

1384463

SEQUENCE LISTING

<110> Roche Diagnostics GmbH  
F. Hoffmann-LaRoche AG  
Ultizyme International Ltd.  
<120> Glucose Oxidase  
<130> 27499 WO  
<160> 33  
<170> PatentIn version 3.1  
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Ser	Asp	Pro	Ser	Lys	Val	Ala	Gly	Lys	Thr	Tyr	Asp	Tyr	Ile	Ile	Ala
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Gly	Gly	Gly	Leu	Thr	Gly	Leu	Thr	Val	Ala	Ala	Lys	Leu	Thr	Glu	Asn
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Pro	Lys	Ile	Lys	Val	Leu	Val	Ile	Glu	Lys	Gly	Phe	Tyr	Glu	Ser	Asn
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Asp	Gly	Ala	Ile	Ile	Glu	Asp	Pro	Asn	Ala	Tyr	Gly	Gln	Ile	Phe	Gly
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Thr	Thr	Val	Asp	Gln	Asn	Tyr	Leu	Thr	Val	Pro	Leu	Ile	Asn	Asn	Arg
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Thr	Asn	Asn	Ile	Lys	Ala	Gly	Lys	Gly	Leu	Gly	Gly	Ser	Thr	Leu	Ile
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Asn	Gly	Asp	Xaa	Trp	Thr	Arg	Pro	Asp	Lys	Val	Gln	Ile	Asp	Ser	Trp
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Glu	Lys	Val	Phe	Gly	Met	Glu	Gly	Trp	Asn	Trp	Asp	Asn	Met	Phe	Glu
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Tyr	Met	Lys	Lys	Ala	Glu	Ala	Ala	Arg	Thr	Pro	Thr	Ala	Ala	Gln	Leu
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Ala	Ala	Gly	His	Ser	Phe	Asn	Ala	Thr	Cys	His	Gly	Thr	Asn	Gly	Thr
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Val	Gln	Ser	Gly	Ala	Arg	Asp	Asn	Gly	Gln	Pro	Trp	Ser	Pro	Ile	Met
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Lys	Ala	Leu	Met	Asn	Thr	Val	Ser	Ala	Leu	Gly	Val	Pro	Val	Gln	Gln
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Pro	Asn	Tyr	Gln	Arg	Ser	Asn	Leu	Glu	Ile	Leu	Thr	Gly	Gln	Met	Val
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Gly	Lys	Val	Leu	Phe	Lys	Gln	Thr	Ala	Ser	Gly	Pro	Gln	Ala	Val	Gly
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Val	Asn	Phe	Gly	Thr	Asn	Lys	Ala	Val	Asn	Phe	Asp	Val	Phe	Ala	Lys
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His	Glu	Val	Leu	Leu	Ala	Ala	Gly	Ser	Ala	Ile	Ser	Pro	Leu	Ile	Leu
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Glu	Tyr	Ser	Gly	Ile	Gly	Leu	Lys	Ser	Val	Leu	Asp	Gln	Ala	Asn	Val
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Thr	Gln	Leu	Leu	Asp	Leu	Pro	Val	Gly	Ile	Asn	Met	Gln	Asp	Gln	Thr
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Thr	Thr	Thr	Val	Ser	Ser	Arg	Ala	Ser	Ser	Ala	Gly	Ala	Gly	Gln	Gly

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Gln	Ala	355	Phe	Xaa	Ala	Asn	360	Phe	Thr	Glu	Thr	Phe	365	Gly	Asp	Tyr	Ala
370	Val					375	Leu	Leu	Asn	Thr	Lys	Leu	380	Asp	Gln	Trp	Ala
Pro	Gln	Ala	Arg	Asp	Leu	390	Gly	Gly	Phe	His	Asn	Val	395	Thr	Ala	Leu	Lys
385	Thr	Val	Ala	Arg	405						410					415	Val
Gln	Tyr	Glu	Asn	Tyr	Arg	Asn	Trp	Leu	425	Leu	Asp	Glu	Asp	Val	430	Ala	Phe
Ala	Glu	Leu	Phe	Met	Asp	Thr	Glu	Gly	Lys	Ile	Asn	Phe	445	Asp	Leu	Trp	
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Pro	Tyr	Leu	Trp	Gln	Phe	Ala	Asn	Asp	Pro	Lys	Phe	Phe	475	Leu	Asn	Glu	
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Phe	Asp	Leu	Leu	Gly	Gln	Ala	Ala	Ala	Ser	Lys	Leu	Ala	Arg	Asp	495	Leu	
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Thr	Ser	Gln	Gly	Ala	Met	Lys	Glu	Tyr	505	Phe	Ala	Gly	Glu	Thr	510	Leu	Pro
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Gly	Tyr	Asn	Leu	Val	Gln	Asn	Ala	Thr	520	Leu	Ser	Gln	Trp	Ser	525	Asp	Tyr
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Val	Leu	Gln	Asn	Phe	Arg	Pro	Asn	Trp	His	Ala	Val	Ser	Ser	Cys	540	Ser	
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Gln	Val	Ser	Ser	His	Val	Met	Thr	Ile	585	Phe	Tyr	Gly	Met	Ala	590	Leu	Lys
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			20					25					30		
Ser	Asp	Pro	Ser	Lys	Val	Ala	Gly	Lys	Thr	Tyr	Asp	Tyr	Ile	Ile	Ala
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Gly	Gly	Gly	Leu	Thr	Gly	Leu	Thr	Val	Ala	Ala	Lys	Leu	Thr	Glu	Asn
		50				55					60				
Pro	Lys	Ile	Lys	Val	Leu	Val	Ile	Glu	Lys	Gly	Phe	Tyr	Glu	Ser	Asn
65					70					75					80
Asp	Gly	Ala	Ile	Ile	Glu	Asp	Pro	Asn	Ala	Tyr	Gly	Gln	Ile	Phe	Gly
			85						90					95	
Thr	Thr	Val	Asp	Gln	Asn	Tyr	Leu	Thr	Val	Pro	Leu	Ile	Asn	Asn	Arg
			100					105					110		
Thr	Asn	Asn	Ile	Lys	Ala	Gly	Lys	Gly	Leu	Gly	Gly	Ser	Thr	Leu	Ile
		115					120					125			
Asn	Gly	Asp	Xaa	Trp	Thr	Arg	Pro	Asp	Lys	Val	Gln	Ile	Asp	Ser	Trp
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Glu	Lys	Val	Phe	Gly	Met	Glu	Gly	Trp	Asn	Trp	Asp	Asn	Met	Phe	Glu
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Tyr	Met	Lys	Lys	Ala	Glu	Ala	Ala	Arg	Thr	Pro	Thr	Ala	Ala	Gln	Val
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Ala	Ala	Gly	His	Ser	Phe	Asn	Ala	Thr	Cys	His	Gly	Thr	Asn	Gly	Thr
Val	Gln	Ser	180	Ala	Arg	Asp	Asn	185	Gln	Pro	Trp	Ser	190	Ile	Met
Lys	Ala	Leu	195	Met	Asn	Thr	Val	200	Ala	Leu	Gly	Val	205	Gln	Gln
Asp	210	Phe	Leu	Cys	Gly	His	215	Pro	Arg	Gly	Val	Ser	220	Met	Asn
225	Leu	Asp	Glu	Asn	Gln	Val	230	Arg	Val	Asp	Ala	Ala	Arg	Ala	Trp
Pro	Asn	Tyr	Gln	Arg	Pro	Asn	Leu	Glu	250	Ile	Leu	Thr	Gly	Gln	Met
Gly	Lys	Val	260	Phe	Lys	Gln	Thr	265	Ala	Ser	Gly	Pro	Gln	Ala	Val
Val	275	Asn	Phe	Gly	Thr	Asn	Lys	280	Ala	Val	Asn	Phe	Asp	Val	Phe
His	290	Glu	Val	Leu	Leu	Ala	310	Ala	Gly	Ser	Ala	Ile	Ser	Pro	Leu
305	Tyr	Ser	Gly	Ile	Gly	Leu	Lys	Ser	Val	315	Leu	Asp	Gln	Ala	Asn
Glu	Thr	Gln	Leu	Leu	Asp	Leu	Pro	Val	Gly	330	Ile	Asn	Met	Gln	Asp
Thr	Thr	Thr	340	Val	Ser	Ser	Arg	Ala	Ser	345	Ala	Ala	Gly	Ala	Gly
Gln	Ala	Val	355	Phe	Xaa	Ala	Asn	Phe	Thr	Glu	Thr	Phe	Gly	Asp	Tyr
Pro	Gln	Ala	370	Arg	Asp	Leu	Leu	Asn	Thr	Lys	Leu	Asp	Gln	Trp	Ala
385	Glu	Thr	Val	Ala	Arg	Gly	Gly	Phe	His	Asn	Val	Thr	Ala	Leu	Lys
Gln	Tyr	Glu	405	Asn	Tyr	Arg	Asn	Trp	Leu	Leu	Asp	Glu	Asp	Val	Ala
Ala	Glu	Leu	420	Phe	Met	Asp	Thr	Glu	Gly	Lys	Ile	Asn	Phe	Asp	Leu
Asp	Leu	Ile	435	Pro	Phe	Thr	Arg	Gly	Ser	Val	His	Ile	Leu	Ser	Ser
Pro	Tyr	Leu	450	Trp	Gln	Phe	Ala	Asn	Asp	Pro	Lys	Phe	Phe	Leu	Asn
465	Phe	Asp	Leu	Leu	Gly	Gln	Ala	Ala	Ala	Ser	Lys	Leu	Ala	Arg	Asp
Thr	Ser	Gln	485	Ala	Met	Lys	Glu	Tyr	Phe	Ala	Gly	Glu	Thr	Leu	Pro
Gly	Tyr	Asn	500	Leu	Val	Gln	Asn	Ala	Thr	Leu	Ser	Gln	Trp	Ser	Asp
Val	Leu	Gln	515	Asn	Phe	Arg	Pro	Asn	Trp	His	Ala	Val	Ser	Ser	Cys
Met	Met	Ser	530	Arg	Glu	Leu	Gly	Gly	Val	Val	Asp	Ala	Thr	Ala	Lys
545	Tyr	Gly	Thr	Gln	Gly	Leu	Arg	Val	Ile	Asp	Gly	Ser	Ile	Pro	Pro
Gln	Val	Ser	565	His	Val	Met	Thr	Ile	Phe	Tyr	Gly	Met	Ala	Leu	Lys
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 Ser Asp Pro Ser Lys Val Ala Gly Lys Thr Tyr Asp Tyr Ile Ile Ala  
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 Gly Gly Gly Leu Thr Gly Leu Thr Val Ala Ala Lys Leu Thr Glu Asn  
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 Pro Lys Ile Lys Val Leu Val Ile Glu Lys Gly Phe Tyr Glu Ser Asn  
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 Asp Gly Ala Ile Ile Glu Asp Pro Asn Ala Tyr Gly Gln Ile Phe Gly  
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 Thr Thr Val Asp Gln Asn Tyr Leu Thr Val Pro Leu Ile Asn Asn Arg  
 100 105 110  
 Thr Asn Asn Ile Lys Ala Gly Lys Gly Leu Gly Gly Ser Thr Leu Ile  
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 Asn Gly Asp Xaa Trp Thr Arg Pro Asp Lys Val Gln Ile Asp Ser Trp  
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 Glu Lys Val Phe Gly Met Glu Gly Trp Asn Trp Asp Ser Met Phe Glu  
 145 150 155 160  
 Tyr Met Lys Lys Ala Glu Ala Ala Arg Ala Pro Thr Ala Ala Gln Leu  
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 Ala Ala Gly His Tyr Phe Asn Ala Thr Cys His Gly Thr Asn Gly Thr  
 180 185 190  
 Val Gln Ser Gly Ala Arg Asp Asn Gly Gln Pro Trp Ser Pro Ile Met  
 195 200 205  
 Lys Ala Leu Met Asn Thr Val Ser Ala Leu Gly Val Pro Val Gln Gln  
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 Asp Phe Leu Cys Gly His Pro Arg Gly Val Ser Met Ile Met Asn Asn  
 225 230 235 240  
 Val Asp Glu Asn Gln Val Arg Val Asp Ala Ala Arg Ala Trp Leu Leu  
 245 250 255  
 Pro Ser Tyr Gln Arg Pro Asn Leu Glu Ile Leu Thr Gly Gln Met Val  
 260 265 270  
 Gly Lys Val Leu Phe Lys Gln Thr Ala Ser Gly Pro Gln Ala Val Gly  
 275 280 285  
 Val Asn Phe Gly Thr Asn Lys Ala Val Asn Phe Asp Val Phe Ala Lys  
 290 295 300  
 His Glu Val Leu Leu Ala Ala Gly Ser Ala Ile Ser Pro Leu Ile Leu  
 305 310 315 320  
 Glu Tyr Ser Gly Ile Gly Leu Lys Ser Val Leu Asp Gln Ala Asn Val  
 325 330 335  
 Thr Gln Leu Leu Asp Leu Pro Val Gly Ile Asn Met Gln Asp Gln Thr  
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 Thr Thr Thr Val Ser Ser Arg Ala Ser Ala Ala Gly Ala Gly Gln Gly  
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 370 375 380  
 Pro Gln Ala Arg Glu Leu Asn Thr Lys Leu Asp Gln Trp Ala Glu  
 385 390 395 400  
 Glu Thr Val Ala Arg Gly Gly Phe His Asn Val Thr Ala Leu Lys Val  
 405 410 415  
 Gln Tyr Glu Asn Tyr Arg Asn Trp Leu Leu Asp Glu Asp Val Ala Phe  
 420 425 430  
 Ala Glu Leu Phe Met Asp Thr Glu Gly Lys Ile Asn Phe Asp Leu Trp  
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 Asp Leu Ile Pro Phe Thr Arg Gly Ser Val His Ile Leu Ser Ser Asp  
 450 455 460  
 Pro Tyr Leu Trp Gln Phe Ala Asn Asp Pro Lys Phe Phe Leu Asn Glu  
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 Phe Asp Leu Leu Gly Gln Ala Ala Ala Ser Lys Leu Ala Arg Asp Leu  
 485 490 495  
 Thr Ser Gln Gly Ala Met Lys Glu Tyr Phe Ala Gly Glu Thr Leu Pro  
 500 505 510  
 Gly Tyr Asn Leu Val Glu Asn Ala Thr Leu Ser Gln Trp Ser Asp Tyr  
 515 520 525  
 Val Leu Gln Asn Phe Arg Pro Asn Trp His Ala Val Ser Ser Cys Ser

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530	Met	Met	Ser	Arg	Glu	Leu	535	Gly	Gly	Val	Val	Asp	540	Ala	Thr	Ala	Lys	Val
545	Tyr	Gly	Thr	Gln	Gly	Leu	550	Arg	Val	Ile	Asp	555	Gly	Ser	Ile	Pro	Pro	Thr
	Gln	Val	Ser	Ser	565	His	Val	Met	Thr	Ile	570	Phe	Tyr	Gly	Met	Ala	Leu	Lys
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Thr	Leu	Leu	Ala	Ile	Pro	Thr	Leu	Phe	Ser	Ala	Ala	Thr	Val	Gln	
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Ala	Tyr	Leu	Pro	Ala	Glu	Gln	Ile	Asp	Val	Gln	Ser	Ser	Leu	Leu	Ser
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Gly	Gly	Leu	Thr	Gly	Leu	Thr	Val	Ala	Ala	Lys	Leu	Thr	Glu	Asn	Pro
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Lys	Ile	Lys	Val	Leu	Val	Ile	Glu	Lys	Gly	Phe	Tyr	Glu	Ser	Asn	Asp
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Gly	Ala	Ile	Ile	Glu	Asp	Pro	Asn	Ala	Tyr	Gly	Gln	Ile	Phe	Gly	Thr
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Thr	Val	Asp	Gln	Asn	Tyr	Leu	Thr	Val	Pro	Leu	Ile	Asn	Asn	Arg	Thr
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Asn	Asn	Ile	Lys	Ala	Gly	Lys	Gly	Leu	Gly	Gly	Ser	Thr	Leu	Ile	Asn
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Gly	Asp	Xaa	Trp	Thr	Arg	Pro	Asp	Lys	Ile	Gln	Ile	Asp	Ser	Trp	Glu
			165					170						175	
Lys	Val	Phe	Gly	Met	Glu	Gly	Trp	Asn	Trp	Asp	Asn	Met	Phe	Glu	Tyr
		180						185					190		
Met	Lys	Lys	Ala	Glu	Ala	Ala	Arg	Pro	Pro	Thr	Asp	Ala	Gln	Leu	Ala
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Ala	Gly	His	Tyr	Phe	Asp	Ala	Thr	Cys	His	Gly	Thr	Asn	Gly	Thr	Val
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Arg	Ser	Gly	Ala	Arg	Asp	Asn	Gly	Lys	Pro	Trp	Ser	Pro	Leu	Met	Lys
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Ala	Leu	Met	Asn	Thr	Val	Ser	Ala	Leu	Gly	Val	Pro	Val	Gln	Gln	Asp
			245						250					255	
Phe	Leu	Cys	Gly	His	Pro	Arg	Gly	Val	Ser	Met	Ile	Met	Asn	Asn	Val
		260					265						270		
Asp	Glu	Asn	Gln	Val	Arg	Ala	Asp	Ala	Ala	Arg	Ala	Trp	Leu	Leu	Pro
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Lys	Val	Leu	Phe	Lys	Gln	Thr	Ala	Ser	Gly	Pro	Lys	Ala	Val	Gly	Val
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Asn	Phe	Gly	Thr	Asn	Lys	Val	Val	Asn	Phe	Asp	Val	Phe	Ala	Lys	His
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Glu	Val	Leu	Leu	Ala	Ala	Gly	Ser	Ala	Ile	Ser	Pro	Leu	Ile	Leu	Glu
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Tyr	Ser	Gly	Ile	Gly	Leu	Lys	Ser	Val	Leu	Asp	Gln	Ala	Asn	Ile	Thr
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Thr	Thr	Val	Ser	Ser	Arg	Ala	Ser	Val	Ala	Gly	Ala	Gly	Gln	Gly	Gln
385					390					395					400
Ala	Val	Phe	Xaa	Ala	Asn	Phe	Thr	Glu	Thr	Phe	Gly	Asp	Tyr	Ala	Pro
				405					410					415	
Gln	Ala	Arg	Glu	Leu	Leu	Asn	Thr	Lys	Leu	Asp	Gln	Trp	Ala	Glu	Glu
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Thr	Val	Ala	Arg	Gly	Gly	Phe	His	Asn	Val	Thr	Ala	Leu	Lys	Val	Gln
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Tyr	Glu	Asn	Tyr	Arg	Asn	Trp	Leu	Leu	Asp	Glu	Asp	Val	Ala	Phe	Ala
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Glu	Leu	Phe	Met	Asp	Thr	Glu	Gly	Lys	Ile	Asn	Phe	Asp	Leu	Trp	Asp
465					470					475					480
Leu	Ile	Pro	Phe	Thr	Arg	Gly	Ser	Val	His	Ile	Leu	Ser	Ser	Asp	Pro
				485					490					495	
Tyr	Leu	Trp	Gln	Phe	Ala	Asn	Asp	Pro	Lys	Phe	Phe	Leu	Asn	Glu	Phe
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Asp	Leu	Leu	Gly	Gln	Ala	Ala	Ala	Ser	Lys	Leu	Ala	His	Asp	Leu	Ser
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Leu	Gln	Asn	Phe	Arg	Pro	Asn	Trp	His	Ala	Val	Ser	Ser	Cys	Ser	Met
				565					570					575	
Met	Ser	Arg	Glu	Leu	Gly	Gly	Val	Val	Asp	Ala	Thr	Ala	Lys	Val	Tyr
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Gly	Thr	Gln	Gly	Leu	Arg	Val	Ile	Asp	Gly	Ser	Ile	Pro	Pro	Thr	Gln
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Val	Ser	His	Val	Met	Thr	Ile	Phe	Tyr	Gly	Met	Ala	Leu	Lys	Val	
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			20				25					30			
Ser	Asp	Pro	Asn	Lys	Val	Ala	Gly	Lys	Thr	Tyr	Asp	Tyr	Ile	Ile	Ala
		35					40					45			
Gly	Gly	Gly	Leu	Thr	Gly	Leu	Thr	Val	Ala	Ala	Lys	Leu	Ser	Glu	Asn
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Pro	Lys	Ile	Lys	Val	Leu	Val	Ile	Glu	Lys	Gly	Phe	Tyr	Glu	Ser	Asn
65					70					75					80
Asp	Gly	Ala	Ile	Ile	Glu	Asp	Ala	Asn	Ala	Tyr	Gly	Gln	Ile	Phe	Gly
				85					90					95	
Thr	Thr	Val	Asp	Gln	Asn	Tyr	Leu	Thr	Val	Pro	Leu	Ile	Asn	Asn	Arg
			100					105					110		
Thr	Ser	Ser	Ile	Lys	Ser	Gly	Lys	Gly	Leu	Gly	Gly	Ser	Thr	Leu	Ile
		115					120					125			
Asn	Gly	Asp	Xaa	Trp	Thr	Arg	Pro	Asp	Lys	Val	Gln	Ile	Asp	Ser	Trp

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130	135	140																	
Glu	Lys	Val	Phe	Gly	Met	Glu	Gly	Trp	Asn	Trp	Asp	Thr	Met	Phe	Glu				
145	Tyr	Met	Lys	Lys	Ala	Glu	Leu	Ala	Arg	Ala	Pro	Thr	Asp	Ala	Gln	Ile			
				165					170						175				
Ala	Ala	Gly	His	Tyr	Phe	Asn	Ala	Thr	Cys	His	Gly	Phe	Asn	Gly	Thr				
			180					185					190						
Ile	His	Ser	Gly	Pro	Arg	Asp	Asn	Gly	Gln	Pro	Trp	Ser	Pro	Ile	Met				
		195					200					205							
Lys	Ala	Leu	Met	Asn	Thr	Thr	Ser	Ala	Leu	Gly	Ile	Pro	Thr	Gln	Gln				
	210					215					220								
Asp	Phe	Leu	Cys	Gly	His	Pro	Arg	Gly	Val	Ser	Met	Ile	Tyr	Asn	Asn				
225					230					235					240				
Leu	Asp	Glu	Asn	Gln	Val	Arg	Ala	Asp	Ala	Gly	Arg	Ala	Trp	Val	Leu				
			245						250					255					
Pro	Asn	Tyr	Gln	Arg	Pro	Asn	Leu	Lys	Ile	Met	Thr	Gly	Gln	Thr	Val				
			260					265					270						
Gly	Lys	Val	Leu	Phe	Asn	Gln	Thr	Ala	Ser	Gly	Pro	Lys	Ala	Val	Gly				
		275					280					285							
Val	Asn	Phe	Gly	Thr	Asn	Lys	Ala	Val	Asn	Phe	Asp	Val	Tyr	Ala	Lys				
	290					295				300									
His	Glu	Val	Leu	Leu	Ala	Gly	Ser	Ala	Ile	Ser	Pro	Leu	Ile	Leu					
305					310					315				320					
Glu	Tyr	Ser	Gly	Ile	Gly	Leu	Lys	Ser	Val	Leu	Asp	Ala	Ala	Asn	Val				
			325						330					335					
Thr	Gln	Leu	Val	Asp	Leu	Pro	Val	Gly	Leu	Asn	Met	Gln	Asp	Gln	Thr				
			340					345					350						
Thr	Thr	Thr	Val	Ser	Ser	Arg	Thr	Asn	Ala	Ala	Gly	Thr	Gly	Gln	Gly				
		355					360					365							
Gln	Ala	Val	Phe	Xaa	Ala	Asn	Phe	Thr	Glu	Val	Phe	Gly	Asp	Tyr	Thr				
	370					375					380								
Pro	Gln	Ala	Arg	Glu	Leu	Leu	Asn	Thr	Lys	Leu	Asp	Gln	Trp	Ala	Glu				
385					390					395					400				
Glu	Thr	Val	Ala	Arg	Gly	Gly	His	Asn	Asn	Val	Thr	Ala	Leu	Lys	Ile				
			405					410						415					
Gln	Tyr	Glu	Asn	Tyr	Arg	Asp	Trp	Leu	Leu	Glu	Glu	Asp	Val	Ala	Tyr				
			420					425					430						
Ala	Glu	Leu	Phe	Met	Asp	Thr	Ser	Gly	Lys	Ile	Asn	Phe	Asp	Leu	Trp				
			435				440					445							
Asp	Leu	Ile	Pro	Phe	Thr	Arg	Gly	Ser	Val	His	Ile	Leu	Ser	Ser	Asp				
	450					455					460								
Pro	Tyr	Leu	Trp	Gln	Tyr	Ala	Asn	Asp	Pro	Lys	Phe	Phe	Leu	Asn	Glu				
465					470					475					480				
Leu	Asp	Leu	Leu	Gly	Gln	Ala	Ala	Ala	Ser	Lys	Leu	Ala	Arg	Glu	Leu				
				485					490					495					
Ser	Thr	Lys	Gly	Ala	Met	Ala	Gln	Tyr	Phe	Ala	Gly	Glu	Thr	Ile	Pro				
			500					505					510						
Gly	Asn	Asn	Leu	Ala	Ala	Asp	Ala	Asn	Leu	Ser	Gln	Trp	Ser	Asp	Tyr				
		515					520					525							
Val	Ile	Gln	Asn	Phe	Arg	Pro	Asn	Trp	His	Ala	Val	Ser	Ser	Cys	Ser				
	530					535					540								
Met	Met	Ala	Lys	Glu	Leu	Gly	Gly	Val	Val	Asp	Ala	Thr	Ala	Lys	Val				
545					550					555				560					
Tyr	Gly	Thr	Gln	Gly	Leu	Arg	Val	Val	Asp	Gly	Ser	Ile	Pro	Pro	Thr				
				565					570					575					
Gln	Val	Ser	Ser	His	Val	Met	Thr	Ile	Phe	Tyr	Gly	Met	Ala	Leu	Lys				
			580					585					590						
Val	Ala	Asp	Ala	Ile	Leu	Ala	Asp	Tyr	Ala	Lys	Ser	Ala							
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 <222> (132)..(132)  
 <223> Xaa is Ser, Ala, Cys, Ile, Asn, Arg, Asp, Thr, Val, Tyr, Glu, His, Met or Gln

<220>  
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 <222> (372)..(372)  
 <223> Xaa is Phe, Ala, Leu, Trp or Tyr, provided that when Xaa132 is Ser, then  
 Xaa372 is not Phe  
 <400> 6

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

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Ser	Ala	Gly	Glu	Met	Lys	Lys	Tyr	Tyr	Ala	Gly	Glu	Thr	Ile	Pro	Gly
			500					505					510		
Asp	Asn	Leu	Pro	Gln	Asp	Ala	Thr	Val	Glu	Gln	Trp	Glu	Asp	Tyr	Val
		515					520					525			
Met	Met	Asn	Phe	Arg	Pro	Asn	Trp	His	Ala	Val	Ser	Thr	Cys	Ser	Met
		530				535					540				
Met	Ser	Arg	Glu	Leu	Gly	Gly	Val	Val	Asp	Ala	Thr	Ala	Lys	Val	Tyr
					550					555					560
Gly	Thr	Gln	Gly	Leu	Arg	Val	Ile	Asp	Gly	Ser	Ile	Pro	Pro	Thr	Gln
				565					570					575	
Val	Ser	Ser	His	Val	Met	Thr	Val	Phe	Tyr	Gly	Met	Ala	Leu	Arg	Ile
			580					585					590		
Ala	Glu	Ser	Val	Leu	Glu	Asp	Tyr	Ala	Lys	Lys	Ala				
		595					600								

<210> 7  
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 <213> Aspergillus terreus  
 <220>  
 <221> MISC\_FEATURE  
 <222> (156)..(156)  
 <223> Xaa is Ser, Ala, Cys, Ile, Asn, Arg, Asp, Thr, Val, Tyr, Glu, His, Met or  
 Gln  
 <220>  
 <221> MISC\_FEATURE  
 <222> (397)..(397)  
 <223> Xaa is Phe, Ala, Leu, Trp or Tyr, provided that when Xaa156 is Ser, then  
 Xaa397 is not Phe  
 <400> 7

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

305 1384463 320  
 Val Asn Phe Asn Val Tyr Ala Asn His Glu Val Leu Leu Ala Ala Gly  
 Ser Ala Ile Ser Pro Leu Ile Leu Glu Tyr Ser Gly Ile Gly Leu Lys  
 Ser Val Leu Asp Lys Ala Asn Val Pro Gln Leu Leu Glu Leu Pro Val  
 Gly Ile Asn Met Gln Asp Gln Thr Thr Thr Thr Val Arg Ala Arg Ser  
 Thr Pro Ala Gly Phe Gly Gln Gly Gln Ala Val Tyr Xaa Ala Asn Phe  
 Thr Glu Thr Phe Gly Glu Asp Ala Pro Tyr Ala Ala Glu Leu Leu Asn  
 Thr Lys Leu Asp Gln Trp Ala Glu Glu Thr Val Ala Arg Gly Gly Ser  
 His Asn Val Thr Ala Leu Lys Val Gln Tyr Glu Asn Tyr Arg Asp Trp  
 Leu Leu Asn Glu Asp Val Ala Tyr Ala Glu Leu Phe Leu Asp Thr Ser  
 Gly Gln Ile Asn Phe Asp Leu Trp Asp Leu Ile Pro Phe Thr Arg Gly  
 Ser Thr His Ile Leu Ser Ser Asp Pro Tyr Leu Trp Gln Phe Ala Asn  
 Asp Pro Lys Phe Phe Asn Glu Leu Asp Leu Leu Gly Gln Ala Ala  
 Ala Ser Arg Leu Ala Arg Thr Leu Gln Asn Ser Gly Ala Met Ala Asn  
 Tyr Phe Asn Gly Glu Ile Ile Pro Gly Ser Glu Leu Pro Tyr Glu Ala  
 Ser Leu Glu Gln Trp Ala Glu Tyr Val Lys Asp Asn Phe Arg Ala Asn  
 Trp His Ala Val Gly Thr Cys Ser Met Met Ser Arg Asp Leu Gly Gly  
 Val Val Asp Ala Thr Ala Lys Val Tyr Asp Thr Gln Gly Leu Arg Val  
 Ile Asp Gly Ser Ile Pro Pro Thr Gln Val Ser Ser His Val Met Thr  
 Ile Phe Tyr Gly Met Ala Leu Arg Ile Ala Glu Ser Ile Leu Glu Asp  
 Tyr Ala Lys Ala

625  
 <210> 8  
 <211> 602  
 <212> PRT  
 <213> Aspergillus terreus  
 <220>  
 <221> MISC\_FEATURE  
 <222> (130)..(130)  
 <223> Xaa is Ser, Ala, Cys, Ile, Asn, Arg, Asp, Thr, Val, Tyr, Glu, His, Met or  
 Gln  
 <220>  
 <221> MISC\_FEATURE  
 <222> (371)..(371)  
 <223> Xaa is Phe, Ala, Leu, Trp or Tyr, provided that when Xaa130 is Ser, then  
 Xaa371 is not Phe  
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Met Arg His Ile Gly Tyr Phe Leu Leu Pro Leu Ala Thr Val Cys Ala  
 1 5 10 15  
 Tyr Leu Val Ser Glu Gln Val Asp Val Gln Ala Ser Leu Leu Thr Asn  
 20 25 30  
 Pro Glu Glu Val Ala Asp Lys Asn Phe Asp Tyr Ile Ile Ala Gly Gly  
 35 40 45  
 Gly Leu Thr Gly Leu Thr Val Ala Ala Lys Leu Thr Glu Asn Pro Asn  
 50 55 60  
 Ile Glu Val Leu Val Ile Glu Lys Gly Phe Tyr Glu Ser Asn Asp Gly  
 65 70 75 80  
 Pro Ile Ile Glu Asp Pro Asn Ala Tyr Gly Gln Ile Phe Gly Thr Thr  
 85 90 95

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Val	Asp	Gln	Asn	Tyr	Leu	Thr	Val	Pro	Leu	Ile	Asn	Asn	Arg	Thr	Asp
			100					105					110		
Asn	Ile	Lys	Ser	Gly	Lys	Gly	Leu	Gly	Gly	Ser	Thr	Leu	Ile	Asn	Gly
		115					120					125			
Asp	Xaa	Trp	Thr	Arg	Pro	Asp	Lys	Val	Gln	Ile	Asp	Ser	Trp	Glu	Thr
	130					135					140				
Val	Phe	Gly	Asn	Glu	Gly	Trp	Asn	Trp	Asp	Asn	Val	Phe	Lys	Tyr	Met
	145				150					155					160
Asn	Gln	Ala	Glu	Arg	Ala	Arg	Ala	Pro	Asn	Ala	Thr	Gln	Ile	Ala	Ala
				165					170					175	
Gly	His	His	Phe	Asp	Pro	Ala	Cys	His	Gly	Phe	Asn	Gly	Thr	Val	His
			180					185					190		
Ala	Gly	Pro	Arg	Asp	Asn	Gly	Gln	Arg	Trp	Ser	Pro	Leu	Met	Lys	Ala
		195					200					205			
Leu	Met	Asn	Thr	Thr	Ser	Ala	Leu	Gly	Val	Pro	Thr	Gln	Val	Asp	Phe
	210					215					220				
His	Cys	Gly	His	Pro	Arg	Gly	Val	Ser	Met	Ile	Pro	Asn	Asn	Leu	Leu
	225				230					235					240
Glu	Asp	Gln	Val	Arg	Ala	Asp	Ala	Ala	His	Glu	Trp	Leu	Leu	Pro	Asn
				245					250					255	
Tyr	Arg	Arg	Lys	Asn	Leu	Lys	Val	Leu	Thr	Gly	Gln	Leu	Val	Gly	Lys
			260					265					270		
Val	Ile	Phe	Asp	Gln	Asp	Ala	Pro	Gly	Leu	Lys	Ala	Ile	Gly	Val	Asn
		275					280					285			
Phe	Gly	Thr	Asn	Lys	Ala	Val	Asn	Phe	Asn	Val	Tyr	Ala	Asn	His	Glu
	290				295						300				
Val	Leu	Leu	Ala	Ala	Gly	Ser	Ala	Ile	Ser	Pro	Leu	Ile	Leu	Glu	Tyr
	305				310					315					320
Ser	Gly	Ile	Gly	Leu	Arg	Ser	Val	Leu	Glu	Lys	Ala	Asn	Val	Pro	Gln
				325					330					335	
Leu	Leu	Glu	Leu	Pro	Val	Gly	Ile	Asn	Met	Gln	Asp	Gln	Thr	Thr	Thr
			340					345					350		
Thr	Val	Arg	Ala	Arg	Ser	Thr	Pro	Ala	Gly	Phe	Gly	Gln	Gly	Gln	Ala
		355					360					365			
Val	Tyr	Xaa	Ala	Asn	Phe	Thr	Glu	Thr	Phe	Glu	Glu	Asp	Ala	Pro	Tyr
	370					375					380				
Ala	Ala	Glu	Leu	Leu	Lys	Thr	Gln	Leu	Asp	Gln	Trp	Ala	Glu	Glu	Thr
	385				390					395					400
Val	Ala	Arg	Gly	Gly	Phe	His	Asn	Val	Thr	Ala	Leu	Lys	Val	Gln	Tyr
				405					410					415	
Glu	Asn	Tyr	Arg	Asp	Trp	Leu	Leu	Asn	Glu	Asp	Val	Ala	Tyr	Ala	Glu
			420					425					430		
Leu	Phe	Leu	Asp	Thr	Ser	Gly	Gln	Ile	Asn	Phe	Asp	Leu	Trp	Asp	Leu
		435				440						445			
Ile	Pro	Phe	Thr	Arg	Gly	Ser	Thr	His	Ile	Leu	Ser	Ser	Asp	Pro	Tyr
	450				455						460				
Leu	Trp	Gln	Phe	Ala	Asn	Asp	Pro	Lys	Phe	Phe	Phe	Asn	Glu	Leu	Asp
	465				470					475					480
Leu	Leu	Gly	Gln	Ala	Ala	Ala	Ser	Arg	Leu	Ala	Arg	Lys	Leu	Gln	Asn
				485					490					495	
Ser	Gly	Ala	Met	Ala	Asn	Tyr	Phe	Asp	Gly	Glu	Ile	Ile	Pro	Gly	Ser
			500					505					510		
Glu	Leu	Pro	Asn	Glu	Ala	Ser	Leu	Glu	Gln	Trp	Ala	Glu	Tyr	Val	Lys
		515					520					525			
Asp	Asn	Phe	Arg	Ala	Asn	Trp	His	Ala	Val	Gly	Thr	Cys	Ser	Met	Met
	530					535					540				
Ser	Lys	Asp	Leu	Gly	Gly	Val	Val	Asp	Ala	Ser	Ala	Lys	Val	Tyr	Asp
	545				550					555					560
Thr	Gln	Arg	Leu	Arg	Val	Ile	Asp	Gly	Ser	Ile	Pro	Pro	Thr	Gln	Val
				565					570					575	
Ser	Ser	His	Val	Met	Thr	Ile	Phe	Tyr	Gly	Met	Ala	Leu	Arg	Ile	Ala
			580					585					590		
Glu	Ser	Ile	Leu	Glu	Asp	Tyr	Ala	Lys	Ala						
			595				600								

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 <212> PRT  
 <213> Aspergillus oryzae

<220>  
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 <222> (133)..(133)  
 <223> Xaa is Ser, Ala, Cys, Ile, Asn, Arg, Asp, Thr, Val, Tyr, Glu, His, Met or Gln  
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 <222> (374)..(374)  
 <223> Xaa is Phe, Ala, Leu, Trp or Tyr, provided that when Xaa133 is Ser, then Xaa374 is not Phe  
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Gln	Asn	Tyr	Ser	Leu	Glu	Lys	His	Phe	Asp	Val	Gln	Ser	Ser	Leu	Ile
			20					25					30		
Ser	Asp	Pro	Lys	Glu	Val	Ser	Glu	Lys	Thr	Phe	Asp	Tyr	Val	Ile	Ala
		35					40					45			
Gly	Gly	Gly	Leu	Thr	Gly	Leu	Thr	Val	Ala	Thr	Lys	Leu	Thr	Glu	Asn
	50					55					60				
Pro	Asp	Ile	Glu	Val	Leu	Val	Ile	Glu	Lys	Gly	Phe	Tyr	Glu	Ser	Asn
65					70					75					80
Cys	Gly	Ser	Ile	Val	Glu	Asp	Leu	Asn	Glu	Tyr	Gly	Asp	Ile	Phe	Gly
			85						90					95	
Thr	Asp	Val	Asp	Gln	Ala	Tyr	Gln	Thr	Val	Pro	Leu	Ala	Val	Asn	Asn
			100					105					110		
Arg	Thr	Glu	Leu	Ile	Arg	Ser	Gly	Asn	Gly	Leu	Gly	Gly	Ser	Thr	Leu
		115					120					125			
Ile	Asn	Gly	Gly	Xaa	Trp	Thr	Arg	Pro	Asp	Lys	Val	Gln	Ile	Asp	Ser
	130					135					140				
Trp	Glu	Arg	Val	Phe	Gly	Asn	Glu	Gly	Trp	Asn	Trp	Asp	Ser	Leu	Phe
145				150					155						160
Glu	Tyr	Met	Lys	Lys	Ala	Glu	His	Ser	Arg	Pro	Pro	Asn	Glu	Ala	Gln
			165					170						175	
Ile	Ala	Ala	Gly	His	Ser	Tyr	Asp	Pro	Ala	Cys	His	Gly	Thr	Asn	Gly
			180					185					190		
Thr	Val	Gln	Ala	Gly	Pro	Arg	Asp	Asn	Gly	Lys	Pro	Trp	Ser	Pro	Ile
		195					200					205			
Met	Lys	Ala	Leu	Ile	Asn	Thr	Ala	Ser	Glu	Arg	Gly	Val	Pro	Thr	Gln
210					215						220				
Gln	Asp	Phe	His	Cys	Gly	His	Pro	Arg	Gly	Val	Ser	Met	Ile	Pro	Asn
				230						235					240
Ala	Val	His	Glu	Asp	Gln	Thr	Arg	Ser	Asp	Thr	Ala	Arg	Glu	Trp	Leu
			245						250					255	
Leu	Pro	Asn	His	Glu	Arg	Pro	Asn	Leu	Lys	Val	Leu	Thr	Gly	Gln	Arg
		260						265					270		
Val	Gly	Lys	Val	Leu	Leu	Asn	Lys	Thr	Glu	Ser	Gly	Ala	Lys	Ala	Thr
		275					280					285			
Gly	Leu	Asn	Phe	Gly	Thr	His	Arg	Lys	Val	Asn	Tyr	Asn	Val	Tyr	Ala
	290					295				300					
Lys	His	Glu	Val	Leu	Leu	Ala	Ala	Gly	Ser	Ala	Ile	Ser	Pro	Leu	Ile
				310					315						320
Leu	Glu	Trp	Ser	Gly	Ile	Gly	Leu	Lys	Asp	Val	Leu	Ser	Ala	Ala	Gly
			325						330					335	
Val	Glu	Gln	Val	Val	Asp	Leu	Pro	Val	Gly	Leu	Asn	Met	Gln	Asp	Gln
			340					345					350		
Thr	Thr	Thr	Asn	Val	Arg	Ser	Gln	Ala	Gln	Ala	Ser	Gly	Ala	Gly	Gln
		355					360					365			
Gly	Gln	Ala	Val	Tyr	Xaa	Ala	Ser	Phe	Asn	Glu	Thr	Phe	Gly	Asp	Tyr
		370				375					380				
Ala	His	Lys	Ala	Met	Glu	Leu	Leu	Asn	Thr	Lys	Leu	Asp	Gln	Trp	Ala
				390						395					400
Glu	Glu	Thr	Val	Arg	Asn	Gly	Gly	Phe	His	Asn	Val	Thr	Ala	Leu	Lys
			405						410					415	
Ile	Gln	Tyr	Glu	Asn	Tyr	Arg	Asp	Trp	Leu	Leu	Asn	Glu	Asp	Val	Ala
			420				425						430		
Phe	Ala	Glu	Leu	Phe	Leu	Asp	Thr	Glu	Gly	Lys	Ile	Asn	Phe	Asp	Leu
		435					440					445			
Trp	Asp	Leu	Ile	Pro	Phe	Thr	Arg	Gly	Ser	Val	His	Ile	Leu	Asn	Gly

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

<210> 10

<211> 605

<212> PRT

<213> Aspergillus flavus

<220>

<221> MISC\_FEATURE

<222> (133)..(133)

<223> Xaa is Ser, Ala, Cys, Ile, Asn, Arg, Asp, Thr, Val, Tyr, Glu, His, Met or Gln

<220>

<221> MISC\_FEATURE

<222> (374)..(374)

<223> Xaa is Phe, Ala, Leu, Trp or Tyr, provided that when Xaa133 is Ser, then Xaa374 is not Phe

<400> 10

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

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

<210> 11

<211> 606

<212> PRT

<213> Aspergillus terreus

<220>

<221> MISC\_FEATURE

<222> (133)..(133)

<223> Xaa is Ser, Ala, Cys, Ile, Asn, Arg, Asp, Thr, Val, Tyr, Glu, His, Met or Gln

<220>

<221> MISC\_FEATURE

<222> (374)..(374)

<223> Xaa is Phe, Ala, Leu, Trp or Tyr, provided that when Xaa133 is Ser, then Xaa374 is not Phe

<400> 11

Met	Lys	Gly	Thr	Phe	Leu	Val	Ser	Ala	Leu	Ala	Phe	Thr	Ala	Ile	Thr
1				5					10					15	

Gln	Ala	Phe	Thr	Pro	Ala	Glu	Gln	Ile	Asp	Val	Gln	Ser	Ser	Leu	Ile
		20					25					30			

Ser	Asp	Pro	Lys	Glu	Val	Ala	Gly	Lys	Glu	Val	Asp	Tyr	Ile	Ile	Ala
		35				40					45				

Gly	Gly	Gly	Leu	Thr	Gly	Leu	Thr	Val	Ala	Ala	Lys	Leu	Thr	Glu	Asp
	50				55						60				

Pro	Asp	Ile	Arg	Val	Leu	Val	Ile	Glu	Lys	Gly	Phe	Tyr	Glu	Ser	Asn
	65				70				75						80

Asn	Gly	Pro	Ile	Ile	Glu	Asp	Leu	Asn	Ala	Tyr	Gly	Asp	Ile	Phe	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



&lt;213&gt; Aspergillus niger

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (110)..(110)

&lt;223&gt; Xaa is Ser, Ala, Cys, Ile, Asn, Arg, Asp, Thr, Val, Tyr, Glu, His, Met or Gln

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (351)..(351)

&lt;223&gt; Xaa is Phe, Ala, Leu, Trp or Tyr, provided that when Xaa110 is Thr, then Xaa351 is not Phe

&lt;400&gt; 12

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Ser Asn Gly Ile Glu Ala Ser Leu Leu Thr Asp Pro Asn Asp Val Ser
1      5      10      15
Gly Arg Thr Val Asp Tyr Ile Ile Ala Gly Gly Gly Leu Thr Gly Leu
20      25      30
Thr Thr Ala Arg Leu Thr Glu Asn Pro Asn Ile Ser Val Leu Val
35      40      45
Ile Glu Ser Gly Ser Tyr Glu Ser Asp Arg Gly Pro Ile Ile Glu Asp
50      55      60
Leu Asn Ala Tyr Gly Asp Ile Phe Gly Ser Ser Val Asp His Ala Tyr
65      70      75      80
Glu Thr Val Glu Leu Ala Thr Asn Asn Gln Thr Ala Leu Ile Arg Ser
85      90      95
Gly Asn Gly Leu Gly Gly Ser Thr Leu Val Asn Gly Gly Xaa Trp Thr
100      105      110
Arg Pro His Lys Ala Gln Val Asp Ser Trp Glu Thr Val Phe Gly Asn
115      120      125
Glu Gly Trp Asn Trp Asp Asn Val Ala Ala Tyr Ser Leu Gln Ala Glu
130      135      140
Arg Ala Arg Ala Pro Asn Ala Lys Gln Ile Ala Ala Gly His Tyr Phe
145      150      155      160
Asn Ala Ser Cys His Gly Thr Asn Gly Thr Val His Ala Gly Pro Arg
165      170      175
Asp Thr Gly Asp Asp Tyr Ser Pro Ile Val Lys Ala Leu Met Ser Ala
180      185      190
Val Glu Asp Arg Gly Val Pro Thr Gln Lys Asp Phe Gly Cys Gly Asp
195      200      205
Pro His Gly Val Ser Met Phe Pro Asn Thr Leu His Glu Asp Gln Val
210      215      220
Arg Ser Asp Ala Ala Arg Glu Trp Leu Leu Pro Asn Tyr Gln Arg Pro
225      230      235      240
Asn Leu Gln Val Leu Thr Gly Gln Tyr Val Gly Lys Val Leu Leu Ser
245      250      255
Gln Asn Gly Thr Thr Pro Arg Ala Val Gly Val Glu Phe Gly Thr His
260      265      270
Lys Gly Asn Thr His Asn Val Tyr Ala Lys His Glu Val Leu Leu Ala
275      280      285
Ala Gly Ser Ala Val Ser Pro Thr Ile Leu Glu Tyr Ser Gly Ile Gly
290      295      300
Met Lys Ser Ile Leu Glu Pro Leu Gly Ile Asp Thr Val Val Asp Leu
305      310      315      320
Pro Val Gly Leu Asn Leu Gln Asp Gln Thr Thr Ala Thr Val Arg Ser
325      330      335
Arg Ile Thr Ser Ala Gly Ala Gly Gln Gly Gln Ala Ala Trp Xaa Ala
340      345      350
Thr Phe Asn Glu Thr Phe Gly Asp Tyr Ser Glu Lys Ala His Glu Leu
355      360      365
Leu Asn Thr Lys Leu Glu Gln Trp Ala Glu Glu Ala Val Ala Arg Gly
370      375      380
Gly Phe His Asn Thr Thr Ala Leu Leu Ile Gln Tyr Glu Asn Tyr Arg
385      390      395      400
Asp Trp Ile Val Asn His Asn Val Ala Tyr Ser Glu Leu Phe Leu Asp
405      410      415
Thr Ala Gly Val Ala Ser Phe Asp Val Trp Asp Leu Leu Pro Phe Thr
420      425      430
Arg Gly Tyr Val His Ile Leu Asp Lys Asp Pro Tyr Leu His His Phe
435      440      445

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Ala	Tyr	Asp	Pro	Gln	Tyr	Phe	Leu	Asn	Glu	Leu	Asp	Leu	Leu	Gly	Gln
450						455					460				
Ala	Ala	Ala	Thr	Gln	Leu	Ala	Arg	Asn	Ile	Ser	Asn	Ser	Gly	Ala	Met
465				470						475					480
Gln	Thr	Tyr	Phe	Ala	Gly	Glu	Thr	Ile	Pro	Gly	Asp	Asn	Leu	Ala	Tyr
			485						490					495	
Asp	Ala	Asp	Leu	Ser	Ala	Trp	Thr	Glu	Tyr	Ile	Pro	Tyr	His	Phe	Arg
			500					505					510		
Pro	Asn	Tyr	His	Gly	Val	Gly	Thr	Cys	Ser	Met	Met	Pro	Lys	Glu	Met
		515					520					525			
Gly	Gly	Val	Val	Asp	Asn	Ala	Ala	Arg	Val	Tyr	Gly	Val	Gln	Gly	Leu
530						535					540				
Arg	Val	Ile	Asp	Gly	Ser	Ile	Pro	Pro	Thr	Gln	Met	Ser	Ser	His	Val
545					550					555					560
Met	Thr	Val	Phe	Tyr	Ala	Met	Ala	Leu	Lys	Ile	Ser	Asp	Ala	Ile	Leu
			565						570					575	
Glu	Asp	Tyr	Ala	Ser	Met	Gln									
			580												

<210> 13

<211> 605

<212> PRT

<213> *Aspergillus niger*

<220>

<221> MISC\_FEATURE

<222> (132)..(132)

<223> Xaa is Ser, Ala, Cys, Ile, Asn, Arg, Asp, Thr, Val, Tyr, Glu, His, Met or Gln

<220>

<221> MISC\_FEATURE

<222> (373)..(373)

<223> Xaa is Phe, Ala, Leu, Trp or Tyr, provided that when Xaa132 is Thr, then Xaa373 is not Phe

<400> 13

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

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

<210> 14  
 <211> 605  
 <212> PRT  
 <213> Apergillus niger  
 <220>  
 <221> MISC\_FEATURE  
 <222> (132)..(132)  
 <223> Xaa is Ser, Ala, Cys, Ile, Asn, Arg, Asp, Thr, Val, Tyr, Glu, His, Met or Gln  
 <220>  
 <221> MISC\_FEATURE  
 <222> (373)..(373)  
 <223> Xaa is Phe, Ala, Leu, Trp or Tyr, provided that when Xaa132 is Thr, then Xaa373 is not Phe  
 <400> 14

Met	Gln	Thr	Leu	Leu	Val	Ser	Ser	Leu	Val	Val	Ser	Leu	Ala	Ala	Ala
1			5					10				15			
Leu	Pro	His	Tyr	Ile	Arg	Ser	Asn	Gly	Ile	Glu	Ala	Ser	Leu	Leu	Thr
		20					25					30			
Asp	Pro	Lys	Asp	Val	Ser	Gly	Arg	Thr	Val	Asp	Tyr	Ile	Ile	Ala	Gly
		35				40					45				
Gly	Gly	Leu	Thr	Gly	Leu	Thr	Thr	Ala	Ala	Arg	Leu	Thr	Glu	Asn	Pro
	50				55					60					
Asn	Ile	Ser	Val	Leu	Val	Ile	Glu	Ser	Gly	Ser	Tyr	Glu	Ser	Asp	Arg
65				70				75						80	
Gly	Pro	Ile	Ile	Glu	Asp	Leu	Asn	Ala	Tyr	Gly	Asp	Ile	Phe	Gly	Ser
			85					90						95	

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

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 <223> Xaa is Ser, Ala, Cys, Ile, Asn, Arg, Asp, Thr, Val, Tyr, Glu, His, Met or Gln  
 <220>  
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 <222> (349)..(349)  
 <223> Xaa is Phe, Ala, Leu, Trp or Tyr, provided that when Xaa108 is Thr, then Xaa349 is not Phe  
 <400> 15  
 Gly Ile Glu Ala Ser Leu Leu Thr Asp Pro Lys Glu Val Ala Gly Arg  
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 Thr Val Asp Tyr Ile Ile Ala Gly Gly Gly Leu Thr Gly Leu Thr Thr  
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 Ala Ala Arg Leu Thr Glu Asn Pro Asp Ile Thr Val Leu Val Ile Glu  
 35 40 45  
 Ser Gly Ser Tyr Glu Ser Asp Arg Gly Pro Ile Ile Glu Asp Leu Asn  
 50 55 60  
 Ala Tyr Gly Asp Ile Phe Gly Ser Ser Val Asp His Ala Tyr Glu Thr  
 65 70 75 80  
 Val Glu Leu Ala Thr Asn Asn Gln Thr Ala Leu Ile Arg Ser Gly Asn  
 85 90 95  
 Gly Leu Gly Gly Ser Thr Leu Val Asn Gly Gly Xaa Trp Thr Arg Pro  
 100 105 110  
 His Lys Ala Gln Val Asp Ser Trp Glu Thr Val Phe Gly Asn Glu Gly  
 115 120 125  
 Trp Asn Trp Asp Ser Val Ala Tyr Ser Leu Gln Ala Glu Arg Ala  
 130 135 140  
 Arg Ala Pro Asn Ala Lys Gln Ile Ala Ala Gly His Tyr Phe Asn Ala  
 145 150 155 160  
 Ser Cys His Gly Ile Asn Gly Thr Val His Ala Gly Pro Arg Asp Thr  
 165 170 175  
 Gly Asp Asp Tyr Ser Pro Ile Val Lys Ala Leu Met Ser Ala Val Glu  
 180 185 190  
 Asp Arg Gly Val Pro Thr Lys Lys Asp Leu Gly Cys Gly Asp Pro His  
 195 200 205  
 Gly Val Ser Met Phe Pro Asn Thr Leu His Glu Asp Gln Val Arg Ser  
 210 215 220  
 Asp Ala Ala Arg Glu Trp Leu Leu Pro Asn Tyr Gln Arg Pro Asn Leu  
 225 230 235 240  
 Gln Val Leu Thr Gly Gln Tyr Val Gly Lys Val Leu Leu Ser Gln Asn  
 245 250 255  
 Ala Thr Thr Pro Arg Ala Val Gly Val Glu Phe Gly Thr His Lys Gly  
 260 265 270  
 Asn Thr His Asn Val Tyr Ala Lys His Glu Val Leu Leu Ala Ala Gly  
 275 280 285  
 Ser Ala Val Ser Pro Thr Ile Leu Glu Tyr Ser Asp Ile Gly Met Lys  
 290 295 300  
 Ser Ile Leu Glu Pro Leu Gly Ile Asp Thr Val Val Asp Leu Pro Val  
 305 310 315 320  
 Gly Leu Asn Leu Gln Asp Gln Thr Thr Ser Thr Val Arg Ser Arg Ile  
 325 330 335  
 Thr Ser Ala Gly Ala Gly Gln Gly Gln Ala Ala Trp Xaa Ala Thr Phe  
 340 345 350  
 Asn Glu Thr Phe Gly Asp Tyr Ala Glu Lys Ala His Glu Leu Leu Asn  
 355 360 365  
 Thr Lys Leu Glu Gln Trp Ala Glu Glu Ala Val Ala Arg Gly Gly Phe  
 370 375 380  
 His Asn Thr Thr Ala Leu Ile Gln Tyr Glu Asn Tyr Arg Asp Trp  
 385 390 395 400  
 Ile Val Lys Asp Asn Val Ala Tyr Ser Glu Leu Phe Leu Asp Thr Ala  
 405 410 415  
 Gly Val Ala Ser Phe Asp Val Trp Asp Leu Leu Pro Phe Thr Arg Gly  
 420 425 430  
 Tyr Val His Ile Leu Asp Lys Asp Pro Tyr Leu Arg His Phe Ala Tyr  
 435 440 445  
 Asp Pro Gln Tyr Phe Leu Asn Glu Leu Asp Leu Leu Gly Gln Ala Ala

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

Tyr Ala Ser

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 <223> Xaa is Ser, Ala, Cys, Ile, Asn, Arg, Asp, Thr, Val, Tyr, Glu, His, Met or Gln  
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 <222> (349)..(349)  
 <223> Xaa is Phe, Ala, Leu, Trp or Tyr, provided that when Xaa108 is Thr, then Xaa349 is not Phe  
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 Gly Ile Glu Ala Ser Leu Leu Thr Asp Pro Lys Glu Val Ala Gly Arg  
 1 5 10 15  
 Thr Val Asp Tyr Ile Ile Ala Gly Gly Gly Leu Thr Gly Leu Thr Thr  
 20 25 30  
 Ala Ala Arg Leu Thr Glu Asn Pro Asp Ile Thr Val Leu Val Ile Glu  
 35 40 45  
 Ser Gly Ser Tyr Glu Ser Asp Arg Gly Pro Ile Ile Glu Asp Leu Asn  
 50 55 60  
 Ala Tyr Gly Asp Ile Phe Gly Ser Ser Val Asp His Ala Tyr Glu Thr  
 65 70 75 80  
 Val Glu Leu Ala Thr Asn Asn Gln Thr Ala Leu Ile Arg Ser Gly Asn  
 85 90 95  
 Gly Leu Gly Gly Ser Thr Leu Val Asn Gly Gly Xaa Trp Thr Arg Pro  
 100 105 110  
 His Lys Ala Gln Val Asp Ser Trp Glu Thr Val Phe Gly Asn Glu Gly  
 115 120 125  
 Trp Asn Trp Asp Ser Val Ala Tyr Ser Leu Gln Ala Glu Arg Ala  
 130 135 140  
 Arg Ala Pro Asn Ala Lys Gln Ile Ala Ala Gly His Tyr Phe Asn Ala  
 145 150 155 160  
 Ser Cys His Gly Ile Asn Gly Thr Val His Ala Gly Pro Arg Asp Thr  
 165 170 175  
 Gly Asp Asp Tyr Ser Pro Ile Val Lys Ala Leu Met Ser Ala Val Glu  
 180 185 190  
 Asp Arg Gly Val Pro Thr Lys Lys Asp Leu Gly Cys Gly Asp Pro His  
 195 200 205  
 Gly Val Ser Met Phe Pro Asn Thr Leu His Glu Asp Gln Val Arg Ser  
 210 215 220  
 Asp Ala Ala Arg Glu Trp Leu Leu Pro Asn Tyr Gln Arg Pro Asn Leu  
 225 230 235 240  
 Gln Val Leu Thr Gly Gln Tyr Val Gly Lys Val Leu Leu Ser Gln Asn  
 245 250 255  
 Ala Thr Thr Pro Arg Ala Val Gly Val Glu Phe Gly Thr His Lys Gly  
 260 265 270  
 Asn Thr His Asn Val Tyr Ala Lys His Glu Val Leu Leu Ala Ala Gly  
 275 280 285

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

<210> 17  
 <211> 605  
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 <222> (132)..(132)  
 <223> Xaa is Ser, Ala, Cys, Ile, Asn, Arg, Asp, Thr, Val, Tyr, Glu, His, Met or  
 Gln  
 <220>  
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 <222> (373)..(373)  
 <223> Xaa is Phe, Ala, Leu, Trp or Tyr, provided that when Xaa132 is Thr, then  
 Xaa373 is not Phe  
 <400> 17

Met Gln Thr Leu Leu Val Ser Ser Leu Val Val Ser Leu Ala Ala Ala  
 1 5 10 15  
 Leu Pro His Tyr Ile Arg Ser Asn Gly Ile Glu Ala Ser Leu Leu Thr  
 20 25 30  
 Asp Pro Lys Asp Val Ser Gly Arg Thr Val Asp Tyr Ile Ile Ala Gly  
 35 40 45  
 Gly Gly Leu Thr Gly Leu Thr Thr Ala Ala Arg Leu Thr Glu Asn Pro  
 50 55 60  
 Asn Ile Ser Val Leu Val Ile Glu Ser Gly Ser Tyr Glu Ser Asp Arg  
 65 70 75 80  
 Gly Pro Ile Ile Glu Asp Leu Asn Ala Tyr Gly Asp Ile Phe Gly Ser  
 85 90 95  
 Ser Val Asp His Ala Tyr Glu Thr Val Glu Leu Ala Thr Asn Asn Gln  
 100 105 110  
 Thr Ala Leu Ile Arg Ser Gly Asn Gly Leu Gly Gly Ser Thr Leu Val

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Asn	Gly	115	Xaa	Trp	Thr	Arg	120	Pro	His	Lys	Ala	Gln	125	Val	Asp	Ser	Trp
130	130	Gly				135	135					140	140				
Glu	Thr	Val	Phe	Gly	Asn	Glu	Gly	Trp	Asn	Trp	Asp	Asn	Val	Ala	Ala	Ala	Ala
145	145				150	150				155	155					160	160
Tyr	Ser	Leu	Gln	Ala	Glu	Arg	Ala	Arg	Ala	Pro	Asn	Ala	Lys	Gln	Ile	Ile	Ile
				165					170							175	175
Ala	Ala	Gly	His	Tyr	Phe	Asn	Ala	Ser	Cys	His	Gly	Val	Asn	Gly	Thr	Thr	Thr
			180					185					190				
Val	His	Ala	Gly	Pro	Arg	Asp	Thr	Gly	Asp	Asp	Tyr	Ser	Pro	Ile	Val	Val	Val
		195					200					205					
Lys	Ala	Leu	Met	Ser	Ala	Val	Glu	Asp	Arg	Gly	Val	Pro	Thr	Lys	Lys	Lys	Lys
		210				215											
Asp	Phe	Gly	Cys	Gly	Asp	Pro	His	Gly	Val	Ser	Met	Phe	Pro	Asn	Thr	Thr	Thr
225	225				230					235						240	240
Leu	His	Glu	Asp	Gln	Val	Arg	Ser	Asp	Ala	Ala	Arg	Glu	Trp	Leu	Leu	Leu	Leu
				245					250						255		
Pro	Asn	Tyr	Gln	Arg	Pro	Asn	Leu	Gln	Val	Leu	Thr	Gly	Gln	Tyr	Val	Val	Val
			260					265									
Gly	Lys	Val	Leu	Leu	Ser	Gln	Asn	Gly	Thr	Thr	Pro	Arg	Ala	Val	Gly	Gly	Gly
		275					280					285					
Val	Glu	Phe	Gly	Thr	His	Lys	Gly	Asn	Thr	His	Asn	Val	Tyr	Ala	Lys	Lys	Lys
		290				295					300						
His	Glu	Val	Leu	Leu	Ala	Gly	Ser	Ala	Val	Val	Ser	Pro	Thr	Ile	Leu	Leu	Leu
305	305				310				315						320		
Glu	Tyr	Ser	Gly	Ile	Gly	Met	Lys	Ser	Ile	Leu	Glu	Pro	Leu	Gly	Ile	Ile	Ile
				325					330					335			
Asp	Thr	Val	Val	Asp	Leu	Pro	Val	Gly	Leu	Asn	Leu	Gln	Asp	Gln	Thr	Thr	Thr
			340					345					350				
Thr	Ala	Thr	Val	Arg	Ser	Arg	Ile	Thr	Ser	Ala	Gly	Ala	Gly	Gln	Gly	Gly	Gly
		355					360					365					
Gln	Ala	Ala	Trp	Xaa	Ala	Thr	Phe	Asn	Glu	Thr	Phe	Gly	Asp	Tyr	Ser	Ser	Ser
		370				375					380						
Glu	Lys	Ala	His	Glu	Leu	Asn	Thr	Lys	Leu	Glu	Gln	Trp	Ala	Glu	Glu	Glu	Glu
385	385				390				395							400	400
Glu	Ala	Val	Ala	Arg	Gly	Gly	Phe	His	Asn	Thr	Thr	Ala	Leu	Leu	Ile	Ile	Ile
			405						410					415			
Gln	Tyr	Glu	Asn	Tyr	Arg	Asp	Trp	Ile	Val	Asn	His	Asn	Val	Ala	Tyr	Tyr	Tyr
			420					425					430				
Ser	Glu	Leu	Phe	Leu	Asp	Thr	Ala	Gly	Val	Ala	Ser	Phe	Asp	Val	Trp	Trp	Trp
		435					440					445					
Asp	Leu	Leu	Pro	Phe	Asp	Arg	Gly	Tyr	Val	His	Ile	Leu	Asp	Lys	Asp	Asp	Asp
		450				455					460						
Pro	Tyr	Leu	His	His	Phe	Ala	Tyr	Asp	Pro	Gln	Tyr	Phe	Leu	Asn	Glu	Glu	Glu
465	465				470					475					480		
Leu	Asp	Leu	Leu	Gly	Gln	Ala	Ala	Ala	Thr	Gln	Leu	Ala	Arg	Asn	Ile	Ile	Ile
			485						490					495			
Ser	Asn	Ser	Gly	Ala	Met	Gln	Thr	Tyr	Phe	Ala	Gly	Glu	Ile	Leu	Pro	Pro	Pro
			500					505					510				
Gly	Asp	Asn	Leu	Ala	Tyr	Asp	Ala	Asp	Leu	Ser	Ala	Trp	Thr	Glu	Tyr	Tyr	Tyr
		515					520					525					
Ile	Pro	Tyr	His	Phe	Arg	Pro	Asn	Tyr	His	Asp	Val	Gly	Thr	Cys	Ser	Ser	Ser
						535					540						
Met	Met	Pro	Lys	Glu	Met	Gly	Ser	Val	Val	Asp	Asn	Ala	Ala	Arg	Val	Val	Val
545	545				550					555					560		
Tyr	Gly	Val	Arg	Gly	Leu	Arg	Val	Ile	Asp	Gly	Ser	Ile	Pro	Pro	Thr	Thr	Thr
				565					570					575			
Gln	Met	Ser	Ser	His	Val	Met	Thr	Val	Phe	Tyr	Ala	Met	Ala	Leu	Lys	Lys	Lys
			580					585					590				
Ile	Ser	Asp	Ala	Ile	Leu	Glu	Asp	Tyr	Ala	Ser	Met	Gln					
		595					600					605					

<210> 18  
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 <222> (108)..(108)

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<223> Xaa is Ser, Ala, Cys, Ile, Asn, Arg, Asp, Thr, Val, Tyr, Glu, His, Met or Gln

<220>

<221> MISC\_FEATURE

<222> (349)..(349)

<223> Xaa is Phe, Ala, Leu, Trp or Tyr, provided that when Xaa108 is Thr, then Xaa349 is not Phe

<400> 18

Gly	Ile	Glu	Ala	Ser	Leu	Leu	Thr	Asp	Pro	Lys	Glu	Ile	Ala	Gly	Cys
1				5					10					15	
Thr	Val	Asp	Tyr	Ile	Ile	Ala	Gly	Gly	Gly	Leu	Thr	Gly	Leu	Thr	Thr
		20					25						30		
Ala	Ala	Arg	Leu	Thr	Glu	Asn	Pro	Asp	Ile	Thr	Val	Leu	Val	Ile	Glu
		35					40					45			
Ser	Gly	Ser	Tyr	Glu	Ser	Asp	Arg	Gly	Pro	Ile	Ile	Glu	Asp	Leu	Asn
	50					55					60				
Ala	Tyr	Gly	Asp	Ile	Phe	Gly	Ser	Ser	Val	Asp	His	Ala	Tyr	Glu	Thr
65					70					75				80	
Val	Glu	Leu	Ala	Thr	Asn	Asn	Gln	Thr	Ala	Leu	Ile	Arg	Ser	Gly	Asn
				85					90					95	
Gly	Leu	Gly	Gly	Ser	Ser	Leu	Val	Asn	Gly	Gly	Xaa	Trp	Thr	Arg	Pro
			100					105					110		
His	Lys	Ala	Gln	Val	Asp	Ser	Trp	Glu	Thr	Val	Phe	Gly	Asn	Glu	Gly
		115					120					125			
Trp	Asn	Trp	Asp	Ser	Val	Ala	Ala	Tyr	Ser	Leu	Gln	Ala	Glu	Arg	Ala
	130					135					140				
Arg	Ala	Pro	Asn	Ala	Lys	Gln	Ile	Ala	Ala	Gly	His	Tyr	Phe	Asn	Ala
145					150					155					160
Ser	Cys	His	Gly	Ile	Asn	Gly	Thr	Val	His	Ala	Gly	Pro	Arg	Asp	Thr
				165					170					175	
Gly	Asp	Asp	Tyr	Ser	Pro	Ile	Val	Lys	Ala	Leu	Met	Ser	Ala	Val	Glu
			180					185					190		
Asp	Arg	Gly	Val	Pro	Thr	Lys	Lys	Asp	Leu	Gly	Cys	Gly	Asp	Pro	His
		195					200					205			
Gly	Val	Ser	Met	Phe	Pro	Asn	Thr	Leu	His	Glu	Asp	Gln	Val	Arg	Ser
	210					215					220				
Asp	Ala	Ala	Arg	Glu	Trp	Leu	Leu	Pro	Asn	Tyr	Gln	Arg	Pro	Asn	Leu
225					230					235					240
Gln	Val	Leu	Thr	Gly	Gln	Tyr	Val	Gly	Lys	Val	Leu	Leu	Ser	Gln	Asn
				245					250					255	
Ala	Thr	Thr	Pro	Arg	Ala	Ile	Gly	Val	Glu	Phe	Gly	Thr	His	Lys	Gly
			260					265					270		
Asn	Thr	His	Asn	Val	Tyr	Ala	Lys	His	Glu	Val	Leu	Leu	Ala	Ala	Gly
		275					280					285			
Ser	Ala	Val	Ser	Pro	Thr	Ile	Leu	Glu	Tyr	Ser	Gly	Ile	Gly	Met	Lys
	290					295					300				
Ser	Ile	Leu	Glu	Pro	Leu	Gly	Ile	Asp	Thr	Val	Val	Asp	Leu	Pro	Val
305					310					315					320
Gly	Leu	Asn	Leu	Gln	Asp	Gln	Thr	Thr	Ser	Thr	Val	Arg	Ser	Arg	Ile
				325					330					335	
Thr	Ser	Ala	Gly	Ala	Gly	Gln	Gly	Gln	Ala	Ala	Trp	Xaa	Ala	Thr	Phe
			340					345					350		
Asn	Glu	Thr	Leu	Gly	Asp	Tyr	Ala	Glu	Lys	Ala	His	Glu	Leu	Leu	Asn
		355					360					365			
Thr	Lys	Leu	Glu	Gln	Trp	Ala	Glu	Glu	Ala	Val	Ala	Arg	Gly	Gly	Phe
	370					375					380				
His	Asn	Thr	Thr	Ala	Leu	Leu	Ile	Gln	Tyr	Glu	Asn	Tyr	Arg	Asp	Trp
385					390					395					400
Ile	Val	Lys	Asp	Asn	Val	Ala	Tyr	Ser	Glu	Leu	Phe	Leu	Asp	Thr	Ala
				405					410					415	
Gly	Val	Ala	Ser	Phe	Gly	Val	Trp	Asp	Leu	Leu	Pro	Phe	Thr	Arg	Gly
			420					425					430		
Tyr	Val	His	Ile	Leu	Asp	Lys	Ala	Pro	Tyr	Leu	Arg	His	Phe	Ala	Tyr
		435					440					445			
Asp	Pro	Gln	Tyr	Phe	Leu	Asn	Glu	Leu	Asp	Leu	Leu	Gly	Gln	Ala	Ala
	450					455					460				
Ala	Thr	Gln	Leu	Ala	Arg	Asn	Ile	Ser	Asn	Ser	Gly	Ala	Met	Gln	Thr
465					470					475					480



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

<210> 19  
 <211> 604  
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 <213> Aspergillus niger  
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 <222> (131)..(131)  
 <223> Xaa is Ser, Ala, Cys, Ile, Asn, Arg, Asp, Thr, Val, Tyr, Glu, His, Met or Gln  
 <220>  
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 <222> (372)..(372)  
 <223> Xaa is Phe, Ala, Leu, Trp or Tyr, provided that when Xaa131 is Thr, then Xaa372 is not Phe  
 <400> 19

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

305 310 1384463 320  
 His Ser Gly Ile Gly Met Lys Ser Ile Leu Asp Thr Val Gly Ile Asp  
 Thr Val Val Asp Leu Pro Val Gly Leu Asn Leu Gln Asp Gln Thr Ile  
 Val Leu Val Ser Ser Arg Ile Thr Ser Ala Gly Ala Gly Gln Gly Gln  
 Val Ala Ile Xaa Ala Thr Phe Asn Glu Thr Phe Gly Asp Tyr Ala Pro  
 Gln Ala His Ala Leu Leu Asp Ala Lys Leu Glu Gln Trp Ala Glu Glu  
 Gly Val Ala Arg Gly Gly Phe His Asn Ala Thr Ala Leu Arg Ile Gln  
 Tyr Glu Asn Tyr Arg Asp Trp Leu Val Asn His Asn Val Ala Tyr Ser  
 Glu Leu Phe Leu Asp Thr Ala Gly Ala Val Ser Phe Thr Ile Trp Asp  
 Leu Ile Pro Phe Thr Arg Gly Tyr Val His Ile Thr Asp Ala Asp Pro  
 Tyr Leu Arg Leu Val Ser Tyr Asp Pro Gln Tyr Phe Leu Asn Glu Leu  
 Asp Leu Tyr Gly Gln Ala Ala Ala Ser Gln Leu Ala Arg Asn Leu Ser  
 Asn Thr Asp Ala Met Gln Thr Tyr Phe Ala Gly Glu Thr Thr Pro Gly  
 Asp Asn Pro Ala Tyr Asp Ala Ser Leu Ser Asp Trp Ala Glu Tyr Ile  
 Lys Tyr Asn Phe Arg Pro Asn Tyr His Gly Val Gly Thr Cys Ser Met  
 Met Lys Lys Glu Leu Gly Gly Val Val Asp Ser Ser Ala Arg Val Tyr  
 Gly Val Asp Ser Leu Arg Val Ile Asp Gly Ser Ile Pro Pro Thr Gln  
 Val Ser Ser His Val Met Thr Val Phe Tyr Ala Met Ala Leu Lys Ile  
 Ser Ala Ala Ile Leu Ala Asp Tyr Ala Ser Ser Gln  
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<210> 20

<211> 619

<212> PRT

<213> Sclerotinia sclerotiorum

<220>

<221> MISC\_FEATURE

<222> (130)..(130)

<223> Xaa is Ser, Ala, Cys, Ile, Asn, Arg, Asp, Thr, Val, Tyr, Glu, His, Met or Gln

<220>

<221> MISC\_FEATURE

<222> (373)..(373)

<223> Xaa is Phe, Ala, Leu, Trp or Tyr, provided that when Xaa130 is Thr, then Xaa373 is not Phe

<400> 20

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 1 5 10 15  
 Ile Ala Ala Ser Pro Pro Pro Asp Leu Ser Cys Ile Ile Asp Asp Pro  
 20 25 30  
 Tyr Lys Ile Lys Asn Ala Thr Phe Asp Tyr Ile Val Ala Gly Gly Gly  
 35 40 45  
 Leu Thr Gly Leu Thr Ala Ala Ile Leu Ser Lys Asn Pro Asn Ile  
 50 55 60  
 Ser Val Leu Val Ile Glu Ala Gly Phe Tyr Glu Ser Asp Gln Gly Pro  
 65 70 75 80  
 Leu Val Glu Asp Val Asn Glu Tyr Gly Lys Ile Phe Gly Ser Thr Val  
 85 90 95  
 Asp Trp Ala Phe Glu Thr Leu Asn Gln Thr Ala Asp Ile Pro Gln Gln  
 100 105 110  
 Thr Ile Arg Ser Gly Arg Gly Leu Gly Gly Ser Thr Leu Ile Asn Gly  
 115 120 125

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 Ala Xaa Trp Thr Arg Pro His Lys Ile Gln Val Asp Ser Trp Glu Lys  
 130 140  
 Val Phe Gly Asn Thr Gly Trp Asn Trp Asn Asn Phe Ser Thr Tyr Met  
 145 150 155 160  
 Lys Ser Ala Glu Asp Val Arg Lys Pro Asn Asp Ala Glu Ile Arg Ala  
 165 170 175  
 Gly His Asn Phe Ile Ser Glu Cys His Gly Lys His Gly Pro Val His  
 180 185 190  
 Val Gly Pro Arg Asn Thr Arg Ala His Tyr Ser Pro Leu Met Lys Ala  
 195 200 205  
 Leu Met Asp Thr Val Ala Leu Ser Gly Ile Pro Thr Lys Arg Asp Phe  
 210 215 220  
 Ser Cys Gly Asn Pro His Gly Val Ser Met Phe Pro Asn Ser Leu His  
 225 230 235 240  
 Ala Asn Trp Asn Gln Thr Arg Ser Asp Ala Gly Arg Glu Met Leu Leu  
 245 250 255  
 Pro Ser Cys Ser Arg Ser Asn Leu Lys Val Leu Val Gly Gln Val Val  
 260 265 270  
 Gly Lys Val Leu Leu Asn Ser Gln Pro Glu Ala Ile Gln Ala His Gly  
 275 280 285  
 Val Gln Phe Gly Thr Asn Arg His Ser Asn Phe Glu Val Tyr Ala Arg  
 290 295 300  
 His Glu Val Leu Leu Ala Gly Ala Leu Ser Ser Pro Leu Ile Leu  
 305 310 315 320  
 Glu Tyr Ser Gly Ile Gly Ile Lys Lys Val Leu Glu Asn Ala Asn Val  
 325 330 335  
 Ser Gln Val Leu Glu Leu Pro Val Gly Ile Asn Val Gln Asp Gln Thr  
 340 345 350  
 Thr Thr Thr Val Arg Ser Glu Ile Asn Asp Leu Gly Tyr Gln Gly  
 355 360 365  
 Gln Ala Ile Tyr Xaa Ala Thr Phe Asn Glu Thr Phe Gly Lys Tyr Ser  
 370 375 380  
 Ser Leu Ala His Asn Leu Leu Asn Lys Asn Leu Lys Arg Trp Ala Arg  
 385 390 395 400  
 Glu Thr Val Asp Asn Gly Gly Phe Asn Asn Ile Thr Ala Leu Ile Ile  
 405 410 415  
 Gln Tyr Glu Asn Tyr Arg Asp Trp Leu Thr Lys Asp Asn Ile Ala Tyr  
 420 425 430  
 Ser Glu Leu Phe Met Asp Thr Glu Gly Ala Ile Asn Phe Asp Leu Trp  
 435 440 445  
 Thr Leu Ile Pro Phe Thr Arg Gly Phe Val His Ile Leu His Arg Asp  
 450 455 460  
 Pro Tyr Leu Arg His Val Met Thr Asn Pro Arg Tyr Phe Gly Asn Glu  
 465 470 475 480  
 Leu Asp Ile Leu Gly Gln Ala Ala Ala Ser Lys Leu Ala Arg Asp Leu  
 485 490 495  
 Ser Asp Ala Gly Ser Met Ala Arg Phe Tyr Glu Lys Glu Val Ile Pro  
 500 505 510  
 Gly Ala Thr Lys Leu Lys Pro Asp Ala Asn Leu Asp Glu Trp Ile Ser  
 515 520 525  
 Tyr Val Lys Gln Asn Phe Arg Pro Asn Tyr His Asn Val Gly Ser Cys  
 530 535 540  
 Ser Met Met Ala Arg Glu Leu Gly Gly Val Val Asn Pro Gln Gly Lys  
 545 550 555 560  
 Val Tyr Asp Val His Gly Leu Arg Val Ile Asp Ala Ser Val Val Pro  
 565 570 575  
 Thr Gln Val Ser Ala His Ile Met Thr Val Leu Tyr Gly Met Ala Val  
 580 585 590  
 Lys Ile Ser Ala Asp Ile Met Val Asp Tyr His Val Lys Met Glu Lys  
 595 600 605  
 Ser Met Leu Glu Thr Ala Lys Leu Glu Leu Lys  
 610 615  
 <210> 21  
 <211> 655  
 <212> PRT  
 <213> Aspergillus niger  
 <220>  
 <221> MISC\_FEATURE

<222> (163)..(163)  
 <223> Xaa is Ser, Ala, Cys, Ile, Asn, Arg, Asp, Thr, Val, Tyr, Glu, His, Met or Gln  
 <220>  
 <221> MISC\_FEATURE  
 <222> (422)..(422)  
 <223> Xaa is Phe, Ala, Leu, Trp or Tyr, provided that when Xaa163 is Thr, then Xaa422 is not Phe  
 <220>  
 <221> MISC\_FEATURE  
 <222> (441)..(441)  
 <223> Xaa is any amino acid  
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 Ala Glu His Phe Gln Val Pro Leu Gln His Thr Ile Ser Pro Cys Ser  
 20 25 30  
 Thr Lys Pro His Thr Ser His Asp Asp Leu Asn His Asn Ile Asn Thr  
 35 40 45  
 Ile Pro His Gly Ile Thr Asp Asp Pro Arg Ser Ile Asp Asn Gln Thr  
 50 55 60  
 Phe Asp Tyr Ile Ile Ala Gly Gly Gly Leu Thr Gly Leu Thr Leu Ala  
 65 70 75 80  
 Ala Lys Leu Val Glu Gln Lys Lys Tyr Thr Val Leu Val Ile Glu Ser  
 85 90 95  
 Gly Phe Tyr Ala Trp Glu Tyr Gly Pro Lys Ile Asp Asp Leu Asn Thr  
 100 105 110  
 Tyr Gly Gln Val Phe Gly Ser Ser Val Asp His Ala Tyr Glu Thr Ser  
 115 120 125  
 Pro Gln Leu Val Gly Asn Asp Gly Glu Thr Gly Leu Asp Lys Asp Ile  
 130 135 140  
 Arg Ile Val Arg Ser Gly Asn Gly Leu Gly Gly Ser Thr Leu Ile Asn  
 145 150 155 160  
 Gly Gly Xaa Trp Thr Arg Pro His Lys Ser Gln Leu Asp Ser Trp Glu  
 165 170 175  
 Glu Val Phe Gly Asn Thr Gly Trp Asn Trp Asp Ala Leu Lys Gly Lys  
 180 185 190  
 Met Asp Glu Ile Glu Val Pro Arg Asp Pro Thr Ser Asp Asp Ile Thr  
 195 200 205  
 Lys Gly Ser Phe His Lys Phe Asp Ala Glu Cys His Asn Lys Glu Pro  
 210 215 220  
 Glu Lys Gly Lys Val Lys Val Gly Ala Arg Asp Arg Lys Tyr Gly Trp  
 225 230 235 240  
 Ser Pro Leu Ile Arg Ala Leu Met His Thr Val Asn Ser Thr Tyr Glu  
 245 250 255  
 Glu Val Val Asn Gln Lys Asp Leu Cys Cys Gly Asp Pro Thr Gly Val  
 260 265 270  
 Ser Met Phe Leu Asn Thr Leu Thr Asn Glu Gln Ile Arg Thr Asp Ala  
 275 280 285  
 Ala Arg Ser Trp Leu Lys Pro Ile Leu Asp Asp Asp Glu Leu Lys Gln  
 290 295 300  
 Tyr Ile Thr Val Leu Thr Gly Glu Leu Val Gly Lys Val His Leu Asn  
 305 310 315 320  
 Glu Ala Asn Pro Ser Glu Thr Gly Thr Glu Phe Lys Ala Lys Gly Val  
 325 330 335  
 Glu Phe Gly Val His Lys Lys Gln Glu Trp Lys Trp Asp Ala Trp Ala  
 340 345 350  
 Arg Lys Glu Val Leu Leu Ala Ala Gly Ser Thr Ile Ser Pro Leu Ile  
 355 360 365  
 Leu Gln Trp Ser Gly Ile Gly Pro Lys Val Trp Leu Asp Ala Ala Gly  
 370 375 380  
 Ile Glu His Lys Leu Glu Leu Pro Val Gly Tyr Asn Leu Gln Asp Gln  
 385 390 395 400  
 Thr Thr Thr Ser Val Val Thr Lys Pro Lys Pro Glu Ala Asn Gly Gln  
 405 410 415  
 Gly Gln Ala Ala Tyr Xaa Ala Thr Phe Ala Glu Ile Phe Gly Lys Asp  
 420 425 430  
 Ala Ser Asp Met Glu Lys Leu Leu Xaa Asp Asp Thr Glu Leu Asp Lys

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Trp	Ala	435	Glu	His	Thr	Val	Asn	440	Gly	His	Gly	Phe	Pro	445	Asp	Lys	Ala	Asn
450	Leu	Leu	Lys	Gln	Tyr	Lys	Asn	455	Tyr	Arg	Asp	Trp	Leu	460	Leu	Leu	Thr	Asp
465	Val	Ser	Tyr	Ala	Glu	470	Leu	Phe	Leu	Asp	Thr	475	Asp	Asn	Ser	Thr	His	480
485	Asp	Leu	Trp	Asn	Leu	Ile	Pro	Phe	Thr	490	Arg	Gly	Tyr	Val	Lys	Ile	Leu	495
500	Asp	Asn	Asp	Pro	Tyr	Leu	Arg	Ser	Phe	505	Glu	Tyr	Asn	Pro	Arg	Tyr	Phe	510
515	Glu	Asn	Ile	Leu	Asp	Leu	Asn	Gly	Gln	520	Ala	Ala	Ala	Thr	Arg	Leu	Ala	525
530	Arg	Gln	Leu	Thr	Asn	Thr	535	Tyr	Asp	Met	Lys	Gln	Tyr	Val	Asp	Lys	Glu	540
545	Gln	Val	Pro	Gly	Arg	Tyr	Val	Pro	Glu	550	Asn	Ala	Asn	Leu	Thr	Glu	Trp	555
560	Ala	Asp	Tyr	Val	Lys	Gln	Asn	Tyr	Arg	565	Ala	Asn	Tyr	His	Gly	Val	Gly	570
575	Thr	Cys	Ser	Met	Met	Lys	Lys	Glu	Leu	580	Gly	Gly	Val	Val	Asp	Pro	Glu	585
590	Ala	Lys	Val	Tyr	Gly	Val	Glu	Gly	Leu	595	Arg	Val	Val	Asp	Gly	Ser	Ile	600
605	Pro	Pro	Thr	Gln	Val	Ser	610	Ser	His	Val	Met	Thr	Val	Phe	Tyr	Ala	Met	615
620	625	Ala	Val	Lys	Ile	Ala	625	Glu	Ser	Val	Ile	Lys	Asp	Ala	Gly	Asn	Ala	630
635	640	645																650

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 <220>  
 <223> primer for point mutation  
 <400> 22  
 cttgataaac ggtgacgcgt ggactcgccc  
 <210> 23  
 <211> 30  
 <212> DNA  
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 <223> primer for point mutation  
 <400> 23  
 gggcgagtcc acgcgtcacc gtttatcaag  
 <210> 24  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> primer for point mutation  
 <400> 24  
 caggcgtct tcgcggccaa ttctactgag  
 <210> 25  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
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 <223> primer for point mutation  
 <400> 25  
 ctcaagtgaat ttggccgcga agacggcctg  
 <210> 26  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> primer for point mutation  
 <400> 26  
 gtcaggcgt cttcctggcc aatttactg ag  
 <210> 27

30

30

30

30

32

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<211> 32
<212> DNA
<213> Artificial Sequence
<220>
<223> primer for point mutation
<400> 27
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<210> 28
<211> 30
<212> DNA
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<223> primer for point mutation
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caggccgtct tcccggccaa tttcactgag
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ctcagtgtgaaa ttggccggga agacggcctg
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<223> primer for point mutation
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caggccgtct tctacgccaa tttcac
<210> 33
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<212> DNA
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<223> primer for point mutation
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gtgaaattgg cgtagaagac ggcctg

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