asp
Thr Ala 50 55 60
ggg cag gag gat tac aac cgg ctg agg cct ctg agc tac cgc
ggc gct 240
Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg
Gly Ala 65 70 75
80
gat gtt ttt gtg ctt gcc ttc tct ctc gtg agc cga gct agc
tat gag 288
Asp Val Phe Val Leu Ala Phe Ser Leu Val Ser Arg Ala Ser
Tyr Glu 85 90
95
aat atc atg aag aag tgg ata ccg gag ctt cag cat tac gcg
ccc gcc 336
Asn Ile Met Lys Lys Trp Ile Pro Glu Leu Gln His Tyr Ala

0070110

Pro Gly													
		100					105					110	
gtg ccg gtt	gtg ctg gta	ggc aca aaa	ctg gat ctt	cgt gaa									
gac aag	384												
Val Pro Val	Val Leu Val	Gly Thr Lys	Leu Asp Leu	Arg Glu									
Asp Lys	115		120									125	
cac tat ttg	ctg gac cac	cct ggc atg	ata ccc gtt	acc aca									
gca cag	432												
His Tyr Leu	Leu Asp His	Pro Gly Met	Ile Pro Val	Thr Thr									
Ala Gln	130		135									140	
ggg gag gaa	ctt cgt aag	caa gtt ggt	gct tta tat	tac ata									
gag tgc	480												
Gly Glu Glu	Leu Arg Lys	Gln Val Gly	Ala Leu Tyr	Tyr Ile									
Glu Cys													
145		150										155	
160													
agc tca aag	aca caa cag	aat gtc aaa	gct gtg ttt	gat gct									
gct atc	528												
Ser Ser Lys	Thr Gln Gln	Asn Val Lys	Ala Val Phe	Asp Ala									
Ala Ile													
	165											170	
175													
aag gta gta	atc cag ccc	cca act aaa	caa aga gaa	aag aag									
aaa aag	576												
Lys Val Val	Ile Gln Pro	Pro Thr Lys	Gln Arg Glu	Lys Lys									
Lys Lys													
	180											190	
aaa cag cgt	cgg gga tgt	tct atg atg	aac ttc ggt	gga agg									
aaa atg	624												
Lys Gln Arg	Arg Gly Cys	Ser Met Met	Asn Phe Gly	Gly Arg									
Lys Met													
	195											205	
cta tgc ttc	aaa tcc tga												
	642												
Leu Cys Phe	Lys Ser												
210													

<210> 721
 <211> 213
 <212> PRT
 <213> Triticum aestivum

<400> 721
 Met Ala Ser Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val
 Seite 1087

0070110

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

0070110

Lys Gln Arg Arg Gly Cys Ser Met Met Asn Phe Gly Gly Arg
 Lys Met
 195 200 205

Leu Cys Phe Lys Ser
 210

<210> 722
 <211> 594
 <212> DNA
 <213> Triticum aestivum

<220>
 <221> CDS
 <222> (1)..(594)

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 ggc gcc 48
 Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala
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 15
 gtc ggc aag act tgc atg ctc atc tcc tac acc tcc aac acc
 ttc ccc 96
 Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
 Phe Pro
 20 25 30
 acc gac tat gtg cca acg gtg ttt gac aac ttc agt gct aat
 gtt gtg 144
 Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
 Val Val
 35 40 45
 gtt gat ggc aac act gtc aac ctc ggg cta tgg gat act gca
 ggt cag 192
 Val Asp Gly Asn Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
 Gly Gln
 50 55 60
 gag gac tac aac aga ctg aga ccg ctg agt tat cgt gga gct
 gat gtc 240
 Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
 Asp Val
 65 70 75
 80
 ttc ctt ctg gcc ttc tcg ctt atc agc aag gcc agc tat gag
 aat gtt 288
 Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
 Asn Val

0070110

85

90

95

tca aag aag tgg ata cct gag ctg aag cat tat gca cca ggt
gtg cct 336
Ser Lys Lys Trp Ile Pro Glu Leu Lys His Tyr Ala Pro Gly
Val Pro

100

105

110

att atc ctc gtg gga aca aag ctt gat ctt cga gat gac aag
cag ttc 384
Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe

115

120

125

ttt gtg gac cat cct ggt gct gtt cct atc act act gct cag
ggg gag 432
Phe Val Asp His Pro Gly Ala Val Pro Ile Thr Thr Ala Gln
Gly Glu

130

135

140

gaa cta aaa aag tta ata ggc gca ccc tac tac atc gaa tgc
agc tcg 480
Glu Leu Lys Lys Leu Ile Gly Ala Pro Tyr Tyr Ile Glu Cys
Ser Ser

145

150

155

160

aag acc caa cta aat gtc aag ggt gta ttt gat gcg gca ata
aag gtg 528
Lys Thr Gln Leu Asn Val Lys Gly Val Phe Asp Ala Ala Ile
Lys Val

165

170

175

gta ctt gcg cca cca aag gcg aag aag aag aaa aag gcg cag
agg ggg 576
Val Leu Ala Pro Pro Lys Ala Lys Lys Lys Lys Lys Ala Gln
Arg Gly

180

185

190

gct tgc tcc atc ttg tga
594
Ala Cys Ser Ile Leu
195

<210> 723

<211> 197

<212> PRT

<213> Triticum aestivum

<400> 723

Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Seite 1090

0070110

Gly	Ala													
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15														
Val	Gly	Lys	Thr	Cys	Met	Leu	Ile	Ser	Tyr	Thr	Ser	Asn	Thr	
Phe	Pro													
			20					25					30	
Thr	Asp	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn	
Val	Val													
		35					40					45		
Val	Asp	Gly	Asn	Thr	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala	
Gly	Gln													
	50					55					60			
Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala	
Asp	Val													
65					70					75				
	80													
Phe	Leu	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Lys	Ala	Ser	Tyr	Glu	
Asn	Val													
				85					90					
95														
Ser	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Lys	His	Tyr	Ala	Pro	Gly	
Val	Pro													
			100					105					110	
Ile	Ile	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys	
Gln	Phe													
		115					120					125		
Phe	Val	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Thr	Thr	Ala	Gln	
Gly	Glu													
	130					135						140		
Glu	Leu	Lys	Lys	Leu	Ile	Gly	Ala	Pro	Tyr	Tyr	Ile	Glu	Cys	
Ser	Ser													
145					150					155				
	160													
Lys	Thr	Gln	Leu	Asn	Val	Lys	Gly	Val	Phe	Asp	Ala	Ala	Ile	
Lys	Val													
				165					170					
175														
Val	Leu	Ala	Pro	Pro	Lys	Ala	Lys	Lys	Lys	Lys	Lys	Ala	Gln	
Arg	Gly													
			180					185					190	
Ala	Cys	Ser	Ile	Leu										

<210> 724
 <211> 639
 <212> DNA
 <213> *Triticum aestivum*

<220>
 <221> CDS
 <222> (1)..(639)

<400> 724
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 ggc gcc 48
 Met Ser Val Thr Lys Phe Ile Lys Cys Val Thr Val Gly Asp
 Gly Ala 1 5 10
 15
 gtc ggc aag acc tgc atg ctc atc tgc tac acc agc aac agg
 ttc ccc 96
 Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser Asn Arg
 Phe Pro 20 25 30
 agc gat tac atc ccc acc gtg ttc gac aac ttc agc gcc aac
 gtc tcc 144
 Ser Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
 Val Ser 35 40 45
 gtc gac ggc aac atc gtc aac ctc ggc ctg tgg gac acc gcc
 ggg caa 192
 Val Asp Gly Asn Ile Val Asn Leu Gly Leu Trp Asp Thr Ala
 Gly Gln 50 55 60
 gag gac tac agc agg ctg agg ccg ctg agc tac aga ggc gcc
 gac gtc 240
 Glu Asp Tyr Ser Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
 Asp Val 65 70 75
 80
 ttc gtg ctc gcc ttc tcc ctc atc agc agc gca agc tac gag
 aat gtc 288
 Phe Val Leu Ala Phe Ser Leu Ile Ser Ser Ala Ser Tyr Glu
 Asn Val 85 90
 95
 ctc aag aag tgg atg cca gag ctc cgc cgg ttc gcg ccc aac
 gtc ccc 336
 Leu Lys Lys Trp Met Pro Glu Leu Arg Arg Phe Ala Pro Asn
 Seite 1092

0070110

Val	Pro												
			100				105					110	
att gtt ctt gtt ggg acc aag cta gat ctg cgt gac cac aga													
gcc tac			384										
Ile Val Leu Val Gly Thr Lys Leu Asp Leu Arg Asp His Arg													
Ala Tyr													
		115				120					125		
ctc gcc gac cat ccc ggt gcc tca gca atc aca act gca cag													
ggt gaa			432										
Leu Ala Asp His Pro Gly Ala Ser Ala Ile Thr Thr Ala Gln													
Gly Glu													
		130				135					140		
gaa ctc agg aag cag atc ggc gcc gca gct tac atc gag tgc													
agc tcg			480										
Glu Leu Arg Lys Gln Ile Gly Ala Ala Ala Tyr Ile Glu Cys													
Ser Ser													
145					150					155			
	160												
aag acg cag cag aac gtc aag gct gtc ttc gac acc gcc atc													
aag gtg			528										
Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Thr Ala Ile													
Lys Val													
			165							170			
175													
gtc ctc caa ccg ccg agg agg agg gag gtg atg gcc gcc agg													
aag aaa			576										
Val Leu Gln Pro Pro Arg Arg Arg Glu Val Met Ala Ala Arg													
Lys Lys													
		180								185			
acc agg cga agc tct gga tgc tcc atc atg cac ttg atg tgt													
ggc agc			624										
Thr Arg Arg Ser Ser Gly Cys Ser Ile Met His Leu Met Cys													
Gly Ser													
		195											
acg tgt gct gct tga										200			
			639										
Thr Cys Ala Ala													
	210												

<210> 725

<211> 212

<212> PRT

<213> Triticum aestivum

<400> 725

Met Ser Val Thr Lys Phe Ile Lys Cys Val Thr Val Gly Asp

0070110

Gly	Ala													
1					5					10				
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Val	Gly	Lys	Thr	Cys	Met	Leu	Ile	Cys	Tyr	Thr	Ser	Asn	Arg	
Phe	Pro													
			20					25					30	
Ser	Asp	Tyr	Ile	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn	
Val	Ser													
		35					40					45		
Val	Asp	Gly	Asn	Ile	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala	
Gly	Gln													
	50					55					60			
Glu	Asp	Tyr	Ser	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala	
Asp	Val													
65					70					75				
	80													
Phe	Val	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Ser	Ala	Ser	Tyr	Glu	
Asn	Val													
				85						90				
95														
Leu	Lys	Lys	Trp	Met	Pro	Glu	Leu	Arg	Arg	Phe	Ala	Pro	Asn	
Val	Pro													
			100					105					110	
Ile	Val	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	His	Arg	
Ala	Tyr													
		115					120					125		
Leu	Ala	Asp	His	Pro	Gly	Ala	Ser	Ala	Ile	Thr	Thr	Ala	Gln	
Gly	Glu													
	130					135						140		
Glu	Leu	Arg	Lys	Gln	Ile	Gly	Ala	Ala	Ala	Tyr	Ile	Glu	Cys	
Ser	Ser													
145					150					155				
	160													
Lys	Thr	Gln	Gln	Asn	Val	Lys	Ala	Val	Phe	Asp	Thr	Ala	Ile	
Lys	Val													
				165					170					
175														
Val	Leu	Gln	Pro	Pro	Arg	Arg	Arg	Glu	Val	Met	Ala	Ala	Arg	
Lys	Lys													
			180					185					190	
Thr	Arg	Arg	Ser	Ser	Gly	Cys	Ser	Ile	Met	His	Leu	Met	Cys	

0070110

Gly Ser 195 200 205

Thr Cys Ala Ala
210

<210> 726
<211> 594
<212> DNA
<213> Triticum aestivum

<220>
<221> CDS
<222> (1)..(594)

<400> 726
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ggc gcc 48
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10
15
gtc ggc aag act tgc ctc ctc atc tcc tac aca tcc aac acc
ttc ccc 96
Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
20 25 30
acc gac tat gtc cca aca gtc ttc gac aac ttc agc gct aac
gtc gtg 144
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
35 40 45
gtt gac ggg agc acc gtc aac ctc gga tta tgg gat act gca
gga caa 192
Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60
gag gac tat aat aga cta cgc cca cta agc tac cga ggt gcc
gat gtc 240
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65 70 75
80
ttc ctg ctc gcc ttt tct ctt atc agc aaa gca agc tac gag
aat gtc 288
Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val

85

90

0070110

95
act aag aag tgg atc cct gag cta cgg cac tat gct cct ggt
gtg ccc 336
Thr Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala Pro Gly
Val Pro

100

105

110

ata att ctt gtt ggg aca aag ctt gat ctg cgg gat gac gag
cag ttt 384
Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Glu
Gln Phe

115

120

125

ttc gtg gat cac cct ggg gct gtt cct att tcc acc gct cag
ggg gaa 432
Phe Val Asp His Pro Gly Ala Val Pro Ile Ser Thr Ala Gln
Gly Glu

130

135

140

gag ctg aag aag gta att ggc gcg acg gcc tac atc gag tgc
agc tca 480
Glu Leu Lys Lys Val Ile Gly Ala Thr Ala Tyr Ile Glu Cys
Ser Ser

145

150

155

160

aaa aca cag cag aac atc aag gcg gtg ttt gat gcg gcg atc
aag gtg 528
Lys Thr Gln Gln Asn Ile Lys Ala Val Phe Asp Ala Ala Ile
Lys Val

165

170

175

gtt ctc cag cct ccg aag cag aag cgg aag aag agg aag tcg
cag aaa 576
Val Leu Gln Pro Pro Lys Gln Lys Arg Lys Lys Arg Lys Ser
Gln Lys

180

185

190

gga tgc agc atc ttg taa
594
Gly Cys Ser Ile Leu
195

<210> 727

<211> 197

<212> PRT

<213> Triticum aestivum

<400> 727

Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala

0070110

1				5				10					
15													
Val	Gly	Lys	Thr	Cys	Leu	Leu	Ile	Ser	Tyr	Thr	Ser	Asn	Thr
Phe	Pro												
			20					25					30
Thr	Asp	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn
Val	Val												
		35					40					45	
Val	Asp	Gly	Ser	Thr	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala
Gly	Gln												
	50					55					60		
Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala
Asp	Val												
65					70					75			
	80												
Phe	Leu	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Lys	Ala	Ser	Tyr	Glu
Asn	Val												
				85					90				
95													
Thr	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Arg	His	Tyr	Ala	Pro	Gly
Val	Pro												
		100						105				110	
Ile	Ile	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Glu
Gln	Phe												
		115					120				125		
Phe	Val	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Ser	Thr	Ala	Gln
Gly	Glu												
	130					135				140			
Glu	Leu	Lys	Lys	Val	Ile	Gly	Ala	Thr	Ala	Tyr	Ile	Glu	Cys
Ser	Ser												
145					150					155			
	160												
Lys	Thr	Gln	Gln	Asn	Ile	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile
Lys	Val												
				165					170				
175													
Val	Leu	Gln	Pro	Pro	Lys	Gln	Lys	Arg	Lys	Lys	Arg	Lys	Ser
Gln	Lys												
			180					185				190	
Gly	Cys	Ser	Ile	Leu									
		195											

0070110

<210> 728
<211> 669
<212> DNA
<213> Triticum aestivum

<220>
<221> CDS
<222> (1)..(669)

<400> 728
atg agc ggc gga gcg gga gcg ggg gcg gcg gcg gcg gcg gcg
gtg agc 48
Met Ser Gly Gly Ala Gly Ala Gly Ala Ala Ala Ala Ala Ala
Val Ser 1 5 10
15
agg ttc atc aag tgc gtg gcc gtg ggc gac ggc gcc gtg ggc
aag acc 96
Arg Phe Ile Lys Cys Val Ala Val Gly Asp Gly Ala Val Gly
Lys Thr 20 25 30
tgc atg ctc atc tgc tac acc tgc aac aag ttc ccc acc gac
tac atc 144
Cys Met Leu Ile Cys Tyr Thr Cys Asn Lys Phe Pro Thr Asp
Tyr Ile 35 40 45
ccc acc gtg ttc gac aac ttc agc gcc aat gtc tcc gtg gac
ggc agc 192
Pro Thr Val Phe Asp Asn Phe Ser Ala Asn Val Ser Val Asp
Gly Ser 50 55 60
atc gtc aac ctc ggc ctc tgg gac acc gca ggt cag gag gat
tac agc 240
Ile Val Asn Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu Asp
Tyr Ser 65 70 75
80
agg ctg agg cct ctg agc tac agg gga gcc gat gtc ttc atc
ctc tcc 288
Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala Asp Val Phe Ile
Leu Ser 85 90
95
ttc tcc ctc acc agc aga gca agc tat gag aat gtg cac aag
aag tgg 336
Phe Ser Leu Thr Ser Arg Ala Ser Tyr Glu Asn Val His Lys
Lys Trp

0070110

100

105

110

atg ccg gag ctt cgc cgg tac gcc ccc ggc att cct gta cta
 ctt gtt 384
 Met Pro Glu Leu Arg Arg Tyr Ala Pro Gly Ile Pro Val Leu
 Leu Val

115 120 125
 gga acc aag ttg gat ctc cga gaa gat aga gca tat ctt gct
 gat cat 432
 Gly Thr Lys Leu Asp Leu Arg Glu Asp Arg Ala Tyr Leu Ala
 Asp His

130 135 140
 gca gct gat tcc atc ata aca act gag cag ggt gag gag ctt
 cgg aga 480
 Ala Ala Asp Ser Ile Ile Thr Thr Glu Gln Gly Glu Glu Leu
 Arg Arg
 145 150 155

160
 caa ata ggt gcg gtg gca tac ata gaa tgc agc tcc aag aca
 caa agg 528
 Gln Ile Gly Ala Val Ala Tyr Ile Glu Cys Ser Ser Lys Thr
 Gln Arg

165 170
 175
 aac att aag gct gtt ttc gac acc gca atc aag gca gtt ctt
 caa cct 576
 Asn Ile Lys Ala Val Phe Asp Thr Ala Ile Lys Ala Val Leu
 Gln Pro

180 185 190
 caa agg cac aag gag gta gcc aga aag gaa att cgg act cgc
 tct agt 624
 Gln Arg His Lys Glu Val Ala Arg Lys Glu Ile Arg Thr Arg
 Ser Ser

195 200 205
 cgg tca gta agg cgc tac ttc tgc ggg agt gtt tgc tta gca
 tag 669
 Arg Ser Val Arg Arg Tyr Phe Cys Gly Ser Val Cys Leu Ala
 210 215 220

<210> 729

<211> 222

<212> PRT

<213> Triticum aestivum

<400> 729

Met Ser Gly Gly Ala Gly Ala Gly Ala Ala Ala Ala Ala Ala
 Val Ser

0070110

1				5				10					
15	Arg	Phe	Ile	Lys	Cys	Val	Ala	Val	Gly	Asp	Gly	Ala	Val
	Lys	Thr											
				20				25					30
	Cys	Met	Leu	Ile	Cys	Tyr	Thr	Cys	Asn	Lys	Phe	Pro	Thr
	Tyr	Ile											Asp
			35					40					45
	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn	Val	Ser	Val
	Gly	Ser											Asp
			50				55					60	
	Ile	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala	Gly	Gln	Glu
	Tyr	Ser											Asp
	65					70					75		
		80											
	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala	Asp	Val	Phe
	Leu	Ser											Ile
					85					90			
	95												
	Phe	Ser	Leu	Thr	Ser	Arg	Ala	Ser	Tyr	Glu	Asn	Val	His
	Lys	Trp											Lys
				100					105				110
	Met	Pro	Glu	Leu	Arg	Arg	Tyr	Ala	Pro	Gly	Ile	Pro	Val
	Leu	Val											Leu
			115					120					125
	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Glu	Asp	Arg	Ala	Tyr	Leu
	Asp	His											Ala
		130					135					140	
	Ala	Ala	Asp	Ser	Ile	Ile	Thr	Thr	Glu	Gln	Gly	Glu	Glu
	Arg	Arg											Leu
	145					150					155		
		160											
	Gln	Ile	Gly	Ala	Val	Ala	Tyr	Ile	Glu	Cys	Ser	Ser	Lys
	Gln	Arg											Thr
					165					170			
	175												
	Asn	Ile	Lys	Ala	Val	Phe	Asp	Thr	Ala	Ile	Lys	Ala	Val
	Gln	Pro											Leu
				180					185				190
	Gln	Arg	His	Lys	Glu	Val	Ala	Arg	Lys	Glu	Ile	Arg	Thr
	Ser	Ser											Arg

0070110
200

195

205

Arg Ser Val Arg Arg Tyr Phe Cys Gly Ser Val Cys Leu Ala
210 215 220

<210> 730
<211> 660
<212> DNA
<213> Triticum aestivum

<220>
<221> CDS
<222> (1)..(660)

<400> 730
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cag gcg 48
Met Asp Ser Ser Ser Ser Ser Thr Ala Ser Ser Ser Gln Ala
Gln Ala
1 5 10
15
cag ccg gac ttc gac tac ctg ttc aag ctc ctc ctc atc ggc
gac tcc 96
Gln Pro Asp Phe Asp Tyr Leu Phe Lys Leu Leu Leu Ile Gly
Asp Ser
20 25 30
ggc gtg ggg aag agc agc ctg ctc ctc cga ttc aca tcg gac
tcc ttc 144
Gly Val Gly Lys Ser Ser Leu Leu Leu Arg Phe Thr Ser Asp
Ser Phe
35 40 45
gag gac cta tcc ccg acc atc ggc gtc gac ttc aag gtg aag
atg gtc 192
Glu Asp Leu Ser Pro Thr Ile Gly Val Asp Phe Lys Val Lys
Met Val
50 55 60
aac att gcc ggc aag aag ctc aag ctc gcc gtc tgg gac acc
gct gga 240
Asn Ile Ala Gly Lys Lys Leu Lys Leu Ala Val Trp Asp Thr
Ala Gly
65 70 75
80
cag gaa cga ttt agg acc ttg acc agc tct tac tac aga ggg
gca caa 288
Gln Glu Arg Phe Arg Thr Leu Thr Ser Ser Tyr Tyr Arg Gly
Ala Gln
85 90
95

0070110

ggg atc atc atg gtg tac gat gtt act cgc cga gaa aca ttc
 acg aat 336
 Gly Ile Ile Met Val Tyr Asp Val Thr Arg Arg Glu Thr Phe
 Thr Asn
 100 105 110

ctc tct gac ata tgg gcc aag gaa att gac ctg tat tcg aca
 aac cag 384
 Leu Ser Asp Ile Trp Ala Lys Glu Ile Asp Leu Tyr Ser Thr
 Asn Gln
 115 120 125

gac tgt ata aag atg ctt gtc gga aac aaa gtg gac aag gaa
 agt gag 432
 Asp Cys Ile Lys Met Leu Val Gly Asn Lys Val Asp Lys Glu
 Ser Glu
 130 135 140

agg gct gtc acc aag aag gaa ggc att gac ttt gcc agg gag
 tat ggg 480
 Arg Ala Val Thr Lys Lys Glu Gly Ile Asp Phe Ala Arg Glu
 Tyr Gly
 145 150 155

160
 tgt tta ttt ctg gaa tgc agt gcg aaa acc aaa gtg aac gtg
 gag cag 528
 Cys Leu Phe Leu Glu Cys Ser Ala Lys Thr Lys Val Asn Val
 Glu Gln
 165 170

175
 tgc ttt gag gag ctc gtg ctg aag ata ttg gac act ccg agc
 ctg ctg 576
 Cys Phe Glu Glu Leu Val Leu Lys Ile Leu Asp Thr Pro Ser
 Leu Leu
 180 185 190

gcg gat gcg tcg tcg ggg gcg aag aag aac atc ttc aag cag
 aag gcg 624
 Ala Asp Ala Ser Ser Gly Ala Lys Lys Asn Ile Phe Lys Gln
 Lys Ala
 195 200 205

cca gag gct gat gct gcg gcg agc ggc tgc tgt tga
 660
 Pro Glu Ala Asp Ala Ala Ala Ser Gly Cys Cys
 210 215

<210> 731
 <211> 219
 <212> PRT
 <213> Triticum aestivum

0070110

<400> 731

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

0070110

180

185

190

Ala Asp Ala Ser Ser Gly Ala Lys Lys Asn Ile Phe Lys Gln
Lys Ala

195

200

205

Pro Glu Ala Asp Ala Ala Ala Ser Gly Cys Cys
210 215

<210> 732

<211> 660

<212> DNA

<213> Triticum aestivum

<220>

<221> CDS

<222> (1)..(660)

<400> 732

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cag gcg 48

Met Asp Ser Ser Ser Ser Ser Thr Ala Ser Ser Ser Gln Ala
Gln Ala

1

5

10

15

cag ccc gac ttc gat tac ctg ttc aag ctc ctc ctc atc ggc
gac tcg 96

Gln Pro Asp Phe Asp Tyr Leu Phe Lys Leu Leu Leu Ile Gly
Asp Ser

20

25

30

ggc gtg ggc aag agc agt ctc ctc ctc cga ttc aca tcc gac
tcc ttc 144

Gly Val Gly Lys Ser Ser Leu Leu Leu Arg Phe Thr Ser Asp
Ser Phe

35

40

45

gag gac cta tcc cca acc atc ggc gtg gac ttc aag gtg aag
atg gtt 192

Glu Asp Leu Ser Pro Thr Ile Gly Val Asp Phe Lys Val Lys
Met Val

50

55

60

aac att gcc ggc aag aag ctc aag ctc gcc gtc tgg gac acc
gct gga 240

Asn Ile Ala Gly Lys Lys Leu Lys Leu Ala Val Trp Asp Thr
Ala Gly

65

70

75

80

cag gaa cgg ttt agg acc ttg acc agc tct tac tac aga ggg
gca caa 288

0070110

Gln	Glu	Arg	Phe	Arg	Thr	Leu	Thr	Ser	Ser	Tyr	Tyr	Arg	Gly
Ala	Gln												
				85					90				
95													
ggg	atc	atc	atg	gtg	tat	gat	gtt	act	cgc	cga	gaa	aca	ttc
acc	aat		336										
Gly	Ile	Ile	Met	Val	Tyr	Asp	Val	Thr	Arg	Arg	Glu	Thr	Phe
Thr	Asn												
			100					105					110
ctc	tct	gac	ata	tgg	gcc	aag	gaa	att	gac	ctg	tat	tcg	acc
aac	cag		384										
Leu	Ser	Asp	Ile	Trp	Ala	Lys	Glu	Ile	Asp	Leu	Tyr	Ser	Thr
Asn	Gln												
		115					120					125	
gac	tgt	ata	aag	atg	ctt	gtc	gga	aac	aaa	gtg	gac	aag	gaa
agt	gag		432										
Asp	Cys	Ile	Lys	Met	Leu	Val	Gly	Asn	Lys	Val	Asp	Lys	Glu
Ser	Glu												
	130					135					140		
agg	gct	gtc	acc	aag	aag	gaa	ggc	gtc	gac	ttt	gcc	agg	gag
tat	ggg		480										
Arg	Ala	val	Thr	Lys	Lys	Glu	Gly	val	Asp	Phe	Ala	Arg	Glu
Tyr	Gly												
145					150					155			
160													
tgt	tta	ttt	ctg	gaa	tgc	agt	gcg	aaa	acc	aaa	gtg	aat	gtg
gag	cag		528										
Cys	Leu	Phe	Leu	Glu	Cys	Ser	Ala	Lys	Thr	Lys	Val	Asn	Val
Glu	Gln												
				165						170			
175													
tgc	ttt	gag	gag	ctt	gtg	ctc	aag	ata	ttg	gac	aca	ccg	agc
ctg	ttg		576										
Cys	Phe	Glu	Glu	Leu	Val	Leu	Lys	Ile	Leu	Asp	Thr	Pro	Ser
Leu	Leu												
			180						185				190
gcg	gat	gca	tcc	tct	ggg	gca	aag	aag	aac	atc	ttc	aag	cag
aag	gcg		624										
Ala	Asp	Ala	Ser	Ser	Gly	Ala	Lys	Lys	Asn	Ile	Phe	Lys	Gln
Lys	Ala												
		195					200					205	
cca	gag	gct	gat	gct	gcg	gcg	agc	ggc	tgc	tgt	tga		
			660										
Pro	Glu	Ala	Asp	Ala	Ala	Ala	Ser	Gly	Cys	Cys			
	210					215							

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<210> 733
 <211> 219
 <212> PRT
 <213> Triticum aestivum

<400> 733
 Met Asp Ser Ser Ser Ser Ser Thr Ala Ser Ser Ser Gln Ala
 Gln Ala
 1 5 10
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 Gln Pro Asp Phe Asp Tyr Leu Phe Lys Leu Leu Leu Ile Gly
 Asp Ser
 20 25 30
 Gly Val Gly Lys Ser Ser Leu Leu Leu Arg Phe Thr Ser Asp
 Ser Phe
 35 40 45
 Glu Asp Leu Ser Pro Thr Ile Gly Val Asp Phe Lys Val Lys
 Met Val
 50 55 60
 Asn Ile Ala Gly Lys Lys Leu Lys Leu Ala Val Trp Asp Thr
 Ala Gly
 65 70 75
 80
 Gln Glu Arg Phe Arg Thr Leu Thr Ser Ser Tyr Tyr Arg Gly
 Ala Gln
 85 90
 95
 Gly Ile Ile Met Val Tyr Asp Val Thr Arg Arg Glu Thr Phe
 Thr Asn
 100 105 110
 Leu Ser Asp Ile Trp Ala Lys Glu Ile Asp Leu Tyr Ser Thr
 Asn Gln
 115 120 125
 Asp Cys Ile Lys Met Leu Val Gly Asn Lys Val Asp Lys Glu
 Ser Glu
 130 135 140
 Arg Ala Val Thr Lys Lys Glu Gly Val Asp Phe Ala Arg Glu
 Tyr Gly
 145 150 155
 160
 Cys Leu Phe Leu Glu Cys Ser Ala Lys Thr Lys Val Asn Val
 Glu Gln

0070110

165

170

175
Cys Phe Glu Glu Leu Val Leu Lys Ile Leu Asp Thr Pro Ser
Leu Leu

180

185

190

Ala Asp Ala Ser Ser Gly Ala Lys Lys Asn Ile Phe Lys Gln
Lys Ala

195

200

205

Pro Glu Ala Asp Ala Ala Ala Ser Gly Cys Cys
210 215

<210> 734

<211> 618

<212> DNA

<213> Triticum aestivum

<220>

<221> CDS

<222> (1)..(618)

<400> 734

atg gcg gcc aac gcc ggc aac aag atc cgc aac gcc aaa ctg
ggt ctt 48
Met Ala Ala Asn Ala Gly Asn Lys Ile Arg Asn Ala Lys Leu
Val Leu

1

5

10

15

ctt gga gat gta ggc gct ggc aaa tcc agc ctg gtg ctt cgg
ttt gta 96
Leu Gly Asp Val Gly Ala Gly Lys Ser Ser Leu Val Leu Arg
Phe Val

20

25

30

aaa gga caa ttt gtt gaa ttc cag gaa tcg aca att gga gcg
gct ttc 144
Lys Gly Gln Phe Val Glu Phe Gln Glu Ser Thr Ile Gly Ala
Ala Phe

35

40

45

ttc tct caa acc ttg gct gtt aat gac gag act gtg aag ttt
gaa atc 192
Phe Ser Gln Thr Leu Ala Val Asn Asp Glu Thr Val Lys Phe
Glu Ile

50

55

60

tgg gat act gct ggg cag gag agg tat cac agc ttg gcc ccc
atg tac 240
Trp Asp Thr Ala Gly Gln Glu Arg Tyr His Ser Leu Ala Pro
Met Tyr

0070110

65	80												70				75			
tat	agg	ggt	gct	gcc	gca	gct	ata	gtt	gtc	tat	gac	atc	tcg							
aac	cag			288																
Tyr	Arg	Gly	Ala	Ala	Ala	Ala	Ile	Val	Val	Tyr	Asp	Ile	Ser							
Asn	Gln																			
	85												90							
95																				
gca	tcc	ttc	acc	cga	gca	aag	aaa	tgg	gtt	caa	gaa	ctt	caa							
gct	caa		336																	
Ala	Ser	Phe	Thr	Arg	Ala	Lys	Lys	Trp	Val	Gln	Glu	Leu	Gln							
Ala	Gln																			
	100												105				110			
gga	aac	cag	aat	aca	gta	gtg	gct	ctt	gct	ggc	aac	aaa	gct							
gat	ttg		384																	
Gly	Asn	Gln	Asn	Thr	Val	Val	Ala	Leu	Ala	Gly	Asn	Lys	Ala							
Asp	Leu																			
	115												120				125			
ctc	gag	gcg	agg	gag	gtt	caa	ata	gag	gaa	gcc	aag	aca	tat							
gcg	cag		432																	
Leu	Glu	Ala	Arg	Glu	Val	Gln	Ile	Glu	Glu	Ala	Lys	Thr	Tyr							
Ala	Gln																			
	130												135				140			
gag	aat	ggc	ctc	ttc	ttc	atg	gaa	acg	tct	gct	aaa	act	gca							
acc	aat		480																	
Glu	Asn	Gly	Leu	Phe	Phe	Met	Glu	Thr	Ser	Ala	Lys	Thr	Ala							
Thr	Asn																			
145	150												155							
160																				
gtg	aat	gac	ata	ttt	tat	gag	att	gcg	aag	aga	ttg	ctt	cag							
ggg	cag		528																	
Val	Asn	Asp	Ile	Phe	Tyr	Glu	Ile	Ala	Lys	Arg	Leu	Leu	Gln							
Gly	Gln																			
	165												170							
175																				
gcg	gcg	cag	aac	cca	cag	acg	gcg	ggg	atg	gtt	ctc	tcc	cag							
aga	ccc		576																	
Ala	Ala	Gln	Asn	Pro	Gln	Thr	Ala	Gly	Met	Val	Leu	Ser	Gln							
Arg	Pro																			
	180												185				190			
aat	gag	aga	gtg	gtc	agc	gcg	gct	tcg	tgc	tgc	tcc	tcc	tga							
			618																	
Asn	Glu	Arg	Val	Val	Ser	Ala	Ala	Ser	Cys	Cys	Ser	Ser								
		195					200					205								

<210> 735

0070110

<211> 205

<212> PRT

<213> Triticum aestivum

<400> 735

Met Ala Ala Asn Ala Gly Asn Lys Ile Arg Asn Ala Lys Leu
Val Leu

1 5 10

15

Leu Gly Asp Val Gly Ala Gly Lys Ser Ser Leu Val Leu Arg
Phe Val

20 25 30

Lys Gly Gln Phe Val Glu Phe Gln Glu Ser Thr Ile Gly Ala
Ala Phe

35 40 45

Phe Ser Gln Thr Leu Ala Val Asn Asp Glu Thr Val Lys Phe
Glu Ile

50 55 60

Trp Asp Thr Ala Gly Gln Glu Arg Tyr His Ser Leu Ala Pro
Met Tyr

65 70 75

80

Tyr Arg Gly Ala Ala Ala Ala Ile Val Val Tyr Asp Ile Ser
Asn Gln

85 90

95

Ala Ser Phe Thr Arg Ala Lys Lys Trp Val Gln Glu Leu Gln
Ala Gln

100 105 110

Gly Asn Gln Asn Thr Val Val Ala Leu Ala Gly Asn Lys Ala
Asp Leu

115 120 125

Leu Glu Ala Arg Glu Val Gln Ile Glu Glu Ala Lys Thr Tyr
Ala Gln

130 135 140

Glu Asn Gly Leu Phe Phe Met Glu Thr Ser Ala Lys Thr Ala
Thr Asn

145 150 155

160

Val Asn Asp Ile Phe Tyr Glu Ile Ala Lys Arg Leu Leu Gln
Gly Gln

165 170

0070110

175
Ala Ala Gln Asn Pro Gln Thr Ala Gly Met Val Leu Ser Gln
Arg Pro
180 185 190

Asn Glu Arg Val Val Ser Ala Ala Ser Cys Cys Ser Ser
195 200 205

<210> 736
<211> 654
<212> DNA
<213> Triticum aestivum

<220>
<221> CDS
<222> (1)..(654)

<400> 736
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cag ccg 48
Met Asp Ser Ser Ser Ser Ser Thr Ala Ser Ser Ser Gln Ala
Gln Pro 1 5 10
15
gac ttt gat tac cta ttc aag ctc ctc ctc atc ggc gac tcc
ggc gtg 96
Asp Phe Asp Tyr Leu Phe Lys Leu Leu Leu Ile Gly Asp Ser
Gly Val 20 25 30
ggg aag agc agt ctc ctc ctc cga ttc aca tcc gac tcc ttc
gag gac 144
Gly Lys Ser Ser Leu Leu Leu Arg Phe Thr Ser Asp Ser Phe
Glu Asp 35 40 45
cta tcc ccg acc atc ggc gtc gac ttc aag gtc aag atg gtc
aac att 192
Leu Ser Pro Thr Ile Gly Val Asp Phe Lys Val Lys Met Val
Asn Ile 50 55 60
gcc ggc aag aag ctc aag ctc gcc gtc tgg gac acc gct gga
cag gaa 240
Ala Gly Lys Lys Leu Lys Leu Ala Val Trp Asp Thr Ala Gly
Gln Glu 65 70 75
80
aga ttc agg acc ttg acc agc tcg tac tac aga ggg gcg caa
ggg atc 288
Arg Phe Arg Thr Leu Thr Ser Ser Tyr Tyr Arg Gly Ala Gln
Seite 1110

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Gly	Ile												
				85					90				
95													
att	atg	gtg	tac	gat	ggt	acc	cgc	cga	gaa	aca	ttc	acg	aat
ctg	tct		336										
Ile	Met	Val	Tyr	Asp	Val	Thr	Arg	Arg	Glu	Thr	Phe	Thr	Asn
Leu	Ser												
			100					105					110
gac	ata	tgg	gcc	aag	gaa	att	gac	ctg	tat	tcg	acc	aat	caa
gac	tgt		384										
Asp	Ile	Trp	Ala	Lys	Glu	Ile	Asp	Leu	Tyr	Ser	Thr	Asn	Gln
Asp	Cys												
		115					120					125	
ata	aag	atg	ctt	gtc	gga	aac	aaa	gtg	gac	aag	gaa	agc	gag
agg	gcc		432										
Ile	Lys	Met	Leu	Val	Gly	Asn	Lys	Val	Asp	Lys	Glu	Ser	Glu
Arg	Ala												
		130				135					140		
gtc	aca	aag	aag	gaa	ggc	att	gac	ttt	gcc	agg	gag	tac	gga
tgt	cta		480										
Val	Thr	Lys	Lys	Glu	Gly	Ile	Asp	Phe	Ala	Arg	Glu	Tyr	Gly
Cys	Leu												
145					150						155		
160													
ttt	ctg	gaa	tgc	agc	gcg	aag	acc	aag	gtg	aac	gtg	gag	cag
tgc	ttt		528										
Phe	Leu	Glu	Cys	Ser	Ala	Lys	Thr	Lys	Val	Asn	Val	Glu	Gln
Cys	Phe												
			165							170			
175													
gag	gag	ctc	gtg	ctg	aag	ata	ttg	gac	acg	ccg	agc	ctg	ttg
gcg	gat		576										
Glu	Glu	Leu	Val	Leu	Lys	Ile	Leu	Asp	Thr	Pro	Ser	Leu	Leu
Ala	Asp												
			180							185			190
gca	tcc	tct	ggg	gcg	aag	aag	aac	atc	ttc	aag	cag	aag	gca
cca	gag		624										
Ala	Ser	Ser	Gly	Ala	Lys	Lys	Asn	Ile	Phe	Lys	Gln	Lys	Ala
Pro	Glu												
		195					200					205	
gct	gat	gct	gcg	gcg	agc	ggc	tgc	tgt	tga				
			654										
Ala	Asp	Ala	Ala	Ala	Ser	Gly	Cys	Cys					
	210					215							

<210> 737

0070110

<211> 217

<212> PRT

<213> Triticum aestivum

<400> 737

Met Asp Ser Ser Ser Ser Ser Thr Ala Ser Ser Ser Gln Ala
Gln Pro

1 5 10

15

Asp Phe Asp Tyr Leu Phe Lys Leu Leu Leu Ile Gly Asp Ser
Gly Val

20 25 30

Gly Lys Ser Ser Leu Leu Leu Arg Phe Thr Ser Asp Ser Phe
Glu Asp

35 40 45

Leu Ser Pro Thr Ile Gly Val Asp Phe Lys Val Lys Met Val
Asn Ile

50 55 60

Ala Gly Lys Lys Leu Lys Leu Ala Val Trp Asp Thr Ala Gly
Gln Glu

65 70 75

80

Arg Phe Arg Thr Leu Thr Ser Ser Tyr Tyr Arg Gly Ala Gln
Gly Ile

85 90

95

Ile Met Val Tyr Asp Val Thr Arg Arg Glu Thr Phe Thr Asn
Leu Ser

100 105 110

Asp Ile Trp Ala Lys Glu Ile Asp Leu Tyr Ser Thr Asn Gln
Asp Cys

115 120 125

Ile Lys Met Leu Val Gly Asn Lys Val Asp Lys Glu Ser Glu
Arg Ala

130 135 140

Val Thr Lys Lys Glu Gly Ile Asp Phe Ala Arg Glu Tyr Gly
Cys Leu

145 150 155

160

Phe Leu Glu Cys Ser Ala Lys Thr Lys Val Asn Val Glu Gln
Cys Phe

165 170

0070110

175
 Glu Glu Leu Val Leu Lys Ile Leu Asp Thr Pro Ser Leu Leu
 Ala Asp
 180 185 190
 Ala Ser Ser Gly Ala Lys Lys Asn Ile Phe Lys Gln Lys Ala
 Pro Glu
 195 200 205
 Ala Asp Ala Ala Ala Ser Gly Cys Cys
 210 215

<210> 738
 <211> 618
 <212> DNA
 <213> Triticum aestivum

<220>
 <221> CDS
 <222> (1)..(618)

<400> 738
 atg agc tcc tcc gag tac gac tac ctc ttc aag ctg ctc ctc
 atc ggc 48
 Met Ser Ser Ser Glu Tyr Asp Tyr Leu Phe Lys Leu Leu Leu
 Ile Gly
 1 5 10
 15
 gac tcc tcc gtc ggc aag tcc tgc ctc ctc ctc cgc ttc gcc
 gac gat 96
 Asp Ser Ser Val Gly Lys Ser Cys Leu Leu Leu Arg Phe Ala
 Asp Asp
 20 25 30
 gcg tac gtc gac acc tac atc agt acc atc ggc gtt gat ttc
 aaa atc 144
 Ala Tyr Val Asp Thr Tyr Ile Ser Thr Ile Gly Val Asp Phe
 Lys Ile
 35 40 45
 cgg acc gtt gag ctc gat ggc aag tcg gtg aag ctg cag att
 tgg gac 192
 Arg Thr Val Glu Leu Asp Gly Lys Ser Val Lys Leu Gln Ile
 Trp Asp
 50 55 60
 aca gca ggc cag gaa agg ttc agg aca ata aca agc agt tac
 tac cgg 240
 Thr Ala Gly Gln Glu Arg Phe Arg Thr Ile Thr Ser Ser Tyr
 Tyr Arg
 65 70 75

0070110

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      80
gga gcg cat gga atc att atc gta tat gac gtg aca gat agg
gaa agc
Gly Ala His Gly Ile Ile Ile Val Tyr Asp Val Thr Asp Arg
Glu Ser
      85
95
ttc aac aat gtc aag cag tgg ttg agt gag atc gat agg tat
gcc agt
Phe Asn Asn Val Lys Gln Trp Leu Ser Glu Ile Asp Arg Tyr
Ala Ser
      100
      105
      110
gac agt gtg tgc aag ctt cta gtg ggg aac aaa tgt gat ttg
gtc gat
Asp Ser Val Cys Lys Leu Leu Val Gly Asn Lys Cys Asp Leu
Val Asp
      115
      120
      125
agt aag gtc gtc gat aca gag gag gcc aag gct ttt gca gaa
tcg ttg
Ser Lys Val Val Asp Thr Glu Glu Ala Lys Ala Phe Ala Glu
Ser Leu
      130
      135
      140
gga atg aat ttt ctt gag aca agt gca aag gaa gcc atc aat
gtg gag
Gly Met Asn Phe Leu Glu Thr Ser Ala Lys Glu Ala Ile Asn
Val Glu
      145
      150
      155
      160
aca gct ttc tta acc atg tca tca gaa atc aag aac aag atg
gcg agc
Thr Ala Phe Leu Thr Met Ser Ser Glu Ile Lys Asn Lys Met
Ala Ser
      165
      170
      175
caa cca acg gcg gag agg aaa tcg acg gtc cat gtt cac atg
aaa ggg
Gln Pro Thr Ala Glu Arg Lys Ser Thr Val His Val His Met
Lys Gly
      180
      185
      190
cag ccc ata cag cag cag aac agc agt tgc tgc tcc tca taa
Gln Pro Ile Gln Gln Gln Asn Ser Ser Cys Cys Ser Ser
      195
      200
      205

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<210> 739

<211> 205

0070110

<212> PRT

<213> Triticum aestivum

<400> 739

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

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Gln Pro Thr Ala Glu Arg Lys Ser Thr Val His Val His Met
Lys Gly
180 185 190

Gln Pro Ile Gln Gln Gln Asn Ser Ser Cys Cys Ser Ser
195 200 205

<210> 740
<211> 642
<212> DNA
<213> Triticum aestivum

<220>
<221> CDS
<222> (1)..(642)

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ggc gac 48
Met Ala Ser Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val
Gly Asp
1 5 10
15
ggc gcc gtc ggc aag acc tgc atg ctc atc tgc tac acc agc
aac aag 96
Gly Ala Val Gly Lys Thr Cys Met Leu Ile Cys Tyr Thr Ser
Asn Lys
20 25 30
ttc ccc acc gac tat ata ccc acg gtg ttc gac aat ttc agc
gca aac 144
Phe Pro Thr Asp Tyr Ile Pro Thr Val Phe Asp Asn Phe Ser
Ala Asn
35 40 45
gtg gtg gcg gac ggc acc acc gtg aat ttg ggc ctt tgg gac
acc gcc 192
Val Val Ala Asp Gly Thr Thr Val Asn Leu Gly Leu Trp Asp
Thr Ala
50 55 60
ggg cag gag gat tac aac agg ctg agg cct ctg agc tac cgg
ggc gct 240
Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg
Gly Ala
65 70 75
80
gat gtt ttt gtg ctt gcc ttc tct ctt gtg agc cga gct agc
tat gag 288
Asp Val Phe Val Leu Ala Phe Ser Leu Val Ser Arg Ala Ser
Tyr Glu

0070110

85

90

95

aat atc atg aag aag tgg ata ccg gag ctt cag cat tac gcg
ccc ggc 336
Asn Ile Met Lys Lys Trp Ile Pro Glu Leu Gln His Tyr Ala
Pro Gly
100 105 110

gtg cct gtt gtg ctg gta ggc aca aaa ctg gat ctt cgt gaa
gac aag 384
Val Pro Val Val Leu Val Gly Thr Lys Leu Asp Leu Arg Glu
Asp Lys
115 120 125

cac tat ttg ctg gac cac cct ggc atg ata ccc gtt acc aca
gca cag 432
His Tyr Leu Leu Asp His Pro Gly Met Ile Pro Val Thr Thr
Ala Gln
130 135 140

ggg gag gaa ctt cgt aag caa gtc ggt gct tta tat tac ata
gag tgc 480
Gly Glu Glu Leu Arg Lys Gln Val Gly Ala Leu Tyr Tyr Ile
Glu Cys
145 150 155

160
agc tca aag aca caa cag aat gtc aaa gct gtg ttt gat gct
gct atc 528
Ser Ser Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala
Ala Ile
165 170

175
aag gta gta atc cag ccc cca act aaa caa aga gaa aag aag
aaa aag 576
Lys Val Val Ile Gln Pro Pro Thr Lys Gln Arg Glu Lys Lys
Lys Lys
180 185 190

aag cag cgt cgt gga tgc tct atg atg aac ttc ggt gga agg
aaa atg 624
Lys Gln Arg Arg Gly Cys Ser Met Met Asn Phe Gly Gly Arg
Lys Met
195 200 205

cta tgc ttc aaa tcc tga
642
Leu Cys Phe Lys Ser
210

<210> 741
<211> 213

0070110

<212> PRT

<213> Triticum aestivum

<400> 741

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

0070110

Lys Val Val Ile Gln Pro Pro Thr Lys Gln Arg Glu Lys Lys
 Lys Lys
 180 185 190

Lys Gln Arg Arg Gly Cys Ser Met Met Asn Phe Gly Gly Arg
 Lys Met
 195 200 205

Leu Cys Phe Lys Ser
 210

<210> 742
 <211> 624
 <212> DNA
 <213> Triticum aestivum

<220>
 <221> CDS
 <222> (1)..(624)

<400> 742
 atg ggc acg acg ccg ggg agc agc tac gac tgc tcc ttc aag
 gtg ctg 48
 Met Gly Thr Thr Pro Gly Ser Ser Tyr Asp Cys Ser Phe Lys
 Val Leu
 1 5 10
 15
 ctc atc ggc gac tcc gcc gtc ggc aag agc agc ctc ctc gtc
 agc ttc 96
 Leu Ile Gly Asp Ser Ala Val Gly Lys Ser Ser Leu Leu Val
 Ser Phe
 20 25 30
 gtc tcc gcc gcc ccc acc aac gac gac atc tcc ccc acc ata
 ggg gtg 144
 Val Ser Ala Ala Pro Thr Asn Asp Asp Ile Ser Pro Thr Ile
 Gly Val
 35 40 45
 gat ttt aaa atc aag ttt ctc act gtt ggg gat aag aaa ttg
 aag ttg 192
 Asp Phe Lys Ile Lys Phe Leu Thr Val Gly Asp Lys Lys Leu
 Lys Leu
 50 55 60
 aca ata tgg gac acc gct ggc cag gag agg ttt agg aca atc
 act agt 240
 Thr Ile Trp Asp Thr Ala Gly Gln Glu Arg Phe Arg Thr Ile
 Thr Ser
 65 70 75
 80

0070110

tct	tac	tac	aga	ggt	gct	cat	gga	att	atc	tta	ggt	tat	gat
gtc	acg		288										
Ser	Tyr	Tyr	Arg	Gly	Ala	His	Gly	Ile	Ile	Leu	Val	Tyr	Asp
Val	Thr												

85

90

95

aag	aga	caa	agt	ttc	aca	aat	ttg	gct	gat	gta	tgg	gcc	aaa
gaa	ata		336										
Lys	Arg	Gln	Ser	Phe	Thr	Asn	Leu	Ala	Asp	Val	Trp	Ala	Lys
Glu	Ile												

100

105

110

gaa	atg	cac	tca	aca	aac	aaa	gag	tgc	gtc	aaa	atg	ctt	ggt
gga	aac		384										
Glu	Met	His	Ser	Thr	Asn	Lys	Glu	Cys	Val	Lys	Met	Leu	Val
Gly	Asn												

115

120

125

aaa	gtg	gac	aag	gat	gag	gac	aga	atg	gta	aca	aca	gaa	gaa
ggt	ctt		432										
Lys	Val	Asp	Lys	Asp	Glu	Asp	Arg	Met	Val	Thr	Thr	Glu	Glu
Gly	Leu												

130

135

140

gcc	ttt	gca	cag	cag	tgt	gga	tgc	ctt	ttt	ctc	gag	agc	agt
gcc	aaa		480										
Ala	Phe	Ala	Gln	Gln	Cys	Gly	Cys	Leu	Phe	Leu	Glu	Ser	Ser
Ala	Lys												

145

150

155

160

aca	aga	gaa	aat	gtg	gag	aaa	tgt	ttt	gaa	gag	ctt	gcg	cta
aag	att		528										
Thr	Arg	Glu	Asn	Val	Glu	Lys	Cys	Phe	Glu	Glu	Leu	Ala	Leu
Lys	Ile												

165

170

175

ctt	gag	gtt	cca	agt	ctg	tcg	gag	gaa	ggc	tcg	tcg	gtc	gtc
aag	agg		576										
Leu	Glu	Val	Pro	Ser	Leu	Ser	Glu	Glu	Gly	Ser	Ser	Val	Val
Lys	Arg												

180

185

190

aac	tcg	ctg	aaa	cag	aag	cat	gag	aag	agc	ggg	ggg	tgc	tgt
cag	tag		624										
Asn	Ser	Leu	Lys	Gln	Lys	His	Glu	Lys	Ser	Gly	Gly	Cys	Cys
Gln													

195

200

205

<210> 743

<211> 207

0070110

<212> PRT

<213> Triticum aestivum

<400> 743

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

0070110

Leu Glu val Pro Ser Leu Ser Glu Glu Gly Ser Ser val val
Lys Arg
180 185 190

Asn Ser Leu Lys Gln Lys His Glu Lys Ser Gly Gly Cys Cys
Gln
195 200 205

<210> 744
<211> 636
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (1)..(636)

<400> 744
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ttc aag 48
Met Ser Ser Ser Ser Gly Gln Ser Ser Gly Tyr Asp Leu Ser
Phe Lys 1 5 10
15
atc ttg ttg atc gga gat tcc ggt gtg gga aaa agt agc cta
ctt gtc 96
Ile Leu Leu Ile Gly Asp Ser Gly Val Gly Lys Ser Ser Leu
Leu Val 20 25 30
agc ttt att tca agt tct gct gaa gat ctt tcc ccc acc att
ggg gtt 144
Ser Phe Ile Ser Ser Ser Ala Glu Asp Leu Ser Pro Thr Ile
Gly Val 35 40 45
gat ttt aag atc aaa acg ctc aca gta ggt ggc aag aga ttg
aaa ttg 192
Asp Phe Lys Ile Lys Thr Leu Thr Val Gly Gly Lys Arg Leu
Lys Leu 50 55 60
acg att tgg gat act gct ggg cag gaa agg ttc agg act cta
aac agt 240
Thr Ile Trp Asp Thr Ala Gly Gln Glu Arg Phe Arg Thr Leu
Asn Ser 65 70 75
80
tct tac tat aga aaa gca cag gga atc att ctc gtt tat gat
gtc aca 288

0070110

Ser	Tyr	Tyr	Arg	Lys	Ala	Gln	Gly	Ile	Ile	Leu	Val	Tyr	Asp
Val	Thr												
				85					90				
95													
agg	aga	gaa	acc	ttt	aca	aac	tta	tct	tta	gtg	tgg	tct	aaa
gaa	gtg		336										
Arg	Arg	Glu	Thr	Phe	Thr	Asn	Leu	Ser	Leu	Val	Trp	Ser	Lys
Glu	Val												
			100					105					110
gaa	ctc	tat	tca	act	aat	cag	aat	tgc	gtg	aag	atg	cta	gtt
gga	aat		384										
Glu	Leu	Tyr	Ser	Thr	Asn	Gln	Asn	Cys	Val	Lys	Met	Leu	Val
Gly	Asn												
		115					120					125	
aaa	gtt	gat	aga	gat	tct	gaa	agg	gtt	gtg	agc	aaa	gaa	gag
ggt	tta		432										
Lys	Val	Asp	Arg	Asp	Ser	Glu	Arg	Val	Val	Ser	Lys	Glu	Glu
Gly	Leu												
	130					135					140		
gca	ctt	gcc	gag	gag	ttg	gga	tgt	ctg	ttt	ttt	gaa	tgt	agt
gcc	aaa		480										
Ala	Leu	Ala	Glu	Glu	Leu	Gly	Cys	Leu	Phe	Phe	Glu	Cys	Ser
Ala	Lys												
145					150					155			
160													
act	cga	gaa	aat	gtg	gag	cgg	tgc	ttc	gag	gaa	ctt	gca	cta
aag	ata		528										
Thr	Arg	Glu	Asn	Val	Glu	Arg	Cys	Phe	Glu	Glu	Leu	Ala	Leu
Lys	Ile												
			165						170				
175													
atg	gaa	gtt	cct	agt	ctt	ttg	gaa	gaa	gga	tct	aca	gca	gtt
aaa	agg		576										
Met	Glu	Val	Pro	Ser	Leu	Leu	Glu	Glu	Gly	Ser	Thr	Ala	Val
Lys	Arg												
			180					185					190
aat	att	cta	aag	caa	caa	caa	caa	ccc	caa	gca	tcc	gaa	ttt
ggt	ggt		624										
Asn	Ile	Leu	Lys	Gln	Gln	Gln	Gln	Pro	Gln	Ala	Ser	Glu	Phe
Gly	Gly												
		195					200					205	
tgt	tgc	tct	taa										
			636										
Cys	Cys	Ser											
	210												

0070110

<210> 745
<211> 211
<212> PRT
<213> Glycine max

<400> 745
Met Ser Ser Ser Ser Gly Gln Ser Ser Gly Tyr Asp Leu Ser
Phe Lys
1 5 10
15
Ile Leu Leu Ile Gly Asp Ser Gly Val Gly Lys Ser Ser Leu
Leu Val
20 25 30
Ser Phe Ile Ser Ser Ser Ala Glu Asp Leu Ser Pro Thr Ile
Gly Val
35 40 45
Asp Phe Lys Ile Lys Thr Leu Thr Val Gly Gly Lys Arg Leu
Lys Leu
50 55 60
Thr Ile Trp Asp Thr Ala Gly Gln Glu Arg Phe Arg Thr Leu
Asn Ser
65 70 75
80
Ser Tyr Tyr Arg Lys Ala Gln Gly Ile Ile Leu Val Tyr Asp
Val Thr
85 90
95
Arg Arg Glu Thr Phe Thr Asn Leu Ser Leu Val Trp Ser Lys
Glu Val
100 105 110
Glu Leu Tyr Ser Thr Asn Gln Asn Cys Val Lys Met Leu Val
Gly Asn
115 120 125
Lys Val Asp Arg Asp Ser Glu Arg Val Val Ser Lys Glu Glu
Gly Leu
130 135 140
Ala Leu Ala Glu Glu Leu Gly Cys Leu Phe Phe Glu Cys Ser
Ala Lys
145 150 155
160
Thr Arg Glu Asn Val Glu Arg Cys Phe Glu Glu Leu Ala Leu
Lys Ile

0070110

165 170
 175
 Met Glu Val Pro Ser Leu Leu Glu Glu Gly Ser Thr Ala Val
 Lys Arg
 180 185 190
 Asn Ile Leu Lys Gln Gln Gln Gln Pro Gln Ala Ser Glu Phe
 Gly Gly
 195 200 205
 Cys Cys Ser
 210

<210> 746
 <211> 663
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (1)..(663)

<400> 746
 atg agc gcg gcg aca gcg gcg gcg gcg agc tcg gtc acc aag
 ttc atc 48
 Met Ser Ala Ala Thr Ala Ala Ala Ala Ser Ser Val Thr Lys
 Phe Ile
 1 5 10
 15
 aag tgc gtc acg gtc ggc gat ggg gcc gtc ggg aag acc tgc
 atg ctc 96
 Lys Cys Val Thr Val Gly Asp Gly Ala Val Gly Lys Thr Cys
 Met Leu
 20 25 30
 atc tgc tac acc tgc aac aag ttc ccc acg gat tat atc ccc
 acc gta 144
 Ile Cys Tyr Thr Cys Asn Lys Phe Pro Thr Asp Tyr Ile Pro
 Thr Val
 35 40 45
 ttt gac aac ttc agc gcc aat gtc tcc gtg ggt ggg agc atc
 gtc aac 192
 Phe Asp Asn Phe Ser Ala Asn Val Ser Val Gly Gly Ser Ile
 Val Asn
 50 55 60
 ttg ggc ctc tgg gac acg gca ggc cag gag gat tac agc agg
 ttg agg 240
 Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu Asp Tyr Ser Arg
 Leu Arg

0070110

65					70					75			
80													
cct	ctc	agc	tac	agg	ggt	gct	gat	gtg	ttc	atc	ctc	tcc	ttc
tcc	ctg			288									
Pro	Leu	Ser	Tyr	Arg	Gly	Ala	Asp	Val	Phe	Ile	Leu	Ser	Phe
Ser	Leu												
				85					90				
95													
gtc	agc	agg	gcg	agc	tat	gag	aac	gtc	ctc	aag	aag	tgg	atg
cca	gag			336									
Val	Ser	Arg	Ala	Ser	Tyr	Glu	Asn	Val	Leu	Lys	Lys	Trp	Met
Pro	Glu												
			100					105				110	
ctt	cg	cga	ttt	tca	cct	act	ggt	cct	gta	ggt	ctt	ggt	gga
acc	aaa			384									
Leu	Arg	Arg	Phe	Ser	Pro	Thr	Val	Pro	Val	Val	Leu	Val	Gly
Thr	Lys												
		115					120				125		
cta	gat	ctc	cg	gaa	gac	aga	tct	tac	ctt	gct	gac	cat	tct
gct	gct			432									
Leu	Asp	Leu	Arg	Glu	Asp	Arg	Ser	Tyr	Leu	Ala	Asp	His	Ser
Ala	Ala												
		130				135					140		
tcc	atc	atc	tct	act	gaa	cag	gga	gaa	gag	ctc	agg	aag	cag
ata	ggc			480									
Ser	Ile	Ile	Ser	Thr	Glu	Gln	Gly	Glu	Glu	Leu	Arg	Lys	Gln
Ile	Gly												
145					150					155			
160													
gct	gtg	gcg	tac	ata	gaa	tgc	agc	tca	aag	aca	cag	agg	aac
gta	aag			528									
Ala	Val	Ala	Tyr	Ile	Glu	Cys	Ser	Ser	Lys	Thr	Gln	Arg	Asn
Val	Lys												
			165							170			
175													
gct	gtg	ttc	gac	act	gca	att	aaa	gta	gtg	ctg	caa	cca	ccg
agg	aga			576									
Ala	Val	Phe	Asp	Thr	Ala	Ile	Lys	Val	Val	Leu	Gln	Pro	Pro
Arg	Arg												
			180					185				190	
aga	gaa	gtt	acc	agg	aag	aaa	atg	aag	aca	agg	tcg	aat	cag
tct	ctg			624									
Arg	Glu	Val	Thr	Arg	Lys	Lys	Met	Lys	Thr	Arg	Ser	Asn	Gln
Ser	Leu												
		195				200					205		
aga	aga	tac	ctc	tgt	gga	agc	gga	tgt	ttc	aca	tcg	taa	

0070110

Arg Arg Tyr Leu Cys Gly Ser Gly Cys Phe Thr Ser
210 215 220

<210> 747
<211> 220
<212> PRT
<213> Zea mays

<400> 747

Met Ser Ala Ala Thr Ala Ala Ala Ala Ser Ser Val Thr Lys
Phe Ile
1 5 10
15
Lys Cys Val Thr Val Gly Asp Gly Ala Val Gly Lys Thr Cys
Met Leu
20 25 30

Ile Cys Tyr Thr Cys Asn Lys Phe Pro Thr Asp Tyr Ile Pro
Thr Val
35 40 45

Phe Asp Asn Phe Ser Ala Asn Val Ser Val Gly Gly Ser Ile
Val Asn
50 55 60

Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu Asp Tyr Ser Arg
Leu Arg
65 70 75

80
Pro Leu Ser Tyr Arg Gly Ala Asp Val Phe Ile Leu Ser Phe
Ser Leu
85 90

95
Val Ser Arg Ala Ser Tyr Glu Asn Val Leu Lys Lys Trp Met
Pro Glu
100 105 110

Leu Arg Arg Phe Ser Pro Thr Val Pro Val Val Leu Val Gly
Thr Lys
115 120 125

Leu Asp Leu Arg Glu Asp Arg Ser Tyr Leu Ala Asp His Ser
Ala Ala
130 135 140

Ser Ile Ile Ser Thr Glu Gln Gly Glu Glu Leu Arg Lys Gln
Ile Gly

0070110

145					150						155		
160	Ala	Val	Ala	Tyr	Ile	Glu	Cys	Ser	Ser	Lys	Thr	Gln	Arg
	Val	Lys											Asn
					165					170			
175	Ala	Val	Phe	Asp	Thr	Ala	Ile	Lys	Val	Val	Leu	Gln	Pro
	Arg	Arg											Pro
				180						185			190
	Arg	Glu	Val	Thr	Arg	Lys	Lys	Met	Lys	Thr	Arg	Ser	Asn
	Ser	Leu											Gln
			195					200				205	
	Arg	Arg	Tyr	Leu	Cys	Gly	Ser	Gly	Cys	Phe	Thr	Ser	
		210					215					220	

<210> 748
 <211> 594
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (1)..(594)

<400> 748													
atg	agc	gcg	tct	cgg	ttc	atc	aag	tgc	gtc	acc	gtg	ggg	gac
ggt	gcc			48									
Met	Ser	Ala	Ser	Arg	Phe	Ile	Lys	Cys	Val	Thr	Val	Gly	Asp
Gly	Ala												
1				5					10				
15													
gtc	gga	aag	acc	tgc	atg	ctc	atc	tcc	tac	aca	tcc	aac	act
ttc	ccc			96									
Val	Gly	Lys	Thr	Cys	Met	Leu	Ile	Ser	Tyr	Thr	Ser	Asn	Thr
Phe	Pro												
			20					25				30	
act	gac	tat	gtt	cca	act	gtg	ttc	gac	aac	ttc	agt	gcc	aat
gtt	gtg		144										
Thr	Asp	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn
Val	Val												
		35				40						45	
gtt	gac	ggg	agc	act	gtc	aac	ttg	ggt	ctg	tgg	gat	aca	gca
gga	caa		192										
Val	Asp	Gly	Ser	Thr	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala
Gly	Gln												
	50					55					60		

0070110

gaa	gat	tac	aat	aga	ctg	cgt	ccg	ttg	agc	tat	cgt	ggg	gct
gat	ggt			240									
Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala
Asp	Val												
65					70					75			
80													
ttt	ctg	ctc	gcc	ttt	tct	ctt	atc	agc	aaa	gca	agc	tat	gag
aat	gtc			288									
Phe	Leu	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Lys	Ala	Ser	Tyr	Glu
Asn	Val												
				85						90			
95													
tct	aag	aag	tgg	ggt	cct	gaa	tta	agg	cac	tat	gct	cct	ggc
gtg	ccc			336									
Ser	Lys	Lys	Trp	Val	Pro	Glu	Leu	Arg	His	Tyr	Ala	Pro	Gly
Val	Pro												
				100				105					110
ata	atc	ctt	ggg	ggg	aca	aaa	ctt	gat	ctg	cgt	gat	gat	aag
cag	ttt			384									
Ile	Ile	Leu	Gly	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys
Gln	Phe												
		115					120					125	
ttt	ggt	gat	cac	cct	ggg	gct	ggt	cca	att	tcc	act	gcc	cag
ggc	gaa			432									
Phe	Val	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Ser	Thr	Ala	Gln
Gly	Glu												
		130				135					140		
gag	ctg	agg	aag	cta	att	ggg	gct	gcc	gcc	tac	atc	gaa	tgc
agt	tca			480									
Glu	Leu	Arg	Lys	Leu	Ile	Gly	Ala	Ala	Ala	Tyr	Ile	Glu	Cys
Ser	Ser												
145					150					155			
160													
aaa	atc	cag	cag	aac	ata	aaa	gca	gtg	ttt	gac	gca	gca	att
aag	gtg			528									
Lys	Ile	Gln	Gln	Asn	Ile	Lys	Ala	Val	Phe	Asp	Ala	Ala	Ile
Lys	Val												
				165						170			
175													
ggt	ctc	cag	cca	cca	aag	caa	aag	aag	agg	aag	aag	aag	gtg
cag	aag			576									
Val	Leu	Gln	Pro	Pro	Lys	Gln	Lys	Lys	Arg	Lys	Lys	Lys	Val
Gln	Lys												
				180				185					190
gga	tgc	acc	att	ttg	taa								
			594										

0070110

Gly Cys Thr Ile Leu
195

<210> 749
<211> 197
<212> PRT
<213> Zea mays

<400> 749
Met Ser Ala Ser Arg Phe Ile Lys Cys Val Thr Val Gly Asp
Gly Ala
1 5 10
15
Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
Phe Pro
20 25 30
Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
Val Val
35 40 45
Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
Gly Gln
50 55 60
Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
Asp Val
65 70 75
80
Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
Asn Val
85 90
95
Ser Lys Lys Trp Val Pro Glu Leu Arg His Tyr Ala Pro Gly
Val Pro
100 105 110
Ile Ile Leu Gly Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
Gln Phe
115 120 125
Phe Val Asp His Pro Gly Ala Val Pro Ile Ser Thr Ala Gln
Gly Glu
130 135 140
Glu Leu Arg Lys Leu Ile Gly Ala Ala Ala Tyr Ile Glu Cys
Ser Ser
145 150 155

0070110

160
 Lys Ile Gln Gln Asn Ile Lys Ala Val Phe Asp Ala Ala Ile
 Lys Val
 165 170
 175
 Val Leu Gln Pro Pro Lys Gln Lys Lys Arg Lys Lys Lys Val
 Gln Lys
 180 185 190
 Gly Cys Thr Ile Leu
 195

<210> 750
 <211> 612
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (1)..(612)

<400> 750
 atg gcg gcc aac ttc ggg aac aag atc cgc aac gcc aag ctg
 gtt ctt 48
 Met Ala Ala Asn Phe Gly Asn Lys Ile Arg Asn Ala Lys Leu
 Val Leu
 1 5 10
 15
 ctt gga gat gta ggc gct ggc aaa tct agc ttg gtt ctt cgg
 ttt gtc 96
 Leu Gly Asp Val Gly Ala Gly Lys Ser Ser Leu Val Leu Arg
 Phe Val
 20 25 30
 aag gga cag ttt gtt gaa ttc cag gaa tca aca atc gga gca
 gct ttc 144
 Lys Gly Gln Phe Val Glu Phe Gln Glu Ser Thr Ile Gly Ala
 Ala Phe
 35 40 45
 ttt tcc cag acc tta gcg gta aat gat gag act gtt aag ttt
 gaa atc 192
 Phe Ser Gln Thr Leu Ala Val Asn Asp Glu Thr Val Lys Phe
 Glu Ile
 50 55 60
 tgg gat act gct ggg cag gag agg tat cat agc ttg gcc ccc
 atg tat 240
 Trp Asp Thr Ala Gly Gln Glu Arg Tyr His Ser Leu Ala Pro
 Met Tyr
 65 70 75

0070110

```

      80
tat agg ggt gca gcc gcc gcc att gtt gtc tat gac atc aca
aat ccg      288
Tyr Arg Gly Ala Ala Ala Ala Ile Val Val Tyr Asp Ile Thr
Asn Pro

      85      90
95
gcc tcc ttc acc cgt gcc aag aaa tgg gtt caa gaa ctt caa
gct caa      336
Ala Ser Phe Thr Arg Ala Lys Lys Trp Val Gln Glu Leu Gln
Ala Gln

      100      105      110

gga aat ccg aat aca ata gtg gct ctt gct ggt aac aag gtt
gat atg      384
Gly Asn Pro Asn Thr Ile Val Ala Leu Ala Gly Asn Lys Val
Asp Met

      115      120      125
cta gat gcg agg cac gtg gca gta gag gaa gca aag acg tat
gcc cag      432
Leu Asp Ala Arg His Val Ala Val Glu Glu Ala Lys Thr Tyr
Ala Gln

      130      135      140
gag aac ggt ctc ttc ttc atg gag aca tct gct aaa act gca
atc aat      480
Glu Asn Gly Leu Phe Phe Met Glu Thr Ser Ala Lys Thr Ala
Ile Asn

      145      150      155
      160
gtg aat gac ata ttt tat gag att gca aag aga ttg ctt caa
ggg caa      528
Val Asn Asp Ile Phe Tyr Glu Ile Ala Lys Arg Leu Leu Gln
Gly Gln

      165      170
175
gag gct cca agt cca cag gct gga att gtt ctg aat cag aga
cca gat      576
Glu Ala Pro Ser Pro Gln Ala Gly Ile Val Leu Asn Gln Arg
Pro Asp

      180      185      190

gag agg atg gtc agc act tcc tcg tgc tgc tca tga
      612
Glu Arg Met Val Ser Thr Ser Ser Cys Cys Ser
      195      200

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<210> 751

<211> 203

0070110

<212> PRT

<213> Zea mays

<400> 751

Met Ala Ala Asn Phe Gly Asn Lys Ile Arg Asn Ala Lys Leu

Val Leu

1

5

10

15

Leu Gly Asp Val Gly Ala Gly Lys Ser Ser Leu Val Leu Arg

Phe Val

20

25

30

Lys Gly Gln Phe Val Glu Phe Gln Glu Ser Thr Ile Gly Ala

Ala Phe

35

40

45

Phe Ser Gln Thr Leu Ala Val Asn Asp Glu Thr Val Lys Phe

Glu Ile

50

55

60

Trp Asp Thr Ala Gly Gln Glu Arg Tyr His Ser Leu Ala Pro

Met Tyr

65

70

75

80

Tyr Arg Gly Ala Ala Ala Ala Ile Val Val Tyr Asp Ile Thr

Asn Pro

85

90

95

Ala Ser Phe Thr Arg Ala Lys Lys Trp Val Gln Glu Leu Gln

Ala Gln

100

105

110

Gly Asn Pro Asn Thr Ile Val Ala Leu Ala Gly Asn Lys Val

Asp Met

115

120

125

Leu Asp Ala Arg His Val Ala Val Glu Glu Ala Lys Thr Tyr

Ala Gln

130

135

140

Glu Asn Gly Leu Phe Phe Met Glu Thr Ser Ala Lys Thr Ala

Ile Asn

145

150

155

160

Val Asn Asp Ile Phe Tyr Glu Ile Ala Lys Arg Leu Leu Gln

Gly Gln

165

170

0070110

175
Glu Ala Pro Ser Pro Gln Ala Gly Ile Val Leu Asn Gln Arg
Pro Asp
180 185 190

Glu Arg Met Val Ser Thr Ser Ser Cys Cys Ser
195 200

<210> 752
<211> 615
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (1)..(615)

<400> 752
atg gcg gca acc gcg ggc ggc aac aag atc cgc aac gcc aag
ctg gtt 48
Met Ala Ala Thr Ala Gly Gly Asn Lys Ile Arg Asn Ala Lys
Leu Val 1 5 10
15
ctt ctt ggg gac gtg ggc gcc ggc aag tcc agc ctg gtc ctc
cgg ttt 96
Leu Leu Gly Asp Val Gly Ala Gly Lys Ser Ser Leu Val Leu
Arg Phe 20 25 30
gtg aaa ggc cag ttc gtc gag ttc cag gaa tcc acc atc ggc
gcg gct 144
Val Lys Gly Gln Phe Val Glu Phe Gln Glu Ser Thr Ile Gly
Ala Ala 35 40 45
ttc ttc tcg cag acc ctg gcg gtg aac gac gag acg gtc aag
ttc gag 192
Phe Phe Ser Gln Thr Leu Ala Val Asn Asp Glu Thr Val Lys
Phe Glu 50 55 60
ata tgg gac acg gcg ggg cag gag cgg tac cac agc ttg gct
ccc atg 240
Ile Trp Asp Thr Ala Gly Gln Glu Arg Tyr His Ser Leu Ala
Pro Met 65 70 75
80
tat tac cgg ggc gct gcg gct gcc ata gtt gtc tac gac atc
acg aac 288
Tyr Tyr Arg Gly Ala Ala Ala Ala Ile Val Val Tyr Asp Ile
Seite 1134

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Thr Asn

85

90

95

gcg gcc tct ttt acg cgt gcg aag aaa tgg gtt caa gaa ctt
 caa gca 336
 Ala Ala Ser Phe Thr Arg Ala Lys Lys Trp Val Gln Glu Leu
 Gln Ala
 100 105 110

caa gga aac tcg aat aca ata gtg gct ctt gcc ggg aac aag
 gct gat 384
 Gln Gly Asn Ser Asn Thr Ile Val Ala Leu Ala Gly Asn Lys
 Ala Asp

115

120

125

ttg tta gat acg agg cag gtg tca gca gat gaa gca aag gcg
 tat gct 432
 Leu Leu Asp Thr Arg Gln Val Ser Ala Asp Glu Ala Lys Ala
 Tyr Ala

130

135

140

caa gag aat ggt ctc ttc ttc atg gaa act tct gcc aaa aca
 gct acc 480
 Gln Glu Asn Gly Leu Phe Phe Met Glu Thr Ser Ala Lys Thr
 Ala Thr

145

150

155

160

aat gtg aac gac gtg ttc tat gag att gcg aag aaa ctg ctt
 caa ggg 528
 Asn Val Asn Asp Val Phe Tyr Glu Ile Ala Lys Lys Leu Leu
 Gln Gly

165

170

175

cag cag gtt cag aac cca caa ggc ggg atg gtt ctc aac cag
 aga cca 576
 Gln Gln Val Gln Asn Pro Gln Gly Gly Met Val Leu Asn Gln
 Arg Pro

180

185

190

cct gag agg atg gtg agc tct tct tcc tgc tgt gcg tga
 615
 Pro Glu Arg Met Val Ser Ser Ser Ser Cys Cys Ala
 195 200

<210> 753

<211> 204

<212> PRT

<213> Zea mays

<400> 753

0070110

Met	Ala	Ala	Thr	Ala	Gly	Gly	Asn	Lys	Ile	Arg	Asn	Ala	Lys
Leu	Val												
1				5					10				
15													
Leu	Leu	Gly	Asp	Val	Gly	Ala	Gly	Lys	Ser	Ser	Leu	Val	Leu
Arg	Phe												
			20					25					30
Val	Lys	Gly	Gln	Phe	Val	Glu	Phe	Gln	Glu	Ser	Thr	Ile	Gly
Ala	Ala												
		35						40				45	
Phe	Phe	Ser	Gln	Thr	Leu	Ala	Val	Asn	Asp	Glu	Thr	Val	Lys
Phe	Glu												
	50					55					60		
Ile	Trp	Asp	Thr	Ala	Gly	Gln	Glu	Arg	Tyr	His	Ser	Leu	Ala
Pro	Met												
65					70					75			
	80												
Tyr	Tyr	Arg	Gly	Ala	Ala	Ala	Ala	Ile	Val	Val	Tyr	Asp	Ile
Thr	Asn												
				85						90			
95													
Ala	Ala	Ser	Phe	Thr	Arg	Ala	Lys	Lys	Trp	Val	Gln	Glu	Leu
Gln	Ala												
			100					105					110
Gln	Gly	Asn	Ser	Asn	Thr	Ile	Val	Ala	Leu	Ala	Gly	Asn	Lys
Ala	Asp												
		115						120				125	
Leu	Leu	Asp	Thr	Arg	Gln	Val	Ser	Ala	Asp	Glu	Ala	Lys	Ala
Tyr	Ala												
	130					135					140		
Gln	Glu	Asn	Gly	Leu	Phe	Phe	Met	Glu	Thr	Ser	Ala	Lys	Thr
Ala	Thr												
145					150					155			
	160												
Asn	Val	Asn	Asp	Val	Phe	Tyr	Glu	Ile	Ala	Lys	Lys	Leu	Leu
Gln	Gly												
				165					170				
175													
Gln	Gln	Val	Gln	Asn	Pro	Gln	Gly	Gly	Met	Val	Leu	Asn	Gln
Arg	Pro												
			180						185				190

0070110

Pro Glu Arg Met Val Ser Ser Ser Ser Cys Cys Ala
195 200

<210> 754
<211> 654
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (1)..(654)

<400> 754
atg agc gcg gcg gcg gcg agc tcg gtc acc aag ttc atc aag
tgc gtc 48
Met Ser Ala Ala Ala Ala Ser Ser Val Thr Lys Phe Ile Lys
Cys Val 1 5 10
15
acg gtc ggc gat ggg gcc gtc ggg aag acc tgc atg ctc atc
tgc tac 96
Thr Val Gly Asp Gly Ala Val Gly Lys Thr Cys Met Leu Ile
Cys Tyr 20 25 30
acc tgc aac aag ttc ccc acg gat tat atc ccc acc gta ttt
gac aac 144
Thr Cys Asn Lys Phe Pro Thr Asp Tyr Ile Pro Thr Val Phe
Asp Asn 35 40 45
ttc agc gcc aat gtc tcc gtg ggt ggg agc atc gtt aac ttg
ggc ctc 192
Phe Ser Ala Asn Val Ser Val Gly Gly Ser Ile Val Asn Leu
Gly Leu 50 55 60
tgg gac acg gca ggc cag gag gat tac agc agg ttg agg cct
ctc agc 240
Trp Asp Thr Ala Gly Gln Glu Asp Tyr Ser Arg Leu Arg Pro
Leu Ser 65 70 75
80
tac agg ggt gcc gat gtg ttc atc ctc tcc ttc tcc ctg gtc
agc agg 288
Tyr Arg Gly Ala Asp Val Phe Ile Leu Ser Phe Ser Leu Val
Ser Arg 85 90
95
gcg agc tat gag aac gtc ctc aag aag tgg atg cca gag ctt

0070110

cgc cga 336
Ala Ser Tyr Glu Asn Val Leu Lys Lys Trp Met Pro Glu Leu
Arg Arg 100 105 110

ttt tca cct act gtt cct gta gtt ctt gtt gga acc aaa cta
gat ctc 384
Phe Ser Pro Thr Val Pro Val Val Leu Val Gly Thr Lys Leu
Asp Leu 115 120 125

cgt gaa gac aga tct tac ctt gct gac cat tct gct gct tcc
atc atc 432
Arg Glu Asp Arg Ser Tyr Leu Ala Asp His Ser Ala Ala Ser
Ile Ile 130 135 140

tct act gaa cag gga gaa gag ctc agg aag cag ata ggc gct
gtg gcg 480
Ser Thr Glu Gln Gly Glu Glu Leu Arg Lys Gln Ile Gly Ala
Val Ala 145 150 155

160
tac ata gaa tgc agc tca aag aca cag agg aac gta aag gct
gtg ttc 528
Tyr Ile Glu Cys Ser Ser Lys Thr Gln Arg Asn Val Lys Ala
Val Phe 165 170

175
gac act gca att aaa gta gtg ctg caa cca ccg agg aga aga
gaa gtt 576
Asp Thr Ala Ile Lys Val Val Leu Gln Pro Pro Arg Arg Arg
Glu Val 180 185 190

acc agg aag aaa atg aag gca agg tcg aat cag tct ctg aga
aga tac 624
Thr Arg Lys Lys Met Lys Ala Arg Ser Asn Gln Ser Leu Arg
Arg Tyr 195 200 205

ctc tgt gga agc gga tgt ttc aca tcg taa
654
Leu Cys Gly Ser Gly Cys Phe Thr Ser
210 215

<210> 755
<211> 217
<212> PRT
<213> Zea mays

0070110

<400> 755

Met	Ser	Ala	Ala	Ala	Ala	Ser	Ser	Val	Thr	Lys	Phe	Ile	Lys
Cys	Val												
1				5					10				
15													
Thr	Val	Gly	Asp	Gly	Ala	Val	Gly	Lys	Thr	Cys	Met	Leu	Ile
Cys	Tyr												
			20					25					30
Thr	Cys	Asn	Lys	Phe	Pro	Thr	Asp	Tyr	Ile	Pro	Thr	Val	Phe
Asp	Asn												
		35					40					45	
Phe	Ser	Ala	Asn	Val	Ser	Val	Gly	Gly	Ser	Ile	Val	Asn	Leu
Gly	Leu												
	50						55				60		
Trp	Asp	Thr	Ala	Gly	Gln	Glu	Asp	Tyr	Ser	Arg	Leu	Arg	Pro
Leu	Ser												
65					70					75			
	80												
Tyr	Arg	Gly	Ala	Asp	Val	Phe	Ile	Leu	Ser	Phe	Ser	Leu	Val
Ser	Arg												
				85					90				
95													
Ala	Ser	Tyr	Glu	Asn	Val	Leu	Lys	Lys	Trp	Met	Pro	Glu	Leu
Arg	Arg												
			100					105				110	
Phe	Ser	Pro	Thr	Val	Pro	Val	Val	Leu	Val	Gly	Thr	Lys	Leu
Asp	Leu												
		115					120					125	
Arg	Glu	Asp	Arg	Ser	Tyr	Leu	Ala	Asp	His	Ser	Ala	Ala	Ser
Ile	Ile												
	130					135					140		
Ser	Thr	Glu	Gln	Gly	Glu	Glu	Leu	Arg	Lys	Gln	Ile	Gly	Ala
Val	Ala												
145					150					155			
	160												
Tyr	Ile	Glu	Cys	Ser	Ser	Lys	Thr	Gln	Arg	Asn	Val	Lys	Ala
Val	Phe												
				165					170				
175													
Asp	Thr	Ala	Ile	Lys	Val	Val	Leu	Gln	Pro	Pro	Arg	Arg	Arg
Glu	Val												
			180					185				190	

0070110

Thr Arg Lys Lys Met Lys Ala Arg Ser Asn Gln Ser Leu Arg
Arg Tyr 195 200 205

Leu Cys Gly Ser Gly Cys Phe Thr Ser
210 215

<210> 756
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 756
atgtctgaaa aggccgtag aagg
24

<210> 757
<211> 26
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 757
ttataaaatt atgcaacagt tagccc
26

<210> 758
<211> 273
<212> PRT
<213> Artificial sequence

<220>
<223> consensus sequence

<220>
<221> variant
<222> (2)..(2)
<223> Xaa in position 2 is any amino acid

<220>
<221> variant

0070110

<222> (4)..(4)

<223> Xaa in position 4 is any amino acid

<220>

<221> variant

<222> (10)..(10)

<223> Xaa in position 10 is any amino acid

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<221> variant

<222> (15)..(15)

<223> Xaa in position 15 is any amino acid

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<221> variant

<222> (18)..(22)

<223> Xaa in position 18 to 22 is any amino acid

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<221> variant

<222> (23)..(25)

<223> Xaa in position 23 to 25 is any or no amino acid

<220>

<221> variant

<222> (28)..(28)

<223> Xaa in position 28 is any amino acid

<220>

<221> variant

<222> (29)..(31)

<223> Xaa in position 29 to 31 is any or no amino acid

<220>

<221> variant

<222> (33)..(33)

<223> Xaa in position 33 is any amino acid

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<221> variant

<222> (38)..(38)

<223> Xaa in position 38 is any amino acid

<220>

<221> variant

<222> (40)..(52)

<223> Xaa in position 40 to 52 is any amino acid

<220>
<221> variant
<222> (53)..(55)
<223> Xaa in position 53 to 55 is any or no amino acid

<220>
<221> variant
<222> (57)..(57)
<223> Xaa in position 57 is any amino acid

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<221> variant
<222> (68)..(68)
<223> Xaa in position 68 is any amino acid

<220>
<221> variant
<222> (76)..(79)
<223> Xaa in position 76 to 79 is any amino acid

<220>
<221> variant
<222> (81)..(84)
<223> Xaa in position 81 to 84 is any amino acid

<220>
<221> variant
<222> (87)..(87)
<223> Xaa in position 87 is any amino acid

<220>
<221> variant
<222> (88)..(92)
<223> Xaa in position 88 to 92 is any or no amino acid

<220>
<221> variant
<222> (94)..(95)
<223> Xaa in position 94 to 95 is any amino acid

<220>
<221> variant
<222> (97)..(98)
<223> Xaa in position 97 to 98 is any amino acid

<220>
<221> variant
<222> (99)..(99)

0070110

<223> Xaa in position 99 is any or no amino acid

<220>

<221> Variant

<222> (101)..(101)

<223> Xaa in position 101 is any amino acid

<220>

<221> Variant

<222> (103)..(104)

<223> Xaa in position 103 to 104 is any amino acid

<220>

<221> Variant

<222> (106)..(113)

<223> Xaa in position 106 to 113 is any amino acid

<220>

<221> Variant

<222> (114)..(118)

<223> Xaa in position 114 to 118 is any or no amino acid

<220>

<221> Variant

<222> (120)..(121)

<223> Xaa in position 120 to 121 is any amino acid

<220>

<221> Variant

<222> (125)..(125)

<223> Xaa in position 125 is any amino acid

<220>

<221> Variant

<222> (127)..(127)

<223> Xaa in position 127 is any amino acid

<220>

<221> Variant

<222> (131)..(139)

<223> Xaa in position 131 to 139 is any amino acid

<220>

<221> Variant

<222> (140)..(172)

<223> Xaa in position 140 to 172 is any or no amino acid

<220>

0070110

<221> Variant
<222> (174)..(181)
<223> Xaa in position 174 to 181 is any amino acid

<220>
<221> Variant
<222> (183)..(183)
<223> Xaa in position 183 is any amino acid

<220>
<221> Variant
<222> (184)..(184)
<223> Xaa in position 184 is any or no amino acid

<220>
<221> Variant
<222> (186)..(186)
<223> Xaa in position 186 is any amino acid

<220>
<221> Variant
<222> (190)..(198)
<223> Xaa in position 190 to 198 is any amino acid

<220>
<221> Variant
<222> (201)..(202)
<223> Xaa in position 201 to 202 is any amino acid

<220>
<221> Variant
<222> (204)..(216)
<223> Xaa in position 204 to 216 is any amino acid

<220>
<221> Variant
<222> (217)..(272)
<223> Xaa in position 217 to 272 is any or no amino acid

<400> 758
Lys Xaa Val Xaa Val Gly Asp Gly Ala Xaa Gly Lys Thr Cys
Xaa Leu
1 5 10
15
Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Pro Xaa Xaa Xaa
Xaa Tyr
20 25 30

0070110

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

0070110

Xaa Xaa Xaa 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 Xaa Xaa Xaa Xaa Xaa Xaa
Xaa Xaa

260 265 270

Cys

<210> 759

<211> 19

<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)..(4)

<223> Xaa in position 3 to 4 is any or no amino acid

<220>

<221> variant

<222> (6)..(9)

<223> Xaa in position 6 to 9 is any amino acid

<220>

<221> variant

<222> (10)..(10)

<223> Xaa in position 10 is any or no amino acid

<220>

<221> variant

<222> (12)..(12)

<223> Xaa in position 12 is Ala, Gly, Gln or Thr

0070110

<220>

<221> Variant

<222> (13)..(13)

<223> Xaa in position 13 is Ile, Leu or Val

<220>

<221> Variant

<222> (14)..(14)

<223> Xaa in position 14 is Phe or Trp

<400> 759

Val Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa
Asp Thr

1 5 10

15

Ala Gly Gln

<210> 760

<211> 17

<212> PRT

<213> Artificial sequence

<220>

<223> protein pattern

<220>

<221> Variant

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<220>

<221> Variant

<222> (5)..(8)

<223> Xaa in position 5 to 8 is any amino acid

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<221> Variant

<222> (9)..(9)

<223> Xaa in position 9 is Gly or Asn

<220>

<221> Variant

<222> (10)..(10)

<223> Xaa in position 10 is Ile, Leu or Val

0070110

<220>
<221> variant
<222> (11)..(12)
<223> Xaa in position 11 to 12 is any amino acid

<220>
<221> variant
<222> (15)..(15)
<223> Xaa in position 15 is Asp, Glu, Gln or Arg

<220>
<221> variant
<222> (16)..(16)
<223> Xaa in position 16 is any amino acid

<400> 760
Glu Cys Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Phe
Xaa Xaa
1 5 10
15
Ala

<210> 761
<211> 12
<212> PRT
<213> Artificial sequence

<220>
<223> protein pattern

<220>
<221> variant
<222> (3)..(3)
<223> Xaa in position 3 is Glu, Gly, Ser or Thr

<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>

0070110

<221> Variant

<222> (11)..(11)

<223> Xaa in position 11 is Asp or Glu

<400> 761

Phe Pro Xaa Xaa Tyr Xaa Pro Thr Val Phe Xaa Asn
1 5 10

<210> 762

<211> 579

<212> DNA

<213> Artificial

<220>

<223> YNL090W codon optimized ORF

<220>

<221> CDS

<222> (1)..(579)

<400> 7621

atg agc gaa aag gca gtc cgc aga aaa cta gtg att ata gga
gac ggt 48
Met Ser Glu Lys Ala Val Arg Arg Lys Leu Val Ile Ile Gly
Asp Gly
1 5 10
15

gct tgc ggt aag acc tca ctt ctt tac gtg ttt acc ttg ggc
aaa ttc 96
Ala Cys Gly Lys Thr Ser Leu Leu Tyr Val Phe Thr Leu Gly
Lys Phe
20 25 30

cct gaa cag tat cat cca aca gtc ttc gag aac tac gta aca
gat tgc 144
Pro Glu Gln Tyr His Pro Thr Val Phe Glu Asn Tyr Val Thr
Asp Cys
35 40 45

aga gtg gac ggg att aag gtt tcc ctt act ctt tgg gat act
gct gga 192
Arg Val Asp Gly Ile Lys Val Ser Leu Thr Leu Trp Asp Thr
Ala Gly

50

55

60

caa gaa gag tat gaa cga ctt agg cca ttt tcg tat tcg aag
 gct gat 240
 Gln Glu Glu Tyr Glu Arg Leu Arg Pro Phe Ser Tyr Ser Lys
 Ala Asp
 65 70 75
 80

ata atc ctt atc gga ttc gct gtc gat aac ttt gag tct ctg
 att aac 288
 Ile Ile Leu Ile Gly Phe Ala Val Asp Asn Phe Glu Ser Leu
 Ile Asn
 85 90
 95

gct aga aca aag tgg gct gat gaa gct ctt aga tac tgt cca
 gat gct 336
 Ala Arg Thr Lys Trp Ala Asp Glu Ala Leu Arg Tyr Cys Pro
 Asp Ala
 100 105 110

cct att gtt ctt gtt gga ctc aag aaa gac ctg aga caa gaa
 gct cac 384
 Pro Ile Val Leu Val Gly Leu Lys Lys Asp Leu Arg Gln Glu
 Ala His
 115 120 125

ttc aag gaa aac gct act gac gaa atg gtg cca att gaa gat
 gca aag 432
 Phe Lys Glu Asn Ala Thr Asp Glu Met Val Pro Ile Glu Asp
 Ala Lys
 130 135 140

caa gtt gca aga gct ata gga gcg aag aaa tat atg gaa tgt
 tct gct 480
 Gln Val Ala Arg Ala Ile Gly Ala Lys Lys Tyr Met Glu Cys
 Ser Ala
 145 150 155
 160

cta acc ggt gaa ggt gtt gat gat gtt ttc gag gtt gct act
 aga acg 528
 Leu Thr Gly Glu Gly Val Asp Asp Val Phe Glu Val Ala Thr
 Seite 1150

0070110

Arg Thr

165

170

175

tct ctc cta atg aag aaa gaa cca gga gcc aac tgt tgt ata
atc ctc 576
Ser Leu Leu Met Lys Lys Glu Pro Gly Ala Asn Cys Cys Ile
Ile Leu

180

185

190

tag

579

<210> 763
<211> 192
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 763

Met Ser Glu Lys Ala Val Arg Arg Lys Leu Val Ile Ile Gly
Asp Gly 5 10
1
15
Ala Cys Gly Lys Thr Ser Leu Leu Tyr Val Phe Thr Leu Gly
Lys Phe 20 25 30
Pro Glu Gln Tyr His Pro Thr Val Phe Glu Asn Tyr Val Thr
Asp Cys 35 40 45
Arg Val Asp Gly Ile Lys Val Ser Leu Thr Leu Trp Asp Thr
Ala Gly 50 55 60
Gln Glu Glu Tyr Glu Arg Leu Arg Pro Phe Ser Tyr Ser Lys
Ala Asp 65 70 75
80
Ile Ile Leu Ile Gly Phe Ala Val Asp Asn Phe Glu Ser Leu
Ile Asn 85 90

0070110

95

Ala Arg Thr Lys Trp Ala Asp Glu Ala Leu Arg Tyr Cys Pro
Asp Ala
100 105 110

Pro Ile Val Leu Val Gly Leu Lys Lys Asp Leu Arg Gln Glu
Ala His
115 120 125

Phe Lys Glu Asn Ala Thr Asp Glu Met Val Pro Ile Glu Asp
Ala Lys
130 135 140

Gln Val Ala Arg Ala Ile Gly Ala Lys Lys Tyr Met Glu Cys
Ser Ala
145 150 155

160
Leu Thr Gly Glu Gly Val Asp Asp Val Phe Glu Val Ala Thr
Arg Thr
165 170

175
Ser Leu Leu Met Lys Lys Glu Pro Gly Ala Asn Cys Cys Ile
Ile Leu
180 185 190

<210> 764

<211> 678

<212> DNA

<213> *Salmonella enterica*

<400> 764

atgaccgccc tttcccaacc gacggccata gatggctatc gctggcttaa
aaatgacatt 60

attcgcggca cttatcagcc ggatgagaaa ctgcggatga gtttattaac
cgcccgctat 120

gcgctcggcg tagggccgct gcgtgaggcg ctgtcgcaac tggtggcgga
acggctggtc 180

accgtgggtga atcaaaaagg ctatcgcggtg gcatccatgt cagaggcgga
actcctcgat 240

atTTTTgacg cgcgcgccaa tatggaagcg atgctgggtac gcctggcgat
tgaacgcggc 300

0070110

gatgatgcgt gggaggcgga gatcctggcg cgagcgcata tgctcagcaa
actggaagcc 360

agcgatgccg gtgaacatat gctcgatgaa tgggatcagc gccaccaggc
gttccattcc 420

gccattgtcg ccgggtgcgg ctcccactat ctgctacaga tgcgcgaacg
cttatttgac 480

ctggcgggccc gctaccgctt tatttggtta cgtgaaaccg ttctgtccgt
cgagatgctg 540

gaagataaac atatccagca tcacacgcta accgaagcga tactggcgcg
cgaggcggca 600

cgcgccagcg aattaatgcg tcagcatttg ctgacgccga ttcccattat
tcgcccaggcg 660

atggcaggga aaatgtag
678

<210> 765

<211> 225

<212> PRT

<213> *Salmonella enterica*

<400> 765

Met Thr Ala Leu Ser Gln Pro Thr Ala Ile Asp Gly Tyr Arg
Trp Leu
1 5 10

15
Lys Asn Asp Ile Ile Arg Gly Thr Tyr Gln Pro Asp Glu Lys
Leu Arg
20 25 30

Met Ser Leu Leu Thr Ala Arg Tyr Ala Leu Gly Val Gly Pro
Leu Arg
35 40 45

Glu Ala Leu Ser Gln Leu Val Ala Glu Arg Leu Val Thr Val
Val Asn
50 55 60

Gln Lys Gly Tyr Arg Val Ala Ser Met Ser Glu Ala Glu Leu
Leu Asp
65 70 75

0070110

80
Ile Phe Asp Ala Arg Ala Asn Met Glu Ala Met Leu Val Arg
Leu Ala
85 90
95
Ile Glu Arg Gly Asp Asp Ala Trp Glu Ala Glu Ile Leu Ala
Arg Ala
100 105 110
His Met Leu Ser Lys Leu Glu Ala Ser Asp Ala Ser Glu His
Met Leu
115 120 125
Asp Glu Trp Asp Gln Arg His Gln Ala Phe His Ser Ala Ile
Val Ala
130 135 140
Gly Cys Gly Ser His Tyr Leu Leu Gln Met Arg Glu Arg Leu
Phe Asp
145 150 155
160
Leu Ala Ala Arg Tyr Arg Phe Ile Trp Leu Arg Glu Thr Val
Leu Ser
165 170
175
Val Glu Met Leu Glu Asp Lys His Ile Gln His His Thr Leu
Thr Glu
180 185 190
Ala Ile Leu Ala Arg Glu Ala Ala Arg Ala Ser Glu Leu Met
Arg Gln
195 200 205
His Leu Leu Thr Pro Ile Pro Ile Ile Arg Gln Ala Met Ala
Gly Lys
210 215 220
Met
225

<210> 766
<211> 774
<212> DNA
<213> Bradyrhizobium japonicum

<400> 766
atgataactga ctggcagcag agggatggca ggacggcgtc ggatgcgtga
gaggggtcaag 60

0070110

ccagcaggtg aaacacgcgc ggctgacgtg ctccaccgga tgcgcgcaga
catcatcagt 120

tgcacgctca agcccggcgc caagctgcgg ttcgaggcgc tacgggacat
ctacgcggtg 180

agctttttcga cgctgaggga ggcgctgtcg cgcctcgtgg ccgaagggct
cgtcacgcgc 240

gaggatcagc gcggccttcgt cgtcgcgccg gtttcgatcg acgatctcaa
cgacctcacc 300

tatgtccgcg tgctcatcga gcgcgaatgc gttgcgctcg cgatcaagaa
cggcgacgac 360

gcctgggagg cggacatcat cggcgcattc caccggatgg atcgcctgca
gaaccggctc 420

ggctccaatt attatctctc ggaagaatgg ggcaagctcc acggcgattt
tcatttttcg 480

cttgttgccg cgtgcggctc gcccaacctc ctggagatcc gccagaagct
gttcgaacgc 540

gcgcaccgct accgccgcat gtcctcgcaa ttccggacca aatggcgcgc
caaggatgtc 600

gagcacaaga tgatcatgga ttcggtcgtc gcgcgcgatg ccgcgaaggc
cgaggagctg 660

atcgagcgcc atatccgcga gacgaccgac aacgtgatca agcacgcagg
ccacctcttc 720

gtcacatccg acgaggaacg cccccgccgc acaagccggg tcgccgctga
atag 774

<210> 767

<211> 257

<212> PRT

<213> Bradyrhizobium japonicum

<400> 767

Met Ile Leu Thr Gly Ser Arg Gly Met Ala Gly Arg Arg Arg
Met Arg

1

5

10

0070110

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

0070110

Val Val Ala Arg Asp Ala Ala Lys Ala Glu Glu Leu Ile Glu
Arg His
210 215 220
Ile Arg Glu Thr Thr Asp Asn Val Ile Lys His Ala Gly His
Leu Phe
225 230 235
240
Val Thr Ser Asp Glu Glu Arg Pro Arg Arg Thr Ser Arg Val
Ala Ala
245 250
255
Glu

<210> 768
<211> 672
<212> DNA
<213> *Oceanicola batsensis*

<400> 768
atgatcttca gccgcggaga gagcgaggac gcaaccgtcg tggccatgct
ggcctcggcc 60
ctgaggcgcg atatctcggt cggcgtgctg ctccccgacc agaaactcag
gatcaatgcg 120
ctgcgacagc gctatggcgg gtcgaaccat tccatgcgcg agacgctgcg
gatgctgagc 180
gccgaggggc tggtcgaggc ttcggcgcaa cgcggttcc gcgtgacctc
ggcgaccgag 240
gacgatctgc gcgacataga actcgtacgg ctggagatcg agaagatcgc
cctcgcccgg 300
gcgctggatg ccggcgatac gggctgggag gggcgggtgg tcgccgcgca
tcacgccttg 360
cgcaaggcgg aggagcgtgt cgcggccaca cccgacgacc tgaccgcgct
tgaatgggac 420
gaaaggtgcc gggctttctc ggccagcctg atctcggcct gtggcagccc
gcggctgac 480
gacctgcagc gcaagttctt cgaccagagc cggcggttcc gcctcgcctt
gctgcgcgag 540

0070110

gacgcgctcg atttcgccgc gcgccgcgac aggcaggagg cgctgggtcgc
cgccgtgctg 600

gcacgcgata cagatgccgc gctcgcgatg ctcgaaaggg acatcgtcgc
ggaactcagg 660

acgggggcgct ga
672

<210> 769

<211> 223

<212> PRT

<213> Oceanicola batsensis

<400> 769

Met Ile Phe Ser Arg Gly Glu Ser Glu Asp Ala Thr Val Val
Ala Met
1 5 10
15

Leu Ala Ser Ala Leu Arg Arg Asp Ile Ser Phe Gly Val Leu
Leu Pro
20 25 30

Asp Gln Lys Leu Arg Ile Asn Ala Leu Arg Gln Arg Tyr Gly
Gly Ser
35 40 45

Asn His Ser Met Arg Glu Thr Leu Arg Met Leu Ser Ala Glu
Gly Leu
50 55 60

Val Glu Ala Ser Ala Gln Arg Gly Phe Arg Val Thr Ser Ala
Thr Glu
65 70 75
80

Asp Asp Leu Arg Asp Ile Glu Leu Val Arg Leu Glu Ile Glu
Lys Ile
85 90

95
Ala Leu Ala Arg Ala Leu Asp Ala Gly Asp Thr Gly Trp Glu
Gly Arg
100 105 110

Val Val Ala Ala His His Ala Leu Arg Lys Ala Glu Glu Arg
Val Ala

0070110
120

115

125

Ala Thr Pro Asp Asp Leu Thr Ala Leu Glu Trp Asp Glu Arg
Cys Arg
130 135 140

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

Asp Leu Gln Arg Lys Phe Phe Asp Gln Ser Arg Arg Phe Arg
Leu Ala
165 170

175
Leu Leu Arg Glu Asp Ala Leu Asp Phe Ala Ala Arg Arg Asp
Arg Gln
180 185 190

Glu Ala Leu Val Ala Ala Val Leu Ala Arg Asp Thr Asp Ala
Ala Leu
195 200 205

Ala Met Leu Glu Arg Asp Ile Val Ala Glu Leu Arg Thr Gly
Arg
210 215 220

<210> 770
<211> 567
<212> DNA
<213> Candida glabrata

<400> 770
atgtccgaga aagctatacg gagaaaattg gtgattatcg gtgatggtgc
gtgcggtaaa 60

acatcgttac tttatgtgtt tacgctgggg aaattccctg aacaatacca
tcctacagtg 120

tttgagaact atgtaacaga ttgtcgcgtt gatgggataa aagtatctct
ggcattgtgg 180

gatacagcag gacaagaaga atacgaaaga ttaagaccat tttcttattc
aggggcagat 240

gtaatactga ttgctttttc tgtggacaat gttgaatctc tacataatgc
caggacaaaa 300

0070110

tgggccgaag aagcgttcag gtactgtcca gatgcacctg tgatacttgt
agggctaaag 360

gaagatttga ggaaatcaaa acaagaaggc atagtttttcg taaatagaga
agatgcagaa 420

caagtagcga aggccattgg ggctaaaaaag tatttggaat gcagtgcggt
gactggtgaa 480

ggtgtcgatg atgttttttga gttggccaca agatcaagct tgctaatagca
caaagaaccg 540

gaccattttt gttgttcgat atcttag
567

<210> 771

<211> 188

<212> PRT

<213> Candida glabrata

<400> 771

Met Ser Glu Lys Ala Ile Arg Arg Lys Leu Val Ile Ile Gly
Asp Gly
1 5 10

15
Ala Cys Gly Lys Thr Ser Leu Leu Tyr Val Phe Thr Leu Gly
Lys Phe
20 25 30

Pro Glu Gln Tyr His Pro Thr Val Phe Glu Asn Tyr Val Thr
Asp Cys
35 40 45

Arg Val Asp Gly Ile Lys Val Ser Leu Ala Leu Trp Asp Thr
Ala Gly
50 55 60

Gln Glu Glu Tyr Glu Arg Leu Arg Pro Phe Ser Tyr Ser Gly
Ala Asp
65 70 75

80
Val Ile Leu Ile Ala Phe Ser Val Asp Asn Val Glu Ser Leu
His Asn
85 90

95

0070110

Ala	Arg	Thr	Lys	Trp	Ala	Glu	Glu	Ala	Phe	Arg	Tyr	Cys	Pro
Asp	Ala												
			100					105					110
Pro	Val	Ile	Leu	Val	Gly	Leu	Lys	Glu	Asp	Leu	Arg	Lys	Ser
Lys	Gln												
		115					120					125	
Glu	Gly	Ile	Val	Phe	Val	Asn	Arg	Glu	Asp	Ala	Glu	Gln	Val
Ala	Lys												
	130					135					140		
Ala	Ile	Gly	Ala	Lys	Lys	Tyr	Leu	Glu	Cys	Ser	Ala	Leu	Thr
Gly	Glu												
145					150					155			
160													
Gly	Val	Asp	Asp	Val	Phe	Glu	Leu	Ala	Thr	Arg	Ser	Ser	Leu
Leu	Met												
				165						170			
175													
His	Lys	Glu	Pro	Asp	His	Phe	Cys	Cys	Ser	Ile	Ser		
180	185												

<210> 772
 <211> 564
 <212> DNA
 <213> Candida albicans

<400> 772
 atgtcagaat cagttagaag aaagctagtt attgttggag acggagcgtg
 tggcaaaacg 60
 tcactactat atgtgtttac ccttggagaa ttccccaccg agtaccatcc
 aactgtgttt 120
 gaaaattatg tcactgattg taggattgat ggcaaaccag tacaattggc
 attatgggat 180
 actgctggtc aagaagaata tgaaagatta cgaccattga gttataacaa
 ttcccatggt 240
 attttgattg catttagttt agatacacca gattcattag ataatgctag
 aagtaagtgg 300
 gttgttgaag tgaaaaaata ttgccccaat actccttatt tgttatgtgg
 tctcaaaaag 360

0070110

gatttgagaa ctgacgaatc tgatcgtggt aattttgtgc aattcgatat
gggacaagcc 420

atggcagatg taattggagc taaaaaatat cttgagagct cggcattgac
aggcgaaggt 480

gtcgatgata tttttgagta cgccgttcgg actagtttgc taaagaatga
taaagccaat 540

acaggatggt gtaccataact ataa
564

<210> 773

<211> 187

<212> PRT

<213> Candida albicans

<400> 773

Met Ser Glu Ser Val Arg Arg Lys Leu Val Ile Val Gly Asp
Gly Ala

1 5 10

15

Cys Gly Lys Thr Ser Leu Leu Tyr Val Phe Thr Leu Gly Glu
Phe Pro

20 25 30

Thr Glu Tyr His Pro Thr Val Phe Glu Asn Tyr Val Thr Asp
Cys Arg

35 40 45

Ile Asp Gly Lys Pro Val Gln Leu Ala Leu Trp Asp Thr Ala
Gly Gln

50 55 60

Glu Glu Tyr Glu Arg Leu Arg Pro Leu Ser Tyr Asn Asn Ser
His Val

65 70 75

80

Ile Leu Ile Ala Phe Ser Leu Asp Thr Pro Asp Ser Leu Asp
Asn Ala

85 90

95

Arg Ser Lys Trp Val Val Glu Val Lys Lys Tyr Cys Pro Asn
Thr Pro

100 105 110

0070110

Tyr Leu Leu Cys Gly Leu Lys Lys Asp Leu Arg Thr Asp Glu
Ser Asp 115 120 125

Arg Val Asn Phe Val Gln Phe Asp Met Gly Gln Ala Met Ala
Asp Val 130 135 140

Ile Gly Ala Lys Lys Tyr Leu Glu Ser Ser Ala Leu Thr Gly
Glu Gly 145 150 155

Val Asp Asp Ile Phe Glu Tyr Ala Val Arg Thr Ser Leu Leu
Lys Asn 160 165 170

175
Asp Lys Ala Asn Thr Gly Cys Cys Thr Ile Leu
180 185

<210> 774
<211> 579
<212> DNA
<213> Strongylocentrotus purpuratus

<400> 774
atggctgcga ttaggaaaaa gttggatcatc gttggagatg gtgcttgtgg
aaagacgcgt 60

ctgctcacag tatttagcaa agaccagtac cccggccagt cagttgagac
ctatgtagct 120

gatatagaag tagatagcaa acagggttgaa ttagcattag tggatacagc
aggtcaggaa 180

gacttcgaca gactgagacc gctcttatat ccagacacag acgttatact
catgtgcttt 240

gctattaaca atccagacag tttagaaaac atcccggaga aatggacacc
agaggtcaag 300

cattcctgtc ccaacgtgcc catcatcctg gtgggtaaca agaaggacct
tcgtaacgac 360

gacaacacca agatggagct gcagcggacc aagaagaccc ccgtcacgta
caacaaggt 420

caccggatgg cagtcaagat caatgctgcc aagtacatgg agtgttcggc
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0070110

cgagaccaac 480

gatggggtga gggaggtctt tgaacggcc acaagggcag cactgcagag
cattgagagc 540

aagaagcgca agaagaagct ttcattgcaag atcttctaa
579

<210> 775

<211> 192

<212> PRT

<213> Strongylocentrotus purpuratus

<400> 775

Met	Ala	Ala	Ile	Arg	Lys	Lys	Leu	Val	Ile	Val	Gly	Asp	Gly
Ala	Cys												
1				5					10				
15													
Gly	Lys	Thr	Arg	Leu	Leu	Thr	Val	Phe	Ser	Lys	Asp	Gln	Tyr
Pro	Gly												
			20					25				30	
Gln	Ser	Val	Glu	Thr	Tyr	Val	Ala	Asp	Ile	Glu	Val	Asp	Ser
Lys	Gln												
		35					40					45	
Val	Glu	Leu	Ala	Leu	Val	Asp	Thr	Ala	Gly	Gln	Glu	Asp	Phe
Asp	Arg												
	50					55					60		
Leu	Arg	Pro	Leu	Leu	Tyr	Pro	Asp	Thr	Asp	Val	Ile	Leu	Met
Cys	Phe												
65					70					75			
80													
Ala	Ile	Asn	Asn	Pro	Asp	Ser	Leu	Glu	Asn	Ile	Pro	Glu	Lys
Trp	Thr												
			85							90			
95													
Pro	Glu	Val	Lys	His	Ser	Cys	Pro	Asn	Val	Pro	Ile	Ile	Leu
Val	Gly												
			100						105			110	
Asn	Lys	Lys	Asp	Leu	Arg	Asn	Asp	Asp	Asn	Thr	Lys	Met	Glu
Leu	Gln												
		115							120			125	

0070110

Arg	Thr	Lys	Lys	Thr	Pro	Val	Thr	Tyr	Asn	Lys	Gly	His	Arg
Met	Ala												
	130					135					140		

Val	Lys	Ile	Asn	Ala	Ala	Lys	Tyr	Met	Glu	Cys	Ser	Ala	Glu
Thr	Asn												
145					150					155			

160													
Asp	Gly	Val	Arg	Glu	Val	Phe	Glu	Thr	Ala	Thr	Arg	Ala	Ala
Leu	Gln												
			165						170				

175													
Ser	Ile	Glu	Ser	Lys	Lys	Arg	Lys	Lys	Lys	Leu	Ser	Cys	Lys
Ile	Phe												
			180					185				190	

<210> 776
 <211> 594
 <212> DNA
 <213> Glycine max

<400> 776
 atgagcgctt ctaggttcac caagtgcgtc actgttgggg atggtgctgt
 gggcaaaacc 60

tgcttgctta tttcctacac cagcaacact ttccccaccg attatgtgcc
 gactgttttt 120

gacaatttca gtgcaaattgt gggtgtcaat gggagcattg tgaatctggg
 tttgtgggat 180

actgctggac aagaggatta taacagatta agacctttga gttaccgtgg
 tgccgatgtt 240

ttcatactgg ctttctctct cataagcaag gccagttatg aaaatgtctc
 taaaaagtgg 300

attccggagt tgaagcatta tgctcctggg gtccccatta ttctgggttg
 cacaagctt 360

gaccttcggg atgataagca gttctgcatt gaccatcctg gtgccgtacc
 tattaccaca 420

gctcagggag aagagcttag gaagctgatt aatgcgccag cttacattga
 atgcagttca 480

0070110

aaaacacagg agaacgtgaa ggcagtcctt gatgcagcca taagagttgt
ccttcaacca 540

cctaagcaga agaaaaagaa gggtaaagca caaaaggcct gttcgatatt
gtga 594

<210> 777
<211> 197
<212> PRT
<213> Glycine max

<400> 777

Met	Ser	Ala	Ser	Arg	Phe	Ile	Lys	Cys	Val	Thr	Val	Gly	Asp
Gly	Ala												
1				5					10				
15													
Val	Gly	Lys	Thr	Cys	Leu	Leu	Ile	Ser	Tyr	Thr	Ser	Asn	Thr
Phe	Pro												
			20					25				30	
Thr	Asp	Tyr	Val	Pro	Thr	Val	Phe	Asp	Asn	Phe	Ser	Ala	Asn
Val	Val												
		35					40					45	
Val	Asn	Gly	Ser	Ile	Val	Asn	Leu	Gly	Leu	Trp	Asp	Thr	Ala
Gly	Gln												
	50					55					60		
Glu	Asp	Tyr	Asn	Arg	Leu	Arg	Pro	Leu	Ser	Tyr	Arg	Gly	Ala
Asp	Val												
65					70					75			
80													
Phe	Ile	Leu	Ala	Phe	Ser	Leu	Ile	Ser	Lys	Ala	Ser	Tyr	Glu
Asn	Val												
			85						90				
95													
Ser	Lys	Lys	Trp	Ile	Pro	Glu	Leu	Lys	His	Tyr	Ala	Pro	Gly
Val	Pro												
			100					105				110	
Ile	Ile	Leu	Val	Gly	Thr	Lys	Leu	Asp	Leu	Arg	Asp	Asp	Lys
Gln	Phe												
		115					120				125		
Cys	Ile	Asp	His	Pro	Gly	Ala	Val	Pro	Ile	Thr	Thr	Ala	Gln
Gly	Glu												

0070110

130	135	140
Glu Leu Arg Lys Leu Ile Asn Ala Pro Ala Tyr Ile Glu Cys		
Ser Ser		
145	150	155
160		
Lys Thr Gln Glu Asn Val Lys Ala Val Phe Asp Ala Ala Ile		
Arg Val		
	165	170
175		
Val Leu Gln Pro Pro Lys Gln Lys Lys Lys Lys Gly Lys Ala		
Gln Lys		
	180	185
		190
Ala Cys Ser Ile Leu		
195		

<210> 778
 <211> 609
 <212> DNA
 <213> Artificial

<220>
 <223> MtN3-like promotor from PAW222qcz

<400> 778
 gaagccacgt catgaagagt atatcatttc agtaatgttt tgagacgcct
 ctataatgct 60
 ttaccaacaa aacaaaacaa aaaaaagaac atttgaaacc atttgtatta
 aaaaaaaaaa 120
 ggtatattag gccataatat tataggtaac atgaaatatc aaatgacacg
 caagagtttt 180
 gtcaaaaatg aaaccatcac acatcagaga ttatggcaaa taatgttttg
 tgtgtctctt 240
 gcttcaccca taacataagc ctctataact ggagagaaga aaaaaaaaaag
 tgagaggggct 300
 aggggtgggaa tttggaagaa tacagttata ttgagcattg agcaagttga
 tagaaagctt 360
 ctcaatttgt acaaaaatttg catccacatg attattaaag acgtagacag
 cacttcttcc 420

0070110

ttctttttttt ctataagttt cttatatatt gttcttcatg ttttaatat
attactttat 480

gtacgcgtct aacagtagtc ctcccaaact gctataaata gaggctcttc
aacgcacctc 540

ttggcagtac aaaaattatt catctcttct aagttctaata tttctaagca
ttcagtaaaa 600

gaactaacc
609