

01 Sequence Listing NZ 11407.204-WO\_ST25 31-MAR-2008  
SEQUENCE LISTING

<110> Novozymes A/S  
<120> FUNGAL PEROXYGENASES AND METHODS OF APPLICATION  
<130> NZ 11407.204-WO  
<160> 59  
<170> PatentIn version 3.5  
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<212> DNA  
<213> Agrocybe aegerita

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<223> chloroperoxidase similar region

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<222> (594)..(1141)  
<223> novel fungal peroxxygenase specific region

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Ile Phe Ala Ala Gly Val Ile Ala Phe Pro Ser His Ala Ser Leu Ala  
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ggc ctc agc gag cag gaa ctg gat gag atc att cct aca ctc gaa att 148  
Gly Leu Ser Glu Gln Glu Leu Asp Glu Ile Ile Pro Thr Leu Glu Ile  
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cga gag cca aca caa cct cct gga cct ccg gag gac acc tct gcc aaa 196  
Arg Glu Pro Thr Gln Pro Pro Gly Pro Pro Glu Asp Thr Ser Ala Lys  
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ttg gtg aat gac aag gat cac cca tgg aag cca ctt cga ccg ggc gac 244  
Leu Val Asn Asp Lys Asp His Pro Trp Lys Pro Leu Arg Pro Gly Asp  
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atc cgt ggg cct tgt ccc ggt ctc aac acg ttg gcg tct cat ggg tac 292  
Ile Arg Gly Pro Cys Pro Gly Leu Asn Thr Leu Ala Ser His Gly Tyr  
35 40 45  
  
ctc ccg aga aac ggg gtt gca act ccg gcg caa att atc aac gct gtc 340  
Leu Pro Arg Asn Gly Val Ala Thr Pro Ala Gln Ile Ile Asn Ala Val  
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cag	gaa	gga	ttc	aac	atg	gat	aat	tca	gtc	gca	ctc	ttt	gcg	acg	tat		388
Gln	Glu	Gly	Phe	Asn	Met	Asp	Asn	Ser	Val	Ala	Leu	Phe	Ala	Thr	Tyr		
	65					70					75						
gag	gca	cac	ctt	atg	gtc	ggc	aat	ctc	ctc	acg	gac	ttg	ctg	agt	atc		436
Glu	Ala	His	Leu	Met	Val	Gly	Asn	Leu	Leu	Thr	Asp	Leu	Leu	Ser	Ile		
	80				85					90					95		
gga	cgc	aag	acg	ccg	ctc	act	ggg	cct	gat	ctc	cca	ccc	cca	gct	aac		484
Gly	Arg	Lys	Thr	Pro	Leu	Thr	Gly	Pro	Asp	Leu	Pro	Pro	Pro	Ala	Asn		
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att	ggt	ggg	ctc	agt	gag	cat	ggg	ctc	ttt	gaa	ggt	gat	gct	agt	atg		532
Ile	Gly	Gly	Leu	Ser	Glu	His	Gly	Leu	Phe	Glu	Gly	Asp	Ala	Ser	Met		
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act	aga	ggt	gac	gca	ttc	ttc	ggc	aac	aat	gat	gag	ttc	aat	gaa	gaa		580
Thr	Arg	Gly	Asp	Ala	Phe	Phe	Gly	Asn	Asn	Asp	Glu	Phe	Asn	Glu	Glu		
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ctc	ttc	caa	cag	ttc	att	gac	tac	agt	aac	cga	ttc	gga	gga	ggg	tac		628
Leu	Phe	Gln	Gln	Phe	Ile	Asp	Tyr	Ser	Asn	Arg	Phe	Gly	Gly	Gly	Tyr		
	145					150					155						
tac	aac	ctt	acg	gtg	gca	gtg	gaa	ctc	cg	ttc	aag	cg	att	cag	gac		676
Tyr	Asn	Leu	Thr	Val	Ala	Val	Glu	Leu	Arg	Phe	Lys	Arg	Ile	Gln	Asp		
				165						170					175		
tcg	att	gcg	acc	aac	ccc	gaa	ttt	aac	ttt	gtc	tcc	ccg	aga	ttc	ttt		724
Ser	Ile	Ala	Thr	Asn	Pro	Glu	Phe	Asn	Phe	Val	Ser	Pro	Arg	Phe	Phe		
				180					185					190			
gct	gcc	tac	ggc	gaa	tct	gtc	gcc	ccc	aat	aac	ttt	ttc	gtc	gat	gga		772
Ala	Ala	Tyr	Gly	Glu	Ser	Val	Ala	Pro	Asn	Asn	Phe	Phe	Val	Asp	Gly		
			195					200					205				
cg	aag	gac	gac	ggg	cat	ttg	gat	atg	gac	gcc	gcc	cg	gga	ttt	ttc		820
Arg	Lys	Asp	Asp	Gly	His	Leu	Asp	Met	Asp	Ala	Ala	Arg	Gly	Phe	Phe		
		210					215					220					
caa	ttc	ggc	cg	atg	cct	gac	ggc	ttc	ttc	cg	cca	aac	gga	acg	aaa		868
Gln	Phe	Gly	Arg	Met	Pro	Asp	Gly	Phe	Phe	Arg	Pro	Asn	Gly	Thr	Lys		
	225					230					235						
ggc	aac	gca	gga	ctc	gat	gac	gtc	gta	cg	gct	cat	ccc	gta	cag	cct		916
Gly	Asn	Ala	Gly	Leu	Asp	Asp	Val	Val	Arg	Ala	His	Pro	Val	Gln	Pro		
					245					250					255		
gga	agg	aat	ctc	ggc	cga	gtc	aac	agc	tac	act	cat	gat	cca	aca	tcc		964
Gly	Arg	Asn	Leu	Gly	Arg	Val	Asn	Ser	Tyr	Thr	His	Asp	Pro	Thr	Ser		
				260					265					270			
gcc	gat	ttc	acc	act	cct	tgc	tta	ttg	tac	gag	aac	ttc	gca	aac	aaa		1012
Ala	Asp	Phe	Thr	Thr	Pro	Cys	Leu	Leu	Tyr	Glu	Asn	Phe	Ala	Asn	Lys		
			275					280					285				
acc	gtc	acg	gca	ctc	tac	ccg	aat	ccg	aag	gga	caa	ctc	cg	aga	gca		1060
Thr	Val	Thr	Ala	Leu	Tyr	Pro	Asn	Pro	Lys	Gly	Gln	Leu	Arg	Arg	Ala		
		290					295					300					
att	aaa	gcg	aat	ctc	cat	ttc	ctc	ttc	ctg	gca	ata	aac	aga	acc	gtc		1108
Ile	Lys	Ala	Asn	Leu	His	Phe	Leu	Phe	Leu	Ala	Ile	Asn	Arg	Thr	Val		
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Gly	Cys	Ala	Glu	Val	Phe	Pro	Tyr	Gly	Arg	Asp							
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1273

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Leu Asp Glu Ile Ile Pro Thr Leu Glu Ile Arg Glu Pro Thr Gln Pro  
 -10 -5 -1 1 5

Pro Gly Pro Pro Glu Asp Thr Ser Ala Lys Leu Val Asn Asp Lys Asp  
 10 15 20

His Pro Trp Lys Pro Leu Arg Pro Gly Asp Ile Arg Gly Pro Cys Pro  
 25 30 35

Gly Leu Asn Thr Leu Ala Ser His Gly Tyr Leu Pro Arg Asn Gly Val  
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Ala Thr Pro Ala Gln Ile Ile Asn Ala Val Gln Glu Gly Phe Asn Met  
 55 60 65

Asp Asn Ser Val Ala Leu Phe Ala Thr Tyr Glu Ala His Leu Met Val  
 70 75 80 85

Gly Asn Leu Leu Thr Asp Leu Leu Ser Ile Gly Arg Lys Thr Pro Leu  
 90 95 100

Thr Gly Pro Asp Leu Pro Pro Pro Ala Asn Ile Gly Gly Leu Ser Glu  
 105 110 115

His Gly Leu Phe Glu Gly Asp Ala Ser Met Thr Arg Gly Asp Ala Phe  
 120 125 130

Phe Gly Asn Asn Asp Glu Phe Asn Glu Glu Leu Phe Gln Gln Phe Ile  
 135 140 145

Asp Tyr Ser Asn Arg Phe Gly Gly Gly Tyr Tyr Asn Leu Thr Val Ala  
 150 155 160 165

Val Glu Leu Arg Phe Lys Arg Ile Gln Asp Ser Ile Ala Thr Asn Pro  
 170 175 180

Glu Phe Asn Phe Val Ser Pro Arg Phe Phe Ala Ala Tyr Gly Glu Ser  
 185 190 195

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Val Ala Pro Asn Asn Phe Phe Val Asp Gly Arg Lys Asp Asp Gly His  
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Leu Asp Met Asp Ala Ala Arg Gly Phe Phe Gln Phe Gly Arg Met Pro  
 215 220 225

Asp Gly Phe Phe Arg Pro Asn Gly Thr Lys Gly Asn Ala Gly Leu Asp  
 230 235 240 245

Asp Val Val Arg Ala His Pro Val Gln Pro Gly Arg Asn Leu Gly Arg  
 250 255 260

Val Asn Ser Tyr Thr His Asp Pro Thr Ser Ala Asp Phe Thr Thr Pro  
 265 270 275

Cys Leu Leu Tyr Glu Asn Phe Ala Asn Lys Thr Val Thr Ala Leu Tyr  
 280 285 290

Pro Asn Pro Lys Gly Gln Leu Arg Arg Ala Ile Lys Ala Asn Leu His  
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Phe Leu Phe Leu Ala Ile Asn Arg Thr Val Gly Cys Ala Glu Val Phe  
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Pro Tyr Gly Arg Asp  
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 Leu Val Phe Ala Ala Arg Val Val Ala Phe Pro Ala Tyr Ala Ser Leu  
 10 15 20 25

gcc ggc ctc agc cag cag gaa ttg gac gct ata atc cca aca ctc gag 147  
 Ala Gly Leu Ser Gln Gln Glu Leu Asp Ala Ile Ile Pro Thr Leu Glu  
 30 35 40

gcc cga gag cca gga tta cct cct ggt cct ctc gag aat agc tct gca 195  
 Ala Arg Glu Pro Gly Leu Pro Pro Gly Pro Leu Glu Asn Ser Ser Ala  
 45 50 55

aag ttg gtg aac gac gag gct cac cca tgg aag ccg ctt cga cct ggc 243  
 Lys Leu Val Asn Asp Glu Ala His Pro Trp Lys Pro Leu Arg Pro Gly  
 60 65 70

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gat	att	cgt	gga	cct	tgc	cct	ggg	ctc	aat	act	ctg	gca	tct	cac	ggg	291
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	75					80					85					
tac	ctc	ccg	aga	aat	ggc	gtt	gca	acc	ccg	gtg	caa	ata	ata	aac	gcg	339
Tyr	Leu	Pro	Arg	Asn	Gly	Val	Ala	Thr	Pro	Val	Gln	Ile	Ile	Asn	Ala	
90					95					100					105	
gtt	cag	gaa	gga	ctc	aat	ttc	gac	aat	caa	gcc	gca	gtc	ttc	gcc	aca	387
Val	Gln	Glu	Gly	Leu	Asn	Phe	Asp	Asn	Gln	Ala	Ala	Val	Phe	Ala	Thr	
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tat	gcg	gcc	cac	ctt	gtg	gac	ggc	aat	ctc	att	acg	gac	ttg	ctg	agc	435
Tyr	Ala	Ala	His	Leu	Val	Asp	Gly	Asn	Leu	Ile	Thr	Asp	Leu	Leu	Ser	
			125					130					135			
atc	gga	cgc	aag	acg	cgg	ctc	act	ggg	cct	gat	cca	cca	ccc	ccc	gct	483
Ile	Gly	Arg	Lys	Thr	Arg	Leu	Thr	Gly	Pro	Asp	Pro	Pro	Pro	Pro	Ala	
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tcc	gtt	ggg	gga	ctc	aat	gag	cat	ggc	acc	ttc	gaa	ggc	gac	gcc	agt	531
Ser	Val	Gly	Gly	Leu	Asn	Glu	His	Gly	Thr	Phe	Glu	Gly	Asp	Ala	Ser	
	155					160					165					
atg	acc	cga	ggg	gac	gca	ttc	ttt	ggc	aac	aac	cac	gat	ttc	aat	gag	579
Met	Thr	Arg	Gly	Asp	Ala	Phe	Phe	Gly	Asn	Asn	His	Asp	Phe	Asn	Glu	
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acg	ctc	ttc	gaa	cag	ttg	gtt	gac	tac	agc	aac	cga	ttt	gga	gga	gga	627
Thr	Leu	Phe	Glu	Gln	Leu	Val	Asp	Tyr	Ser	Asn	Arg	Phe	Gly	Gly	Gly	
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aaa	tac	aat	ctt	acc	gtc	gcg	ggg	gag	ctc	cgt	ttc	aag	cgc	att	caa	675
Lys	Tyr	Asn	Leu	Thr	Val	Ala	Gly	Glu	Leu	Arg	Phe	Lys	Arg	Ile	Gln	
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Asp	Ser	Ile	Ala	Thr	Asn	Pro	Asn	Phe	Ser	Phe	Val	Asp	Phe	Arg	Phe	
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Phe	Thr	Ala	Tyr	Gly	Glu	Thr	Thr	Phe	Pro	Ala	Asn	Leu	Phe	Val	Asp	
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Gly	Arg	Arg	Asp	Asp	Gly	Gln	Leu	Asp	Met	Asp	Ala	Ala	Arg	Ser	Phe	
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Phe	Gln	Phe	Ser	Arg	Met	Pro	Asp	Asp	Phe	Phe	Arg	Ala	Pro	Ser	Pro	
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aga	agt	ggc	aca	gga	gtc	gag	gta	gtt	ata	cag	gct	cat	cct	atg	cag	915
Arg	Ser	Gly	Thr	Gly	Val	Glu	Val	Val	Ile	Gln	Ala	His	Pro	Met	Gln	
			285				290						295			
ccc	gga	aga	aat	gtc	ggc	aag	atc	aac	agc	tac	acc	gtc	gac	cca	aca	963
Pro	Gly	Arg	Asn	Val	Gly	Lys	Ile	Asn	Ser	Tyr	Thr	Val	Asp	Pro	Thr	
		300					305					310				
tcc	tct	gac	ttt	tcc	acc	ccc	tgc	ttg	atg	tac	gag	aaa	ttc	gtc	aac	1011
Ser	Ser	Asp	Phe	Ser	Thr	Pro	Cys	Leu	Met	Tyr	Glu	Lys	Phe	Val	Asn	
	315					320					325					
ata	acg	gtc	aag	tca	ctc	tac	ccg	aat	ccg	acg	gtg	cac	gtt	cgc	aaa	1059
Ile	Thr	Val	Lys	Ser	Leu	Tyr	Pro	Asn	Pro	Thr	Val	His	Val	Arg	Lys	
330					335					340					345	
gcc	ctt	aat	acg	aat	ctc	gat	ttc	ttc	ttc	cag	gga	gtc	gcc	gct	gga	1107

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Ala Leu Asn Thr Asn Leu Asp Phe Phe Phe Gln Gly Val Ala Ala Gly  
350 355 360

tgt acc cag gtc ttc cca tac ggg cga gat tgatatgata gagacaagag 1157  
Cys Thr Gln Val Phe Pro Tyr Gly Arg Asp  
365 370

agagtgtttc gacagtagcg gttctcaatt tgaatagttt gcagacatct gcttgtgtaa 1217

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aaaaaaaa 1284

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Leu Asp Ala Ile Ile Pro Thr Leu Glu Ala Arg Glu Pro Gly Leu Pro  
35 40 45

Pro Gly Pro Leu Glu Asn Ser Ser Ala Lys Leu Val Asn Asp Glu Ala  
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His Pro Trp Lys Pro Leu Arg Pro Gly Asp Ile Arg Gly Pro Cys Pro  
65 70 75 80

Gly Leu Asn Thr Leu Ala Ser His Gly Tyr Leu Pro Arg Asn Gly Val  
85 90 95

Ala Thr Pro Val Gln Ile Ile Asn Ala Val Gln Glu Gly Leu Asn Phe  
100 105 110

Asp Asn Gln Ala Ala Val Phe Ala Thr Tyr Ala Ala His Leu Val Asp  
115 120 125

Gly Asn Leu Ile Thr Asp Leu Leu Ser Ile Gly Arg Lys Thr Arg Leu  
130 135 140

Thr Gly Pro Asp Pro Pro Pro Pro Ala Ser Val Gly Gly Leu Asn Glu  
145 150 155 160

His Gly Thr Phe Glu Gly Asp Ala Ser Met Thr Arg Gly Asp Ala Phe  
165 170 175

Phe Gly Asn Asn His Asp Phe Asn Glu Thr Leu Phe Glu Gln Leu Val  
180 185 190

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Asp Tyr Ser Asn Arg Phe Gly Gly Gly Lys Tyr Asn Leu Thr Val Ala  
195 200 205

Gly Glu Leu Arg Phe Lys Arg Ile Gln Asp Ser Ile Ala Thr Asn Pro  
210 215 220

Asn Phe Ser Phe Val Asp Phe Arg Phe Phe Thr Ala Tyr Gly Glu Thr  
225 230 235 240

Thr Phe Pro Ala Asn Leu Phe Val Asp Gly Arg Arg Asp Asp Gly Gln  
245 250 255

Leu Asp Met Asp Ala Ala Arg Ser Phe Phe Gln Phe Ser Arg Met Pro  
260 265 270

Asp Asp Phe Phe Arg Ala Pro Ser Pro Arg Ser Gly Thr Gly Val Glu  
275 280 285

Val Val Ile Gln Ala His Pro Met Gln Pro Gly Arg Asn Val Gly Lys  
290 295 300

Ile Asn Ser Tyr Thr Val Asp Pro Thr Ser Ser Asp Phe Ser Thr Pro  
305 310 315 320

Cys Leu Met Tyr Glu Lys Phe Val Asn Ile Thr Val Lys Ser Leu Tyr  
325 330 335

Pro Asn Pro Thr Val His Val Arg Lys Ala Leu Asn Thr Asn Leu Asp  
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ttcagcttca taccataccc aagaacgtgt ctcgcccatt tacaggatgat ctggaggatga	180
ggtttataaa tagaacggac tataagcgga ctaaccttgg acgttatata gtgcaaacct	240
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gatcattgtc acgagtataa gatagggtgtg tgtaggcgtc gaattccaac aattcagtcg	540
tgcata atg gct cgc ctt act ttc ctc gca gct att gcc ctg gca tta Met Ala Arg Leu Thr Phe Leu Ala Ala Ile Ala Leu Ala Leu	588
1 5 10	
tct tcc acc act gta cta gca ttc cca tca tac ggc tcc ctt gct ggg Ser Ser Thr Thr Val Leu Ala Phe Pro Ser Tyr Gly Ser Leu Ala Gly	636
15 20 25 30	
ctt tca gag gcg gaa tta gac cgt att att ccc ttg cta gaa gct cgt Leu Ser Glu Ala Glu Leu Asp Arg Ile Ile Pro Leu Leu Glu Ala Arg	684
35 40 45	
aac gct ggc cct cct cct gga cca ctg aag aat act tca aca aaa ttg Asn Ala Gly Pro Pro Pro Gly Pro Leu Lys Asn Thr Ser Thr Lys Leu	732
50 55 60	
gtc aac gac aag aac cac ccc tgg aag cct ctc gga tat ggc gat att Val Asn Asp Lys Asn His Pro Trp Lys Pro Leu Gly Tyr Gly Asp Ile	780
65 70 75	
cga ggt cct tgc cct ggg tta aac aca ctg gcc tcc cat ggg Arg Gly Pro Cys Pro Gly Leu Asn Thr Leu Ala Ser His Gly	822
80 85 90	
gtgagttcgg acatttatgg ttacgtttca tcggagttaa ttgtaactgt tttattcgtg	882
cag tgg ctt cct cga aac ggc atc gct act ccg gcg caa att gtc aac Trp Leu Pro Arg Asn Gly Ile Ala Thr Pro Ala Gln Ile Val Asn	930
95 100 105	
gcg gtg cag gaa g gtctgtgtt cgactaattg ctgacaattg atattgattg	983
Ala Val Gln Glu	
110	
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115 120 125	
gct gcg cat ctc gtt gac ggc aat cag gtc acg gac ttg ctt agc atc Ala Ala His Leu Val Asp Gly Asn Gln Val Thr Asp Leu Leu Ser Ile	1080
130 135 140	
ggg gga aag acg cct caa aca ggc cct gac ccg ccc gcg cct gcc att Gly Gly Lys Thr Pro Gln Thr Gly Pro Asp Pro Pro Ala Pro Ala Ile	1128
145 150 155	
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160 165	
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170	
agt atg act cga g gtatgatcat cgccccgata attagatgac aattgaaccg	1279
Ser Met Thr Arg	
175	
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180 185	

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190

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Phe Ser Ala Phe Ser Asn Lys Phe Gly Gly Gly Tyr Tyr  
195 200 205

aat ttg agc gta gca gcc gag ttt aga tgg cag cgc att caa gaa tct 1479  
Asn Leu Ser Val Ala Ala Glu Phe Arg Trp Gln Arg Ile Gln Glu Ser  
210 215 220

att gcg acg aac cca aac ttt tct ctc atc tcc ccc cgt tac ttc acg 1527  
Ile Ala Thr Asn Pro Asn Phe Ser Leu Ile Ser Pro Arg Tyr Phe Thr  
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gcg tat gcc gag tcc gtg ttt ccc ctg gta ttc ttc gtc gac ggc cgc 1575  
Ala Tyr Ala Glu Ser Val Phe Pro Leu Val Phe Phe Val Asp Gly Arg  
240 245 250

gta tca gac gga cgg ctt agc cta ccg aac gcg cgt ggg ttc ttc cag 1623  
Val Ser Asp Gly Arg Leu Ser Leu Pro Asn Ala Arg Gly Phe Phe Gln  
255 260 265 270

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Asn Ser Gln Met Pro Lys Asp Phe Phe Arg Pro Asn Gln Ser Ile Gly  
275 280 285

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

Leu Asn Thr His Ala Val Phe Glu Gly Asp Ala Ser Met Thr Arg Gly  
165 170 175

Asp Ala Phe Phe Gly Asp Asn His Ser Phe Asn Glu Thr Gln Phe Asp  
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Glu Phe Ser Ala Phe Ser Asn Lys Phe Gly Gly Gly Tyr Tyr Asn Leu  
195 200 205

Ser Val Ala Ala Glu Phe Arg Trp Gln Arg Ile Gln Glu Ser Ile Ala  
210 215 220

Thr Asn Pro Asn Phe Ser Leu Ile Ser Pro Arg Tyr Phe Thr Ala Tyr  
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Ala Glu Ser Val Phe Pro Leu Val Phe Phe Val Asp Gly Arg Val Ser  
245 250 255

Asp Gly Arg Leu Ser Leu Pro Asn Ala Arg Gly Phe Phe Gln Asn Ser  
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Gln Met Pro Lys Asp Phe Phe Arg Pro Asn Gln Ser Ile Gly Leu Asn  
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Glu Ile Gly Asp Gly Ile Ser Ala Ile Ala Ser Ala His Pro Ile Ala  
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Pro Gly Lys Asn Glu Gly Val Gly Asn Tyr Val Leu Asp Pro Thr Ser  
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Ala Asp Phe Asp His Phe Cys Leu Leu Tyr Ile Asn Phe Val Asn Gln  
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Thr Val Lys Ser Leu Tyr Pro Asn Pro Lys Gly Val Leu Leu Asp Ala  
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Cys Glu Gln Ile Phe Pro Tyr Gly Lys  
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Val Ser His Leu Ser Leu Val Leu Gly Phe Pro Ala Tyr Ala Ser Leu	
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Ile Val Phe Pro Pro Pro Pro Pro Glu Pro Ile Lys Asp Pro Trp Leu	
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Lys Leu Val Asn Asp Arg Ala His Pro Trp Arg Pro Leu Arg Arg Gly	
65 70 75 80	
gat gtc aga gga ccc tgc ccg ggg ttg aat acg ttg gca tcc cat ggg	288
Asp Val Arg Gly Pro Cys Pro Gly Leu Asn Thr Leu Ala Ser His Gly	
85 90 95	
tat ctt cct cga gat ggt gtg gcg act cca gct caa atc atc act gcc	336
Tyr Leu Pro Arg Asp Gly Val Ala Thr Pro Ala Gln Ile Ile Thr Ala	
100 105 110	
gtc caa gaa ggc ttc aac atg gag tac ggg atc gcg aca ttc gtc acc	384
Val Gln Glu Gly Phe Asn Met Glu Tyr Gly Ile Ala Thr Phe Val Thr	
115 120 125	
tac gct gcc cac ctc gtc gat gga aac cca ctc acc aat ctc atc agc	432
Tyr Ala Ala His Leu Val Asp Gly Asn Pro Leu Thr Asn Leu Ile Ser	
130 135 140	
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145 150 155 160	

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acg ctt tgg gag cag ttc aag gac tac agt aac cgc tat gga ggt gga Thr Leu Trp Glu Gln Phe Lys Asp Tyr Ser Asn Arg Tyr Gly Gly Gly 195 200 205	624
cga tac aac cta act gcg gct gct gag ctt cgc tgg gca cgt atc cag Arg Tyr Asn Leu Thr Ala Ala Glu Leu Arg Trp Ala Arg Ile Gln 210 215 220	672
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ttc aca gcc tac gcc gaa tcc gtt ttc cca atc aac ttc ttc acg gac Phe Thr Ala Tyr Ala Glu Ser Val Phe Pro Ile Asn Phe Phe Thr Asp 245 250 255	768
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gcc tac cct atc cag ccg ggc tac aat gca gat ggg aag gtg aac aac Ala Tyr Pro Ile Gln Pro Gly Tyr Asn Ala Asp Gly Lys Val Asn Asn 305 310 315 320	960
tac gtc ctc gac ccg act tcc gcg gat ttc aca aag ttc tgt ctg ctg Tyr Val Leu Asp Pro Thr Ser Ala Asp Phe Thr Lys Phe Cys Leu Leu 325 330 335	1008
tac gag aac ttt gtg ttg aag act gtg aag ggg ctc tat cca aat ccg Tyr Glu Asn Phe Val Leu Lys Thr Val Lys Gly Leu Tyr Pro Asn Pro 340 345 350	1056
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cag tcg ttc cct ggg tcg gga ggc tgc ccg cag gtc ttc ccc tgg ggc Gln Ser Phe Pro Gly Ser Gly Gly Cys Pro Gln Val Phe Pro Trp Gly 370 375 380	1152
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 Page 13

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Ile Val Phe Pro Pro Pro Pro Pro Glu Pro Ile Lys Asp Pro Trp Leu
          50          55          60
Lys Leu Val Asn Asp Arg Ala His Pro Trp Arg Pro Leu Arg Arg Gly
          65          70          75          80
Asp Val Arg Gly Pro Cys Pro Gly Leu Asn Thr Leu Ala Ser His Gly
          85          90          95
Tyr Leu Pro Arg Asp Gly Val Ala Thr Pro Ala Gln Ile Ile Thr Ala
          100          105          110
Val Gln Glu Gly Phe Asn Met Glu Tyr Gly Ile Ala Thr Phe Val Thr
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Tyr Ala Ala His Leu Val Asp Gly Asn Pro Leu Thr Asn Leu Ile Ser
          130          135          140
Ile Gly Gly Lys Thr Arg Lys Thr Gly Pro Asp Pro Pro Pro Pro Ala
          145          150          155          160
Ile Val Gly Gly Leu Asn Thr His Ala Val Phe Glu Gly Asp Ala Ser
          165          170          175
Met Thr Arg Gly Asp Phe His Leu Gly Asp Asn Phe Asn Phe Asn Gln
          180          185          190
Thr Leu Trp Glu Gln Phe Lys Asp Tyr Ser Asn Arg Tyr Gly Gly Gly
          195          200          205
Arg Tyr Asn Leu Thr Ala Ala Ala Glu Leu Arg Trp Ala Arg Ile Gln
          210          215          220
Gln Ser Met Ala Thr Asn Gly Gln Phe Asp Phe Thr Ser Pro Arg Tyr
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Phe Thr Ala Tyr Ala Glu Ser Val Phe Pro Ile Asn Phe Phe Thr Asp
          245          250          255
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Ser Ala Leu Ser Phe Phe Arg Asp His Arg Tyr Pro Lys Asp Phe His
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Ala Tyr Pro Ile Gln Pro Gly Tyr Asn Ala Asp Gly Lys Val Asn Asn  
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Tyr Val Leu Asp Pro Thr Ser Ala Asp Phe Thr Lys Phe Cys Leu Leu  
325 330 335

Tyr Glu Asn Phe Val Leu Lys Thr Val Lys Gly Leu Tyr Pro Asn Pro  
340 345 350

Lys Gly Phe Leu Arg Lys Ala Leu Glu Thr Asn Leu Glu Tyr Phe Tyr  
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tcc aag cgc cag ctc gag acg att atc ccc gga ctg ccg gtt gtc aac	144
Ser Lys Arg Gln Leu Glu Thr Ile Ile Pro Gly Leu Pro Val Val Asn	
35 40 45	
cct ggc cct cca cct ggg ccg tta gcg gat tcc acc ttg aag ttg gtc	192
Pro Gly Pro Pro Pro Gly Pro Leu Ala Asp Ser Thr Leu Lys Leu Val	
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aat gat gcg gcg cat ccg tat cag gcg cct agg ccg cat ttg gat cat	240
Asn Asp Ala Ala His Pro Tyr Gln Ala Pro Arg Pro His Leu Asp His	
65 70 75 80	
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Arg Gly Pro Cys Pro Gly Leu Asn Thr Leu Ala Asn His Gly Tyr Leu	
85 90 95	
ccc agg tcg ggt atc gcg acg cca gct cag atc gtt cag gct gtt atg	336
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tac aat ctc aca gct gca act gaa ctc cga tac cag cgc atc cag cag Tyr Asn Leu Thr Ala Ala Thr Glu Leu Arg Tyr Gln Arg Ile Gln Gln 210 215 220	672
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gac ttt gtg aac gat att gtc gtt gca ctc tat ccg aat ccg acg ggt Asp Phe Val Asn Asp Ile Val Val Ala Leu Tyr Pro Asn Pro Thr Gly 305 310 315 320	960
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Pro Gly Pro Pro Pro Gly Pro Leu Ala Asp Ser Thr Leu Lys Leu Val  
50 55 60

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Arg Gly Pro Cys Pro Gly Leu Asn Thr Leu Ala Asn His Gly Tyr Leu  
85 90 95

Pro Arg Ser Gly Ile Ala Thr Pro Ala Gln Ile Val Gln Ala Val Met  
100 105 110

Glu Gly Phe Asn Met Glu Asn Thr Phe Ala Lys Phe Val Thr Tyr Ala  
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Ala Phe Leu Val Asp Gly Asn Pro Ile Thr Asn Leu Met Ser Ile Gly  
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Val Gly Gly Leu Asn Thr His Ala Val Phe Glu Gly Asp Thr Ser Met  
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Thr Arg Gly Asp Phe His Phe Gly Asp Asn His Ser Phe Asn Gln Thr  
180 185 190

Leu Phe Asp Gln Phe Val Glu Tyr Ser Asn Ile His Gly Gly Gly Phe  
195 200 205

Tyr Asn Leu Thr Ala Ala Thr Glu Leu Arg Tyr Gln Arg Ile Gln Gln  
210 215 220

Ser Ile Ala Thr Asn Pro Glu Met Ser Phe Val Ser Pro Arg Trp Phe  
225 230 235 240

Thr Ala Ile Leu Leu Gln Asp Glu Lys Phe Pro Asp Asp Phe His Arg  
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Ala Pro Gly Pro Phe Ser Phe Glu Gly Leu Gly Tyr Leu Val Thr Arg  
260 265 270

Arg Pro Met Pro Pro Gly Arg Asn Val Gly Gly Val Asp Asn Tyr Val  
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305 310 315 320

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Lys Leu Val Asn Asp Lys Ala His Pro Phe Lys Pro Leu Lys Lys Gly	
65 70 75 80	
gac gtc cgt gga cca tgt cct gga ttg aac acc cta gcc tcc cat ggg	288
Asp Val Arg Gly Pro Cys Pro Gly Leu Asn Thr Leu Ala Ser His Gly	
85 90 95	
tac ctc ccc cgc aac ggt gtc gcc agc cca tcc cag atc att gac gcc	336
Tyr Leu Pro Arg Asn Gly Val Ala Ser Pro Ser Gln Ile Ile Asp Ala	
100 105 110	
gtc caa gaa ggt ttc aac atg gag aac gag ctg gct agg ttt acg acc	384
Val Gln Glu Gly Phe Asn Met Glu Asn Glu Leu Ala Arg Phe Thr Thr	
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Tyr Val Ala His Leu Val Asp Gly Asn Leu Val Thr Asp Leu Leu Ser	
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gag ctg ttt gac cag ttc aag aat ttc agc gcg gtg tac gga aac ggc Glu Leu Phe Asp Gln Phe Lys Asn Phe Ser Ala Val Tyr Gly Asn Gly 195 200 205	624
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gac agc ttg ggc agt ctt ctc gat ttc tgc ggg ttc tac gag aac ttt Asp Ser Leu Gly Ser Leu Leu Asp Phe Cys Gly Phe Tyr Glu Asn Phe 325 330 335	1008
gtc aac aag acg ctc aag gca ctg tac ccc aac ccc aag ggc gtg ttg Val Asn Lys Thr Leu Lys Ala Leu Tyr Pro Asn Pro Lys Gly Val Leu 340 345 350	1056
agg agg aat ctc aat atc aac ctc cag ttc ttc ttc gag tcc ttg ccc Arg Arg Asn Leu Asn Ile Asn Leu Gln Phe Phe Phe Glu Ser Leu Pro 355 360 365	1104
aag gac gag agc ggt acc cct gtc tgc acc cag gtg ttc ccc tac gga Lys Asp Glu Ser Gly Thr Pro Val Cys Thr Gln Val Phe Pro Tyr Gly 370 375 380	1152
cgt aac tga Arg Asn 385	1161

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His Arg Val Pro Pro Pro Pro Pro Gly Pro Pro Ala Phe Thr Gly Ala
          50          55          60
Lys Leu Val Asn Asp Lys Ala His Pro Phe Lys Pro Leu Lys Lys Gly
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Asp Val Arg Gly Pro Cys Pro Gly Leu Asn Thr Leu Ala Ser His Gly
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Tyr Leu Pro Arg Asn Gly Val Ala Ser Pro Ser Gln Ile Ile Asp Ala
          100          105          110
Val Gln Glu Gly Phe Asn Met Glu Asn Glu Leu Ala Arg Phe Thr Thr
          115          120          125
Tyr Val Ala His Leu Val Asp Gly Asn Leu Val Thr Asp Leu Leu Ser
          130          135          140
Ile Gly Glu Lys Thr Arg Lys Thr Gly Pro Asp Pro Pro Pro Pro Ala
          145          150          155          160
Ile Val Gly Gly Leu Asn Asn His Gly Thr Phe Glu Gly Asp Ala Ser
          165          170          175
Leu Thr Arg Gly Asp Ala Phe Phe Gly Asp Asn His Asn Phe Asn Gln
          180          185          190
Glu Leu Phe Asp Gln Phe Lys Asn Phe Ser Ala Val Tyr Gly Asn Gly
          195          200          205
Phe Phe Asn Met Thr Val Ala Gly Glu Leu Arg Phe His Arg Ile Gln
          210          215          220
Gln Ser Ile Ala Thr Asn Pro Glu Phe Ser Leu Val Gly Leu Arg His
          225          230          235          240
Leu Thr Ala Tyr Ala Glu Ala Ser Phe Pro Ser Leu Phe Phe Val Asp
          245          250          255
Gly Arg Lys Thr Gly Ala Glu Ala Gly Gln Leu Asp Met Ala Thr Ala
          260          265          270
Glu Ser Phe Phe Arg Asp Met Met Tyr Pro Pro Asp Phe Phe Arg Pro
          275          280          285

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Ala Ala Pro Val Ala Gly Asp Ala Gly Ala Ile Phe Leu Ala His Pro  
290 295 300

Phe Gln Pro Gly Arg Asn Val Gly Gly Val Asn Asn Phe Thr Val Asp  
305 310 315 320

Asp Ser Leu Gly Ser Leu Leu Asp Phe Cys Gly Phe Tyr Glu Asn Phe  
325 330 335

Val Asn Lys Thr Leu Lys Ala Leu Tyr Pro Asn Pro Lys Gly Val Leu  
340 345 350

Arg Arg Asn Leu Asn Ile Asn Leu Gln Phe Phe Phe Glu Ser Leu Pro  
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Lys Asp Glu Ser Gly Thr Pro Val Cys Thr Gln Val Phe Pro Tyr Gly  
370 375 380

Arg Asn  
385

<210> 13  
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<220>  
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aat gga acc aag ctt gtg aac gac gaa gat cac cct ttc atg cct ccg	96
Asn Gly Thr Lys Leu Val Asn Asp Glu Asp His Pro Phe Met Pro Pro	
20 25 30	
agg aag ggg gat gcc cgt gga ccg tgt cct ggg ttg aat act ttg gcg	144
Arg Lys Gly Asp Ala Arg Gly Pro Cys Pro Gly Leu Asn Thr Leu Ala	
35 40 45	
tcg cac ggg tac ctc ccc cgt aat ggc ata gcc act ccc gct cag atc	192
Ser His Gly Tyr Leu Pro Arg Asn Gly Ile Ala Thr Pro Ala Gln Ile	
50 55 60	
atc aac gcc gtt caa gaa ggc ttc aat atg gag aac gag atc gcc agg	240
Ile Asn Ala Val Gln Glu Gly Phe Asn Met Glu Asn Glu Ile Ala Arg	
65 70 75 80	
ttc acg acc tac acc gcg cat ctc atg gac ggg aat ctg gtc act gac	288
Phe Thr Thr Tyr Thr Ala His Leu Met Asp Gly Asn Leu Val Thr Asp	
85 90 95	
ttg ctc agt atc ggg ccg aag acg ccc aag act gga cct gac cca cct	336
Leu Leu Ser Ile Gly Pro Lys Thr Pro Lys Thr Gly Pro Asp Pro Pro	
100 105 110	

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ccc cct gcc atc gtt gga gga ttg aac aac cat ggt act ttc gaa ggc Pro Pro Ala Ile Val Gly Gly Leu Asn Asn His Gly Thr Phe Glu Gly 115 120 125	384
gac gcg agt ctg tct cgg gca gac gct ttc ttt ggc gat aac cat agc Asp Ala Ser Leu Ser Arg Ala Asp Ala Phe Phe Gly Asp Asn His Ser 130 135 140	432
ttt gac caa gag ctg ttc gac cag ttc agg aat ttc agc gcg atc tac Phe Asp Gln Glu Leu Phe Asp Gln Phe Arg Asn Phe Ser Ala Ile Tyr 145 150 155 160	480
gga aac ggt ttc ttc aat atg aca gtc gcc gcc gag ctc agg ttc cac Gly Asn Gly Phe Phe Asn Met Thr Val Ala Ala Glu Leu Arg Phe His 165 170 175	528
cgt atc caa cag tcc atc gct acc aac ccc gaa ttc tcc ttc gct gga Arg Ile Gln Gln Ser Ile Ala Thr Asn Pro Glu Phe Ser Phe Ala Gly 180 185 190	576
ctc cgt cac att acc gcc tac gct gaa gcc tct ttc cct ccg atc ttc Leu Arg His Ile Thr Ala Tyr Ala Glu Ala Ser Phe Pro Pro Ile Phe 195 200 205	624
ttc gtc gat ggg cgg aag acc ggt gct gag gcg gga caa ctc gac atg Phe Val Asp Gly Arg Lys Thr Gly Ala Glu Ala Gly Gln Leu Asp Met 210 215 220	672
gcc gcc gcg gag agc ttc ttc aag cac atg atg tac cct ccc gac ttc Ala Ala Ala Glu Ser Phe Phe Lys His Met Met Tyr Pro Pro Asp Phe 225 230 235 240	720
cac cgc cct gcg gaa ccc gtc aac agc gat gcg cag gcc gta ttt gaa His Arg Pro Ala Glu Pro Val Asn Ser Asp Ala Gln Ala Val Phe Glu 245 250 255	768
gtt cat cct ttc caa ccc ggg agg aac gtc gga ggg gtc aac aac tat Val His Pro Phe Gln Pro Gly Arg Asn Val Gly Gly Val Asn Asn Tyr 260 265 270	816
acc gtt gat gag agt ttg ggt ggt ctg ttg gat ttc tgc ggg ttc tac Thr Val Asp Glu Ser Leu Gly Gly Leu Leu Asp Phe Cys Gly Phe Tyr 275 280 285	864
gag aac ttt gtg aac aag acg atc aag ggt ttg tat ccc aac ccc acg Glu Asn Phe Val Asn Lys Thr Ile Lys Gly Leu Tyr Pro Asn Pro Thr 290 295 300	912
ggc gtt ttg aag agg aat ttg aat att aat ctc gat ttc ctc ttt gag Gly Val Leu Lys Arg Asn Leu Asn Ile Asn Leu Asp Phe Leu Phe Glu 305 310 315 320	960
gcg ttg ccg aag gct ggt gac ggg tct caa ccg tgt act caa gtt ttc Ala Leu Pro Lys Ala Gly Asp Gly Ser Gln Pro Cys Thr Gln Val Phe 325 330 335	1008
cct tac gga cac gat tag Pro Tyr Gly His Asp 340	1026

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 <211> 341  
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 <213> Coprinopsis cinerea okayama7#130

<400> 14

Met Leu Lys Pro Arg Val Pro Pro Pro Pro Pro Gly Pro Leu Ala Phe  
 Page 22

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

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



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cac ctc cgc cgt cgc cgt atc gag caa tcc att gcc acc aac ccc gaa 528  
His Leu Arg Arg Arg Arg Ile Glu Gln Ser Ile Ala Thr Asn Pro Glu  
165 170 175

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Phe Asp Phe Thr Ser Pro Arg Phe Phe Thr Ala Phe Ala Glu Ser Ser  
180 185 190

ttc cct tac tcg ttc ttc gtc gac ggc cgt atc acc gag cgt ccc gga 624  
Phe Pro Tyr Ser Phe Phe Val Asp Gly Arg Ile Thr Glu Arg Pro Gly  
195 200 205

ggc ctc agt atg gag aat gcc act ctc ttc ttc agg gac cac aag atg 672  
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35 40 45

Thr Pro Ala Gln Ile Ile Asn Ala Ile Val Glu Gly Phe Asn Phe Asn  
50 55 60

Tyr Glu Gly Ala Val Phe Val Thr Tyr Phe Ala His Ile Val Asp Gly  
65 70 75 80

Asn Leu Val Thr Asp Leu Leu Ser Ile Gly Gly Lys Thr Asn Leu Thr  
85 90 95

Gly Glu Asp Thr Gly Ala Pro Ala Ile Ile Gly Gly Leu Asn Thr His  
100 105 110

Ser Val Phe Glu Gly Asp Ala Ser Met Thr Arg Asp Asp Phe His Phe  
115 120 125

Gly Asp Asn His Ser Phe Asn Gln Thr Leu Phe Asp Gln Phe Val Glu  
130 135 140

Tyr Ser Asn Thr Tyr Gly Gly Gly Phe Tyr Asn Gln Glu Val Ala Gly  
145 150 155 160

His Leu Arg Arg Arg Arg Ile Glu Gln Ser Ile Ala Thr Asn Pro Glu

Phe Asp Phe Thr Ser Pro Arg Phe Phe Thr Ala Phe Ala Glu Ser Ser  
180 185 190

Phe Pro Tyr Ser Phe Phe Val Asp Gly Arg Ile Thr Glu Arg Pro Gly  
195 200 205

Gly Leu Ser Met Glu Asn Ala Thr Leu Phe Phe Arg Asp His Lys Met  
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Pro Asp Asp Phe Trp  
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Gly Leu Asn Val Leu Asp Ile Tyr Arg Ala Ser Gly Ser Pro Pro Ala  
20 25 30  
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Gly Arg Asn Val Asn Gly Thr Asn Thr Phe Thr Pro Asp Pro Asn Ser  
35 40 45  
gcg gat ttc gat aat cct tgt gaa ctc tac tac gac tac gtc aac agg 192  
Ala Asp Phe Asp Asn Pro Cys Glu Leu Tyr Tyr Asp Tyr Val Asn Arg  
50 55 60  
ata gtg aag agt ctt tac ccc aac ccc act ggg atc ctc agg gac aac 240  
Ile Val Lys Ser Leu Tyr Pro Asn Pro Thr Gly Ile Leu Arg Asp Asn  
65 70 75 80  
ctg aat atc gcc ctc ggg cat gtg ttt gac tcc atg gac ttc ggc gat 288  
Leu Asn Ile Ala Leu Gly His Val Phe Asp Ser Met Asp Phe Gly Asp  
85 90 95  
tgc gag cag ttg ttc cct tat ggg cgc taggtccgtg tatatagatt 335  
Cys Glu Gln Leu Phe Pro Tyr Gly Arg  
100 105  
tgccgaggtt ctattaccct atccttctgc tgccctccgag cttcatttta ggctcgtcct 395  
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Gly Arg Asn Val Asn Gly Thr Asn Thr Phe Thr Pro Asp Pro Asn Ser
35          40          45
Ala Asp Phe Asp Asn Pro Cys Glu Leu Tyr Tyr Asp Tyr Val Asn Arg
50          55          60
Ile Val Lys Ser Leu Tyr Pro Asn Pro Thr Gly Ile Leu Arg Asp Asn
65          70          75          80
Leu Asn Ile Ala Leu Gly His Val Phe Asp Ser Met Asp Phe Gly Asp
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Cys Glu Gln Leu Phe Pro Tyr Gly Arg
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<210> 19

<211> 325

<212> PRT

<213> Coprinus radians DSM888

<400> 19

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

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Gly Asp Asn His Ser Phe Asn Gln Thr Leu Phe Asp Gln Phe Val Glu  
130 135 140

Tyr Ser Asn Thr Tyr Gly Gly Gly Phe Tyr Asn Gln Glu Val Ala Gly  
145 150 155 160

His Leu Arg Arg Arg Arg Ile Glu Gln Ser Ile Ala Thr Asn Pro Glu  
165 170 175

Phe Asp Phe Thr Ser Pro Arg Phe Phe Thr Ala Phe Ala Glu Ser Ser  
180 185 190

Phe Pro Tyr Ser Phe Phe Val Asp Gly Arg Ile Thr Glu Arg Pro Gly  
195 200 205

Gly Leu Ser Met Glu Asn Ala Thr Leu Phe Phe Arg Asp His Lys Met  
210 215 220

Pro Asp Asp Phe Trp Arg Ala Pro Glu Pro Thr Gly Gly Leu Asn Val  
225 230 235 240

Leu Asp Ile Tyr Arg Ala Ser Gly Ser Pro Pro Ala Gly Arg Asn Val  
245 250 255

Asn Gly Thr Asn Thr Phe Thr Pro Asp Pro Asn Ser Ala Asp Phe Asp  
260 265 270

Asn Pro Cys Glu Leu Tyr Tyr Asp Tyr Val Asn Arg Ile Val Lys Ser  
275 280 285

Leu Tyr Pro Asn Pro Thr Gly Ile Leu Arg Asp Asn Leu Asn Ile Ala  
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Leu Gly His Val Phe Asp Ser Met Asp Phe Gly Asp Cys Glu Gln Leu  
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Phe Pro Tyr Gly Arg  
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36

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<220>
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<400> 22
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<223> AP2-primer

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<210> 26
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<223> heel-specific primer

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<212> DNA

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

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<210> 28

<211> 14

<212> DNA

<213> Artificial sequence

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<223> Primer Cop5-For

<400> 28

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<210> 29

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<212> DNA

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<220>

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

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18

<210> 30

<211> 20

<212> DNA

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<221> misc\_feature  
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<210> 33  
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<210> 34  
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<400> 34  
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<210> 35  
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<210> 36  
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<210> 37  
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<212> DNA  
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<220>  
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<210> 39  
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<212> DNA  
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<220>  
<223> Specific primer 2Aap-Rev2

<400> 39  
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<222> (2)..(3)  
<223> Xaa can be any naturally occurring amino acid

<220>  
<221> VARIANT  
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<223> The amino acid may be Tyr or Phe.

<220>  
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<223> The amino acid may be Ala or Asn.

<220>  
<221> misc\_feature  
<222> (7)..(7)  
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<220>  
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<223> The amino acid may be Phe, His or Tyr.

<220>  
<221> VARIANT  
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<223> The amino acid may be Gly or Asn.

<220>  
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<222> (12)..(12)

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<223> Xaa can be any naturally occurring amino acid

<220>

<221> VARIANT

<222> (13)..(13)

<223> The amino acid may be Tyr or Phe.

<400> 40

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<210> 41

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<212> PRT

<213> Artificial sequence

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<223> Peroxygenase motif II

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<221> VARIANT

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<220>

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<222> (7)..(8)

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<221> misc\_feature

<222> (11)..(11)

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<220>

<221> VARIANT

<222> (12)..(12)

<223> The amino acid may be Glu or His.

<220>

<221> VARIANT

<222> (13)..(13)

<223> The amino acid may be Leu or Phe.

<400> 41

Gly Xaa Gly Xaa Xaa Asn Xaa Xaa Xaa Ala Xaa Xaa Xaa Arg  
1 5 10

<210> 42

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<211> 12  
 <212> PRT  
 <213> Artificial sequence  
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 <220>  
 <221> misc\_feature  
 <222> (2)..(3)  
 <223> Xaa can be any naturally occurring amino acid  
 <220>  
 <221> VARIANT  
 <222> (6)..(6)  
 <223> The amino acid may be Gln or Glu.  
 <220>  
 <221> VARIANT  
 <222> (7)..(7)  
 <223> The amino acid may be Asp, Glu or Gln.  
 <220>  
 <221> VARIANT  
 <222> (9)..(9)  
 <223> The amino acid may be Ile or Met.  
 <400> 42

Arg Xaa Xaa Arg Ile Xaa Xaa Ser Xaa Ala Thr Asn  
 1 5 10

<210> 43  
 <211> 10  
 <212> PRT  
 <213> Artificial sequence  
 <220>  
 <223> Peroxygenase motif IV  
 <220>  
 <221> VARIANT  
 <222> (2)..(2)  
 <223> The amino acid may be Ile or Met.  
 <220>  
 <221> VARIANT  
 <222> (6)..(6)  
 <223> The amino acid may be Pro or Gly.  
 <220>  
 <221> VARIANT  
 <222> (7)..(7)  
 <223> The amino acid may be Glu, Gln or Asn.  
 <220>  
 <221> VARIANT  
 <222> (8)..(8)  
 <223> The amino acid may be Phe or Met.  
 <220>  
 <221> VARIANT  
 <222> (9)..(9)  
 <223> The amino acid may be Ser, Asp or Asn.  
 <220>

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<221> VARIANT  
 <222> (10)..(10)  
 <223> The amino acid may be Phe or Leu.

<400> 43

Ser Xaa Ala Thr Asn Xaa Xaa Xaa Xaa Xaa  
 1 5 10

<210> 44  
 <211> 7  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Peroxygenase motif V

<220>  
 <221> VARIANT  
 <222> (2)..(2)  
 <223> The amino acid may be Pro, Asp or Lys.

<220>  
 <221> VARIANT  
 <222> (3)..(3)  
 <223> The amino acid may be Asp or Gly.

<220>  
 <221> VARIANT  
 <222> (5)..(5)  
 <223> The amino acid may be His, Phe or Trp.

<220>  
 <221> VARIANT  
 <222> (7)..(7)  
 <223> The amino acid may be Ala or Pro.

<400> 44

Pro Xaa Xaa Phe Xaa Arg Xaa  
 1 5

<210> 45  
 <211> 11  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Peroxygenase motif VI

<220>  
 <221> VARIANT  
 <222> (1)..(1)  
 <223> The amino acid may be Thr or Ile.

<220>  
 <221> misc\_feature  
 <222> (2)..(4)  
 <223> Xaa can be any naturally occurring amino acid

<220>  
 <221> VARIANT  
 <222> (10)..(10)  
 <223> The amino acid may be Thr or Lys.

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<220>

<221> VARIANT

<222> (11)..(11)

<223> The amino acid may be Gly or Val.

<400> 45

Xaa Xaa Xaa Xaa Leu Tyr Pro Asn Pro Xaa Xaa  
1 5 10

<210> 46

<211> 40

<212> DNA

<213> Artificial sequence

<220>

<223> Primer AaP1F

<400> 46

acacaactgg ggatccacca tgaaatactt cagcctgttc 40

<210> 47

<211> 36

<212> DNA

<213> Artificial sequence

<220>

<223> Primer AaP1R

<400> 47

agatctcgag aagcttaatc tcgcccgtac gggaat 36

<210> 48

<211> 41

<212> DNA

<213> Artificial sequence

<220>

<223> Primer AaP2F

<400> 48

acacaactgg ggatccacca tgaaatattt tcccctgttc c 41

<210> 49

<211> 36

<212> DNA

<213> Artificial sequence

<220>

<223> Primer AaP2R

<400> 49

agatctcgag aagcttaatc tcgcccgtat gggaag 36

<210> 50

<211> 39

<212> DNA

<213> Artificial sequence

<220>

<223> Forward Primer

<400> 50

acacaactgg ggatccacca tggctcgctt tactttcct 39

01 Sequence Listing NZ 11407.204-WO\_ST25 31-MAR-2008

<210> 51  
 <211> 38  
 <212> DNA  
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 <220>  
 <223> Reverse primer  
  
 <400> 51  
 agatctcgag aagcttactt tccataaggg aagatctg 38  
  
 <210> 52  
 <211> 39  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
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 <400> 52  
 acacaactgg ggatccacca tgatctcgac ctcgaagca 39  
  
 <210> 53  
 <211> 35  
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 <223> Reverse primer  
  
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 agatctcgag aagcttaatc actcttgccc caggg 35  
  
 <210> 54  
 <211> 38  
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 <400> 54  
 acacaactgg ggatccacca tggtttcgtg caagctcc 38  
  
 <210> 55  
 <211> 37  
 <212> DNA  
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 <223> Reverse primer  
  
 <400> 55  
 agatctcgag aagcttacag tgtaccatac ggtttca 37  
  
 <210> 56  
 <211> 38  
 <212> DNA  
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 <220>  
 <223> Forward primer

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<400> 56  
acacaactgg ggatccacca tgaacggtct gttcgcca 38

<210> 57  
<211> 36  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Reverse primer

<400> 57  
agatctcgag aagcttagtt acgtccgtag gggaac 36

<210> 58  
<211> 38  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Forward primer

<400> 58  
acacaactgg ggatccacca tgctcaaacc gcgtgttc 38

<210> 59  
<211> 37  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Reverse primer

<400> 59  
agatctcgag aagcttaatc gtgtccgtaa gggaaaa 37