

SEQUENCE LISTING

<110> GlaxoSmithKline LLC

<120> HOST CELLS AND METHODS OF USE

<130> PU65411

<150> 61/773329

<151> 2013-03-06

<160> 10

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 651

<212> PRT

<213> Artificial Sequence

<220>

<223> heterologous polypeptide

<400> 1

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

PU65411PCT

			260					265				270					
Ala	Trp	Ala	Val	Ala	Arg	Leu	Ser	Gln	Arg	Phe	Pro	Lys	Ala	Glu	Phe		
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Ala	Glu	Val	Ser	Lys	Leu	Val	Thr	Asp	Leu	Thr	Lys	Val	His	Thr	Glu		
	290					295					300						
Cys	Cys	His	Gly	Asp	Leu	Leu	Glu	Cys	Ala	Asp	Asp	Arg	Ala	Asp	Leu		
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Ala	Lys	Tyr	Ile	Cys	Glu	Asn	Gln	Asp	Ser	Ile	Ser	Ser	Lys	Leu	Lys		
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Glu	Cys	Cys	Glu	Lys	Pro	Leu	Leu	Glu	Lys	Ser	His	Cys	Ile	Ala	Glu		
			340					345					350				
Val	Glu	Asn	Asp	Glu	Met	Pro	Ala	Asp	Leu	Pro	Ser	Leu	Ala	Ala	Asp		
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Phe	Val	Glu	Ser	Lys	Asp	Val	Cys	Lys	Asn	Tyr	Ala	Glu	Ala	Lys	Asp		
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Tyr	Ser	Val	Val	Leu	Leu	Leu	Arg	Leu	Ala	Lys	Thr	Tyr	Glu	Thr	Thr		
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Leu	Glu	Lys	Cys	Cys	Ala	Ala	Ala	Asp	Pro	His	Glu	Cys	Tyr	Ala	Lys		
			420					425					430				
Val	Phe	Asp	Glu	Phe	Lys	Pro	Leu	Val	Glu	Glu	Pro	Gln	Asn	Leu	Ile		
	435					440						445					
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Asn	Ala	Leu	Leu	Val	Arg	Tyr	Thr	Lys	Lys	Val	Pro	Gln	Val	Ser	Thr		
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Pro	Thr	Leu	Val	Glu	Val	Ser	Arg	Asn	Leu	Gly	Lys	Val	Gly	Ser	Lys		
			485					490					495				
Cys	Cys	Lys	His	Pro	Glu	Ala	Lys	Arg	Met	Pro	Cys	Ala	Glu	Asp	Tyr		
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Leu	Ser	Val	Val	Leu	Asn	Gln	Leu	Cys	Val	Leu	His	Glu	Lys	Thr	Pro		
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Val	Ser	Asp	Arg	Val	Thr	Lys	Cys	Cys	Thr	Glu	Ser	Leu	Val	Asn	Arg		
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Arg	Pro	Cys	Phe	Ser	Ala	Leu	Glu	Val	Asp	Glu	Thr	Tyr	Val	Pro	Lys		
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Glu	Phe	Asn	Ala	Glu	Thr	Phe	Thr	Phe	His	Ala	Asp	Ile	Cys	Thr	Leu		
			565					570					575				
Ser	Glu	Lys	Glu	Arg	Gln	Ile	Lys	Lys	Gln	Thr	Ala	Leu	Val	Glu	Leu		
			580					585					590				
Val	Lys	His	Lys	Pro	Lys	Ala	Thr	Lys	Glu	Gln	Leu	Lys	Ala	Val	Met		
	595					600						605					
Asp	Asp	Phe	Ala	Ala	Phe	Val	Glu	Lys	Cys	Cys	Lys	Ala	Asp	Asp	Lys		
	610					615					620						
Glu	Thr	Cys	Phe	Ala	Glu	Glu	Gly	Lys	Lys	Leu	Val	Ala	Ala	Ser	Gln		
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<210> 2

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> albumin fusion protein

PU65411PCT

<220>
 <221> VARIANT
 <222> 31
 <223> Xaa = Any Amino Acid

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 <213> Artificial Sequence

<220>
 <223> S. cerevisiae

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 agcaatgaaa cattatcccg cttggaggaa atgcatccaa attggaaata tgaacatgat 180
 gttcgagggc taccaaacca ttatgttttt tcaaaagagt tgctaaaatt gggcaaaaaga 240
 tcatcattag aagagttaca gggggataac aacgaccaca tattatctgt ccatgattta 300
 ttcccgcgta acgacctatt taagagacta ccggtgcctg ctccaccaat ggactcaagc 360
 ttgttaccgg taaaagaagc tgaggataaa ctacagcataa atgatccgct ttttgagagg 420
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 aatgttaacg cacaacctg gttttacctg ccaacattgt atgtttccca gtccacaaac 1440
 tccacggaag agacattaga atccgtcata accatatcag aaaaaagtct tcaagatgct 1500
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 gaaactttcg tctttggaaa cgataaagag gaggttgaac cagctgctac agaaagtacc 1860
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 tcaaggagaa ggatcagaag gtcaagagcg gaaacgtatg aattcgatat cattgataca 2160
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PU65411PCT

gaaaacggtg	atgctgaaca	tacaattgat	agtgtactaa	caaacgaaaa	tccatttagt	2340
gaccctataa	agcaaaagtt	cccaaatgac	gccaacgcag	aatctgcttc	caataaatta	2400
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 $\langle 210 \rangle$ 4

<211> 814

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> S. cerevisiae

<400> 4

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

His 370	Ser	Ser	Asp	Ile	Asn	Gly 375	Arg	Cys	Ser	Asn	Ser 380	His	Gly	Gly	Thr
Ser 385	Ala	Ala	Ala	Pro	Leu 390	Ala	Ala	Gly	Val	Tyr 395	Thr	Leu	Leu	Leu	Glu 400
Ala	Asn	Pro	Asn	Leu 405	Thr	Trp	Arg	Asp	Val 410	Gln	Tyr	Leu	Ser	Ile	Leu
Ser	Ala	Val	Gly 420	Leu	Glu	Lys	Asn	Ala 425	Asp	Gly	Asp	Trp	Arg	Asp	Ser
Ala	Met	Gly 435	Lys	Lys	Tyr	Ser	His 440	Arg	Tyr	Gly	Phe	Gly	Lys	Ile	Asp
Ala	His 450	Lys	Leu	Ile	Glu	Met 455	Ser	Lys	Thr	Trp	Glu	Asn	Val	Asn	Ala
Gln 465	Thr	Trp	Phe	Tyr	Leu 470	Pro	Thr	Leu	Tyr	Val 475	Ser	Gln	Ser	Thr	Asn
Ser	Thr	Glu	Glu	Thr 485	Leu	Glu	Ser	Val	Ile 490	Thr	Ile	Ser	Glu	Lys	Ser
Leu	Gln	Asp	Ala 500	Asn	Phe	Lys	Arg	Ile 505	Glu	His	Val	Thr	Val	Thr	Val
Asp	Ile	Asp 515	Thr	Glu	Ile	Arg	Gly 520	Thr	Thr	Thr	Val	Asp 525	Leu	Ile	Ser
Pro	Ala 530	Gly	Ile	Ile	Ser	Asn 535	Leu	Gly	Val	Val	Arg 540	Pro	Arg	Asp	Val
Ser 545	Ser	Glu	Gly	Phe	Lys 550	Asp	Trp	Thr	Phe	Met 555	Ser	Val	Ala	His	Trp 560
Gly	Glu	Asn	Gly 565	Val	Gly	Asp	Trp	Lys	Ile 570	Lys	Val	Lys	Thr	Thr	Glu
Asn	Gly	His	Arg 580	Ile	Asp	Phe	His	Ser 585	Trp	Arg	Leu	Lys	Leu	Phe	Gly
Glu	Ser	Ile 595	Asp	Ser	Ser	Lys	Thr 600	Glu	Thr	Phe	Val	Phe 605	Gly	Asn	Asp
Lys	Glu 610	Glu	Val	Glu	Pro	Ala 615	Ala	Thr	Glu	Ser	Thr 620	Val	Ser	Gln	Tyr
Ser 625	Ala	Ser	Ser	Thr	Ser 630	Ile	Ser	Ile	Ser	Ala 635	Thr	Ser	Thr	Ser	Ser
Ile	Ser	Ile	Gly 645	Val	Glu	Thr	Ser	Ala	Ile 650	Pro	Gln	Thr	Thr	Thr	Ala
Ser	Thr	Asp	Pro 660	Asp	Ser	Asp	Pro	Asn 665	Thr	Pro	Lys	Lys	Leu	Ser	Ser
Pro	Arg 675	Gln	Ala	Met	His	Tyr	Phe 680	Leu	Thr	Ile	Phe 685	Leu	Ile	Gly	Ala
Thr	Phe 690	Leu	Val	Leu	Tyr	Phe 695	Met	Phe	Phe	Met	Lys 700	Ser	Arg	Arg	Arg
Ile 705	Arg	Arg	Ser	Arg	Ala 710	Glu	Thr	Tyr	Glu	Phe 715	Asp	Ile	Ile	Asp	Thr
Asp	Ser	Glu	Tyr 725	Asp	Ser	Thr	Leu	Asp	Asn 730	Gly	Thr	Ser	Gly	Ile	Thr
Glu	Pro	Glu	Glu 740	Val	Glu	Asp	Phe	Asp 745	Phe	Asp	Leu	Ser	Asp	Glu	Asp
His	Leu 755	Ala	Ser	Leu	Ser	Ser	Ser 760	Glu	Asn	Gly	Asp 765	Ala	Glu	His	Thr
Ile	Asp 770	Ser	Val	Leu	Thr	Asn 775	Glu	Asn	Pro	Phe	Ser 780	Asp	Pro	Ile	Lys
Gln 785	Lys	Phe	Pro	Asn	Asp 790	Ala	Asn	Ala	Glu	Ser 795	Ala	Ser	Asn	Lys	Leu
Gln	Glu	Leu	Gln 805	Pro	Asp	Val	Pro	Pro	Ser 810	Ser	Gly	Arg	Ser		

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 <213> Artificial Sequence

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 <223> *S. cerevisiae*

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 aaaaacatta ccttggccca gatcgactgt actgaaaacc aggatctgtg tatggaacac 300
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 aagctttcta tttacttgcc ctccgccatg gacgagcctg tagtatacaa cggttaagaaa 660
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 tttggtgaaa tcgacggttc cgttttcgcc caatacgtcg aaagcggttt gcctttgggt 780
 tacttattct acaatgacga ggaagaattg gaagaataca agcctctctt taccgagttg 840
 gccaaaaaga acagaggctt aatgaacttt gttagcatcg atgccagaaa attcggcaga 900
 cacgccggca acttgaacat gaaggaacaa ttccctctat ttgccatcca cgacatgact 960
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 aagatcgtgt tggagtctaa ggctattgaa tctttggtta aggacttctt gaaaggtgat 1080
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 tactatgccc catggtgtgg tcaactgtaag agattggccc caacttacca agaactagct 1260
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 aagtccgaat ctgttggtga ccaaggttca agatccttgg actctttatt cgacttcac 1440
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<210> 6
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 <212> PRT
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<220>
 <223> *S. cerevisiae*

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

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Glu	Ala	Ile	Val	Gln	Phe	Met	Ile	Lys	Gln	Ser	Gln	Pro	Ala	Val	Ala	
		130				135					140					
Val	Val	Ala	Asp	Leu	Pro	Ala	Tyr	Leu	Ala	Asn	Glu	Thr	Phe	Val	Thr	
145					150					155					160	
Pro	Val	Ile	Val	Gln	Ser	Gly	Lys	Ile	Asp	Ala	Asp	Phe	Asn	Ala	Thr	
				165					170					175		
Phe	Tyr	Ser	Met	Ala	Asn	Lys	His	Phe	Asn	Asp	Tyr	Asp	Phe	Val	Ser	
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Ala	Glu	Asn	Ala	Asp	Asp	Asp	Phe	Lys	Leu	Ser	Ile	Tyr	Leu	Pro	Ser	
		195					200					205				
Ala	Met	Asp	Glu	Pro	Val	Val	Tyr	Asn	Gly	Lys	Lys	Ala	Asp	Ile	Ala	
		210				215					220					
Asp	Ala	Asp	Val	Phe	Glu	Lys	Trp	Leu	Gln	Val	Glu	Ala	Leu	Pro	Tyr	
225					230					235					240	
Phe	Gly	Glu	Ile	Asp	Gly	Ser	Val	Phe	Ala	Gln	Tyr	Val	Glu	Ser	Gly	
				245					250					255		
Leu	Pro	Leu	Gly	Tyr	Leu	Phe	Tyr	Asn	Asp	Glu	Glu	Glu	Leu	Glu	Glu	
			260					265					270			
Tyr	Lys	Pro	Leu	Phe	Thr	Glu	Leu	Ala	Lys	Lys	Asn	Arg	Gly	Leu	Met	
		275					280					285				
Asn	Phe	Val	Ser	Ile	Asp	Ala	Arg	Lys	Phe	Gly	Arg	His	Ala	Gly	Asn	
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		370				375					380					
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Tyr	Tyr	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Arg	Leu	Ala	Pro	Thr	Tyr	
			405					410						415		
Gln	Glu	Leu	Ala	Asp	Thr	Tyr	Ala	Asn	Ala	Thr	Ser	Asp	Val	Leu	Ile	
			420					425					430			
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Val	Val	Tyr	Gln	Gly	Ser	Arg	Ser	Leu	Asp	Ser	Leu	Phe	Asp	Phe	Ile	
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<210> 7

<211> 1692

<212> DNA

<213> Artificial Sequence

<220>

<223> *S. cerevisiae*

<400> 7

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<211> 563

<212> PRT

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<223> *S. cerevisiae*

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Ala Phe Asn Asp Thr His Phe Cys Lys Val Asp Arg Asn Asp His Val
35           40           45
Ser Pro Ser Cys Asn Val Thr Phe Asn Glu Leu Asn Ala Ile Asn Glu
50           55           60
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65           70           75           80
Tyr Phe Arg Leu Asp Leu Tyr Lys Gln Cys Ser Phe Trp Asp Ala Asn
85           90           95
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	290					295					300				
Lys	Met	Asp	Asn	Val	Ile	Ser	Gln	Leu	Asp	Thr	Lys	Ile	Phe	Asn	Glu
305					310					315					320
Asp	Leu	Val	Phe	Ala	Asn	Asp	Leu	Ser	Leu	Thr	Leu	Lys	Asp	Glu	Phe
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Arg	Ser	Arg	Phe	Lys	Asn	Val	Thr	Lys	Ile	Met	Asp	Cys	Val	Gln	Cys
			340					345					350		
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		355					360					365			
Ala	Leu	Lys	Ile	Leu	Phe	Glu	Ile	Asn	Asp	Ala	Asp	Glu	Phe	Thr	Lys
	370					375					380				
Gln	His	Ile	Val	Gly	Lys	Leu	Thr	Lys	Tyr	Glu	Leu	Ile	Ala	Leu	Leu
385					390					395					400
Gln	Thr	Phe	Gly	Arg	Leu	Ser	Glu	Ser	Ile	Glu	Ser	Val	Asn	Met	Phe
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Glu	Lys	Met	Tyr	Gly	Lys	Arg	Leu	Asn	Gly	Ser	Glu	Asn	Arg	Leu	Ser
			420					425					430		
Ser	Phe	Phe	Gln	Asn	Asn	Phe	Phe	Asn	Ile	Leu	Lys	Glu	Ala	Gly	Lys
		435					440					445			
Ser	Ile	Arg	Tyr	Thr	Ile	Glu	Asn	Ile	Asn	Ser	Thr	Lys	Glu	Gly	Lys
	450					455					460				
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PU65411PCT

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<212> PRT

<213> Artificial Sequence

<220>

<223> KEX2 leader sequence

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<223> KEX leader sequence

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Tyr	Ser	Gly	Ser	Leu	Asp	Lys	Arg								
				20											