

SEQUENCE LISTING

<110> DSM IP Assets B.V.

<120> Improved production of secreted proteins by filamentous fungi

<130> 25115WO

<160> 63

<170> WIPO Extractor Vers 1.0 - <http://www.biomax.com/>

<210> 1

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<212> DNA

<213> *Aspergillus niger*

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<213> *Aspergillus niger*

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Val Lys Lys Arg Lys Ser Trp Gly Gln Glu Leu Pro Val Pro Lys Thr	
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Arg Arg Ile Glu Arg Val Leu Arg Asn Arg Ala Ala Ala Gln Thr Ser	
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Phe Ala Phe Asp Val Leu Asp Gly Gly Asp Leu Ser Ala Phe Pro Phe	
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 <212> PRT
 <213> *Aspergillus niger*

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 <213> *Aspergillus niger*

<400> 4

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Asp Glu Glu Ser Pro Lys Ala Ile Leu Phe Thr Glu Lys Gly Thr Thr	
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Ser Pro Leu Leu Arg Ala Leu Ala Ile Asp Phe Leu Gly Ser Ile Gln	
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gaa ccg agt gag ccg gac gca gag ctc ccg gct ccg gcc aag gac gcc			1008
Glu Pro Ser Glu Pro Asp Ala Glu Leu Pro Ala Pro Ala Lys Asp Ala			
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Leu Leu Ser Leu Ala Glu Ile Ser His Lys His Ala Val Arg Lys Ser			
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Lys Leu Phe Pro Phe Tyr Ser Val Pro Ala Ile Asn Ser Gly Ala Lys			
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gtt gaa gaa ccc gtc gag gag aag ccg gcg gtc gac cac gac gaa ttg			1392
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 <213> Aspergillus niger

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 His Thr Ser Ile Val Glu Phe Tyr Ala Pro Trp Cys Gly His Cys Gln
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 65 70 75 80
 Ala Lys Val Ala Ala Val Asn Cys Asp Tyr Asp Asp Asn Lys Pro Phe
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 Pro Gly Lys Lys Pro Gly Lys Pro Arg Val Glu Asp Tyr Lys Gly Ala

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 Asp Pro Ala Val Thr Tyr Thr Ala Arg Lys Glu Thr Thr Leu Tyr Thr
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 Ile Asp Ala Arg Thr Gly Asn Ile Leu Arg Val Phe Ser Ser Arg Gly
 225 230 235 240
 Pro Ile Ser Ser Gly Gln Glu Cys Arg Lys Val Asp Gly Leu Asp Val
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 Val Glu Tyr Thr Val Ala Ile Gln Asn Thr Glu Thr Gly Asp Pro Ile
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 Cys Thr Leu Lys Tyr Ser Glu Trp Thr Ala Asn Asn Arg Asp Met Asp
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 Leu Gln Ser Gln Tyr Leu Arg Thr Met Asp Gln Ser His Ile Tyr Ser
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 Met His Asp Gly Val Leu Gly Phe Asp His Ser Arg Met Asp Arg
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 Pro Arg Tyr Thr Gln Arg Phe Ser Ser Pro Val Val Arg Val Phe Asp
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Glu	Ser	Val	Ala	Pro	Arg	Val	Met	Gly	Pro	Asp	Met	Asp	Phe	Leu	Arg		
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Thr	Gly	Ser	Lys	Met	Leu	Asp	Leu	Leu	Arg	Ala	Leu	Arg	Asn	Lys	Arg		
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<211> 2332

<212> DNA

<213> *Aspergillus niger*

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atc atg ggc tat gcc cat gct gag gag acc gag aag aag ccc gag acc	96
Ile Met Gly Tyr Ala His Ala Glu Glu Thr Glu Lys Lys Pro Glu Thr	
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acc tcc ttg gcc gag aag cct acc ttc acc ccc acc tcc atc gag gct	144
Thr Ser Leu Ala Glu Lys Pro Thr Phe Thr Pro Thr Ser Ile Glu Ala	
35 40 45	
cct ttc ttg gag cag ttc acc gat gac tgg gac tcc cgg tgg act ccc	192
Pro Phe Leu Glu Gln Phe Thr Asp Asp Trp Asp Ser Arg Trp Thr Pro	
50 55 60	
tct cac gct aag aag gag gac tcc aag tcc gag gaa gac tgg gcc tat	240
Ser His Ala Lys Lys Glu Asp Ser Lys Ser Glu Glu Asp Trp Ala Tyr	

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ggt ggt gaa tgg tcc gtc gag gag ccc act gtc ctc aag ggt atg gag	288						
Val Gly Glu Trp Ser Val Glu Glu Pro Thr Val Leu Lys Gly Met Glu							
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ggt gac aag ggt ctc gtc gtc aag aac gtc gct gcc cac cac gcc atc	336						
Gly Asp Lys Gly Leu Val Val Lys Asn Val Ala Ala His His Ala Ile							
		100		105		110	
tcg gct aag ttt ccc aag aag atc gac aac aag gac aag act ctg gtc	384						
Ser Ala Lys Phe Pro Lys Lys Ile Asp Asn Lys Asp Lys Thr Leu Val							
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gtc cag tat gag gtg aag ccg cag aac tcc ctt gtc tgc ggt ggt gcc	432						
Val Gln Tyr Glu Val Lys Pro Gln Asn Ser Leu Val Cys Gly Gly Ala							
		130		135		140	
tac ctg aag ctc ctc cag gac aac aag cag ctc cac ctc gac gag ttc	480						
Tyr Leu Lys Leu Leu Gln Asp Asn Lys Gln Leu His Leu Asp Glu Phe							
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tcg aac gcg tct ccc tac gtg atc atg ttc ggt ccc gac aag tgt ggt	528						
Ser Asn Ala Ser Pro Tyr Val Ile Met Phe Gly Pro Asp Lys Cys Gly							
		165		170		175	
gcc acc aac aag gtt cac ttc atc ttc cgt cac aag aac ccc aag acc	576						
Ala Thr Asn Lys Val His Phe Ile Phe Arg His Lys Asn Pro Lys Thr							
		180		185		190	
ggc gag tac gag gag aag cac ctt aag gca cct ccc gcc gcc cgt acc	624						
Gly Glu Tyr Glu Glu Lys His Leu Lys Ala Pro Pro Ala Ala Arg Thr							
		195		200		205	
tcc aag gtt acc tcc gtt tac acc ctg gtc gtc aac ccc gat cag acc	672						
Ser Lys Val Thr Ser Val Tyr Thr Leu Val Val Asn Pro Asp Gln Thr							
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Phe Gln Ile Leu Ile Asp Gly Glu Ser Val Lys Glu Gly Ser Leu Leu							
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gag gac ttc aac ccc cct gtc aac ccc gag aag gag atc gac gac ccc	768						
Glu Asp Phe Asn Pro Pro Val Asn Pro Glu Lys Glu Ile Asp Asp Pro							
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aag gac aag aag ccc gcc gac tgg gtt gat gag gcc aag atc ccc gac	816						
Lys Asp Lys Lys Pro Ala Asp Trp Val Asp Glu Ala Lys Ile Pro Asp							
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cct gag gct acg aag ccc gag gac tgg gac gag gag gct ccc ttc gag	864						
Pro Glu Ala Thr Lys Pro Glu Asp Trp Asp Glu Glu Ala Pro Phe Glu							
		275		280		285	
att gtc gag gag gag gct acc att ccc gag gac tgg ctc gag gag gag	912						
Ile Val Asp Glu Glu Ala Thr Ile Pro Glu Asp Trp Leu Glu Asp Glu							
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ccc act agc atc cct gac cct gag gcc gag aag ccc gag gac tgg gat	960						
Pro Thr Ser Ile Pro Asp Pro Glu Ala Glu Lys Pro Glu Asp Trp Asp							
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gat gag gag gat ggc gac tgg gtt cct ccc act gtt ccc aac ccc aag	1008						
Asp Glu Glu Asp Gly Asp Trp Val Pro Pro Thr Val Pro Asn Pro Lys							
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tgc cag gat gcc tcc gga tgt ggt cct tgg tct ccc cct atg aag aag	1056						
Cys Gln Asp Ala Ser Gly Cys Gly Pro Trp Ser Pro Pro Met Lys Lys							
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aac cct gac tac aag ggc aag tgg tct gct ccc ttg att gac aac ccg	1104						
Asn Pro Asp Tyr Lys Gly Lys Trp Ser Ala Pro Leu Ile Asp Asn Pro							
		355		360		365	
gcc tac aag gga ccc tgg gcc ccc cgc aag att gcc aac ccc gcc tac	1152						
Ala Tyr Lys Gly Pro Trp Ala Pro Arg Lys Ile Ala Asn Pro Ala Tyr							

370	375	380	
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Phe Glu Asp Lys Thr Pro Ser Asn Phe Glu Pro Met Gly Ala Ile Gly			
385	390	395	400
ttc gag att tgg acc atg cag aac gac atc ctg ttc gac aac atc tac			1248
Phe Glu Ile Trp Thr Met Gln Asn Asp Ile Leu Phe Asp Asn Ile Tyr			
	405	410	415
gtt ggt cac tcc gcc gag gat gcc gag aag ctg cgc cag gag acc ttc			1296
Val Gly His Ser Ala Glu Asp Ala Glu Lys Leu Arg Gln Glu Thr Phe			
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gat gtc aag cac ccc att gag ctg gct gag gag gag gcc aac aag ccc			1344
Asp Val Lys His Pro Ile Glu Leu Ala Glu Glu Glu Ala Asn Lys Pro			
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aag cct gaa gag aag gcc gcc gaa ccc agc gtt agc ttc aag gaa gac			1392
Lys Pro Glu Glu Lys Ala Ala Glu Pro Ser Val Ser Phe Lys Glu Asp			
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Pro Val Gly His Ile Lys Glu Lys Val Asp Asn Phe Val Arg Leu Ser			
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aag cag gac ccc atc aac gcc gtg aag cag gtt cct gac gtt gcc ggt			1488
Lys Gln Asp Pro Ile Asn Ala Val Lys Gln Val Pro Asp Val Ala Gly			
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ggg ctt gcc gct gtt ctc gtc aca atg atc ctt gtc atc gtc gga gcc			1536
Gly Leu Ala Ala Val Leu Val Thr Met Ile Leu Val Ile Val Gly Ala			
	500	505	510
gtt ggt gcc agc acc ccg gcc cct gcc ccc gcc aag aag ggc aag gag			1584
Val Gly Ala Ser Thr Pro Ala Pro Ala Pro Ala Lys Lys Gly Lys Glu			
	515	520	525
gct gct ggt gct acc aag gag aag act ggt gcg gcc tcc agc tcc tcc			1632
Ala Ala Gly Ala Thr Lys Glu Lys Thr Gly Ala Ala Ser Ser Ser Ser			
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gca gac act ggc aag ggt ggt gct acc aag cgc act acc cgc tct tct			1680
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gcc gag taa			1689
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<211> 562

<212> PRT

<213> Aspergillus niger

<400> 12

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Pro Phe Leu Glu Gln Phe Thr Asp Asp Trp Asp Ser Arg Trp Thr Pro	
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Ser His Ala Lys Lys Glu Asp Ser Lys Ser Glu Glu Asp Trp Ala Tyr	
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Val	Gly	Glu	Trp	Ser	Val	Glu	Glu	Pro	Thr	Val	Leu	Lys	Gly	Met	Glu	
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Ser	Ala	Lys	Phe	Pro	Lys	Lys	Ile	Asp	Asn	Lys	Asp	Lys	Thr	Leu	Val	
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Glu	Asp	Phe	Asn	Pro	Pro	Val	Asn	Pro	Glu	Lys	Glu	Ile	Asp	Asp	Pro	
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Pro	Glu	Ala	Thr	Lys	Pro	Glu	Asp	Trp	Asp	Glu	Glu	Ala	Pro	Phe	Glu	
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	290					295					300					
Pro	Thr	Ser	Ile	Pro	Asp	Pro	Glu	Ala	Glu	Lys	Pro	Glu	Asp	Trp	Asp	
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Cys	Gln	Asp	Ala	Ser	Gly	Cys	Gly	Pro	Trp	Ser	Pro	Pro	Met	Lys	Lys	
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Val	Gly	His	Ser	Ala	Glu	Asp	Ala	Glu	Lys	Leu	Arg	Gln	Glu	Thr	Phe	
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Gly	Leu	Ala	Ala	Val	Leu	Val	Thr	Met	Ile	Leu	Val	Ile	Val	Gly	Ala	
			500					505					510			
Val	Gly	Ala	Ser	Thr	Pro	Ala	Pro	Ala	Pro	Ala	Lys	Lys	Gly	Lys	Glu	
		515					520					525				
Ala	Ala	Gly	Ala	Thr	Lys	Glu	Lys	Thr	Gly	Ala	Ala	Ser	Ser	Ser	Ser	

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 <213> *Aspergillus niger*

<400> 13

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attctgatag	tgtgatttctg	aatgattccc	tccttgaata	atatggagac	agtctgatgc	2040
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Ser Asn Ser Leu Val Tyr Ala Asp Ser Ala Pro Ser Ser Ser Pro Val	
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gct ctc cct cgc gat ttc aag cct ccc caa gtg ttt aag aac gcc aat	144
Ala Leu Pro Arg Asp Phe Lys Pro Pro Gln Val Phe Lys Asn Ala Asn	
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ctt gtc cgc aac acc aat ttg gag aag gga tac cta cgt gag acc gtc	192
Leu Val Arg Asn Thr Asn Leu Glu Lys Gly Tyr Leu Arg Glu Thr Val	
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aat gtt gtc gtt gag aat gtg gac aag aag ccg cag tcc gac tac tac	240
Asn Val Val Val Glu Asn Val Asp Lys Lys Pro Gln Ser Asp Tyr Tyr	
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ttg tcc ttc cca tcc gac ctt tac gac aag gtc ggt gcc cta gaa gtc	288
Leu Ser Phe Pro Ser Asp Leu Tyr Asp Lys Val Gly Ala Leu Glu Val	
85 90 95	
cgt gat aaa tcg gct cct gaa cag gga cgc ttc gaa gtg gaa gct act	336
Arg Asp Lys Ser Ala Pro Glu Gln Gly Arg Phe Glu Val Glu Ala Thr	
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gag ttc gac tca agc agg gac ttc cag tac ttc gtt gtt cac ctc ccc	384
Glu Phe Asp Ser Ser Arg Asp Phe Gln Tyr Phe Val Val His Leu Pro	
115 120 125	
aag cct ctc gcc cct tcg tcg cag atc act ctg ggc atc tcc tac tcc	432
Lys Pro Leu Ala Pro Ser Ser Gln Ile Thr Leu Gly Ile Ser Tyr Ser	
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gcc ctc aac acc ctg aag ccc cgt cct gcg gcc atc agc cag aat gat	480
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Arg Gln Tyr Leu Ala Tyr Ala Phe Ser Ala Tyr Ala Pro Ser Ala Tyr	
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Thr Thr Thr Thr Gln Lys Thr Lys Ile Lys Phe Pro Ser Thr Asn Val	
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ccc gac tac acc tcc acg gac ctg acg tcg ggc gcg gat cca gag cgc	624
Pro Asp Tyr Thr Ser Thr Asp Leu Thr Ser Gly Ala Asp Pro Glu Arg	
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Gln Gly Ala Thr Tyr Thr Tyr Gly Pro Tyr Ala Asp Val Ala Pro Glu	
210 215 220	
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Thr Thr Tyr Pro Ala Ser Val Arg Tyr Glu Phe Thr Lys Pro Val Ile	
225 230 235 240	
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Thr Ala Thr Leu Leu Glu Arg Asp Leu Glu Val Ser His Trp Gly Gly	
245 250 255	
aac ctg gcg acg gaa gag cgc tac tgg ctg cgc aac aac ggc tcc aag	816
Asn Leu Ala Thr Glu Glu Arg Tyr Trp Leu Arg Asn Asn Gly Ser Lys	
260 265 270	
ctc acc gac aac ttc aac cgc gtg gaa tgg acc atc agc agc tac cag	864
Leu Thr Asp Asn Phe Asn Arg Val Glu Trp Thr Ile Ser Ser Tyr Gln	
275 280 285	
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Gln	Leu	Pro	Ser	Ser	Ala	Ile	Arg	Glu	Leu	Lys	Ile	Pro	Leu	Lys	Pro		
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Gly	Ser	Val	Asp	Pro	Tyr	Phe	Thr	Asp	Asp	Ile	Gly	Asn	Val	Ser	Thr		
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agc	cgc	tac	cgt	ccc	gga	aag	gtc	cgc	aac	cgt	gac	gcc	tcc	ctg	gag		1008
Ser	Arg	Tyr	Arg	Pro	Gly	Lys	Val	Pro	Asn	Arg	Asp	Ala	Ser	Leu	Glu		
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ctt	cgt	ccc	cgg	ttc	ccc	atc	ttc	ggc	gga	tgg	aac	tac	agc	ttc	cgc		1056
Leu	Arg	Pro	Arg	Phe	Pro	Ile	Phe	Gly	Gly	Trp	Asn	Tyr	Ser	Phe	Arg		
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Ile	Gly	Trp	Asn	Asn	Asp	Leu	Ser	Ala	Phe	Leu	Arg	Lys	Ala	Val	Thr		
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Gly	Ala	Asp	Ser	Tyr	Val	Leu	Lys	Val	Pro	Phe	Ile	Glu	Gly	Pro	Lys		
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Val	Ser	Glu	Gly	Ile	Gln	Tyr	Glu	Lys	Ala	Val	Val	Arg	Ile	Ile	Leu		
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ccc	gag	ggt	gcc	cgg	aac	gtc	cgc	tac	gag	ctc	ctc	gag	aag	gcg	act		1248
Pro	Glu	Gly	Ala	Arg	Asn	Val	Arg	Tyr	Glu	Leu	Leu	Glu	Lys	Ala	Thr		
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agc	aat	ggt	ctc	ccc	ggt	gcg	aac	cag	atc	cag	act	gag	ctc	acc	agc		1296
Ser	Asn	Gly	Leu	Pro	Gly	Ala	Asn	Gln	Ile	Gln	Thr	Glu	Leu	Thr	Ser		
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cac	aag	act	ttc	atg	gat	acc	cta	gga	cgc	acg	gcg	ctg	act	ttg	acc		1344
His	Lys	Thr	Phe	Met	Asp	Thr	Leu	Gly	Arg	Thr	Ala	Leu	Thr	Leu	Thr		
		435					440						445				
gtg	gag	gag	ttg	act	gat	gag	gcc	cgt	gac	tcg	cag	ata	gtg	gtc	act		1392
Val	Glu	Glu	Leu	Thr	Asp	Glu	Ala	Arg	Asp	Ser	Gln	Ile	Val	Val	Thr		
	450					455					460						
tac	gac	tac	tct	ctg	tgg	gat	gga	ttg	cgc	aag	ccc	gtg	acc	atc	acg		1440
Tyr	Asp	Tyr	Ser	Leu	Trp	Asp	Gly	Leu	Arg	Lys	Pro	Val	Thr	Ile	Thr		
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gcg	ggg	ctg	ttc	acc	gtg	ttt	gtt	gcc	gcg	tgg	gcg	att	gga	aat	att		1488
Ala	Gly	Leu	Phe	Thr	Val	Phe	Val	Ala	Ala	Trp	Ala	Ile	Gly	Asn	Ile		
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 Ala Leu Pro Arg Asp Phe Lys Pro Pro Gln Val Phe Lys Asn Ala Asn
 35 40 45

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Arg	Asp	Lys	Ser	Ala	Pro	Glu	Gln	Gly	Arg	Phe	Glu	Val	Glu	Ala	Thr
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Pro	Glu	Gly	Ala	Arg	Asn	Val	Arg	Tyr	Glu	Leu	Leu	Glu	Lys	Ala	Thr
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		420						425					430		
His	Lys	Thr	Phe	Met	Asp	Thr	Leu	Gly	Arg	Thr	Ala	Leu	Thr	Leu	Thr
		435					440					445			
Val	Glu	Glu	Leu	Thr	Asp	Glu	Ala	Arg	Asp	Ser	Gln	Ile	Val	Val	Thr
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Tyr	Asp	Tyr	Ser	Leu	Trp	Asp	Gly	Leu	Arg	Lys	Pro	Val	Thr	Ile	Thr
465					470					475					480
Ala	Gly	Leu	Phe	Thr	Val	Phe	Val	Ala	Ala	Trp	Ala	Ile	Gly	Asn	Ile
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<212> DNA

<213> *Aspergillus niger*

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<210> 17

<211> 1548

<212> DNA

<213> *Aspergillus niger*

<220>

<221> CDS

<222> (1)..(1548)

<400> 17

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Val Val Ala Ala Asp Thr Glu Ser Asp Val Ile Ser Leu Asp Gln	
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gac aca ttt gag agc ttc atg aac gag cac ggt ctc gtg ctt gcc gaa	144
Asp Thr Phe Glu Ser Phe Met Asn Glu His Gly Leu Val Leu Ala Glu	
35 40 45	
ttc ttt gct cct tgg tgt ggc cac tgt aaa gcc ctc gca cca aag tat	192
Phe Phe Ala Pro Trp Cys Gly His Cys Lys Ala Leu Ala Pro Lys Tyr	
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Glu Glu Ala Ala Thr Glu Leu Lys Ala Lys Asn Ile Pro Leu Val Lys	
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Val Asp Cys Thr Ala Glu Glu Asp Leu Cys Arg Ser Gln Gly Val Glu	
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Gly Tyr Pro Thr Leu Lys Ile Phe Arg Gly Val Asp Ser Ser Lys Pro	
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tac cag ggc gct agg caa aca gaa tca atc gtt tcc tac atg att aag	384
Tyr Gln Gly Ala Arg Gln Thr Glu Ser Ile Val Ser Tyr Met Ile Lys	
115 120 125	
cag tca ctt cct gca gta tcc tcc gtg aac gag gag aat tta gaa gag	432
Gln Ser Leu Pro Ala Val Ser Ser Val Asn Glu Glu Asn Leu Glu Glu	
130 135 140	
atc aag acc atg gac aag att gtc gtg atc ggt tat atc ccg tcc gag	480
Ile Lys Thr Met Asp Lys Ile Val Val Ile Gly Tyr Ile Pro Ser Glu	
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Asp Gln Glu Thr Tyr Gln Ala Phe Glu Lys Tyr Ala Glu Ser Gln Arg	
165 170 175	
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Asp Asn Tyr Leu Phe Ala Ala Thr Asp Asp Ala Ala Ile Ala Lys Ser	
180 185 190	
gaa ggt gtc gag cag ccc tcc atc gtg ctc tat aag gac ttc gat gag	624
Glu Gly Val Glu Gln Pro Ser Ile Val Leu Tyr Lys Asp Phe Asp Glu	
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Lys Lys Ala Val Tyr Asp Gly Glu Ile Glu Gln Glu Ala Ile His Ser	
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Trp Val Lys Ser Ala Ser Thr Pro Leu Val Gly Glu Ile Gly Pro Glu	
225 230 235 240	
acc tac tct ggc tat att ggg gct gga gtc cca ttg gcc tat atc ttt	768
Thr Tyr Ser Gly Tyr Ile Gly Ala Gly Val Pro Leu Ala Tyr Ile Phe	
245 250 255	
gcc gag acc aag gag gag cgc gaa aag tac acc gaa gac ttc aag cct	816
Ala Glu Thr Lys Glu Glu Arg Glu Lys Tyr Thr Glu Asp Phe Lys Pro	
260 265 270	
att gcc cag aag cac aag ggt gct atc aac att gct act att gac gcc	864
Ile Ala Gln Lys His Lys Gly Ala Ile Asn Ile Ala Thr Ile Asp Ala	
275 280 285	
aag atg ttc ggt gcc cac gct gga aac ctc aac cta gac tct cag aag	912
Lys Met Phe Gly Ala His Ala Gly Asn Leu Asn Leu Asp Ser Gln Lys	
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Phe Pro Ala Phe Ala Ile Gln Asp Pro Ala Lys Asn Ala Lys Tyr Pro	
305 310 315 320	
tat gac cag gcc aag gaa ttg aat gcc gac gag gtt gaa aag ttc atc	1008
Tyr Asp Gln Ala Lys Glu Leu Asn Ala Asp Glu Val Glu Lys Phe Ile	
325 330 335	
cag gat gtt ctg gat ggg aag gtc gag cct agc atc aag tcg gaa cct	1056
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Tyr Ala Pro Trp Cys Gly His Cys Lys Ala Leu Ala Pro Lys Tyr Asp	
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Glu Leu Ala Ala Leu Tyr Ala Asp His Pro Asp Leu Ala Ala Lys Val	
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Thr Ile Ala Lys Ile Asp Ala Thr Ala Asn Asp Val Pro Asp Pro Ile	
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acc gga ttc cct acc ctc aga ctc tac ccg gcc ggt gcc aag gac tcc	1344
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Pro Ile Glu Tyr Ser Gly Ser Arg Thr Val Glu Asp Leu Ala Asn Phe	
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gtg aag gag aat ggc aaa cac aac gtt gac gcc ctc aat gtc gct tcc	1440
Val Lys Glu Asn Gly Lys His Asn Val Asp Ala Leu Asn Val Ala Ser	
465 470 475 480	
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Glu Glu Thr Gln Glu Gly Gly Asp Val Thr Glu Ala Ala Pro Ser Ala	
485 490 495	
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<210> 18
 <211> 515
 <212> PRT
 <213> *Aspergillus niger*

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		35				40				45					
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Val	Asp	Cys	Thr	Ala	Glu	Glu	Asp	Leu	Cys	Arg	Ser	Gln	Gly	Val	Glu
				85					90					95	
Gly	Tyr	Pro	Thr	Leu	Lys	Ile	Phe	Arg	Gly	Val	Asp	Ser	Ser	Lys	Pro
			100					105					110		
Tyr	Gln	Gly	Ala	Arg	Gln	Thr	Glu	Ser	Ile	Val	Ser	Tyr	Met	Ile	Lys
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Gln	Ser	Leu	Pro	Ala	Val	Ser	Ser	Val	Asn	Glu	Glu	Asn	Leu	Glu	Glu
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Asp	Gln	Glu	Thr	Tyr	Gln	Ala	Phe	Glu	Lys	Tyr	Ala	Glu	Ser	Gln	Arg
				165					170					175	
Asp	Asn	Tyr	Leu	Phe	Ala	Ala	Thr	Asp	Asp	Ala	Ala	Ile	Ala	Lys	Ser
			180					185					190		
Glu	Gly	Val	Glu	Gln	Pro	Ser	Ile	Val	Leu	Tyr	Lys	Asp	Phe	Asp	Glu
		195					200					205			
Lys	Lys	Ala	Val	Tyr	Asp	Gly	Glu	Ile	Glu	Gln	Glu	Ala	Ile	His	Ser
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Thr	Tyr	Ser	Gly	Tyr	Ile	Gly	Ala	Gly	Val	Pro	Leu	Ala	Tyr	Ile	Phe
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Ala	Glu	Thr	Lys	Glu	Glu	Arg	Glu	Lys	Tyr	Thr	Glu	Asp	Phe	Lys	Pro
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Ile	Ala	Gln	Lys	His	Lys	Gly	Ala	Ile	Asn	Ile	Ala	Thr	Ile	Asp	Ala
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Lys	Met	Phe	Gly	Ala	His	Ala	Gly	Asn	Leu	Asn	Leu	Asp	Ser	Gln	Lys
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Tyr	Asp	Gln	Ala	Lys	Glu	Leu	Asn	Ala	Asp	Glu	Val	Glu	Lys	Phe	Ile
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Gln	Asp	Val	Leu	Asp	Gly	Lys	Val	Glu	Pro	Ser	Ile	Lys	Ser	Glu	Pro
			340					345					350		
Val	Pro	Glu	Ser	Gln	Glu	Gly	Pro	Val	Thr	Val	Val	Val	Ala	His	Ser
		355					360					365			
Tyr	Lys	Asp	Leu	Val	Ile	Asp	Asn	Asp	Lys	Asp	Val	Leu	Leu	Glu	Phe
	370					375					380				
Tyr	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Ala	Leu	Ala	Pro	Lys	Tyr	Asp
385					390					395					400
Glu	Leu	Ala	Ala	Leu	Tyr	Ala	Asp	His	Pro	Asp	Leu	Ala	Ala	Lys	Val
				405					410					415	
Thr	Ile	Ala	Lys	Ile	Asp	Ala	Thr	Ala	Asn	Asp	Val	Pro	Asp	Pro	Ile
			420					425					430		
Thr	Gly	Phe	Pro	Thr	Leu	Arg	Leu	Tyr	Pro	Ala	Gly	Ala	Lys	Asp	Ser
		435					440					445			
Pro	Ile	Glu	Tyr	Ser	Gly	Ser	Arg	Thr	Val	Glu	Asp	Leu	Ala	Asn	Phe
	450					455					460				
Val	Lys	Glu	Asn	Gly	Lys	His	Asn	Val	Asp	Ala	Leu	Asn	Val	Ala	Ser
465					470					475					480
Glu	Glu	Thr	Gln	Glu	Gly	Gly	Asp	Val	Thr	Glu	Ala	Ala	Pro	Ser	Ala
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 Asp Glu Leu
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<210> 19
 <211> 2113
 <212> DNA
 <213> *Aspergillus niger*

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 ccggtttctc gatctcatca agcccttcac gcccctcctc ccggaggtgg ccgccccgga 360
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<210> 20
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 <213> *Aspergillus niger*

<220>
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<400> 20

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

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Lys	Leu	Leu	Gly	Val	Trp	Glu	Pro	Arg	Glu	Gly	Ser	Ala	Gln	Leu	His		
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gcc	gcc	tcc	ggc	att	gcc	tac	tac	atg	tct	cct	ccc	ctg	aac	ttc	aag	1056	
Ala	Ala	Ser	Gly	Ile	Ala	Tyr	Tyr	Met	Ser	Pro	Pro	Leu	Asn	Phe	Lys		
			340					345					350				
gag	gcc	ctt	ctt	gac	ccc	att	cac	acc	gcc	gtt	tac	atc	acc	ttc	atg	1104	
Glu	Ala	Leu	Leu	Asp	Pro	Ile	His	Thr	Ala	Val	Tyr	Ile	Thr	Phe	Met		
		355				360					365						
ctg	gtt	gct	tgt	gct	ctc	ttc	tcc	aag	acc	tgg	att	gag	gtt	tcc	ggc	1152	
Leu	Val	Ala	Cys	Ala	Leu	Phe	Ser	Lys	Thr	Trp	Ile	Glu	Val	Ser	Gly		
	370				375						380						
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Ser	Ala	Pro	Arg	Asp	Val	Ala	Lys	Gln	Leu	Lys	Asp	Gln	Gly	Leu	Val		
385				390						395					400		
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Met	Ala	Gly	His	Arg	Glu	Gln	Ser	Met	Tyr	Lys	Glu	Leu	Lys	Arg	Val		
			405					410						415			
atc	cct	act	gct	gct	gct	ttc	ggt	ggt	gcc	tgc	att	ggt	gcc	ctg	tcc	1296	
Ile	Pro	Thr	Ala	Ala	Ala	Phe	Gly	Gly	Ala	Cys	Ile	Gly	Ala	Leu	Ser		
			420				425					430					
gtc	gct	tct	gac	ctg	ctt	ggt	gct	ctt	ggc	agc	ggt	act	ggt	atc	ctc	1344	
Val	Ala	Ser	Asp	Leu	Leu	Gly	Ala	Leu	Gly	Ser	Gly	Thr	Gly	Ile	Leu		
		435				440					445						
ctt	gcc	gtt	acg	att	ata	tac	gga	tac	ttt	gaa	att	gcc	gcc	cgt	gag	1392	
Leu	Ala	Val	Thr	Ile	Ile	Tyr	Gly	Tyr	Phe	Glu	Ile	Ala	Ala	Arg	Glu		
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ggc	gac	att	gga	tcg	ggc	ctc	aag	ggc	ctt	gtt	ccg	ggt	aac	tag		1437	
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<210> 21

<211> 478

<212> PRT

<213> Aspergillus niger

<400> 21

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Leu	Met	Trp	Thr	Gly	Leu	Thr	Leu	Leu	Ile	Phe	Leu	Val	Met	Ser	Gln		
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Met	Pro	Leu	Tyr	Gly	Ile	Val	Ser	Ser	Asp	Thr	Ser	Asp	Pro	Leu	Tyr		
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Trp	Leu	Arg	Met	Met	Leu	Ala	Ser	Asn	Arg	Gly	Thr	Leu	Met	Glu	Leu		
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Gly	Ile	Thr	Pro	Ile	Ile	Ser	Ser	Gly	Met	Val	Phe	Gln	Leu	Leu	Ala		
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Gly Thr His Leu Ile Asp Val Asn Leu Asp Leu Lys Thr Asp Arg Glu
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 Gln Ala Cys Val Tyr Val Leu Thr Gly Leu Tyr Gly Gln Pro Ser Asp
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 Gly Leu Val Val Ile Leu Leu Asp Glu Leu Leu Gln Lys Gly Tyr Gly
 165 170 175
 Leu Gly Ser Gly Ile Ser Leu Phe Ile Ala Thr Asn Ile Cys Glu Ser
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 Pro Glu Phe Glu Gly Ala Ile Ile Ala Leu Phe His Leu Leu Leu Thr
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 Trp Ser Asp Lys Gln Arg Ala Leu Arg Glu Ala Phe Tyr Arg Gln Asn
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 Val Ile Tyr Leu Gln Gly Phe Arg Val Glu Ile Pro Val Lys Ser Ser
 260 265 270
 Arg Gln Arg Gly Met Arg Gly Ser Tyr Pro Val Arg Leu Phe Tyr Thr
 275 280 285
 Ser Asn Met Pro Ile Met Leu Gln Ser Ala Leu Cys Ser Asn Ile Phe
 290 295 300
 Leu Ile Ser Gln Met Leu Tyr Ser Arg Phe Ser Asp Asn Leu Leu Val
 305 310 315 320
 Lys Leu Leu Gly Val Trp Glu Pro Arg Glu Gly Ser Ala Gln Leu His
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 340 345 350
 Glu Ala Leu Leu Asp Pro Ile His Thr Ala Val Tyr Ile Thr Phe Met
 355 360 365
 Leu Val Ala Cys Ala Leu Phe Ser Lys Thr Trp Ile Glu Val Ser Gly
 370 375 380
 Ser Ala Pro Arg Asp Val Ala Lys Gln Leu Lys Asp Gln Gly Leu Val
 385 390 395 400
 Met Ala Gly His Arg Glu Gln Ser Met Tyr Lys Glu Leu Lys Arg Val
 405 410 415
 Ile Pro Thr Ala Ala Ala Phe Gly Gly Ala Cys Ile Gly Ala Leu Ser
 420 425 430
 Val Ala Ser Asp Leu Leu Gly Ala Leu Gly Ser Gly Thr Gly Ile Leu
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<210> 22

<211> 5117

<212> DNA

<213> *Aspergillus niger*

<400> 22

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60

120

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Cys Asn Asn Pro Met Thr Lys Glu Pro Lys Leu Asp Arg Ala Arg Arg	
1425 1430 1435 1440	
cag gta cct gag tgg acg gag tat gat gat gag att gcg gcc ttg tcg	4368
Gln Val Pro Glu Trp Thr Glu Tyr Asp Asp Glu Ile Ala Ala Leu Ser	
1445 1450 1455	
aag aga gtt gcc gct gag aag cag cag ggg cag gtg gag gaa gaa agg	4416
Lys Arg Val Ala Ala Glu Lys Gln Gln Gly Gln Val Glu Glu Glu Arg	
1460 1465 1470	
gcc ggt gaa tcg tac cct gac gag gat gag gag ggc gag act tcc tct	4464
Ala Gly Glu Ser Tyr Pro Asp Glu Asp Glu Glu Gly Glu Thr Ser Ser	
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Gly Trp Asp Lys Asp Glu Leu	
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<210> 24

<211> 1495

<212> PRT

<213> *Aspergillus niger*

<400> 24

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

Cys	Phe	Gln	Ala	Ala	Thr	Gln	Asp	Arg	Ser	Pro	Arg	Leu	Glu	Lys	Val
545					550					555					560
Ser	Leu	Ser	Leu	Asp	Glu	Val	Leu	Asn	Asn	Ala	Val	Tyr	Asp	Ala	Thr
				565					570					575	
Val	Ser	Lys	Thr	Thr	Ala	Tyr	Leu	Asn	Arg	Leu	Gly	Met	Lys	His	Glu
			580					585					590		
Pro	Ser	His	Ala	Phe	Val	Asn	Gly	Ile	Pro	Val	Thr	Arg	Asn	Asp	Lys
		595					600					605			
Trp	Ala	Gln	Glu	Met	Ser	Thr	Lys	Ile	Ser	Lys	Asp	Thr	Gln	Leu	Ile
	610					615					620				
Gln	Gln	Lys	Ile	Ala	Asp	Ala	Glu	Val	Asp	Glu	Asp	Thr	Trp	Leu	Pro
625					630					635					640
Glu	Leu	Phe	Leu	Ser	Gln	Ala	Phe	Asp	Arg	Arg	Asn	Pro	Ala	Ile	Val
				645					650					655	
Pro	Glu	Asp	Pro	Lys	Glu	Ile	Arg	Ala	Val	Asp	Leu	Val	Gln	Leu	Ala
			660					665					670		
Asp	Ser	Gln	Glu	Lys	Leu	Phe	Ser	Gln	Ile	Pro	Arg	Leu	Gly	Leu	Asp
		675					680					685			
Glu	Ser	Asn	Ala	Leu	Glu	Ser	Ala	His	Ala	Ile	Val	Val	Gly	Asn	Phe
	690					695					700				
Asp	Glu	Lys	Ser	Gly	Tyr	Glu	Leu	Leu	Ser	Ala	Ala	Leu	Glu	Ser	Arg
705				710						715					720
Lys	Thr	His	Gly	Glu	Val	Glu	Met	Leu	Phe	Leu	His	Asn	Pro	Lys	Leu
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Glu	Ala	Ser	Pro	Ala	Ser	Arg	Ser	Val	Ala	Val	Arg	Arg	Leu	Leu	Asn
			740					745					750		
Gly	Gly	Lys	Glu	Val	Asp	Ala	Ser	Gln	Ile	Leu	Glu	Ala	Ile	Ala	Ser
		755					760					765			
Ser	Ala	Ser	Pro	Ala	Asp	Glu	Glu	Ala	Gly	Asp	Ala	Ala	Leu	Phe	Trp
	770					775					780				
Glu	Ala	Gln	Arg	Ala	Val	Val	Glu	Glu	Leu	Gly	Leu	Ala	Pro	Gly	Glu
785				790						795					800
Arg	Ala	Leu	Val	Ile	Asn	Gly	Arg	Val	Val	Gly	Pro	Ile	Ala	Glu	Asp
			805						810					815	
Thr	Ala	Leu	Thr	Ser	Glu	Asp	Leu	Asp	Gln	Leu	Leu	Ile	Tyr	Glu	Lys
			820					825					830		
Gln	Lys	Arg	Ile	Thr	Pro	Val	Ala	Lys	Ala	Val	Lys	Ala	Leu	Glu	Phe
		835					840					845			
Asp	Glu	Lys	Leu	Ser	Asp	Pro	Leu	Asp	Phe	Ala	Lys	Leu	Thr	Ser	Leu
	850					855					860				
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865					870					875					880
Thr	Ser	Asp	Ile	Arg	Leu	Asn	Leu	Phe	Asn	Arg	Trp	Asn	Asp	Ser	Gln
			885						890					895	
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			900					905					910		
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Tyr	Val	Leu	Asp	Ser	Glu	Pro	Ser	Phe	Asn	Glu	Asp	Gly	Ser	Val	Ser
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Arg	Pro	Thr	Ala	Ser	Phe	Ser	Gly	Val	Pro	Val	Glu	Ala	Leu	Leu	Thr
			980					985					990		
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Ile His Asp Leu Asp Asn	Ile Lys Leu Ser Ser Val	Lys Asp Gly Ser
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Ser Arg Asp Met Thr Thr	Lys Ser Pro Pro Arg	Gly Val Gln Leu Val
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Asn Leu Gly Tyr Phe Gln	Phe Lys Ala Gln Pro	Gly Leu Trp Asn Ile
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Asn Leu Lys Pro Gly Arg	Ser Glu Arg Ile Phe	Thr Leu Asp Ser Val
1090	1095	1100
Gly Ser Leu Gly Tyr Asn	Pro Gln Pro Gly Asp	Glu Asn Asn Glu Val
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Ala Leu Leu Ser Phe Gln	Gly Arg Thr Leu Phe	Pro Arg Val Ser Arg
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Lys Lys Gly Tyr Glu Thr	Glu Asp Val Leu Glu	Thr Asn Pro Lys Pro
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Gly Ser Ala Met Asp Tyr	Met Asn Lys Gly Phe	Asn Phe Ala Ser Gly
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Gln Ala Asp Ile Asn Ile	Phe Ser Val Ala Ser	Gly His Leu Tyr Glu
1185	1190	1195
Arg Met Leu Asn Ile Met	Met Val Ser Val Met	Arg Asn Thr Asn His
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Ser Val Lys Phe Trp Phe	Ile Glu Gln Phe Leu	Ser Pro Ser Phe Lys
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Ser Phe Leu Pro His Leu	Ala Lys Glu Tyr Asn	Phe Ser Tyr Glu Met
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Val Thr Tyr Lys Trp Pro	His Trp Leu Arg Ala	Gln Lys Glu Lys Gln
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Arg Glu Ile Trp Gly Tyr	Lys Ile Leu Phe Leu	Asp Val Leu Phe Pro
1265	1270	1275
Leu Asp Leu Asp Lys Val	Ile Phe Val Asp Ala	Asp Gln Ile Val Arg
1285	1290	1295
Thr Asp Met Tyr Asp Leu	Val Ser Leu Asp Leu	Glu Gly Ala Pro Tyr
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Gly Phe Thr Pro Met Cys	Asp Ser Arg His Glu	Met Glu Gly Phe Arg
1315	1320	1325
Phe Trp Lys Gln Gly Tyr	Trp Lys Asn Phe Leu	Arg Gly Gln Pro Tyr
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His Ile Ser Ala Leu Tyr	Val Val Asp Leu Asn	Arg Phe Arg Ala Ile
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Ala Ala Gly Asp Arg Leu	Arg Gly Gln Tyr Gln	Met Leu Ser Ala Asp
1365	1370	1375
Pro Glu Ser Leu Ser Asn	Leu Asp Gln Asp Leu	Pro Asn His Met Gln
1380	1385	1390
His His Ile Pro Ile Lys	Ser Leu Pro Gln Glu	Trp Leu Trp Cys Glu
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Thr Trp Cys Ser Asp Glu	Ser Gln Ser Gln Ala	Arg Thr Ile Asp Leu
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Cys Asn Asn Pro Met Thr	Lys Glu Pro Lys Leu	Asp Arg Ala Arg Arg
1425	1430	1435
Gln Val Pro Glu Trp Thr	Glu Tyr Asp Asp Glu	Ile Ala Ala Leu Ser
1445	1450	1455

Lys Arg Val Ala Ala Glu Lys Gln Gln Gly Gln Val Glu Glu Glu Arg
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 Ala Gly Glu Ser Tyr Pro Asp Glu Asp Glu Glu Gly Glu Thr Ser Ser
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 <212> DNA
 <213> *Aspergillus niger*

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 Ser Ser Lys Cys Val Leu Ile Trp Ala Ile His Arg Asn Lys Ser Ala
 20 25 30

gaa gga gtc tcc ctt ctg acg cag atg ctc tat gct ttg gtg ttc gtg	144
Glu Gly Val Ser Leu Leu Thr Gln Met Leu Tyr Ala Leu Val Phe Val	
35 40 45	
act cgt tat ctc gac ctt ttc tcg aag gca gga tgg aag cac ttc tac	192
Thr Arg Tyr Leu Asp Leu Phe Ser Lys Ala Gly Trp Lys His Phe Tyr	
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ctc gta ttc ttc aag cta ttt tat atc atc tcc tcg ttc tac gtt ata	240
Leu Val Phe Phe Lys Leu Phe Tyr Ile Ile Ser Ser Phe Tyr Val Ile	
65 70 75 80	
tac ctg atg atg aga gta ttt ccc cgg aca cgg gaa agg gag cga gcc	288
Tyr Leu Met Met Arg Val Phe Pro Arg Thr Arg Glu Arg Glu Arg Ala	
85 90 95	
tgg aag atg gct ata ata tcg gtc gct cta tct ctg gtt ctg gct cct	336
Trp Lys Met Ala Ile Ile Ser Val Ala Leu Ser Leu Val Leu Ala Pro	
100 105 110	
ata tct att gtc atc ttc tat cgt ggt tat ccc gat aga tgg ttc acg	384
Ile Ser Ile Val Ile Phe Tyr Arg Gly Tyr Pro Asp Arg Trp Phe Thr	
115 120 125	
gag act tgc tgg act ttc tcg att ata tta gag tcc gtc tgt gtt ctc	432
Glu Thr Cys Trp Thr Phe Ser Ile Ile Leu Glu Ser Val Cys Val Leu	
130 135 140	
cct caa ttg ttg ctc ttg cgc caa acg acc gtt ccg aca gtc atc gat	480
Pro Gln Leu Leu Leu Leu Arg Gln Thr Thr Val Pro Thr Val Ile Asp	
145 150 155 160	
tca tac tac ctg ctt atg ctg gga tcc tac cgt gcc ttc tat att ctc	528
Ser Tyr Tyr Leu Leu Met Leu Gly Ser Tyr Arg Ala Phe Tyr Ile Leu	
165 170 175	
aat tgg ctt gtg cgg gga ctg ggc tct gag ggt cat tgg gac gta att	576
Asn Trp Leu Val Arg Gly Leu Gly Ser Glu Gly His Trp Asp Val Ile	
180 185 190	
gca gac ctc tac ggt gtc atc cag acg gct ttc tac gtc gat ttc gcc	624
Ala Asp Leu Tyr Gly Val Ile Gln Thr Ala Phe Tyr Val Asp Phe Ala	
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Trp Val Tyr Tyr Ser Arg Gln Arg Val Lys Leu Arg Asn Gly Gly Val	
210 215 220	
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Val Asp Ser Glu Asp Phe Arg His Ser Trp Leu Val Ser Lys Ile Leu	
225 230 235 240	
aat ttc cgg cag cga agg agt gca gat gag gag cag aat ttg aac gac	768
Asn Phe Arg Gln Arg Arg Ser Ala Asp Glu Glu Gln Asn Leu Asn Asp	
245 250 255	
gag gac gtg gag gat gag gaa gtt gct ggt ggc ggt aga ccc agg aac	816
Glu Asp Val Glu Asp Glu Glu Val Ala Gly Gly Gly Arg Pro Arg Asn	
260 265 270	
aac cgc tgg gga gca atg ggg atc tcc gtc tcg gcc gac gat acg cta	864
Asn Arg Trp Gly Ala Met Gly Ile Ser Val Ser Ala Asp Asp Thr Leu	
275 280 285	
gga aac cat cgt ggg aca agc caa gac gag agt ctg gaa ggg ttc tta	912
Gly Asn His Arg Gly Thr Ser Gln Asp Glu Ser Leu Glu Gly Phe Leu	
290 295 300	
gaa gat gaa gaa gac gac gag gac aat aac ggg tac cct gtg aac ggg	960
Glu Asp Glu Glu Asp Glu Asp Asn Asn Gly Tyr Pro Val Asn Gly	
305 310 315 320	
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<210> 27
 <211> 335
 <212> PRT
 <213> Aspergillus niger

<400> 27
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 Thr Arg Tyr Leu Asp Leu Phe Ser Lys Ala Gly Trp Lys His Phe Tyr
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 65 70 75 80
 Tyr Leu Met Met Arg Val Phe Pro Arg Thr Arg Glu Arg Glu Arg Ala
 85 90 95
 Trp Lys Met Ala Ile Ile Ser Val Ala Leu Ser Leu Val Leu Ala Pro
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 Ile Ser Ile Val Ile Phe Tyr Arg Gly Tyr Pro Asp Arg Trp Phe Thr
 115 120 125
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 Pro Gln Leu Leu Leu Leu Arg Gln Thr Thr Val Pro Thr Val Ile Asp
 145 150 155 160
 Ser Tyr Tyr Leu Leu Met Leu Gly Ser Tyr Arg Ala Phe Tyr Ile Leu
 165 170 175
 Asn Trp Leu Val Arg Gly Leu Gly Ser Glu Gly His Trp Asp Val Ile
 180 185 190
 Ala Asp Leu Tyr Gly Val Ile Gln Thr Ala Phe Tyr Val Asp Phe Ala
 195 200 205
 Trp Val Tyr Tyr Ser Arg Gln Arg Val Lys Leu Arg Asn Gly Gly Val
 210 215 220
 Val Asp Ser Glu Asp Phe Arg His Ser Trp Leu Val Ser Lys Ile Leu
 225 230 235 240
 Asn Phe Arg Gln Arg Arg Ser Ala Asp Glu Glu Gln Asn Leu Asn Asp
 245 250 255
 Glu Asp Val Glu Asp Glu Glu Val Ala Gly Gly Gly Arg Pro Arg Asn
 260 265 270
 Asn Arg Trp Gly Ala Met Gly Ile Ser Val Ser Ala Asp Asp Thr Leu
 275 280 285
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 305 310 315 320
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 <212> DNA
 <213> Aspergillus niger

<400> 28

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cag	atc	ccc	tac	gat	gtc	atc	tgg	ctg	gac	atc	gaa	tat	acc	gat	gac	1296
Gln	Ile	Pro	Tyr	Asp	Val	Ile	Trp	Leu	Asp	Ile	Glu	Tyr	Thr	Asp	Asp	
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Arg	Lys	Tyr	Phe	Thr	Trp	Asp	Pro	Leu	Ser	Phe	Pro	Asp	Pro	Ile	Ser	
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Lys	Ser	Lys	Asp	Leu	Ala	Thr	Lys	Asn	Lys	Asp	Gly	Glu	Ile	Tyr	Asp	
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Arg	Arg	Pro	Phe	Ile	Leu	Thr	Arg	Ser	Tyr	Tyr	Ala	Gly	Ala	Gln	Arg	
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Phe	Ala	Gly	Ala	Asp	Val	Gly	Gly	Phe	Phe	Gln	Asn	Pro	Ser	Lys	Glu	
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Ala	His	Ala	His	Ile	Asp	Thr	Arg	Arg	Arg	Glu	Pro	Tyr	Leu	Ile	Ala	
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<210> 32
 <211> 1707
 <212> DNA
 <213> *Aspergillus niger*

<220>
 <221> CDS
 <222> (1)..(1707)

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Met	Ile	Leu	Pro	Gln	Gly	Ser	Leu	Phe	Leu	Val	Ser	Ile	Ala	Ala	Cys	
1				5					10					15		
tcg	acc	gtc	gtg	gct	gcg	gcg	ggt	gat	gcc	tcc	tct	cgt	ccc	cgg	ggt	96
Ser	Thr	Val	Val	Ala	Ala	Ala	Gly	Asp	Ala	Ser	Ser	Arg	Pro	Arg	Gly	
			20					25					30			
gta	ggt	ccc	gaa	ttc	gcc	aag	ttc	tac	aag	gat	acc	acc	acc	ttc	acg	144
Val	Gly	Pro	Glu	Phe	Ala	Lys	Phe	Tyr	Lys	Asp	Thr	Thr	Thr	Phe	Thr	
			35				40						45			
tgc	atc	tcc	cac	cca	gcc	atc	cag	atc	ccc	ttc	tcc	gcc	gtg	aac	gat	192
Cys	Ile	Ser	His	Pro	Ala	Ile	Gln	Ile	Pro	Phe	Ser	Ala	Val	Asn	Asp	
			50				55						60			
gat	tac	tgt	gac	tgt	ccg	gat	ggc	agt	gat	gag	cct	ggc	aca	tct	gcc	240
Asp	Tyr	Cys	Asp	Cys	Pro	Asp	Gly	Ser	Asp	Glu	Pro	Gly	Thr	Ser	Ala	
					70					75					80	
tgt	gcc	ttc	ctg	tct	cgc	aac	tcc	gcc	cta	aca	ccg	ggt	gag	cgc	ccc	288
Cys	Ala	Phe	Leu	Ser	Arg	Asn	Ser	Ala	Leu	Thr	Pro	Gly	Glu	Arg	Pro	

				85				90				95					
ggc	agc	gac	gat	ctc	gag	ctg	aca	tcc	gcc	ctg	ccg	ggt	ttc	tac	tgc		336
Gly	Ser	Asp	Asp	Leu	Glu	Leu	Thr	Ser	Ala	Leu	Pro	Gly	Phe	Tyr	Cys		
			100					105					110				
aag	aac	aag	ggc	cac	aag	ccc	ggc	tac	gtc	ccc	ttc	cag	cgg	gtc	aat		384
Lys	Asn	Lys	Gly	His	Lys	Pro	Gly	Tyr	Val	Pro	Phe	Gln	Arg	Val	Asn		
		115					120					125					
gac	ggc	atc	tgt	gac	tat	gag	ctc	tgc	tgc	gac	ggc	agt	gac	gag	tgg		432
Asp	Gly	Ile	Cys	Asp	Tyr	Glu	Leu	Cys	Cys	Asp	Gly	Ser	Asp	Glu	Trp		
	130					135					140						
gcc	cgc	cct	ggc	ggc	acc	aag	tgt	gaa	gac	aag	tgc	aag	gag	atc	ggc		480
Ala	Arg	Pro	Gly	Gly	Thr	Lys	Cys	Glu	Asp	Lys	Cys	Lys	Glu	Ile	Gly		
	145				150					155					160		
aag	gaa	tgg	cgg	aag	aag	gag	gag	aag	aga	cag	aag	tcc	atg	act	gcg		528
Lys	Glu	Trp	Arg	Lys	Lys	Glu	Glu	Lys	Arg	Gln	Lys	Ser	Met	Thr	Ala		
			165					170						175			
gct	ttg	aag	aag	aag	aag	gat	ctg	ctt	gtg	gag	gct	ggt	aga	cag	cag		576
Ala	Leu	Lys	Lys	Lys	Lys	Asp	Leu	Leu	Val	Glu	Ala	Gly	Arg	Gln	Gln		
			180				185						190				
aag	gag	gtc	gag	gac	aat	atc	aag	cgt	ctg	gaa	gtt	gaa	att	cag	gcc		624
Lys	Glu	Val	Glu	Asp	Asn	Ile	Lys	Arg	Leu	Glu	Val	Glu	Ile	Gln	Ala		
		195					200					205					
cag	gag	ctg	aag	gtc	aat	gat	ctt	cag	gcg	gag	ctg	gag	gag	gtg	gag		672
Gln	Glu	Leu	Lys	Val	Asn	Asp	Leu	Gln	Ala	Glu	Leu	Glu	Glu	Val	Glu		
		210				215					220						
cag	cag	gag	gcg	agc	aag	gtc	gtg	aag	ggc	aag	acg	gcg	ggc	aag	gtt		720
Gln	Gln	Glu	Ala	Ser	Lys	Val	Val	Lys	Gly	Lys	Thr	Ala	Gly	Lys	Val		
		225			230				235						240		
aat	gtg	ctt	gct	ggg	ttg	gct	aag	agc	cgg	gtt	gag	gag	ctt	cga	aac		768
Asn	Val	Leu	Ala	Gly	Leu	Ala	Lys	Ser	Arg	Val	Glu	Glu	Leu	Arg	Asn		
			245					250					255				
gcc	ctg	atg	gac	gtc	cgc	aag	gag	cgt	gat	gat	acc	cgt	gcc	cgt	gtg		816
Ala	Leu	Met	Asp	Val	Arg	Lys	Glu	Arg	Asp	Asp	Thr	Arg	Ala	Arg	Val		
		260					265					270					
aag	gag	ctc	gaa	gag	att	ctg	tct	aag	ttc	aag	gtg	gaa	tac	aac	cct		864
Lys	Glu	Leu	Glu	Glu	Ile	Leu	Ser	Lys	Phe	Lys	Val	Glu	Tyr	Asn	Pro		
		275				280						285					
aac	ttc	aac	gat	gag	ggc	gtt	aag	cgc	gct	gtg	cgc	agc	tgg	gaa	gac		912
Asn	Phe	Asn	Asp	Glu	Gly	Val	Lys	Arg	Ala	Val	Arg	Ser	Trp	Glu	Asp		
	290				295						300						
tac	gcc	gcc	aag	ggc	acc	ctt	gag	ggc	gcc	gtg	aac	aac	gct	cag	gac		960
Tyr	Ala	Ala	Lys	Gly	Thr	Leu	Glu	Gly	Ala	Val	Asn	Asn	Ala	Gln	Asp		
	305				310				315						320		
cgt	gat	ttg	gat	gaa	att	gct	aag	ccc	gat	gat	gag	aag	gcg	ggc	atc		1008
Arg	Asp	Leu	Asp	Glu	Ile	Ala	Lys	Pro	Asp	Asp	Glu	Lys	Ala	Gly	Ile		
		325						330					335				
aac	tgg	gaa	cag	tgg	gag	aat	gaa	gag	gat	ggg	tgt	gag	gct	ggt	ctt		1056
Asn	Trp	Glu	Gln	Trp	Glu	Asn	Glu	Glu	Asp	Gly	Cys	Glu	Ala	Gly	Leu		
		340					345					350					
gtc	tac	cag	ctg	gca	gcc	tac	ctt	ccg	cct	tct	ttg	gtc	gag	ttt	atc		1104
Val	Tyr	Gln	Leu	Ala	Ala	Tyr	Leu	Pro	Pro	Ser	Leu	Val	Glu	Phe	Ile		
	355					360						365					
gaa	ggc	aag	gtg	ctc	ttc	gtc	aga	ggg	ctc	ttg	gaa	gat	aac	gga	att		1152
Glu	Gly	Lys	Val	Leu	Phe	Val	Arg	Gly	Leu	Leu	Glu	Asp	Asn	Gly	Ile		
	370				375				380								
cta	ccc	aag	gcg	gcc	gag	act	tct	acg	tcc	gaa	tcc	aag	gtt	gtg	tca		1200
Leu	Pro	Lys	Ala	Ala	Glu	Thr	Ser	Thr	Ser	Glu	Ser	Lys	Val	Val	Ser		

385		390		395		400	
gaa gcc cga gaa gcc gtg aag tca gca gag aag gag ctt gga gac aag							1248
Glu Ala Arg Glu Ala Val Lys Ser Ala Glu Lys Glu Leu Gly Asp Lys							
	405		410		415		
cag aag cag ctg aag gat cac aag tcc gat ctt gag acg gac tat ggt							1296
Gln Lys Gln Leu Lys Asp His Lys Ser Asp Leu Glu Thr Asp Tyr Gly							
	420		425		430		
gtc gga tcc atc ttc cgt gcc ctc aag ggc gtt tgc atc tcc aag gac							1344
Val Gly Ser Ile Phe Arg Ala Leu Lys Gly Val Cys Ile Ser Lys Asp							
	435		440		445		
tcg ggt gag tac acg tat gag cac tgc ttc ctg gac cag aca aaa cag							1392
Ser Gly Glu Tyr Thr Tyr Glu His Cys Phe Leu Asp Gln Thr Lys Gln							
	450		455		460		
att cca aag aag ggc ggc gga tcc aca cgc atg ggc aag tac acc ggc							1440
Ile Pro Lys Lys Gly Gly Gly Ser Thr Arg Met Gly Lys Tyr Thr Gly							
	465		470		475		480
att ggg tcg gtc agt gtt gat gtg ctc aac gag gcg ggc gag att gtc							1488
Ile Gly Ser Val Ser Val Asp Val Leu Asn Glu Ala Gly Glu Ile Val							
	485		490		495		
ccc gaa gac agg gtc act ctt cag tac gcc aac gga caa ggc tgc tgg							1536
Pro Glu Asp Arg Val Thr Leu Gln Tyr Ala Asn Gly Gln Gly Cys Trp							
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aat gga ccg gcc cgc tcg acg acg gtc atc ctg aca tgc ggc gaa gag							1584
Asn Gly Pro Ala Arg Ser Thr Thr Val Ile Leu Thr Cys Gly Glu Glu							
	515		520		525		
gat gcg atc ctg aag gtg gcc gaa gac gag aag tgc gtg tac tcg atg							1632
Asp Ala Ile Leu Lys Val Ala Glu Asp Glu Lys Cys Val Tyr Ser Met							
	530		535		540		
cat gtc acg tcg ccg gcc gtg tgt ccc gga ggc gat gag ggc gca act							1680
His Val Thr Ser Pro Ala Val Cys Pro Gly Gly Asp Glu Gly Ala Thr							
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gcc ccg aac cgc aag gat gag ctg tga							1707
Ala Pro Asn Arg Lys Asp Glu Leu							
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<210> 33

<211> 568

<212> PRT

<213> Aspergillus niger

<400> 33

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

Ala Pro Asn Arg Lys Asp Glu Leu
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<210> 34

<211> 2343

<212> DNA

<213> *Aspergillus niger*

<400> 34

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taagtcgata	caacgctcgg	gcatacgctt	ggactgcatg	ttgtagaccg	gacttggctg	360
attcattctc	atctctacca	gattgacccc	actgccatgg	tgtccgacgc	ttgtgtctcc	420
tacgccacta	togatcatct	gaacgatcaa	gtctacacc	tcctccaatc	cattacgcaa	480
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gacgacattc	cgtaaacatg	gcgcgcggag	gagctcagta	aactcgaggg	acccaaagca	660
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aagagctggg	tcaatgcacc	aaagacattg	taagtgtagg	catacgatga	cctccacagt	1980
ttcctatata	ctaactgggc	attgcagctt	cgagatcgcc	gtcctggagg	ttgctcgggt	2040
atggaactac	tggtctgggtc	tgctgtgcc	gccacgggtc	tggaggatcc	agcttcccaa	2100
gcgacccacc	cctccaacac	ccccgaccca	tgaggagctc	tagacggtag	aagtgggcaa	2160
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actaatcttt	ttccgatctg	tttgggccgg	cgttggtgac	gatgcctggt	gggaaatcgc	2280
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<210> 35

<211> 1803

<212> DNA

<213> *Aspergillus niger*

<220>

<221> CDS

<222> (1)..(1803)

<400> 35

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

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Trp	His	Pro	Asn	Leu	Gln	Cys	Phe	Lys	Asp	Arg	Leu	His	Asp	His	Pro	
	290					295					300					
gag	cgc	atc	tcg	aac	ctg	tac	ttc	aac	tac	gcg	ctg	gtc	tcg	cgc	gcc	960
Glu	Arg	Ile	Ser	Asn	Leu	Tyr	Phe	Asn	Tyr	Ala	Leu	Val	Ser	Arg	Ala	
	305				310					315					320	
gtg	gcg	aag	ctg	cag	aaa	cac	cta	cac	aac	tac	aac	tac	tgc	gtc	ggc	1008
Val	Ala	Lys	Leu	Gln	Lys	His	Leu	His	Asn	Tyr	Asn	Tyr	Cys	Val	Gly	
				325					330					335		
gat	ccg	gtc	cag	gat	gcc	atg	act	agg	gag	aag	gtc	tcc	aag	ttg	acc	1056
Asp	Pro	Val	Gln	Asp	Ala	Met	Thr	Arg	Glu	Lys	Val	Ser	Lys	Leu	Thr	
			340					345					350			
tcg	acc	ttg	gct	gac	cgc	cct	caa	att	ttc	gac	gag	aac	gtc	atg	ttc	1104
Ser	Thr	Leu	Ala	Asp	Arg	Pro	Gln	Ile	Phe	Asp	Glu	Asn	Val	Met	Phe	
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cag	gat	ccc	agc	tcc	gct	ggc	ctg	aag	gaa	gac	ttc	cgc	aac	cga	ttc	1152
Gln	Asp	Pro	Ser	Ser	Ala	Gly	Leu	Lys	Glu	Asp	Phe	Arg	Asn	Arg	Phe	
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cgc	aac	gtc	agt	cgc	ctg	atg	gac	tgc	gtc	ggg	tgc	gac	aaa	tgc	cgc	1200
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Leu	Trp	Gly	Lys	Leu	Gln	Val	Asn	Gly	Tyr	Gly	Thr	Ala	Leu	Lys	Val	
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ctg	ttc	gag	tac	gac	gag	act	aag	aac	ggc	gag	aac	ccg	ttg	ctg	cgc	1296
Leu	Phe	Glu	Tyr	Asp	Glu	Thr	Lys	Asn	Gly	Glu	Asn	Pro	Leu	Leu	Arg	
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cgg	act	gag	ctg	gtg	gca	ctg	atc	aat	acc	ctt	ggc	cgc	att	tct	cac	1344
Arg	Thr	Glu	Leu	Val	Ala	Leu	Ile	Asn	Thr	Leu	Gly	Arg	Ile	Ser	His	
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Ser	Ile	Ala	Ala	Val	Arg	Ser	Phe	His	Arg	Ala	Met	Asp	Val	Gly	Asp	
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Gly	Glu	Val	Phe	Thr	Ile	Pro	Ala	Ser	Ile	Ala	Ser	Lys	Glu	Arg	Gly	
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Gly	Lys	Lys	Lys	Thr	Arg	Arg	Leu	Leu	Lys	Asp	Gly	Gly	Ser	Thr	Phe	
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Tyr	Tyr	Glu	Asp	Gly	Asp	Asp	Asp	Asn	Phe	Val	Tyr	Ile	Thr	Glu	Lys	
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Leu	Pro	Trp	Glu	Lys	Val	Arg	Val	Arg	Arg	Asp	Thr	Asp	Thr	Val	Trp	
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gat	gat	att	aag	gcc	gag	ttt	tct	atg	atc	tgg	gac	att	tac	gtc	tat	1632
Asp	Asp	Ile	Lys	Ala	Glu	Phe	Ser	Met	Ile	Trp	Asp	Ile	Tyr	Val	Tyr	
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gtg	ctg	aag	agc	tgg	gtc	aat	gca	cca	aag	aca	ttc	ttc	gag	atc	gcc	1680
Val	Leu	Lys	Ser	Trp	Val	Asn	Ala	Pro	Lys	Thr	Phe	Phe	Glu	Ile	Ala	
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Val	Leu	Glu	Val	Ala	Arg	Val	Trp	Asn	Tyr	Trp	Leu	Gly	Leu	Pro	Val	
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ccg	cca	cgg	tcc	tgg	agg	atc	cag	ctt	ccc	aag	cga	ccc	acc	cct	cca	1776
Pro	Pro	Arg	Ser	Trp	Arg	Ile	Gln	Leu	Pro	Lys	Arg	Pro	Thr	Pro	Pro	

aca ccc ccg acc cat gag gag ctc tag 1803

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

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Thr Thr Arg Gly Leu Leu Arg Ile Ile Ile Leu Ala Thr Ile Ala Ala															
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gct gct gtg tcc agt cgt ctg ttc agt gtg atc cga ttc gag agt att	144														
Ala Ala Val Ser Ser Arg Leu Phe Ser Val Ile Arg Phe Glu Ser Ile															
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atc cac gag ttc gac ccc tgg ttc aac ttc cgc gca aca aaa tac ctg	192														
Ile His Glu Phe Asp Pro Trp Phe Asn Phe Arg Ala Thr Lys Tyr Leu															
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Val Ser His Gly Phe Glu Ser Phe Trp Asp Trp Phe Asp Asp Arg Thr	
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Trp His Pro Leu Gly Arg Val Thr Gly Gly Thr Leu Tyr Pro Gly Leu	
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atg gtg acc agc ggt gtt att tac cac gtc ttg cgg ttc ctc act atc	336
Met Val Thr Ser Gly Val Ile Tyr His Val Leu Arg Phe Leu Thr Ile	
100 105 110	
cct gtc gac atc cgt aac atc tgt gtc ttg ctt gcc ccg ggt ttc tcc	384
Pro Val Asp Ile Arg Asn Ile Cys Val Leu Leu Ala Pro Gly Phe Ser	
115 120 125	
ggt ttg acc gcg ctg gca atg tac ttc ctg act cgc gag atg gcg aca	432
Gly Leu Thr Ala Leu Ala Met Tyr Phe Leu Thr Arg Glu Met Ala Thr	
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Gly Tyr Ile Ser Arg Ser Val Ala Gly Ser Tyr Asp Asn Glu Ala Ile	
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gcc att ttc ctg ctg gta ttc acc ttc ttc ctg tgg atc aag gct gtt	576
Ala Ile Phe Leu Leu Val Phe Thr Phe Phe Leu Trp Ile Lys Ala Val	
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aag aat ggc tcc atc atg tgg ggt tct ctg gcg gcc ttg ttc tac ggc	624
Lys Asn Gly Ser Ile Met Trp Gly Ser Leu Ala Ala Leu Phe Tyr Gly	
195 200 205	
tac atg gtg tct gcc tgg ggt ggt tat gtc ttc atc act aac ttg atc	672
Tyr Met Val Ser Ala Trp Gly Tyr Val Phe Ile Thr Asn Leu Ile	
210 215 220	
cct ctg cac gtt ttc gtt ctt ctg tgc atg ggc aga tac agc tcg cgt	720
Pro Leu His Val Phe Val Leu Leu Cys Met Gly Arg Tyr Ser Ser Arg	
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atc tat atc agt tat acc act tgg tat gct ctg gga act ctg gcc agt	768
Ile Tyr Ile Ser Tyr Thr Thr Trp Tyr Ala Leu Gly Thr Leu Ala Ser	
245 250 255	
atg cag att cct ttc gtc gga ttc ctg ccg att cgc aac agt gac cac	816
Met Gln Ile Pro Phe Val Gly Phe Leu Pro Ile Arg Asn Ser Asp His	
260 265 270	
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Met Ser Ala Leu Gly Val Phe Gly Leu Ile Gln Leu Val Ala Phe Ala	
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Asp Phe Val Arg Gly Phe Ile Pro Gly Arg His Phe Gln Arg Leu Leu	
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Thr Thr Met Ile Ile Val Val Phe Gly Ile Ala Phe Val Gly Leu Val	
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Val Leu Thr Val Ser Gly Val Ile Ala Pro Trp Ser Gly Arg Phe Tyr	
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Tyr Ser Ser Pro Ser Val Val Leu Ala Ser Arg Leu Pro Asp Gly Ser	
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Gln His Ile Ile Asp Asp Tyr Arg Glu Ala Tyr Tyr Trp Leu Arg Gln	
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aac acc gag cac aac gcc aag atc atg tcc tgg tgg gat tac ggc tac	1632
Asn Thr Glu His Asn Ala Lys Ile Met Ser Trp Trp Asp Tyr Gly Tyr	
530 535 540	
cag att ggt ggt atg gcg gac cgc cct acc ctg gtt gac aac aac acg	1680
Gln Ile Gly Gly Met Ala Asp Arg Pro Thr Leu Val Asp Asn Asn Thr	
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tgg aac aac acc cac att gcc act gtc ggt aag gcg atg agc tct cgt	1728
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Glu Glu Val Ser Tyr Pro Ile Leu Arg Gln His Asp Val Asp Tyr Val	
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Leu Val Val Phe Gly Gly Leu Leu Gly Tyr Ser Gly Asp Asp Ile Asn	
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aag ttc ctg tgg atg gtc cgt atc gct gaa ggt atc tgg ccc gac gag	1872
Lys Phe Leu Trp Met Val Arg Ile Ala Glu Gly Ile Trp Pro Asp Glu	
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Val Lys Glu Arg Asp Phe Phe Thr Ala Arg Gly Glu Tyr Arg Val Asp	
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Asp Gly Ala Thr Pro Thr Met Arg Asn Ser Leu Met Tyr Lys Met Ser	
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Tyr Tyr Asn Phe Asn Ser Leu Phe Gly Pro Gly Gln Ala Val Asp Arg	
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385					390					395					400
Ala	Ser	Tyr	Phe	Ala	Gly	Val	Met	Val	Arg	Leu	Met	Leu	Thr	Leu	Thr
				405					410					415	
Pro	Ile	Val	Cys	Val	Ala	Ala	Ala	Leu	Ala	Leu	Ser	Thr	Ile	Leu	Asp
			420					425					430		
Thr	Tyr	Val	Phe	Ala	Lys	Asn	Gly	Pro	Asn	Pro	Arg	Ala	Lys	Ala	Asn
		435					440					445			
Asp	Asp	Thr	Ser	Asp	Gly	Leu	Arg	Ser	Thr	Arg	Lys	Pro	Asp	Val	Gly
	450					455					460				
Val	Thr	Ser	Tyr	Leu	Ser	Lys	Ala	Val	Met	Thr	Ser	Ser	Val	Val	Ile
465					470					475					480
Tyr	Leu	Leu	Leu	Phe	Val	Ala	His	Cys	Thr	Trp	Val	Thr	Ser	Asn	Ala
				485					490					495	
Tyr	Ser	Ser	Pro	Ser	Val	Val	Leu	Ala	Ser	Arg	Leu	Pro	Asp	Gly	Ser
			500					505					510		
Gln	His	Ile	Ile	Asp	Asp	Tyr	Arg	Glu	Ala	Tyr	Tyr	Trp	Leu	Arg	Gln
		515					520					525			
Asn	Thr	Glu	His	Asn	Ala	Lys	Ile	Met	Ser	Trp	Trp	Asp	Tyr	Gly	Tyr
	530					535						540			
Gln	Ile	Gly	Gly	Met	Ala	Asp	Arg	Pro	Thr	Leu	Val	Asp	Asn	Asn	Thr
545					550					555					560
Trp	Asn	Asn	Thr	His	Ile	Ala	Thr	Val	Gly	Lys	Ala	Met	Ser	Ser	Arg
				565					570					575	
Glu	Glu	Val	Ser	Tyr	Pro	Ile	Leu	Arg	Gln	His	Asp	Val	Asp	Tyr	Val
				580				585				590			
Leu	Val	Val	Phe	Gly	Gly	Leu	Leu	Gly	Tyr	Ser	Gly	Asp	Asp	Ile	Asn
		595					600					605			
Lys	Phe	Leu	Trp	Met	Val	Arg	Ile	Ala	Glu	Gly	Ile	Trp	Pro	Asp	Glu
	610					615					620				
Val	Lys	Glu	Arg	Asp	Phe	Phe	Thr	Ala	Arg	Gly	Glu	Tyr	Arg	Val	Asp
625					630					635					640
Asp	Gly	Ala	Thr	Pro	Thr	Met	Arg	Asn	Ser	Leu	Met	Tyr	Lys	Met	Ser
				645					650					655	
Tyr	Tyr	Asn	Phe	Asn	Ser	Leu	Phe	Gly	Pro	Gly	Gln	Ala	Val	Asp	Arg
			660					665					670		
Val	Arg	Gly	Ser	Arg	Leu	Pro	Ala	Glu	Gly	Pro	Gln	Leu	Asn	Thr	Leu
		675					680					685			
Glu	Glu	Ala	Phe	Thr	Ser	Glu	Asn	Trp	Ile	Ile	Arg	Ile	Tyr	Lys	Val
	690					695					700				
Lys	Asp	Leu	Asp	Asn	Leu	Gly	Arg	Asp	His	Asn	Asn	Ala	Val	Ala	Phe

705		710		715		720									
Asp	Lys	Gly	His	Lys	Arg	Lys	Arg	Ala	Thr	Lys	Arg	Lys	Gly	Pro	Arg
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Val	Leu	Arg	Thr	Glu											
				740											

<210> 40
 <211> 1546
 <212> DNA
 <213> Aspergillus niger

<400> 40

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aggaccattt	gctattgaca	agtaacattg	tcaatcgccc	tgcttctact	tctccctaaa	180
ccaaaaccac	accatccatc	atggtccgtc	tcagcaatct	cgtgagctgc	ctcggcctgg	240
cctccgcggt	caccgcagca	gtggtcgatc	togtcccaa	gaacttcgac	gacgtcgtcc	300
tcaagtccgg	caagcccgtc	ctggttgaat	tcttcgctcc	ctggtgcggc	cactgcaaga	360
acctcgcggc	cgtgtatgaa	gagctgggccc	aggcattcgc	ccatgcctcc	gacaaggcca	420
ccgtcggcaa	ggttgatgcg	gacgagcacc	gagacttggt	ccgcaagttc	gggtgtccagg	480
gattccccac	gctaaagtgg	ttcgacggaa	agagtgcaga	gccggaggat	tacaagggtg	540
gtcgtgattt	ggagagtctg	tcttcgttca	tctctgagaa	gacgggcgtc	aagccccgtg	600
gtcctaagaa	ggagcccagc	aaggtggaga	tgctgaacga	cgcgactttc	aagggcgctg	660
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accgtaccgt	tggcggcgga	ctcgacacca	aggccggcac	cattgctagc	ctggacgagc	1080
tgattgccag	caattctgct	gctgacctgg	ccgccgcagt	caagaaggct	gctacggagc	1140
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agtatgccgc	taaggagctt	gctcgtctgg	agaagatcct	ggccaagggt	ggatcggccc	1260
ctgagaaggt	ggatgacctt	atctcccgcg	gcaacatcct	tcgcaagttt	gttggtgagg	1320
agaaggaggc	caaggatgag	ctgtagatat	tgtatggatt	atgacttggt	tagctagggt	1380
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gatgcgaaca	gtaaaccatc	catttcccat	tcccatgtat	gtatacacia	gaacataaga	1500
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<210> 41
 <211> 1080
 <212> DNA
 <213> Aspergillus niger

<220>
 <221> CDS
 <222> (1)..(1080)

<400> 41

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Met	Val	Arg	Leu	Ser	Asn	Leu	Val	Ser	Cys	Leu	Gly	Leu	Ala	Ser	Ala	
1				5				10					15			
gtc	acc	gca	gca	gtg	gtc	gat	ctc	gtc	ccc	aag	aac	ttc	gac	gac	gtc	96
Val	Thr	Ala	Ala	Val	Val	Asp	Leu	Val	Pro	Lys	Asn	Phe	Asp	Asp	Val	
			20					25				30				
gtc	ctc	aag	tcc	ggc	aag	ccc	gct	ctg	gtt	gaa	ttc	ttc	gct	ccc	tgg	144

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

Asp Leu Ile Ser Arg Ser Asn Ile Leu Arg Lys Phe Val Gly Glu Glu
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 aag gag gcc aag gat gag ctg tag
 Lys Glu Ala Lys Asp Glu Leu
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1080

<210> 42
 <211> 359
 <212> PRT
 <213> *Aspergillus niger*

<400> 42
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 Val Leu Lys Ser Gly Lys Pro Ala Leu Val Glu Phe Phe Ala Pro Trp
 35 40 45
 Cys Gly His Cys Lys Asn Leu Ala Pro Val Tyr Glu Glu Leu Gly Gln
 50 55 60
 Ala Phe Ala His Ala Ser Asp Lys Val Thr Val Gly Lys Val Asp Ala
 65 70 75 80
 Asp Glu His Arg Asp Leu Gly Arg Lys Phe Gly Val Gln Gly Phe Pro
 85 90 95
 Thr Leu Lys Trp Phe Asp Gly Lys Ser Asp Glu Pro Glu Asp Tyr Lys
 100 105 110
 Gly Gly Arg Asp Leu Glu Ser Leu Ser Ser Phe Ile Ser Glu Lys Thr
 115 120 125
 Gly Val Lys Pro Arg Gly Pro Lys Lys Glu Pro Ser Lys Val Glu Met
 130 135 140
 Leu Asn Asp Ala Thr Phe Lys Gly Ala Val Gly Gly Asp Asn Asp Val
 145 150 155 160
 Leu Val Ala Phe Thr Ala Pro Trp Cys Gly His Cys Lys Asn Leu Ala
 165 170 175
 Pro Thr Trp Glu Ala Leu Ala Asn Asp Phe Val Leu Glu Pro Asn Val
 180 185 190
 Val Ile Ala Lys Val Asp Ala Asp Ala Glu Asn Gly Lys Ala Thr Ala
 195 200 205
 Arg Glu Gln Gly Val Ser Gly Tyr Pro Thr Ile Lys Phe Phe Pro Lys
 210 215 220
 Gly Ser Thr Glu Ser Val Pro Tyr Glu Gly Ala Arg Ser Glu Gln Ala
 225 230 235 240
 Phe Ile Asp Phe Leu Asn Glu Lys Thr Gly Thr His Arg Thr Val Gly
 245 250 255
 Gly Gly Leu Asp Thr Lys Ala Gly Thr Ile Ala Ser Leu Asp Glu Leu
 260 265 270
 Ile Ala Ser Thr Ser Ala Ala Asp Leu Ala Ala Ala Val Lys Lys Ala
 275 280 285
 Ala Thr Glu Leu Lys Asp Lys Tyr Ala Gln Tyr Tyr Val Lys Val Ala
 290 295 300
 Asp Lys Leu Ser Gln Asn Ala Glu Tyr Ala Ala Lys Glu Leu Ala Arg
 305 310 315 320
 Leu Glu Lys Ile Leu Ala Lys Gly Gly Ser Ala Pro Glu Lys Val Asp
 325 330 335

Asp Leu Ile Ser Arg Ser Asn Ile Leu Arg Lys Phe Val Gly Glu Glu
 340 345 350
 Lys Glu Ala Lys Asp Glu Leu
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<210> 43
 <211> 2673
 <212> DNA
 <213> *Aspergillus niger*

<400> 43
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 attcaacttt ctacacacaac atgaagaact ggtggctgtg gcgtttcctg ccgttggcgc 240
 ttctgtagtc ctcttactgt ggagcttagc cgcatacgc gatagcaact gacctccaag 300
 catcactttc cagtgttctt gcaggcgctt gcggatgaat acaatggaca gcacgacaca 360
 caaaaaccct taacagatgt tgttcttgaa tcatatgcac atgctgagtc ctcgagcggg 420
 cccgagggct ctgacgttct accgggacac ggtaagcggc cctgtgcatg acgccagcgc 480
 acccatcctt gctaacaact agtgatttga tgtgccata gtacacgtcg aaaatgccct 540
 tcaaatcctc cgagagagca agatccccat tgtcgtcac gagaaaccgt ccggccttct 600
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 gccgatgga acacacaagc aaaagctcga tccaaatggt gcaaaggctg cgaatgaact 720
 taaggttgcg gcgcaagaac accaaaacc ccatgcaatg ttctcttag cggaaatgaa 780
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 ggggtgctggg ggtgcggtgg agcgcgacca ggctaaggcc ctgttatacc acacctttgc 960
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 tattgaatac ttccgatcgg gaccgcccgg tggccataac atgatccgcg agtcctaccg 1140
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 tcagcatgag ctaggactga tgtacctgca tggctatggt gtgacaccag atgcgttcag 1620
 agctgcatca caatttaagg ctgcggctga gcaggacttc ccggcggtg aaacgagact 1680
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 tccttttcgc tgagaaaccc gaacaatcac acttacacac taatgcagaa gtgaggtcgc 2520
 atcgacactt gaaggaattc atcgccactt ttatccagaa caacgaggaa gaagaggccg 2580
 ccttccgcgc ccagatgtac aaacaggacg aggaggacga actcatgtcg aataatcgcc 2640
 ttgacgacca ccgcgaagac ggctactatg atg 2673

<210> 44
 <211> 2070
 <212> DNA
 <213> *Aspergillus niger*

<220>
 <221> CDS
 <222> (1)..(2070)

<400> 44
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 Met Lys Asn Trp Trp Leu Trp Arg Phe Leu Pro Leu Ala Leu His Val
 1 5 10 15
 gtt cct gaa tca tat gca cat gct gag tcc tcg agc ggg ccc gag ggc 96
 Val Pro Glu Ser Tyr Ala His Ala Glu Ser Ser Ser Gly Pro Glu Gly
 20 25 30
 tct gac gtt cta ccg gga cac gta cac gtc gaa aat gcc ctt caa atc 144
 Ser Asp Val Leu Pro Gly His Val His Val Glu Asn Ala Leu Gln Ile
 35 40 45
 ctc cga gag agc aag atc ccc att gtc gct cac gag aaa ccg tcc ggc 192
 Leu Arg Glu Ser Lys Ile Pro Ile Val Ala His Glu Lys Pro Ser Gly
 50 55 60
 ctt ctg ggg tac acc tgg cat tac gcc caa gaa gcc ttc cga ctc cta 240
 Leu Leu Gly Tyr Thr Trp His Tyr Ala Gln Glu Ala Phe Arg Leu Leu
 65 70 75 80
 ttt atg aat gga cca cag ccg gat gga aca cac aag caa aag ctc gat 288
 Phe Met Asn Gly Pro Gln Pro Asp Gly Thr His Lys Gln Lys Leu Asp
 85 90 95
 cca aat gtt gca aag gct gcg aat gaa ctt aag gtt gcg gcg caa gaa 336
 Pro Asn Val Ala Lys Ala Ala Asn Glu Leu Lys Val Ala Ala Gln Glu
 100 105 110
 cac caa aac ccc gat gca atg ttc ctc tta gcg gaa atg aac ttc tac 384
 His Gln Asn Pro Asp Ala Met Phe Leu Leu Ala Glu Met Asn Phe Tyr
 115 120 125
 ggc aac ttc acc cac ccg aga gat ttc aag cag gcg ttt cat tgg tac 432
 Gly Asn Phe Thr His Pro Arg Asp Phe Lys Gln Ala Phe His Trp Tyr
 130 135 140
 caa act ctg gcg tca tcg act gga aac agt acg gcg caa tat atg ctt 480
 Gln Thr Leu Ala Ser Ser Thr Gly Asn Ser Thr Ala Gln Tyr Met Leu
 145 150 155 160
 ggg ttt atg tat gca acg ggt gtc ggg ggt gcg gtg gag cgc gac cag 528
 Gly Phe Met Tyr Ala Thr Gly Val Gly Gly Ala Val Glu Arg Asp Gln
 165 170 175
 gct aag gcc ctg tta tac cac acc ttt gcg gct gaa gcg ggc aat acg 576
 Ala Lys Ala Leu Leu Tyr His Thr Phe Ala Ala Glu Ala Gly Asn Thr
 180 185 190
 aag tcg gaa atg acc ctc gcg tat cgc tac cac gct gga att ggg gct 624
 Lys Ser Glu Met Thr Leu Ala Tyr Arg Tyr His Ala Gly Ile Gly Ala
 195 200 205
 cct aga gat tgc gat caa gcg act tac tac tat aag aag gtg gct gat 672
 Pro Arg Asp Cys Asp Gln Ala Thr Tyr Tyr Tyr Lys Lys Val Ala Asp
 210 215 220
 aag gct att gaa tac ttc cga tcg gga ccg ccc ggt ggc cat aac atg 720
 Lys Ala Ile Glu Tyr Phe Arg Ser Gly Pro Pro Gly Gly His Asn Met
 225 230 235 240
 atc cgc gag tcc tac cgt tgg gcg gac gaa gag ggt ggt gtt tat ggt 768

Ile	Arg	Glu	Ser	Tyr	Arg	Trp	Ala	Asp	Glu	Glu	Gly	Gly	Val	Tyr	Gly	
				245					250					255		
gaa	ggc	gct	agt	gta	tcg	act	gcc	gta	cgc	gat	gga	acg	cat	tcg	agc	816
Glu	Gly	Ala	Ser	Val	Ser	Thr	Ala	Val	Arg	Asp	Gly	Thr	His	Ser	Ser	
				260					265					270		
acg	gaa	gcc	agc	ttg	gaa	gac	gtc	ttg	gag	tac	ctg	gat	ttg	atg	tcg	864
Thr	Glu	Ala	Ser	Leu	Glu	Asp	Val	Leu	Glu	Tyr	Leu	Asp	Leu	Met	Ser	
		275					280					285				
aga	aag	ggc	gaa	ctg	aag	gct	act	ttc	agc	ttg	ggc	aag	atg	cat	tac	912
Arg	Lys	Gly	Glu	Leu	Lys	Ala	Thr	Phe	Ser	Leu	Gly	Lys	Met	His	Tyr	
	290					295					300					
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Glu	Gly	Gly	Arg	Gly	Leu	Pro	Arg	Asn	Phe	Arg	Lys	Ser	Met	Asn	Tyr	
305				310					315						320	
ttc	cga	cag	gtc	gcc	aag	cgg	tat	tgg	aat	aaa	gat	gga	tcg	gtg	aac	1008
Phe	Arg	Gln	Val	Ala	Lys	Arg	Tyr	Trp	Asn	Lys	Asp	Gly	Ser	Val	Asn	
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ccc	aac	cat	cct	gtt	ggc	gtt	gaa	aag	ctc	gct	tcg	aaa	gca	gca	ggc	1056
Pro	Asn	His	Pro	Val	Gly	Val	Glu	Lys	Leu	Ala	Ser	Lys	Ala	Ala	Gly	
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His	Ile	Gly	Met	Met	Tyr	Leu	Arg	Gly	Glu	Gly	Val	Glu	Gln	Asn	Phe	
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gca	acc	gct	cag	act	tgg	ttt	agg	cgt	gga	ctc	gcg	aat	ggc	gat	gct	1152
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ctc	tgt	cag	cat	gag	cta	gga	ctg	atg	tac	ctg	cat	ggc	tat	ggc	gtg	1200
Leu	Cys	Gln	His	Glu	Leu	Gly	Leu	Met	Tyr	Leu	His	Gly	Tyr	Gly	Val	
385				390						395					400	
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Thr	Pro	Asp	Ala	Phe	Arg	Ala	Ala	Ser	Gln	Phe	Lys	Ala	Ala	Ala	Glu	
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cag	gac	ttc	ccg	gcg	gct	gaa	acg	aga	ctg	ggc	ctg	ttt	cta	gac		1296
Gln	Asp	Phe	Pro	Ala	Ala	Glu	Thr	Arg	Leu	Gly	Ala	Leu	Phe	Leu	Asp	
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Gln	Gly	Asp	Val	Gln	Thr	Ala	Thr	Arg	Tyr	Phe	Glu	Leu	Ala	Ala	Arg	
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Trp	Gly	Trp	Met	Glu	Ala	Phe	Tyr	Tyr	Leu	Ala	Glu	Leu	Ser	Asn	Asn	
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Gly	Val	Gly	Arg	Lys	Arg	His	Cys	Gly	Met	Ala	Ala	Ser	Tyr	Tyr	Lys	
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Met	Val	Ala	Glu	Arg	Ala	Glu	Val	Ile	His	Ser	Ser	Phe	Glu	Glu	Ala	
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Asn	Thr	Ala	Tyr	Glu	Asn	Gly	Asp	Lys	Glu	Arg	Ala	Leu	Ile	Pro	Ala	
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Leu	Met	Ala	Ala	Glu	Gln	Gly	Tyr	Glu	His	Ala	Gln	Ser	Asn	Val	Ala	
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Phe	Leu	Leu	Asp	Glu	Gln	Arg	Ser	Leu	Phe	Ala	Ile	Asp	Thr	Ile	Leu	
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cca	gga	gct	aag	aag	agc	aga	ccg	gct	ttg	ctg	cgg	aat	gca	gcg	ctg	1680

Pro Gly Ala Lys Lys Ser Arg Pro Ala Leu Leu Arg Asn Ala Ala Leu	
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gct ctt atc tat tgg aca cgt tcc gcc aaa cag gcg aac atc gac tcc	1728
Ala Leu Ile Tyr Trp Thr Arg Ser Ala Lys Gln Ala Asn Ile Asp Ser	
565 570 575	
ttg ctc aag atg ggc gat tac tac ctg gcg ggc atg gga att gct gcg	1776
Leu Leu Lys Met Gly Asp Tyr Tyr Leu Ala Gly Met Gly Ile Ala Ala	
580 585 590	
gat gcg gag aag gcc tcg acc tgc tac cac aca gca gcc gaa gtg cac	1824
Asp Ala Glu Lys Ala Ser Thr Cys Tyr His Thr Ala Ala Glu Val His	
595 600 605	
tat agc gca cag gcg tac tgg aat ctg gga tgg atg cat gag aat ggc	1872
Tyr Ser Ala Gln Ala Tyr Trp Asn Leu Gly Trp Met His Glu Asn Gly	
610 615 620	
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Val Ala Val Asp Gln Asp Phe His Met Ala Lys Arg Tyr Tyr Asp Leu	
625 630 635	
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Ala Leu Glu Thr Ser Ser Glu Ala Tyr Leu Pro Val Lys Leu Ser Leu	
645 650 655	
ctt aaa ctg cgg atg cgg gga tac tgg aac tgg ctc acg aac gga gac	2016
Leu Lys Leu Arg Met Arg Gly Tyr Trp Asn Trp Leu Thr Asn Gly Asp	
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atc aac cct atc cga gag gaa gaa ggt aag gaa ccc caa cat cct ttt	2064
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cgc tga	2070
Arg	

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 <211> 689
 <212> PRT
 <213> Aspergillus niger

<400> 45

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

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

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Tyr	Ser	Ala	Gln	Ala	Tyr	Trp	Asn	Leu	Gly	Trp	Met	His	Glu	Asn	Gly	
610					615					620						
Val	Ala	Val	Asp	Gln	Asp	Phe	His	Met	Ala	Lys	Arg	Tyr	Tyr	Asp	Leu	
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Ala	Leu	Glu	Thr	Ser	Ser	Glu	Ala	Tyr	Leu	Pro	Val	Lys	Leu	Ser	Leu	
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Leu	Lys	Leu	Arg	Met	Arg	Gly	Tyr	Trp	Asn	Trp	Leu	Thr	Asn	Gly	Asp	
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<211> 2326

<212> DNA

<213> *Aspergillus niger*

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Ser Ile Val Leu His Val Leu Cys Pro Ser Leu Pro Pro Pro Asn Arg																		
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Phe Thr Leu His Asp Ile Ser Pro Ser Thr Thr Ile Ser Thr Leu Lys																		
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Ala Arg Ile Ala Gln Thr Ile Pro Ser Glu Pro Ser Pro Glu Thr Gln																		
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agg ctg ata tac cgg ggg aag ccc ctt acg aac gac gcc gtg gcg cta	240																	
Arg Leu Ile Tyr Arg Gly Lys Pro Leu Thr Asn Asp Ala Val Ala Leu																		
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Asn Asp Val Leu Glu Ser Ser Asn Asp Thr Glu Tyr Ser Ile His Leu																		
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gtc ctt cct cct gcc cca gtt ccc cat gct tca act tct gcc aga gct	336																	
Val Leu Pro Pro Ala Pro Val Pro His Ala Ser Thr Ser Ala Arg Ala																		
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Pro Ala Pro Met Pro Arg Gly Ala Ser Gly Asn Pro Ala Pro Gln Ser																		
115 120 125																		
cca ttc tca tcg aac cga ttc acg ccg caa cac ctg cct cac gga caa	432																	
Pro Phe Ser Ser Asn Arg Phe Thr Pro Gln His Leu Pro His Gly Gln																		
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Ile Asp Met Gln Glu Arg Gly Gly Pro Leu Gly Gly Val Ala Ala Gly																		
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acc gcg ggg gct act tcc cac tcg acc aca tcc acg act acg aca gct	624																	
Thr Ala Gly Ala Thr Ser His Ser Thr Thr Ser Thr Thr Thr Ala																		
195 200 205																		
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Ser Phe Ala Gln Gln Pro Ala Trp Pro His Val Thr Pro Gly Leu Ser																		
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cac cca gga cat tcg tcc atc tca tct gat ttc aca atg gct tcc ggc	720																	

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Ser	Ser	Gly	Thr	Ala	Asn	Val	His	Ser	Asn	Leu	Pro	Glu	Glu	Val	Arg	
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Leu	Arg	Leu	Gln	Ile	Leu	Arg	Asn	Gln	Ile	Ala	Phe	Gly	Glu	Glu	Gln	
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Leu	Asn	Arg	Gly	Val	Ala	Pro	Pro	Met	Asp	His	Ile	Ile	Arg	Ile	Arg	
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Thr	Gln	Leu	Phe	Ala	Leu	Leu	Asp	Asp	Gln	Tyr	Gln	Asn	Pro	His	Ala	
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Glu	Arg	Asp	Gly	Ser	Ile	Glu	Ser	Leu	Leu	Thr	Arg	Val	Phe	Asn	Ile	
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tat	acc	cgc	gct	gat	cag	ctc	cgc	gtc	tca	caa	gct	aga	acc	atg	ccc	1008
Tyr	Thr	Arg	Ala	Asp	Gln	Leu	Arg	Val	Ser	Gln	Ala	Arg	Thr	Met	Pro	
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aca	cct	gtt	cta	tct	gga	cct	ccc	aat	ccc	gca	cca	ggg	cag	gct	cct	1056
Thr	Pro	Val	Leu	Ser	Gly	Pro	Pro	Asn	Pro	Ala	Pro	Gly	Gln	Ala	Pro	
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Pro	Arg	Gly	Ala	Glu	Thr	Met	Gln	Ser	Ser	Leu	Asp	Thr	Leu	Arg	Ala	
	370					375					380					
atg	cac	tcc	ccg	acc	gga	gcc	tct	gcg	cct	cgt	aca	ggt	gct	cca	ccg	1200
Met	His	Ser	Pro	Thr	Gly	Ala	Ser	Ala	Pro	Arg	Thr	Gly	Ala	Pro	Pro	
	385			390						395					400	
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Glu	Ile	His	Asn	Ala	Asn	Ala	Val	Val	Met	Glu	Asn	Ile	Val	Arg	Gln	
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gcc	gta	ctc	aac	caa	cgc	atc	gaa	aac	aac	ggg	caa	ttg	agc	ttc	aca	1296
Ala	Val	Leu	Asn	Gln	Arg	Ile	Glu	Asn	Asn	Gly	Gln	Leu	Ser	Phe	Thr	
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cgc	aat	ctc	cga	cgc	atg	tgg	cta	ttt	gtg	cgc	ttg	tat	ttc	ttc	tgc	1344
Arg	Asn	Leu	Arg	Arg	Met	Trp	Leu	Phe	Val	Arg	Leu	Tyr	Phe	Phe	Cys	
	435					440						445				
tac	atg	ttc	agc	gaa	ccg	ggc	aca	tgg	tct	cgc	gtg	gtg	tat	gta	acc	1392
Tyr	Met	Phe	Ser	Glu	Pro	Gly	Thr	Trp	Ser	Arg	Val	Val	Tyr	Val	Thr	
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cta	gcc	gtc	ctt	gtc	tca	ctc	ctg	tca	gaa	acc	ggg	atc	cca	cag	cag	1440
Leu	Ala	Val	Leu	Val	Ser	Leu	Leu	Ser	Glu	Thr	Gly	Ile	Pro	Gln	Gln	
	465				470					475					480	
ttg	tac	cga	atg	ctt	gtg	gcg	cca	gtg	caa	cga	cac	ctg	gaa	gga	ctg	1488
Leu	Tyr	Arg	Met	Leu	Val	Ala	Pro	Val	Gln	Arg	His	Leu	Glu	Gly	Leu	
			485					490						495		
gtt	cat	ttc	gct	ccg	gac	gaa	ccg	act	cca	gca	cca	cct	ggc	acg	cag	1536
Val	His	Phe	Ala	Pro	Asp	Glu	Pro	Thr	Pro	Ala	Pro	Pro	Gly	Thr	Gln	
		500						505					510			
tca	act	ggg	caa	ggg	aac	gtt	ccc	act	gct	cag	cca	acc	gga	atg	cga	1584
Ser	Thr	Gly	Gln	Gly	Asn	Val	Pro	Thr	Ala	Gln	Pro	Thr	Gly	Met	Arg	
		515					520					525				
cac	cag	ctg	cgc	cgc	gta	gaa	cgg	tcc	ttg	gcg	ctt	ttc	att	gca	agc	1632

His	Gln	Leu	Arg	Arg	Val	Glu	Arg	Ser	Leu	Ala	Leu	Phe	Ile	Ala	Ser		
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Leu	Val	Pro	Gly	Val	Gly	Glu	Arg	His	Val	Glu	Val	Arg	Asn	Ala	Ala		
545					550					555					560		
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Glu	Ala	Ala	Arg	Asn	Ala	Glu	Arg	Ala	Arg	Glu	Glu	Glu	Glu	Arg	Arg		
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cga	cag	gag	gaa	gag	gcc	acc	aac	gca	ggc	acg	act	ggg	gag	gct	cag		1776
Arg	Gln	Glu	Glu	Glu	Ala	Thr	Asn	Ala	Gly	Thr	Thr	Gly	Glu	Ala	Gln		
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gca	cag	gca	cag	gag	agc	agc	gag	aac	gaa	cag	aga	gaa	acg	ggg	gag		1824
Ala	Gln	Ala	Gln	Glu	Ser	Ser	Glu	Asn	Glu	Gln	Arg	Glu	Thr	Gly	Glu		
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aat	gca	ccc	aac	acg	ata	ccc	caa	act	gag	aat	tag						1860
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 <212> PRT
 <213> Aspergillus niger

<400> 48

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Phe	Thr	Leu	His	Asp	Ile	Ser	Pro	Ser	Thr	Thr	Ile	Ser	Thr	Leu	Lys		
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Ala	Arg	Ile	Ala	Gln	Thr	Ile	Pro	Ser	Glu	Pro	Ser	Pro	Glu	Thr	Gln		
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Arg	Leu	Ile	Tyr	Arg	Gly	Lys	Pro	Leu	Thr	Asn	Asp	Ala	Val	Ala	Leu		
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Asn	Asp	Val	Leu	Glu	Ser	Ser	Asn	Asp	Thr	Glu	Tyr	Ser	Ile	His	Leu		
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Val	Leu	Pro	Pro	Ala	Pro	Val	Pro	His	Ala	Ser	Thr	Ser	Ala	Arg	Ala		
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Pro	Ala	Pro	Met	Pro	Arg	Gly	Ala	Ser	Gly	Asn	Pro	Ala	Pro	Gln	Ser		
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Pro	Phe	Ser	Ser	Asn	Arg	Phe	Thr	Pro	Gln	His	Leu	Pro	His	Gly	Gln		
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Glu	Ile	Arg	Tyr	Arg	Gly	Pro	Ala	Leu	Pro	Ala	Val	Pro	His	Glu	Ala		
145					150					155					160		
Glu	Ile	Gly	Leu	Ala	Leu	Arg	Arg	Asn	Ile	Glu	Ala	Ile	Arg	Arg	Gln		
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Ile	Asp	Met	Gln	Glu	Arg	Gly	Gly	Pro	Leu	Gly	Gly	Val	Ala	Ala	Gly		
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Thr	Ala	Gly	Ala	Thr	Ser	His	Ser	Thr	Thr	Ser	Thr	Thr	Thr	Thr	Ala		
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Ser	Phe	Ala	Gln	Gln	Pro	Ala	Trp	Pro	His	Val	Thr	Pro	Gly	Leu	Ser		
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His	Pro	Gly	His	Ser	Ser	Ile	Ser	Ser	Asp	Phe	Thr	Met	Ala	Ser	Gly		
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Ser	Ser	Gly	Thr	Ala	Asn	Val	His	Ser	Asn	Leu	Pro	Glu	Glu	Val	Arg	
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Leu	Arg	Leu	Gln	Ile	Leu	Arg	Asn	Gln	Ile	Ala	Phe	Gly	Glu	Glu	Gln	
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Leu	Asn	Arg	Gly	Val	Ala	Pro	Pro	Met	Asp	His	Ile	Ile	Arg	Ile	Arg	
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Thr	Gln	Leu	Phe	Ala	Leu	Leu	Asp	Asp	Gln	Tyr	Gln	Asn	Pro	His	Ala	
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Glu	Arg	Asp	Gly	Ser	Ile	Glu	Ser	Leu	Leu	Thr	Arg	Val	Phe	Asn	Ile	
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Tyr	Thr	Arg	Ala	Asp	Gln	Leu	Arg	Val	Ser	Gln	Ala	Arg	Thr	Met	Pro	
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Thr	Pro	Val	Leu	Ser	Gly	Pro	Pro	Asn	Pro	Ala	Pro	Gly	Gln	Ala	Pro	
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Met	His	Ser	Pro	Thr	Gly	Ala	Ser	Ala	Pro	Arg	Thr	Gly	Ala	Pro	Pro	
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Glu	Ile	His	Asn	Ala	Asn	Ala	Val	Val	Met	Glu	Asn	Ile	Val	Arg	Gln	
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Ala	Val	Leu	Asn	Gln	Arg	Ile	Glu	Asn	Asn	Gly	Gln	Leu	Ser	Phe	Thr	
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Arg	Asn	Leu	Arg	Arg	Met	Trp	Leu	Phe	Val	Arg	Leu	Tyr	Phe	Phe	Cys	
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Glu	Ala	Ala	Arg	Asn	Ala	Glu	Arg	Ala	Arg	Glu	Glu	Glu	Glu	Arg	Arg	
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Arg	Gln	Glu	Glu	Glu	Ala	Thr	Asn	Ala	Gly	Thr	Thr	Gly	Glu	Ala	Gln	
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Ala	Gln	Ala	Gln	Glu	Ser	Ser	Glu	Asn	Glu	Gln	Arg	Glu	Thr	Gly	Glu	
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<212> DNA

<213> Aspergillus niger

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60

120

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<211> 2331

<212> DNA

<213> *Aspergillus niger*

<220>

<221> CDS

<222> (1)..(2331)

<400> 50

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

gac att gtt aca gga gcc agt gac cga atc aca cgc gtg ttt agc agg	912
Asp Ile Val Thr Gly Ala Ser Asp Arg Ile Thr Arg Val Phe Ser Arg	
290 295 300	
agc cag gag cgc gtg gca agc cca gaa gta gta caa cag ttc gag aag	960
Ser Gln Glu Arg Val Ala Ser Pro Glu Val Val Gln Gln Phe Glu Lys	
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Thr Val Lys Glu Ser Ala Ile Pro Glu Gln Gln Ile Gly Lys Ile Asn	
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aaa gat aag ctt ccg ggt acg gag ttt ctc agg cag aaa tcc ggg acc	1056
Lys Asp Lys Leu Pro Gly Thr Glu Phe Leu Arg Gln Lys Ser Gly Thr	
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Lys Asp Gly Gln Val Gln Met Ile Arg Glu Ala Asp Gly Ser Val Thr	
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Ala His Thr Trp Ser Ala Ala Ser Arg Glu Trp Val Ala Val Gly Thr	
370 375 380	
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Gln Asp Tyr Asp Tyr Val Phe Asp Val Asp Val Glu Asp Gly Lys Pro	
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ccc ctc aaa ttg cca tac aac gtc tct caa aac ccc tac gag gct gcg	1296
Pro Leu Lys Leu Pro Tyr Asn Val Ser Gln Asn Pro Tyr Glu Ala Ala	
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acc aag ttt atc cag gac aac gaa ctg tcg atg aat tac ctt gat caa	1344
Thr Lys Phe Ile Gln Asp Asn Glu Leu Ser Met Asn Tyr Leu Asp Gln	
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Val Ala Gln Phe Ile Val Gln Asn Thr Gln Gly Ala Thr Leu Glu Arg	
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Arg Tyr Arg Pro Glu Asp Ala Gln Ser Pro Pro Ala Pro Glu Ala Arg	
465 470 475 480	
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Pro Lys Val Leu Pro Gln Lys Thr Tyr Leu Ser Ile Lys Ser Ala Asn	
485 490 495	
ctt aaa ctg atc gct aag aag ttg caa gag ctg aac caa cac gtc ata	1536
Leu Lys Leu Ile Ala Lys Lys Leu Gln Glu Leu Asn Gln His Val Ile	
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Ser Ser Gly Ser Lys Asp Leu Ser Leu Ser Pro Ser Glu Leu Glu Thr	
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Val Ala Thr Leu Cys Gly Gln Leu Glu Ser Ser Asn Val Glu Gln Ser	
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Pro Ala Val Glu Ala Gly Val Val Leu Leu Tyr Lys Val Ala Thr Val	
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Trp Pro Val Ala Ser Arg Leu Pro Gly Leu Asp Leu Leu Arg Leu Ser	
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Ala Ala Ala Thr Pro Val Thr Ala Thr Ala Asp Tyr Asp Gly Lys Asp	
580 585 590	

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Leu Ile Ser Gly Ile Lys Ser Ser Gly Val Phe Asp Ser Pro Phe Asn	
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Leu Val Leu Leu Gly Glu Leu Thr Thr Leu Ile Thr Gly Glu Lys Asp	
690 695 700	
tct gaa gca gtc tac cgc ggc ctt gtg gct cta ggg acc ttg atc aag	2160
Ser Glu Ala Val Tyr Arg Gly Leu Val Ala Leu Gly Thr Leu Ile Lys	
705 710 715 720	
gga cta ggg gaa gaa gtc agg act gcg gcc aag gaa gtg tac gat gtc	2208
Gly Leu Gly Glu Glu Val Arg Thr Ala Ala Lys Glu Val Tyr Asp Val	
725 730 735	
gat gat gtt ttg aag aag gtt tca agc tct ggt ctt ggt aaa gaa cca	2256
Asp Asp Val Leu Lys Lys Val Ser Ser Ser Gly Leu Gly Lys Glu Pro	
740 745 750	
aga atc aag ggt atc ata ggc gag atc aag gag tcg tta tca tca agg	2304
Arg Ile Lys Gly Ile Ile Gly Glu Ile Lys Glu Ser Leu Ser Ser Arg	
755 760 765	
tat aaa atg ttg agg ccc ggg tct taa	2331
Tyr Lys Met Leu Arg Pro Gly Ser	
770 775	

<210> 51

<211> 776

<212> PRT

<213> Aspergillus niger

<400> 51

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

Pro Ala Val Glu Ala Gly Val Val Leu Leu Tyr Lys Val Ala Thr Val
 545 550 555 560
 Trp Pro Val Ala Ser Arg Leu Pro Gly Leu Asp Leu Leu Arg Leu Ser
 565 570 575
 Ala Ala Ala Thr Pro Val Thr Ala Thr Ala Asp Tyr Asp Gly Lys Asp
 580 585 590
 Leu Ile Ser Gly Ile Lys Ser Ser Gly Val Phe Asp Ser Pro Phe Asn
 595 600 605
 Val Asn Asn Ala Met Leu Ser Ile Arg Met Leu Ala Asn Leu Phe Glu
 610 615 620
 Thr Asp Ala Gly Arg Asp Leu Ala Thr Ser Lys Phe Glu Gln Ile Leu
 625 630 635 640
 Ser Gly Val Lys Ser Ala Leu Thr Asn Ser Gly Thr Thr Pro Asn Arg
 645 650 655
 Asn Leu Thr Ile Ala Ile Thr Thr Leu Tyr Ile Asn Phe Ala Val Tyr
 660 665 670
 Leu Thr Ser Ala Gly Arg Glu Ser Met Pro Glu Ser Ser Glu Gln Ala
 675 680 685
 Leu Val Leu Leu Gly Glu Leu Thr Thr Leu Ile Thr Gly Glu Lys Asp
 690 695 700
 Ser Glu Ala Val Tyr Arg Gly Leu Val Ala Leu Gly Thr Leu Ile Lys
 705 710 715 720
 Gly Leu Gly Glu Glu Val Arg Thr Ala Ala Lys Glu Val Tyr Asp Val
 725 730 735
 Asp Asp Val Leu Lys Lys Val Ser Ser Ser Gly Leu Gly Lys Glu Pro
 740 745 750
 Arg Ile Lys Gly Ile Ile Gly Glu Ile Lys Glu Ser Leu Ser Ser Arg
 755 760 765
 Tyr Lys Met Leu Arg Pro Gly Ser
 770 775

<210> 52

<211> 2505

<212> DNA

<213> *Aspergillus niger*

<400> 52

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cctcccctcc	tcggtggtgt	gtatgtctgt	aacgggcctt	ttatcttcgt	gaacagtta	180
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gtgaaacctg	aagcattgcg	tttgctgtgc	tggtctttga	tcctcctccc	ccacactgca	300
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tacagcggtc	tttttcatcc	ctcctcttgt	gtgtcgcgcc	tgcaatgtgg	tgatcatccc	480
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tggggcaacc	ttcccacccg	cctctccctt	tccttcctgt	ttcctgtccc	tccgaggtag	1020
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cgtcagcggt	atctcgaagc	acaagatctg	gggtggtatgt	attctagcca	tggccgtttt	1140
ggagacgacg	ttgggttttg	ttcattcggt	gactggttct	aggccaatgc	tggtgattct	1200

cgctctgtac	tgggtgtcaa	gggtcgcgca	aagcctctgt	catttgacca	caagcctcag	1260
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gaatgaacgg	gagggaactc	ctgggcctca	gtctaaggat	acttctcgaa	cggacgccgc	2220
tgagatatcg	gagtcgccgt	ctaccaccgc	ggagggttcg	tccggcagtg	gccctggaac	2280
gccgcaaaag	cctacgagtt	cgtagtcatg	atggatctct	tgcatttctc	cttaatatgt	2340
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cctttttttc	ttattttggg	tctttgaaaa	ccaccgcgtg	gtgattctac	gactgtgccc	2460
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<210> 53

<211> 1275

<212> DNA

<213> *Aspergillus niger*

<220>

<221> CDS

<222> (1)..(1275)

<400> 53

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ggt caa gat gag tgc tgt ata tac ggt gtt tcc gcc atg caa gga tgg	96
Gly Gln Asp Glu Cys Cys Ile Tyr Gly Val Ser Ala Met Gln Gly Trp	
20 25 30	
cga atc agc atg gag gat gcc cat gcc gct gtc ctc gac ctc cag gcc	144
Arg Ile Ser Met Glu Asp Ala His Ala Ala Val Leu Asp Leu Gln Ala	
35 40 45	
aag tac tcc gag cag gat gaa aag ccg acc gac ccc gat aaa cga ctc	192
Lys Tyr Ser Glu Gln Asp Glu Lys Pro Thr Asp Pro Asp Lys Arg Leu	
50 55 60	
gct ttc ttt ggt gta tat gac ggg cac ggt gga gac aaa gta gca tta	240
Ala Phe Phe Gly Val Tyr Asp Gly His Gly Gly Asp Lys Val Ala Leu	
65 70 75 80	
ttc gcc gga gaa aac gtc cac aag atc gtc gcg aag cag gac tcc ttt	288
Phe Ala Gly Glu Asn Val His Lys Ile Val Ala Lys Gln Asp Ser Phe	
85 90 95	
gcc aaa ggt gat atc gaa cag gcc ctg aag gat ggc ttc ctc gct acc	336
Ala Lys Gly Asp Ile Glu Gln Ala Leu Lys Asp Gly Phe Leu Ala Thr	
100 105 110	
gac cgg gct att ttg gaa gac ccg aaa tat gag gag gaa gtg tct ggc	384
Asp Arg Ala Ile Leu Glu Asp Pro Lys Tyr Glu Glu Glu Val Ser Gly	

	115		120		125		
tgc	acc gca gcc gtc agc gtt atc tcg aag cac aag atc tgg gtg gcc					432	
Cys	Thr Ala Ala Val Ser Val Ile Ser Lys His Lys Ile Trp Val Ala						
	130		135		140		
aat	gct ggt gat tct cgc tct gta ctg ggt gtc aag ggt cgc gca aag					480	
Asn	Ala Gly Asp Ser Arg Ser Val Leu Gly Val Lys Gly Arg Ala Lys						
	145		150		155		160
cct	ctg tca ttt gac cac aag cct cag aat gaa ggc gag aaa gcc cgt					528	
Pro	Leu Ser Phe Asp His Lys Pro Gln Asn Glu Gly Glu Lys Ala Arg						
	165		170		175		
atc	agc gct gct ggt ggt ttc gtt gac ttc ggc cgt gtc aac ggc aac					576	
Ile	Ser Ala Ala Gly Gly Phe Val Asp Phe Gly Arg Val Asn Gly Asn						
	180		185		190		
ctg	gcc ttg tcg cgg gcc att ggt gac ttc gag ttc aag aag agc ccc					624	
Leu	Ala Leu Ser Arg Ala Ile Gly Asp Phe Glu Phe Lys Lys Ser Pro						
	195		200		205		
gag	ttg tct cct gag cag cag atc gtc act gcc tat ccc gac gtc act					672	
Glu	Leu Ser Pro Glu Gln Gln Ile Val Thr Ala Tyr Pro Asp Val Thr						
	210		215		220		
gtg	cac gat ctc agt gac gat gac gag ttc ctc gta att gcc tgt gac					720	
Val	His Asp Leu Ser Asp Asp Asp Glu Phe Leu Val Ile Ala Cys Asp						
	225		230		235		240
ggt	atc tgg gat tgt cag tcc tcc caa tca gtg gtg gaa ttc gtc cgc					768	
Gly	Ile Trp Asp Cys Gln Ser Ser Gln Ser Val Val Glu Phe Val Arg						
	245		250		255		
cgt	ggg att gcc gcg aag cag gat ctg tat cgg atc tgt gag aac atg					816	
Arg	Gly Ile Ala Ala Lys Gln Asp Leu Tyr Arg Ile Cys Glu Asn Met						
	260		265		270		
atg	gac aac tgc ctg gcc tcc aac agt gaa acc ggc ggc gtt ggc tgc					864	
Met	Asp Asn Cys Leu Ala Ser Asn Ser Glu Thr Gly Gly Val Gly Cys						
	275		280		285		
gac	aat atg aca atg gtc atc atc ggt ctc ctg aac gct gag ttc cgc					912	
Asp	Asn Met Thr Met Val Ile Ile Gly Leu Leu Asn Ala Glu Phe Arg						
	290		295		300		
ggc	ccc ggt atc cgg aat caa ttc gag gag aac ccg gat gac ttt gac					960	
Gly	Pro Gly Ile Arg Asn Gln Phe Glu Glu Asn Pro Asp Asp Phe Asp						
	305		310		315		320
atg	gaa aac gac cgt gcg cgt ggc ttc agc gtc cgc tcg ggc cgc atc					1008	
Met	Glu Asn Asp Arg Ala Arg Gly Phe Ser Val Arg Ser Gly Arg Ile						
	325		330		335		
atc	ctc ttg ggg gac ggc act gaa ttg att ccg gag cag aac gat gac					1056	
Ile	Leu Leu Gly Asp Gly Thr Glu Leu Ile Pro Glu Gln Asn Asp Asp						
	340		345		350		
gaa	ctc ttt gat cag gct gag gaa gac cag gac ctt gtc aat cag gtg					1104	
Glu	Leu Phe Asp Gln Ala Glu Glu Asp Gln Asp Leu Val Asn Gln Val						
	355		360		365		
cac	cgt gat tcg cct gat gcg gct cgg aat gaa cgg gag gga act cct					1152	
His	Arg Asp Ser Pro Asp Ala Ala Arg Asn Glu Arg Glu Gly Thr Pro						
	370		375		380		
ggg	cct cag tct aag gat act tct cga acg gac gcc gct gag ata tcg					1200	
Gly	Pro Gln Ser Lys Asp Thr Ser Arg Thr Asp Ala Ala Glu Ile Ser						
	385		390		395		400
gag	tcg ccg tct acc acc gcg gag ggt tcg tcc ggc agt ggc cct gga					1248	
Glu	Ser Pro Ser Thr Thr Ala Glu Gly Ser Ser Gly Ser Gly Pro Gly						
	405		410		415		
acg	ccg caa aag cct acg agt tcg tag					1275	
Thr	Pro Gln Lys Pro Thr Ser Ser						

<210> 54
 <211> 424
 <212> PRT
 <213> *Aspergillus niger*

<400> 54

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

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His	Arg	Asp	Ser	Pro	Asp	Ala	Ala	Arg	Asn	Glu	Arg	Glu	Gly	Thr	Pro
	370					375					380				
Gly	Pro	Gln	Ser	Lys	Asp	Thr	Ser	Arg	Thr	Asp	Ala	Ala	Glu	Ile	Ser
385					390					395					400
Glu	Ser	Pro	Ser	Thr	Thr	Ala	Glu	Gly	Ser	Ser	Gly	Ser	Gly	Pro	Gly
				405					410					415	
Thr	Pro	Gln	Lys	Pro	Thr	Ser	Ser								
			420												

<210> 55
 <211> 1209
 <212> DNA
 <213> *Aspergillus niger*

<400> 55

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ttcgtcgcat	cgtaaccgccc	accgagcaa	cctccccct	aagttaatcc	caacgttcgc	180
aactctacta	cccatcaatt	atggccgcca	tctggggtaa	cggcgggcag	gctggccagt	240
tcccgtctga	gcaatgggtc	tatgaaatgc	cccctgtaac	tcgatgggtg	acagcagcca	300
cagttgccac	ttcagtcttg	gtccaatgtc	acgtcctcac	cccattccag	ctgttttata	360
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cctatacttc	ggaccactca	atctcgactt	actatttcat	gtgttcttct	tgcagcgata	540
ctcgcgcctc	ttggaggaat	catcgggcg	atcgccggcc	cacttctcgt	ggcttctgtt	600
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cttcctagga	atgctggtct	tcaccgcccc	ctatctcccc	tgggttctga	tggcattcag	780
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caacgtcaac	ggggaattcg	ccgctgctgc	tgcacccgaa	gttcggtgag	ctatttgtgc	1020
acccactgg	ggcatttact	gcatggcgat	gcaaagaatc	gtccgcgtaa	tcgctctgga	1080
aacgtcagca	tatatgtgtg	tactgccaac	tactcgcgcc	gacacgcgcg	aagcatgaga	1140
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<210> 56
 <211> 741
 <212> DNA
 <213> *Aspergillus niger*

<220>
 <221> CDS
 <222> (1)..(741)

<400> 56

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1			5					10					15			
gag	caa	tgg	ttc	tat	gaa	atg	ccc	cct	gta	act	cga	tgg	tgg	aca	gca	96
Glu	Gln	Trp	Phe	Tyr	Glu	Met	Pro	Val	Thr	Arg	Trp	Trp	Thr	Ala		
			20					25				30				
gcc	aca	gtt	gcc	act	tca	gtc	ttg	gtc	caa	tgt	cac	gtc	ctc	acc	cca	144
Ala	Thr	Val	Ala	Thr	Ser	Val	Leu	Val	Gln	Cys	His	Val	Leu	Thr	Pro	
		35					40					45				

ttc cag ctg ttt tat agc ttc cgc gca gtc tat gtt aag tct cag tat	192
Phe Gln Leu Phe Tyr Ser Phe Arg Ala Val Tyr Val Lys Ser Gln Tyr	
50 55 60	
tgg cgt ctg ttc aca acc ttc cta tac ttc gga cca ctc aat ctc gac	240
Trp Arg Leu Phe Thr Phe Leu Tyr Phe Gly Pro Leu Asn Leu Asp	
65 70 75 80	
tta cta ttt cat gtg ttc ttc ttg cag cga tac tcg cgc ctc ttg gag	288
Leu Leu Phe His Val Phe Phe Leu Gln Arg Tyr Ser Arg Leu Leu Glu	
85 90 95	
gaa tca tcg ggg cga tcg ccg gcc cac ttc tcg tgg ctt ctg ttc tac	336
Glu Ser Ser Gly Arg Ser Pro Ala His Phe Ser Trp Leu Leu Phe Tyr	
100 105 110	
gcc atg gcc tct ctc ctc gtc ctc tcg cca ttt ctc tcc ctt cca ttc	384
Ala Met Ala Ser Leu Leu Val Leu Ser Pro Phe Leu Ser Leu Pro Phe	
115 120 125	
ctg ggc acg gct ctc tct tcc agt ctg gtc tac atc tgg agt cgt cgc	432
Leu Gly Thr Ala Leu Ser Ser Ser Leu Val Tyr Ile Trp Ser Arg Arg	
130 135 140	
aac ccg gaa act cgc ctc agc ttc cta gga atg ctg gtc ttc acc gcc	480
Asn Pro Glu Thr Arg Leu Ser Phe Leu Gly Met Leu Val Phe Thr Ala	
145 150 155 160	
ccc tat ctc ccc tgg gtt ctg atg gca ttc agc ctg gtc gtc cat ggc	528
Pro Tyr Leu Pro Trp Val Leu Met Ala Phe Ser Leu Val Val His Gly	
165 170 175	
atc gtg ccc aag gat gaa atc tgc ggc gtt gtc gtc ggc cac gtc tgg	576
Ile Val Pro Lys Asp Glu Ile Cys Gly Val Val Val Gly His Val Trp	
180 185 190	
tac ttc ttc aac gat gtt tac cct tcg ctt cac ggt ggt cac cgt cct	624
Tyr Phe Phe Asn Asp Val Tyr Pro Ser Leu His Gly Gly His Arg Pro	
195 200 205	
ttc gat cct cct atg tgg tgg gtg cgt ctg ttt gag tca ggg ccc ggg	672
Phe Asp Pro Pro Met Trp Trp Val Arg Leu Phe Glu Ser Gly Pro Gly	
210 215 220	
gaa cga ggc acc gac gct gcc aac gtc aac ggg gaa ttc gcc gct gct	720
Glu Arg Gly Thr Asp Ala Ala Asn Val Asn Gly Glu Phe Ala Ala Ala	
225 230 235 240	
gct gca ccc gaa gtt cgg tga	741
Ala Ala Pro Glu Val Arg	
245	

<210> 57

<211> 246

<212> PRT

<213> *Aspergillus niger*

<400> 57

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Ala Thr Val Ala Thr Ser Val Leu Val Gln Cys His Val Leu Thr Pro	
35 40 45	
Phe Gln Leu Phe Tyr Ser Phe Arg Ala Val Tyr Val Lys Ser Gln Tyr	
50 55 60	

Trp	Arg	Leu	Phe	Thr	Thr	Phe	Leu	Tyr	Phe	Gly	Pro	Leu	Asn	Leu	Asp
65					70					75					80
Leu	Leu	Phe	His	Val	Phe	Phe	Leu	Gln	Arg	Tyr	Ser	Arg	Leu	Leu	Glu
			85						90					95	
Glu	Ser	Ser	Gly	Arg	Ser	Pro	Ala	His	Phe	Ser	Trp	Leu	Leu	Phe	Tyr
			100					105					110		
Ala	Met	Ala	Ser	Leu	Leu	Val	Leu	Ser	Pro	Phe	Leu	Ser	Leu	Pro	Phe
		115					120					125			
Leu	Gly	Thr	Ala	Leu	Ser	Ser	Ser	Leu	Val	Tyr	Ile	Trp	Ser	Arg	Arg
	130					135						140			
Asn	Pro	Glu	Thr	Arg	Leu	Ser	Phe	Leu	Gly	Met	Leu	Val	Phe	Thr	Ala
145					150					155					160
Pro	Tyr	Leu	Pro	Trp	Val	Leu	Met	Ala	Phe	Ser	Leu	Val	Val	His	Gly
				165					170					175	
Ile	Val	Pro	Lys	Asp	Glu	Ile	Cys	Gly	Val	Val	Val	Gly	His	Val	Trp
			180					185					190		
Tyr	Phe	Phe	Asn	Asp	Val	Tyr	Pro	Ser	Leu	His	Gly	Gly	His	Arg	Pro
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Phe	Asp	Pro	Pro	Met	Trp	Trp	Val	Arg	Leu	Phe	Glu	Ser	Gly	Pro	Gly
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<211> 2538

<212> DNA

<213> *Aspergillus niger*

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<212> DNA

<213> *Aspergillus niger*

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