

# SEQUENCE LISTING

<110> DSM IP Assets B.V.

<120> METHOD FOR REDUCING THE EXPRESSION OF A GENE IN A FILAMENTOUS FUNGAL CELL

<130> 25146WO

<160> 175

<170> PatentIn version 3.1

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<211> 3809

<212> DNA

<213> *Aspergillus niger*

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<213> Aspergillus niger

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Gln Pro Asn Leu Gln Leu His Arg Tyr Glu Val Arg Val Ser Arg Ser	
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<212> DNA

<213> *Aspergillus niger*

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 <213> *Aspergillus niger*

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Gly Pro Gln Pro Ala Gly Lys Tyr Ile Ser Val Ala Asp Phe Phe Leu							
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caa aat tac aat atc caa tgc gac cca aag atg cct gtt gta aac gtt	1440						
Gln Asn Tyr Asn Ile Gln Cys Asp Pro Lys Met Pro Val Val Asn Val							
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Gly Thr Arg Glu Asn Pro Ser Tyr Leu Pro Val Glu Val Cys Glu Val							
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Val Pro Gly Gln Gln Ala Asn Thr Lys Leu Thr Pro Asn Gln Thr Arg							
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aat atg ctt aac ttt gct gtg cga agc cca ccg cat aat gct cag tca	1584						
Asn Met Leu Asn Phe Ala Val Arg Ser Pro Pro His Asn Ala Gln Ser							
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Ile Ala Ala Gln Gly Thr Asp Val Leu Gly Leu Gly Ala Ser Pro Asn							

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ccc acc ctc gtg gat ttc ggt atc cag aat gat gtc cgg ttg atc acc			1680
Pro Thr Leu Val Asp Phe Gly Ile Gln Asn Asp Val Arg Leu Ile Thr			
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gta cct gga cga gta cta ccg gcg cct agc gtt ctg tac aga gac gag			1728
Val Pro Gly Arg Val Leu Pro Ala Pro Ser Val Leu Tyr Arg Asp Glu			
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aat agg ccg aat caa aag ccg atc aag ccc ttt tca gga agt tgg aac			1776
Asn Arg Pro Asn Gln Lys Pro Ile Lys Pro Phe Ser Gly Ser Trp Asn			
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Met Arg Ser Ile Arg Phe Ser Thr Ser Thr Lys Leu Pro Ser Trp Thr			
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tgg ctt tcc ctg gac tac gaa ggc gcg aga tat cca gcc atc aga cct			1872
Trp Leu Ser Leu Asp Tyr Glu Gly Ala Arg Tyr Pro Ala Ile Arg Pro			
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gaa gac ttg agc gcg aac ctg aaa ggc ttt acg gac aag ttg aac gag			1920
Glu Asp Leu Ser Ala Asn Leu Lys Gly Phe Thr Asp Lys Leu Asn Glu			
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Ile Gly Val Ile Ala Ser Pro Pro Lys Ser Gly Ala Ala Thr Leu Leu			
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acg agg agg gga tcc gac aat gag gtt aga gaa tac aat acg aag gcc			2016
Thr Arg Arg Gly Ser Asp Asn Glu Val Arg Glu Tyr Asn Thr Lys Ala			
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Lys Arg Ala Cys Asp Leu Thr His Gly Val Arg Asn Val Asn Val Val			
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Ala Asp Lys Phe Arg Lys Pro Asn Asn Asp Gln Tyr Trp Ala Asn Val			
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ggg ctc aaa ttc aac ctc aag ctg gga gga aac aac cag ctc att gat			2256
Gly Leu Lys Phe Asn Leu Lys Leu Gly Gly Asn Asn Gln Leu Ile Asp			
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Pro Lys Glu Leu Gly Leu Ile Gly Gln Asn Lys Thr Met Leu Val Gly			
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Val Asp Val Thr His Pro Ser Pro Gly Ser Ser Ala Ala Pro Ser			
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Val Ala Gly Met Val Ala Ser Ile Asp Ser Thr Leu Gly Gln Trp Pro			
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gcg gag ctt cgt atc caa aag ccc ccg gaa gaa atg gtc gcc gag ctt			2448
Ala Glu Leu Arg Ile Gln Lys Pro Arg Glu Glu Met Val Ala Glu Leu			
	805	810	815
gac gcc atg cta aag gct cat ctt cga cgc tgg gtt cgt aac cgc aag			2496
Asp Ala Met Leu Lys Ala His Leu Arg Arg Trp Val Arg Asn Arg Lys			
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acc tac ccg gag aat atc atc gta tac cgc gat ggt gta tcg gaa ggt			2544
Thr Tyr Pro Glu Asn Ile Ile Val Tyr Arg Asp Gly Val Ser Glu Gly			

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<212> PRT

<213> Aspergillus niger

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<212> DNA

<213> *Aspergillus niger*

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<213> Aspergillus niger

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

Ala	Arg	Ala	Gly	Asn	Ser	Ala	Asp	Thr	Met	Gly	Trp	Thr	Asp	Glu	Glu		
305					310					315					320		
aag	gca	tat	cta	tta	gat	atc	gtc	tcg	aaa	cta	ccc	atc	ccg	aat	att	1008	
Lys	Ala	Tyr	Leu	Leu	Asp	Ile	Val	Ser	Lys	Leu	Pro	Ile	Pro	Asn	Ile		
				325					330					335			
gat	ctc	acc	cac	tca	gac	cca	gat	aga	ata	cct	att	tcg	tcg	aag	ttc	1056	
Asp	Leu	Thr	His	Ser	Asp	Pro	Asp	Arg	Ile	Pro	Ile	Ser	Ser	Lys	Phe		
			340					345					350				
cgc	tcc	ctg	ctg	gaa	ttc	ttg	gat	aca	aag	ggc	gag	ccc	aac	ttc	tct	1104	
Arg	Ser	Leu	Leu	Glu	Phe	Leu	Asp	Thr	Lys	Gly	Glu	Pro	Asn	Phe	Ser		
		355					360					365					
ggc	ctg	ata	ttt	gct	aaa	cag	agg	gct	aca	gtg	agc	gtc	atg	gaa	aag	1152	
Gly	Leu	Ile	Phe	Ala	Lys	Gln	Arg	Ala	Thr	Val	Ser	Val	Met	Glu	Lys		
		370				375					380						
cta	ctg	tcc	att	cat	cct	gtg	acg	aaa	cat	cgt	ttt	cga	tgc	gct	tcc	1200	
Leu	Leu	Ser	Ile	His	Pro	Val	Thr	Lys	His	Arg	Phe	Arg	Cys	Ala	Ser		
385					390					395					400		
ttc	gtc	ggc	tgg	tcc	ggc	ggg	ggg	agc	aaa	gac	gtt	ttg	ggg	gag	ctc	1248	
Phe	Val	Gly	Trp	Ser	Gly	Gly	Gly	Ser	Lys	Asp	Val	Leu	Gly	Glu	Leu		
			405					410						415			
ctg	gac	gcc	cgt	atg	cag	cgt	gat	aca	ctg	agc	gag	ttc	cgg	acc	ggg	1296	
Leu	Asp	Ala	Arg	Met	Gln	Arg	Asp	Thr	Leu	Ser	Glu	Phe	Arg	Thr	Gly		
			420					425					430				
cag	aaa	aac	ctg	att	att	gcg	acg	gat	gtg	ctg	gag	gaa	ggc	att	gac	1344	
Gln	Lys	Asn	Leu	Ile	Ile	Ala	Thr	Asp	Val	Leu	Glu	Glu	Gly	Ile	Asp		
		435				440					445						
att	agc	gct	tgc	agt	gtg	gtg	gtg	tgc	ttt	gat	aag	ccg	ccg	aac	ttg	1392	
Ile	Ser	Ala	Cys	Ser	Val	Val	Val	Cys	Phe	Asp	Lys	Pro	Pro	Asn	Leu		
		450				455					460						
aaa	tcg	ttc	gtg	cag	aga	cga	ggg	cgc	gcg	cgc	cac	agg	caa	tca	acc	1440	
Lys	Ser	Phe	Val	Gln	Arg	Arg	Gly	Arg	Ala	Arg	His	Arg	Gln	Ser	Thr		
465					470					475					480		
tac	gct	ata	atg	ttt	gct	aca	gat	gat	gaa	tct	tct	gca	ctg	agc	aag	1488	
Tyr	Ala	Ile	Met	Phe	Ala	Thr	Asp	Asp	Glu	Ser	Ser	Ala	Leu	Ser	Lys		
				485					490					495			
tgg	gag	gac	ctg	gaa	cag	gca	atg	ata	gaa	gcg	tac	gag	gat	gac	gaa	1536	
Trp	Glu	Asp	Leu	Glu	Gln	Ala	Met	Ile	Glu	Ala	Tyr	Glu	Asp	Asp	Glu		
		500						505					510				
agg	cga	ctg	cgc	gag	gcg	tgg	gcc	ctg	gag	gcc	atc	aac	gaa	gaa	gtg	1584	
Arg	Arg	Leu	Arg	Glu	Ala	Trp	Ala	Leu	Glu	Ala	Ile	Asn	Glu	Glu	Val		
		515					520					525					
gtg	gaa	agg	ctt	gag	gtg	caa	tcg	acc	ggc	gct	gtc	ttg	acg	gct	gac	1632	
Val	Glu	Arg	Leu	Glu	Val	Gln	Ser	Thr	Gly	Ala	Val	Leu	Thr	Ala	Asp		
		530				535					540						
act	gcc	gtt	gca	cat	ctc	aac	cat	ttc	tgc	gca	gtc	ctg	ccg	cgt	caa	1680	
Thr	Ala	Val	Ala	His	Leu	Asn	His	Phe	Cys	Ala	Val	Leu	Pro	Arg	Gln		
545					550					555					560		
ccg	tat	gcg	agt	aat	gag	ccc	gag	ttc	tca	tac	gag	aag	gac	gat	gcg	1728	
Pro	Tyr	Ala	Ser	Asn	Glu	Pro	Glu	Phe	Ser	Tyr	Glu	Lys	Asp	Asp	Ala		
				565					570					575			
gac	cta	ttg	aga	ggc	act	gtc	act	cta	ccg	tcc	tgc	gtc	cat	ccc	gga	1776	
Asp	Leu	Leu	Arg	Gly	Thr	Val	Thr	Leu	Pro	Ser	Cys	Val	His	Pro	Gly		
			580					585					590				
gtc	cgt	cgt	att	cag	ggc	cag	cga	tgg	tgg	cag	acc	gag	cga	gca	gcc	1824	
Val	Arg	Arg	Ile	Gln	Gly	Gln	Arg	Trp	Trp	Gln	Thr	Glu	Arg	Ala	Ala		
		595					600					605					
cgg	aaa	gaa	gca	gcc	ttt	caa	gcc	tat	aaa	cgt	ctc	tac	gag	ttt	ggg	1872	

Arg	Lys	Glu	Ala	Ala	Phe	Gln	Ala	Tyr	Lys	Arg	Leu	Tyr	Glu	Phe	Gly	
610						615					620					
ctt	ctg	agc	gat	cat	cta	ctt	ccg	ttt	aag	agg	aat	tta	gag	ctc	aaa	1920
Leu	Leu	Ser	Asp	His	Leu	Leu	Pro	Phe	Lys	Arg	Asn	Leu	Glu	Leu	Lys	
625					630					635					640	
gag	acc	gat	ctt	acc	aat	tta	cca	gcc	ctt	gtg	gaa	gta	tcg	gag	cag	1968
Glu	Thr	Asp	Leu	Thr	Asn	Leu	Pro	Ala	Leu	Val	Glu	Val	Ser	Glu	Gln	
				645					650					655		
tac	gat	cct	tgg	gtc	gac	tgg	gct	tgt	tcc	tgg	tca	tct	ccc	gat	gtc	2016
Tyr	Asp	Pro	Trp	Val	Asp	Trp	Ala	Cys	Ser	Trp	Ser	Ser	Pro	Asp	Val	
			660					665					670			
cac	caa	acg	cga	att	gcc	ata	aag	cac	aac	ggg	gac	tca	cgc	atg	tgt	2064
His	Gln	Thr	Arg	Ile	Ala	Ile	Lys	His	Asn	Gly	Asp	Ser	Arg	Met	Cys	
			675				680					685				
atc	agg	ttg	act	agt	cca	acg	agc	ctg	cct	cca	ggt	gaa	cca	atg	acc	2112
Ile	Arg	Leu	Thr	Ser	Pro	Thr	Ser	Leu	Pro	Pro	Val	Glu	Pro	Met	Thr	
			690			695					700					
tta	ttc	tgg	gat	agc	gag	aca	ata	tat	acg	ttg	gat	ttc	gac	aaa	cca	2160
Leu	Phe	Trp	Asp	Ser	Glu	Thr	Ile	Tyr	Thr	Leu	Asp	Phe	Asp	Lys	Pro	
705					710					715					720	
aag	cga	atg	aaa	gaa	att	gcc	gct	gaa	agc	att	gaa	aat	atg	aga	ctg	2208
Lys	Arg	Met	Lys	Glu	Ile	Ala	Ala	Glu	Ser	Ile	Glu	Asn	Met	Arg	Leu	
			725					730						735		
gca	acc	gcg	cta	tac	ctc	cag	gct	gca	agc	tct	agg	caa	atg	agg	cct	2256
Ala	Thr	Ala	Leu	Tyr	Leu	Gln	Ala	Ala	Ser	Ser	Arg	Gln	Met	Arg	Pro	
			740				745						750			
gaa	caa	gat	ttt	gtg	act	ttg	ttt	gga	ccg	gac	ctt	act	gac	ctt	gag	2304
Glu	Gln	Asp	Phe	Val	Thr	Leu	Phe	Gly	Pro	Asp	Leu	Thr	Asp	Leu	Glu	
			755			760						765				
ttg	gca	gaa	tgg	ctc	aac	aag	cac	gca	gga	gac	gag	cct	gcg	cta	gag	2352
Leu	Ala	Glu	Trp	Leu	Asn	Lys	His	Ala	Gly	Asp	Glu	Pro	Ala	Leu	Glu	
			770			775					780					
gtc	tac	tct	cgc	aag	gac	ttt	cct	acg	gtc	atg	ggc	att	gtg	cgg	gac	2400
Val	Tyr	Ser	Arg	Lys	Asp	Phe	Pro	Thr	Val	Met	Gly	Ile	Val	Arg	Asp	
785					790					795					800	
cgt	tca	cgc	tac	aat	gag	ccc	atg	ctt	ttc	aaa	agg	tgg	gtt	gtg	tct	2448
Arg	Ser	Arg	Tyr	Asn	Glu	Pro	Met	Leu	Phe	Lys	Arg	Trp	Val	Val	Ser	
				805				810						815		
gga	caa	gat	gac	acg	ccc	ata	gtc	gaa	ctt	gaa	tgc	gac	gcc	gtc	ccc	2496
Gly	Gln	Asp	Asp	Thr	Pro	Ile	Val	Glu	Leu	Glu	Cys	Asp	Ala	Val	Pro	
			820					825					830			
aag	cga	cgg	aac	ctg	ttg	cat	cgg	caa	aca	tta	gct	gct	aag	cag	cct	2544
Lys	Arg	Arg	Asn	Leu	Leu	His	Arg	Gln	Thr	Leu	Ala	Ala	Lys	Gln	Pro	
			835				840						845			
gat	agt	gaa	aca	cct	gcc	atc	tcc	tcg	aag	ata	cgg	ctt	att	ctt	gcg	2592
Asp	Ser	Glu	Thr	Pro	Ala	Ile	Ser	Ser	Lys	Ile	Arg	Leu	Ile	Leu	Ala	
			850			855						860				
gaa	aat	tgc	acc	ata	gac	aaa	ctc	ccc	tac	gcc	gaa	acc	atc	ttc	ggc	2640
Glu	Asn	Cys	Thr	Ile	Asp	Lys	Leu	Pro	Tyr	Ala	Glu	Thr	Ile	Phe	Gly	
865					870					875					880	
cgc	ttc	ata	tcg	gtt	ata	ctg	gat	aga	cta	gaa	gct	aca	ttg	gtt	gca	2688
Arg	Phe	Ile	Ser	Val	Ile	Leu	Asp	Arg	Leu	Glu	Ala	Thr	Leu	Val	Ala	
				885				890						895		
act	aga	cta	tgt	gaa	acg	att	cta	cgc	gat	cta	gaa	ttt	tcc	agc	att	2736
Thr	Arg	Leu	Cys	Glu	Thr	Ile	Leu	Arg	Asp	Leu	Glu	Phe	Ser	Ser	Ile	
			900					905					910			
cgt	cat	att	atc	aca	gcc	atc	acc	gcg	cca	agt	gcg	caa	tca	ctt	acc	2784

Arg	His	Ile	Ile	Thr	Ala	Ile	Thr	Ala	Pro	Ser	Ala	Gln	Ser	Leu	Thr		
		915					920					925					
aac	tat	cag	cga	tac	gag	ttc	ttc	gga	gac	tcg	gtc	ctc	aaa	ttc	acc	2832	
Asn	Tyr	Gln	Arg	Tyr	Glu	Phe	Phe	Gly	Asp	Ser	Val	Leu	Lys	Phe	Thr		
	930					935					940						
gtc	tca	tgc	cag	ctt	ttc	ttc	cag	cac	ccc	aac	tgg	cac	gag	ggc	tac	2880	
Val	Ser	Cys	Gln	Leu	Phe	Phe	Gln	His	Pro	Asn	Trp	His	Glu	Gly	Tyr		
945					950					955					960		
ctt	tca	gaa	ggg	cga	gac	gag	atc	gtc	cag	aac	tcc	cgt	cta	gca	cga	2928	
Leu	Ser	Glu	Gly	Arg	Asp	Glu	Ile	Val	Gln	Asn	Ser	Arg	Leu	Ala	Arg		
				965					970					975			
gcc	gct	ctc	gac	gcc	ggc	ctc	gac	gcc	ttc	atc	atg	aac	aag	atg	ttc	2976	
Ala	Ala	Leu	Asp	Ala	Gly	Leu	Asp	Ala	Phe	Ile	Met	Asn	Lys	Met	Phe		
			980					985					990				
act	cct	cgc	aaa	tgg	agt	gcc	ccc	ctc	atc	tcc	gaa	aag	atc	agc	ctc	3024	
Thr	Pro	Arg	Lys	Trp	Ser	Ala	Pro	Leu	Ile	Ser	Glu	Lys	Ile	Ser	Leu		
	995					1000						1005					
acc	ccc	aag	cag	cga	aca	atg	tcc	acc	aaa	gtg	cta	gcc	gac	gta	gtc	3072	
Thr	Pro	Lys	Gln	Arg	Thr	Met	Ser	Thr	Lys	Val	Leu	Ala	Asp	Val	Val		
	1010					1015					1020						
gaa	gcc	cta	atc	gga	gca	tcc	tac	att	gac	gga	ggc	ttc	gcc	gca	gca	3120	
Glu	Ala	Leu	Ile	Gly	Ala	Ser	Tyr	Ile	Asp	Gly	Gly	Phe	Ala	Ala	Ala		
1025					1030					1035					1040		
cac	gca	tgc	att	cat	cgc	ttc	ctc	ccc	gaa	gtc	aac	ctc	gag	aac	atc	3168	
His	Ala	Cys	Ile	His	Arg	Phe	Leu	Pro	Glu	Val	Asn	Leu	Glu	Asn	Ile		
			1045					1050					1055				
gac	cgc	acc	aca	gcc	ccg	atg	ccc	aaa	gac	ggc	gtc	acg	aac	cac	acc	3216	
Asp	Arg	Thr	Thr	Ala	Pro	Met	Pro	Lys	Asp	Gly	Val	Thr	Asn	His	Thr		
		1060					1065					1070					
ctc	aac	gac	gac	cac	cta	atg	gcc	cac	atc	ggc	tac	acc	ttc	acc	aac	3264	
Leu	Asn	Asp	Asp	His	Leu	Met	Ala	His	Ile	Gly	Tyr	Thr	Phe	Thr	Asn		
		1075					1080					1085					
aaa	tcc	ctc	ctc	gtc	gaa	tcc	ctc	acc	cac	cca	tcc	tgc	caa	ttc	gac	3312	
Lys	Ser	Leu	Leu	Val	Glu	Ser	Leu	Thr	His	Pro	Ser	Cys	Gln	Phe	Asp		
	1090					1095					1100						
aca	acc	acc	caa	tcc	tac	caa	cgc	ctc	gaa	ttc	ctc	ggc	gac	gcc	gtc	3360	
Thr	Thr	Thr	Gln	Ser	Tyr	Gln	Arg	Leu	Glu	Phe	Leu	Gly	Asp	Ala	Val		
	1105				1110					1115					1120		
ctc	gac	atg	gcc	atc	atg	tcg	acc	ctt	ctc	tcc	cac	cca	cgc	gag	atc	3408	
Leu	Asp	Met	Ala	Ile	Met	Ser	Thr	Leu	Leu	Ser	His	Pro	Arg	Glu	Ile		
			1125					1130						1135			
ccc	caa	ggc	cta	atg	acc	aag	ata	aaa	cac	gcc	gta	gta	aac	gca	aac	3456	
Pro	Gln	Gly	Leu	Met	Thr	Lys	Ile	Lys	His	Ala	Val	Val	Asn	Ala	Asn		
		1140					1145					1150					
ctc	ctc	gcc	ttc	tgc	atg	gaa	ttc	gcc	ctc	acc	gaa	aaa	cgc	acc		3504	
Leu	Leu	Ala	Phe	Cys	Met	Glu	Phe	Ala	Leu	Thr	Glu	Lys	Arg	Thr			
		1155				1160					1165						
aac	gtg	caa	gtc	acc	ccc	acc	gga	acc	gta	acc	ctc	aac	ccc	tcc	aca	3552	
Asn	Val	Gln	Val	Thr	Pro	Thr	Gly	Thr	Val	Thr	Leu	Asn	Pro	Ser	Thr		
	1170					1175					1180						
gaa	cac	atc	gaa	ctc	tgg	cgt	ttc	atg	cga	tac	caa	ggc	gcc	cat	cta	3600	
Glu	His	Ile	Glu	Leu	Trp	Arg	Phe	Met	Arg	Tyr	Gln	Gly	Ala	His	Leu		
	1185				1190					1195					1200		
caa	aca	gcc	cgc	gac	ctc	gct	cta	tcc	cgc	cac	agc	tcc	ctc	cgc	gga	3648	
Gln	Thr	Ala	Arg	Asp	Leu	Ala	Leu	Ser	Arg	His	Ser	Ser	Leu	Arg	Gly		
				1205					1210					1215			
tcc	atc	atc	cac	ggc	ctt	aaa	cac	tcc	cca	tcc	tac	ccc	tgg	aaa	tcc	3696	

Ser	Ile	Ile	His	Gly	Leu	Lys	His	Ser	Pro	Ser	Tyr	Pro	Trp	Lys	Ser		
			1220					1225					1230				
ctt	tcc	cag	ctc	aac	gcc	gat	aaa	ttc	ttc	tcc	gat	atc	att	gaa	agt	3744	
Leu	Ser	Gln	Leu	Asn	Ala	Asp	Lys	Phe	Phe	Ser	Asp	Ile	Ile	Glu	Ser		
		1235					1240					1245					
atc	ctc	ggc	gct	atc	ttc	atc	gat	tcg	cat	ggg	aat	ctg	gcg	gaa	tgt	3792	
Ile	Leu	Gly	Ala	Ile	Phe	Ile	Asp	Ser	His	Gly	Asn	Leu	Ala	Glu	Cys		
		1250					1255				1260						
gag	aaa	ttc	ctt	gaa	cgg	ctc	ggg	ctt	ttg	agg	tac	ttg	aga	cgg	att	3840	
Glu	Lys	Phe	Leu	Glu	Arg	Leu	Gly	Leu	Leu	Arg	Tyr	Leu	Arg	Arg	Ile		
					1270					1275					1280		
ctt	aag	gat	gag	gtg	gat	gtt	atg	cat	cca	cgg	aat	atc	gcg	cag	cag	3888	
Leu	Lys	Asp	Glu	Val	Asp	Val	Met	His	Pro	Arg	Asn	Ile	Ala	Gln	Gln		
				1285					1290					1295			
atg	gcg	aag	ggg	gag	att	cgg	ttt	gag	gtc	ctc	cgc	gtg	ccg	aat	gaa	3936	
Met	Ala	Lys	Gly	Glu	Ile	Arg	Phe	Glu	Val	Leu	Arg	Val	Pro	Asn	Glu		
			1300					1305				1310					
ggg	ggg	ggg	ggc	ggg	gag	gat	gat	gga	gcg	acg	tat	cgg	tgt	acg	gtg	3984	
Gly	Gly	Gly	Gly	Gly	Glu	Asp	Asp	Gly	Ala	Thr	Tyr	Arg	Cys	Thr	Val		
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<400> 12

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Lys Arg Met Lys Glu	Ile Ala Ala Glu Ser	Ile Glu Asn Met Arg Leu
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<213> *Aspergillus niger*

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agcctagcgg	cagttccccc	tgaagtgtac	cactttcttt	ctgggtccgtc	gctcgggctc	6300
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caactcgact	ggcggaatag	acgacgacgg	agctttatta	tgaaccctta	gattactttc	6420
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tgaaccacc	cgtttaatcc	taccatcccg	aagccgacac	cgcgccatt	tcccgtaaac	6540
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<212> DNA

<213> *Aspergillus niger*

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48

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

305	gtg gcc agg cgt cca	310	gtg gag aga gta	315	tgg tcc ttc aac aag ttg	320	gag	1008
Val Ala Arg Arg	Pro Val Glu Arg	Val Trp Ser Phe Asn Lys	Leu Glu					
	325	330	335					
caa ccg ttc gcc act agc ctg tat aag cac ctt gaa gat cgt ttt gga	1056							
Gln Pro Phe Ala Thr Ser Leu Tyr Lys His Leu Glu Asp Arg Phe Gly								
	340	345	350					
gac atg gcg tgc ctg gag ggt ata ttc aga ttt gct tgg cag gcc agc	1104							
Asp Met Ala Cys Leu Glu Gly Ile Phe Arg Phe Ala Trp Gln Ala Ser								
	355	360	365					
tct gag cta ggc cga tgg tgt tca gat cga gca tgg gct cgt gct tta	1152							
Ser Glu Leu Gly Arg Trp Cys Ser Asp Arg Ala Trp Ala Arg Ala Leu								
	370	375	380					
gca gat gat gtg ttg ccc aaa ctc gaa ggt agt gtt cgc aag act gca	1200							
Ala Asp Asp Val Leu Pro Lys Leu Glu Gly Ser Val Arg Lys Thr Ala								
	385	390	395					
aac tca gaa aca tca tcc aat gtg ccc gaa agt gcc tat aag gag atc	1248							
Asn Ser Glu Thr Ser Ser Asn Val Pro Glu Ser Ala Tyr Lys Glu Ile								
	405	410	415					
ttg cgg ata acg gaa gct agt gag att gtg aag agc tat gct ttc agc	1296							
Leu Arg Ile Thr Glu Ala Ser Glu Ile Val Lys Ser Tyr Ala Phe Ser								
	420	425	430					
agt cct gag act ttt ggc caa ctt agc ccc aaa gtg caa gtc ctt cgt	1344							
Ser Pro Glu Thr Phe Gly Gln Leu Ser Pro Lys Val Gln Val Leu Arg								
	435	440	445					
gaa gag ctt gcc cgc tac ttt gga cga cag acg gaa aca aaa tgc att	1392							
Glu Glu Leu Ala Arg Tyr Phe Gly Arg Gln Thr Glu Thr Lys Cys Ile								
	450	455	460					
gtc ttt acg cag aag cgc tac aca gct ttg att ctg gct gaa ctt ttt	1440							
Val Phe Thr Gln Lys Arg Tyr Thr Ala Leu Ile Leu Ala Glu Leu Phe								
	465	470	475					
caa acc ctg aat att cct ttt ctt cgg cct ggt gtg ctt att ggt gtc	1488							
Gln Thr Leu Asn Ile Pro Phe Leu Arg Pro Gly Val Leu Ile Gly Val								
	485	490	495					
cgg tct ggg gat tta gca gga atg aac ata acg ttt cgt cag caa ttt	1536							
Arg Ser Gly Asp Leu Ala Gly Met Asn Ile Thr Phe Arg Gln Gln Phe								
	500	505	510					
att tcc ttg gtc aag ttc aga acc ggt gag atc aat tgc ttg ttt gct	1584							
Ile Ser Leu Val Lys Phe Arg Thr Gly Glu Ile Asn Cys Leu Phe Ala								
	515	520	525					
aca tct gtc gct gaa gag gga ctt gat att cct gac tgt aat ctg gtc	1632							
Thr Ser Val Ala Glu Glu Gly Leu Asp Ile Pro Asp Cys Asn Leu Val								
	530	535	540					
gtt agg ttt gac ttg tat caa acg ttg atc cag tac gtg caa agc cgt	1680							
Val Arg Phe Asp Leu Tyr Gln Thr Leu Ile Gln Tyr Val Gln Ser Arg								
	545	550	555					
ggg cgt gcg aga cat ttc aat tca acg tat gcg agt atg gtc gaa aga	1728							
Gly Arg Ala Arg His Phe Asn Ser Thr Tyr Ala Ser Met Val Glu Arg								
	565	570	575					
ggg aat ttg gag cat gag cag agg cta ctt gag gtc caa gat gct gaa	1776							
Gly Asn Leu Glu His Glu Gln Arg Leu Leu Glu Val Gln Asp Ala Glu								
	580	585	590					
aaa atg atg caa agc ttt tgc aga act ctt ccc gaa gat agg tta cta	1824							
Lys Met Met Gln Ser Phe Cys Arg Thr Leu Pro Glu Asp Arg Leu Leu								
	595	600	605					
tat ggg ttt gac cat gac ctt gat aca gtg ttg cag aaa gac gag ggc	1872							
Tyr Gly Phe Asp His Asp Leu Asp Thr Val Leu Gln Lys Asp Glu Gly								

610	aac agg acc ttt aga atc	615	aaa tct aca ggt gct	620	aag cta acc tat cat	1920
	Asn Arg Thr Phe Arg Ile		Lys Ser Thr Gly Ala		Lys Leu Thr Tyr His	
625		630		635		640
	tca gca acc gcg ata ctt		gct cgc tac gct agt		tct ttg caa tac gaa	1968
	Ser Ala Thr Ala Ile Leu		Ala Arg Tyr Ala Ser		Ser Leu Gln Tyr Glu	
		645		650		655
	aag gaa ttt tcc gcc caa		gta aca tac gtg gtc		ctt cct atc aac ggt	2016
	Lys Glu Phe Ser Ala Gln		Val Thr Val Val Leu		Pro Ile Asn Gly	
		660		665		670
	gcc ttt gtc tgc gaa gta		att ctg cct gaa aaa		tca cct atc cgg ggt	2064
	Ala Phe Val Cys Glu Val		Ile Leu Pro Glu Lys		Ser Pro Ile Arg Gly	
		675		680		685
	ctt aca gga agc cca gca		atg aag aag tcc att		gcg aag cgg tct gcg	2112
	Leu Thr Gly Ser Pro Ala		Met Lys Lys Ser Ile		Ala Lys Arg Ser Ala	
		690		695		700
	gct ttt gat act tgt ctc		ttg ctt cga aaa aac		aag ttg ctc gat gac	2160
	Ala Phe Asp Thr Cys Leu		Leu Leu Leu Arg Lys		Asn Lys Leu Leu Asp	
		705		710		715
	cat ttc aat tcg ata tat		cat cgc cgc ctt ccg		gca atg cgt aat gcg	2208
	His Phe Asn Ser Ile Tyr		His Arg Arg Leu Pro		Ala Met Arg Asn Ala	
		725		730		735
	aaa ctt gca ata aca tct		aag cgc acc agc cag		tat gac atg ata tcg	2256
	Lys Leu Ala Ile Thr Ser		Lys Arg Thr Ser Gln		Tyr Asp Met Ile Ser	
		740		745		750
	aag ccg tcg ttg tgg ggc		cgg aaa caa gga atg		cca cca aag gag ctt	2304
	Lys Pro Ser Leu Trp Gly		Arg Lys Gln Gly Met		Pro Pro Lys Glu Leu	
		755		760		765
	cat ggc act ttt atc acg		ttc ttg cca tcg atg		caa cta tcg cac gag	2352
	His Gly Thr Phe Ile Thr		Phe Leu Pro Ser Met		Gln Leu Ser His Glu	
		770		775		780
	ccc gca cct ttg cta cta		ttc aca cga gag aga		cta cca cac ttt ccg	2400
	Pro Ala Pro Leu Leu Leu		Phe Thr Arg Glu Arg		Leu Pro His Phe Pro	
		785		790		795
	gag ttt ccc atc ttc ctc		gat gat gat gta gag		act aca ata atc acg	2448
	Glu Phe Pro Ile Phe Leu		Asp Asp Asp Val Glu		Thr Thr Ile Ile Thr	
		805		810		815
	act cct ttg gag aaa cag		cta tta ctt tca gaa		aaa gag gtg gac gcc	2496
	Thr Pro Leu Glu Lys Gln		Leu Leu Leu Ser Glu		Lys Glu Val Asp Ala	
		820		825		830
	ctc aca gtg ttt act ctt		cgt gtt ttt cgt gac		gtc ttc cac aag acc	2544
	Leu Thr Val Phe Thr Leu		Arg Val Phe Arg Asp		Val Phe His Lys Thr	
		835		840		845
	tac gac aaa gag ccc gaa		aag atg gct tac tgg		ctg gcc ccg gca aag	2592
	Tyr Asp Lys Glu Pro Glu		Lys Met Ala Tyr Trp		Leu Ala Pro Ala Lys	
		850		855		860
	gtt caa agc tca tac ctc		ccg tca tat gac cca		agg cag att ctt gac	2640
	Val Gln Ser Ser Tyr Leu		Pro Pro Ser Tyr Asp		Pro Arg Gln Ile Leu	
		865		870		875
	tgg gag agc ctc acc tat		gtg cgc gac aac gat		agt att cca ttt tct	2688
	Trp Glu Ser Leu Thr Tyr		Val Arg Asp Asn Asp		Ser Ile Pro Phe Ser	
		885		890		895
	acg aat gca gac cca gag		agc tgg gta gat cta		ttc gtg ttc gat gcc	2736
	Thr Asn Ala Asp Pro Glu		Ser Trp Val Asp Leu		Phe Val Phe Asp Ala	
		900		905		910
	tgg gat gga cga tgc cga		ttt ttc aca gta ggg		gtc gag cat agt ctg	2784
	Trp Asp Gly Arg Cys Arg		Phe Phe Thr Val Gly		Val Glu His Ser Leu	

	915		920		925	
act	ccc tct tct cct cca cca cca ttt gta gcc cgg cgc aga cac atg	2832				
Thr	Pro Ser Ser Pro Pro Pro Pro Phe Val Ala Arg Arg Arg His Met					
	930	935	940			
aac	gat gtc atg aat tac tgt ctg agt ctc tca aag aac tcc agg gct	2880				
Asn	Asp Val Met Asn Tyr Cys Leu Ser Leu Ser Lys Asn Ser Arg Ala					
	945	950	955	960		
aag	ttt ttg tcg acc tgt cac tgg gac caa cct gtc cta aga gca gag	2928				
Lys	Phe Leu Ser Thr Cys His Trp Asp Gln Pro Val Leu Arg Ala Glu					
	965	970	975			
ctc	gta cga ctc cgc aga aac ctt tta gac aaa atg aca gac acc gag	2976				
Leu	Val Arg Leu Arg Arg Asn Leu Leu Asp Lys Met Thr Asp Thr Glu					
	980	985	990			
aga	gat gtg gag aca agg tgc ttc atc tgt att gag cct ttg aaa gta	3024				
Arg	Asp Val Glu Thr Arg Cys Phe Ile Cys Ile Glu Pro Leu Lys Val					
	995	1000	1005			
tct	gct atc cct gca tct aca gca ttc tcc tgt ctc gca ttt cct gca	3072				
Ser	Ala Ile Pro Ala Ser Thr Ala Phe Ser Cys Leu Ala Phe Pro Ala					
	1010	1015	1020			
att	atc tct aga att gat gcg tac ctt att tct ctt caa ggc tgc gag	3120				
Ile	Ile Ser Arg Ile Asp Ala Tyr Leu Ile Ser Leu Gln Gly Cys Glu					
	1025	1030	1035	1040		
agc	ctg aac ttt acc gtc aag ctg gat ctt gcc ctt gaa gca ttc acg	3168				
Ser	Leu Asn Phe Thr Val Lys Leu Asp Leu Ala Leu Glu Ala Phe Thr					
	1045	1050	1055			
aaa	gac tcc gat aat acc gac gag cac cgg gcc cag cag atc cat gtc	3216				
Lys	Asp Ser Asp Asn Thr Asp Glu His Arg Ala Gln Gln Ile His Val					
	1060	1065	1070			
caa	cga gga atg gga aga aac tac gag cgt cta gag ttt ctg ggg gac	3264				
Gln	Arg Gly Met Gly Arg Asn Tyr Glu Arg Leu Glu Phe Leu Gly Asp					
	1075	1080	1085			
tgc	ttc ctg aag atg gct acc tcg att gct ctc ttc acg caa aac cca	3312				
Cys	Phe Leu Lys Met Ala Thr Ser Ile Ala Leu Phe Thr Gln Asn Pro					
	1090	1095	1100			
gat	gac gat gag ttt gac tac cac gtg aac cgg atg tgt cta atc tgc	3360				
Asp	Asp Asp Glu Phe Asp Tyr His Val Asn Arg Met Cys Leu Ile Cys					
	1105	1110	1115	1120		
aac	aag aac ctc ttc aac gca gct gtg gat aag gag atc tat aag tat	3408				
Asn	Lys Asn Leu Phe Asn Ala Ala Val Asp Lys Glu Ile Tyr Lys Tyr					
	1125	1130	1135			
atc	cgt agt cga gga ttt tca aga cat aca tgg tat cca gag ggc ctg	3456				
Ile	Arg Ser Arg Gly Phe Ser Arg His Thr Trp Tyr Pro Glu Gly Leu					
	1140	1145	1150			
aag	ttg cta caa ggc aaa gat cac agt aga aag gca acc aca gag agc	3504				
Lys	Leu Leu Gln Gly Lys Asp His Ser Arg Lys Ala Thr Thr Glu Ser					
	1155	1160	1165			
aaa	cat gcc ctc gca gag aaa aca att gcc gat gtt tgc gaa gct tta	3552				
Lys	His Ala Leu Ala Glu Lys Thr Ile Ala Asp Val Cys Glu Ala Leu					
	1170	1175	1180			
ata	ggg gcg gct ttg ctt tcc ggt ggt cct gac cat cga ttt gac atg	3600				
Ile	Gly Ala Ala Leu Leu Ser Gly Gly Pro Asp His Arg Phe Asp Met					
	1185	1190	1195	1200		
gct	gtc aaa gca gtg act act ctg gtg aat agt ccc agc cac aaa gcc	3648				
Ala	Val Lys Ala Val Thr Thr Leu Val Asn Ser Pro Ser His Lys Ala					
	1205	1210	1215			
gag	cga tgg aag gac tac att tct ttc tat aca ata ccg aaa tat cag	3696				
Glu	Arg Trp Lys Asp Tyr Ile Ser Phe Tyr Thr Ile Pro Lys Tyr Gln					

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cgg cga gca gca gat ggt gcc gag cta tac ctt tct cga aaa att gaa			3744
Arg Arg Ala Ala Asp Gly Ala Glu Leu Tyr Leu Ser Arg Lys Ile Glu			
1235	1240	1245	
gag aag ctg agc tac cgc ttc cgg tac cca acg ctt ctg gga tca gct			3792
Glu Lys Leu Ser Tyr Arg Phe Arg Tyr Pro Thr Leu Leu Gly Ser Ala			
1250	1255	1260	
ttc act cat cct tcg tat cca tcc gca tgg gcc aaa gtg ccc tgc tat			3840
Phe Thr His Pro Ser Tyr Pro Ser Ala Trp Ala Lys Val Pro Cys Tyr			
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cag cgc ttg gag ttt ctt ggt gac tca ctg att gac atg gtg tgc gtg			3888
Gln Arg Leu Glu Phe Leu Gly Asp Ser Leu Ile Asp Met Val Cys Val			
1285	1290	1295	
gaa gac ttg ttt gcc aga ttc cct gac cga gac ccc cag tgg ctc aca			3936
Glu Asp Leu Phe Ala Arg Phe Pro Asp Arg Asp Pro Gln Trp Leu Thr			
1300	1305	1310	
gaa cac aaa atg gcc atg gta tcc aac aag ttt ctg ggt gcg tta gct			3984
Glu His Lys Met Ala Met Val Ser Asn Lys Phe Leu Gly Ala Leu Ala			
1315	1320	1325	
gtg aag ctg ggg ctc cat acg cat cta aaa tat ttt agc gct ccg ttg			4032
Val Lys Leu Gly Leu His Thr His Leu Lys Tyr Phe Ser Ala Pro Leu			
1330	1335	1340	
cag tct cag att act cag tac gcc gaa gag atc cag aca gcg gag ggc			4080
Gln Ser Gln Ile Thr Gln Tyr Ala Glu Glu Ile Gln Thr Ala Glu Gly			
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gaa agt gag ggc gcg gtg gac tat tgg acc gtg act aaa gac cct cct			4128
Glu Ser Glu Gly Ala Val Asp Tyr Trp Thr Val Thr Lys Asp Pro Pro			
1365	1370	1375	
aag tgc ttg ccc gac atg gtt gaa gcg tat gta ggg gca gtt ttt gtt			4176
Lys Cys Leu Pro Asp Met Val Glu Ala Tyr Val Gly Ala Val Phe Val			
1380	1385	1390	
gac tct gat ttt aac ttc gag gta att gag aga ttc ttc cgg gac tac			4224
Asp Ser Asp Phe Asn Phe Glu Val Ile Glu Arg Phe Phe Arg Asp Tyr			
1395	1400	1405	
att aaa ccc ttt ttc gag gat atg gca att tat gac acc ttc gcg aat			4272
Ile Lys Pro Phe Phe Glu Asp Met Ala Ile Tyr Asp Thr Phe Ala Asn			
1410	1415	1420	
aag cat ccg acg act ttc ttg cac aac cga ctg act aat gag ttt ggc			4320
Lys His Pro Thr Thr Phe Leu His Asn Arg Leu Thr Asn Glu Phe Gly			
1425	1430	1435	1440
tgc gtg aat tat tgt cta aaa gct ggt gag atg ccc agt atc gat ggg			4368
Cys Val Asn Tyr Cys Leu Lys Ala Gly Glu Met Pro Ser Ile Asp Gly			
1445	1450	1455	
gcc ccg gct ggg gtt tta gcg gcc gtg atc gtg cat gat gtt gtc atc			4416
Ala Pro Ala Gly Val Leu Ala Ala Val Ile Val His Asp Val Val Ile			
1460	1465	1470	
gcc gaa ggt acg gca aca tct ggt cgc tat gct aaa gtc aag gcc agt			4464
Ala Glu Gly Thr Ala Thr Ser Gly Arg Tyr Ala Lys Val Lys Ala Ser			
1475	1480	1485	
gag aag gcg ctg gca gtg cta gac gaa ata tcg tct gca gaa ttc cag			4512
Glu Lys Ala Leu Ala Val Leu Asp Glu Ile Ser Ser Ala Glu Phe Gln			
1490	1495	1500	
agg aaa ttt cgc tgt gat tgt cga gag tca gga gat tcg gca aga ctc			4560
Arg Lys Phe Arg Cys Asp Cys Arg Glu Ser Gly Asp Ser Ala Arg Leu			
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Asp Ile Gly Thr Ala Ile			



<210> 15  
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 <212> PRT  
 <213> *Aspergillus niger*

<400> 15

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			20					25					30		
Thr	Met	Thr	Glu	Asp	Leu	Gln	Glu	Asp	Asp	Gly	Ser	Ser	Asp	Glu	Ser
		35					40					45			
Asp	Asn	Asp	Glu	Arg	Glu	Asp	His	Ser	Lys	Thr	Gly	Val	Ser	Gln	Gln
	50					55					60				
Arg	Ile	Thr	Gln	Asn	Ala	Lys	Phe	Lys	Ala	Leu	Leu	Ala	Gln	Arg	Ala
65					70				75						80
Asp	Thr	Gly	Pro	Ile	His	Asp	Val	Ser	Val	Thr	His	Asp	Leu	Pro	Asp
				85				90						95	
Ala	Gln	Leu	Ser	Thr	Ala	His	Leu	Val	Ala	Lys	Gln	Asp	Leu	Gly	Ile
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Gly	Thr	Leu	Asp	Pro	Arg	Glu	Tyr	Gln	Leu	Glu	Leu	Phe	Glu	Arg	Ala
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Lys	Val	Gln	Asn	Thr	Ile	Ala	Val	Leu	Asp	Thr	Gly	Ser	Gly	Lys	Thr
	130					135					140				
Leu	Ile	Ala	Val	Leu	Leu	Lys	His	Thr	Leu	Glu	Lys	Glu	Leu	Asn	
145					150				155						160
Asp	Arg	Met	Glu	Gly	Lys	Pro	His	Arg	Ile	Ala	Phe	Phe	Leu	Val	Asp
				165				170						175	
Ser	Val	Thr	Leu	Ala	Tyr	Gln	Gln	Ala	Ala	Val	Leu	Arg	Asn	Asn	Leu
			180					185					190		
Asp	Gln	Ser	Val	Gly	His	Phe	Phe	Gly	Ala	Met	Gly	Thr	Asp	Leu	Trp
		195					200					205			
Ser	Lys	Ser	Val	Trp	Asp	Gln	His	Phe	Gln	Lys	Asn	Met	Val	Ile	Val
	210					215					220				
Cys	Thr	Ala	Glu	Ile	Leu	Asn	Gln	Cys	Leu	Leu	Asn	Ser	Tyr	Ile	Lys
225					230					235					240
Met	Ser	Gln	Ile	Asn	Ile	Leu	Ile	Phe	Asp	Glu	Ala	His	His	Thr	Lys
				245				250						255	
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Ser Glu Asp Ala Glu Asn Pro Leu Ala Met Ser Arg His Ile Asn His	
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gac cag cac cgc tac cgc caa aca atg atg tac aca gcc acc atg ccc	1776
Asp Gln His Arg Tyr Arg Gln Thr Met Met Tyr Thr Ala Thr Met Pro	
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acc gcc gtc gaa cgc atc gcc cga aaa tac ctc cgc cgt ccg gca atc	1824
Thr Ala Val Glu Arg Ile Ala Arg Lys Tyr Leu Arg Arg Pro Ala Ile	
595 600 605	
gtc acg atc ggc tcc gcc ggc gaa gcc gtc gac acc gtc gag cag cgc	1872
Val Thr Ile Gly Ser Ala Gly Glu Ala Val Asp Thr Val Glu Gln Arg	
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Val Glu Met Ile Ala Gly Glu Asp Lys Arg Lys Lys Arg Leu Gly Asp	
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Ile Leu Ser Ser Gly Glu Phe Arg Ala Pro Ile Ile Val Phe Val Asn	
645 650 655	

atc aag cgc aac tgc gat gcc atc gct cgc gaa atc aaa cag tgg gga	2016
Ile Lys Arg Asn Cys Asp Ala Ile Ala Arg Glu Ile Lys Gln Trp Gly	
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Phe Ser Ser Val Thr Leu His Gly Ser Lys Thr Gln Asp Gln Arg Glu	
675 680 685	
gcc gcc ctc gcg tcc gtt agg aat gga acc aca gat gtc ctg gta gct	2112
Ala Ala Leu Ala Ser Val Arg Asn Gly Thr Thr Asp Val Leu Val Ala	
690 695 700	
acg gat ctg gcg ggt cgt ggt atc gat gtg ccg gat gtt agt ctc gtc	2160
Thr Asp Leu Ala Gly Arg Gly Ile Asp Val Pro Asp Val Ser Leu Val	
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Val Asn Phe Asn Met Ala Thr Ser Ile Glu Ser Tyr Thr His Arg Ile	
725 730 735	
ggg cgt acc ggt cgt gcc ggg aag agt ggt gtg gct att act ttc ttg	2256
Gly Arg Thr Gly Arg Ala Gly Lys Ser Gly Val Ala Ile Thr Phe Leu	
740 745 750	
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Gly Asn Glu Asp Ala Asp Val Met Tyr Asp Leu Lys Gln Met Leu Met	
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Lys Ser Pro Ile Ser Arg Val Pro Glu Glu Leu Arg Lys His Glu Ala	
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Ala Gln Ser Lys Pro Thr Arg Gly Phe Ser Ser Lys Lys Asn Asn Glu	
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<210> 18

<211> 810

<212> PRT

<213> Aspergillus niger

<400> 18

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Pro Lys Lys Lys Lys Val Gly Trp Gly Thr Lys Arg Pro Ala Pro Thr	
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Ser Glu His Ala Ser Asn Gly Val Asp Arg Ser Ala Thr His Ser Pro	
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Ser Val Ser Ser Glu Gly Pro Asn Gly Asp Ala Arg Ser Ile Pro Thr	



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Ala	Met	Arg	His	Ser	Gln	Ser	His	Asn	Lys	Asn	Tyr	Asp	Leu	Ala	Pro
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Met	Glu	Arg	Arg	Arg	Arg	Glu	Glu	Ser	Thr	Arg	Asn	Gln	Leu	Asp	Lys
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His	Trp	Ser	Glu	Lys	Lys	Leu	Glu	His	Met	Arg	Glu	Arg	Asp	Trp	Arg
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 Phe Ser Ser Val Thr Leu His Gly Ser Lys Thr Gln Asp Gln Arg Glu  
 675 680 685  
 Ala Ala Leu Ala Ser Val Arg Asn Gly Thr Thr Asp Val Leu Val Ala  
 690 695 700  
 Thr Asp Leu Ala Gly Arg Gly Ile Asp Val Pro Asp Val Ser Leu Val  
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 Gly Arg Thr Gly Arg Ala Gly Lys Ser Gly Val Ala Ile Thr Phe Leu  
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 Gly Asn Glu Asp Ala Asp Val Met Tyr Asp Leu Lys Gln Met Leu Met  
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<210> 19

<211> 2802

<212> DNA

<213> *Aspergillus niger*

<400> 19

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<211> 600

<212> DNA

<213> *Aspergillus niger*

<220>

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<400> 20

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Phe	Val	Ile	Pro	Ile	Ile	Gly	Met	Met	Ala	Tyr	Phe	Val	His	Gly	Tyr	
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ctc	aat	gca	aac	cag	att	acc	cct	gcc	tac	att	ctc	gtc	ctc	ttc	atc	144
Leu	Asn	Ala	Asn	Gln	Ile	Thr	Pro	Ala	Tyr	Ile	Leu	Val	Leu	Phe	Ile	
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Phe	Phe	Gly	Ala	Phe	Ile	Ala	Gly	Val	Tyr	Glu	Leu	Arg	Phe	Ile	Ala	
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ggg	gcc	aat	tgc	tct	cat	tgg	gat	gga	ggt	tcg	gtg	tat	att	tcg	ctg	336
Gly	Ala	Asn	Cys	Ser	His	Trp	Asp	Gly	Gly	Ser	Val	Tyr	Ile	Ser	Leu	
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His Ile Asp Lys Thr Cys Ala Met Leu Lys Ala Ser Phe Ala Leu Gly	
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ata att gaa gtc gtt ttc ttc ttc tgg aca gct atc ctg gct ctc gcc	480
Ile Ile Glu Val Val Phe Phe Phe Trp Thr Ala Ile Leu Ala Leu Ala	
145 150 155 160	
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Ile Tyr Lys Arg Pro Glu Val Val Val Lys Glu Thr Thr Val Arg Arg	
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Arg Arg Gln Gln Tyr Val Val	
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 <213> Aspergillus niger

<400> 21

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Val Ser Val Ile Ala Ala Phe Trp Cys Leu Asp Thr Leu Ile Arg Phe	
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Ser Thr Thr Lys Arg Ser Ala Met Phe Val Ala Phe Ile Asp Leu Leu	
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Phe Phe Gly Ala Phe Ile Ala Gly Val Tyr Glu Leu Arg Phe Ile Ala	
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Gly Ala Asn Cys Ser His Trp Asp Gly Gly Ser Val Tyr Ile Ser Leu	
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Gly Pro Phe Gly Tyr Tyr Gly Tyr Arg Thr Asp Asn Pro Leu Ser Phe	
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Ile Ile Glu Val Val Phe Phe Trp Thr Ala Ile Leu Ala Leu Ala	
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<210> 22  
 <211> 6651  
 <212> DNA

<213> *Aspergillus niger*

<400> 22

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<211> 802

<212> DNA

<213> *Aspergillus niger*

<220>

<221> CDS

<222> (1)..(802)

<400> 26

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aac	ccc	cgc	gac	acg	aag	caa	aac	ctc	cag	gca	atc	acc	tcc	atc	gtt	96
Asn	Pro	Arg	Asp	Thr	Lys	Gln	Asn	Leu	Gln	Ala	Ile	Thr	Ser	Ile	Val	
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ccc	gac	ctg	acc	gaa	gac	ctg	ctc	tcc	tct	gtc	gat	cag	cct	cta	gaa	144
Pro	Asp	Leu	Thr	Glu	Asp	Leu	Leu	Ser	Ser	Val	Asp	Gln	Pro	Leu	Glu	
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atc	cgc	aag	tgc	ccc	aag	aca	gac	cgc	gac	tac	ctc	ctc	tgt	gac	tac	192
Ile	Arg	Lys	Cys	Pro	Lys	Thr	Asp	Arg	Asp	Tyr	Leu	Leu	Cys	Asp	Tyr	
	50					55				60						
aac	cgc	gac	gga	gat	agc	tat	cgg	tcg	ccc	tgg	agc	aat	gaa	ttc	gat	240
Asn	Arg	Asp	Gly	Asp	Ser	Tyr	Arg	Ser	Pro	Trp	Ser	Asn	Glu	Phe	Asp	
65					70				75					80		
ccc	ccg	ttg	gaa	gac	gga	act	gtt	ccc	agt	gaa	aga	gtg	aga	aag	ctt	288
Pro	Pro	Leu	Glu	Asp	Gly	Thr	Val	Pro	Ser	Glu	Arg	Val	Arg	Lys	Leu	
			85					90					95			
gag	gtc	gcc	gcc	aac	gag	gct	ttc	gat	gtc	tac	cgg	gag	ctg	tac	tac	336
Glu	Val	Ala	Ala	Asn	Glu	Ala	Phe	Asp	Val	Tyr	Arg	Glu	Leu	Tyr	Tyr	
		100						105					110			
gag	ggt	gga	gta	ggc	agc	gtg	tac	ttt	tgg	gac	ttg	gac	gat	gga	ttc	384
Glu	Gly	Gly	Val	Gly	Ser	Val	Tyr	Phe	Trp	Asp	Leu	Asp	Asp	Gly	Phe	
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gct	ggc	gtt	atc	cta	ttg	aag	aag	gga	gtt	acg	cca	ggg	gct	aag	agc	432
Ala	Gly	Val	Ile	Leu	Leu	Lys	Lys	Gly	Val	Thr	Pro	Gly	Ala	Lys	Ser	
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tct	ggg	gag	tgg	gac	agt	atc	cac	gtc	ttc	gag	gct	acc	gac	aga	gcg	480
Ser	Gly	Glu	Trp	Asp	Ser	Ile	His	Val	Phe	Glu	Ala	Thr	Asp	Arg	Ala	
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cgc	atg	tcc	cac	tac	aag	ctg	act	agc	acc	gtc	atc	ctg	cac	ttg	gct	528
Arg	Met	Ser	His	Tyr	Lys	Leu	Thr	Ser	Thr	Val	Ile	Leu	His	Leu	Ala	
			165					170					175			
aat	gaa	act	gag	gct	ttg	ggg	gag	atg	gac	ctg	agt	ggg	aac	atg	acc	576

Asn	Glu	Thr	Glu	Ala	Leu	Gly	Glu	Met	Asp	Leu	Ser	Gly	Asn	Met	Thr		
			180					185					190				
cgc	caa	ggt	gga	ggt	gga	tct	tcc	cgt	cga	gtc	gga	tgc	gag	cca	cgt		624
Arg	Gln	Val	Glu	Val	Asp	Leu	Pro	Val	Glu	Ser	Asp	Ala	Ser	His	Val		
		195					200					205					
cgc	caa	tgt	tgg	tcg	act	tgt	tga	gga	cat	gga	ggt	gaa	gat	gag	gaa		672
Ala	Asn	Val	Gly	Arg	Leu	Val	Glu	Asp	Met	Glu	Leu	Lys	Met	Arg	Asn		
		210				215					220						
ctt	gct	gca	gga	ggt	ata	ctt	cgg	caa	ggc	taa	gga	tgt	cgt	ggg	tga		720
Leu	Leu	Gln	Glu	Val	Tyr	Phe	Gly	Lys	Ala	Lys	Asp	Val	Val	Gly	Glu		
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act	tcg	gag	tct	ccc	ctc	ctt	gtc	cga	gtc	gaa	cag	aga	tcg	ggc	tac		768
Leu	Arg	Ser	Gly	Leu	Pro	Ser	Leu	Ser	Glu	Ser	Asn	Arg	Asp	Arg	Ala		
				245					250					255			
cca	cct	gga	gat	gat	ccg	gtc	tat	gca	cag	cta	g						802
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<210> 27

<211> 267

<212> PRT

<213> *Aspergillus niger*

<400> 27

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			20					25					30				
Pro	Asp	Leu	Thr	Glu	Asp	Leu	Leu	Ser	Ser	Val	Asp	Gln	Pro	Leu	Glu		
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Ile	Arg	Lys	Cys	Pro	Lys	Thr	Asp	Arg	Asp	Tyr	Leu	Leu	Cys	Asp	Tyr		
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Glu	Val	Ala	Ala	Asn	Glu	Ala	Phe	Asp	Val	Tyr	Arg	Glu	Leu	Tyr	Tyr		
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Glu	Gly	Gly	Val	Gly	Ser	Val	Tyr	Phe	Trp	Asp	Leu	Asp	Asp	Gly	Phe		
	115					120					125						
Ala	Gly	Val	Ile	Leu	Leu	Lys	Lys	Gly	Val	Thr	Pro	Gly	Ala	Lys	Ser		
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Ser	Gly	Glu	Trp	Asp	Ser	Ile	His	Val	Phe	Glu	Ala	Thr	Asp	Arg	Ala		
145				150					155					160			
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Asn	Glu	Thr	Glu	Ala	Leu	Gly	Glu	Met	Asp	Leu	Ser	Gly	Asn	Met	Thr		
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Arg	Gln	Val	Glu	Val	Asp	Leu	Pro	Val	Glu	Ser	Asp	Ala	Ser	His	Val		
		195				200						205					
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Leu	Leu	Gln	Glu	Val	Tyr	Phe	Gly	Lys	Ala	Lys	Asp	Val	Val	Gly	Glu		
225				230					235					240			
Leu	Arg	Ser	Gly	Leu	Pro	Ser	Leu	Ser	Glu	Ser	Asn	Arg	Asp	Arg	Ala		
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 <213> *Aspergillus niger*

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<210> 29

<211> 1230  
 <212> DNA  
 <213> *Aspergillus niger*

<220>  
 <221> CDS  
 <222> (1)..(1230)

<400> 29

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

aat ctg tca tgg gaa ctc tgg cta gac gaa gcc cgg cac att cgc ctg	816
Asn Leu Ser Trp Glu Leu Trp Leu Asp Glu Ala Arg His Ile Arg Leu	
260 265 270	
aga tac gaa gag gcc gta ttc tcg gca aga aac aat tac tcc gag cac	864
Arg Tyr Glu Glu Ala Val Phe Ser Ala Arg Asn Asn Tyr Ser Glu His	
275 280 285	
cct ata gac cca ctg agt gaa cta gag gtc ttt att ggg tcc gtc atg	912
Pro Ile Asp Pro Leu Ser Glu Leu Glu Val Phe Ile Gly Ser Val Met	
290 295 300	
aac aaa ggt gta cag acc cgt cgg cag cgt gat caa tct aac aaa ctc	960
Asn Lys Gly Val Gln Thr Arg Arg Gln Arg Asp Gln Ser Asn Lys Leu	
305 310 315 320	
gcc gat gaa ttc gat cgc atc tct act tgg att gtg ggt cag atg cgc	1008
Ala Asp Glu Phe Asp Arg Ile Ser Thr Trp Ile Val Gly Gln Met Arg	
325 330 335	
gca ggg agc tcg tcc gag tca cca ata acc agt gtg tcg gat caa ctc	1056
Ala Gly Ser Ser Ser Glu Ser Pro Ile Thr Ser Val Ser Asp Gln Leu	
340 345 350	
aaa cct ctg gag ttt tgt ctc gcc tgc atc cat gtc ggt ggt gag agc	1104
Lys Pro Leu Glu Phe Cys Leu Ala Cys Ile His Val Gly Gly Glu Ser	
355 360 365	
aac aag gat ccc gcg cgc cgt cgt agg gaa gtg tac ggt gag att aaa	1152
Asn Lys Asp Pro Ala Arg Arg Arg Arg Glu Val Tyr Gly Glu Ile Lys	
370 375 380	
agc ttc cgg gtg gtt gca gcg tgt gct ttg ctg ttt gag ctt gac ctc	1200
Ser Phe Arg Val Val Ala Ala Cys Ala Leu Leu Phe Glu Leu Asp Leu	
385 390 395 400	
atc gaa aag ggg aga aag cga aag ttc taa	1230
Ile Glu Lys Gly Arg Lys Arg Lys Phe	
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<210> 30

<211> 409

<212> PRT

<213> *Aspergillus niger*

<400> 30

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



145					150					155				160
Lys	Pro	Phe	Arg	Pro	Asp	Phe	Met	Ala	Leu	Gly	Pro	Val	Ala	Arg Ile
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His	Asn	Lys	Ser	Asp	Ile	Glu	Leu	Glu	Glu	Tyr	Val	Ile	Gln	Ala Ala
			180					185					190	
Tyr	Asp	Glu	Asp	Asp	Asp	Met	Glu	Pro	Phe	His	Lys	Tyr	Tyr	Arg Ser
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Glu	Lys	Ile	Leu	Gly	Lys	Leu	Tyr	Arg	Gly	Val	Asp	Glu	Arg	Gln Ile
	210					215					220			
Trp	Gln	Glu	Asp	Ile	Gln	Ser	Lys	Val	Gln	Pro	Asn	Glu	Asp	Glu Phe
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	ctt	aag	atc	aag	acg	cca	acg	ggc	gag	cct	cca	tcg	gct	ttt	cag	ttc	1968	
	Leu	Lys	Ile	Lys	Thr	Pro	Thr	Gly	Glu	Pro	Pro	Ser	Ala	Phe	Gln	Phe		
					645					650					655			
	cg	ctc	ggg	ggc	tgt	aag	gg	atg	ctt	gct	g	tct	tcc	gat	gcc	cag	2016	
	Arg	Leu	Gly	Gly	Cys	Lys	Gly	Met	Leu	Ala	Val	Ser	Ser	Asp	Ala	Gln		
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	ccg	caa	gag	atc	cac	att	cga	gag	agt	caa	aat	aag	ttt	ccg	acc	gtc	2064	
	Pro	Gln	Glu	Ile	His	Ile	Arg	Glu	Ser	Gln	Asn	Lys	Phe	Pro	Thr	Val		
				675				680					685					
	cat	aat	ggc	ttg	gat	att	att	cga	tgg	tct	cag	ttc	tca	atg	gct	act	2112	
	His	Asn	Gly	Leu	Asp	Ile	Ile	Arg	Trp	Ser	Gln	Phe	Ser	Met	Ala	Thr		
		690				695						700						
	ttg	aac	cg	cag	ctg	ata	ctt	gtc	atg	tct	acc	ctc	ggg	g	ccc	gac	2160	
	Leu	Asn	Arg	Gln	Leu	Ile	Leu	Val	Met	Ser	Thr	Leu	Gly	Val	Pro	Asp		
	705				710					715					720			
	gag	gtg	ttt	cat	gct	aag	ctc	aag	tcc	atg	ctg	cg	gct	ctc	gat	gag	2208	
	Glu	Val	Phe	His	Ala	Lys	Leu	Lys	Ser	Met	Leu	Arg	Ala	Leu	Asp	Glu		
				725					730					735				
	gcc	atg	gaa	agt	gac	tcc	cga	gca	atc	gag	gta	ctc	aaa	aag	tac	gtt	2256	
	Ala	Met	Glu	Ser	Asp	Ser	Arg	Ala	Ile	Glu	Val	Leu	Lys	Lys	Tyr	Val		
				740				745					750					
	gat	ccg	aat	cag	acg	act	ctg	acc	gtc	agt	caa	atg	gta	tct	gat	gg	2304	
	Asp	Pro	Asn	Gln	Thr	Thr	Leu	Thr	Val	Ser	Gln	Met	Val	Ser	Asp	Gly		
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	Phe	Arg	Arg	Ser	Lys	Glu	Pro	Phe	Leu	Thr	Ser	Ile	Leu	Ala	Leu	Trp		

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Arg Thr Trp His Ile Lys Tyr Leu Lys Glu Lys Ala Lys Ile Val Ile			
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gat aaa ggc aca aat cta cta gga gtt atg gat gag acg ggg att ctc			2448
Asp Lys Gly Thr Asn Leu Leu Gly Val Met Asp Glu Thr Gly Ile Leu			
	805	810	815
aag ggc tac ttc tat gat aag ata cca aag aaa gac gct tct ctc gag			2496
Lys Gly Tyr Phe Tyr Asp Lys Ile Pro Lys Lys Asp Ala Ser Leu Glu			
	820	825	830
cag aag ctg gca gca tta cca gag ata ttt ctt cag att cct cgt tca			2544
Gln Lys Leu Ala Ala Leu Pro Glu Ile Phe Leu Gln Ile Pro Arg Ser			
	835	840	845
gaa gcc tcc gag gac ggt gca aca tat gaa gtc atc gaa ggg ctc tgt			2592
Glu Ala Ser Glu Asp Gly Ala Thr Tyr Glu Val Ile Glu Gly Leu Cys			
	850	855	860
ata ttg gca cga aat ccc tct ctt cac cca ggt gac att cgt gtg gtc			2640
Ile Leu Ala Arg Asn Pro Ser Leu His Pro Gly Asp Ile Arg Val Val			
	865	870	875
agg gca gtc aac gtg cct gag ttg cac agc ctc cgt gat gtg gtc gtc			2688
Arg Ala Val Asn Val Pro Glu Leu His Ser Leu Arg Asp Val Val Val			
	885	890	895
tta ccg caa acc ggc gat cga gat atc gcc agc atg tgt tcc ggt gga			2736
Leu Pro Gln Thr Gly Asp Arg Asp Ile Ala Ser Met Cys Ser Gly Gly			
	900	905	910
gac ctc gat ggt gat gac tac ctg att atc tgg gat cag gat cta att			2784
Asp Leu Asp Gly Asp Asp Tyr Leu Ile Ile Trp Asp Gln Asp Leu Ile			
	915	920	925
cac aag gat tgg ttc cta gac cca atg cgc tat aca agc aac aag gcc			2832
His Lys Asp Trp Phe Leu Asp Pro Met Arg Tyr Thr Ser Asn Lys Ala			
	930	935	940
cag gat cta gac cac gat gtc acc gtc gat gag gtc act tct ttc ttc			2880
Gln Asp Leu Asp His Asp Val Thr Val Asp Glu Val Thr Ser Phe Phe			
	945	950	955
gtc atg tac atg aaa aat gac agc ctt cca acg atc gct cac gcc cat			2928
Val Met Tyr Met Lys Asn Asp Ser Leu Pro Thr Ile Ala His Ala His			
	965	970	975
gtt gcc tgg gca gat cag ctt gag gat ggc gtc aac gaa gaa aag tgt			2976
Val Ala Trp Ala Asp Gln Leu Glu Asp Gly Val Asn Glu Glu Lys Cys			
	980	985	990
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Ile Arg Leu Ala Gln Leu His Ser Asp Ala Val Asp Tyr Asn Lys Thr			
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Gly Arg Pro Ala Ile Met Thr Arg Asn Leu Gln Pro Arg Arg Trp Pro			
	1010	1015	1020
cac ttc atg gag aag cct aag ccg aaa gac cta att tat cac tcc gaa			3120
His Phe Met Glu Lys Pro Lys Pro Lys Asp Leu Ile Tyr His Ser Glu			
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aag atc ctc ggt cag ctt tat gac gcc gtg gag agg gtg gac ttc gtg			3168
Lys Ile Leu Gly Gln Leu Tyr Asp Ala Val Glu Arg Val Asp Phe Val			
	1045	1050	1055
cca agc ctg gag atg cct ttc gac gag cgt atc ctg aac tgt tcg atc			3216
Pro Ser Leu Glu Met Pro Phe Asp Glu Arg Ile Leu Asn Cys Ser Ile			
	1060	1065	1070
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Glu Val Asn Glu Asp Leu Tyr Thr Phe Ala Lys Asn Leu Lys Val Glu			

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cac gac aca gcc ata cgg cgg atc atg gca cag cac gag atc aag acc			3312
His Asp Thr Ala Ile Arg Arg Ile Met Ala Gln His Glu Ile Lys Thr			
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Glu Phe Glu Ile Trp Ser Thr Phe Ile Leu Asn His Ser Gln Met Ser			
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aag gac tac aaa ttc cac gaa gag att ggt gca att tca gcc gcg cac			3408
Lys Asp Tyr Lys Phe His Glu Glu Ile Gly Ala Ile Ser Ala Ala His			
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Arg Glu Thr Phe Arg Lys Gln Cys Tyr Asn Lys Val Glu Gly Arg Thr			
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Phe Glu Leu Leu Ala Pro Leu Ala Val Ala Met Tyr Arg Val Thr His			
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Glu Glu Met Thr Gln Ala Leu Arg Lys His Arg Glu Lys Ser Pro Gln			
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His Gly Thr Pro Lys Ile Asn Gln Leu Pro Leu Ile Ser Phe Pro Trp			
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Ile Leu Pro His Ile Leu Gly Arg Val Ala Arg Gly Leu Tyr Asp Val			
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tat caa cct gca gca ctc aac ccc gat cct gtg gaa cat ggc ccg gcc			3696
Tyr Gln Pro Ala Ala Leu Asn Pro Asp Pro Val Glu His Gly Pro Ala			
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Lys Val Arg Gln Ala Ala Asp Lys Pro Asp Thr Leu Tyr Glu Asp Pro			
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Phe Gly Leu Phe Thr Asp Glu Glu Arg Ala Ala Asn Ala Ser His Ala			
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Gln Pro Ile Ser Thr Ala Gly Pro Ser Thr Gly His Ala Ser Ala Glu			
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agt agc gag agc atc atc gat caa ctc ctt gat ata ggc atc tca gac			3888
Ser Ser Glu Ser Ile Ile Asp Gln Leu Leu Asp Ile Gly Ile Ser Asp			
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Val Pro Ala Leu Ser Pro Ser Pro Pro Ser Ala Ser Ser Thr Pro			
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Gly Arg Glu Gln Ile Ser Leu Leu Asp Ile Asp Asp Asn Val Thr Phe			
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Ser Glu Leu Pro Lys Met Val Lys Pro Val Ile Ala Ser Pro Ala Ala			
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Thr Pro Leu Val Glu Glu Asn Val Glu Gly Glu Asp Glu Cys Glu Glu			
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atc ctt gag gag gaa gac gaa ctt gaa cct act gct ctc gat aaa ctc			4128
Ile Leu Glu Glu Glu Asp Glu Leu Glu Pro Thr Ala Leu Asp Lys Leu			
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Ser	Asp	Ile	Asn	Ala	Thr	Phe	His	Glu	Pro	Gly	Ser	Trp	Arg	Asp	Ser
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Asp	Cys	Trp	Tyr	Arg	Gln	Thr	His	Ile	Val	His	Asn	Pro	Leu	Ser	Leu
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Ile	Glu	Asp	Thr	Asp	Arg	Phe	Ile	Gln	Trp	Asp	Asp	Arg	Gln	Glu	Arg
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Pro	Phe	Pro	Val	Arg	Tyr	Gln	Leu	Glu	Val	Cys	Ile	Ser	Asn	Gly	Tyr	385	390	395	400
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Leu	Gly	Glu	Ala	Lys	Ala	Arg	Lys	Leu	Leu	Glu	Asn	Val	Ala	Gly	Gln	420	425		430
Lys	His	Gln	Tyr	Tyr	Asp	Pro	Met	Lys	Ile	Phe	Asp	Leu	Pro	Phe	Val	435	440		445
Arg	Gly	Ile	Arg	Ala	Thr	Lys	Ala	Lys	Ile	Pro	Pro	Tyr	Cys	Cys	His	450	455		460
Met	Arg	Ser	Ala	Thr	Ile	Thr	Pro	Ser	Thr	Val	Tyr	Tyr	Asn	Leu	Pro	465	470		475
Ser	Val	Asp	Ile	Ser	Asn	Arg	Ile	Ile	Arg	Arg	Tyr	Met	Glu	His	Ala	485	490		495
Asp	Arg	Phe	Leu	Arg	Val	Arg	Phe	Thr	Asp	Glu	Lys	Leu	Tyr	Gly	Arg	500	505		510
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Phe	Ala	Pro	Leu	Pro	Asp	Leu	Thr	Ala	Ala	Asn	Ile	Arg	Ala	Trp	Met	565	570		575
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Gly	Gln	Cys	Phe	Ser	Thr	Thr	Arg	Ala	Val	Ala	Gly	Cys	Pro	Val	Gln	595	600		605
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Pro	Gln	Glu	Ile	His	Ile	Arg	Glu	Ser	Gln	Asn	Lys	Phe	Pro	Thr	Val	675	680		685
His	Asn	Gly	Leu	Asp	Ile	Ile	Arg	Trp	Ser	Gln	Phe	Ser	Met	Ala	Thr	690	695		700
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Glu	Val	Phe	His	Ala	Lys	Leu	Lys	Ser	Met	Leu	Arg	Ala	Leu	Asp	Glu	725	730		735
Ala	Met	Glu	Ser	Asp	Ser	Arg	Ala	Ile	Glu	Val	Leu	Lys	Lys	Tyr	Val	740	745		750
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Asp	Lys	Gly	Thr	Asn	Leu	Leu	Gly	Val	Met	Asp	Glu	Thr	Gly	Ile	Leu	805	810		815
Lys	Gly	Tyr	Phe	Tyr	Asp	Lys	Ile	Pro	Lys	Lys	Asp	Ala	Ser	Leu	Glu	820	825		830
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Cys	Arg	Arg	Val	Gln	Ile	Phe	Ala	Tyr	Phe	Asn	Glu	Tyr	Phe	Arg	Arg	
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gca	aga	ctg	caa	tgc	ctc	atg	tga	caa	ctg	caa	gtc	cga	ctc	tgt	ctt	3360
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Glu	Leu	His	Asp	Phe	Ser	His	Tyr	Ala	Val	Ser	Ala	Ile	Lys	Val	Val	



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Asn	Ile	Phe	Arg	Gly	Ser	Val	Lys	Arg	Phe	Arg	Ser	Pro	Gln	His	Arg	
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Gln	Ala	Pro	Gly	Tyr	Gly	Asp	Gly	Ser	Gly	Leu	Glu	Leu	Gly	Glu	Ala	
	1155					1160					1165					
aga	acg	act	att	cca	cag	act	tct	agg	cga	ggg	ggc	tct	tgt	tga	aga	3600
Glu	Arg	Leu	Phe	His	Arg	Leu	Leu	Gly	Glu	Gly	Ala	Leu	Val	Glu	Glu	
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gaa	tgt	cgt	caa	tgg	aag	taa	att	tgc	cat	tca	ata	tat	caa	agt	ggg	3648
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acg	ccg	tgc	cgc	tga	ttt	cga	gag	tgg	gcg	gtg	caa	act	aaa	gct	tga	3696
Arg	Arg	Ala	Ala	Asp	Phe	Glu	Ser	Gly	Arg	Cys	Lys	Leu	Lys	Leu	Asp	
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cgt	gcg	agt	ctc	gcc	gaa	tgg	aaa	ggc	cag	gaa	gtc	caa	ttc	ggg	atc	3744
Val	Arg	Val	Ser	Pro	Asn	Gly	Lys	Ala	Arg	Lys	Ser	Asn	Ser	Gly	Ser	
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Arg	Thr	Asp	Gly	Gly	Asn	Lys	Glu	Tyr	Gln	Pro	Gln	Ser	Thr	Asn	Val	
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ctc	gtc	acc	tgt	aca	agc	ggc	aaa	cca	acg	ccg	tct	atc	tcg	ctt	ccg	3840
Ser	Ser	Pro	Val	Gln	Ala	Ala	Asn	Gln	Arg	Arg	Leu	Ser	Arg	Phe	Arg	
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Tyr	Gln	Gly	Gly	Ala	Gly	Asp	Thr	Thr	Asp	Asp	Asp	Ala	Asp	Ser	Asp	
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tgg	ggt	cga	aag	agt	acg	aat	cgc	cgg	caa	acc	agc	aca	gga	gag	gcg	3936
Gly	Phe	Glu	Arg	Val	Arg	Ile	Ala	Gly	Lys	Pro	Ala	Gln	Glu	Arg	Arg	
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Asp	Pro	Leu	His	Lys	Ala	Val	Ala	Glu	Asp	Phe	Met	Val	Tyr	Ala	Lys	
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Phe	Thr	Asp	Ser	Val	Leu	Arg	Glu	Met	Val	Ile	Val	Phe	Pro	Lys	Asp	
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Tyr	Ala	Glu	Leu	Lys	Lys	Glu	Gln	Asp	Asp	Ala	Asp	Gly	Val	Val	Pro	
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ggt cag cga tgg cgg aat ctt tac gga tca tcc gtc tac att taa tgt							4368
Phe Ser Asp Gly Gly Ile Phe Thr Asp His Pro Ser Thr Phe Asn Val							
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gga tga gac cct gtc aag tgc tta ttt ctc tac cca gaa cac tgc tgg							4416
Asp Glu Thr Leu Ser Ser Arg Tyr Phe Ser Thr Gln Asn Thr Ala Gly							
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cct cga ctc cga cga cga gga tga tgg ccc cgg aaa gtc cag tag acc							4464
Leu Asp Ser Asp Asp Glu Asp Asp Gly Pro Gly Lys Ser Ser Arg Pro							
	1475		1480		1485		
tcg ggc tcg gaa gcg tca aac aac caa acg ccc tcg ccg cca aaa cgc							4512
Arg Ala Arg Lys Arg Gln Thr Thr Lys Arg Pro Arg Arg Gln Asn Ala							
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tgc ccc tag atc cag ggc aaa atc gac ggg agc ccg cag aaa atc tgg							4560
Ala Pro Arg Ser Arg Ala Lys Ser Thr Gly Ala Arg Arg Lys Ser Gly							
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tga tcg tgc tga caa tcg ctc ctc tgc ccc tcg gaa aac gac caa agc							4608
Asp Arg Ala Asp Asn Arg Ser Ser Ala Pro Arg Lys Thr Thr Lys Ala							
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Lys Pro Ser Thr Ser Arg Ile Gly Met Met Pro Ile							
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<211> 1548

<212> PRT

<213> Aspergillus niger

<400> 36

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Gly Thr Leu Ala His Gln Pro Glu Asp Ile Pro Phe Pro Thr Asp Asp	
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Leu Gln Pro Glu Val Lys Pro Ala Asp Thr Asp His Val Asp Glu Lys	
65 70 75 80	
Ala Glu Val Asp Ser Asp Thr Val Met Ala Arg Leu Leu Leu Thr Pro	
85 90 95	
Ala Ser Ala Arg Lys Pro Arg Met Leu Ser Leu Ser Lys Asp Ala Gly	
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Ala Pro Thr Pro Lys Pro Leu Lys Ser Ser Gln Ser Val Lys Ser Pro	
115 120 125	
Phe Lys Gly Arg Glu Asn Gly Pro Asp Arg Val Ile Lys Asp Leu Gln	
130 135 140	
Ser Pro Arg Ser Pro Leu Arg Ser Pro Lys Thr Ser Leu Thr Pro Phe	
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Gly Ser Lys Gln Pro Leu Asn Thr Asn Ser Pro Leu Phe Asp Ser Asp	
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Ile Asp Thr Ile Asp Leu Thr Gly Asp Leu Asn Gln Thr Thr Leu Ser	
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Ser Asp Thr Phe Asp Gly Phe Glu Glu Pro Gln Arg Leu Trp Thr Glu	
195 200 205	
Asp Ala Ala Ser Arg Arg Glu Pro Leu Glu Lys Arg Gly Lys Lys Arg	

210	215	220
Lys Ser Asp Asp Tyr Val Ser Asp Leu Val Ser Pro Arg Lys Asn Gly		
225	230	235
Ser Lys Thr Arg Ser Pro Leu Lys Ala Val Glu Ser Ala Lys Thr Pro		
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Arg Ser Thr Ser Thr Arg Leu Gln Pro Gly Lys Ser Pro Arg Thr Thr		
	260	265
Arg Lys Asp Ile Leu Thr Arg Ala Asp Gly Pro Ser Gly Leu Pro Ser		
	275	280
Leu Ser Gln Ser Ser Arg Val Gly His Val Ile Ala Asp Ser Asp Asp		
	290	295
Asp Asp Gly Asp Glu Asn Leu Phe Asp Asp Trp Val Pro Asp Gly Asp		
305	310	315
Gly Pro Thr Leu Asn Ser Asn Glu Ser Leu Tyr Pro Ile Leu Pro Asn		
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Gln Asp Ser Ser Asp Glu His Ala Pro Pro Ser Pro Ala Arg Lys Lys		
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Thr Arg Ala Ser Pro Trp Ala Pro Asp Ala Met Asp Val Val Pro Ser		
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Ser Ile Leu Pro Pro Arg Lys Asp Thr His Ile Ser Pro Lys Pro Ile		
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Thr His Val Pro Ala Thr Thr Asp Ser Pro Ser Ser Gln Pro Gln Asn		
385	390	395
Glu Asp Val Ala Met Phe Leu Ser Leu Ser Ala Asp Ser Leu Glu Gly		
	405	410
Ala Ile Ala Thr Leu Lys Ser Thr Leu Thr Lys Asn Ser Glu Ile Val		
	420	425
Tyr Glu Arg Ala Met Arg Gly Glu Leu Ala Pro Asp Leu Ile Ala Glu		
	435	440
Asn Lys Thr Leu Thr Asp Arg Ile Glu Ala Ile Asn Leu Leu Lys Gln		
	450	455
Gln Arg Val Thr Tyr Gln Ser Tyr Asp Leu Lys Arg Asn Lys Leu Lys		
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Lys Arg Leu Met Gln Val Ile Thr Gln Gly Gly Asp Pro Ser Glu Met		
	485	490
Pro Glu Leu Val Glu Ser Arg Glu Ala Thr Thr Gln Leu Gln Lys Val		
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Glu Ser Asp Ile Gln His Leu Leu Ala Arg Ser Lys Leu Leu Ser Ile		
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Pro Leu Leu Asp Val Arg Pro Leu Arg Tyr Lys Ala Asp His Pro Thr		
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Thr Leu Ser Arg Pro Ser Pro Val Leu Ile Ser Ala Leu Asp Asp Thr		
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Thr Ile Ser Gly Val Ser Ser Arg Ser His Ala Pro Ser Thr Val Asp		
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Tyr Ser Asn Ser Arg Ser Glu Ile Ser Thr Arg Val Ser Asp Leu Ser		
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Phe Lys Asn Thr Asn Gly Thr Ser Ser Ile Arg Ala Phe Asn Tyr Asp		
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Asp Pro Thr Thr Leu Asp Asp Asp Ala Phe Thr Arg Thr Met Gly		
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Ser Pro Thr Arg Pro Ala Val Asp Ala Asp Glu Phe Asp Leu Asp Asp		
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Glu Asp Met Leu Glu Ala Ala Gly Phe Leu Asp Glu Gly Tyr Ser Leu		
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Ala Thr Asp Asn His Gly Phe His Asn Arg Lys Val Phe Ala Glu Thr		
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Ser	Gly	Asn	Ala	Ser	Arg	Thr	Pro	Leu	Ser	Gln	Pro	Lys	Ser	Gln	Gly	
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His	Asn	Ala	Leu	Trp	Asn	Gln	His	Pro	Trp	Ser	Lys	Asp	Val	Arg	Asn	
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Ala	Leu	Lys	Asp	Arg	Phe	His	Leu	Arg	Gly	Phe	Arg	Leu	Asn	Gln	Leu	
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Glu	Ala	Ile	Asp	Ala	Thr	Leu	Ser	Gly	Lys	Asp	Thr	Phe	Val	Leu	Met	
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Pro	Thr	Gly	Gly	Lys	Ser	Leu	Cys	Tyr	Gln	Leu	Pro	Ser	Val	Val		
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Thr	Ser	Gly	Ser	Thr	Arg	Gly	Val	Thr	Ile	Val	Ile	Ser	Pro	Leu	Leu	
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Ser	Leu	Met	Gln	Asp	Gln	Val	Ser	His	Leu	Asn	Arg	Leu	Asn	Ile	Lys	
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Ala	Tyr	Leu	Leu	Asn	Gly	Glu	Thr	Pro	Lys	Glu	Gln	Arg	Gln	Trp	Ile	
785					790					795					800	
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Ala	Leu	Thr	Ala	Thr	Ala	Thr	Glu	Asn	Val	Lys	Val	Asp	Val	Ile	His	
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Asn	Leu	Arg	Met	Glu	Gly	Cys	Glu	Val	Phe	Ser	Gln	Ser	Phe	Asn	Arg	
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Pro	Asn	Leu	Thr	Tyr	Glu	Val	Arg	Ile	Lys	Lys	Lys	Gly	Thr	Glu	Leu	
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Leu	Ala	Ser	Ile	Ala	Asp	Thr	Ile	Lys	Thr	Ser	Tyr	Ala	Asn	Lys	Ser	
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Gly	Ile	Val	Tyr	Cys	Leu	Ser	Arg	Lys	Thr	Cys	Glu	Lys	Val	Ala	Ser	
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Gly	Leu	Arg	Asp	Asp	Tyr	Arg	Ile	Lys	Ala	Glu	His	Tyr	His	Ala	Gly	
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Arg	Gln	Met	Leu	His	Asn	Val	Val	Gln	Tyr	Cys	Glu	Asn	Arg	Ser	Asp	
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Cys	Arg	Arg	Val	Gln	Ile	Phe	Ala	Tyr	Phe	Asn	Glu	Tyr	Phe	Arg	Arg	
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Gln	Asp	Cys	Asn	Ala	Ser	Cys	Asp	Asn	Cys	Lys	Ser	Asp	Ser	Val	Phe	
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Glu	Leu	His	Asp	Phe	Ser	His	Tyr	Ala	Val	Ser	Ala	Ile	Lys	Val	Val	

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	1315					1320						1325			
Asp	Pro	Leu	His	Lys	Ala	Val	Ala	Glu	Asp	Phe	Met	Val	Tyr	Ala	Lys
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Leu	Asp	Ser	Asp	Asp	Glu	Asp	Asp	Gly	Pro	Gly	Lys	Ser	Ser	Arg	Pro
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<211> 2810

<212> DNA

<213> *Aspergillus niger*

<400> 37

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<213> *Aspergillus niger*

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Val Ile Thr Ala Ala Ile Asn Gly His Asp Val Phe Leu Gln Ala Asn
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Thr Ser Phe Gly Lys Ser Leu Cys Phe Gln Leu Pro Ala Val Ile Ser
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65      70      75      80
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Gln Val Lys Ala Leu Gln Ala Leu Gly Ile Ala Val Ala Thr Ile Asn
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145      150      155      160
ggc cat gac ttt cgg ccg gcg tac aaa gaa ctg ggc tgg ttc aag caa      528
Gly His Asp Phe Arg Pro Ala Tyr Lys Glu Leu Gly Trp Phe Lys Gln
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Tyr His Ala Gly Leu Ser Ser Glu Asp Arg Thr Arg Ile Gln Ser Glu	
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<213> Aspergillus niger



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Thr Ser Phe Gly Lys Ser Leu Cys Phe Gln Leu Pro Ala Val Ile Ser
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His Gly Val Thr Val Val Ile Ser Pro Leu Leu Ala Leu Met Thr Asp
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Gln Val Lys Ala Leu Gln Ala Leu Gly Ile Ala Val Ala Thr Ile Asn
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<212> DNA

<213> *Aspergillus niger*

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<221> CDS

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Asp Ile Pro Ser Pro Glu Asp Leu Gln Ala Met Ser Gln Tyr Val Leu	
180 185 190	
gaa tat ggg caa gaa ttt gac caa ttc cga cag acc gct ccg ctg aaa	624
Glu Tyr Gly Gln Glu Phe Asp Gln Phe Arg Gln Thr Ala Pro Leu Lys	
195 200 205	
ttg aag ata ttc ttc gag gga gcg cct acg aag gtc aac ggc gaa gaa	672
Leu Lys Ile Phe Phe Glu Gly Ala Pro Thr Lys Val Asn Gly Glu Glu	
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ttc aag gta gtc gag tcg gcc gtg gtt gcg ttg ccc gat acc cag aag	720
Phe Lys Val Val Glu Ser Ala Val Val Ala Leu Pro Asp Thr Gln Lys	
225 230 235 240	
caa ctt gtt cgc atc ggg tat agc cat cac ggc atg agt tgc ttc aag	768
Gln Leu Val Arg Ile Gly Tyr Ser His His Gly Met Ser Cys Phe Lys	
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gat gag aat gac aag gaa ttt aag aag atc ttc aat ccg ctg aag tcc	816
Asp Glu Asn Asp Lys Glu Phe Lys Lys Ile Phe Asn Pro Leu Lys Ser	
260 265 270	
tgg ttg ggt agt ctt ccg agt ccg gaa gag aag ggc act gtt aac aat	864
Trp Leu Gly Ser Leu Pro Ser Pro Glu Glu Lys Gly Thr Val Asn Asn	
275 280 285	
atc tcg aat gcc tcg ttc gcg ggg tct aac aac tct ggc ttg cag ctt	912
Ile Ser Asn Ala Ser Phe Ala Gly Ser Asn Asn Ser Gly Leu Gln Leu	
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 <212> PRT  
 <213> Aspergillus niger

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 Glu Leu Val Gly Val Arg Asn Gly Asp Val Val Arg His Pro Ser Ser  
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 Lys Arg Pro Ile Ile Phe Ile Ala His Cys Leu Gly Gly Leu Ile Cys  
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 Glu His Ala Leu Val Arg Ala Ala Asn Asp Asp Asp Lys Lys Gln Val  
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 Pro Ala Asn Ile Ser Glu Ala Thr Lys Tyr Phe Arg Leu Ala Gln Gln  
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 Asp Ile Pro Ser Pro Glu Asp Leu Gln Ala Met Ser Gln Tyr Val Leu  
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 Glu Tyr Gly Gln Glu Phe Asp Gln Phe Arg Gln Thr Ala Pro Leu Lys  
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 225 230 235 240  
 Gln Leu Val Arg Ile Gly Tyr Ser His His Gly Met Ser Cys Phe Lys  
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 Asp Glu Asn Asp Lys Glu Phe Lys Lys Ile Phe Asn Pro Leu Lys Ser  
 260 265 270  
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 275 280 285  
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 <211> 2171  
 <212> DNA  
 <213> Aspergillus niger

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gcg	ccc	gca	caa	gag	agc	gat	gtc	gaa	tct	tcc	acc	cca	gag	caa	acg	96
Ala	Pro	Ala	Gln	Glu	Ser	Asp	Val	Glu	Ser	Ser	Thr	Pro	Glu	Gln	Thr	
			20				25				30					
caa	gaa	cca	gaa	gca	caa	gag	caa	gaa	caa	gaa	gag	gga	cag	tcc	aag	144
Gln	Glu	Pro	Glu	Ala	Gln	Glu	Gln	Glu	Gln	Glu	Glu	Gly	Gln	Ser	Lys	
		35					40					45				

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Thr Phe Lys Glu Leu Gly Ile Ile Glu Gln Leu Cys Glu Ala Cys Glu	
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acc atg ggc tac aaa gca cct aca cct att cag cgg gag tcg att cct	240
Thr Met Gly Tyr Lys Ala Pro Thr Pro Ile Gln Arg Glu Ser Ile Pro	
65 70 75 80	
ctg gct ctt aaa ggc cgt gat ttg atc ggt ctt gca gag acc gga agt	288
Leu Ala Leu Lys Gly Arg Asp Leu Ile Gly Leu Ala Glu Thr Gly Ser	
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gga aag acg gca gcg ttt gct ctt ccc atc ctc caa gcc ttg atg gaa	336
Gly Lys Thr Ala Ala Phe Ala Leu Pro Ile Leu Gln Ala Leu Met Glu	
100 105 110	
aag ccc caa ccc ttc ttc ggc ctc gtc ctc gcc cca acc cga gaa ctc	384
Lys Pro Gln Pro Phe Phe Gly Leu Val Leu Ala Pro Thr Arg Glu Leu	
115 120 125	
gcc tac cag atc tcc aaa tct ttc gag tcc cta ggc gcc agc atg ggt	432
Ala Tyr Gln Ile Ser Lys Ser Phe Glu Ser Leu Gly Ala Ser Met Gly	
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gtg cga agc tgc gtc atc gtc ggt ggc atg gac atg gtc tct cag tca	480
Val Arg Ser Cys Val Ile Val Gly Gly Met Asp Met Val Ser Gln Ser	
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Ile Ser Leu Gly Lys Lys Pro His Ile Ile Val Ala Thr Pro Gly Arg	
165 170 175	
ctt ctg gac cac ctc gag aac acc aag ggc ttc tcc ctc cgc aac ctg	576
Leu Leu Asp His Leu Glu Asn Thr Lys Gly Phe Ser Leu Arg Asn Leu	
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aag tac ctg gtg atg gac gaa gcg gat cga ctt ctt gac atg gac ttc	624
Lys Tyr Leu Val Met Asp Glu Ala Asp Arg Leu Leu Asp Met Asp Phe	
195 200 205	
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Gly Pro Leu Leu Asp Lys Ile Leu Lys Val Leu Pro Arg Glu Arg Arg	
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Thr Phe Leu Phe Ser Ala Thr Met Ser Ser Lys Val Glu Ser Leu Gln	
225 230 235 240	
cgt gcc tcc ctc tcc aat ccg ctc cgt gtc tct gtc tcc aca agc aaa	768
Arg Ala Ser Leu Ser Asn Pro Leu Arg Val Ser Val Ser Thr Ser Lys	
245 250 255	
tac cag acc gtc tcg act ctc ctc caa tct tac ctc ttc att ccc cag	816
Tyr Gln Thr Val Ser Thr Leu Leu Gln Ser Tyr Leu Phe Ile Pro Gln	
260 265 270	
aag cac aag gac ctg tac ctt gtc tac ctg ttg aac gaa ttc gcc ggc	864
Lys His Lys Asp Leu Tyr Leu Val Tyr Leu Leu Asn Glu Phe Ala Gly	
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cag agt act atc atc ttc acg agg acg gtg aac gag acg cag aga ctt	912
Gln Ser Thr Ile Ile Phe Thr Arg Thr Val Asn Glu Thr Gln Arg Leu	
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gcg ttc ttg ctt cgt gcg ctt ggc ttc ggc gct atc ccg ctg cat gga	960
Ala Phe Leu Leu Arg Ala Leu Gly Phe Gly Ala Ile Pro Leu His Gly	
305 310 315 320	
cag ctt tca cag tct gct cgt ctc ggt gcg ctg ggc aag ttc cgt gct	1008
Gln Leu Ser Gln Ser Ala Arg Leu Gly Ala Leu Gly Lys Phe Arg Ala	
325 330 335	
cgt agt cgg aat att ctt gtc gcg acg gat gtg gct gct cgt ggt ttg	1056
Arg Ser Arg Asn Ile Leu Val Ala Thr Asp Val Ala Ala Arg Gly Leu	
340 345 350	

gat att ccg tcc gtt gat gtt gtg ctt aac ttt gat ttg ccg ggt gat	1104
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355 360 365	
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Ser Pro Ser Tyr Val His Arg Val Gly Arg Thr Ala Arg Ala Gly Lys	
370 375 380	
agt ggt ctt gct atc agc ttt gtc gcc cag tac gat gtt gag gtt tgg	1200
Ser Gly Leu Ala Ile Ser Phe Val Ala Gln Tyr Asp Val Glu Val Trp	
385 390 395 400	
ctg agg atc gaa ggt gct ttg ggc aag aag ctc aag gaa tac gac tgc	1248
Leu Arg Ile Glu Gly Ala Leu Gly Lys Lys Leu Lys Glu Tyr Asp Cys	
405 410 415	
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Pro Lys Asp Glu Val Met Val Leu Gly Glu Asn Val Ala Glu Ala Gln	
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Arg Gln Ala Ile Met Asp Met Lys Asp Tyr Asn Glu Lys Lys Gly Ser	
435 440 445	
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<210> 45

<211> 467

<212> PRT

<213> *Aspergillus niger*

<400> 45

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



97

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<213> *Aspergillus niger*

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<221> CDS  
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Thr Leu Ser Asp Asp Glu Asn Asp Thr Leu Asn Gln Leu Glu Glu Glu  
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ggc gag ggc gac gat ggt gcg cta gcc acg gga tcg aaa acg aag aag 144  
Gly Glu Gly Asp Asp Gly Ala Leu Ala Thr Gly Ser Lys Thr Lys Lys  
35 40 45  
cgc aag aga gat gat gct gcg gcg gcg cag cag gag aag ggg aag aac 192  
Arg Lys Arg Asp Asp Ala Ala Ala Ala Gln Gln Glu Lys Gly Lys Asn  
50 55 60  
aag aag gtg aag aag cag gaa caa cag caa caa gca caa cag aag 240  
Lys Lys Val Lys Lys Gln Glu Gln Gln Gln Gln Ala Gln Gln Lys  
65 70 75 80  
aaa aag aag gga aag aat gcc cct gtt cag gag gaa gag gat gag gat 288  
Lys Lys Lys Gly Lys Asn Ala Pro Val Gln Glu Glu Glu Asp Glu Asp  
85 90 95  
gaa gag gag gaa gag gat cag ggt gaa gat gat ggc gcg ctt aat tcg 336  
Glu Glu Glu Glu Glu Asp Gln Gly Glu Asp Asp Gly Ala Leu Asn Ser  
100 105 110  
gat ttc gag ttc gat gtc ggc ggt gct gcg aat gag gtt agg gat ttc 384  
Asp Phe Glu Phe Asp Val Gly Gly Ala Ala Asn Glu Val Arg Asp Phe  
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gat ggg tgg gag gtt aat ggt aat gag gag ggt aag ggt ggg gat aag 432  
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Lys Ala Val Asp Ile Asp Asp Ile Ile Ser Arg Arg Gln Ala Lys Lys  
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Asp	Phe	Glu	Phe	Asp	Val	Gly	Gly	Ala	Ala	Asn	Glu	Val	Arg	Asp	Phe
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Glu	Ala	Glu	Leu	Ile	Arg	Lys	Gln	Lys	Lys	Lys	Lys	Gln	Lys	Gln	Glu
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Asp	Glu	Gln	Met	Asp	Glu	Asp	Asp	Asp	Asp	Ala	Ala	Ser	Asp	Asp	Asp
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Ser	Val	Ala	Thr	Pro	Val	Met	His	Pro	Asp	Asp	Ile	Ala	Ser	Asp	Arg
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Asp	Ser	Asp	Glu	Glu	Ser	Gln	Val	Asp	Ala	Glu	Glu	Glu	Glu	Lys	Arg
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Lys	Ala	Phe	Phe	Ala	Pro	Glu	Glu	Lys	Thr	Ser	Glu	Ser	Ala	Met	
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Leu	Arg	Gly	Leu	Ala	Gly	Val	Asn	Phe	Ser	Asn	Pro	Thr	Pro	Ile	Gln
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Ala	Val	Thr	Gly	Ser	Gly	Lys	Thr	Ala	Ala	Phe	Val	Val	Pro	Ile	Leu
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Glu	Arg	Leu	Leu	Phe	Arg	Pro	Arg	Lys	Val	Pro	Thr	Ser	Arg	Val	Ala
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Asp	Ser	Arg	Gln	Arg	Gln	Glu	Ala	Gly	Ala	Gly	Trp	Lys	Lys	Gly	Arg	
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 tcc tct gac tcg gag gtc gag cag acc gaa ctg caa tcc cgc gcc ccc 96



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

Lys	Gln	Thr	Tyr	Leu	Lys	Val	Pro	Met	Thr	His	Arg	Glu	Ala	Phe	Leu	
				325					330					335		
cac	gtc	ctc	ctc	tcc	acg	gaa	gcg	aac	gcc	tcc	aaa	cca	gcc	atc	atc	1056
His	Val	Leu	Leu	Ser	Thr	Glu	Ala	Asn	Ala	Ser	Lys	Pro	Ala	Ile	Ile	
				340				345					350			
ttc	tgc	aac	cac	acc	aag	acg	gcg	gac	ttg	ctg	gag	cgc	atg	ctc	cgc	1104
Phe	Cys	Asn	His	Thr	Lys	Thr	Ala	Asp	Leu	Leu	Glu	Arg	Met	Leu	Arg	
		355					360					365				
agg	ctg	tct	cac	cgc	gtt	aca	tcc	ctg	cat	agt	ctg	ctg	ccg	cag	tcg	1152
Arg	Leu	Ser	His	Arg	Val	Ser	Leu	His	Ser	Ser	Leu	Leu	Pro	Gln	Ser	
		370				375					380					
gag	cgc	aat	gcc	aat	ctg	gcg	agg	ttc	aga	gcg	tcc	gcg	gcg	agg	ttg	1200
Glu	Arg	Asn	Ala	Asn	Leu	Ala	Arg	Phe	Arg	Ala	Ser	Ala	Ala	Arg	Leu	
385					390					395					400	
ctc	gtt	gcg	acg	gat	gtg	gcg	tcc	cgt	ggt	ttg	gat	att	ccg	tcg	gtg	1248
Leu	Val	Ala	Thr	Asp	Val	Ala	Ser	Arg	Gly	Leu	Asp	Ile	Pro	Ser	Val	
				405					410					415		
gag	ttg	gtg	gtc	aat	ttt	gat	gtg	ccc	agg	aat	ccg	gat	gat	tat	gtg	1296
Glu	Leu	Val	Val	Asn	Phe	Asp	Val	Pro	Arg	Asn	Pro	Asp	Asp	Tyr	Val	
				420				425					430			
cat	cgg	gtt	ggt	cga	acg	gcg	cgt	gca	ggg	aga	aag	ggt	gag	tcg	gtc	1344
His	Arg	Val	Gly	Arg	Thr	Ala	Arg	Ala	Gly	Arg	Lys	Gly	Glu	Ser	Val	
		435					440					445				
acg	ctt	gtt	ggg	caa	cgg	gat	gtg	agt	ctg	gtg	ttg	gcg	att	gag	gag	1392
Thr	Leu	Val	Gly	Gln	Arg	Asp	Val	Ser	Leu	Val	Leu	Ala	Ile	Glu	Glu	
		450				455					460					
agg	gtg	ggt	agg	cag	atg	gag	gag	tgg	agt	gag	gag	ggt	gtt	agt	gtt	1440
Arg	Val	Gly	Arg	Gln	Met	Glu	Glu	Trp	Ser	Glu	Glu	Gly	Val	Ser	Val	
		465			470					475					480	
gag	ggt	agg	gtt	gtt	agg	acg	ggt	gtg	ttg	aag	gag	gtt	ggt	gag	gcc	1488
Glu	Gly	Arg	Val	Val	Arg	Thr	Gly	Val	Leu	Lys	Glu	Val	Gly	Glu	Ala	
				485				490						495		
aag	aga	gag	gct	gcg	ggt	gag	att	gag	gag	ggg	aga	gat	gtg	ttg	gga	1536
Lys	Arg	Glu	Ala	Ala	Gly	Glu	Ile	Glu	Glu	Gly	Arg	Asp	Val	Leu	Gly	
			500					505					510			
agg	aag	agg	aat	aag	ttg	aag	aag	gtg	cgg	tag						1569
Arg	Lys	Arg	Asn	Lys	Leu	Lys	Lys	Val	Arg							
		515					520									

<210> 51

<211> 522

<212> PRT

<213> *Aspergillus niger*

<400> 51

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			20					25					30			
Lys	Arg	Arg	Arg	Leu	Ser	Glu	Ser	Ser	Thr	Asp	Ser	Tyr	Val	Ala	Pro	
		35					40					45				
Ala	Pro	Leu	Pro	Thr	Leu	Ser	Arg	Ile	Lys	Lys	Lys	Gly	Ala	Asp	Glu	
	50					55					60					
Glu	Asn	Lys	Pro	Ala	Thr	Ser	Asp	Lys	Asp	Glu	Pro	Val	Leu	Ile	Lys	
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Asp	Ala	Leu	Glu	Ile	Gly	Leu	Asn	Asp	Ala	Gln	Asn	Ser	Phe	Ala	Ser	

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Leu	Asn	Val	Ala	Pro	Trp	Leu	Ile	Gly	Ser	Leu	Thr	Thr	Met	Ala	Val		
			100					105					110				
Arg	Lys	Pro	Thr	Ala	Ile	Gln	Lys	Ala	Cys	Ile	Pro	Glu	Ile	Leu	Asn		
		115					120					125					
Gly	Arg	Asp	Cys	Ile	Gly	Gly	Ser	Arg	Thr	Gly	Ser	Gly	Lys	Thr	Ile		
	130				135					140							
Ala	Phe	Ser	Val	Pro	Met	Leu	Gln	Lys	Trp	Ala	Glu	Asp	Pro	Phe	Gly		
145					150					155					160		
Ile	Phe	Gly	Leu	Val	Leu	Thr	Pro	Thr	Arg	Glu	Leu	Ala	Leu	Gln	Ile		
			165						170					175			
Tyr	Glu	Gln	Ile	Lys	Ala	Ile	Ser	Ala	Pro	Gln	Ser	Met	Lys	Pro	Leu		
			180					185					190				
Leu	Ile	Thr	Gly	Gly	Thr	Asp	Met	Arg	Pro	Gln	Ala	Val	Ala	Leu	Ala		
		195					200					205					
Gln	Arg	Pro	His	Val	Val	Ile	Ala	Thr	Pro	Gly	Arg	Leu	Ala	Asp	His		
	210					215				220							
Ile	Asn	Thr	Ser	Gly	Ser	Asp	Thr	Ile	Arg	Gly	Leu	Lys	Arg	Val	Arg		
225				230						235				240			
Met	Val	Val	Leu	Asp	Glu	Ala	Asp	Arg	Leu	Leu	Ala	Pro	Gly	His	Gly		
			245						250					255			
Ser	Met	Leu	Pro	Asp	Val	Glu	Thr	Cys	Leu	Ser	Ala	Leu	Pro	Pro	Ser		
			260					265					270				
Ser	Glu	Arg	Gln	Thr	Leu	Leu	Phe	Thr	Ala	Thr	Leu	Thr	Pro	Glu	Val		
	275						280					285					
Arg	Ala	Leu	Lys	Ser	Met	Pro	Arg	Pro	Ser	Thr	Lys	Pro	Pro	Ile	Phe		
	290				295					300							
Val	Thr	Glu	Ile	Ser	Thr	Glu	Asn	Asn	Ala	Ser	Ile	Pro	Pro	Thr	Leu		
305					310					315					320		
Lys	Gln	Thr	Tyr	Leu	Lys	Val	Pro	Met	Thr	His	Arg	Glu	Ala	Phe	Leu		
			325						330					335			
His	Val	Leu	Leu	Ser	Thr	Glu	Ala	Asn	Ala	Ser	Lys	Pro	Ala	Ile	Ile		
			340					345					350				
Phe	Cys	Asn	His	Thr	Lys	Thr	Ala	Asp	Leu	Leu	Glu	Arg	Met	Leu	Arg		
	355						360					365					
Arg	Leu	Ser	His	Arg	Val	Thr	Ser	Leu	His	Ser	Leu	Leu	Pro	Gln	Ser		
	370					375					380						
Glu	Arg	Asn	Ala	Asn	Leu	Ala	Arg	Phe	Arg	Ala	Ser	Ala	Ala	Arg	Leu		
385				390					395					400			
Leu	Val	Ala	Thr	Asp	Val	Ala	Ser	Arg	Gly	Leu	Asp	Ile	Pro	Ser	Val		
			405						410					415			
Glu	Leu	Val	Val	Asn	Phe	Asp	Val	Pro	Arg	Asn	Pro	Asp	Asp	Tyr	Val		
			420					425					430				
His	Arg	Val	Gly	Arg	Thr	Ala	Arg	Ala	Gly	Arg	Lys	Gly	Glu	Ser	Val		
	435					440						445					
Thr	Leu	Val	Gly	Gln	Arg	Asp	Val	Ser	Leu	Val	Leu	Ala	Ile	Glu	Glu		
	450					455					460						
Arg	Val	Gly	Arg	Gln	Met	Glu	Glu	Trp	Ser	Glu	Glu	Gly	Val	Ser	Val		
465				470						475				480			
Glu	Gly	Arg	Val	Val	Arg	Thr	Gly	Val	Leu	Lys	Glu	Val	Gly	Glu	Ala		
			485						490					495			
Lys	Arg	Glu	Ala	Ala	Gly	Glu	Ile	Glu	Glu	Gly	Arg	Asp	Val	Leu	Gly		
			500					505					510				
Arg	Lys	Arg	Asn	Lys	Leu	Lys	Lys	Val	Arg								
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<210> 52  
 <211> 1951  
 <212> DNA  
 <213> *Aspergillus niger*

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 ttttgcttgt aattaggagc gctgtgtggg ggtgtatctt gctttcgtag tgacattgca 180  
 gataagctaa aactgtgaaa ggcgctacaa aatactatag aacgtcaa atcatcgacat 240  
 tctcagagcc catcagtga gctgaaatac tcatcattct aagttctcct gcactgagaa 300  
 acccctcctc atctctagta gtcattccgca gtgatataaa atccaagcca aagcggcaga 360  
 aaacctgccc cacaatttct cttttcagct ttgtttccct gacgtaacat tcatcaactc 420  
 atctctccca catcgcgaaat ccatttcaat tatcatccac cacaacatat cagataataa 480  
 acaaataatc catcatgac gatcacaaca tcttcgaaga cctgcaggcc aagattgacg 540  
 aggaggccgc ggtccgcgat gtaagttgac ccgtgcccgc gccaaagcga gagacaaaac 600  
 cgaaagcaaa gcgccgttgt gttacaaga tgtacaggag cttcacgata ttgtgcagac 660  
 gcttgctaga aagggtactt acctacttac ctatccctat atgaattctc agaattggga 720  
 ttatctcgat ttgagattcg tcgactgact attaggatcg gattatagga agatctaccc 780  
 aggctattct ttcgcgagct cattctactc ccactgatca gtgtatgatt gactcctctc 840  
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 atgacgcaac caaggagatc atcgcccaga gggatgaagt atctcggttg aagactgtgg 960  
 cggacaagca cccgttttcc aagtacaatg ggggtgtggac gcgcgagttg cagaaccttg 1020  
 tgcgtgcccc ttctgttact ggggttttgtt tattgcagac gagagcta at cagccaatca 1080  
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 cagctcctct tcgtttctga cgatagaaga ggttggaat ttcctgggtg gtaggttctc 1200  
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 tacagggttaa gaagggtggag gatgtcgttt acgatctctc tttgcgcaat ttgattccca 1680  
 agggtagcgc tgcggcgtaa attaaacaca gagacttaaa ttagcatatg atatgaacat 1740  
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 cctagagtaa tgtaacaacc attatataat actcagtata taaaagacag cagctgcaac 1860  
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 tattaatata gtacttcctc cgacacacac a 1951

<210> 53  
 <211> 708  
 <212> DNA  
 <213> *Aspergillus niger*

<220>  
 <221> CDS  
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<400> 53  
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 gag gcc gcg gtc cgc gat gag ctt cac gat att gtg cag acg ctt gct 96  
 Glu Ala Ala Val Arg Asp Glu Leu His Asp Ile Val Gln Thr Leu Ala  
 20 25 30

aga aag gga aga tct acc cag gct att ctt tcg cga gct cat tct act	144
Arg Lys Gly Arg Ser Thr Gln Ala Ile Leu Ser Arg Ala His Ser Thr	
35 40 45	
ccc act gat cag ttg aaa ccc gtt ctc gat gac gca acc aag gag atc	192
Pro Thr Asp Gln Leu Lys Pro Val Leu Asp Asp Ala Thr Lys Glu Ile	
50 55 60	
atc gcc cag agg gat gaa gta tct cgg ttg aag act gtg gcg gac aag	240
Ile Ala Gln Arg Asp Glu Val Ser Arg Leu Lys Thr Val Ala Asp Lys	
65 70 75 80	
cac ccg ttt tac aag tac aat ggg gtg tgg acg cgc gag ttg cag aac	288
His Pro Phe Tyr Lys Tyr Asn Gly Val Trp Thr Arg Glu Leu Gln Asn	
85 90 95	
ctt gtc tcg tcg atc gag ctc tgc gct tgg cta ggc gga ctg gaa gag	336
Leu Val Ser Ser Ile Glu Leu Cys Ala Trp Leu Gly Gly Leu Glu Glu	
100 105 110	
tac aag acg aac agc tcc tct tcg ttt ctg acg ata gaa gag gtt gga	384
Tyr Lys Thr Asn Ser Ser Ser Ser Phe Leu Thr Ile Glu Glu Val Gly	
115 120 125	
aat ttc ctg ggt gtc ccc gtg aat ctc aaa gaa cag gat gcc ttc cat	432
Asn Phe Leu Gly Val Pro Val Asn Leu Lys Glu Gln Asp Ala Phe His	
130 135 140	
ctc act att gag gag tat ttg ctt gcg ctg att tcc atg gtc gag gag	480
Leu Thr Ile Glu Glu Tyr Leu Leu Ala Leu Ile Ser Met Val Glu Glu	
145 150 155 160	
ctg gcc cgt ctg gct gtc aac tcg gtc act ctg ggt gac tat acc cgg	528
Leu Ala Arg Leu Ala Val Asn Ser Val Thr Leu Gly Asp Tyr Thr Arg	
165 170 175	
ccg gtg caa att ggc aac ttc atc aag gat ttg ttt gcg ggc ttc cag	576
Pro Val Gln Ile Gly Asn Phe Ile Lys Asp Leu Phe Ala Gly Phe Gln	
180 185 190	
ttg ctg aac ctg aag aat gat att ttg cgg aag agg agt gat gga att	624
Leu Leu Asn Leu Lys Asn Asp Ile Leu Arg Lys Arg Ser Asp Gly Ile	
195 200 205	
aaa tac agt gtt aag aag gtg gag gat gtc gtt tac gat ctc tct ttg	672
Lys Tyr Ser Val Lys Lys Val Glu Asp Val Val Tyr Asp Leu Ser Leu	
210 215 220	
cgc aat ttg att ccc aag ggt agc gct gcg gcg taa	708
Arg Asn Leu Ile Pro Lys Gly Ser Ala Ala Ala	
225 230 235	

<210> 54

<211> 235

<212> PRT

<213> *Aspergillus niger*

<400> 54

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Arg Lys Gly Arg Ser Thr Gln Ala Ile Leu Ser Arg Ala His Ser Thr	
35 40 45	
Pro Thr Asp Gln Leu Lys Pro Val Leu Asp Asp Ala Thr Lys Glu Ile	
50 55 60	
Ile Ala Gln Arg Asp Glu Val Ser Arg Leu Lys Thr Val Ala Asp Lys	
65 70 75 80	

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

<210> 55

<211> 4547

<212> DNA

<213> *Aspergillus niger*

<400> 55

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caagcgagcg	cgccacctga	tccgatggcc	agggccattt	taccagagg	tcctgtatca	180
tggatagcag	gcacgaaaat	gccgagaaaag	gaggggtgag	tcggttacta	gcgttcagga	240
ttcaggcagt	cgactcgctc	ctggtgtttt	gcaagaggat	gagtagtgag	gagtcgtaat	300
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Pro Ser Val Val His Gln Asp Leu Gln Ala Asn Gly Lys Leu Lys Asn	
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Pro Tyr Val Gly Phe Asn Glu Leu Asp Ala Arg Trp Val Asn Glu Lys	
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Ser Arg Ile Val Leu Ala Phe Asp Gly Leu Asp Thr Phe Ala Lys Val	
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<213> *Aspergillus niger*

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Phe	Val	Met	Gln	Ala	Ala	Arg	Trp	Ile	Arg	Lys	Arg	Cys	Asp	Glu	Val	
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Gln	Pro	Ser	Ser	Gln	Ala	Arg	Pro	Ser	Ala	Thr	Ala	Ser	Ala	Thr	Ala	
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Gln	Lys	Val	Met	Thr	Pro	Ile	Pro	Phe	Asn	Asn	Arg	Asp	Ala	Ile	Ala	
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Thr	His	Glu	Glu	Thr	Arg	Gln	His	Thr	Glu	Asn	His	Pro	Glu	Arg	Ser	
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Ser	Ile	Met	Ser	Thr	Ala	Lys	Lys	Leu	Arg	Asp	Pro	Ala	Gly	Thr	Gln
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Tyr	Phe	Gly	Gln	Lys	Ser	Pro	Leu	Thr	Tyr	Leu	Asp	Val	Glu	His	Ile
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Ser	Leu	Glu	Arg	Phe	Thr	Asp	Ala	Arg	Gly	Glu	Leu	Pro	Ser	Arg	Tyr
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Met Gly Asp Glu Lys Lys Gly Gln Tyr Val Thr Val Ala Glu Tyr Phe		
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Lys Arg Gln Tyr Asn Met Pro Leu Arg Glu Gly Gln Met Pro Val		
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Leu Asn Val Gly Thr Leu Asp Arg Pro Val Tyr Leu Pro Ala Glu Leu		
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Cys Glu Ala Leu Pro Gly Gln Pro Cys Thr Ala Glu Leu Gly Leu Ile		
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Gln Arg Gln Asn Met Ile Lys Phe Ser Cys Arg Arg Pro Pro Gln Asn		
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Tyr Asp Ser Ile Met Thr Glu Gly Leu Asn Leu Met Gly Ile Ser Gly		
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Gly His Thr Lys Ala Val Gly Ile Lys Pro Gly Lys Glu Met Ile Thr		
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Ser	Gly	Asn	Leu	Pro	Gln	Asn	Ile	Leu	Val	Tyr	Arg	Asp	Gly	Val	Ser	
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Asp	Glu	Ile	Phe	Thr	Asn	Ser	Lys	Ala	Asn	Pro	Asp	Arg	Lys	Pro	Val	
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 <212> DNA  
 <213> *Penicillium chrysogenum*

<400> 122

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Gln	Pro	Val	Val	Val	Pro	Gly	Ala	Pro	Glu	Ser	Lys	Gly	Asn	Lys	Gly		
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Lys	Lys	Gly	Lys	Lys	Ala	Pro	Thr	Ala	Gly	Pro	Ala	Glu	Ala	Gly	Arg		
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Tyr	Ile	Thr	Val	Ala	Asp	Phe	Phe	Lys	Lys	Glu	Tyr	Asn	Met	Ala	Leu		
				485				490						495			
aat	gca	aac	ctc	cca	gtg	gtg	aat	gtc	ggg	tct	cgt	gac	aga	cct	gtc	1536	
Asn	Ala	Asn	Leu	Pro	Val	Val	Asn	Val	Gly	Ser	Arg	Asp	Arg	Pro	Val		
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Tyr	Leu	Pro	Val	Glu	Val	Cys	Asp	Val	Glu	Ala	Gly	Gln	Pro	Ala	Lys		
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Ser	Lys	Leu	Ser	Gly	Asp	Gln	Thr	Ala	Ser	Met	Leu	Arg	Phe	Ala	Val		
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Val	Gly	Val	Leu	Gly	Leu	Gly	Glu	Pro	Leu	Asn	Ala	Thr	Leu	Ser	Ala		
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Phe	Gly	Val	Asn	Ser	Ser	Thr	Glu	Leu	Ile	Thr	Val	Pro	Gly	Arg	Val		
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Leu	Pro	Ala	Pro	Ser	Val	Thr	Tyr	Arg	Asp	Gly	Asn	Arg	Thr	Lys	Glu		
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Lys	Ala	Ala	Pro	Met	Lys	Ser	Trp	Thr	Tyr	Leu	Tyr	Ile	Asp	Gln	Glu		
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Ala	Gly	Phe	Arg	Lys	Thr	Leu	Lys	Asp	Met	Gly	Met	Ser	Val	Asp	Pro	
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		675					680					685				
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Asp	Leu	Glu	Glu	Ala	Val	Val	Glu	Leu	Lys	Asn	Lys	Leu	Asn	Pro	Val	
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Val	Lys	Gln	Val	Cys	Asp	Val	Arg	Val	Gly	Ile	Arg	Asn	Val	Asn	Val	
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Gly	Leu	Lys	Ile	Asn	Leu	Lys	Leu	Gly	Gly	Ala	Asn	Gln	Ala	Leu	Arg	
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Thr	Gln	Asp	Leu	Gly	Ile	Ile	Ser	Glu	Gly	Lys	Thr	Met	Leu	Val	Gly	
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Ile	Asp	Val	Thr	His	Pro	Ser	Pro	Gly	Ser	Ala	Ser	Thr	Ala	Pro	Ser	
785					790					795					800	
gtc	gca	ggc	atc	gtc	gcc	tcc	gtg	gac	gga	acg	ctc	gcc	caa	tgg	ccc	2448
Val	Ala	Gly	Ile	Val	Ala	Ser	Val	Asp	Gly	Thr	Leu	Ala	Gln	Trp	Pro	
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gcc	gag	atc	cgc	gtc	caa	ggc	gcc	cgc	caa	gaa	atg	gtc	gcc	gac	ctc	2496
Ala	Glu	Ile	Arg	Val	Gln	Gly	Ala	Arg	Gln	Glu	Met	Val	Ala	Asp	Leu	
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gaa	acc	ctc	ctg	gcc	gga	cgt	ctc	cag	cac	tgg	cgc	aag	cta	aac	aaa	2544
Glu	Thr	Leu	Leu	Ala	Gly	Arg	Leu	Gln	His	Trp	Arg	Lys	Leu	Asn	Lys	
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Ser	Leu	Pro	Glu	Asn	Ile	Ile	Val	Tyr	Arg	Asp	Gly	Val	Ser	Glu	Gly	
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Gln	Tyr	Asn	Lys	Val	Ile	Asp	Glu	Glu	Leu	Pro	Leu	Leu	Gln	Glu	Ala	
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Cys	Lys	Lys	Thr	Tyr	Pro	Ala	Asp	Gln	Thr	Lys	Lys	Gly	Leu	Pro	Arg	
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Thr	Thr	Glu	Gln	Asp	Ser	Asn	Arg	Glu	Asn	Pro	Ile	Pro	Gly	Thr	Val	
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Val	Asp	Arg	Gly	Val	Ser	Glu	Pro	Arg	Asp	Trp	Asp	Phe	Phe	Leu	Gln	
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ccc	ggc	gca	gct	gat	gtc	ctc	cag	gac	ctc	act	cac	aag	atg	tgc	tac		2976
Pro	Gly	Ala	Ala	Asp	Val	Leu	Gln	Asp	Leu	Thr	His	Lys	Met	Cys	Tyr		
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Met	Phe	Gly	Arg	Ala	Thr	Lys	Ala	Val	Ser	Val	Cys	Pro	Pro	Ala	Tyr		
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Tyr	Ala	Asp	Leu	Val	Cys	Thr	Arg	Ala	Arg	Cys	Phe	Leu	Ser	Asp	Leu		
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Phe	Asp	Pro	Leu	Pro	Val	Asp	Ser	Thr	Ala	Gly	Ser	Thr	Ser	Gly	Thr		
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gag	ggc	gcg	gcg	gat	atg	aac	cgc	agg	gat	gat	gtc	aac	atc	cat	cct		3168
Glu	Gly	Ala	Ala	Asp	Met	Asn	Arg	Arg	Asp	Asp	Val	Asn	Ile	His	Pro		
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aac	att	gcc	gag	act	atg	ttc	tac	atc	tag								3198
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<212> PRT

<213> *Penicillium chrysogenum*

<400> 124

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Gly	Asp	Arg	Gly	Arg	Gly	Arg	Gly	Gly	Gly	Asp	Phe	Arg	Gly	Gly	Arg		
			85					90						95			
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Gly	Glu	Pro	Ile	Pro	Pro	Pro	Asn	Pro	Thr	Val	Thr	Lys	Thr	Glu	Asn		
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Asp	Leu	Ala	Lys	Ala	Leu	Ala	Val	Ser	Ser	Lys	Lys	Thr	Pro	Arg	Gln		
	130					135					140						
Ala	Lys	Tyr	Pro	Glu	Arg	Pro	Gly	Tyr	Gly	Thr	Ala	Gly	Arg	Pro	Val		
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Phe	Arg	Tyr	His	Ile	Ser	Ile	Ala	Ala	Asp	Ser	Thr	Gly	Arg	Ala	Ala		
			180					185					190				
Pro	Val	Gly	Lys	Lys	Ala	Arg	His	Ile	Val	Arg	Leu	Leu	Leu	Glu	Glu		
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His	Phe	Pro	Glu	Gln	Lys	Asn	Ser	Ile	Ala	Ser	Asp	Phe	Arg	Ser	Thr		
	210					215					220						
Leu	Val	Ser	Cys	Val	Lys	Leu	Thr	Glu	Gly	Lys	Phe	Asp	Val	Arg	Tyr		



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Lys	Glu	His	Leu	Asp	Asp	Asp	Tyr	Leu	Asp	Pro	Pro	Arg	Val	His
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Val	Thr	Cys	Gln	Tyr	Thr	Gly	Glu	Leu	Asn	Pro	Ala	Asp	Leu	Val
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Tyr	Leu	Thr	Ser	Thr	Ser	Ala	Gly	Ala	Met	Leu	Glu	Ser	Lys	Ser
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Asp	Thr	Met	Glu	Ser	Phe	Asn	Leu	Gly	Gly	Leu	Ser	Val	Leu	Arg
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Gly	Phe	Phe	Val	Ser	Val	Arg	Ala	Ala	Thr	Ala	Arg	Val	Leu	Leu
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Val	Gln	Val	Lys	Tyr	Leu	Ala	Cys	Tyr	Asn	Glu	Gly	Pro	Leu	Val
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Val	Ile	Gln	Gly	Tyr	Gly	Asn	Arg	Asn	Thr	Tyr	Arg	Leu	Glu	Lys
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Leu	Lys	Ser	Leu	Arg	Val	Arg	Ile	Thr	His	Ile	Thr	Arg	Lys	Asn
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Arg	Gly	Gln	Pro	Arg	Pro	Arg	Ile	Arg	Pro	Ile	Tyr	Gly	Leu	Ala
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Arg	Gly	Asp	Gly	Gly	Ser	Ser	Pro	Asn	Ala	Pro	Lys	Val	Ser	Arg
			420					425					430	His
Gly	Ala	Gly	Pro	Gln	Asp	Val	Gln	Phe	Phe	Leu	Ala	Glu	Ser	Ser
		435					440					445		Pro
Gln	Pro	Val	Val	Val	Pro	Gly	Ala	Pro	Glu	Ser	Lys	Gly	Asn	Lys
	450					455					460			Gly
Lys	Lys	Gly	Lys	Lys	Ala	Pro	Thr	Ala	Gly	Pro	Ala	Glu	Ala	Gly
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Tyr	Ile	Thr	Val	Ala	Asp	Phe	Phe	Lys	Lys	Glu	Tyr	Asn	Met	Ala
				485					490					495
Asn	Ala	Asn	Leu	Pro	Val	Val	Asn	Val	Gly	Ser	Arg	Asp	Arg	Pro
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Tyr	Leu	Pro	Val	Glu	Val	Cys	Asp	Val	Glu	Ala	Gly	Gln	Pro	Ala
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Ser	Lys	Leu	Ser	Gly	Asp	Gln	Thr	Ala	Ser	Met	Leu	Arg	Phe	Ala
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Phe	Gly	Val	Asn	Ser	Ser	Thr	Glu	Leu	Ile	Thr	Val	Pro	Gly	Arg
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His	Lys	Pro	Gly	Lys	Arg	Val	Phe	Leu	Thr	Gly	Lys	Asn	Asp	Ala
		675					680					685		Asn

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 Phe Ile Leu Gly Ile Leu Tyr Thr Lys Asp Thr Gly Val Tyr Asn Cys  
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 Val Lys Gln Val Cys Asp Val Arg Val Gly Ile Arg Asn Val Asn Val  
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 Leu Ala Glu Lys Leu Ala Asn Ser Asn Asp Gln Tyr Asn Ala Asn Val  
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 Gly Leu Lys Ile Asn Leu Lys Leu Gly Gly Ala Asn Gln Ala Leu Arg  
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 Thr Gln Asp Leu Gly Ile Ile Ser Glu Gly Lys Thr Met Leu Val Gly  
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 Ile Asp Val Thr His Pro Ser Pro Gly Ser Ala Ser Thr Ala Pro Ser  
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 Ala Glu Ile Arg Val Gln Gly Ala Arg Gln Glu Met Val Ala Asp Leu  
 820 825 830  
 Glu Thr Leu Leu Ala Gly Arg Leu Gln His Trp Arg Lys Leu Asn Lys  
 835 840 845  
 Ser Leu Pro Glu Asn Ile Ile Val Tyr Arg Asp Gly Val Ser Glu Gly  
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 Thr Thr Glu Gln Asp Ser Asn Arg Glu Asn Pro Ile Pro Gly Thr Val  
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 930 935 940  
 Ala His Ser Ala Leu Gln Gly Thr Ala Arg Pro Ala His Tyr Phe Thr  
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 Val Trp Asp Glu Ile Phe Tyr Pro Arg Tyr Pro Ala Asn Ser Gly Gly  
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 Pro Gly Ala Ala Asp Val Leu Gln Asp Leu Thr His Lys Met Cys Tyr  
 980 985 990  
 Met Phe Gly Arg Ala Thr Lys Ala Val Ser Val Cys Pro Pro Ala Tyr  
 995 1000 1005  
 Tyr Ala Asp Leu Val Cys Thr Arg Ala Arg Cys Phe Leu Ser Asp Leu  
 1010 1015 1020  
 Phe Asp Pro Leu Pro Val Asp Ser Thr Ala Gly Ser Thr Ser Gly Thr  
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Asn	Asp	Leu	Glu	Gly	Met	Ile	Asn	Asp	His	Cys	Tyr	Gln	Tyr	Ile	Arg	
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tcg	aca	acc	tcc	gtc	tct	gtc	cac	cct	gca	atc	tac	tat	gcc	cac	ttg	2544

Ser	Thr	Thr	Ser	Val	Ser	Val	His	Pro	Ala	Ile	Tyr	Tyr	Ala	His	Leu	
		835					840					845				
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Ile	Ser	Val	Arg	Ala	Arg	His	His	Glu	Asp	Val	Pro	Ile	Thr	Ser	Gly	
		850					855					860				
ccc	caa	agt	ggc	ccg	gag	gtg	aaa	atg	acg	aac	ccg	aag	ccc	aag	gag	2640
Pro	Gln	Ser	Gly	Pro	Glu	Val	Lys	Met	Thr	Asn	Pro	Lys	Pro	Lys	Glu	
865						870				875					880	
cct	cga	gcc	aag	aga	ttg	ctt	ccc	att	gaa	ggc	acc	tca	aac	agg	ctg	2688
Pro	Arg	Ala	Lys	Arg	Leu	Leu	Pro	Ile	Glu	Gly	Thr	Ser	Asn	Arg	Leu	
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<210> 127

<211> 903

<212> PRT

<213> *Penicillium chrysogenum*

<400> 127

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





Trp	Gly	Gly	Lys	Met	Cys	Val	Val	Val	Ala	Asn	Lys	Arg	His	His	Leu
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Arg	Ala	Phe	Pro	Asp	Pro	Lys	Asn	Arg	Ala	Ala	Ala	Asp	Ser	His	Gly
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Asp	Trp	Asp	Phe	Leu	Leu	Tyr	Thr	His	Ile	Ala	Leu	Gln	Gly	Thr	Thr
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Arg	Pro	Val	His	Tyr	His	Val	Leu	Leu	Asp	Glu	Met	Gly	Leu	Lys	Pro
			805						810					815	
Asn	Asp	Leu	Glu	Gly	Met	Ile	Asn	Asp	His	Cys	Tyr	Gln	Tyr	Ile	Arg
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Ser	Thr	Thr	Ser	Val	Ser	Val	His	Pro	Ala	Ile	Tyr	Tyr	Ala	His	Leu
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Ile	Ser	Val	Arg	Ala	Arg	His	His	Glu	Asp	Val	Pro	Ile	Thr	Ser	Gly
	850					855					860				
Pro	Gln	Ser	Gly	Pro	Glu	Val	Lys	Met	Thr	Asn	Pro	Lys	Pro	Lys	Glu
865					870					875					880
Pro	Arg	Ala	Lys	Arg	Leu	Leu	Pro	Ile	Glu	Gly	Thr	Ser	Asn	Arg	Leu
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<210> 128

<211> 5357

<212> DNA

<213> *Penicillium chrysogenum*

<400> 128

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ccattgcgac	aacgcactca	gtcagtcctc	aaaattttctc	gtggaagggc	aggccatcct	180
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<210> 129

<211> 4182

<212> DNA

<213> *Penicillium chrysogenum*

<220>

<221> CDS

<222> (1) .. (4182)

<400> 129

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ggg	tac	caa	ctc	gaa	atg	tta	gag	gct	agc	cgc	aag	gaa	aat	atc	att	96
Gly	Tyr	Gln	Leu	Glu	Met	Leu	Glu	Ala	Ser	Arg	Lys	Glu	Asn	Ile	Ile	
			20					25						30		
gtc	gcg	atg	gac	aca	ggg	agt	gga	aaa	act	cat	atg	cat	ggt	tcc	agc	144
Val	Ala	Met	Asp	Thr	Gly	Ser	Gly	Lys	Thr	His	Met	His	Val	Ser	Ser	
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ttt	acc	ttt	tgt	cgg	cac	gtt	ttc	ctg	act	ggt	ttc	ttt	agt	gcc	att	192
Phe	Thr	Phe	Cys	Arg	His	Val	Phe	Leu	Thr	Val	Phe	Phe	Ser	Ala	Ile	
			50			55					60					
ctt	cgg	atc	ata	gat	gag	ctt	gag	aac	tcc	gat	tct	cca	gac	aaa	ctt	240
Leu	Arg	Ile	Ile	Asp	Glu	Leu	Glu	Asn	Ser	Asp	Ser	Pro	Asp	Lys	Leu	
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att	tgg	ttt	ttg	gcc	ccg	act	gtc	gca	ttg	agc	ctt	caa	cag	cat	gaa	288
Ile	Trp	Phe	Leu	Ala	Pro	Thr	Val	Ala	Leu	Ser	Leu	Gln	Gln	His	Glu	
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gtt	atc	act	agc	cag	atc	ctc	tct	gtg	aaa	acc	aaa	att	tta	act	ggg	336
Val	Ile	Thr	Ser	Gln	Ile	Leu	Ser	Val	Lys	Thr	Lys	Ile	Leu	Thr	Gly	
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Ala	Leu	Gly	His	Gly	Phe	Val	Arg	Met	Ser	Arg	Leu	Ala	Leu	Leu	Val	
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ttt	gat	gag	gct	cat	cat	tgc	aca	aaa	cgc	cat	ccg	gcg	aac	aag	att	528
Phe	Asp	Glu	Ala	His	His	Cys	Thr	Lys	Arg	His	Pro	Ala	Asn	Lys	Ile	
				165				170						175		
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Met	Gln	Asn	His	Tyr	His	Pro	Thr	Leu	Leu	Arg	Ser	Gly	Pro	Asn	Ala	
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gta	cct	cga	att	ttg	gga	ctc	act	gct	agt	cca	gtg	gtc	cgg	tcg	agc	624
Val	Pro	Arg	Ile	Leu	Gly	Leu	Thr	Ala	Ser	Pro	Val	Val	Arg	Ser	Ser	
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Gln Asn Glu Leu Glu Thr Ile Glu Ser Asn Leu Asn Ala Ile Cys Lys	
210 215 220	
act cca cgc gtc cat cgc act gag ctt ttg gaa aac acc cat cgc cct	720
Thr Pro Arg Val His Arg Thr Glu Leu Leu Glu Asn Thr His Arg Pro	
225 230 235 240	
cac ctt gag cgt gtc aat tac ata agt ttt gac gaa gcg cat tat ggt	768
His Leu Glu Arg Val Asn Tyr Ile Ser Phe Asp Glu Ala His Tyr Gly	
245 250 255	
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Ser Gly Ser Arg Leu Leu Leu Pro Leu Ile Glu Cys Cys Arg Ala Tyr	
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Asn Ile Glu Asp Asp Pro Trp Val Glu Ser Leu Arg Ser Lys Asp His	
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Thr Val Glu Leu Thr Lys Ala Leu Thr Thr Gly Lys Thr Phe Cys Ser	
290 295 300	
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Leu Gly Gly Trp Ala Val Asp Phe Phe Ile Ser Ala Ser Ile Asp Gln	
325 330 335	
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Leu Gln Arg Ser Met Gln Asp Ala Ser Glu Met Ser His Leu Asp Gln	
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355 360 365	
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Val Ser Ala Glu Glu Ser Asn His Val Ser Val Lys Leu Glu Met Leu	
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ctc aac ttc ctt gag aaa atg gat agg cct ggg ttt tcc ggg ctg cta	1200
Leu Asn Phe Leu Glu Lys Met Asp Arg Pro Gly Phe Ser Gly Leu Leu	
385 390 395 400	
ttt gcc aag cag aga gca act gtc agt gtg tta gct cgc att cta tcc	1248
Phe Ala Lys Gln Arg Ala Thr Val Ser Val Leu Ala Arg Ile Leu Ser	
405 410 415	
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Ile His Pro Lys Thr Arg Asp Arg Phe Gln Cys Ala Ala Tyr Val Gly	
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Phe	Asp	Glu	Ala	His	His	Cys	Thr	Lys	Arg	His	Pro	Ala	Asn	Lys	Ile
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Thr	Val	Glu	Leu	Thr	Lys	Ala	Leu	Thr	Thr	Gly	Lys	Thr	Phe	Cys	Ser
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<213> *Penicillium chrysogenum*

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Lys	His	Trp	Ser	Glu	Lys	Arg	Leu	Asp	Leu	Met	Arg	Glu	Arg	Asp	Trp
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<212> DNA

<213> *Penicillium chrysogenum*

<220>

<221> CDS

<222> (1) .. (621)

<400> 138

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Val	Ser	Val	Val	Ala	Ile	Phe	Trp	Ala	Leu	Asp	Thr	Leu	Ile	Arg	Phe	
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Ser	Thr	Thr	Lys	Arg	Ser	Ala	Ser	Phe	Val	Ala	Phe	Val	Asp	Leu	Leu	
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<210> 139

<211> 206

<212> PRT

<213> *Penicillium chrysogenum*

<400> 139

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<210> 140  
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 <213> *Penicillium chrysogenum*

<400> 140

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<210> 141

<211> 2049

<212> DNA

<213> *Penicillium chrysogenum*

<220>

<221> CDS

<222> (1) .. (2049)

<400> 141

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His Ala Pro Gln Gly Asn Ala Pro Val Gly Arg Ala Ala Tyr Ile Pro	
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ccc cac ctt cgt cag cgt ggt ccc ggc cct gcc ccc agt gct aac gct	144
Pro His Leu Arg Gln Arg Gly Pro Gly Pro Ala Pro Ser Ala Asn Ala	
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ggt gct cct tct ggc ttc ggt ggt cct cgg tac agt aca cga aag act	192
Gly Ala Pro Ser Gly Phe Gly Gly Pro Arg Tyr Ser Thr Arg Lys Thr	
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gaa cat cgt gaa gcg gca act gat ttt gtg tct tct agt gac ggt ggc	240
Glu His Arg Glu Ala Ala Thr Asp Phe Val Ser Ser Ser Asp Gly Gly	
65 70 75 80	
aac tgg gcc aac gct aac gct ccc aac ttc agc cct cgt ggc ccc gcg	288
Asn Trp Ala Asn Ala Asn Ala Pro Asn Phe Ser Pro Arg Gly Pro Ala	
85 90 95	
aac ggt atg acc agc tgg act ccc gac gga aaa ctc cga ccc ttc aat	336



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His	Leu	Ile	Ala	Asn	Ile	Lys	Leu	Ala	Ser	Tyr	Val	Ile	Pro	Thr	Pro	
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<212> PRT

<213> *Penicillium chrysogenum*

<400> 142

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Trp	Arg	Asp	Gly	Lys	His	Val	Pro	Gly	Pro	Ala	Asn	Ala	Arg	Leu	Glu
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Arg	Glu	Leu	Phe	Gly	Val	Pro	Asn	Asp	Pro	Ser	Lys	Gln	Gln	Thr	Gly
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Asn	Arg	Asp	Gly	Asp	Ser	Tyr	Arg	Ser	Pro	Trp	Ser	Asn	Glu	Phe	Asp	
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<210> 145

<211> 266

<212> PRT

<213> *Penicillium chrysogenum*

<400> 145

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<210> 146

<211> 5564

<212> DNA

<213> *Penicillium chrysogenum*

<400> 146

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<210> 147  
 <211> 4107  
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<213> Penicillium chrysogenum

<220>

<221> CDS

<222> (1) .. (4107)

<400> 147

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Lys	Phe	Phe	Lys	Gly	Val	Thr	Asp	Ser	Arg	Ile	Pro	Asn	Tyr	Cys	Cys	
			450			455					460					
ttc	atg	cg	acc	gcg	cga	atc	aca	cca	act	aca	att	tac	tac	aac	act	1440
Phe	Met	Arg	Thr	Ala	Arg	Ile	Thr	Pro	Thr	Thr	Ile	Tyr	Tyr	Asn	Thr	
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cca	act	gta	gac	atc	tca	aac	cga	gtc	gtg	cg	gaa	tgg	tct	aca	aaa	1488
Pro	Thr	Val	Asp	Ile	Ser	Asn	Arg	Val	Val	Arg	Glu	Trp	Ser	Thr	Lys	
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ggt	aca	cct	ggg	cg	ttt	ctt	cga	gtt	cga	ttt	aca	gat	gag	aag	act	1536
Gly	Thr	Pro	Gly	Arg	Phe	Leu	Arg	Val	Arg	Phe	Thr	Asp	Glu	Lys	Thr	
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gaa	ggt	cg	atc	aat	gct	tca	cag	aga	ggt	tgc	aac	gac	gaa	gtc	tac	1584
Glu	Gly	Arg	Ile	Asn	Ala	Ser	Gln	Arg	Gly	Cys	Asn	Asp	Glu	Val	Tyr	
			515				520						525			
acc	cg	gtc	aaa	agg	aca	ctg	gcc	aac	ggc	atc	gcc	att	gga	gat	cg	1632
Thr	Arg	Val	Lys	Arg	Thr	Leu	Ala	Asn	Gly	Ile	Ala	Ile	Gly	Asp	Arg	
			530			535					540					
cac	tac	gag	ttc	ctc	gca	ttc	ggc	aac	tct	cag	ttc	cg	gag	cat	ggc	1680
His	Tyr	Glu	Phe	Leu	Ala	Phe	Gly	Asn	Ser	Gln	Phe	Arg	Glu	His	Gly	
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gca	tac	ttc	gtt	gca	cca	gat	gcc	ggt	atc	tca	gcg	gga	act	atc	cg	1728
Ala	Tyr	Phe	Val	Ala	Pro	Asp	Ala	Gly	Ile	Ser	Ala	Gly	Thr	Ile	Arg	

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Ala	Trp	Met	Gly	Gln	Phe	Asn	His	Ile	Arg	Asn	Val	Ala	Lys	Tyr	Thr		
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gca	aga	cta	ggg	caa	tgc	ttt	tcg	acc	acc	cga	gct	ttc	act	gga	tcc		1824
Ala	Arg	Leu	Gly	Gln	Cys	Phe	Ser	Thr	Thr	Arg	Ala	Phe	Thr	Gly	Ser		
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tct	gtt	caa	act	att	ccg	tgc	gac	gac	att	atc	cgc	aac	ggc	ttc	aca		1872
Ser	Val	Gln	Thr	Ile	Pro	Cys	Asp	Asp	Ile	Ile	Arg	Asn	Gly	Phe	Thr		
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ttc	tcc	gac	ggg	gtt	gga	aag	att	tcc	aaa	ttc	ctc	gcc	cag	atg	gtc		1920
Phe	Ser	Asp	Gly	Val	Gly	Lys	Ile	Ser	Lys	Phe	Leu	Ala	Gln	Met	Val		
	625				630					635					640		
aca	tcc	cag	cac	gat	att	aag	act	ctc	act	gga	gaa	cct	cca	tca	gct		1968
Thr	Ser	Gln	His	Asp	Ile	Lys	Thr	Leu	Thr	Gly	Glu	Pro	Pro	Ser	Ala		
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ttc	cag	ttt	cgt	ctt	ggg	gga	gcc	aag	ggc	atg	ctg	gtg	gtc	tcg	aca		2016
Phe	Gln	Phe	Arg	Leu	Gly	Gly	Ala	Lys	Gly	Met	Leu	Val	Val	Ser	Thr		
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gac	cct	ctg	ccc	cag	gag	gta	cac	att	cga	cca	agt	cag	caa	aag	ttt		2064
Asp	Pro	Leu	Pro	Gln	Glu	Val	His	Ile	Arg	Pro	Ser	Gln	Gln	Lys	Phe		
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gaa	acc	agt	caa	gcc	ggc	ttg	gag	atc	atc	cgt	tgg	tcc	cag	tat	tct		2112
Glu	Thr	Ser	Gln	Ala	Gly	Leu	Glu	Ile	Ile	Arg	Trp	Ser	Gln	Tyr	Ser		
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Leu	Ala	Thr	Leu	Asn	Arg	Gln	Ile	Ile	Leu	Val	Leu	Ser	Ala	Leu	Gly		
	705			710					715					720			
atc	cca	gat	gaa	gtc	ttc	cat	agt	aaa	ctc	aat	acc	atg	ttg	ggg	agc		2208
Ile	Pro	Asp	Glu	Val	Phe	His	Ser	Lys	Leu	Asn	Thr	Met	Leu	Gly	Ser		
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Phe	His	Arg	Ala	Met	Leu	Asn	Asp	Ser	Lys	Ala	Ile	Asn	Leu	Leu	Gln		
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aag	tac	atc	gat	cca	aac	caa	atg	acc	cta	acc	tta	gcc	cag	atg	gta		2304
Lys	Tyr	Ile	Asp	Pro	Asn	Gln	Met	Thr	Leu	Thr	Leu	Ala	Gln	Met	Val		
		755				760						765					
tct	gat	ggc	ttc	cga	cga	aat	gag	gag	ccg	ttt	gtc	aat	aca	atg	ctc		2352
Ser	Asp	Gly	Phe	Arg	Arg	Asn	Glu	Glu	Pro	Phe	Val	Asn	Thr	Met	Leu		
	770				775						780						
gag	ctc	tgg	aaa	tcc	tgg	cat	ctc	aag	cac	ctt	aaa	gag	aaa	gca	aag		2400
Glu	Leu	Trp	Lys	Ser	Trp	His	Leu	Lys	His	Leu	Lys	Glu	Lys	Ala	Lys		
	785			790				795						800			
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Ile	Ala	Ile	Asp	Gln	Gly	Ala	Asn	Val	Leu	Gly	Val	Met	Asp	Glu	Thr		
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Gly	Val	Leu	Lys	Gly	Tyr	Phe	Arg	Lys	Glu	Leu	Pro	Ser	Arg	Arg	Ala		
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tcg	tat	gca	gag	aaa	ctg	gcc	gct	ctt	cct	gag	ata	ttt	gtg	cag	gtc		2544
Ser	Tyr	Ala	Glu	Lys	Leu	Ala	Ala	Leu	Pro	Glu	Ile	Phe	Val	Gln	Val		
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tgc	cgg	cta	gat	gga	ggg	ggg	gag	tat	gaa	gtc	att	gaa	ggg	ctc	tgc		2592
Cys	Arg	Leu	Asp	Gly	Gly	Gly	Glu	Tyr	Glu	Val	Ile	Glu	Gly	Leu	Cys		
	850				855						860						
att	ctg	gca	cgc	aac	cct	tcg	ctt	cac	cct	gga	gat	atc	cgt	gtg	gtt		2640
Ile	Leu	Ala	Arg	Asn	Pro	Ser	Leu	His	Pro	Gly	Asp	Ile	Arg	Val	Val		

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cga gca gta aac	cga tca gag ctg cac	gca ctc cgg gac gtg gtt gtg	2688				
Arg Ala Val Asn	Arg Ser Glu Leu His	Ala Leu Arg Asp Val Val Val					
	885	890	895				
ctt ccc caa act	ggc gac cag gac att	gcg agc atg tgc tcc ggg ggt	2736				
Leu Pro Gln Thr	Gly Asp Gln Asp Ile	Ala Ser Met Cys Ser Gly Gly					
	900	905	910				
gat ctc gat ggt	gat gac tac ctc gtt att	tgg gac ccc aat ctg atc	2784				
Asp Leu Asp Gly	Asp Asp Tyr Leu Val	Ile Trp Asp Pro Asn Leu Ile					
	915	920	925				
ccc gca aac tgg	ttc gtc gag tgc atg gac tac	aag ggt tcc aaa gcg	2832				
Pro Ala Asn Trp	Phe Val Glu Cys Met Asp	Tyr Lys Gly Ser Lys Ala					
	930	935	940				
cca gac ctt gat	cat gat gtg act gtt gat	gag atc act tca ttc ttc	2880				
Pro Asp Leu Asp	His Asp Val Thr Val	Asp Glu Ile Thr Ser Phe Phe					
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gtc acc tat atg	aag aat gac tgc ctt ccc	cga att gcg cac gct cat	2928				
Val Thr Tyr Met	Lys Asn Asp Cys Leu	Pro Arg Ile Ala His Ala His					
	965	970	975				
tta gct tgg gct	gac aga ctc ccg agg	ggc gtt tgg gaa gac aag tgc	2976				
Leu Ala Trp Ala	Asp Arg Leu Pro Arg	Gly Val Trp Glu Asp Lys Cys					
	980	985	990				
att cgt ctc gcc	cag ctt cat tct gat	gca gtg gac tat aac aag agc	3024				
Ile Arg Leu Ala	Gln Leu His Ser Asp	Ala Val Asp Tyr Asn Lys Ser					
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Gly Ala His Ala	Arg Met Ala Arg Ser	Leu Asp Pro Lys Phe Trp Pro					
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His Phe Met Glu	Lys Arg Phe Lys Arg	Pro Ser Ser Ile Tyr Lys Ser					
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acc aaa atc ctc	ggc caa ctc tac gac	gca gtg ata acg cct gac ttc	3168				
Thr Lys Ile Leu	Gly Gln Leu Tyr Asp	Ala Val Ile Thr Pro Asp Phe					
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Val Pro Lys Leu	Glu Lys Pro Phe Asp	Ser Arg Ile Leu Glu Ser Pro					
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ctg gct ccg gca	agt gag gcc tac atg	gag tac gcc cgt gag ctc aag	3264				
Leu Ala Pro Ala	Ser Glu Ala Tyr Met	Glu Tyr Ala Arg Glu Leu Lys					
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Val Ile Lys Asp	Tyr Lys Met Gln Glu	Asp Leu Gly Arg Ile Val Gly					
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aca ctc cgc cgc	gga ttc cgc cac cag	tgc tat gac aaa gtc ggc cgt	3456				
Thr Leu Arg Arg	Gly Phe Arg His Gln	Cys Tyr Asp Lys Val Gly Arg					
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Gln Glu Gln Val	Ala Ala Ala Leu Glu	Ala Arg Arg Asn Glu Ala Leu					

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Gln Arg Glu Asp Val Ser Ile Ala Glu Val Asn Ser Thr Glu Leu Pro			
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ctc att agc ttc cct tgg att ttc cct gac gtc ctc ggt gat gtt gcg			3648
Leu Ile Ser Phe Pro Trp Ile Phe Pro Asp Val Leu Gly Asp Val Ala			
1205	1210	1215	
acg ggc cgg gcg cga cag gcc atg atc tca gac gga caa gag agc gct			3696
Thr Gly Arg Ala Arg Gln Ala Met Ile Ser Asp Gly Gln Ser Ala			
1220	1225	1230	
gat tct gcg aag cct atc ggc gag ggt ttg gtc ttc act cac aag cag			3744
Asp Ser Ala Lys Pro Ile Gly Glu Gly Leu Val Phe Thr His Lys Gln			
1235	1240	1245	
atc ctc aag att gtt gag gat atg gat ggg gac atc aaa tcg acc gct			3792
Ile Leu Lys Ile Val Glu Asp Met Asp Gly Asp Ile Lys Ser Thr Ala			
1250	1255	1260	
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Glu Asn Met Lys Leu Lys Asp Pro Lys Asn Met Glu Pro Lys Ala Glu			
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Ala Gly Ser Asn Ser Ala Pro Pro Asp Gln Glu Leu Ile Ala Arg Arg			
1285	1290	1295	
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Arg Ile Asp Lys Thr Lys Pro Lys Gln Lys Ser Glu Asp Arg Asp Thr			
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Gly Leu Tyr Ile Glu Glu Asp Asp Glu Lys Glu Gly Gly Val Ala Ile			
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Gly Ser Ala Lys Thr Glu Glu Lys Ile Asp Lys Arg Glu Ala Val Thr			
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Pro Val Leu Asp Leu Pro Val Arg Asp Trp Ile Thr Trp Arg Ser Trp	
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Arg Thr Cys Ala Val Asp Leu Leu Asn Leu Pro Arg Glu Met Asn Thr	
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His Asp Ile Tyr Asp Ala Phe His Arg Tyr Gly Asn Met Ile Ser Ile	
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Asp Leu Trp Glu Asp Ala Ser Gly Arg Pro Asp Cys Lys Gly Arg Ile	
85 90 95	

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Cys	Cys	Gly	Asp	Ser	Asn	Gly	Thr	Ile	Gln	Ser	Pro	Val	Arg	Pro	Asp		
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Asn	Leu	Ala	Tyr	Pro	Arg	Cys	Val	Val	Asp	Val	Met	Arg	Lys	Cys	Leu		
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Phe	Leu	Tyr	Phe	Arg	Val	Gly	Ile	Arg	Gly	Ser	Asp	Thr	Ala	Asp	Val		
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Asn	Gln	His	Asp	His	Arg	Val	Lys	Ile	Thr	Phe	Leu	Gln	Leu	Thr	Gln		
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Ile	Tyr	Gln	Gln	Tyr	Asp	Lys	Ala	Thr	Arg	Glu	Arg	Ser	Leu	Leu	Ile		
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Val	Leu	Asp	Ser	Ala	Ala	Ile	Trp	His	Arg	Lys	Ala	Lys	Asp	Ile	Gln		
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Ser	Thr	Leu	Thr	Glu	Pro	Leu	Ser	Trp	Arg	Glu	Glu	Asp	Ser	Trp	Tyr		
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Arg	Gln	Thr	Ser	Val	Thr	His	Asn	Pro	Asn	Ser	Leu	Lys	Thr	Leu	Pro		
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Ala	Asn	Leu	Lys	Lys	Thr	Gly	His	Ile	Ile	Asp	Leu	Gly	Arg	Trp	Asn		
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				325				330						335			
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			340					345					350				
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Ser	Asn	Lys	Ala	Ser	Ala	Leu	Leu	Gln	Asp	Leu	Gly	Asn	Gln	Asn	Tyr		
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Leu	His	Leu	Pro	Phe	Lys	Val	Arg	Tyr	Gln	Leu	Glu	Val	Cys	Leu	Ser		
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Leu	Lys	Gly	Leu	Gly	Asp	Asp	Gln	Ala	Thr	Arg	Leu	Leu	Glu	Phe	Val		
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Ala	Thr	Glu	Lys	Lys	Gln	Tyr	Leu	Ala	Pro	Met	Glu	Ile	Phe	Asp	Leu		
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Lys	Phe	Lys	Gly	Val	Thr	Asp	Ser	Arg	Ile	Pro	Asn	Tyr	Cys	Cys			
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Thr	Arg	Val	Lys	Arg	Thr	Leu	Ala	Asn	Gly	Ile	Ala	Ile	Gly	Asp	Arg		
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	Leu	Pro	Gln	Thr	Gly	Asp	Gln	Asp	Ile	Ala	Ser	Met	Cys	Ser	Gly	Gly
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		660		665		670	
gga gga aag tct cta tgt tat caa tta cct tct gtg gta acg ggt gga	2064						
Gly Gly Lys Ser Leu Cys Tyr Gln Leu Pro Ser Val Val Thr Gly Gly							
		675		680		685	
cgc acc aca ggg gta aca atc gtt ata tcc cca ttg ttg agt ctg atg	2112						
Arg Thr Thr Gly Val Thr Ile Val Ile Ser Pro Leu Leu Ser Leu Met							

690	695	700	
gag gat cag gta tca cac ctg cgg aaa ctg aac att aag gcc ttc atg			2160
Glu Asp Gln Val Ser His Leu Arg Lys Leu Asn Ile Lys Ala Phe Met			
705	710	715	720
gtc aac ggc gac acc aac ccg gag gaa aaa tcc tgg atc atg agc cag			2208
Val Asn Gly Asp Thr Asn Pro Glu Glu Lys Ser Trp Ile Met Ser Gln			
	725	730	735
ctc tcg aac gca gct ggc gag ggg atg gag gtc ttg tac att act cct			2256
Leu Ser Asn Ala Ala Gly Glu Gly Met Glu Val Leu Tyr Ile Thr Pro			
	740	745	750
gag atg ctc agt aaa agc caa gcc ttg atc aga gcc ctt gag aag ctt			2304
Glu Met Leu Ser Lys Ser Gln Ala Leu Ile Arg Ala Leu Glu Lys Leu			
	755	760	765
cac gga aga aac aga cta gca cgc ctc gtc atc gac gag gct cac tgc			2352
His Gly Arg Asn Arg Leu Ala Arg Leu Val Ile Asp Glu Ala His Cys			
	770	775	780
gtc agc caa tgg gga cac gat ttc cga cct gat tac aag gag cta gga			2400
Val Ser Gln Trp Gly His Asp Phe Arg Pro Asp Tyr Lys Glu Leu Gly			
	785	790	800
gag gtt cga gcc agg ttc cct ggt gta cca gtc atg gcc ttg acg gcc			2448
Glu Val Arg Ala Arg Phe Pro Gly Val Pro Val Met Ala Leu Thr Ala			
	805	810	815
acc gcc act gag aat gtc aaa gtt gac gtg atg cat aat ctt aaa atc			2496
Thr Ala Thr Glu Asn Val Lys Val Asp Val Met His Asn Leu Lys Ile			
	820	825	830
act gac tgt gaa gtg ttc ttg caa agt ttt aac cgt cct aac ctc acc			2544
Thr Asp Cys Glu Val Phe Leu Gln Ser Phe Asn Arg Pro Asn Leu Thr			
	835	840	845
tac gag gta cgg tcg aag gga aag aat gac gag gtt ctg gcc agc atg			2592
Tyr Glu Val Arg Ser Lys Gly Lys Asn Asp Glu Val Leu Ala Ser Met			
	850	855	860
gcg gag acc att aca agc tca tat cag aat cag tgc gga att atc tac			2640
Ala Glu Thr Ile Thr Ser Ser Tyr Gln Asn Gln Cys Gly Ile Ile Tyr			
	865	870	875
tgc ctc tcg cga aag aca tgc gac aag gtt gca gag gat cta cag aag			2688
Cys Leu Ser Arg Lys Thr Cys Asp Lys Val Ala Glu Asp Leu Gln Lys			
	885	890	895
aag tac cac ctc aag gcg ctc gct tat cat gcc ggt atg tca gcc aag			2736
Lys Tyr His Leu Lys Ala Leu Ala Tyr His Ala Gly Met Ser Ala Lys			
	900	905	910
gta aaa tcg gaa gct cag agg aag tgg cag atg ggc cgg gtg cat atc			2784
Val Lys Ser Glu Ala Gln Arg Lys Trp Gln Met Gly Arg Val His Ile			
	915	920	925
att gtt gcc acc att gca ttc gga atg gga att gac aag gcc gat gtg			2832
Ile Val Ala Thr Ile Ala Phe Gly Met Gly Ile Asp Lys Ala Asp Val			
	930	935	940
cga ttc gtc atg cac cac agt atc ccg aag agt ctc gag ggg tat tat			2880
Arg Phe Val Met His His Ser Ile Pro Lys Ser Leu Glu Gly Tyr Tyr			
	945	950	955
caa gaa acc ggt cgt gct ggt cga gac ggc aaa cgt tct ggc tgc tat			2928
Gln Glu Thr Gly Arg Ala Gly Arg Asp Gly Lys Arg Ser Gly Cys Tyr			
	965	970	975
ctt tac ttc gga tac aaa gac aca gca acc ttg aag cgg atg atc gat			2976
Leu Tyr Phe Gly Tyr Lys Asp Thr Ala Thr Leu Lys Arg Met Ile Asp			
	980	985	990
gca gga gat ggc aat ggt cag caa aag gct cgt caa aaa cag atg ttg			3024
Ala Gly Asp Gly Asn Gly Gln Gln Lys Ala Arg Gln Lys Gln Met Leu			

	995		1000		1005											
cga	aac	gtg	gtt	caa	tat	tgt	gag	aac	cgt	agc	gat	tgc	aga	cga	gtg	3072
Arg	Asn	Val	Val	Gln	Tyr	Cys	Glu	Asn	Arg	Ser	Asp	Cys	Arg	Arg	Val	
	1010					1015					1020					
caa	gtc	ctc	gcc	tat	ttt	gcg	gaa	tac	ttc	cgc	cga	gag	gac	tgc	aac	3120
Gln	Val	Leu	Ala	Tyr	Phe	Ala	Glu	Tyr	Phe	Arg	Arg	Glu	Asp	Cys	Asn	
1025					1030				1035					1040		
aac	act	tgt	gat	aac	tgc	aag	tcc	gat	ctg	gtg	ttt	gag	ctc	cat	gac	3168
Asn	Thr	Cys	Asp	Asn	Cys	Lys	Ser	Asp	Leu	Val	Phe	Glu	Leu	His	Asp	
				1045					1050					1055		
ttt	act	gaa	cag	gcg	tcc	tgg	gcc	atc	aag	att	gtg	cga	caa	ttc	cag	3216
Phe	Thr	Glu	Gln	Ala	Ser	Trp	Ala	Ile	Lys	Ile	Val	Arg	Gln	Phe	Gln	
			1060				1065						1070			
aac	gca	aag	gag	aag	gtg	act	gtg	cta	tac	tgc	agt	gac	ata	ctt	cgc	3264
Asn	Ala	Lys	Glu	Lys	Val	Thr	Val	Leu	Tyr	Cys	Ser	Asp	Ile	Leu	Arg	
	1075						1080					1085				
ggg	gac	tgc	aaa	cgg	cct	aaa	gct	cca	gag	cat	cgc	atg	atg	ccg	gga	3312
Gly	Asp	Cys	Lys	Arg	Pro	Lys	Ala	Pro	Glu	His	Arg	Met	Met	Pro	Gly	
1090					1095				1100							
tac	ggg	aag	gga	tct	gac	ctc	gac	cgt	gga	gca	gcc	gaa	cgt	ctg	ttc	3360
Tyr	Gly	Lys	Gly	Ser	Asp	Leu	Asp	Arg	Gly	Ala	Ala	Glu	Arg	Leu	Phe	
1105				1110				1115						1120		
tac	cgg	ctg	ctg	ggt	gaa	gac	gca	ttg	gcc	gaa	gac	aat	gtg	atc	aat	3408
Tyr	Arg	Leu	Leu	Gly	Glu	Asp	Ala	Leu	Ala	Glu	Asp	Asn	Val	Ile	Asn	
				1125				1130						1135		
aaa	agt	gat	ttt	gct	att	caa	tat	ctc	att	ctc	ggc	cgc	cgt	gcg	gca	3456
Lys	Ser	Asp	Phe	Ala	Ile	Gln	Tyr	Leu	Ile	Leu	Gly	Arg	Arg	Ala	Ala	
			1140				1145						1150			
gag	tat	gag	agt	ggg	cag	cga	aag	atg	aaa	cta	ctg	ggt	cgc	gcg	tcg	3504
Glu	Tyr	Glu	Ser	Gly	Gln	Arg	Lys	Met	Lys	Leu	Leu	Val	Arg	Ala	Ser	
1155					1160							1165				
ccg	aat	agc	aag	gct	aaa	ggc	aag	agc	aaa	cct	tcg	gct	gcc	gca	cag	3552
Pro	Asn	Ser	Lys	Ala	Lys	Gly	Lys	Ser	Lys	Pro	Ser	Ala	Ala	Ala	Gln	
1170					1175							1180				
aag	aaa	aag	tct	ggc	ggc	gat	cct	cag	tcc	acc	atg	gtc	tct	tct	cca	3600
Lys	Lys	Lys	Ser	Gly	Gly	Asp	Pro	Gln	Ser	Thr	Met	Val	Ser	Ser	Pro	
1185				1190					1195					1200		
gtg	caa	gct	gcc	caa	gac	cgc	cgc	ctt	gac	cgt	tat	caa	tat	acc	ggt	3648
Val	Gln	Ala	Ala	Gln	Asp	Arg	Arg	Leu	Asp	Arg	Tyr	Gln	Tyr	Thr	Gly	
				1205				1210						1215		
gtt	cca	gct	gca	cgt	ctc	tcg	gtc	gat	gag	gat	agt	gat	ggc	ttc	gag	3696
Val	Pro	Ala	Ala	Arg	Leu	Ser	Val	Asp	Glu	Asp	Ser	Asp	Gly	Phe	Glu	
				1220				1225						1230		
ccg	att	cga	acc	acc	ggc	aag	cct	cgc	cgc	gca	aac	aca	cac	gaa	atg	3744
Pro	Ile	Arg	Thr	Thr	Gly	Lys	Pro	Arg	Arg	Ala	Asn	Thr	His	Glu	Met	
				1235			1240						1245			
ggc	cct	cca	atc	acc	agc	gat	cag	aaa	ttg	gat	caa	ctt	gat	cat	atg	3792
Gly	Pro	Pro	Ile	Thr	Ser	Asp	Gln	Lys	Leu	Asp	Gln	Leu	Asp	His	Met	
1250					1255						1260					
cat	cgt	gta	gtt	gtg	gag	gac	ttc	caa	gag	cat	gcc	aaa	atc	atg	ctt	3840
His	Arg	Val	Val	Val	Glu	Asp	Phe	Gln	Glu	His	Ala	Lys	Ile	Met	Leu	
1265					1270				1275					1280		
caa	gat	ctt	gtc	gtt	aag	aag	ggc	ctt	cgg	tgc	caa	ccg	ttc	tct	gat	3888
Gln	Asp	Leu	Val	Val	Lys	Lys	Gly	Leu	Arg	Cys	Gln	Pro	Phe	Ser	Asp	
				1285				1290						1295		
cag	gta	cta	cgt	gat	atg	ggc	atc	tcc	ttc	ccc	tca	agt	aaa	tac	tct	3936
Gln	Val	Leu	Arg	Asp	Met	Gly	Ile	Ser	Phe	Pro	Ser	Ser	Lys	Tyr	Ser	

	1300	1305	1310	
tct ttc atc aat ttg gaa cac caa gct aac aac gag ata gat ctt act				3984
Ser Phe Ile Asn Leu Glu His Gln Ala Asn Asn Glu Ile Asp Leu Thr				
	1315	1320	1325	
gag ctt tct gcg atc ccg gga atc gac caa gat aag gtg aag cgc tat				4032
Glu Leu Ser Ala Ile Pro Gly Ile Asp Gln Asp Lys Val Lys Arg Tyr				
	1330	1335	1340	
ggc cgg cag atc ctg gga ctg gtt gat aat gca aag cgg cgc tac ctg				4080
Gly Arg Gln Ile Leu Gly Leu Val Asp Asn Ala Lys Arg Arg Tyr Leu				
	1345	1350	1355	1360
gaa atg aag cag gaa gca gag acc ggc ggc att gtt ccg gat ccc aac				4128
Glu Met Lys Gln Glu Ala Glu Thr Gly Gly Ile Val Pro Asp Pro Asn				
	1365	1370	1375	
cac cat aat gtc atc aat ctc agc agc agt gat gag tat agt gac gac				4176
His His Asn Val Ile Asn Leu Ser Ser Ser Asp Glu Tyr Ser Asp Asp				
	1380	1385	1390	
gac ttg ttc atg gat gat gtt tct gtc ttc aat ctg gac aat cct gtt				4224
Asp Leu Phe Met Asp Asp Val Ser Val Phe Asn Leu Asp Asn Pro Val				
	1395	1400	1405	
tca acc gca ccc agc aat gcg gct gaa aat atc aca agc cgt tac ttc				4272
Ser Thr Ala Pro Ser Asn Ala Ala Glu Asn Ile Thr Ser Arg Tyr Phe				
	1410	1415	1420	
cct cca gca gca tct ccg ggg tat gac tct ggt gac gac tgg gaa tca				4320
Pro Pro Ala Ala Ser Pro Gly Tyr Asp Ser Gly Asp Asp Trp Glu Ser				
	1425	1430	1435	1440
ggt act gcg cct tcc ggc tcg aag agt cgc aag cgc cag cct gct agt				4368
Gly Thr Ala Pro Ser Gly Ser Lys Ser Arg Lys Arg Gln Pro Ala Ser				
	1445	1450	1455	
gga aaa cga ccg tca agg cgt aaa tat ggc tcc gct ggc agc tgg aag				4416
Gly Lys Arg Pro Ser Arg Arg Lys Tyr Gly Ser Ala Gly Ser Trp Lys				
	1460	1465	1470	
ggc aaa agc gca cga cca aag gcc aaa tcc ggc gat cgt cct aca agc				4464
Gly Lys Ser Ala Arg Pro Lys Ala Lys Ser Gly Asp Arg Pro Thr Ser				
	1475	1480	1485	
cag tca tct gcc ccg cga aag aat gcc agg gcc aaa acg cca aag tct				4512
Gln Ser Ser Ala Pro Arg Lys Asn Ala Arg Ala Lys Thr Pro Lys Ser				
	1490	1495	1500	
acg att gga atg atg cct att tga				4536
Thr Ile Gly Met Met Pro Ile				
1505	1510			

<210> 151

<211> 1511

<212> PRT

<213> Penicillium chrysogenum

<400> 151

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Gly Asn Pro Val Gln Pro Pro Leu Ala Gln Ile Ser Leu Pro Glu Arg	
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Asn Asn His Val Ser Gln Gln Ser Ile Pro Pro Thr Asp Glu Phe Ala	
35 40 45	
Ala Leu Asp Asp Ile Leu Glu Asp Ala Glu Asn Glu Thr Asp Ile Ser	
50 55 60	
Met Ala Arg Leu Leu Pro Gln Ser Ala Ser Lys Pro Arg Met Leu Ser	

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



His	Leu	Pro	Arg	Thr	Ser	Pro	Lys	Lys	Ala	Lys	Glu	Thr	Asn	Arg	Ala	530	535	540
Ser	Ser	Tyr	Glu	Asn	Cys	Ile	Ser	Arg	Asn	Met	Gly	Thr	Pro	Pro	Leu	545	550	555
Asp	Ser	Met	Glu	Leu	Asp	Glu	Phe	Asp	Trp	Asn	Val	Ser	Asp	Asp	Asp	565	570	575
Ile	Leu	Glu	Ala	Ala	Glu	Gly	Phe	Asp	Gly	Ala	Asp	Gln	Ile	Pro	Val	580	585	590
Arg	Glu	Gln	Ala	Thr	Gln	Asn	Arg	Arg	Val	Phe	Ala	Glu	Thr	Ser	Gly	595	600	605
Asn	Val	Pro	Lys	Ala	Pro	Val	Pro	Lys	Lys	Ser	Pro	Gly	His	Ser	Ala	610	615	620
Phe	Trp	Ser	Asn	His	Pro	Trp	Ser	Gln	Glu	Val	Arg	Lys	Val	Leu	Lys	625	630	635
Glu	Arg	Phe	His	Leu	Arg	Gly	Phe	Arg	Pro	Asn	Gln	Leu	Glu	Ala	Ile	645	650	655
Asp	Ala	Thr	Leu	Ala	Gly	Lys	Asp	Thr	Phe	Ile	Leu	Met	Pro	Thr	Gly	660	665	670
Gly	Gly	Lys	Ser	Leu	Cys	Tyr	Gln	Leu	Pro	Ser	Val	Val	Thr	Gly	Gly	675	680	685
Arg	Thr	Thr	Gly	Val	Thr	Ile	Val	Ile	Ser	Pro	Leu	Leu	Ser	Leu	Met	690	695	700
Glu	Asp	Gln	Val	Ser	His	Leu	Arg	Lys	Leu	Asn	Ile	Lys	Ala	Phe	Met	705	710	715
Val	Asn	Gly	Asp	Thr	Asn	Pro	Glu	Glu	Lys	Ser	Trp	Ile	Met	Ser	Gln	725	730	735
Leu	Ser	Asn	Ala	Ala	Gly	Glu	Gly	Met	Glu	Val	Leu	Tyr	Ile	Thr	Pro	740	745	750
Glu	Met	Leu	Ser	Lys	Ser	Gln	Ala	Leu	Ile	Arg	Ala	Leu	Glu	Lys	Leu	755	760	765
His	Gly	Arg	Asn	Arg	Leu	Ala	Arg	Leu	Val	Ile	Asp	Glu	Ala	His	Cys	770	775	780
Val	Ser	Gln	Trp	Gly	His	Asp	Phe	Arg	Pro	Asp	Tyr	Lys	Glu	Leu	Gly	785	790	795
Glu	Val	Arg	Ala	Arg	Phe	Pro	Gly	Val	Pro	Val	Met	Ala	Leu	Thr	Ala	805	810	815
Thr	Ala	Thr	Glu	Asn	Val	Lys	Val	Asp	Val	Met	His	Asn	Leu	Lys	Ile	820	825	830
Thr	Asp	Cys	Glu	Val	Phe	Leu	Gln	Ser	Phe	Asn	Arg	Pro	Asn	Leu	Thr	835	840	845
Tyr	Glu	Val	Arg	Ser	Lys	Gly	Lys	Asn	Asp	Glu	Val	Leu	Ala	Ser	Met	850	855	860
Ala	Glu	Thr	Ile	Thr	Ser	Ser	Tyr	Gln	Asn	Gln	Cys	Gly	Ile	Ile	Tyr	865	870	875
Cys	Leu	Ser	Arg	Lys	Thr	Cys	Asp	Lys	Val	Ala	Glu	Asp	Leu	Gln	Lys	885	890	895
Lys	Tyr	His	Leu	Lys	Ala	Leu	Ala	Tyr	His	Ala	Gly	Met	Ser	Ala	Lys	900	905	910
Val	Lys	Ser	Glu	Ala	Gln	Arg	Lys	Trp	Gln	Met	Gly	Arg	Val	His	Ile	915	920	925
Ile	Val	Ala	Thr	Ile	Ala	Phe	Gly	Met	Gly	Ile	Asp	Lys	Ala	Asp	Val	930	935	940
Arg	Phe	Val	Met	His	His	Ser	Ile	Pro	Lys	Ser	Leu	Glu	Gly	Tyr	Tyr	945	950	955
Gln	Glu	Thr	Gly	Arg	Ala	Gly	Arg	Asp	Gly	Lys	Arg	Ser	Gly	Cys	Tyr	965	970	975
Leu	Tyr	Phe	Gly	Tyr	Lys	Asp	Thr	Ala	Thr	Leu	Lys	Arg	Met	Ile	Asp			





agatcaaagg gttagacaca aggcaaactg ctagactttc tttagcacaa agagatctga	2400
aagagattaa cgaaaagtaa tcgctgtgtc accctcgttt ttgcaaacga ccaggacatg	2460
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 <211> 1527  
 <212> DNA  
 <213> *Penicillium chrysogenum*

<220>  
 <221> CDS  
 <222> (1) .. (1527)

<400> 153																		
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Met	Asp	Arg	Asn	Pro	Ala	Val	Thr	Arg	Gln	Thr	Ala	Asn	Met	Arg	Trp			
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gtc	ttg	aaa	cac	acc	ttc	aaa	aag	aat	gat	ttc	cgt	cca	ctt	caa	cga		96	
Val	Leu	Lys	His	Thr	Phe	Lys	Lys	Asn	Asp	Phe	Arg	Pro	Leu	Gln	Arg			
			20					25				30						
gaa	gtg	atc	tca	tcc	gtt	att	gaa	gga	cac	gat	gtc	ttt	ctc	caa	gca		144	
Glu	Val	Ile	Ser	Ser	Val	Ile	Glu	Gly	His	Asp	Val	Phe	Leu	Gln	Ala			
			35				40				45							
tgc	act	tcg	ttc	gga	aaa	agc	ttg	tgt	tat	caa	ctc	ccc	gcg	gta	ctg		192	
Cys	Thr	Ser	Phe	Gly	Lys	Ser	Leu	Cys	Tyr	Gln	Leu	Pro	Ala	Val	Leu			
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aaa	gat	tgg	ggc	ttg	act	gtc	gtc	ggt	tgt	cca	ctt	ctc	tca	ttg	atg		240	
Lys	Asp	Trp	Gly	Leu	Thr	Val	Val	Val	Cys	Pro	Leu	Leu	Ser	Leu	Met			
65				70				75						80				
acc	gac	caa	gta	aat	aca	ttg	aaa	gct	ctt	ggg	gtg	gca	gtc	gct	acg		288	
Thr	Asp	Gln	Val	Asn	Thr	Leu	Lys	Ala	Leu	Gly	Val	Ala	Val	Ala	Thr			
				85				90						95				
atc	aac	tcc	aat	act	act	cat	gat	gag	aga	cag	cga	ggt	ttt	gaa	gac		336	
Ile	Asn	Ser	Asn	Thr	Thr	His	Asp	Glu	Arg	Gln	Arg	Val	Phe	Glu	Asp			
			100				105					110						
atg	ctt	tgc	ggc	cac	ccg	agc	aca	cgc	ctt	cta	tac	gtc	aca	ccg	gaa		384	
Met	Leu	Cys	Gly	His	Pro	Ser	Thr	Arg	Leu	Leu	Tyr	Val	Thr	Pro	Glu			
		115				120					125							
ttg	tgc	cag	aca	gac	aac	ttc	cgc	cgc	cgt	ctg	ctc	ata	ggt	cac	aaa		432	
Leu	Cys	Gln	Thr	Asp	Asn	Phe	Arg	Arg	Arg	Leu	Leu	Ile	Val	His	Lys			
	130				135					140								
caa	ggt	cag	ctc	atc	cgc	ggt	gcc	atc	gat	gag	gca	cat	tgt	ata	agt		480	
Gln	Gly	Gln	Leu	Ile	Arg	Val	Ala	Ile	Asp	Glu	Ala	His	Cys	Ile	Ser			
145				150				155						160				
gaa	tgg	ggt	cat	gac	ttc	cgc	cca	gct	tac	aaa	gag	ctg	ggc	tgg	ttc		528	
Glu	Trp	Gly	His	Asp	Phe	Arg	Pro	Ala	Tyr	Lys	Glu	Leu	Gly	Trp	Phe			
			165					170					175					
aga	agg	aat	ctc	gtc	gat	ccg	act	gtc	cca	atc	acg	gcc	ttg	aca	gcg		576	
Arg	Arg	Asn	Leu	Val	Asp	Pro	Thr	Val	Pro	Ile	Thr	Ala	Leu	Thr	Ala			
			180				185						190					
aca	gcg	acc	ccg	cga	ggt	cgc	tcg	gac	atg	atc	aac	atc	ttg	ggg	ttg		624	
Thr	Ala	Thr	Pro	Arg	Val	Arg	Ser	Asp	Met	Ile	Asn	Ile	Leu	Gly	Leu			
		195				200					205							
gat	ctt	gag	aat	ctc	cgc	ctg	ttc	aac	act	cca	tcg	gac	cgt	cca	aat		672	
Asp	Leu	Glu	Asn	Leu	Arg	Leu	Phe	Asn	Thr	Pro	Ser	Asp	Arg	Pro	Asn			

210	215	220	
att cac tac gag gta cgg tat ctc gca gat ttc gct ggc gac agc gac			720
Ile His Tyr Glu Val Arg Tyr Leu Ala Asp Phe Ala Gly Asp Ser Asp			
225	230	235	240
agt gca gaa gac agt caa cta caa aac ctg ctc aga tgg ctt aag ggc			768
Ser Ala Glu Asp Ser Gln Leu Gln Asn Leu Leu Arg Trp Leu Lys Gly			
	245	250	255
atc cga acc cga cga gag gcc cga ctt ggc agc aga gtg aca ctg ctc			816
Ile Arg Thr Arg Arg Glu Ala Arg Leu Gly Ser Arg Val Thr Leu Leu			
	260	265	270
cct cca atg tca gga atc gtc tat gta ggg acc cgg gct atg gct gag			864
Pro Pro Met Ser Gly Ile Val Tyr Val Gly Thr Arg Ala Met Ala Glu			
	275	280	285
cat ctt gcc agt cgg cta tcc tcg gac gaa atg gtc atg gcc gtg gca			912
His Leu Ala Ser Arg Leu Ser Ser Asp Glu Met Val Met Ala Val Ala			
	290	295	300
tac cac gcc ggc gtg gaa gcc acc aag cgt gcg cac att caa tca aca			960
Tyr His Ala Gly Val Glu Ala Thr Lys Arg Ala His Ile Gln Ser Thr			
	310	315	320
tgg aag tcg tct cgg cca gtc cag cca gct gat ggg gaa agg aca ccc			1008
Trp Lys Ser Ser Arg Pro Val Gln Pro Ala Asp Gly Glu Arg Thr Pro			
	325	330	335
gtt ttc tcc att att gtg gca acc aat gcc ttc ggg atg gga att gat			1056
Val Phe Ser Ile Ile Val Ala Thr Asn Ala Phe Gly Met Gly Ile Asp			
	340	345	350
aac ccc gat gtc cgc ttt gtc gtg cat tgg acg cca ccg cga agc ttc			1104
Asn Pro Asp Val Arg Phe Val Val His Trp Thr Pro Pro Arg Ser Phe			
	355	360	365
gaa agt ttc gtt caa gag tcg ggc cgt gca ggt cga gat ggc cgc gcc			1152
Glu Ser Phe Val Gln Glu Ser Gly Arg Ala Gly Arg Asp Gly Arg Ala			
	370	375	380
gct gcc tca ctt gtc tac tac gga atc caa gaa agg aac ttc ata gag			1200
Ala Ala Ser Leu Val Tyr Tyr Gly Ile Gln Glu Arg Asn Phe Ile Glu			
	385	390	395
acc atg atc tac cgg gat aca gaa tct cac cgt gcg aat ggc ccc gaa			1248
Thr Met Ile Tyr Arg Asp Thr Glu Ser His Arg Ala Asn Gly Pro Glu			
	405	410	415
aat cga gag gcc aag ctt gaa agc ttc ggc aag gtc att cga tac tgt			1296
Asn Arg Glu Ala Lys Leu Glu Ser Phe Gly Lys Val Ile Arg Tyr Cys			
	420	425	430
gag agt atc agg agg tgt aga cat gaa ctg atc aaa gag ttc ttc ggt			1344
Glu Ser Ile Arg Arg Cys Arg His Glu Leu Ile Lys Glu Phe Phe Gly			
	435	440	445
gac ttc gag ctg gaa gaa atg ggg tcc caa ctg ccg gcc agg gag gcc			1392
Asp Phe Glu Leu Glu Glu Met Gly Ser Gln Leu Pro Ala Arg Glu Ala			
	450	455	460
gta tca gtt acg agc tcg tcc cct tgc gac ttt gcc tgc gat ttt tgc			1440
Val Ser Val Thr Ser Ser Ser Pro Cys Asp Phe Ala Cys Asp Phe Cys			
	465	470	475
aaa gag ggt cgt gcc ggg ttg gca aaa cgc cgg gag aaa atg gca tct			1488
Lys Glu Gly Arg Ala Gly Leu Ala Lys Arg Arg Glu Lys Met Ala Ser			
	485	490	495
gag act cag atg gct ctc cta tat gcg gat ttc gat tga			1527
Glu Thr Gln Met Ala Leu Leu Tyr Ala Asp Phe Asp			
	500	505	

<210> 154  
 <211> 508  
 <212> PRT  
 <213> Penicillium chrysogenum

<400> 154

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

				405					410					415			
Asn	Arg	Glu	Ala	Lys	Leu	Glu	Ser	Phe	Gly	Lys	Val	Ile	Arg	Tyr	Cys		
			420					425					430				
Glu	Ser	Ile	Arg	Arg	Cys	Arg	His	Glu	Leu	Ile	Lys	Glu	Phe	Phe	Gly		
		435				440						445					
Asp	Phe	Glu	Leu	Glu	Glu	Met	Gly	Ser	Gln	Leu	Pro	Ala	Arg	Glu	Ala		
	450				455						460						
Val	Ser	Val	Thr	Ser	Ser	Pro	Cys	Asp	Phe	Ala	Cys	Asp	Phe	Cys			
465				470				475						480			
Lys	Glu	Gly	Arg	Ala	Gly	Leu	Ala	Lys	Arg	Arg	Glu	Lys	Met	Ala	Ser		
			485				490						495				
Glu	Thr	Gln	Met	Ala	Leu	Leu	Tyr	Ala	Asp	Phe	Asp						
			500					505									

<210> 155  
 <211> 2028  
 <212> DNA  
 <213> *Penicillium chrysogenum*

<400> 155

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atcttgcggc	cccacattaa	attatttttt	gagatagctg	accatcgaca	accaacaact	180
tcttttttcc	ataaaataca	aatcaaatat	gccgattacc	aagaaacgca	aggctcgaca	240
cgcgagacct	gctgcacctg	ttgaagacag	cgacgcttca	tcaaattgcaa	gctcttcaag	300
cccccaacc	accgctgaga	accccgacat	tggagatagc	gagccccaag	ccactgctga	360
tgacccaat	gtcaaagatg	ccacctccga	gactgagccc	agcgctacta	ccgcccctaa	420
gacattcaaa	gaactgggccc	tgattgactc	gctctgcgag	gcctgcgaca	agatgggata	480
caaggcccct	acaccaatcc	agtcggaatc	aatcccgtcg	gcactgcagg	gtcgtgatat	540
tattggatta	gctgaaacag	gatctggaat	aactgcctcc	ttcgtttctac	caattcttca	600
aggtttgtgc	atatttgacg	acatacatct	tcatatacga	ttctaaccag	tcttctagcg	660
ctcatggaga	aaccccagtc	attctttggg	ctcgtactgg	ccccaaaccg	tgaactggca	720
taccagattt	cactagcatg	cgagtccttt	ggtgcaacaa	tcaacgtcag	atccaccacg	780
ttggctcgcg	gcatggacat	ggttcctcag	tcgatcgctt	tgggcaagaa	acctcacatc	840
atcgttgcta	cgcccggcag	acttctcgac	cacctcgaga	atacaaaagg	cttctccctc	900
cgagcttgta	agttcctcgt	catggatgaa	gcagacagac	tcctcgatat	ggatttcggc	960
cccattctcg	ataagatcct	gaaggtcctg	ccgcgcgagc	gcagaacctt	cctattctcc	1020
gccactttga	gttcaaagg	tgaatctctc	cagcgagcct	ccctgtcaaa	tccggcccgc	1080
gtctcgatct	cttctagcaa	gtatgctacc	gtggagaccc	tccagcaaac	ctatctcctt	1140
cgtccttata	aacacaagga	catctacctt	gtctacctcc	tccacgaatt	tatcggccag	1200
tccgtcatta	tcttcatgcg	cacggttcat	gagacgcagc	gtggttgctt	tctgctgcgc	1260
ggtctaggct	tcggcgcaat	ccctctgcat	ggccagatgt	ctcaatctgc	acgtctggga	1320
gcattgggaa	aattccgatc	gaaaagtgcg	gagatcctgg	ttgccaccga	cgttgctgct	1380
cgtggtctag	atattccctc	tgtggactgt	gttttgaact	ttgacttgcc	aaccgacagt	1440
aagacctata	ttcaccgagt	aggccgtacg	gcacgtgccg	gaaagtctgg	aaccgccatc	1500
tcttttgtca	cgcaatatga	cgtggaaata	tggcagcgta	tagaggctgc	catgggcaaa	1560
gagttggccg	aataccccgc	tccgaaagat	gaggccatgg	tctttgctga	gcaagtgagc	1620
gcttcgcagc	gtgatgccat	tcaggcgatg	aagcactacg	acgagaagaa	gggcgctaag	1680
ggcaaaggaa	agttctcggt	caagggcaag	cgaagtcgcg	atgccatgga	ccaggaagag	1740
ggctagaatt	ccatcctggc	tcatttgctt	ttcttgatata	tgaatatggg	ctatcttacg	1800
aatttggggc	gtttaagtat	gtaatatgaa	agaatccata	gatttcatta	ctgcgtcaaa	1860
atgatatcga	atattttcct	ggaccatatt	tccaggggtc	catagagttg	aaggatatccg	1920
ctgcctaaag	tcacaaaggc	cagtgtataa	attgtaatat	agcctagaaa	cagtgggtccc	1980
taggggcatt	tgtcaagacc	gaagatccca	ttggactagg	gaatctat		2028

<210> 156  
 <211> 1482  
 <212> DNA  
 <213> *Penicillium chrysogenum*

<220>  
 <221> CDS  
 <222> (1) .. (1482)

<400> 156

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



				245					250				255				
tca	aag	gtt	gaa	tct	ctc	cag	cga	gcc	tcc	ctg	tca	aat	ccg	gcc	cgc		816
Ser	Lys	Val	Glu	Ser	Leu	Gln	Arg	Ala	Ser	Leu	Ser	Asn	Pro	Ala	Arg		
			260					265					270				
gtc	tcg	atc	tct	tct	agc	aag	tat	gct	acc	gtg	gag	acc	ctc	cag	caa		864
Val	Ser	Ile	Ser	Ser	Ser	Lys	Tyr	Ala	Thr	Val	Glu	Thr	Leu	Gln	Gln		
		275					280					285					
acc	tat	ctc	ctt	cgt	cct	tat	aaa	cac	aag	gac	atc	tac	ctt	gtc	tac		912
Thr	Tyr	Leu	Leu	Arg	Pro	Tyr	Lys	His	Lys	Asp	Ile	Tyr	Leu	Val	Tyr		
	290					295				300							
ctc	ctc	cac	gaa	ttt	atc	ggc	cag	tcc	gtc	att	atc	ttc	atg	cgc	acg		960
Leu	Leu	His	Glu	Phe	Ile	Gly	Gln	Ser	Val	Ile	Ile	Phe	Met	Arg	Thr		
305				310					315						320		
gtt	cat	gag	acg	cag	cgt	gtt	gct	ttt	ctg	ctg	cgc	ggg	cta	ggc	ttc		1008
Val	His	Glu	Thr	Gln	Arg	Val	Ala	Phe	Leu	Leu	Arg	Gly	Leu	Gly	Phe		
				325				330					335				
ggc	gca	atc	cct	ctg	cat	ggc	cag	atg	tct	caa	tct	gca	cgt	ctg	gga		1056
Gly	Ala	Ile	Pro	Leu	His	Gly	Gln	Met	Ser	Gln	Ser	Ala	Arg	Leu	Gly		
			340				345					350					
gca	ttg	gga	aaa	ttc	cga	tcg	aaa	agt	cgc	gag	atc	ctg	gtt	gcc	acc		1104
Ala	Leu	Gly	Lys	Phe	Arg	Ser	Lys	Ser	Arg	Glu	Ile	Leu	Val	Ala	Thr		
		355					360				365						
gac	gtt	gct	gct	cgt	ggg	cta	gat	att	ccc	tct	gtg	gac	tgt	gtt	ttg		1152
Asp	Val	Ala	Ala	Arg	Gly	Leu	Asp	Ile	Pro	Ser	Val	Asp	Cys	Val	Leu		
	370				375				380								
aac	ttt	gac	ttg	cca	acc	gac	agt	aag	acc	tat	att	cac	cga	gta	ggc		1200
Asn	Phe	Asp	Leu	Pro	Thr	Asp	Ser	Lys	Thr	Tyr	Ile	His	Arg	Val	Gly		
385				390					395					400			
cgt	acg	gca	cgt	gcc	gga	aag	tct	gga	acc	gcc	atc	tct	ttt	gtc	acg		1248
Arg	Thr	Ala	Arg	Ala	Gly	Lys	Ser	Gly	Thr	Ala	Ile	Ser	Phe	Val	Thr		
			405					410					415				
caa	tat	gac	gtg	gaa	ata	tgg	cag	cgt	ata	gag	gct	gcc	atg	ggc	aaa		1296
Gln	Tyr	Asp	Val	Glu	Ile	Trp	Gln	Arg	Ile	Glu	Ala	Ala	Met	Gly	Lys		
			420				425					430					
gag	ttg	gcc	gaa	tac	ccc	gct	ccg	aaa	gat	gag	gcc	atg	gtc	ttt	gct		1344
Glu	Leu	Ala	Glu	Tyr	Pro	Ala	Pro	Lys	Asp	Glu	Ala	Met	Val	Phe	Ala		
		435				440					445						
gag	caa	gtg	agc	gct	tcg	cag	cgt	gat	gcc	att	cag	gcg	atg	aag	cac		1392
Glu	Gln	Val	Ser	Ala	Ser	Gln	Arg	Asp	Ala	Ile	Gln	Ala	Met	Lys	His		
	450					455				460							
tac	gac	gag	aag	aag	ggc	gct	aag	ggc	aaa	gga	aag	ttc	tcg	ttc	aag		1440
Tyr	Asp	Glu	Lys	Lys	Gly	Ala	Lys	Gly	Lys	Gly	Lys	Phe	Ser	Phe	Lys		
465				470				475						480			
ggc	aag	cga	agt	cgc	gat	gcc	atg	gac	cag	gaa	gag	ggc	tag				1482
Gly	Lys	Arg	Ser	Arg	Asp	Ala	Met	Asp	Gln	Glu	Glu	Gly					
			485					490									

<210> 157  
 <211> 493  
 <212> PRT  
 <213> Penicillium chrysogenum

<400> 157  
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 Pro Val Glu Asp Ser Asp Ala Ser Ser Asn Ala Ser Ser Ser Ser Pro

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		35					40					45			
Thr	Ala	Asp	Asp	Pro	Asn	Val	Lys	Asp	Ala	Thr	Ser	Glu	Thr	Glu	Pro
	50					55					60				
Ser	Ala	Thr	Thr	Ala	Pro	Lys	Thr	Phe	Lys	Glu	Leu	Gly	Leu	Ile	Asp
65					70					75				80	
Ser	Leu	Cys	Glu	Ala	Cys	Asp	Lys	Met	Gly	Tyr	Lys	Ala	Pro	Thr	Pro
				85					90					95	
Ile	Gln	Ser	Glu	Ser	Ile	Pro	Leu	Ala	Leu	Gln	Gly	Arg	Asp	Ile	Ile
			100					105					110		
Gly	Leu	Ala	Glu	Thr	Gly	Ser	Gly	Lys	Thr	Ala	Ser	Phe	Val	Leu	Pro
		115					120					125			
Ile	Leu	Gln	Ala	Leu	Met	Glu	Lys	Pro	Gln	Ser	Phe	Phe	Gly	Leu	Val
	130					135					140				
Leu	Ala	Pro	Thr	Arg	Glu	Leu	Ala	Tyr	Gln	Ile	Ser	Leu	Ala	Cys	Glu
145					150					155					160
Ser	Leu	Gly	Ala	Thr	Ile	Asn	Val	Arg	Ser	Thr	Thr	Leu	Val	Gly	Gly
				165					170					175	
Met	Asp	Met	Val	Pro	Gln	Ser	Ile	Ala	Leu	Gly	Lys	Lys	Pro	His	Ile
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<212> DNA

<213> *Penicillium chrysogenum*

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<400> 159

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





<210> 161  
 <211> 2291  
 <212> DNA  
 <213> *Penicillium chrysogenum*

<400> 161

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atttttctga	cggtacatta	gttgcatgtt	ttgtgcctta	caaaccaggc	cgccaacccc	180
caccgcttgt	tggagataac	tttttctgcc	gcaaaattat	ttcgtcctga	tagacagtcg	240
caaacaagat	ggcgcccccg	atcacagaga	atccagagtt	cgaggactct	gatgtatctg	300
ataattccga	tgtggaacag	cccgatgtcg	acgaccgagc	ccccaagcgt	cgccgtctct	360
cagagtcgtc	caacgactca	tacgtcgcac	ctgcgcgcgt	ccctaccctc	tctcgtatca	420
agaagaaggg	tgaggtagag	aaggagcccg	agtcaaagga	agaggaaccc	gttcttatta	480
gcgatgcaat	tgagcttggg	aaacagagt	ggctgtccac	tttcgcagaa	ttggatgtcg	540
caccttggct	tgtctcttcg	ttggccacaa	tggcgatcaa	acggccaact	gctattcaga	600
aggcttgtat	tcctgagatt	ctaaagggga	aagactgtat	tggtggaagt	cgcactgggt	660
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cccggccgac	tagccgacca	catcaaaacg	tccggagaag	acacagtggc	cggtctccgc	1020
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ggcaacaagc	caccgatctt	catgaccgag	atcggcaccg	agaaccaagg	caagatcccg	1260
ccaaccctca	agcagacata	cctaaaggtc	ccgatgacgc	accgcgaggc	cttccctgcat	1320
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atatttagcg	atcttctttc	tgggatttga	cctgaagtct	atacctatgt	gcattttgtg	1980
gtatttggtt	caacttcctc	atcctataat	tgttcaaacg	cacaaatggg	atcattttatc	2040
gcaacgtata	gacgaattat	tctaattgctg	catgcttcca	aaaagggata	ccggttgcca	2100
tgctaggact	aacacttgaa	gtatatcaac	gtatctcgat	atgcacgttt	gaccctttac	2160
atcatgcaat	acattgcctt	gggaaatggc	tgctatccat	tgcaatgcga	cttatttact	2220
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atgcagccga	a					2291

<210> 162  
 <211> 1563  
 <212> DNA  
 <213> *Penicillium chrysogenum*

<220>  
 <221> CDS  
 <222> (1) .. (1563)

<400> 162

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





Glu Ala Ala Gly Glu Ile Asp Glu Gly Arg Asp Ile Leu Gly Arg Lys  
500 505 510  
Arg Asn Lys Leu Lys Lys Val Arg  
515 520

<210> 164  
<211> 2176  
<212> DNA  
<213> *Penicillium chrysogenum*

<400> 164  
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gttcgcggcgt tcttctttgt ttctttttgt ttccgcggag tcaacttttg aggagtgaat 180  
acaagtcaca ttcaagtctc tttttctgag gtccaatata tttcaaaaca gcttagaatc 240  
gttacaagct ttatcaatta tcccgcgggt gatagttgta cgccgcagtc gtaaatacata 300  
gccgtaaatc atagtaagag tgcctcaaat gaccttcacc tggaggaaat tttctcttca 360  
gaaagtaaaa tatatttcag gaagtgtctat gaaagctcac catataagtt tcaactggaa 420  
taaagaatgg tggcatattg cgcaagctat cctcattttt taagatggat ttgacgtaac 480  
gcgcttccaa caccacatct cgcagatctg ccttcaatcc tctcaagtac ctatctacaa 540  
ccacaacaaa gcagcaaaat gattgaccaa cgcatttttg agaatctcca gacgaagatc 600  
gatgaggaga ccaccgtccg ggatgtaggt cttaccaatg cgtcctgacc ttggtgaatt 660  
cttcgcgcgc caagcctaca ccggagcaag acccttgggc caggaaatcc gacaggtagc 720  
taacaatttt gataggagct acatgagatt gtccaaaaac tcgctagaag aggtactttc 780  
tgcaattcgt gacttcgacc cggacttcca ggcgttcac ctgtcgggga cggcactccc 840  
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aggctatcct gtcgcgagct cattctacgc ctgtctgatca gtgtaagtta ttatctatat 960  
caggtggctc gatgagagtg ctgggtacat ttgatctttg gactcgctgc togatcacta 1020  
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cgggcctcat gttaaggggg ggtaggatat agaccaagg aactgatata gcgacgactt 1980  
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aattcccatc gttagaccga atcgtaaacc gaaaagaac agtatgtcac aagcagaagc 2100  
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cacctcaagc acagcc 2176

<210> 165  
<211> 708  
<212> DNA  
<213> *Penicillium chrysogenum*

<220>

<221> CDS

<222> (1)..(708)

<400> 165

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Met Ile Asp Gln Arg Ile Phe Glu Asn Leu Gln Thr Lys Ile Asp Glu	
1 5 10 15	
gag acc acc gtc cgg gat gag cta cat gag att gtc caa aaa ctc gct	96
Glu Thr Thr Val Arg Asp Glu Leu His Glu Ile Val Gln Lys Leu Ala	
20 25 30	
aga aga ggg cgt tcc aca cag gct atc ctg tgc cga gct cat tct acg	144
Arg Arg Gly Arg Ser Thr Gln Ala Ile Leu Ser Arg Ala His Ser Thr	
35 40 45	
cct gct gat cag ttg aag ccc gtg ctt gac gat gtc acc aag gaa att	192
Pro Ala Asp Gln Leu Lys Pro Val Leu Asp Asp Val Thr Lys Glu Ile	
50 55 60	
ctt gct cag aag gaa gag gtc act cgc ctg aag gcc gtg gca gac caa	240
Leu Ala Gln Lys Glu Glu Val Thr Arg Leu Lys Ala Val Ala Asp Gln	
65 70 75 80	
cat ccc ttc tac aag tac aac ggg cta tgg agt cgt gag ctg caa aac	288
His Pro Phe Tyr Lys Tyr Asn Gly Leu Trp Ser Arg Glu Leu Gln Asn	
85 90 95	
ctg gtc gcc tct atc gag ctt tgc gca tgg ctg gga ggg ctg cag gag	336
Leu Val Ala Ser Ile Glu Leu Cys Ala Trp Leu Gly Gly Leu Gln Glu	
100 105 110	
cac aag gga cct agc tca aca tct ttc atg acc att gag gat gtg ggc	384
His Lys Gly Pro Ser Ser Thr Ser Phe Met Thr Ile Glu Asp Val Gly	
115 120 125	
aag ttc ctg gac att cct gtc aac cta aag gag cag gat gcc ttc cac	432
Lys Phe Leu Asp Ile Pro Val Asn Leu Lys Glu Gln Asp Ala Phe His	
130 135 140	
ctg acg att gag gaa tac cta ttg gcg ctc att gcc atg gtt gag gaa	480
Leu Thr Ile Glu Glu Tyr Leu Leu Ala Leu Ile Ala Met Val Glu Glu	
145 150 155 160	
ctg gct cgc ttg gct gtc aat tca gtc acc ctg ggt gat tac acc cgt	528
Leu Ala Arg Leu Ala Val Asn Ser Val Thr Leu Gly Asp Tyr Thr Arg	
165 170 175	
ccc atg cag att ggc aac ttt gtc aag gaa ttg ttc gct ggg ttc cag	576
Pro Met Gln Ile Gly Asn Phe Val Lys Glu Leu Phe Ala Gly Phe Gln	
180 185 190	
ctc tta aac ttg aag aac gat atc ctg cgc aag cgc agc gac ggt atc	624
Leu Leu Asn Leu Lys Asn Asp Ile Leu Arg Lys Arg Ser Asp Gly Ile	
195 200 205	
aag tac agc gtc aag aag gtt gag gat gtg gtc tac gat ctg tcc cta	672
Lys Tyr Ser Val Lys Lys Val Glu Asp Val Val Tyr Asp Leu Ser Leu	
210 215 220	
cgt aat ctg gtt cct aag ggt agt tca tct gct tga	708
Arg Asn Leu Val Pro Lys Gly Ser Ser Ser Ala	
225 230 235	

<210> 166

<211> 235

<212> PRT

<213> *Penicillium chrysogenum*

<400> 166

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

<210> 167

<211> 5836

<212> DNA

<213> *Penicillium chrysogenum*

<400> 167

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ggaggagcta	ttttaaggct	ctgtacagca	gtgacggatg	ggatttagat	ttagattatt	180
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cagttctcag	aggattccta	gatcagctca	aagttaaata	tcgccgtaag	gtaacgtcaa	300
ccgtggacaa	agtcattgtt	cctattcaac	acagacataa	aaacacggga	caagatcatt	360
cccgataatc	tcttaatagg	cataaagaac	atcaccagca	ctaggcggag	caccctgct	420
gatcttcttg	tctgtattct	gcagccacca	cctcaaaacg	gaccataaaa	gtttggctcg	480
tgcacaagtt	gaaaacctcg	atctcgagga	gaaacttagg	gcggccgaag	ctaaagcatc	540
tcgcttcgag	gaggctgtag	tatcagcgga	agctgaaatc	cacgaccgaa	attcaactat	600
ctaggaagcg	caaatcacca	ttcaacttta	tcaacaggat	atattgaact	agatagctat	660
tgccgagtgc	tatcagacta	aatgtttcca	gcgctcgaat	gtattagggc	aaatgatgac	720
attcttacaa	gacactatat	ctaagactaa	gtgagaattg	gtacagtaat	attcgaattc	780
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gccacacgcc	ggtgagttag	tagttgggtg	ggtgaccacc	agcgaatcct	cactgttgta	960
tgTTTTtTgtt	ttctTTTTtTg	tttctTTTTtTg	gactatctca	tgattcggtt	tctggaacac	1020
actgcgtgta	acccgggtat	ttttgaaagc	agttgtgcat	attcctactc	aatgctagcc	1080
gataagcaac	ttgggtTTTTt	cggggatatt	cacgtgcaag	gcgctgccag	gggaagcgtc	1140

caggcctctt	tgattatctc	caggatatcg	attcgttaac	actgtcgtgt	atgtagttga	1200
aggctgtcaa	tgaattgcat	ccgtggaata	ttgacttggg	tgaagactcc	gatggtgacc	1260
caatggaaac	tagatgggga	ggacttgata	gataagggtg	agcatgagtc	ttgttgcatg	1320
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gaacccttta	cagtgtgtga	aagagtcggt	gagaccaggc	ctaagatgct	caaagttgcc	1560
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<211> 2538

<212> DNA

<213> *Penicillium chrysogenum*

<220>

<221> CDS

<222> (1) .. (2538)

<400> 168

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<212> PRT

<213> *Penicillium chrysogenum*

<400> 169

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Gly Ser Gln Thr Leu Tyr Glu Val Ser Val Ser Leu Ser Cys Asn Gly		270
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Asn Glu Val His Gln Val Ser Lys Lys Ile Gly Ile Arg Ser Ala Glu		285
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Asn Gly Val Asp Ile Phe Cys Gly Gly Ser Cys Trp Ile Pro Ala Asp		320
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Ser Leu Leu Pro Ser Ile Ser Ala Glu Arg Tyr Arg Lys Trp Ile Glu		335
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Leu Met Val Ala Gly Gly Gln Val Met Thr Arg Val Trp Gly Gly Gly		350
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Ile Tyr Glu Asp Asp Ala Phe Tyr Asp Ala Cys Asp Glu Leu Gly Val		365
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Leu Val Trp Gln Asp Phe Met Phe Ala Cys Gly Asn Tyr Pro Val Trp		380
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Pro Glu Leu Leu Asp Ser Val Arg Gln Glu Ala Ala Tyr Asn Ile Arg		400
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Arg Leu Arg His Arg Pro Ser Ile Val Ile Tyr Val Gly Asn Asn Glu		415
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Asp Tyr Gln Phe Gln Glu Ile Ser Gly Leu Thr Tyr Asn Tyr Glu Asp		430
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Lys Asp Pro Glu Ser Trp Leu Lys Tyr Asp Phe Pro Ala Arg Tyr Ile		445
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Tyr Glu Lys Ile Leu Pro Glu Val Val Ala Glu Tyr Ser Pro Ser Ile		460
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Phe Tyr His Pro Gly Ser Pro Trp Gly Asp Gly Lys Val Thr Thr Asp		480
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Pro Thr Val Gly Asp Ile His Gln Trp Asn Val Trp His Gly Thr Gln		495
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Phe Gly Met Val Gly Phe Pro His Met Ser Thr Ile Glu Tyr Phe Val		525
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Gln Asn Glu Lys Asp Lys His Pro Gln Ser Gln Val Met Asp Phe His		540
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Gln Pro Lys Pro Ala Tyr Tyr Thr Val Lys Arg Val Met Gln Pro Val		640
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<212> DNA

<213> *Penicillium chrysogenum*

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Gln Gln Asp Leu Ile Ala Asn Lys Lys Leu Asp Asp Pro Tyr Val Gly
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ttc aaa gaa ttg gat gcc cgc tgg gtc aac gag aag tca tgg gtc tac      192
Phe Lys Glu Leu Asp Ala Arg Trp Val Asn Glu Lys Ser Trp Val Tyr
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Arg Asn Val Val Gln Lys Pro Ser Thr Pro Ala Gly Ser Ser Ile Val
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ctg gtc ttc gat ggt ctt gat acc ttt gcc aag gtc aag ctg gat gga      288
Leu Val Phe Asp Gly Leu Asp Thr Phe Ala Lys Val Lys Leu Asp Gly
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Val Thr Lys Ala Leu Glu Ala Glu Gly Glu His Thr Leu Glu Ile Glu
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Phe Asp Cys Ala Leu Ile Lys Ala Arg Glu Leu Arg Ala Lys Asp Thr
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Thr His Lys Trp Val Gly Phe Asn Gly Asp Pro Ser Arg Met Ala Ala
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cgg aaa gcc cag tac cac tgg ggc tgg gac tgg ggt cca gtg ttg atg      528
Arg Lys Ala Gln Tyr His Trp Gly Trp Asp Trp Gly Pro Val Leu Met
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Thr Ala Gly Ile Trp Arg Ala Val Arg Phe Glu Val Tyr Gln Ala Arg
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Ala Glu Val Thr Ala Ala Ile Asp Val Glu Ser Val Gly Asp Gly Asp
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Tyr Thr Ala Gln Val Ser Leu Gly Leu Lys Gly Lys Glu Ile Ala Ser
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Gln	Glu	Gly	Val	Gln	Leu	Glu	Asp	Asn	Ala	Ile	Asp	Ile	Val	Pro	Gly	
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 Tyr Asp Val Ser Val Ser Leu Leu Arg Asn Gly Glu Gln Val Asp Gln  
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Tyr	Tyr	Ala	Val	Lys	Arg	Val	Met	Asn	Pro	Ile	Ala	Val	Gly	Val	Arg		
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785					790					795					800		
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 <213> *Penicillium chrysogenum*

<400> 173

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att	gca	tat	att	tac	atg	acg	aac	tgc	gct	ctg	ttg	act	ctc	aac	atg	576
Ile	Ala	Tyr	Ile	Tyr	Met	Thr	Asn	Cys	Ala	Leu	Leu	Thr	Leu	Asn	Met	
		180						185					190			
ttc	ctc	ccc	agc	atg	ggc	atc	gag	tcc	cag	tcg	gag	gtc	atg	caa	cag	624
Phe	Leu	Pro	Ser	Met	Gly	Ile	Glu	Ser	Gln	Ser	Glu	Val	Met	Gln	Gln	
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ctg	gat	tcc	cag	ttc	ccg	gga	tgt	ggt	atg	agc	aac	ctt	gta	gaa	agt	672
Leu	Asp	Ser	Gln	Phe	Pro	Gly	Cys	Val	Met	Ser	Asn	Leu	Val	Glu	Ser	
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aac	ctt	gcc	ttg	ggc	atc	cgc	acg	cag	ttc	ttt	atc	atg	gaa	tta	gaa	768
Asn	Leu	Ala	Leu	Gly	Ile	Arg	Thr	Gln	Phe	Phe	Ile	Met	Glu	Leu	Glu	
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aga	cgc	caa	cat	gag	cag	gac	ttc	aat	cca	ctc	tct	atc	ttg	agg	cag	816
Arg	Arg	Gln	His	Glu	Gln	Asp	Phe	Asn	Pro	Leu	Ser	Ile	Leu	Arg	Gln	
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atc	ttc	gct	atg	gac	ctt	gca	ccc	agc	gaa	gac	gac	tcc	cct	gct	tct	864
Ile	Phe	Ala	Met	Asp	Leu	Ala	Pro	Ser	Glu	Asp	Asp	Ser	Pro	Ala	Ser	
		275					280					285				
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Phe	Arg	Gly	Phe	Asn	Leu	Pro	Gly	Val	Leu	Gln	Asp	Glu	Asp	Gly	His	
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ctt	cca	gaa	tac	cta	cct	gaa	agg	ttt	ctc	atc	gcc	atc	agc	gac	agg	960
Leu	Pro	Glu	Tyr	Leu	Pro	Glu	Arg	Phe	Leu	Ile	Ala	Ile	Ser	Asp	Arg	
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ttc	aat	gag	ctt	cac	gag	gaa	att	tct	gag	tgg	gat	agc	ctt	gat	att	1008
Phe	Asn	Glu	Leu	His	Glu	Glu	Ile	Ser	Glu	Trp	Asp	Ser	Leu	Asp	Ile	
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gat	ggc	ctg	agg	aag	gca	tac	aga	tgg	cga	tcg	ttt	gaa	cgg	gac	ctt	1056
Asp	Gly	Leu	Arg	Lys	Ala	Tyr	Arg	Trp	Arg	Ser	Phe	Glu	Arg	Asp	Leu	
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gca	cgt	tgg	gta	tat	gct	cgt	gac	aga	gaa	atc	aag	gac	gac	atc	aga	1104
Ala	Arg	Trp	Val	Tyr	Ala	Arg	Asp	Arg	Glu	Ile	Lys	Asp	Asp	Ile	Arg	
		355					360					365				
cgg	ttg	tca	gaa	aga	ttg	cgt	atc	tca	ccc	agc	cct	cgt	cgc	ctt	act	1152

Arg	Leu	Ser	Glu	Arg	Leu	Arg	Ile	Ser	Pro	Ser	Pro	Arg	Arg	Leu	Thr	
370						375					380					
tct	gtc	cca	gct	gga	act	ccc	aat	cgg	cgt	cca	gga	tcg	aca	gtg	cct	1200
Ser	Val	Pro	Ala	Gly	Thr	Pro	Asn	Arg	Arg	Pro	Gly	Ser	Thr	Val	Pro	
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Pro	Ser	Gly	Asp	Ile	Ser	Arg	Pro	Arg	Pro	Leu	Pro	Gln	Gln	Thr	His	
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Ser	Pro	Gln	Lys	Glu	Arg	Leu	Val	Asn	Ala	Pro	Gly	Ala	Asn	Arg	Ala	
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ccc	cag	gcg	gag	acg	gta	gtg	cag	gca	gaa	cag	tca	gcc	cag	gcg	ggc	1344
Pro	Gln	Ala	Glu	Thr	Val	Val	Gln	Ala	Glu	Gln	Ser	Ala	Gln	Ala	Gly	
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Asn	Ile	Pro	Gly	Asp	Ile	Ala	Ser	Arg	Ser	Gly	Ile	Thr	Ser	Gln	Thr	
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Asp	Pro	Gly	Arg	Arg	Lys	Ser	Lys	Ser	Asn	Tyr	Arg	Asp	Pro	Ala	Ser	
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Leu	Ala	Ala	Leu	Met	Arg	Arg	Gln	Ala	Thr	Ser	Arg	Pro	Gln	Pro	Ala	
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Val	Thr	Gln	Ala	Asp	Pro	Ser	Ala	Asn	Arg	Gly	Val	Asp	Ser	Val	Glu	
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Ile	Gln	Gln	Ser	Pro	Asp	Met	Thr	Tyr	Arg	Asp	Ile	Gly	Asp	Glu	Ser	
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Thr	Tyr	Val	Asn	Asn	Asp	Glu	Asp	Leu	Asp	Leu	Gly	Gln	Gly	Pro	Glu	
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cct	gat	gtt	atg	aca	tcg	acc	agc	ccc	cct	acc	tcc	tct	aga	atc	ggt	1776
Pro	Asp	Val	Met	Thr	Ser	Thr	Ser	Pro	Pro	Thr	Ser	Ser	Arg	Ile	Gly	
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Arg	Val	Ser	His	Asn	Pro	Asn	Pro	Arg	Phe	Phe	Asp	Ser	Pro	Arg	Asp	
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Gly	Asn	Thr	Gln	Arg	Ser	Val	Pro	Ala	Ala	Arg	Arg	Phe	Leu	Asp	Lys	
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Gln	Ser	Asn	Ala	Arg	Val	Val	Ser	Pro	Ile	Ser	Gln	Tyr	Asp	Ala	Pro	
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Asp	Pro	Pro	Asp	Asp	Asp	Leu	Ser	Asp	Glu	Ser	Asp	Val	Glu	Phe	Glu	
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Gln	Asn	Asn	Gln	Asp	Leu	Asp	Pro	Arg	Arg	Arg	Val	Glu	Lys	Pro	Gln		
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Gln	Lys	Leu	Pro	Ala	Ala	Lys	Arg	Gln	Arg	Pro	Glu	Asp	Asn	Ala	Gly		
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Ser	Asp	Asp	Ile	Thr	Asp	Asp	Glu	Thr	Ala	Val	Glu	Gln	Tyr	Glu	Ala		
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ccc	act	agg	acc	cag	gg	ccc	tgg	gca	gcc	tcc	aac	tcc	cag	gct	gcg		2304
Pro	Thr	Arg	Thr	Gln	Gly	Pro	Trp	Ala	Ala	Ser	Asn	Ser	Gln	Ala	Ala		
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ctt	gtc	aat	cg	aga	gtt	cga	ggg	gcg	acc	cac	aga	tgg	aca	gag	gaa		2352
Leu	Val	Asn	Arg	Arg	Val	Arg	Gly	Ala	Thr	His	Arg	Trp	Thr	Glu	Glu		
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Glu	Asp	Glu	Arg	Leu	Ile	Tyr	Leu	Leu	Gly	Ile	Tyr	Gly	Thr	Ser	Tyr		
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tcc	gcc	ata	aag	aag	caa	gac	aac	gct	tgt	ccc	ccg	tct	gaa	ggc	ggc		2448
Ser	Ala	Ile	Lys	Lys	Gln	Asp	Asn	Ala	Cys	Pro	Pro	Ser	Glu	Gly	Gly		
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ccc	atg	ctt	gag	cgt	cg	tct	cag	gtt	aat	tgt	aaa	gat	cgt	gct	cg		2496
Pro	Met	Leu	Glu	Arg	Arg	Ser	Gln	Val	Asn	Cys	Lys	Asp	Arg	Ala	Arg		
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<211> 840

<212> PRT

<213> *Penicillium chrysogenum*

<400> 175

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Ile	Ala	Pro	Arg	His	Val	Val	Pro	Glu	Ser	Pro	Glu	Asn	His	Glu	Gly		
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His	Thr	Asn	Val	Ser	Gly	Thr	Thr	Leu	Gly	His	Asn	Asp	Val	Glu	Pro		
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Val	Gly	Ser	Gln	Val	Ala	Asp	Lys	Ile	Ala	Thr	His	Leu	Pro	Phe	Val		
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Gln	Gln	Gln	Ala	Thr	Leu	Val	Met	Ser	Leu	Leu	Val	Arg	Pro	Glu	Leu		
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Asn	Pro	Asp	Ser	Leu	Ala	Ala	Glu	Ser	Lys	Arg	Leu	Leu	Asp	Ser	Asn		
			115				120					125					
His	Pro	Asn	Arg	Lys	Arg	Leu	Arg	Arg	Ser	Val	Glu	Gly	Leu	Thr	Asp		

130	135	140
Glu Leu Glu Asp Ser	Pro Leu Ser Arg Asp	Gly Arg Ser Phe Leu Asp
145	150	155
Ile Ser Gln Ala Arg	Arg Leu Leu Ser Pro	Ala Gln Leu Asp Ala Ser
165	170	175
Ile Ala Tyr Ile Tyr	Met Thr Asn Cys Ala	Leu Leu Thr Leu Asn Met
180	185	190
Phe Leu Pro Ser Met	Gly Ile Glu Ser Gln	Ser Glu Val Met Gln Gln
195	200	205
Leu Asp Ser Gln Phe	Pro Gly Cys Val Met	Ser Asn Leu Val Glu Ser
210	215	220
Ser Met Thr Arg Asp	Ile Gly Ala Ser Asn	Thr Thr Glu Thr Thr Phe
225	230	235
Asn Leu Ala Leu Gly	Ile Arg Thr Gln Phe	Phe Ile Met Glu Leu Glu
245	250	255
Arg Arg Gln His Glu	Gln Asp Phe Asn Pro	Leu Ser Ile Leu Arg Gln
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Phe Arg Gly Phe Asn	Leu Pro Gly Val Leu	Gln Asp Glu Asp Gly His
290	295	300
Leu Pro Glu Tyr Leu	Pro Glu Arg Phe Leu	Ile Ala Ile Ser Asp Arg
305	310	315
Phe Asn Glu Leu His	Glu Glu Ile Ser Glu	Trp Asp Ser Leu Asp Ile
325	330	335
Asp Gly Leu Arg Lys	Ala Tyr Arg Trp Arg	Ser Phe Glu Arg Asp Leu
340	345	350
Ala Arg Trp Val Tyr	Ala Arg Asp Arg Glu	Ile Lys Asp Asp Ile Arg
355	360	365
Arg Leu Ser Glu Arg	Leu Arg Ile Ser Pro	Ser Pro Arg Arg Leu Thr
370	375	380
Ser Val Pro Ala Gly	Thr Pro Asn Arg Arg	Pro Gly Ser Thr Val Pro
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Pro Ser Gly Asp Ile	Ser Arg Pro Arg Pro	Leu Pro Gln Gln Thr His
405	410	415
Ser Pro Gln Lys Glu	Arg Leu Val Asn Ala	Pro Gly Ala Asn Arg Ala
420	425	430
Pro Gln Ala Glu Thr	Val Val Gln Ala Glu	Gln Ser Ala Gln Ala Gly
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Asn Ile Pro Gly Asp	Ile Ala Ser Arg Ser	Gly Ile Thr Ser Gln Thr
450	455	460
Val Pro Glu Gln Ser	Val Ser Asn Gln Val	Ala Gln Thr Val Ser Lys
465	470	475
Asp Pro Gly Arg Arg	Lys Ser Lys Ser Asn	Tyr Arg Asp Pro Ala Ser
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Leu Ala Ala Leu Met	Arg Arg Gln Ala Thr	Ser Arg Pro Gln Pro Ala
500	505	510
Ser Asn Val Ala Ser	Gln Ala Gln Asn Ile	Ser Thr Gly Thr Asn Ile
515	520	525
Val Thr Gln Ala Asp	Pro Ser Ala Asn Arg	Gly Val Asp Ser Val Glu
530	535	540
Ile Gln Gln Ser Pro	Asp Met Thr Tyr Arg	Asp Ile Gly Asp Glu Ser
545	550	555
Thr Tyr Val Asn Asn	Asp Glu Asp Leu Asp	Leu Gly Gln Gly Pro Glu
565	570	575
Pro Asp Val Met Thr	Ser Thr Ser Pro Pro	Thr Ser Ser Arg Ile Gly
580	585	590

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Gly	Asn	Thr	Gln	Arg	Ser	Val	Pro	Ala	Ala	Arg	Arg	Phe	Leu	Asp	Lys
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Ser	Pro	Gly	Asn	Gln	Phe	Thr	Val	Leu	Gly	Lys	Arg	Asn	Arg	Asn	Ala
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Asp	Pro	Pro	Asp	Asp	Asp	Leu	Ser	Asp	Glu	Ser	Asp	Val	Glu	Phe	Glu
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Gln	Asn	Asn	Gln	Asp	Leu	Asp	Pro	Arg	Arg	Arg	Val	Glu	Lys	Pro	Gln
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Gln	Lys	Leu	Pro	Ala	Ala	Lys	Arg	Gln	Arg	Pro	Glu	Asp	Asn	Ala	Gly
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Asn	Gln	Pro	Ile	Ser	Thr	Gln	Gly	Ala	Gln	Arg	Val	Gln	Arg	Ala	Glu
				725				730						735	
Ser	Asp	Asp	Ile	Thr	Asp	Asp	Glu	Thr	Ala	Val	Glu	Gln	Tyr	Glu	Ala
			740					745					750		
Pro	Thr	Arg	Thr	Gln	Gly	Pro	Trp	Ala	Ala	Ser	Asn	Ser	Gln	Ala	Ala
		755					760						765		
Leu	Val	Asn	Arg	Arg	Val	Arg	Gly	Ala	Thr	His	Arg	Trp	Thr	Glu	Glu
	770					775					780				
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785					790					795					800
Ser	Ala	Ile	Lys	Lys	Gln	Asp	Asn	Ala	Cys	Pro	Pro	Ser	Glu	Gly	Gly
			805						810					815	
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			820					825					830		
Asn	Leu	Lys	Lys	Lys	Tyr	Leu	Arg								
		835					840								