

SEQUENCE LISTING

<110> Ghanshani, Sanjiv
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 Liu, Li
 Steward, Lance E.

<120> Methods of Intracellular Conversion of
 Single-Chain Proteins into their Di-chain Form

<130> 18469 (BOT)

<150> US 61/286,963

<151> 2010-01-25

<150> PCT/US11/22272

<151> 2011-01-24

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<170> FastSEQ for windows Version 4.0

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 Page 8

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 Gly Ile Gly Ile Phe Ser Ile Lys Asn Ile Val Ser Lys Asn Lys Tyr
 1205 1210 1215
 Cys Ser Gln Ile Phe Ser Ser Phe Arg Glu Asn Thr Met Leu Leu Ala
 1220 1225 1230
 Asp Ile Tyr Lys Pro Trp Arg Phe Ser Phe Lys Asn Ala Tyr Thr Pro
 1235 1240 1245
 Val Ala Val Thr Asn Tyr Glu Thr Lys Leu Leu Ser Thr Ser Ser Phe
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 Phe Asn Ile Met Lys Asn Ile Trp Ile Ile Pro Glu Arg Asn Val Ile
 35 40 45
 Gly Thr Thr Pro Gln Asp Phe His Pro Pro Thr Ser Leu Lys Asn Gly
 50 55 60
 Asp Ser Ser Tyr Tyr Asp Pro Asn Tyr Leu Gln Ser Asp Glu Glu Lys
 65 70 75 80
 Asp Arg Phe Leu Lys Ile Val Thr Lys Ile Phe Asn Arg Ile Asn Asn
 85 90 95
 Asn Leu Ser Gly Gly Ile Leu Leu Glu Glu Leu Ser Lys Ala Asn Pro
 100 105 110
 Tyr Leu Gly Asn Asp Asn Thr Pro Asp Asn Gln Phe His Ile Gly Asp
 115 120 125
 Ala Ser Ala Val Glu Ile Lys Phe Ser Asn Gly Ser Gln Asp Ile Leu
 130 135 140
 Leu Pro Asn Val Ile Ile Met Gly Ala Glu Pro Asp Leu Phe Glu Thr
 145 150 155 160
 Asn Ser Ser Asn Ile Ser Leu Arg Asn Asn Tyr Met Pro Ser Asn His
 165 170 175
 Gly Phe Gly Ser Ile Ala Ile Val Thr Phe Ser Pro Glu Tyr Ser Phe
 180 185 190
 Arg Phe Asn Asp Asn Ser Met Asn Glu Phe Ile Gln Asp Pro Ala Leu
 195 200 205
 Thr Leu Met His Glu Leu Ile His Ser Leu His Gly Leu Tyr Gly Ala
 210 215 220
 Lys Gly Ile Thr Thr Lys Tyr Thr Ile Thr Gln Lys Gln Asn Pro Leu
 225 230 235 240
 Ile Thr Asn Ile Arg Gly Thr Asn Ile Glu Glu Phe Leu Thr Phe Gly
 245 250 255
 Gly Thr Asp Leu Asn Ile Ile Thr Ser Ala Gln Ser Asn Asp Ile Tyr
 260 265 270
 Thr Asn Leu Leu Ala Asp Tyr Lys Lys Ile Ala Ser Lys Leu Ser Lys
 275 280 285
 Val Gln Val Ser Asn Pro Leu Asn Pro Tyr Lys Asp Val Phe Glu
 290 295 300
 Ala Lys Tyr Gly Leu Asp Lys Asp Ala Ser Gly Ile Tyr Ser Val Asn
 305 310 315 320
 Ile Asn Lys Phe Asn Asp Ile Phe Lys Lys Leu Tyr Ser Phe Thr Glu

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

865 Tyr Pro Thr Asn Lys 870 Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu Ser 880
 Glu Val Asn Ile 885 Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys Tyr 895
 Lys Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp Asn 910
 Lys Ile Val Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Arg 925
 Asp Asn Asn Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Ile Ile 940
 945 Trp Thr Leu Gln Asp Asn Ala Gly Ile Asn Gln Lys Leu Ala Phe Asn 955
 Tyr Gly Asn Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe 970
 Val Thr Ile Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn 985
 Gly Asn Leu Ile Asp Gln Lys Ser Ile Leu Asn Leu Gly Asn Ile His 990
 1010 Val Ser Asp Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Thr Arg 1005
 1025 Tyr Ile Gly Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp Glu 1035
 Thr Glu Ile Gln Thr Leu Tyr Ser Asn Glu Pro Asn Thr Asn Ile Leu 1050
 Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr Leu 1065
 Leu Asn Val Leu Lys Pro Asn Asn Phe Ile Asp Arg Arg Lys Asp Ser 1080
 1090 Thr Leu Ser Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn Arg 1100
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 Thr Asn Asp Asn Leu Val Arg Lys Asn Asp Gln Val Tyr Ile Asn Phe 1130
 Val Ala Ser Lys Thr His Leu Phe Pro Leu Tyr Ala Asp Thr Ala Thr 1145
 Thr Asn Lys Glu Lys Thr Ile Lys Ile Ser Ser Ser Gly Asn Arg Phe 1160
 1170 Asn Gln Val Val Val Met Asn Ser Val Gly Asn Asn Cys Thr Met Asn 1180
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 Asp Thr Val Val Ala Ser Thr Trp Tyr Tyr Thr His Met Arg Asp His 1210
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 35 40 45
 Arg Asn Thr Ile Gly Thr Asn Pro Ser Asp Phe Asp Pro Pro Ala Ser
 50 55 60
 Leu Lys Asn Gly Ser Ser Ala Tyr Tyr Asp Pro Asn Tyr Leu Thr Thr
 65 70 75 80
 Asp Ala Glu Lys Asp Arg Tyr Leu Lys Thr Thr Ile Lys Leu Phe Lys

Arg	Ile	Asn	Ser	85	Asn	Pro	Ala	Gly	Lys	90	Val	Leu	Leu	Gln	Glu	95	Ile	Ser
Tyr	Ala	Lys	100	Tyr	Leu	Gly	Asn	105	Asp	His	Thr	Pro	Ile	110	Asp	Glu	Phe	
Ser	Pro	Val	Thr	Arg	Thr	Thr	Ser	Val	Asn	Ile	Lys	Leu	Ser	Thr	Asn			
Val	Glu	Ser	Ser	Met	Leu	Leu	Asn	Leu	Val	140	Gly	Ala	Gly	Pro				
Asp	Ile	Phe	Glu	Ser	Cys	Cys	Tyr	Pro	Val	Arg	Lys	Leu	Ile	Asp	Pro			
Asp	Val	Val	Tyr	Asp	Pro	Ser	Asn	Tyr	Gly	Phe	Gly	Ser	Ile	Asn	Ile			
Val	Thr	Phe	Ser	Pro	Glu	Tyr	Glu	Tyr	Thr	Phe	Asn	Asp	Ile	Ser	Gly			
Gly	His	Asn	Ser	Ser	Thr	Glu	Ser	Phe	Ile	Ala	Asp	Pro	Ala	Ile	Ser			
Leu	Ala	His	Glu	Leu	Ile	His	Ala	Leu	His	Gly	Leu	Tyr	Gly	Ala	Arg			
Gly	Val	Thr	Tyr	Glu	Thr	Ile	Glu	Val	Lys	Gln	Ala	Pro	Leu	Met				
Ile	Ala	Glu	Lys	Pro	Ile	Arg	Leu	Glu	Glu	Phe	Leu	Thr	Phe	Gly	Gly			
Gln	Asp	Leu	Asn	Ile	Ile	Thr	Ser	Ala	Met	Lys	Glu	Lys	Ile	Tyr	Asn			
Asn	Leu	Leu	Ala	Asn	Tyr	Glu	Lys	Ile	Ala	Thr	Arg	Leu	Ser	Glu	Val			
Asn	Ser	Ala	Pro	Pro	Glu	Tyr	Asp	Ile	Asn	Glu	Tyr	Lys	Asp	Tyr	Phe			
Gln	Trp	Lys	Tyr	Gly	Leu	Asp	Lys	Asn	Ala	Asp	Gly	Ser	Tyr	Thr	Val			
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Glu	Ser	Asp	Leu	Ala	Asn	Lys	Phe	Lys	Val	Lys	Cys	Arg	Asn	Thr	Tyr			
Phe	Ile	Lys	Tyr	Glu	Phe	Leu	Lys	Val	Pro	Asn	Leu	Leu	Asp	Asp	Asp			
Ile	Tyr	Thr	Val	Ser	Glu	Gly	Phe	Asn	Ile	Gly	Asn	Leu	Ala	Val	Asn			
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Pro	Asp	Lys	Gly	Leu	Val	Glu	Lys	Ile	Val	Lys	Phe	Cys	Lys	Ser	Val			
Ile	Pro	Arg	Lys	Gly	Thr	Lys	Ala	Pro	Pro	Arg	Leu	Cys	Ile	Arg	Val			
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Asn	Asp	Ile	Asn	Thr	Pro	Lys	Glu	Ile	Asp	Asp	Thr	Thr	Asn	Leu	Asn			
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Gln	Thr	Ile	Pro	Gln	Ile	Ser	Asn	Arg	Thr	Leu	Asn	Thr	Leu	Val	Gln			
Asp	Asn	Ser	Tyr	Val	Pro	Arg	Tyr	Asp	Ser	Asn	Gly	Thr	Ser	Glu	Ile			
Glu	Glu	Tyr	Asp	Val	Val	Asp	Phe	Asn	Val	Phe	Phe	Tyr	Leu	His	Ala			
Gln	Lys	Val	Pro	Glu	Gly	Glu	Thr	Asn	Ile	Ser	Leu	Thr	Ser	Ser	Ile			
Asp	Thr	Ala	Leu	Leu	Glu	Glu	Ser	Lys	Asp	Ile	Phe	Phe	Ser	Ser	Glu			
Phe	Ile	Asp	Thr	Ile	Asn	Lys	Pro	Val	Asn	Ala	Ala	Leu	Phe	Ile	Asp			
Trp	Ile	Ser	Lys	Val	Ile	Arg	Asp	Phe	Thr	Thr	Glu	Ala	Thr	Gln	Lys			
Ser	Thr	Val	Asp	Lys	Ile	Ala	Asp	Ile	Ser	Leu	Ile	Val	Pro	Tyr	Val			
Gly	Leu	Ala	Leu	Asn	Ile	Ile	Ile	Glu	Ala	Glu	Lys	Gly	Asn	Phe	Glu			

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	Glu	Leu	Thr	Ile	660	Pro	Val	Ile	Leu	665	Thr						670		
	Asp	Ser	Tyr	Glu	Asn	Lys	Asn	Lys	Ala	Ile	Lys	Ala	Ile	Asn	Asn	Ser			
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	Leu	Ile	Glu	Arg	Glu	Ala	Lys	Trp	Lys	Glu	Ile	Tyr	700	Ser	Trp	Ile	Val		
		690						695											
	Ser	Asn	Trp	Leu	Thr	Arg	Ile	Asn	Thr	Gln	Phe	Asn	Lys	Arg	Lys	Glu			
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	Gln	Met	Tyr	Gln	Ala	Leu	Gln	Asn	Gln	Val	Asp	Ala	Ile	Lys	Thr	Ala			
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	Ile	Glu	Tyr	Lys	Tyr	Asn	Asn	Tyr	Thr	Ser	Asp	Glu	Lys	Asn	Arg	Leu			
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	Glu	Ser	Glu	Tyr	Asn	Ile	Asn	Asn	Ile	Glu	Glu	Glu	Leu	Asn	Lys	Lys			
			755					760					765						
	Val	Ser	Leu	Ala	Met	Lys	Asn	Ile	Glu	Arg	Phe	Met	Thr	Glu	Ser	Ser			
		770						775				780							
	Ile	Ser	Tyr	Leu	Met	Lys	Leu	Ile	Asn	Glu	Ala	Lys	Val	Gly	Lys	Leu			
785						790					795								
	Lys	Lys	Tyr	Asp	Asn	His	Val	Lys	Ser	Asp	Leu	Leu	Asn	Tyr	Ile	Leu			
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	Asp	His	Arg	Ser	Ile	Leu	Gly	Glu	Gln	Thr	Asn	Glu	Leu	Ser	Asp	Leu			
					820					825									
	Val	Thr	Ser	Thr	Leu	Asn	Ser	Ser	Ile	Pro	Phe	Glu	Leu	Ser	Ser	Tyr			
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	Thr	Asn	Asp	Lys	Ile	Leu	Ile	Ile	Tyr	Phe	Asn	Arg	Leu	Tyr	Lys	Lys			
		850						855				860							
	Ile	Lys	Asp	Ser	Ser	Ile	Leu	Asp	Met	Arg	Tyr	Glu	Asn	Asn	Lys	Phe			
865						870					875								
	Ile	Asp	Ile	Ser	Gly	Tyr	Gly	Ser	Asn	Ile	Ser	Ile	Asn	Gly	Asn	Val			
					885					890									
	Tyr	Ile	Tyr	Ser	Thr	Asn	Arg	Asn	Gln	Phe	Gly	Ile	Tyr	Asn	Ser	Arg			
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	Leu	Ser	Glu	Val	Asn	Ile	Ala	Gln	Asn	Asn	Asp	Ile	Ile	Tyr	Asn	Ser			
			915					920					925						
	Arg	Tyr	Gln	Asn	Phe	Ser	Ile	Ser	Phe	Trp	Val	Arg	Ile	Pro	Lys	His			
		930						935				940							
	Tyr	Lys	Pro	Met	Asn	His	Asn	Arg	Glu	Tyr	Thr	Ile	Ile	Asn	Cys	Met			
945						950					955								
	Gly	Asn	Asn	Asn	Ser	Gly	Trp	Lys	Ile	Ser	Leu	Arg	Thr	Val	Arg	Asp			
					965					970									
	Cys	Glu	Ile	Ile	Trp	Thr	Leu	Gln	Asp	Thr	Ser	Gly	Asn	Lys	Glu	Asn			
					980				985										
	Leu	Ile	Phe	Arg	Tyr	Glu	Glu	Leu	Asn	Arg	Ile	Ser	Asn	Tyr	Ile	Asn			
			995					1000					1005						
	Lys	Trp	Ile	Phe	Val	Thr	Ile	Thr	Asn	Asn	Arg	Leu	Gly	Asn	Ser	Arg			
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	Ile	Tyr	Ile	Asn	Gly	Asn	Leu	Ile	Val	Glu	Lys	Ser	Ile	Ser	Asn	Leu			
1025						1030					1035								
	Gly	Asp	Ile	His	Val	Ser	Asp	Asn	Ile	Leu	Phe	Lys	Ile	Val	Gly	Cys			
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	Asp	Asp	Glu	Thr	Val	Gly	Ile	Arg	Tyr	Phe	Lys	Val	Phe	Asn	Thr				
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	Glu	Leu	Asp	Lys	Thr	Glu	Ile	Glu	Thr	Leu	Tyr	Ser	Asn	Glu	Pro	Asp			
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	Pro	Ser	Ile	Leu	Lys	Asn	Tyr	Trp	Gly	Asn	Tyr	Leu	Leu	Tyr	Asn	Lys			
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	Lys	Tyr	Tyr	Leu	Phe	Asn	Leu	Leu	Arg	Lys	Asp	Lys	Tyr	Ile	Thr	Leu			
1105						1110					1115								
	Asn	Ser	Gly	Ile	Leu	Asn	Ile	Asn	Gln	Gln	Arg	Gly	Val	Thr	Glu	Gly			
					1125					1130									
	Ser	Val	Phe	Leu	Asn	Tyr	Lys	Leu	Tyr	Glu	Gly	Val	Glu	Val	Ile	Ile			
					1140				1145				1150						
	Arg	Lys	Asn	Gly	Pro	Ile	Asp	Ile	Ser	Asn	Thr	Asp	Asn	Phe	Val	Arg			
			1155					1160					1165						
	Lys	Asn	Asp	Leu	Ala	Tyr	Ile	Asn	Val	Val	Asp	Arg	Gly	Val	Glu	Tyr			

1170 1175 1180
 Arg Leu Tyr Ala Asp Thr Lys Ser Glu Lys Glu Lys Ile Ile Arg Thr
 1185 1190 1195 1200
 Ser Asn Leu Asn Asp Ser Leu Gly Gln Ile Ile Val Met Asp Ser Ile
 1205 1210 1215
 Gly Asn Asn Cys Thr Met Asn Phe Gln Asn Asn Asn Gly Ser Asn Ile
 1220 1225 1230
 Gly Leu Leu Gly Phe His Ser Asn Asn Leu Val Ala Ser Ser Trp Tyr
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 Tyr Tyr Lys Ala Phe Arg Ile Ile Asp Arg Ile Trp Ile Val Pro Glu
 35 40 45
 Arg Phe Thr Tyr Gly Phe Gln Pro Asp Gln Phe Asn Ala Ser Thr Gly
 50 55 60
 Val Phe Ser Lys Asp Val Tyr Glu Tyr Tyr Asp Pro Thr Tyr Leu Lys
 65 70 75 80
 Thr Asp Ala Glu Lys Asp Lys Phe Leu Lys Thr Met Ile Lys Leu Phe
 85 90 95
 Asn Arg Ile Asn Ser Lys Pro Ser Gly Gln Arg Leu Leu Asp Met Ile
 100 105 110
 Val Asp Ala Ile Pro Tyr Leu Gly Asn Ala Ser Thr Pro Pro Asp Lys
 115 120
 Phe Ala Ala Asn Val Ala Asn Val Ser Ile Asn Lys Lys Ile Ile Gln
 130 135 140
 Pro Gly Ala Glu Asp Gln Ile Lys Gly Leu Met Thr Asn Leu Ile Ile
 145 150 155
 Phe Gly Pro Gly Pro Val Leu Ser Asp Asn Phe Thr Asp Ser Met Ile
 165 170 175
 Met Asn Gly His Ser Pro Ile Ser Glu Gly Phe Gly Ala Arg Met Met
 180 185 190
 Ile Arg Phe Cys Pro Ser Cys Leu Asn Val Phe Asn Asn Val Gln Glu
 195 200 205
 Asn Lys Asp Thr Ser Ile Phe Ser Arg Arg Ala Tyr Phe Ala Asp Pro
 210 215 220
 Ala Leu Thr Leu Met His Glu Leu Ile His Val Leu His Gly Leu Tyr
 225 230 235
 Gly Ile Lys Ile Ser Asn Leu Pro Ile Thr Pro Asn Thr Lys Glu Phe
 245 250 255
 Phe Met Gln His Ser Asp Pro Val Gln Ala Glu Glu Leu Tyr Thr Phe
 260 265 270
 Gly Gly His Asp Pro Ser Val Ile Ser Pro Ser Thr Asp Met Asn Ile
 275 280 285
 Tyr Asn Lys Ala Leu Gln Asn Phe Gln Asp Ile Ala Asn Arg Leu Asn
 290 295 300
 Ile Val Ser Ser Ala Gln Gly Ser Gly Ile Asp Ile Ser Leu Tyr Lys
 305 310 315
 Gln Ile Tyr Lys Asn Lys Tyr Asp Phe Val Glu Asp Pro Asn Gly Lys
 325 330 335
 Tyr Ser Val Asp Lys Asp Lys Phe Asp Lys Leu Tyr Lys Ala Leu Met
 340 345 350
 Phe Gly Phe Thr Glu Thr Asn Leu Ala Gly Glu Tyr Gly Ile Lys Thr
 355 360 365
 Arg Tyr Ser Tyr Phe Ser Glu Tyr Leu Pro Pro Ile Lys Thr Glu Lys

370	Leu	Leu	Asp	Asn	Thr	Ile	375	Tyr	Thr	Gln	Asn	Glu	380	Gly	Phe	Asn	Ile	Ala
385	Ser	Lys	Asn	Leu	Lys	390	Thr	Glu	Phe	Asn	Gly	395	Gln	Asn	Lys	Ala	Val	Asn
	Lys	Glu	Ala	Tyr	Glu	405	Glu	Ile	Ser	Leu	Glu	410	His	Leu	Val	Ile	Tyr	Arg
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465	Thr	Gln	Asn	Asn	Thr	470	Ile	Glu	Asn	475	Asn	Phe	480	Ser	Ile	Asp	Gln	Leu
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	Glu	Ser	Thr	Gln	Lys	595	Ser	Thr	Ile	600	Asp	Lys	605	Val	Ser	Asp	Val	Ser
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625	Lys	Glu	Asn	Phe	Lys	630	Asn	Ala	Phe	635	Glu	Ile	640	Gly	Gly	Ala	Ala	Ile
	Met	Glu	Phe	Ile	Pro	645	Glu	Leu	Ile	650	Val	Pro	655	Ile	Val	Gly	Phe	Phe
	Leu	Glu	Ser	Tyr	Val	660	Gly	Asn	Lys	665	Gly	His	670	Ile	Ile	Met	Thr	Ile
	Asn	Ala	Leu	Lys	Lys	675	Arg	Asp	Gln	680	Lys	Trp	685	Thr	Asp	Met	Tyr	Gly
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	Lys	Ile	Ile	Glu	Asp	725	Gln	Tyr	Asn	730	Arg	Tyr	735	Ser	Glu	Glu	Asp	Lys
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	Thr	Asn	Glu	Leu	Tyr	805	Leu	Leu	Asp	810	Glu	Val	815	Asn	Ile	Leu	Lys	Ser
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	Thr	Lys	Asp	Thr	Ile	835	Leu	Ile	Gln	840	Val	Phe	845	Asn	Asn	Tyr	Ile	Ser
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 Ser Cys Ile Lys Asn Asp Ser Gly Trp Lys Val Ser Ile Lys Gly Asn
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 Arg Ile Ile Trp Thr Leu Ile Asp Val Asn Ala Lys Ser Lys Ser Ile
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 Phe Phe Glu Tyr Ser Ile Lys Asp Asn Ile Ser Asp Tyr Ile Asn Lys
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 Ile Lys Lys Ala Ser Asn Ser Arg Asn Ile Asn Asn Asp Asn Ile Val
 1155 1160 1165
 Arg Glu Gly Asp Tyr Ile Tyr Leu Asn Ile Asp Asn Ile Ser Asp Glu
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 Ser Tyr Arg Val Tyr Val Leu Val Asn Ser Lys Glu Ile Gln Thr Gln
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 Arg Tyr Glu Phe Gly Thr Lys Pro Glu Asp Phe Asn Pro Pro Ser Ser
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 Leu Ile Glu Gly Ala Ser Glu Tyr Tyr Asp Pro Asn Tyr Leu Arg Thr
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 Asp Ser Asp Lys Asp Arg Phe Leu Gln Thr Met Val Lys Leu Phe Asn

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 Tyr Glu Gly Asn Phe 645 Ile Gly Ala Leu 650 Glu Thr Thr Gly Val Val Leu 655
 Leu Leu Glu Tyr Ile Pro Glu Ile Thr Leu Pro Val Ile Ala Ala Leu 670
 Ser Ile Ala Glu Ser Ser Thr Gln Lys Glu Lys Ile Ile Lys Thr Ile 685
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 Lys Lys Ile Ile Asp Tyr Glu Tyr Lys Ile Tyr Ser Gly Pro Asp Lys 735
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 Lys Ala Asn Lys Ala Met Ile Asn Ile Asn Ile Phe Met Arg Glu Ser 765
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 Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Lys Lys Leu Glu 815
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 Lys Asn Leu Asp Cys Trp Val Asp Asn Glu Glu Asp Ile Asp Val Ile 845
 865 Leu Lys Lys Ser Thr Ile Leu Asn Leu Asp Ile Asn Asn Asp Ile Ile 860
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 Thr Asn Asp
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 Leu Asp Ser Gly Ser Ser Ala Tyr Tyr Asp Pro Asn Tyr Leu Thr Thr
 65 70 75 80
 Asp Ala Glu Lys Asp Arg Phe Leu Lys Thr Val Ile Lys Leu Phe Asn
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 Arg Ile Asn Ser Asn Pro Ala Gly Gln Val Leu Leu Glu Glu Ile Lys
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 Asn Gly Lys Pro Tyr Leu Gly Asn Asp His Thr Ala Val Asn Glu Phe
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 Cys Ala Asn Asn Arg Ser Thr Ser Val Glu Ile Lys Glu Ser Asn Gly
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 Asn Ile Leu Glu Cys Ser Thr Phe Pro Val Arg Ile Phe Pro Asn Asn
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 Ile Ala Tyr Asp Pro Ser Glu Lys Gly Phe Gly Ser Ile Gln Leu Met
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 Ser Phe Ser Thr Glu Tyr Glu Tyr Ala Phe Asn Asp Asn Thr Asp Leu
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 Phe Ile Ala Asp Pro Ala Ile Ser Leu Ala His Glu Leu Ile His Val
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 Leu His Gly Leu Tyr Gly Ala Lys Gly Val Thr Asn Lys Lys Val Ile
 225 230 235 240
 Glu Val Asp Gln Gly Ala Leu Met Ala Ala Glu Lys Asp Ile Lys Ile
 245 250 255
 Glu Glu Phe Ile Thr Phe Gly Gly Gln Asp Leu Asn Ile Ile Thr Asn
 260 265 270
 Ser Thr Asn Gln Lys Ile Tyr Val Ile Leu Leu Ser Asn Tyr Thr Ala
 275 280 285
 Ile Ala Ser Arg Leu Ser Gln Val Asn Arg Asn Asn Ser Ala Leu Asn
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 Thr Thr Tyr Tyr Lys Asn Phe Phe Gln Trp Lys Tyr Gly Leu Asp Gln
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 Asp Ser Asn Gly Asn Tyr Thr Val Asn Ile Ser Lys Phe Asn Ala Ile

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Gln	Val	Lys	340	Asn	Arg	Ser	Asn	Tyr	345	Leu	Phe	His	Phe	Lys	350	Pro	Phe	Arg
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Asn	Ile	Gly	370	Ser	Leu	Arg	Val	Asn	375	Asn	Asn	Gly	Gln	Asn	380	Ile	Asn	Leu
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745	Arg	Phe	Leu	Thr	Glu	Ser	Ser	Ile	750	Ser	Tyr	Leu	Met	Lys	755	Leu	Ile	Asn
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790	Ser	Val	Pro	Glu	Leu	Asn	Asn	Leu	795	Val	Ser	Asn	Thr	Leu	800	Asn	Asn	Ser
805	Ile	Pro	Phe	Glu	Leu	Ser	Glu	Tyr	810	Thr	Asn	Asp	Lys	Ile	815	Leu	Ile	His
820	Ile	Leu	Ile	Arg	Phe	Tyr	Lys	Arg	825	Ile	Ile	Asp	Ser	Ser	830	Ile	Leu	Asn
835	Met	Lys	Tyr	Glu	Asn	Asn	Arg	Phe	840	Ile	Asp	Ser	Ser	Gly	845	Tyr	Gly	Ser
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865 Asn Ile Ser Ile 870 Asn Gly Asp Ile Tyr Ile Tyr Ser Thr Asn Arg Asn 880
 Gln Phe Gly Ile 885 Tyr Ser Ser Arg Leu 890 Ser Glu Val Asn Ile Thr Gln 895
 Asn Asn Thr Ile Ile Tyr Asn Ser Arg Tyr Gln Asn Phe Ser Val Ser 910
 Phe Trp Val Arg Ile Pro Lys Tyr Asn Asn Leu Lys Asn Leu Asn Asn 925
 Glu Tyr Thr Ile Ile Asn Cys Met Arg Asn Asn Asn Ser Gly Trp Lys 940
 945 Ile Ser Leu Asn Tyr Asn Asn Ile Ile Trp Thr Leu Gln Asp Thr Thr 955
 Gly Asn Asn Gln Lys Leu Val Phe Asn Tyr Thr Gln Met Ile Asp Ile 970
 Ser Asp Tyr Ile Asn Lys Trp Thr Phe Val Thr Ile Thr Asn Asn Arg 985
 Leu Gly His Ser Lys Leu Tyr Ile Asn Gly Asn Leu Thr Asp Gln Lys 990
 1010 Ser Ile Leu Asn Leu Gly Asn Ile His Val Asp Asp Asn Ile Leu Phe 1005
 1025 Lys Ile Val Gly Cys Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe 1035
 Lys Ile Phe Asn Met Glu Leu Asp Lys Thr Glu Ile Glu Thr Leu Tyr 1050
 His Ser Glu Pro Asp Ser Thr Ile Leu Lys Asp Phe Trp Gly Asn Tyr 1065
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 Phe Asn Ile Met Lys Asn Ile Trp Ile Ile Pro Glu Arg Asn Val Ile
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 Gly Thr Ile Pro Gln Asp Phe Leu Pro Pro Thr Ser Leu Lys Asn Gly
 50 55 60
 Asp Ser Ser Tyr Tyr Asp Pro Asn Tyr Leu Gln Ser Asp Gln Glu Lys
 Page 23

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	Ala	Ser	Ala	115	Val	Pro	Ile	Gln	Phe	120	Ser	Asn	Gly	Ser	125	Gln	Ser	Ile	
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145	Asn	Ser	Ser	150	Asn	Ile	Ser	Leu	Arg	155	Asn	Tyr	Met	Pro	Ser	Asn	His		
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	Phe	Asp	Leu	325	Ala	Thr	Lys	Phe	Gln	330	Val	Lys	Cys	Arg	Gln	Thr	Tyr		
	Gly	Gln	Tyr	340	Lys	Tyr	Phe	Lys	Leu	345	Ser	Asn	Leu	Leu	Asn	Asp	Ser		
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 Leu Glu Leu Leu Gly Ala Gly Ile Leu Leu Glu Phe Glu Pro Glu Leu
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 Leu Ile Pro Thr Ile Leu Val Phe Thr Ile Lys Ser Phe Leu Gly Ser
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 Ser Asp Asn Lys Asn Lys Val Ile Lys Ala Ile Asn Asn Ala Leu Lys
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 Glu Arg Asp Glu Lys Trp Lys Glu Val Tyr Ser Phe Ile Val Ser Asn
 675 680 685
 Trp Met Thr Lys Ile Asn Thr Gln Phe Asn Lys Arg Lys Glu Gln Met
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 Lys Tyr Asp Ile Glu Gln Ile Glu Asn Glu Leu Asn Gln Lys Val Ser
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 Val Thr Ile Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn
 995 1000 1005
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 Val Ser Asp Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Thr Arg
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 Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr Leu
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 Leu Asn Val Leu Lys Pro Asn Asn Phe Ile Asn Arg Arg Thr Asp Ser
 1090 1095 1100
 Thr Leu Ser Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn Arg
 1105 1110 1115 1120
 Leu Tyr Ser Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asn Ser Ser
 1125 1130 1135
 Thr Asn Asp Asn Leu Val Arg Lys Asn Asp Gln Val Tyr Ile Asn Phe
 1140 1145 1150
 Val Ala Ser Lys Thr His Leu Leu Pro Leu Tyr Ala Asp Thr Ala Thr

1155 1160 1165
 Thr Asn Lys Glu Lys Thr Ile Lys Ile Ser Ser Ser Gly Asn Arg Phe
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 Asn Gln Val Val Val Met Asn Ser Val Gly Asn Cys Thr Met Asn Phe
 1185 1190 1195 1200
 Lys Asn Asn Asn Gly Asn Asn Ile Gly Leu Leu Gly Phe Lys Ala Asp
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 Gln Glu Lys
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<400> 11
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 35 40 45
 Asp Ala Ala Phe Gly Lys Ser His Glu Ala Arg Gly Thr Leu Lys Ile
 50 55 60
 Ile Ser Gly Ala Thr Tyr Asn Pro His Leu Gln Asp Lys Leu Ser Val
 65 70 75 80
 Asp Phe Lys Val Leu Ala Phe Asp Ile Gln Gln Met Ile Asp Asp Ile
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 Phe Gln Ser Ser Asn Leu Lys Asn Glu Tyr Lys Asn Ser Arg Val Leu
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 Gln Phe Glu Asn Gly Ser Ile Ile Val Ile Phe Asp Leu Leu Phe Asp
 115 120 125
 Gln Trp Val Ser Asp Lys Asn Val Lys Glu Glu Leu Ile Gln Gly Ile
 130 135 140
 Glu Ala Asn Lys Ser Ser Gln Leu Val Thr Phe His Ile Asp Leu Asn
 145 150 155 160
 Ser Ile Asp Ile Thr Ala Ser Leu Glu Asn Phe Ser Thr Ile Ser Pro
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 Ala Thr Thr Ser Glu Lys Leu Thr Thr Ser Ile Pro Leu Ala Thr Pro
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 Gly Asn Val Ser Ile Glu Cys Pro Pro Asp Ser Arg Leu Cys Ala Asp
 195 200 205
 Ala Leu Lys Cys Ile Ala Ile Asp Leu Phe Cys Asp Gly Glu Leu Asn
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 Cys Pro Asp Gly Ser Asp Glu Asp Asn Lys Thr Cys Ala Thr Ala Cys
 225 230 235 240
 Asp Gly Arg Phe Leu Leu Thr Gly Ser Ser Gly Ser Phe Glu Ala Leu
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 His Tyr Pro Lys Pro Ser Asn Asn Thr Ser Ala Val Cys Arg Trp Ile
 260 265 270
 Ile Arg Val Asn Gln Gly Leu Ser Ile Gln Leu Asn Phe Asp Tyr Phe
 275 280 285
 Asn Thr Tyr Tyr Ala Asp Val Leu Asn Ile Tyr Glu Gly Met Gly Ser
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 Ser Lys Ile Leu Arg Ala Ser Leu Trp Ser Asn Asn Pro Gly Ile Ile
 305 310 315 320
 Arg Ile Phe Ser Asn Gln Val Thr Ala Thr Phe Leu Ile Gln Ser Asp
 325 330 335
 Glu Ser Asp Tyr Ile Gly Phe Lys Val Thr Tyr Thr Ala Phe Asn Ser
 340 345 350
 Lys Glu Leu Asn Asn Tyr Glu Lys Ile Asn Cys Asn Phe Glu Asp Gly
 355 360 365
 Phe Cys Phe Trp Ile Gln Asp Leu Asn Asp Asp Asn Glu Trp Glu Arg

370	Thr	Gln	Gly	Ser	Thr	Phe	Pro	Pro	Ser	Thr	Gly	Pro	Thr	Phe	Asp	His
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	Gly	Gly	Arg	Arg	Glu	Arg	Val	Gly	Leu	Leu	Thr	Leu	Pro	Leu	Asp	Pro
				420					425					430		
	Thr	Pro	Glu	Gln	Ala	Cys	Leu	Ser	Phe	Trp	Tyr	Tyr	Met	Tyr	Gly	Glu
			435					440					445			
	Asn	Val	Tyr	Lys	Leu	Ser	Ile	Asn	Ile	Ser	Ser	Asp	Gln	Asn	Met	Glu
			450					455				460				
	Lys	Thr	Ile	Phe	Gln	Lys	Glu	Gly	Asn	Tyr	Gly	Gln	Asn	Trp	Asn	Tyr
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	Leu	Thr	Tyr	Gly	Ile	Cys	Asn	Val	Ser	Val	Tyr	Pro	Glu	Pro	Thr	Leu
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	Val	Pro	Thr	Pro	Pro	Pro	Glu	Leu	Pro	Thr	Asp	Cys	Gly	Gly	Pro	His
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	Asp	Leu	Trp	Glu	Pro	Asn	Thr	Phe	Thr	Ser	Ile	Asn	Phe	Pro	Asn	
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	Gly	Lys	Asn	Ile	Gln	Leu	His	Phe	Gln	Glu	Phe	Asp	Leu	Glu	Asn	Ile
				580					585					590		
	Ala	Asp	Val	Val	Glu	Ile	Arg	Asp	Gly	Glu	Gly	Asp	Asp	Ser	Leu	Phe
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	Leu	Ala	Val	Tyr	Thr	Gly	Pro	Gly	Pro	Val	Asn	Asp	Val	Phe	Ser	Thr
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	Thr	Asn	Arg	Met	Thr	Val	Leu	Phe	Ile	Thr	Asp	Asn	Met	Leu	Ala	Lys
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	Glu	Pro	Cys	Lys	Glu	Asp	Asn	Phe	Gln	Cys	Lys	Asp	Gly	Glu	Cys	Ile
				660					665					670		
	Pro	Leu	Val	Asn	Leu	Cys	Asp	Gly	Phe	Pro	His	Cys	Lys	Asp	Gly	Ser
			675					680					685			
	Asp	Glu	Ala	His	Cys	Val	Arg	Leu	Phe	Asn	Gly	Thr	Thr	Asp	Ser	Ser
			690				695					700				
	Gly	Leu	Val	Gln	Phe	Arg	Ile	Gln	Ser	Ile	Trp	His	Val	Ala	Cys	Ala
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	Leu	Gly	Thr	Gly	Asn	Ser	Ser	Val	Pro	Thr	Phe	Ser	Thr	Gly	Gly	Gly
				740					745					750		
	Pro	Tyr	Val	Asn	Leu	Asn	Thr	Ala	Pro	Asn	Gly	Ser	Leu	Ile	Leu	Thr
			755					760					765			
	Pro	Ser	Gln	Gln	Cys	Leu	Glu	Asp	Ser	Leu	Ile	Leu	Leu	Gln	Cys	Asn
			770				775						780			
	Tyr	Lys	Ser	Cys	Gly	Lys	Lys	Leu	Val	Thr	Gln	Glu	Val	Ser	Pro	Lys
785	Ile	Val	Gly	Gly	Ser	Asp	Ser	Arg	Glu	Gly	Ala	Trp	Pro	Trp	Val	Val
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	Ala	Leu	Tyr	Phe	Asp	Asp	Gln	Gln	Val	Cys	Gly	Ala	Ser	Leu	Val	Ser
				820					825					830		
	Arg	Asp	Trp	Leu	Val	Ser	Ala	Ala	His	Cys	Val	Tyr	Gly	Arg	Asn	Met
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	Glu	Pro	Ser	Lys	Trp	Lys	Ala	Val	Leu	Gly	Leu	His	Met	Ala	Ser	Asn
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	Leu	Thr	Ser	Pro	Gln	Ile	Glu	Thr	Arg	Leu	Ile	Asp	Gln	Ile	Val	Ile
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	His	Leu	Glu	Met	Lys	Val	Asn	Tyr	Thr	Asp	Tyr	Ile	Gln	Pro	Ile	Cys
			900						905					910		
	Leu	Pro	Glu	Glu	Asn	Gln	Val	Phe	Pro	Pro	Gly	Arg	Ile	Cys	Ser	Ile

915 920 925
 Ala Gly Trp Gly Ala Leu Ile Tyr Gln Gly Ser Thr Ala Asp Val Leu
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 Gln Glu Ala Asp Val Pro Leu Leu Ser Asn Glu Lys Cys Gln Gln Gln
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 Met Pro Glu Tyr Asn Ile Thr Glu Asn Met Val Cys Ala Gly Tyr Glu
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 Ala Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Met
 980 985 990
 Cys Gln Glu Asn Asn Arg Trp Leu Leu Ala Gly Val Thr Ser Phe Gly
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 <213> Human rhinovirus C

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 Ile Asp Gly Arg Leu Val Arg Val Leu Lys Gln Gln Val Leu Thr Asp
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 Met Asn Asp Val Asp Thr Glu Val Thr Val Leu Trp Leu Asp Gln Asn
 65 70 75 80
 Glu Lys Phe Arg Asp Ile Arg Arg Phe Ile Pro Glu His Gln Gln Asp
 85 90 95
 Trp His Asn Ile His Leu Ala Thr Asn Val Thr Lys Phe Pro Met Leu
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 Asn Val Glu Val Gly His Thr Val Pro Tyr Gly Glu Ile Asn Leu Ser
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 Gly Asn Ala Thr Cys Arg Leu Tyr Lys Tyr Asp Tyr Pro Thr Gln Pro
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 Gly Gln Cys Gly Ala Val Leu Ala Asn Thr Gly Asn Ile Ile Gly Ile
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 <213> Human enterovirus 71

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 Ile Glu His Lys Leu Val Asn Val Leu Asp Ala Val Glu Leu Val Asp
 50 55 60
 Glu Gln Gly Val Asn Leu Glu Leu Thr Leu Ile Thr Leu Asp Thr Asn
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 Page 28

<210> 14
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<213> Potyvirus

Page 29

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Gln	Ala	Pro	Phe	Thr	His	Val	Leu	Ala	Val	Ser	Glu	Ile	Leu
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Gly	Asn	Lys	Leu	Thr	Gly	Ala	Asp	Leu	Glu	Glu	Ala	Ser	Thr
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Leu	Glu	Ile	Ala	Arg	Phe	Leu	Asn	Asn	Arg	Thr	Glu	Asn	Met
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Gly	His	Leu	Gly	Ser	Phe	Arg	Asn	Lys	Ile	Ser	Ser	Lys	Ala
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Asn	Asn	Ala	Leu	Met	Cys	Asp	Asn	Gln	Leu	Asp	Gln	Asn	Gly
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Ile	Trp	Gly	Leu	Arg	Gly	Ala	His	Ala	Lys	Arg	Phe	Leu	Lys
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Phe	Thr	Glu	Ile	Asp	Pro	Asn	Glu	Gly	Tyr	Asp	Lys	Tyr	Val
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Lys	His	Ile	Arg	Gly	Ser	Arg	Lys	Leu	Ala	Ile	Gly	Asn	Leu
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Ser	Thr	Asp	Phe	Gln	Thr	Leu	Arg	Gln	Gln	Ile	Gln	Gly	Glu
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Glu	Arg	Lys	Glu	Ile	Gly	Asn	His	Cys	Ile	Ser	Met	Arg	Asn
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Tyr	Val	Tyr	Pro	Cys	Cys	Cys	Val	Thr	Leu	Glu	Asp	Gly	Lys
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Tyr	Ser	Asp	Leu	Lys	His	Pro	Thr	Lys	Arg	His	Leu	Val	Ile
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Ser	Gly	Asp	Ser	Lys	Tyr	Leu	Asp	Leu	Pro	Val	Leu	Asn	Glu
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Met	Tyr	Ile	Ala	Asn	Glu	Gly	Tyr	Cys	Tyr	Met	Asn	Ile	Phe
				645					650				655
Leu	Leu	Val	Asn	Val	Lys	Glu	Glu	Asp	Ala	Lys	Asp	Phe	Thr
			660					665				670	
Ile	Arg	Asp	Thr	Ile	Val	Pro	Lys	Leu	Gly	Ala	Trp	Pro	Thr
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Asp	Val	Ala	Thr	Ala	Cys	Tyr	Leu	Leu	Ser	Ile	Leu	Tyr	Pro
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Leu	Arg	Ala	Glu	Leu	Pro	Arg	Ile	Leu	Val	Asp	His	Asp	Asn
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Met	His	Val	Leu	Asp	Ser	Tyr	Gly	Ser	Arg	Thr	Thr	Gly	Tyr
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Leu	Lys	Met	Asn	Thr	Thr	Ser	Gln	Leu	Ile	Glu	Phe	Val	His
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Leu	Glu	Ser	Glu	Met	Lys	Thr	Tyr	Asn	Val	Gly	Gly	Met	Asn
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Val	Val	Thr	Gln	Gly	Ala	Ile	Glu	Met	Leu	Ile	Lys	Ser	Ile
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Pro	His	Leu	Met	Lys	Gln	Leu	Leu	Glu	Glu	Glu	Pro	Tyr	Ile
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Thr	Phe	Glu	Gln	Ala	Leu	Gln	Met	Trp	Leu	Pro	Asn	Thr	Met
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Ala	Asp	Leu	Phe	Val	Gln	Gln	Arg	Asn	Leu	Ile	Asn	Glu	Tyr
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Val	Ile	Leu	Asp	Asn	Leu	Ile	Asp	Gly	Val	Arg	Val	Asn	His
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Ser	Leu	Ala	Met	Glu	Ile	Val	Thr	Ile	Lys	Leu	Ala	Thr	Gln
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His	Glu	Met	Leu	Glu	Lys	Asn	Tyr	Val	Lys	Ala	Leu	Lys	Asp
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Asp	Glu	Leu	Thr	Trp	Leu	Glu	Lys	Phe	Ser	Ala	Ile	Arg	His

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 Asp Cys Gly Gly His Ile Asp Leu Ser Val Lys Ser Leu Phe Lys Phe
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 His Leu Glu Leu Leu Lys Gly Thr Ile Ser Arg Ala Val Asn Gly Gly
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 Ala Arg Lys Val Arg Val Ala Lys Asn Ala Met Thr Lys Gly Val Phe
 995 1000 1005
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 Ser Ser Val Leu Ser Leu Leu Thr Phe Leu Phe Gln Ile Asp Cys
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 Met Ile Arg Ala His Arg Glu Ala Lys Val Ala Ala Gln Leu Gln Lys
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 Glu Ser Glu Trp Asp Asn Ile Ile Asn Arg Thr Phe Gln Tyr Ser Lys
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 Leu Glu Asn Pro Ile Gly Tyr Arg Ser Thr Ala Glu Glu Arg Leu Gln
 1075 1080 1085
 Ser Glu His Pro Glu Ala Phe Glu Tyr Tyr Lys Phe Cys Ile Gly Lys
 1090 1095 1100
 Glu Asp Leu Val Glu Gln Ala Lys Gln Pro Glu Ile Ala Tyr Phe Glu
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 Arg Ser Asp Gly Val Phe Lys Ile Leu Asn Lys Phe Lys Gly Ile Leu
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 Asp Glu Leu His Lys Thr Ser Leu Pro Gly Val Thr Phe Lys Gln Trp
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 Ser Glu Ile Ser His Ser Pro Ala Arg Asp Phe Leu Val Arg Gly Ala
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 Val Gly Ser Gly Lys Ser Thr Gly Leu Pro Tyr His Leu Ser Lys Arg
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 Met Arg Gly Lys Ser Thr Phe Gly Ser Ser Pro Ile Thr Val Met Thr
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 Ser Gly Phe Ala Leu His His Phe Ala Arg Asn Ile Ala Glu Val Lys
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 Thr Tyr Asp Phe Val Ile Ile Asp Glu Cys His Val Asn Asp Ala Ser
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 Ala Ile Ala Phe Arg Asn Leu Leu Phe Glu His Glu Phe Glu Gly Lys
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 Val Leu Lys Val Ser Ala Thr Pro Pro Gly Arg Glu Val Glu Phe Thr
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 Glu Phe Val Ser Leu Gln Gly Thr Gly Ala Asn Ala Asp Val Ile Ser
 1395 1400 1405
 Cys Gly Asp Asn Ile Leu Val Tyr Val Ala Ser Tyr Asn Asp Val Asp
 1410 1415 1420
 Ser Leu Gly Lys Leu Leu Val Gln Lys Gly Tyr Lys Val Ser Lys Ile
 1425 1430 1435 1440
 Asp Gly Arg Thr Met Lys Ser Gly Gly Thr Glu Ile Ile Thr Glu Gly
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 Thr Ser Val Lys Lys His Phe Ile Val Ala Thr Asn Ile Ile Glu Asn
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 Val Pro Val Leu Asp Val Asp Asn Arg Ala Val Gln Tyr Asn Lys Thr
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 Gly Ile Arg Ile Pro Phe Val Cys Lys Glu Ile Pro Asp Ser Leu His
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 Glu Glu Ile Trp His Ile Val Val Ala His Lys Gly Asp Ser Gly Ile
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 Gly Arg Leu Thr Ser Val Gln Ala Ala Lys Val Val Tyr Thr Leu Gln
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 Thr Asp Val His Ser Ile Ala Arg Thr Leu Ala Cys Ile Asn Arg Arg
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 Ile Ala Asp Glu Gln Met Lys Gln Ser His Phe Glu Ala Ala Thr Gly
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 Asp Gln Asp Val Thr Gly Ile Ile Gln Asp Phe Asn His Leu Glu Thr
 1780 1785 1790
 Ile Tyr Leu Gln Ser Asp Ser Glu Val Ala Lys His Leu Lys Leu Lys
 1795 1800 1805
 Ser His Trp Asn Lys Ser Gln Ile Thr Arg Asp Ile Ile Ile Ala Leu
 1810 1815 1820
 Ser Val Leu Ile Gly Gly Gly Trp Met Leu Ala Thr Tyr Phe Lys Asp
 1825 1830 1835 1840
 Lys Phe Asn Glu Pro Val Tyr Phe Gln Gly Lys Lys Asn Gln Lys His
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 Lys Leu Lys Met Arg Glu Ala Arg Gly Ala Arg Gly Gln Tyr Glu Val
 1860 1865 1870
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 1875 1880 1885
 Asn Lys Gly Lys Arg Lys Gly Thr Thr Arg Gly Met Gly Ala Lys Ser
 1890 1895 1900
 Arg Lys Phe Ile Asn Met Tyr Gly Phe Asp Pro Thr Asp Phe Ser Tyr
 1905 1910 1915 1920
 Ile Arg Phe Val Asp Pro Leu Thr Gly His Thr Ile Asp Glu Ser Thr
 1925 1930 1935
 Asn Ala Pro Ile Asp Leu Val Gln His Glu Phe Gly Lys Val Arg Thr
 1940 1945 1950
 Arg Met Leu Ile Asp Asp Glu Ile Glu Pro Gln Ser Leu Ser Thr His
 1955 1960 1965
 Thr Thr Ile His Ala Tyr Leu Val Asn Ser Gly Thr Lys Lys Val Leu
 1970 1975 1980
 Lys Val Asp Leu Thr Pro His Ser Ser Leu Arg Ala Ser Glu Lys Ser
 1985 1990 1995 2000
 Thr Ala Ile Met Gly Phe Pro Glu Arg Glu Asn Glu Leu Arg Gln Thr
 2005 2010 2015
 Gly Met Ala Val Pro Val Ala Tyr Asp Gln Leu Pro Pro Lys Asn Glu

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 2130 2135 2140
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 Met Val Ser Asp Thr Ser Cys Thr Phe Pro Ser Ser Asp Gly Ile Phe
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 Trp Lys His Trp Ile Gln Thr Lys Asp Gly Gln Cys Gly Ser Pro Leu
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 Val Ser Thr Arg Asp Gly Phe Ile Val Gly Ile His Ser Ala Ser Asn
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 2290 2295 2300
 Val Thr Lys His Val Val Lys Gly Lys Cys Pro Leu Phe Glu Leu Tyr
 2305 2310 2315 2320
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 Phe Pro Thr Val Asn Tyr Ile Thr Asp Pro Glu Glu Ile Phe Ser Ala
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 Glu Ala Leu Ser Glu Leu Thr Leu Asp Glu Gln Glu Ala Met Leu Lys
 2420 2425 2430
 Ala Ser Cys Leu Arg Leu Tyr Thr Gly Lys Leu Gly Ile Trp Asn Gly
 2435 2440 2445
 Ser Leu Lys Ala Glu Leu Arg Pro Ile Glu Lys Val Glu Asn Asn Lys
 2450 2455 2460
 Thr Arg Thr Phe Thr Ala Ala Pro Ile Asp Thr Leu Leu Ala Gly Lys
 2465 2470 2475 2480
 Val Cys Val Asp Asp Phe Asn Asn Gln Phe Tyr Asp Leu Asn Ile Lys
 2485 2490 2495
 Ala Pro Trp Thr Val Gly Met Thr Lys Phe Tyr Gln Gly Trp Asn Glu
 2500 2505 2510
 Leu Met Glu Ala Leu Pro Ser Gly Trp Val Tyr Cys Asp Ala Asp Gly
 2515 2520 2525
 Ser Gln Phe Asp Ser Ser Leu Thr Pro Phe Leu Ile Asn Ala Val Leu
 2530 2535 2540
 Lys Val Arg Leu Ala Phe Met Glu Glu Trp Asp Ile Gly Glu Gln Met
 2545 2550 2555 2560
 Leu Arg Asn Leu Tyr Thr Glu Ile Val Tyr Thr Pro Ile Leu Thr Pro

2565 2570 2575
 Asp Gly Thr Ile Ile Lys Lys His Lys Gly Asn Asn Ser Gly Gln Pro
 2580 2585 2590
 Ser Thr Val Val Asp Asn Thr Leu Met Val Ile Ile Ala Met Leu Tyr
 2595 2600 2605
 Thr Cys Glu Lys Cys Gly Ile Asn Lys Glu Glu Ile Val Tyr Tyr Val
 2610 2615 2620
 Asn Gly Asp Asp Leu Leu Ile Ala Ile His Pro Asp Lys Ala Glu Arg
 2625 2630 2635 2640
 Leu Ser Arg Phe Lys Glu Ser Phe Gly Glu Leu Gly Leu Lys Tyr Glu
 2645 2650 2655
 Phe Asp Cys Thr Thr Arg Asp Lys Thr Gln Leu Trp Phe Met Ser His
 2660 2665 2670
 Arg Ala Leu Glu Arg Asp Gly Met Tyr Ile Pro Lys Leu Glu Glu Glu
 2675 2680 2685
 Arg Ile Val Ser Ile Leu Glu Trp Asp Arg Ser Lys Glu Pro Ser His
 2690 2695 2700
 Arg Leu Glu Ala Ile Cys Ala Ser Met Ile Glu Ala Trp Gly Tyr Asp
 2705 2710 2715 2720
 Lys Leu Val Glu Glu Ile Arg Asn Phe Tyr Ala Trp Val Leu Glu Gln
 2725 2730 2735
 Ala Pro Tyr Ser Gln Leu Ala Glu Glu Gly Lys Ala Pro Tyr Leu Ala
 2740 2745 2750
 Glu Thr Ala Leu Lys Phe Leu Tyr Thr Ser Gln His Gly Thr Asn Ser
 2755 2760 2765
 Glu Ile Glu Glu Tyr Leu Lys Val Leu Tyr Asp Tyr Asp Ile Pro Thr
 2770 2775 2780
 Thr Glu Asn Leu Tyr Phe Gln Ser Gly Thr Val Asp Ala Gly Ala Asp
 2785 2790 2795 2800
 Ala Gly Lys Lys Lys Asp Gln Lys Asp Asp Lys Val Ala Glu Gln Ala
 2805 2810 2815
 Ser Lys Asp Arg Asp Val Asn Ala Gly Thr Ser Gly Thr Phe Ser Val
 2820 2825 2830
 Pro Arg Ile Asn Ala Met Ala Thr Lys Leu Gln Tyr Pro Arg Met Arg
 2835 2840 2845
 Gly Glu Val Val Val Asn Leu Asn His Leu Leu Gly Tyr Lys Pro Gln
 2850 2855 2860
 Gln Ile Asp Leu Ser Asn Ala Arg Ala Thr His Glu Gln Phe Ala Ala
 2865 2870 2875 2880
 Trp His Gln Ala Val Met Thr Ala Tyr Gly Val Asn Glu Glu Gln Met
 2885 2890 2895
 Lys Ile Leu Leu Asn Gly Phe Met Val Trp Cys Ile Glu Asn Gly Thr
 2900 2905 2910
 Ser Pro Asn Leu Asn Gly Thr Trp Val Met Met Asp Gly Glu Asp Gln
 2915 2920 2925
 Val Ser Tyr Pro Leu Lys Pro Met Val Glu Asn Ala Gln Pro Thr Leu
 2930 2935 2940
 Arg Gln Ile Met Thr His Phe Ser Asp Leu Ala Glu Ala Tyr Ile Glu
 2945 2950 2955 2960
 Met Arg Asn Arg Glu Arg Pro Tyr Met Pro Arg Tyr Gly Leu Gln Arg
 2965 2970 2975
 Asn Ile Thr Asp Met Ser Leu Ser Arg Tyr Ala Phe Asp Phe Tyr Glu
 2980 2985 2990
 Leu Thr Ser Lys Thr Pro Val Arg Ala Arg Glu Ala His Met Gln Met
 2995 3000 3005
 Lys Ala Ala Ala Val Arg Asn Ser Gly Thr Arg Leu Phe Gly Leu Asp
 3010 3015 3020
 Gly Asn Val Gly Thr Ala Glu Glu Asp Thr Glu Arg His Thr Ala His
 3025 3030 3035 3040
 Asp Val Asn Arg Asn Met His Thr Leu Leu Gly Val Arg Gln
 3045 3050

<210> 15
 <211> 242
 <212> PRT
 <213> Potyvirus

<400> 15
 Gly Glu Ser Leu Phe Lys Gly Pro Arg Asp Tyr Asn Pro Ile Ser Ser
 1 5 10 15
 Thr Ile Cys His Leu Thr Asn Glu Ser Asp Gly His Thr Thr Ser Leu
 20 25 30
 Tyr Gly Ile Gly Phe Gly Pro Phe Ile Ile Thr Asn Lys His Leu Phe
 35 40 45
 Arg Arg Asn Asn Gly Thr Leu Leu Val Gln Ser Leu His Gly Val Phe
 50 55 60
 Lys Val Lys Asn Thr Thr Thr Leu Gln Gln His Leu Ile Asp Gly Arg
 65 70 75 80
 Asp Met Ile Ile Ile Arg Met Pro Lys Asp Phe Pro Pro Phe Pro Gln
 85 90 95
 Lys Leu Lys Phe Arg Glu Pro Gln Arg Glu Glu Arg Ile Cys Leu Val
 100 105 110
 Thr Thr Asn Phe Gln Thr Lys Ser Met Ser Ser Met Val Ser Asp Thr
 115 120 125
 Ser Cys Thr Phe Pro Ser Ser Asp Gly Ile Phe Trp Lys His Trp Ile
 130 135 140
 Gln Thr Lys Asp Gly Gln Cys Gly Ser Pro Leu Val Ser Thr Arg Asp
 145 150 155 160
 Gly Phe Ile Val Gly Ile His Ser Ala Ser Asn Phe Thr Asn Thr Asn
 165 170 175
 Asn Tyr Phe Thr Ser Val Pro Lys Asn Phe Met Glu Leu Leu Thr Asn
 180 185 190
 Gln Glu Ala Gln Gln Trp Val Ser Gly Trp Arg Leu Asn Ala Asp Ser
 195 200 205
 Val Leu Trp Gly Gly His Lys Val Phe Met Ser Lys Pro Glu Glu Pro
 210 215 220
 Phe Gln Pro Val Lys Glu Ala Thr Gln Leu Met Asn Glu Leu Val Tyr
 225 230 235 240
 Ser Gln

<210> 16
 <211> 242
 <212> PRT
 <213> Potyvirus

<220>
 <221> VARIANT
 <222> 216
 <223> S219N

<400> 16
 Gly Glu Ser Leu Phe Lys Gly Pro Arg Asp Tyr Asn Pro Ile Ser Ser
 1 5 10 15
 Thr Ile Cys His Leu Thr Asn Glu Ser Asp Gly His Thr Thr Ser Leu
 20 25 30
 Tyr Gly Ile Gly Phe Gly Pro Phe Ile Ile Thr Asn Lys His Leu Phe
 35 40 45
 Arg Arg Asn Asn Gly Thr Leu Leu Val Gln Ser Leu His Gly Val Phe
 50 55 60
 Lys Val Lys Asn Thr Thr Thr Leu Gln Gln His Leu Ile Asp Gly Arg
 65 70 75 80
 Asp Met Ile Ile Ile Arg Met Pro Lys Asp Phe Pro Pro Phe Pro Gln
 85 90 95
 Lys Leu Lys Phe Arg Glu Pro Gln Arg Glu Glu Arg Ile Cys Leu Val
 100 105 110
 Thr Thr Asn Phe Gln Thr Lys Ser Met Ser Ser Met Val Ser Asp Thr
 115 120 125
 Ser Cys Thr Phe Pro Ser Ser Asp Gly Ile Phe Trp Lys His Trp Ile
 130 135 140
 Gln Thr Lys Asp Gly Gln Cys Gly Ser Pro Leu Val Ser Thr Arg Asp
 145 150 155 160
 Gly Phe Ile Val Gly Ile His Ser Ala Ser Asn Phe Thr Asn Thr Asn
 165 170 175

Asn Tyr Phe Thr Ser Val Pro Lys Asn Phe Met Glu Leu Leu Thr Asn
 180 185 190
 Gln Glu Ala Gln Gln Trp Val Ser Gly Trp Arg Leu Asn Ala Asp Ser
 195 200 205
 Val Leu Trp Gly Gly His Lys Val Phe Met Asn Lys Pro Glu Glu Pro
 210 215 220
 Phe Gln Pro Val Lys Glu Ala Thr Gln Leu Met Asn Glu Leu Val Tyr
 225 230 235 240
 Ser Gln

<210> 17
 <211> 242
 <212> PRT
 <213> Potyvirus

<220>
 <221> VARIANT
 <222> 56
 <223> L56V

<220>
 <221> VARIANT
 <222> 135
 <223> S135G

<220>
 <221> VARIANT
 <222> 219
 <223> S219N

<400> 17
 Gly Glu Ser Leu Phe Lys Gly Pro Arg Asp Tyr Asn Pro Ile Ser Ser
 1 5 10 15
 Thr Ile Cys His Leu Thr Asn Glu Ser Asp Gly His Thr Thr Ser Leu
 20 25 30
 Tyr Gly Ile Gly Phe Gly Pro Phe Ile Ile Thr Asn Lys His Leu Phe
 35 40 45
 Arg Arg Asn Asn Gly Thr Leu Val Val Gln Ser Leu His Gly Val Phe
 50 55 60
 Lys Val Lys Asn Thr Thr Thr Leu Gln Gln His Leu Ile Asp Gly Arg
 65 70 75 80
 Asp Met Ile Ile Ile Arg Met Pro Lys Asp Phe Pro Pro Phe Pro Gln
 85 90 95
 Lys Leu Lys Phe Arg Glu Pro Gln Arg Glu Glu Arg Ile Cys Leu Val
 100 105 110
 Thr Thr Asn Phe Gln Thr Lys Ser Met Ser Ser Met Val Ser Asp Thr
 115 120 125
 Ser Cys Thr Phe Pro Ser Gly Asp Gly Ile Phe Trp Lys His Trp Ile
 130 135 140
 Gln Thr Lys Asp Gly Gln Cys Gly Ser Pro Leu Val Ser Thr Arg Asp
 145 150 155 160
 Gly Phe Ile Val Gly Ile His Ser Ala Ser Asn Phe Thr Asn Thr Asn
 165 170 175
 Asn Tyr Phe Thr Ser Val Pro Lys Asn Phe Met Glu Leu Leu Thr Asn
 180 185 190
 Gln Glu Ala Gln Gln Trp Val Ser Gly Trp Arg Leu Asn Ala Asp Ser
 195 200 205
 Val Leu Trp Gly Gly His Lys Val Phe Met Asn Lys Pro Glu Glu Pro
 210 215 220
 Phe Gln Pro Val Lys Glu Ala Thr Gln Leu Met Asn Glu Leu Val Tyr
 225 230 235 240
 Ser Gln

<210> 18

<211> 242
<212> PRT
<213> Potyvirus

<220>
<221> VARIANT
<222> 17
<223> T17V

<220>
<221> VARIANT
<222> 68
<223> N68D

<220>
<221> VARIANT
<222> 77
<223> I77V

<220>
<221> VARIANT
<222> 219
<223> S219N

<400> 18
Gly Glu Ser Leu Phe Lys Gly Pro Arg Asp Tyr Asn Pro Ile Ser Ser
1 5 10 15
Ser Ile Cys His Leu Thr Asn Glu Ser Asp Gly His Thr Thr Ser Leu
20 25 30
Tyr Gly Ile Gly Phe Gly Pro Phe Ile Ile Thr Asn Lys His Leu Phe
35 40 45
Arg Arg Asn Asn Gly Thr Leu Leu Val Gln Ser Leu His Gly Val Phe
50 55 60
Lys Val Lys Asp Thr Thr Thr Leu Gln Gln His Leu Val Asp Gly Arg
65 70 75 80
Asp Met Ile Ile Ile Arg Met Pro Lys Asp Phe Pro Pro Phe Pro Gln
85 90 95
Lys Leu Lys Phe Arg Glu Pro Gln Arg Glu Glu Arg Ile Cys Leu Val
100 105 110
Thr Thr Asn Phe Gln Thr Lys Ser Met Ser Ser Met Val Ser Asp Thr
115 120 125
Ser Cys Thr Phe Pro Ser Ser Asp Gly Ile Phe Trp Lys His Trp Ile
130 135 140
Gln Thr Lys Asp Gly Gln Cys Gly Ser Pro Leu Val Ser Thr Arg Asp
145 150 155 160
Gly Phe Ile Val Gly Ile His Ser Ala Ser Asn Phe Thr Asn Thr Asn
165 170 175
Asn Tyr Phe Thr Ser Val Pro Lys Asn Phe Met Glu Leu Leu Thr Asn
180 185 190
Gln Glu Ala Gln Gln Trp Val Ser Gly Trp Arg Leu Asn Ala Asp Ser
195 200 205
Val Leu Trp Gly Gly His Lys Val Phe Met Asn Lys Pro Glu Glu Pro
210 215 220
Phe Gln Pro Val Lys Glu Ala Thr Gln Leu Met Asn Glu Leu Val Tyr
225 230 235 240
Ser Gln

<210> 19
<211> 242
<212> PRT
<213> Potyvirus

<220>
<221> VARIANT
<222> 44
<223> N44V

<220>
 <221> VARIANT
 <222> 56
 <223> L56V

<220>
 <221> VARIANT
 <222> 135
 <223> S135G

<220>
 <221> VARIANT
 <222> 219
 <223> S219N

<400> 19
 Gly Glu Ser Leu Phe Lys Gly Pro Arg Asp Tyr Asn Pro Ile Ser Ser
 1 5 10 15
 Thr Ile Cys His Leu Thr Asn Glu Ser Asp Gly His Thr Thr Ser Leu
 20 25 30
 Tyr Gly Ile Gly Phe Gly Pro Phe Ile Ile Thr Val Lys His Leu Phe
 35 40 45
 Arg Arg Asn Asn Gly Thr Leu Val Val Gln Ser Leu His Gly Val Phe
 50 55 60
 Lys Val Lys Asn Thr Thr Thr Leu Gln Gln His Leu Ile Asp Gly Arg
 65 70 75 80
 Asp Met Ile Ile Ile Arg Met Pro Lys Asp Phe Pro Pro Phe Pro Gln
 85 90 95
 Lys Leu Lys Phe Arg Glu Pro Gln Arg Glu Glu Arg Ile Cys Leu Val
 100 105 110
 Thr Thr Asn Phe Gln Thr Lys Ser Met Ser Ser Met Val Ser Asp Thr
 115 120 125
 Ser Cys Thr Phe Pro Ser Gly Asp Gly Ile Phe Trp Lys His Trp Ile
 130 135 140
 Gln Thr Lys Asp Gly Gln Cys Gly Ser Pro Leu Val Ser Thr Arg Asp
 145 150 155 160
 Gly Phe Ile Val Gly Ile His Ser Ala Ser Asn Phe Thr Asn Thr Asn
 165 170 175
 Asn Tyr Phe Thr Ser Val Pro Lys Asn Phe Met Glu Leu Leu Thr Asn
 180 185 190
 Gln Glu Ala Gln Gln Trp Val Ser Gly Trp Arg Leu Asn Ala Asp Ser
 195 200 205
 Val Leu Trp Gly Gly His Lys Val Phe Met Asn Lys Pro Glu Glu Pro
 210 215 220
 Phe Gln Pro Val Lys Glu Ala Thr Gln Leu Met Asn Glu Leu Val Tyr
 225 230 235 240
 Ser Gln

<210> 20
 <211> 242
 <212> PRT
 <213> Potyvirus

<220>
 <221> VARIANT
 <222> 56
 <223> L56V

<220>
 <221> VARIANT
 <222> 68
 <223> N68D

<220>
 <221> VARIANT

<222> 135
<223> S135G

<220>
<221> VARIANT
<222> 219
<223> S219N

<400> 20
Gly Glu Ser Leu Phe Lys Gly Pro Arg Asp Tyr Asn Pro Ile Ser Ser
1 5 10 15
Thr Ile Cys His Leu Thr Asn Glu Ser Asp Gly His Thr Thr Ser Leu
20 25 30
Tyr Gly Ile Gly Phe Gly Pro Phe Ile Ile Thr Asn Lys His Leu Phe
35 40 45
Arg Arg Asn Asn Gly Thr Leu Val Val Gln Ser Leu His Gly Val Phe
50 55 60
Lys Val Lys Asp Thr Thr Thr Leu Gln Gln His Leu Ile Asp Gly Arg
65 70 75 80
Asp Met Ile Ile Ile Arg Met Pro Lys Asp Phe Pro Pro Phe Pro Gln
85 90 95
Lys Leu Lys Phe Arg Glu Pro Gln Arg Glu Glu Arg Ile Cys Leu Val
100 105 110
Thr Thr Asn Phe Gln Thr Lys Ser Met Ser Ser Met Val Ser Asp Thr
115 120 125
Ser Cys Thr Phe Pro Ser Gly Asp Gly Ile Phe Trp Lys His Trp Ile
130 135 140
Gln Thr Lys Asp Gly Gln Cys Gly Ser Pro Leu Val Ser Thr Arg Asp
145 150 155 160
Gly Phe Ile Val Gly Ile His Ser Ala Ser Asn Phe Thr Asn Thr Asn
165 170 175
Asn Tyr Phe Thr Ser Val Pro Lys Asn Phe Met Glu Leu Leu Thr Asn
180 185 190
Gln Glu Ala Gln Gln Trp Val Ser Gly Trp Arg Leu Asn Ala Asp Ser
195 200 205
Val Leu Trp Gly Gly His Lys Val Phe Met Asn Lys Pro Glu Glu Pro
210 215 220
Phe Gln Pro Val Lys Glu Ala Thr Gln Leu Met Asn Glu Leu Val Tyr
225 230 235 240
Ser Gln

<210> 21
<211> 242
<212> PRT
<213> Potyvirus

<220>
<221> VARIANT
<222> 17
<223> T17S

<220>
<221> VARIANT
<222> 56
<223> L56V

<220>
<221> VARIANT
<222> 68
<223> N68D

<220>
<221> VARIANT
<222> 77
<223> I77V

<220>
 <221> VARIANT
 <222> 219
 <223> S219N

<400> 21
 Gly Glu Ser Leu Phe Lys Gly Pro Arg Asp Tyr Asn Pro Ile Ser Ser
 1 5 10 15
 Ser Ile Cys His Leu Thr Asn Glu Ser Asp Gly His Thr Thr Ser Leu
 20 25 30
 Tyr Gly Ile Gly Phe Gly Pro Phe Ile Ile Thr Asn Lys His Leu Phe
 35 40 45
 Arg Arg Asn Asn Gly Thr Leu Val Val Gln Ser Leu His Gly Val Phe
 50 55 60
 Lys Val Lys Asp Thr Thr Thr Leu Gln Gln His Leu Val Asp Gly Arg
 65 70 75 80
 Asp Met Ile Ile Ile Arg Met Pro Lys Asp Phe Pro Pro Phe Pro Gln
 85 90 95
 Lys Leu Lys Phe Arg Glu Pro Gln Arg Glu Glu Arg Ile Cys Leu Val
 100 105 110
 Thr Thr Asn Phe Gln Thr Lys Ser Met Ser Ser Met Val Ser Asp Thr
 115 120 125
 Ser Cys Thr Phe Pro Ser Ser Asp Gly Ile Phe Trp Lys His Trp Ile
 130 135 140
 Gln Thr Lys Asp Gly Gln Cys Gly Ser Pro Leu Val Ser Thr Arg Asp
 145 150 155 160
 Gly Phe Ile Val Gly Ile His Ser Ala Ser Asn Phe Thr Asn Thr Asn
 165 170 175
 Asn Tyr Phe Thr Ser Val Pro Lys Asn Phe Met Glu Leu Leu Thr Asn
 180 185 190
 Gln Glu Ala Gln Gln Trp Val Ser Gly Trp Arg Leu Asn Ala Asp Ser
 195 200 205
 Val Leu Trp Gly Gly His Lys Val Phe Met Asn Lys Pro Glu Glu Pro
 210 215 220
 Phe Gln Pro Val Lys Glu Ala Thr Gln Leu Met Asn Glu Leu Val Tyr
 225 230 235 240
 Ser Gln

<210> 22
 <211> 242
 <212> PRT
 <213> Potyvirus

<220>
 <221> VARIANT
 <222> 17
 <223> T17S

<220>
 <221> VARIANT
 <222> 68
 <223> N68D

<220>
 <221> VARIANT
 <222> 77
 <223> I77V

<220>
 <221> VARIANT
 <222> 135
 <223> S135G

<220>
 <221> VARIANT
 <222> 219

<223> S219N

<400> 22

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

<210> 23

<211> 242

<212> PRT

<213> Potyvirus

<220>

<221> VARIANT

<222> 17

<223> T17S

<220>

<221> VARIANT

<222> 44

<223> N44V

<220>

<221> VARIANT

<222> 56

<223> L56V

<220>

<221> VARIANT

<222> 68

<223> N68D

<220>

<221> VARIANT

<222> 77

<223> I77V

<220>

<221> VARIANT
 <222> 135
 <223> S135G

<220>
 <221> VARIANT
 <222> (219)... (219)
 <223> S219N

<400> 23
 Gly Glu Ser Leu Phe Lys Gly Pro Arg Asp Tyr Asn Pro Ile Ser Ser
 1 5 10 15
 Ser Ile Cys His Leu Thr Asn Glu Ser Asp Gly His Thr Thr Ser Leu
 20 25 30
 Tyr Gly Ile Gly Phe Gly Pro Phe Ile Ile Thr Val Lys His Leu Phe
 35 40 45
 Arg Arg Asn Asn Gly Thr Leu Val Val Gln Ser Leu His Gly Val Phe
 50 55 60
 Lys Val Lys Asp Thr Thr Thr Leu Gln Gln His Leu Val Asp Gly Arg
 65 70 75 80
 Asp Met Ile Ile Ile Arg Met Pro Lys Asp Phe Pro Pro Phe Pro Gln
 85 90 95
 Lys Leu Lys Phe Arg Glu Pro Gln Arg Glu Glu Arg Ile Cys Leu Val
 100 105 110
 Thr Thr Asn Phe Gln Thr Lys Ser Met Ser Ser Met Val Ser Asp Thr
 115 120 125
 Ser Cys Thr Phe Pro Ser Gly Asp Gly Ile Phe Trp Lys His Trp Ile
 130 135 140
 Gln Thr Lys Asp Gly Gln Cys Gly Ser Pro Leu Val Ser Thr Arg Asp
 145 150 155 160
 Gly Phe Ile Val Gly Ile His Ser Ala Ser Asn Phe Thr Asn Thr Asn
 165 170 175
 Asn Tyr Phe Thr Ser Val Pro Lys Asn Phe Met Glu Leu Leu Thr Asn
 180 185 190
 Gln Glu Ala Gln Gln Trp Val Ser Gly Trp Arg Leu Asn Ala Asp Ser
 195 200 205
 Val Leu Trp Gly Gly His Lys Val Phe Met Asn Lys Pro Glu Glu Pro
 210 215 220
 Phe Gln Pro Val Lys Glu Ala Thr Gln Leu Met Asn Glu Leu Val Tyr
 225 230 235 240
 Ser Gln

<210> 24
 <211> 3023
 <212> PRT
 <213> Potyvirus

<400> 24
 Met Ala Ala Thr Met Ile Phe Gly Ser Phe Thr His Asp Leu Leu Gly
 1 5 10 15
 Lys Ala Met Ser Thr Ile His Ser Ala Val Thr Ala Glu Lys Asp Ile
 20 25 30
 Phe Ser Ser Ile Lys Glu Arg Leu Glu Arg Lys Arg His Gly Lys Ile
 35 40 45
 Cys Arg Met Lys Asn Gly Ser Ile Tyr Ile Lys Ala Ala Ser Ser Thr
 50 55 60
 Lys Val Glu Lys Ile Asn Ala Ala Lys Lys Leu Ala Asp Asp Lys
 65 70 75 80
 Ala Ala Phe Leu Lys Ala Gln Pro Thr Ile Val Asp Lys Ile Ile Val
 85 90 95
 Asn Glu Lys Ile Gln Val Val Glu Ala Glu Glu Val His Lys Arg Glu
 100 105 110
 Asp Val Gln Thr Val Phe Phe Lys Lys Thr Lys Lys Arg Ala Pro Lys
 115 120 125
 Leu Arg Ala Thr Cys Ser Ser Ser Gly Leu Asp Asn Leu Tyr Asn Ala
 130 135 140

Val	Ala	Asn	Ile	Ala	Lys	Ala	Ser	Ser	Leu	Arg	Val	Glu	Val	Ile	His
145					150					155					160
Lys	Lys	Arg	Val	Cys	Gly	Glu	Phe	Lys	Gln	Thr	Arg	Phe	Gly	Arg	Ala
				165					170					175	
Leu	Phe	Ile	Asp	Val	Ala	His	Ala	Lys	Gly	His	Arg	Arg	Arg	Ile	Asp
			180					185					190		
Cys	Arg	Met	His	Arg	Arg	Glu	Gln	Arg	Thr	Met	His	Met	Phe	Met	Arg
		195						200				205			
Lys	Thr	Thr	Lys	Thr	Glu	Val	Arg	Ser	Lys	His	Leu	Arg	Lys	Gly	Asp
	210				215						220				
Ser	Gly	Ile	Val	Leu	Leu	Thr	Gln	Lys	Ile	Lys	Gly	His	Leu	Ser	Gly
225					230					235					240
Val	Arg	Asp	Glu	Phe	Phe	Ile	Val	Arg	Gly	Thr	Cys	Asp	Asp	Ser	Leu
			245						250					255	
Leu	Glu	Ala	Arg	Ala	Arg	Phe	Ser	Gln	Ser	Ile	Thr	Leu	Arg	Ala	Thr
			260					265					270		
His	Phe	Ser	Thr	Gly	Asp	Ile	Phe	Trp	Lys	Gly	Phe	Asn	Ala	Ser	Phe
		275					280					285			
Gln	Glu	Gln	Lys	Ala	Ile	Gly	Leu	Asp	His	Thr	Cys	Thr	Ser	Asp	Leu
	290				295						300				
Pro	Val	Glu	Ala	Cys	Gly	His	Val	Ala	Ala	Leu	Met	Cys	Gln	Ser	Leu
305					310					315					320
Phe	Pro	Cys	Gly	Lys	Ile	Thr	Cys	Lys	Arg	Cys	Ile	Ala	Asn	Leu	Ser
			325						330					335	
Asn	Leu	Asp	Phe	Asp	Thr	Phe	Ser	Glu	Leu	Gln	Gly	Asp	Arg	Ala	Met
			340					345					350		
Arg	Ile	Leu	Asp	Val	Met	Arg	Ala	Arg	Phe	Pro	Ser	Phe	Thr	His	Thr
		355					360					365			
Ile	Arg	Phe	Leu	His	Asp	Leu	Phe	Thr	Gln	Arg	Arg	Val	Thr	Asn	Pro
	370					375					380				
Asn	Thr	Ala	Ala	Phe	Arg	Glu	Ile	Leu	Arg	Leu	Ile	Gly	Asp	Arg	Asn
385					390					395					400
Glu	Ala	Pro	Phe	Ala	His	Val	Asn	Arg	Leu	Asn	Glu	Ile	Leu	Leu	Leu
			405						410				415		
Gly	Ser	Lys	Ala	Asn	Pro	Asp	Ser	Leu	Ala	Lys	Ala	Ser	Asp	Ser	Leu
			420					425					430		
Leu	Glu	Leu	Ala	Arg	Tyr	Leu	Asn	Asn	Arg	Thr	Glu	Asn	Ile	Arg	Asn
	435					440						445			
Gly	Ser	Leu	Lys	His	Phe	Arg	Asn	Lys	Ile	Ser	Ser	Lys	Ala	His	Ser
	450					455					460				
Asn	Leu	Ala	Leu	Ser	Cys	Asp	Asn	Gln	Leu	Asp	Gln	Asn	Gly	Asn	Phe
465					470					475					480
Leu	Trp	Gly	Leu	Ala	Gly	Ile	Ala	Ala	Lys	Arg	Phe	Leu	Asn	Asn	Tyr
			485						490					495	
Phe	Glu	Thr	Ile	Asp	Pro	Glu	Gln	Gly	Tyr	Asp	Lys	Tyr	Val	Ile	Arg
			500					505					510		
Lys	Asn	Pro	Asn	Gly	Glu	Arg	Lys	Leu	Ala	Ile	Gly	Asn	Phe	Ile	Ile
	515						520					525			
Ser	Thr	Asn	Leu	Glu	Lys	Leu	Arg	Asp	Gln	Leu	Glu	Gly	Glu	Ser	Ile
	530					535					540				
Ala	Arg	Val	Gly	Ile	Thr	Glu	Glu	Cys	Val	Ser	Arg	Lys	Asp	Gly	Asn
545					550					555					560
Tyr	Arg	Tyr	Pro	Cys	Cys	Val	Thr	Leu	Glu	Asp	Gly	Ser	Pro	Met	
			565						570				575		
Tyr	Ser	Glu	Leu	Lys	Met	Pro	Thr	Lys	Asn	His	Leu	Val	Ile	Gly	Asn
		580						585					590		
Ser	Gly	Asp	Pro	Lys	Tyr	Leu	Asp	Leu	Pro	Gly	Glu	Ile	Ser	Asn	Leu
	595						600					605			
Met	Tyr	Ile	Ala	Lys	Glu	Gly	Tyr	Cys	Tyr	Ile	Asn	Ile	Phe	Leu	Ala
	610					615					620				
Met	Leu	Val	Asn	Val	Asp	Glu	Ala	Asn	Ala	Lys	Asp	Phe	Thr	Lys	Arg
625					630					635					640
Val	Arg	Asp	Glu	Ser	Val	Gln	Lys	Leu	Gly	Lys	Trp	Pro	Ser	Leu	Ile
			645						650					655	
Asp	Val	Ala	Thr	Glu	Cys	Ala	Leu	Leu	Ser	Thr	Tyr	Tyr	Pro	Ala	Ala
		660						665					670		
Ala	Ser	Ala	Glu	Leu	Pro	Arg	Leu	Leu	Val	Asp	His	Ala	Gln	Lys	Thr
	675						680					685			

Ile His Val Val Asp Ser Tyr Gly Ser Leu Asn Thr Gly Tyr His Ile
 690 695 700
 Leu Lys Ala Asn Thr Val Ser Gln Leu Glu Lys Phe Ala Ser Asn Thr
 705 710 715 720
 Leu Glu Ser Pro Met Ala Gln Tyr Lys Val Gly Gly Leu Val Tyr Ser
 725 730 735
 Glu Asn Asn Asp Ala Ser Ala Val Lys Ala Leu Thr Gln Ala Ile Phe
 740 745 750
 Arg Pro Asp Val Leu Ser Glu Leu Ile Glu Lys Glu Pro Tyr Leu Met
 755 760 765
 Val Phe Ala Leu Val Ser Pro Gly Ile Leu Met Ala Met Ser Asn Ser
 770 775 780
 Gly Ala Leu Glu Phe Gly Ile Ser Lys Trp Ile Ser Ser Asp His Ser
 785 790 795 800
 Leu Val Arg Met Ala Ser Ile Leu Lys Thr Leu Ala Ser Lys Val Ser
 805 810 815
 Val Ala Asp Thr Leu Ala Leu Gln Lys His Ile Met Arg Gln Asn Ala
 820 825 830
 Asn Phe Leu Cys Gly Glu Leu Ile Asn Gly Phe Gln Lys Lys Lys Ser
 835 840 845
 Tyr Thr His Ala Thr Arg Phe Leu Leu Met Ile Ser Glu Glu Asn Glu
 850 855 860
 Met Asp Asp Pro Val Leu Asn Ala Gly Tyr Arg Val Leu Glu Ala Ser
 865 870 875 880
 Ser His Glu Ile Met Glu Lys Thr Tyr Leu Ala Leu Leu Glu Thr Ser
 885 890 895
 Trp Ser Asp Leu Ser Leu Tyr Gly Lys Phe Lys Ser Ile Trp Phe Thr
 900 905 910
 Arg Lys His Phe Gly Arg Tyr Lys Ala Glu Leu Phe Pro Lys Glu Gln
 915 920 925
 Thr Asp Leu Gln Gly Arg Tyr Ser Asn Ser Leu Arg Phe His Tyr Gln
 930 935 940
 Ser Thr Leu Lys Arg Leu Arg Asn Lys Gly Ser Leu Cys Arg Glu Arg
 945 950 955 960
 Phe Leu Glu Ser Ile Ser Ser Ala Arg Arg Arg Thr Thr Cys Ala Val
 965 970 975
 Phe Ser Leu Leu His Lys Ala Phe Pro Asp Val Leu Lys Phe Ile Asn
 980 985 990
 Thr Leu Val Ile Val Ser Leu Ser Met Gln Ile Tyr Tyr Met Leu Val
 995 1000 1005
 Ala Ile Ile His Glu His Arg Ala Ala Lys Ile Lys Ser Ala Gln Leu
 1010 1015 1020
 Glu Glu Arg Val Leu Glu Asp Lys Thr Met Leu Leu Tyr Asp Asp Phe
 1025 1030 1035 1040
 Lys Ala Lys Leu Pro Glu Gly Ser Phe Glu Glu Phe Leu Glu Tyr Thr
 1045 1050 1055
 Arg Gln Arg Asp Lys Glu Val Tyr Glu Tyr Leu Met Met Glu Thr Thr
 1060 1065 1070
 Glu Ile Val Glu Phe Gln Ala Lys Asn Thr Gly Gln Ala Ser Leu Glu
 1075 1080 1085
 Arg Ile Ile Ala Phe Val Ser Leu Thr Leu Met Leu Phe Asp Asn Glu
 1090 1095 1100
 Arg Ser Asp Cys Val Tyr Lys Ile Leu Thr Lys Phe Lys Gly Ile Leu
 1105 1110 1115 1120
 Gly Ser Val Glu Asn Asn Val Arg Phe Gln Ser Leu Asp Thr Ile Val
 1125 1130 1135
 Pro Thr Gln Glu Glu Lys Asn Met Val Ile Asp Phe Glu Leu Asp Ser
 1140 1145 1150
 Asp Thr Ala His Thr Pro Gln Met Gln Glu Gln Thr Phe Ser Asp Trp
 1155 1160 1165
 Trp Ser Asn Gln Ile Ala Asn Asn Arg Val Val Pro His Tyr Arg Thr
 1170 1175 1180
 Glu Gly Tyr Phe Met Gln Phe Thr Arg Asn Thr Ala Ser Ala Val Ser
 1185 1190 1195 1200
 His Gln Ile Ala His Asn Glu His Lys Asp Ile Ile Leu Met Gly Ala
 1205 1210 1215
 Val Gly Ser Gly Lys Ser Thr Gly Leu Pro Thr Asn Leu Cys Lys Phe
 1220 1225 1230

Gly Gly Val Leu Leu Leu Glu Pro Thr Arg Pro Leu Ala Glu Asn Val
 1235 1240 1245
 Thr Lys Gln Met Arg Gly Ser Pro Phe Phe Ala Ser Pro Thr Leu Arg
 1250 1255 1260
 Met Arg Asn Leu Ser Thr Phe Gly Ser Ser Pro Ile Thr Val Met Thr
 1265 1270 1275 1280
 Thr Gly Phe Ala Leu His Phe Phe Ala Asn Asn Val Lys Glu Phe Asp
 1285 1290 1295
 Arg Tyr Gln Phe Ile Ile Phe Asp Glu Phe His Val Leu Asp Ser Asn
 1300 1305 1310
 Ala Ile Ala Phe Arg Asn Leu Cys His Glu Tyr Ser Tyr Asn Gly Lys
 1315 1320 1325
 Ile Ile Lys Val Ser Ala Thr Pro Pro Gly Arg Glu Cys Asp Leu Thr
 1330 1335 1340
 Thr Gln Tyr Pro Val Glu Leu Leu Ile Glu Glu Gln Leu Ser Leu Arg
 1345 1350 1355 1360
 Asp Phe Val Asp Ala Gln Gly Thr Asp Ala His Ala Asp Val Val Lys
 1365 1370 1375
 Lys Gly Asp Asn Ile Leu Val Tyr Val Ala Ser Tyr Asn Glu Val Asp
 1380 1385 1390
 Gln Leu Ser Lys Met Leu Asn Glu Arg Gly Phe Leu Val Thr Lys Val
 1395 1400 1405
 Asp Gly Arg Thr Met Lys Leu Gly Gly Val Glu Ile Ile Thr Lys Gly
 1410 1415 1420
 Ser Ser Ile Lys Lys His Phe Ile Val Ala Thr Asn Ile Ile Glu Asn
 1425 1430 1435 1440
 Gly Val Thr Leu Asp Val Asp Val Val Val Asp Phe Gly Leu Lys Val
 1445 1450 1455
 Val Pro Asn Leu Asp Ser Asp Asn Arg Leu Val Ser Tyr Cys Lys Ile
 1460 1465 1470
 Pro Ile Ser Leu Gly Glu Arg Ile Gln Arg Phe Gly Arg Val Gly Arg
 1475 1480 1485
 Asn Lys Pro Gly Val Ala Leu Arg Ile Gly Glu Thr Ile Lys Gly Leu
 1490 1495 1500
 Val Glu Ile Pro Ser Met Ile Ala Thr Glu Ala Ala Phe Leu Cys Phe
 1505 1510 1515 1520
 Val Tyr Gly Leu Pro Val Thr Thr Gln Asn Val Ser Thr Ser Ile Leu
 1525 1530 1535
 Ser Gln Val Ser Val Arg Gln Ala Arg Val Met Cys Gln Phe Glu Leu
 1540 1545 1550
 Pro Ile Phe Tyr Thr Ala His Leu Val Arg Tyr Asp Gly Ala Met His
 1555 1560 1565
 Pro Ala Ile His Asn Ala Leu Lys Arg Phe Lys Leu Arg Asp Ser Glu
 1570 1575 1580
 Ile Asn Leu Asn Thr Leu Ala Ile Pro Thr Ser Ser Ser Lys Thr Trp
 1585 1590 1595 1600
 Tyr Thr Gly Lys Cys Tyr Lys Gln Leu Val Gly Arg Leu Asp Ile Pro
 1605 1610 1615
 Asp Glu Ile Lys Ile Pro Phe Tyr Thr Lys Glu Val Pro Glu Lys Val
 1620 1625 1630
 Pro Glu Gln Ile Trp Asp Val Met Val Lys Phe Ser Ser Asp Ala Gly
 1635 1640 1645
 Phe Gly Arg Met Thr Ser Ala Ala Ala Cys Lys Val Ala Tyr Thr Leu
 1650 1655 1660
 Gln Thr Asp Ile His Ser Ile Gln Arg Thr Val Gln Ile Ile Asp Arg
 1665 1670 1675 1680
 Leu Leu Glu Asn Glu Met Lys Lys Arg Asn His Phe Asn Leu Val Val
 1685 1690 1695
 Asn Gln Ser Cys Ser Ser His Phe Met Ser Leu Ser Ser Ile Met Ala
 1700 1705 1710
 Ser Leu Arg Ala His Tyr Ala Lys Asn His Thr Gly Gln Asn Ile Glu
 1715 1720 1725
 Ile Leu Gln Lys Ala Lys Ala Gln Leu Leu Glu Phe Ser Asn Leu Ala
 1730 1735 1740
 Ile Asp Pro Ser Thr Thr Glu Ala Leu Arg Asp Phe Gly Tyr Leu Glu
 1745 1750 1755 1760
 Ala Val Arg Phe Gln Ser Glu Ser Glu Met Ala Arg Gly Leu Lys Leu
 1765 1770 1775

Ser Gly His Trp Lys Trp Ser Leu Ile Ser Arg Asp Leu Ile Val Val
 1780 1785 1790
 Ser Gly Val Gly Ile Gly Leu Gly Cys Met Leu Trp Gln Phe Phe Lys
 1795 1800 1805
 Glu Lys Met His Glu Pro Val Lys Phe Gln Gly Lys Ser Arg Arg Arg
 1810 1815 1820
 Leu Gln Phe Arg Lys Ala Arg Asp Asp Lys Met Gly Tyr Ile Met His
 1825 1830 1835 1840
 Gly Glu Gly Asp Thr Ile Glu His Phe Phe Gly Ala Ala Tyr Thr Lys
 1845 1850 1855
 Lys Gly Lys Ser Lys Gly Lys Thr His Gly Ala Gly Thr Lys Ala His
 1860 1865 1870
 Lys Phe Val Asn Met Tyr Gly Val Ser Pro Asp Glu Tyr Ser Tyr Val
 1875 1880 1885
 Arg Tyr Leu Asp Pro Val Thr Gly Ala Thr Leu Asp Glu Ser Pro Met
 1890 1895 1900
 Thr Asp Leu Asn Ile Val Gln Glu His Phe Gly Glu Ile Arg Arg Glu
 1905 1910 1915 1920
 Ala Ile Leu Ala Asp Ala Met Ser Pro Gln Gln Arg Asn Lys Gly Ile
 1925 1930 1935
 Gln Ala Tyr Phe Val Arg Asn Ser Thr Met Pro Ile Leu Lys Val Asp
 1940 1945 1950
 Leu Thr Pro His Ile Pro Leu Lys Val Cys Glu Ser Asn Asn Ile Ala
 1955 1960 1965
 Gly Phe Pro Glu Arg Glu Gly Glu Leu Arg Arg Thr Gly Pro Thr Glu
 1970 1975 1980
 Thr Leu Pro Phe Asp Ala Leu Pro Pro Glu Lys Gln Glu Val Ala Phe
 1985 1990 1995 2000
 Glu Ser Lys Ala Leu Lys Gly Val Arg Asp Phe Asn Pro Ile Ser
 2005 2010 2015
 Ala Cys Val Trp Leu Leu Glu Asn Ser Ser Asp Gly His Ser Glu Arg
 2020 2025 2030
 Leu Phe Gly Ile Gly Phe Gly Pro Tyr Ile Ile Ala Asn Gln His Leu
 2035 2040 2045
 Phe Arg Arg Asn Asn Gly Glu Leu Thr Ile Lys Thr Met His Gly Glu
 2050 2055 2060
 Phe Lys Val Lys Asn Ser Thr Gln Leu Gln Met Lys Pro Val Glu Gly
 2065 2070 2075 2080
 Arg Asp Ile Ile Val Ile Lys Met Ala Lys Asp Phe Pro Pro Phe Pro
 2085 2090 2095
 Gln Lys Leu Lys Phe Arg Gln Pro Thr Ile Lys Asp Arg Val Cys Met
 2100 2105 2110
 Val Ser Thr Asn Phe Gln Gln Lys Ser Val Ser Ser Leu Val Ser Glu
 2115 2120 2125
 Ser Ser His Ile Val His Lys Glu Asp Thr Ser Phe Trp Gln His Trp
 2130 2135 2140
 Ile Thr Thr Lys Asp Gly Gln Cys Gly Ser Pro Leu Val Ser Ile Ile
 2145 2150 2155 2160
 Asp Gly Asn Ile Leu Gly Ile His Ser Leu Thr His Thr Thr Asn Gly
 2165 2170 2175
 Ser Asn Tyr Phe Val Glu Phe Pro Glu Lys Phe Val Ala Thr Tyr Leu
 2180 2185 2190
 Asp Ala Ala Asp Gly Trp Cys Lys Asn Trp Lys Phe Asn Ala Asp Lys
 2195 2200 2205
 Ile Ser Trp Gly Ser Phe Thr Leu Val Glu Asp Ala Pro Glu Asp Asp
 2210 2215 2220
 Phe Met Ala Lys Lys Thr Val Ala Ala Ile Met Asp Asp Leu Val Arg
 2225 2230 2235 2240
 Thr Gln Gly Glu Lys Arg Lys Trp Met Leu Glu Ala Ala His Thr Asn
 2245 2250 2255
 Ile Gln Pro Val Ala His Leu Gln Ser Gln Leu Val Thr Lys His Ile
 2260 2265 2270
 Val Lys Gly Arg Cys Lys Met Phe Ala Leu Tyr Leu Gln Glu Ash Ala
 2275 2280 2285
 Asp Ala Arg Asp Phe Phe Lys Ser Phe Met Gly Ala Tyr Gly Pro Ser
 2290 2295 2300
 His Leu Asn Lys Glu Ala Tyr Ile Lys Asp Ile Met Lys Tyr Ser Lys
 2305 2310 2315 2320

Gln Ile Val Val Gly Ser Val Asp Cys Asp Thr Phe Glu Ser Ser Leu
 2325 2330 2335
 Lys Val Leu Ser Arg Lys Met Lys Glu Trp Gly Phe Glu Asn Leu Glu
 2340 2345 2350
 Tyr Val Thr Asp Glu Gln Thr Ile Lys Asn Ala Leu Asn Met Asp Ala
 2355 2360 2365
 Ala Val Gly Ala Leu Tyr Ser Gly Lys Lys Lys Gln Tyr Phe Glu Asp
 2370 2375 2380
 Leu Ser Asp Asp Ala Val Ala Asn Leu Val Gln Lys Ser Cys Leu Arg
 2385 2390 2395 2400
 Leu Phe Lys Asn Lys Leu Gly Val Trp Asn Gly Ser Leu Lys Ala Glu
 2405 2410 2415
 Leu Arg Pro Phe Glu Lys Leu Ile Glu Asn Lys Thr Arg Thr Phe Thr
 2420 2425 2430
 Ala Ala Pro Ile Glu Thr Leu Leu Gly Gly Lys Val Cys Val Asp Asp
 2435 2440 2445
 Phe Asn Asn His Phe Tyr Ser Lys His Ile Gln Cys Pro Trp Ser Val
 2450 2455 2460
 Gly Met Thr Lys Phe Tyr Gly Gly Trp Asn Glu Leu Leu Gly Lys Leu
 2465 2470 2475 2480
 Pro Asp Gly Trp Val Tyr Cys Asp Ala Asp Gly Ser Gln Phe Asp Ser
 2485 2490 2495
 Ser Leu Ser Pro Tyr Leu Ile Asn Ala Val Leu Arg Leu Arg Leu Ser
 2500 2505 2510
 Ser Met Glu Trp Asp Val Gly Gln Lys Met Leu Gln Asn Leu Tyr
 2515 2520 2525
 Thr Glu Ile Val Tyr Thr Pro Ile Ser Thr Pro Asp Gly Thr Ile Val
 2530 2535 2540
 Lys Lys Phe Lys Gly Asn Asn Ser Gly Gln Pro Ser Thr Val Val Asp
 2545 2550 2555 2560
 Asn Thr Leu Met Val Val Leu Ala Met Tyr Tyr Ala Leu Ser Lys Leu
 2565 2570 2575
 Gly Val Asp Ile Asn Ser Gln Glu Asp Val Cys Lys Phe Phe Ala Asn
 2580 2585 2590
 Gly Asp Asp Leu Ile Ile Ala Ile Ser Pro Glu Leu Glu His Val Leu
 2595 2600 2605
 Asp Gly Phe Gln Gln His Phe Ser Asp Leu Gly Leu Asn Tyr Asp Phe
 2610 2615 2620
 Ser Ser Arg Thr Arg Asp Lys Lys Glu Leu Trp Phe Met Ser His Arg
 2625 2630 2635 2640
 Ala Leu Ser Lys Asp Gly Ile Leu Ile Pro Lys Leu Glu Pro Glu Arg
 2645 2650 2655
 Ile Val Ser Ile Leu Glu Trp Asp Arg Ser Ala Glu Pro His His Arg
 2660 2665 2670
 Leu Glu Ala Ile Cys Ala Ser Met Ile Glu Ala Trp Gly Tyr Thr Asp
 2675 2680 2685
 Leu Leu Gln Asn Ile Arg Arg Phe Tyr Lys Trp Thr Ile Glu Gln Glu
 2690 2695 2700
 Pro Tyr Arg Ser Leu Ala Glu Gln Gly Leu Ala Pro Tyr Leu Ser Glu
 2705 2710 2715 2720
 Val Ala Leu Arg Arg Leu Tyr Thr Ser Gln Ile Ala Thr Asp Asn Glu
 2725 2730 2735
 Leu Thr Asp Tyr Tyr Lys Glu Ile Leu Ala Asn Asn Glu Phe Leu Arg
 2740 2745 2750
 Glu Thr Val Arg Phe Gln Ser Asp Thr Val Asp Ala Gly Lys Asp Lys
 2755 2760 2765
 Ala Arg Asp Gln Lys Leu Ala Asp Lys Pro Thr Leu Ala Ile Asp Arg
 2770 2775 2780
 Thr Lys Asp Lys Asp Val Asn Thr Gly Thr Ser Gly Thr Phe Ser Ile
 2785 2790 2795 2800
 Pro Arg Leu Lys Lys Ala Ala Met Asn Met Lys Leu Pro Lys Val Gly
 2805 2810 2815
 Gly Ser Ser Val Val Asn Leu Asp His Leu Leu Thr Tyr Lys Pro Ala
 2820 2825 2830
 Gln Glu Phe Val Val Asn Thr Arg Ala Thr His Ser Gln Phe Lys Ala
 2835 2840 2845
 Trp His Thr Asn Val Met Ala Glu Leu Glu Leu Asn Glu Glu Gln Met
 2850 2855 2860

Lys Ile Val Leu Asn Gly Phe Met Ile Trp Cys Ile Glu Asn Gly Thr
 2865 2870 2875 2880
 Ser Pro Asn Ile Ser Gly Val Trp Thr Met Met Asp Gly Asp Glu Gln
 2885 2890 2895
 Val Glu Tyr Pro Ile Glu Pro Met Val Lys His Ala Asn Pro Ser Leu
 2900 2905 2910
 Arg Gln Ile Met Lys His Phe Ser Asn Leu Ala Glu Ala Tyr Ile Arg
 2915 2920 2925
 Met Arg Asn Ser Glu Gln Val Tyr Ile Pro Arg Tyr Gly Leu Gln Arg
 2930 2935 2940
 Gly Leu Val Asp Arg Asn Leu Ala Pro Phe Ala Phe Asp Phe Phe Glu
 2945 2950 2955 2960
 Val Asn Gly Ala Thr Pro Val Arg Ala Arg Glu Ala His Ala Gln Met
 2965 2970 2975
 Lys Ala Ala Ala Leu Arg Asn Ser Gln Gln Arg Met Phe Cys Leu Asp
 2980 2985 2990
 Gly Ser Val Ser Gly Gln Glu Glu Asn Thr Glu Arg His Thr Val Asp
 2995 3000 3005
 Asp Val Asn Ala Gln Met His His Leu Leu Gly Val Lys Gly Val
 3010 3015 3020

<210> 25
 <211> 381
 <212> PRT
 <213> Bacillus subtilis

<400> 25
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 1 5 10 15
 Ile Phe Thr Met Ala Phe Ser Asn Met Ser Ala Gln Ala Ala Gly Lys
 20 25 30
 Ser Ser Thr Glu Lys Lys Tyr Ile Val Gly Phe Lys Gln Thr Met Ser
 35 40 45
 Ala Met Ser Ser Ala Lys Lys Lys Asp Val Ile Ser Glu Lys Gly Gly
 50 55 60
 Lys Val Gln Lys Gln Phe Lys Tyr Val Asn Ala Thr Ala Thr Leu
 65 70 75 80
 Asp Glu Lys Ala Val Lys Glu Leu Lys Gln Asp Pro Ser Val Ala Tyr
 85 90 95
 Val Glu Glu Asp His Ile Ala His Glu Tyr Ala Gln Ser Val Pro Tyr
 100 105 110
 Gly Ile Ser Gln Ile Lys Ala Pro Ala Leu His Ser Gln Gly Tyr Thr
 115 120 125
 Gly Ser Asn Val Lys Val Ala Val Ile Asp Ser Gly Ile Asp Ser Ser
 130 135 140
 His Pro Asp Leu Asn Val Lys Gly Gly Ala Ser Phe Val Pro Ser Glu
 145 150 155 160
 Thr Asn Pro Tyr Gln Asp Gly Ser Ser His Gly Thr His Val Ala Gly
 165 170 175
 Thr Ile Ala Ala Leu Asn Asn Thr Ile Gly Val Leu Gly Val Ala Pro
 180 185 190
 Asn Ala Ser Leu Tyr Ala Val Lys Val Leu Asp Ser Thr Gly Ser Gly
 195 200 205
 Gln Tyr Ser Trp Ile Ile Asn Gly Ile Glu Trp Ala Ile Ser Asn Asn
 210 215 220
 Met Asp Val Ile Asn Met Ser Leu Gly Gly Pro Ser Gly Ser Thr Ala
 225 230 235 240
 Leu Lys Thr Val Val Asp Lys Ala Val Ser Ser Gly Ile Val Val Ala
 245 250 255
 Ala Ala Ala Gly Asn Glu Gly Ser Ser Gly Ser Thr Ser Thr Val Gly
 260 265 270
 Tyr Pro Ala Lys Tyr Pro Ser Thr Ile Ala Val Gly Ala Val Asn Ser
 275 280 285
 Ser Asn Gln Arg Ala Ser Phe Ser Ser Ala Gly Ser Glu Leu Asp Val
 290 295 300
 Met Ala Pro Gly Val Ser Ile Gln Ser Thr Leu Pro Gly Gly Thr Tyr
 305 310 315 320

Gly Ala Tyr Asn Gly Thr Ser Met Ala Thr Pro His Val Ala Gly Ala
 325 330 335
 Ala Ala Leu Ile Leu Ser Lys His Pro Thr Trp Thr Asn Ala Gln Val
 340 345 350
 Arg Asp Arg Leu Glu Ser Thr Ala Thr Tyr Leu Gly Ser Phe Tyr
 355 360 365
 Tyr Gly Lys Gly Leu Ile Asn Val Gln Ala Ala Ala Gln
 370 375 380

<210> 26
 <211> 277
 <212> PRT
 <213> Rattus norvegicus

<400> 26
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 Glu Thr Lys Thr Ile His Gly Ser Lys Ser Met Asp Ser Gly Ile Tyr
 20 25 30
 Leu Asp Ser Ser Tyr Lys Met Asp Tyr Pro Glu Met Gly Leu Cys Ile
 35 40 45
 Ile Ile Asn Asn Lys Asn Phe His Lys Ser Thr Gly Met Ser Ala Arg
 50 55 60
 Asn Gly Thr Asp Val Asp Ala Ala Asn Leu Arg Glu Thr Phe Met Ala
 65 70 75 80
 Leu Lys Tyr Glu Val Arg Asn Lys Asn Asp Leu Thr Arg Glu Glu Ile
 85 90 95
 Met Glu Leu Met Asp Ser Val Ser Lys Glu Asp His Ser Lys Arg Ser
 100 105 110
 Ser Phe Val Cys Val Ile Leu Ser His Gly Asp Glu Gly Val Ile Phe
 115 120 125
 Gly Thr Asn Gly Pro Val Asp Leu Lys Lys Leu Thr Ser Phe Phe Arg
 130 135 140
 Gly Asp Tyr Cys Arg Ser Leu Thr Gly Lys Pro Lys Leu Phe Ile Ile
 145 150 155 160
 Gln Ala Cys Arg Gly Thr Glu Leu Asp Cys Gly Ile Glu Thr Asp Ser
 165 170 175
 Gly Thr Asp Asp Met Ala Cys Gln Lys Ile Pro Val Glu Ala Asp
 180 185 190
 Phe Leu Tyr Ala Tyr Ser Thr Ala Pro Gly Tyr Tyr Ser Trp Arg Asn
 195 200 205
 Ser Arg Asp Gly Ser Trp Phe Ile Gln Ser Leu Cys Ala Met Leu Lys
 210 215 220
 Leu Tyr Ala His Lys Leu Glu Phe Met His Ile Leu Thr Arg Val Asn
 225 230 235 240
 Arg Lys Val Ala Thr Glu Phe Glu Ser Phe Ser Leu Asp Ala Thr Phe
 245 250 255
 His Ala Lys Lys Gln Ile Pro Cys Ile Val Ser Met Leu Thr Lys Glu
 260 265 270
 Leu Tyr Phe Tyr His
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<210> 27
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Tobacco Etch virus protease cleavage site -
 consensus sequence

<220>
 <221> VARIANT
 <222> 2, 3, 5
 <223> xaa can be any amino acid

<400> 27
Glu Xaa Xaa Tyr Xaa Gln Gly
1 5

<210> 28
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Tobacco Etch Virus protease cleavage site
consensus sequence

<220>
<221> VARIANT
<222> 2, 3, 5
<223> Xaa can be any amino acid

<400> 28
Glu Xaa Xaa Tyr Xaa Gln Ser
1 5

<210> 29
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Tobacco Etch Virus protease cleavage site

<400> 29
Glu Asn Leu Tyr Phe Gln Gly
1 5

<210> 30
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Tobacco Etch Virus protease cleavage site

<400> 30
Glu Asn Leu Tyr Phe Gln Ser
1 5

<210> 31
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Tobacco Etch Virus protease cleavage site

<400> 31
Glu Asn Ile Tyr Thr Gln Gly
1 5

<210> 32
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Tobacco Etch Virus protease cleavage site

<400> 32
Glu Asn Ile Tyr Thr Gln Ser
1 5

<210> 33
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Tobacco Etch Virus protease cleavage site

<400> 33
Glu Asn Ile Tyr Leu Gln Gly
1 5

<210> 34
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Tobacco Etch Virus protease cleavage site

<400> 34
Glu Asn Ile Tyr Leu Gln Ser
1 5

<210> 35
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Tobacco Etch Virus protease cleavage site

<400> 35
Glu Asn Val Tyr Phe Gln Gly
1 5

<210> 36
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Tobacco Etch Virus protease cleavage site

<400> 36
Glu Asn Val Tyr Ser Gln Ser
1 5

<210> 37
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Tobacco Etch Virus protease cleavage site

<400> 37
Glu Asn Val Tyr Ser Gln Gly
1 5

<210> 38
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Tobacco Etch Virus protease cleavage site

<400> 38
Glu Asn Val Tyr Ser Gln Ser
1 5

<210> 39
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Tobacco Vein Mottling Virus protease cleavage site
consensus sequence

<220>
<221> VARIANT
<222> 1, 2
<223> Xaa can be any amino acid

<400> 39
Xaa Xaa Val Arg Phe Gln Gly
1 5

<210> 40
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Tobacco Vein Mottling Virus protease cleavage site
consensus sequence

<220>
<221> VARIANT
<222> 1, 2
<223> Xaa can be any amino acid

<400> 40
Xaa Xaa Val Arg Phe Gln Ser
1 5

<210> 41
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Tobacco Vein Mottling Virus protease cleavage site

<400> 41
Glu Thr Val Arg Phe Gln Gly
1 5

<210> 42
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Tobacco Vein Mottling Virus protease cleavage site

<400> 42
Glu Thr Val Arg Phe Gln Ser
1 5

<210> 43
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Tobacco Vein Mottling Virus protease cleavage site

<400> 43
Asn Asn Val Arg Phe Gln Gly
1 5

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

<220>
<223> Tobacco Vein Mottling Virus protease cleavage site

<400> 44
Asn Asn Val Arg Phe Gln Ser
1 5

<210> 45
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Human Rhinovirus 3C protease cleavage site
consensus sequence

<220>
<221> VARIANT
<222> 1
<223> Xaa can be amino acid, with D or E preferred

<220>
<221> VARIANT
<222> 2
<223> Xaa can be G, A, V, L, I, M, S or T

<400> 45
Xaa Xaa Leu Phe Gln Gly Pro
1 5

<210> 46
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Human Rhinovirus 3C protease cleavage site

<400> 46
Glu Ala Leu Phe Gln Gly Pro
1 5

<210> 47
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Human Rhinovirus 3C protease cleavage site

<400> 47
Glu Val Leu Phe Gln Gly Pro
1 5

<210> 48
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Human Rhinovirus 3C protease cleavage site

<400> 48
Glu Leu Leu Phe Gln Gly Pro
1 5

<210> 49
<211> 7
<212> PRT
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<220>
<223> Human Rhinovirus 3C protease cleavage site

<400> 49
Asp Ala Leu Phe Gln Gly Pro
1 5

<210> 50
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Human Rhinovirus 3C protease cleavage site

<400> 50
Asp Val Leu Phe Gln Gly Pro
1 5

<210> 51
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Human Rhinovirus 3C protease cleavage site

<400> 51
Asp Leu Leu Phe Gln Gly Pro
1 5

<210> 52
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> subtilisin protease cleavage site consensus
sequence

<220>
<221> VARIANT
<222> 1, 2, 3, 4
<223> Xaa can be any amino acid

<400> 52
Xaa Xaa Xaa Xaa His Tyr
1 5

<210> 53
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> subtilisin protease cleavage site consensus
sequence

<220>
<221> VARIANT
<222> 1, 2, 3, 4
<223> Xaa can be any amino acid

<400> 53
Xaa Xaa Xaa Xaa His Tyr
1 5

<210> 54
<211> 2
<212> PRT
<213> Artificial Sequence

<220>
<223> subtilisin protease cleavage site

<400> 54
His Tyr
1

<210> 55
<211> 2
<212> PRT
<213> Artificial Sequence

<220>
<223> subtilisin protease cleavage site

<400> 55
Tyr His
1

<210> 56
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> subtilisin protease cleavage site

<400> 56
Pro Gly Ala Ala His Tyr
1 5

<210> 57
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Caspase 3 protease cleavage site consensus
sequence

<220>
<221> VARIANT
<222> 2
<223> Xaa can be any amino acid with E preferred

<220>
<221> VARIANT
<222> 3
<223> Xaa can be any amino acid

<220>
<221> VARIANT
<222> 5
<223> Xaa can be any amino acid with G or S preferred

<400> 57
Asp Xaa Xaa Asp Xaa
1 5

<210> 58
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Caspase 3 protease cleavage site

<400> 58
Asp Glu Val Asp Gly
1 5

<210> 59
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Caspase 3 protease cleavage site

<400> 59
Asp Glu Val Asp Ser
1 5

<210> 60
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Caspase 3 protease cleavage site

<400> 60
Asp Glu Pro Asp Gly
1 5

<210> 61
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Caspase 3 protease cleavage site

<400> 61
Asp Glu Pro Asp Ser
1 5

<210> 62
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Caspase 3 protease cleavage site

<400> 62
Asp Glu Leu Asp Gly
1 5

<210> 63
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Caspase 3 protease cleavage site

<400> 63
Asp Glu Leu Asp Ser
1 5

<210> 64
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Enterokinase protease cleavage site consensus
sequence

<400> 64
Asp Asp Asp Asp Lys
1 5

<210> 65
 <211> 753
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Codon-optimized TEV open reading frame

<400> 65
 atgggcgaat ctctgttcaa ggggtccgct gattataacc cgatatcttc tactatttgt 60
 catctgacta acgaaagcga cggccacacg acttctctgt acggtatcgg tttcgggtccg 120
 ttcatcatta ccaacaagca tctgttccgc cgtaacaacg gtaccctgct ggttcaatct 180
 ctgcacggcg tcttcaagggt aaaaaatacc actacgctgc agcagcacct gattgacggc 240
 cgtgacatga tcatcatccg catgccgaaa gattttccgc cgttcccgcg aaaactgaag 300
 tttcgtgaac cgcaacgcga agaacgtatt tgcctgggta ccaccaactt tcagacccaaa 360
 agcatgtctt ctatggtttc cgatacctct tgcaccttcc caagctctga cggtattttc 420
 tggaaacatt ggatccagac caaagatggg cagtgcggct ctccgctggg gtctacgcgt 480
 gacggtttca tcgttggtat ccattctgct tctaacttca ctaacactaa caactacttt 540
 acttccgttc cgaaaaactt catggagctg ctgactaacc aagaggccca gcagtgggtg 600
 tccggttggc gcctgaacgc agattctgta ctgtgggggt gtcataaggt attcatgaac 660
 aaaccggagg agccgttcca gccggtcaaa gaggcgaccc agctgatgaa cgaactgggt 720
 tactctcagg gtcaccacca tcaccaccat taa 753

<210> 66
 <211> 250
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TEV protease (S219N) with amino-terminus
 polyhistidine affinity tag

<400> 66
 Met Gly Glu Ser Leu Phe Lys Gly Pro Arg Asp Tyr Asn Pro Ile Ser
 1 5 10 15
 Ser Thr Ile Cys His Leu Thr Asn Glu Ser Asp Gly His Thr Thr Ser
 20 25 30
 Leu Tyr Gly Ile Gly Phe Gly Pro Phe Ile Ile Thr Asn Lys His Leu
 35 40 45
 Phe Arg Arg Asn Asn Gly Thr Leu Leu Val Gln Ser Leu His Gly Val
 50 55 60
 Phe Lys Val Lys Asn Thr Thr Leu Gln Gln His Leu Ile Asp Gly
 65 70 75 80
 Arg Asp Met Ile Ile Ile Arg Met Pro Lys Asp Phe Pro Pro Phe Pro
 85 90 95
 Gln Lys Leu Lys Phe Arg Glu Pro Gln Arg Glu Glu Arg Ile Cys Leu
 100 105 110
 Val Thr Thr Asn Phe Gln Thr Lys Ser Met Ser Ser Met Val Ser Asp
 115 120 125
 Thr Ser Cys Thr Phe Pro Ser Ser Asp Gly Ile Phe Trp Lys His Trp
 130 135 140
 Ile Gln Thr Lys Asp Gly Gln Cys Gly Ser Pro Leu Val Ser Thr Arg
 145 150 155 160
 Asp Gly Phe Ile Val Gly Ile His Ser Ala Ser Asn Phe Thr Asn Thr
 165 170 175
 Asn Asn Tyr Phe Thr Ser Val Pro Lys Asn Phe Met Glu Leu Leu Thr
 180 185 190
 Asn Gln Glu Ala Gln Gln Trp Val Ser Gly Trp Arg Leu Asn Ala Asp
 195 200 205
 Ser Val Leu Trp Gly Gly His Lys Val Phe Met Asn Lys Pro Glu Glu
 210 215 220
 Pro Phe Gln Pro Val Lys Glu Ala Thr Gln Leu Met Asn Glu Leu Val
 225 230 235 240
 Tyr Ser Gln Gly His His His His His His
 245 250

<210> 67

<211> 753
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Codon-optimized TEV open reading frame

<400> 67
 atgggtcacc accatcacca ccatggcgaa tctctgttca aggggtccgcg tgattataac 60
 ccgatatctt ctactatttg tcatctgact aacgaaaagcg acggccacac gacttctctg 120
 tacgggtatcg gtttcgggtcc gttcatcatt accaacaagc atctgttccg ccgtaacaac 180
 ggtaccctgg tggttcaatc tctgcacggc gtcttcaagg taaaaaatac cactacgctg 240
 cagcagcacc tgattgacgg ccgtgacatg atcatcatcc gcatgccgaa agattttccg 300
 ccgttcccgc aaaaactgaa gtttcgtgaa ccgcaacgcg aagaacgtat ttgcctggtt 360
 accaccaact ttcagaccaa aagcatgtct tctatgggtt ccgatacctc ttgcaccttc 420
 ccaagcggtg acggtatttt ctggaaacat tggatccaga ccaaagatgg tcagtgcggc 480
 tctccgctgg tgtctacgcg tgacgggtttc atcggttgga tccattctgc ttctaacttc 540
 actaacacta acaactactt tacttccggt ccgaaaaaact tcatggagct gctgactaac 600
 caagaggccc agcagtgggt gtccgggttg cgctgaacg cagattctgt actgtgggtt 660
 ggtcataagg tattcatgaa caaacggag gagccgttcc agccggtcaa agaggcgacc 720
 cagctgatga acgaactggt ttactctcag taa 753

<210> 68
 <211> 250
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TEV protease (L56V, S135G, S219N) with
 amino-terminus polyhistidine affinity tag

<400> 68
 Met Gly His His His His His Gly Glu Ser Leu Phe Lys Gly Pro
 1 5 10 15
 Arg Asp Tyr Asn Pro Ile Ser Ser Thr Ile Cys His Leu Thr Asn Glu
 20 25 30
 Ser Asp Gly His Thr Thr Ser Leu Tyr Gly Ile Gly Phe Gly Pro Phe
 35 40 45
 Ile Ile Thr Asn Lys His Leu Phe Arg Arg Asn Asn Gly Thr Leu Val
 50 55 60
 Val Gln Ser Leu His Gly Val Phe Lys Val Lys Asn Thr Thr Thr Leu
 65 70 75 80
 Gln Gln His Leu Ile Asp Gly Arg Asp Met Ile Ile Ile Arg Met Pro
 85 90 95
 Lys Asp Phe Pro Pro Phe Pro Gln Lys Leu Lys Phe Arg Glu Pro Gln
 100 105 110
 Arg Glu Glu Arg Ile Cys Leu Val Thr Thr Asn Phe Gln Thr Lys Ser
 115 120 125
 Met Ser Ser Met Val Ser Asp Thr Ser Cys Thr Phe Pro Ser Gly Asp
 130 135 140
 Gly Ile Phe Trp Lys His Trp Ile Gln Thr Lys Asp Gly Gln Cys Gly
 145 150 155 160
 Ser Pro Leu Val Ser Thr Arg Asp Gly Phe Ile Val Gly Ile His Ser
 165 170 175
 Ala Ser Asn Phe Thr Asn Thr Asn Asn Tyr Phe Thr Ser Val Pro Lys
 180 185 190
 Asn Phe Met Glu Leu Leu Thr Asn Gln Glu Ala Gln Gln Trp Val Ser
 195 200 205
 Gly Trp Arg Leu Asn Ala Asp Ser Val Leu Trp Gly Gly His Lys Val
 210 215 220
 Phe Met Asn Lys Pro Glu Glu Pro Phe Gln Pro Val Lys Glu Ala Thr
 225 230 235 240
 Gln Leu Met Asn Glu Leu Val Tyr Ser Gln
 245 250

<210> 69
 <211> 753

<212> DNA
<213> Artificial Sequence

<220>
<223> Codon-optimized TEV open reading frame

<400> 69
atgggtcacc accatcacca ccatggcgaa tctctgttca aggggtccgcg tgattataac 60
ccgatatctt cttctatttg tcacttgact aacgaaagcg acggccacac gacttctctg 120
tacggtatcg gtttcgggtcc gttcatcatt accaacaagc atctgttccg ccgtaacaac 180
gggtaccctgc tgggttcaatc tctgcacggc gtcttcaagg taaaagacac cactacgctg 240
cagcagcacc tgggtcgacgg ccgtgacatg atcatcatcc gcatgccgaa agattttccg 300
ccgttcccgcc aaaaactgaa gtttcgtgaa ccgcaacgcg aagaacgtat ttgcctgggt 360
accaccaact ttcagaccaa aagcatgtct tctatgggtt ccgataacct ttgcaccttc 420
ccaagctctg acgggtatttt ctggaaacat tggatccaga ccaaagatgg tcagtgcggc 480
tctccgctgg tgtctacgcg tgacgggtttc atcgttggta tccattctgc ttctaacttc 540
actaacacta acaactactt tacttccgtt ccgaaaaact tcatggagct gctgactaac 600
caagaggccc agcagtggtt gtccggttgg cgctggaacg cagattctgt actgtggggg 660
ggtcataagg tattcatgaa caaacgggag gagccgttcc agccgggtcaa agaggcgacc 720
cagctgatga acgaactggt ttactctcag taa 753

<210> 70
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> TEV protease (T17S, N68D, I77V, S219N) with
amino-terminus polyhistidine affinity tag

<400> 70
Met Gly His His His His His His Gly Glu Ser Leu Phe Lys Gly Pro
1 5 10 15
Arg Asp Tyr Asn Pro Ile Ser Ser Ser Ile Cys His Leu Thr Asn Glu
20 25 30
Ser Asp Gly His Thr Thr Ser Leu Tyr Gly Ile Gly Phe Gly Pro Phe
35 40 45
Ile Ile Thr Asn Lys His Leu Phe Arg Arg Asn Asn Gly Thr Leu Leu
50 55 60
Val Gln Ser Leu His Gly Val Phe Lys Val Lys Asp Thr Thr Thr Leu
65 70 75 80
Gln Gln His Leu Val Asp Gly Arg Asp Met Ile Ile Ile Arg Met Pro
85 90 95
Lys Asp Phe Pro Pro Phe Pro Gln Lys Leu Lys Phe Arg Glu Pro Gln
100 105 110
Arg Glu Glu Arg Ile Cys Leu Val Thr Thr Asn Phe Gln Thr Lys Ser
115 120 125
Met Ser Ser Met Val Ser Asp Thr Ser Cys Thr Phe Pro Ser Ser Asp
130 135 140
Gly Ile Phe Trp Lys His Trp Ile Gln Thr Lys Asp Gly Gln Cys Gly
145 150 155 160
Ser Pro Leu Val Ser Thr Arg Asp Gly Phe Ile Val Gly Ile His Ser
165 170 175
Ala Ser Asn Phe Thr Asn Thr Asn Tyr Phe Thr Ser Val Pro Lys
180 185 190
Asn Phe Met Glu Leu Leu Thr Asn Gln Glu Ala Gln Gln Trp Val Ser
195 200 205
Gly Trp Arg Leu Asn Ala Asp Ser Val Leu Trp Gly His Lys Val
210 215 220
Phe Met Asn Lys Pro Glu Glu Pro Phe Gln Pro Val Lys Glu Ala Thr
225 230 235 240
Gln Leu Met Asn Glu Leu Val Tyr Ser Gln
245 250

<210> 71
<211> 753
<212> DNA

<213> Artificial Sequence

<220>

<223> Codon-optimized TEV open reading frame

<400> 71

```
atgggtcacc accatcacca ccatggcgaa tctctgttca aggggtccgcg tgattataac 60
ccgatatctt ctactatttg tcatctgact aacgaaagcg acggccacac gacttctctg 120
tacgggtatcg gtttcgggtcc gtatcatcatt accgtgaagc atctgttccg ccgtaacaac 180
gggtaccctgg tggttcaatc tctgcacggc gtcttcaagg taaaaaatac cactacgctg 240
cagcagcacc tgattgacgg ccgtgacatg atcatcatcc gcatgccgaa agattttccg 300
ccgttcccg caaaaactgaa gtttcgtgaa ccgcaacgcg aagaacgtat ttgcctgggt 360
accaccaact ttcagaccaa aagcatgtct tctatgggtt ccgatacctc ttgcaccttc 420
ccaagcgggt acggtatttt ctggaaacat tggatccaga ccaaagatgg tcagtgcggc 480
tctccgctgg tgtctacgcg tgacgggttt atcgttggta tccattctgc ttctaacttc 540
actaacacta acaactactt tacttccggt ccgaaaaact tcatggagct gctgactaac 600
caagaggccc agcagtgggt gtccgggttg cgcctgaacg cagattctgt actgtggggt 660
ggtcataaag tattcatgaa caaacgggag gagccgttcc agccgggtcaa agaggcgacc 720
cagctgatga acgaactggt ttactctcag taa 753
```

<210> 72

<211> 250

<212> PRT

<213> Artificial Sequence

<220>

<223> TEV protease (N44V, L56V, S135G, S219N) with amino-terminus polyhistidine affinity tag

<400> 72

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

<210> 73

<211> 753

<212> DNA

<213> Artificial Sequence

<220>

<223> Codon-optimized TEV open reading frame

<400> 73

```
atgggtcacc accatcacca ccatggcgaa tctctgttca aggggtccgcg tgattataac 60
ccgatatctt ctactatttg tcatctgact aacgaaagcg acggccacac gacttctctg 120
tacggtatcg gtttcgggtcc gttcatcatt accaacaagc atctgttccg ccgtaacaac 180
gggtaccctgg tggttcaatc tctgcacggc gtcttcaagg taaaagacac cactacgctg 240
cagcagcacc tgattgacgg ccgtgacatg atcatcatcc gcatgccgaa agattttccg 300
ccgttcccgc aaaaactgaa gtttcgtgaa ccgcaacgcg aagaacgtat ttgcctgggt 360
accaccaact ttcagaccaa aagcatgtct tctatggttt ccgatacctc ttgcaccttc 420
ccaagcggtg acggtatttt ctggaaacat tggatccaga ccaaagatgg tcagtgcggc 480
tctccgctgg tgtctacgcg tgacgggttc atcgttggtg tccattctgc ttctaacttc 540
actaacacta acaactactt tacttccgtt ccgaaaaact tcatggagct gctgactaac 600
caagaggccc agcagtgggt gtccggttgg cgcctgaacg cagattctgt actgtggggg 660
ggtcataagg tattcatgaa caaacccggag gagccgttcc agccgggtcaa agaggcgacc 720
cagctgatga acgaactggg ttactctcag taa 753
```

<210> 74

<211> 250

<212> PRT

<213> Artificial Sequence

<220>

<223> TEV protease (L56V, N68D, S135G, S219N) with amino-terminus polyhistidine affinity tag

<400> 74

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

<210> 75

<211> 753

<212> DNA

<213> Artificial Sequence

<220>
 <223> Codon-optimized TEV open reading frame

<400> 75
 atgggtcacc accatcacca ccatggcgaa tctctgttca aggggtccgcg tgattataac 60
 ccgatatctt ctctctatttg tcatctgact aacgaaagcg acggccacac gacttctctg 120
 tacgggtatcg gtttcgggtcc gttcatcatt accaacaagc atctgttccg ccgtaacaac 180
 ggtaccctgg tgggttcaatc tctgcacggc gtcttcaagg taaaagacac cactacgctg 240
 cagcagcacc tgggtcgacgg ccgtgacatg atcatcatcc gcatgccgaa agattttccg 300
 ccgttcccgc aaaaactgaa gtttcgtgaa ccgcaacgcg aagaacgtat ttgcctgggt 360
 accaccaact ttcagaccaa aagcatgtct tctatgggtt ccgatacctc ttgcaccttc 420
 ccaagctctg acgggtatttt ctggaaacat tggatccaga ccaaagatgg tcagtgcggc 480
 tctccgctgg tgtctacgcg tgacgggttc atcgttggtg tccattctgc ttctaacttc 540
 actaacacta acaactactt tacttccggt ccgaaaaact tcatggagct gctgactaac 600
 caagaggccc agcagtgggt gtccggttgg cgctgaacg cagattctgt actgtggggt 660
 ggtcataagg tattcatgaa caaacggag gagccgttcc agccggtcaa agaggcgacc 720
 cagctgatga acgaactggt ttactctcag taa 753

<210> 76
 <211> 250
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TEV protease (T17S, L56V, N68D, I77V, S219N) with
 amino-terminus polyhistidine affinity tag

<400> 76
 Met Gly His His His His His Gly Glu Ser Leu Phe Lys Gly Pro
 1 5 10 15
 Arg Asp Tyr Asn Pro Ile Ser Ser Ser Ile Cys His Leu Thr Asn Glu
 20 25 30
 Ser Asp Gly His Thr Thr Ser Leu Tyr Gly Ile Gly Phe Gly Pro Phe
 35 40 45
 Ile Ile Thr Asn Lys His Leu Phe Arg Arg Asn Asn Gly Thr Leu Val
 50 55 60
 Val Gln Ser Leu His Gly Val Phe Lys Val Lys Asp Thr Thr Thr Leu
 65 70 75 80
 Gln Gln His Leu Val Asp Gly Arg Asp Met Ile Ile Ile Arg Met Pro
 85 90 95
 Lys Asp Phe Pro Pro Phe Pro Gln Lys Leu Lys Phe Arg Glu Pro Gln
 100 105 110
 Arg Glu Glu Arg Ile Cys Leu Val Thr Asn Phe Gln Thr Lys Ser
 115 120 125
 Met Ser Ser Met Val Ser Asp Thr Ser Cys Thr Phe Pro Ser Ser Asp
 130 135 140
 Gly Ile Phe Trp Lys His Trp Ile Gln Thr Lys Asp Gly Gln Cys Gly
 145 150 155 160
 Ser Pro Leu Val Ser Thr Arg Asp Gly Phe Ile Val Gly Ile His Ser
 165 170 175
 Ala Ser Asn Phe Thr Asn Thr Asn Asn Tyr Phe Thr Ser Val Pro Lys
 180 185 190
 Asn Phe Met Glu Leu Leu Thr Asn Gln Glu Ala Gln Gln Trp Val Ser
 195 200 205
 Gly Trp Arg Leu Asn Ala Asp Ser Val Leu Trp Gly Gly His Lys Val
 210 215 220
 Phe Met Asn Lys Pro Glu Glu Pro Phe Gln Pro Val Lys Glu Ala Thr
 225 230 235 240
 Gln Leu Met Asn Glu Leu Val Tyr Ser Gln
 245 250

<210> 77
 <211> 753
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Codon-optimized TEV open reading frame

<400> 77

```
atgggtcacc accatcacca ccatggcgaa tctctgttca aggggtccgcg tgattataac 60
ccgatatctt cttctatctt tcattctgact aacgaaagcg acggccacac gacttctctg 120
tacgggtatcg gtttcgggtcc gttcatcatt accaacaagc atctgttccg ccgtaacaac 180
ggtagcctgc tgggtcaatc tctgcacggc gtcttcaagg taaaagacac cactacgctg 240
cagcagcacc tggtcgacgg ccgtgacatg atcatcatcc gcatgccgaa agattttccg 300
ccgttcccgc aaaaactgaa gtttcgtgaa ccgcaacgcg aagaacgtat ttgcctgggt 360
accaccaact ttcagaccaa aagcatgtct tctatgggtt ccgatacctc ttgcaccttc 420
ccaagcgggtg acggtatctt ctggaacatg tggatccaga ccaaagatgg tcagtgcggc 480
tctccgctgg tgtctacgcg tgacgggtttc atcgttggtg tccattctgc ttctaacttc 540
actaacacta acaactactt tacttccggt ccgaaaaact tcattggagct gctgactaac 600
caagaggccc agcagtgggt gtccgggttg cgcctgaacg cagattctgt actgtggggg 660
gggtcataagg tattcatgaa caaacgggag gagccgttcc agccgggtcaa agaggcgacc 720
cagctgatga acgaactggg ttactctcag taa 753
```

<210> 78

<211> 250

<212> PRT

<213> Artificial Sequence

<220>

<223> TEV protease (T17S, N68D, I77V, S135G, S219N) with amino-terminus polyhistidine affinity tag

<400> 78

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

<210> 79

<211> 753

<212> DNA

<213> Artificial Sequence

<220>

<223> Codon-optimized TEV open reading frame

```

<400> 79
atgggCGaAt ctctgttcaa gggTccgcgt gattataacc cgatatcttc ttctatttgt 60
catctgacta acgaaagcga cggccacacg acttctctgt acggtatcgg tttcgggtccg 120
ttcatcatta ccgtgaagca tctgttccgc cgtaacaacg gtaccctggg ggttcaatct 180
ctgcacggcg tcttcaaggt aaaagacacc actacgctgc agcagcacct ggtcgacggc 240
cgtgacatga tcatcatccg catgccgaaa gattttccgc cgttcccgcg aaaactgaag 300
tttcgtgaac cgcaacgcga agaacgtatt tgcctgggta ccaccaactt tcagacacaa 360
agcatgtctt ctatgggttc cgatacctct tgcaccttcc caagcgggtg cggatatttc 420
tggaacatt ggatccagac caaagatggg cagtgcggct ctccgctggg gtctacgcgt 480
gacggtttca tctgttggtat ccattctgct tctaacttca ctaacactaa caactacttt 540
acttccgttc cgaaaaactt catggagctg ctgactaacc aagaggccca gcagtgggtg 600
tccggttggc gcctgaacgc agattctgta ctgtgggggt gtcataaggt attcatgaac 660
aaaccggagg agccgttcca gccggtcaaa gaggcgacc agctgatgaa cgaactgggt 720
tactctcagg gtcaccacca tcaccacat taa 753

```

```

<210> 80
<211> 250
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> TEV protease (T17S, N44V, L56V, N68D, I77V, S135G,
S219N) with carboxyl-terminus polyhistidine
affinity tag

```

```

<400> 80
Met Gly Glu Ser Leu Phe Lys Gly Pro Arg Asp Tyr Asn Pro Ile Ser
1 5 10 15
Ser Ser Ile Cys His Leu Thr Asn Glu Ser Asp Gly His Thr Thr Ser
20 25 30
Leu Tyr Gly Ile Gly Phe Gly Pro Phe Ile Ile Thr Val Lys His Leu
35 40 45
Phe Arg Arg Asn Asn Gly Thr Leu Val Val Gln Ser Leu His Gly Val
50 55 60
Phe Lys Val Lys Asp Thr Thr Thr Leu Gln Gln His Leu Val Asp Gly
65 70 75 80
Arg Asp Met Ile Ile Ile Arg Met Pro Lys Asp Phe Pro Pro Phe Pro
85 90 95
Gln Lys Leu Lys Phe Arg Glu Pro Gln Arg Glu Glu Arg Ile Cys Leu
100 105 110
Val Thr Thr Asn Phe Gln Thr Lys Ser Met Ser Ser Met Val Ser Asp
115 120 125
Thr Ser Cys Thr Phe Pro Ser Gly Asp Gly Ile Phe Trp Lys His Trp
130 135 140
Ile Gln Thr Lys Asp Gly Gln Cys Gly Ser Pro Leu Val Ser Thr Arg
145 150 155 160
Asp Gly Phe Ile Val Gly Ile His Ser Ala Ser Asn Phe Thr Asn Thr
165 170 175
Asn Asn Tyr Phe Thr Ser Val Pro Lys Asn Phe Met Glu Leu Leu Thr
180 185 190
Asn Gln Glu Ala Gln Gln Trp Val Ser Gly Trp Arg Leu Asn Ala Asp
195 200 205
Ser Val Leu Trp Gly Gly His Lys Val Phe Met Asn Lys Pro Glu Glu
210 215 220
Pro Phe Gln Pro Val Lys Glu Ala Thr Gln Leu Met Asn Glu Leu Val
225 230 235 240
Tyr Ser Gln Gly His His His His His
245 250

```

```

<210> 81
<211> 753
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Codon-optimized TEV open reading frame

```

```

<400> 81
atgggtcacc accatcacca ccatggcgaa tctctgttca aggggtccgcg tgattataac 60
ccgatatctt cttctatttg tcatctgact aacgaaagcg acggccacac gacttctctg 120
tacgggtatcg gtttcgggtcc gttcatcatt accgtgaagc atctgttccg ccgtaacaac 180
gggtaccctgg tggttcaatc tctgcacggc gtcttcaagg taaaagacac cactacgctg 240
cagcagcacc tgggtcgacgg ccgtgacatg atcatcatcc gcatgccgaa agattttccg 300
ccgttcccgc aaaaactgaa gtttcgtgaa ccgcaacgcg aagaacgtat ttgcctgggt 360
accaccaact ttcagaccaa aagcatgtct tctatgggtt ccgatacctc ttgcaccttc 420
ccaagcggtg acggtatttt ctggaaacat tggatccaga ccaaagatgg tcagtgcggc 480
tctccgctgg tgtctacgcg tgacgggttc atcgttggta tccattctgc ttctaacttc 540
actaacacta acaactactt tacttccggt ccgaaaaact tcatggagct gctgactaac 600
caagaggccc agcagtgggt gtccgggttg cgcctgaacg cagattctgt actgtggggg 660
ggtcataagg tattcatggt gaaaccggag gagccgttcc agccgggtcaa agaggcgacc 720
cagctgatga acgaactggt ttactctcag taa 753

```

```

<210> 82
<211> 250
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> TEV protease (T17S, N44V, L56V, N68D, I77V, S135G,
S219V) with amino-terminus polyhistidine affinity
tag

```

```

<400> 82
Met Gly His His His His His His Gly Glu Ser Leu Phe Lys Gly Pro
1 5 10 15
Arg Asp Tyr Asn Pro Ile Ser Ser Ser Ile Cys His Leu Thr Asn Glu
20 25 30
Ser Asp Gly His Thr Thr Ser Leu Tyr Gly Ile Gly Phe Gly Pro Phe
35 40 45
Ile Ile Thr Val Lys His Leu Phe Arg Arg Asn Asn Gly Thr Leu Val
50 55 60
Val Gln Ser Leu His Gly Val Phe Lys Val Lys Asp Thr Thr Thr Leu
65 70 75 80
Gln Gln His Leu Val Asp Gly Arg Asp Met Ile Ile Ile Arg Met Pro
85 90 95
Lys Asp Phe Pro Pro Phe Pro Gln Lys Leu Lys Phe Arg Glu Pro Gln
100 105 110
Arg Glu Glu Arg Ile Cys Leu Val Thr Thr Asn Phe Gln Thr Lys Ser
115 120 125
Met Ser Ser Met Val Ser Asp Thr Ser Cys Thr Phe Pro Ser Gly Asp
130 135 140
Gly Ile Phe Trp Lys His Trp Ile Gln Thr Lys Asp Gly Gln Cys Gly
145 150 155 160
Ser Pro Leu Val Ser Thr Arg Asp Gly Phe Ile Val Gly Ile His Ser
165 170 175
Ala Ser Asn Phe Thr Asn Thr Asn Asn Tyr Phe Thr Ser Val Pro Lys
180 185 190
Asn Phe Met Glu Leu Leu Thr Asn Gln Glu Ala Gln Gln Trp Val Ser
195 200 205
Gly Trp Arg Leu Asn Ala Asp Ser Val Leu Trp Gly Gly His Lys Val
210 215 220
Phe Met Val Lys Pro Glu Glu Pro Phe Gln Pro Val Lys Glu Ala Thr
225 230 235 240
Gln Leu Met Asn Glu Leu Val Tyr Ser Gln
245 250

```

```

<210> 83
<211> 753
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Codon-optimized TEV open reading frame

```

```

<400> 83
atgggtcacc accatcacca ccatggcgaa tctctgttca aggggtccgcg tgattataac 60
ccgataatctt ctcttatttg tcatctgact aacgaaagcg acggccacac gacttctctg 120
tacgggtatcg gtttcgggtcc gttcatcatt accgtgaagc atctgttccg ccgtaacaac 180
gggtaccctgg tgggttcaatc tctgcacggc gtcttcaagg taaaagacac cactacgctg 240
cagcagcacc tgggtcgacgg ccgtgacatg atcatcatcc gcatgccgaa agattttccg 300
ccgttcccgcc aaaaactgaa gtttcgtgaa ccgcaacgcg aagaacgtat ttgcctgggt 360
accaccaact ttcagaccaa aagcatgtct tctatggttt ccgatacctc ttgcaccttc 420
ccaagcgggtg acgggtatctt ctggaaacat tggatccaga ccaaagatgg tcagtgcggc 480
tctccgctgg tgtctacgcg tgacgggtttc atcgttggtg tccattctgc ttctaacttc 540
actaacacta acaactactt tacttccgtt ccgaaaaact tcatggagct gctgactaac 600
caagaggccc agcagtgggt gtccggttgg cgcctgaacg cagattctgt actgtggggt 660
ggtcataagg tattcatgaa caaacggag gagccgttcc agccgggtcaa agaggcgacc 720
cagctgatga acgaactggg ttactctcag taa 753

```

```

<210> 84
<211> 250
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> TEV protease (T17S, N44V, L56V, N68D, I77V, S135G,
S219N) with amino-terminus polyhistidine affinity
tag

```

```

<400> 84
Met Gly His His His His His Gly Glu Ser Leu Phe Lys Gly Pro
1 5 10 15
Arg Asp Tyr Asn Pro Ile Ser Ser Ser Ile Cys His Leu Thr Asn Glu
20 25 30
Ser Asp Gly His Thr Thr Ser Leu Tyr Gly Ile Gly Phe Gly Pro Phe
35 40 45
Ile Ile Thr Val Lys His Leu Phe Arg Arg Asn Asn Gly Thr Leu Val
50 55 60
Val Gln Ser Leu His Gly Val Phe Lys Val Lys Asp Thr Thr Thr Leu
65 70 75 80
Gln Gln His Leu Val Asp Gly Arg Asp Met Ile Ile Ile Arg Met Pro
85 90 95
Lys Asp Phe Pro Pro Phe Pro Gln Lys Leu Lys Phe Arg Glu Pro Gln
100 105 110
Arg Glu Glu Arg Ile Cys Leu Val Thr Thr Asn Phe Gln Thr Lys Ser
115 120 125
Met Ser Ser Met Val Ser Asp Thr Ser Cys Thr Phe Pro Ser Gly Asp
130 135 140
Gly Ile Phe Trp Lys His Trp Ile Gln Thr Lys Asp Gly Gln Cys Gly
145 150 155 160
Ser Pro Leu Val Ser Thr Arg Asp Gly Phe Ile Val Gly Ile His Ser
165 170 175
Ala Ser Asn Phe Thr Asn Thr Asn Asn Tyr Phe Thr Ser Val Pro Lys
180 185 190
Asn Phe Met Glu Leu Leu Thr Asn Gln Glu Ala Gln Gln Trp Val Ser
195 200 205
Gly Trp Arg Leu Asn Ala Asp Ser Val Leu Trp Gly Gly His Lys Val
210 215 220
Phe Met Asn Lys Pro Glu Glu Pro Phe Gln Pro Val Lys Glu Ala Thr
225 230 235 240
Gln Leu Met Asn Glu Leu Val Tyr Ser Gln
245 250

```

```

<210> 85
<211> 750
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Native TEV open reading frame

```

```

<400> 85
atgcatcacc atcaccacca tggagaaagc ttgtttaagg gaccacgtga ttacaacccg 60
atatcgagca ccatttgtca ttgtacgaat gaatctgatg ggcacacaac atcgttgtat 120
ggatattggat ttgttcctt catcattaca aacaagcact tgtttcgccg taataatgga 180
acactgttgg tccaatcact acatgggtga ttcaagggtca agaacaccac gactttgcaa 240
caacacctca ttgatgggag ggacatgata attattcgca tgcctaagga tttcccacca 300
tttcctcaaa agctgaaatt tagagagcca caaagggaag agcgcatctg tcttgtgaca 360
accaacttcc aaactaagag catgtctagc atggtgtcag acactagtgt cacattccct 420
tcatctgatg gcatattctg gaagcattgg atccaaacca aggatgggca gtgtggcagt 480
ccattagtat caactagaga tgggttcatt gttggtatac actcagcatc gaatttcacc 540
aacacaaaca attatttcac aagcgtgccg aaaaacttca tgggaattgt gacaaatcag 600
gaggcgcagc agtggggttag tggttggcga ttaaatgctg actcagtatt gtgggggggc 660
cataaagttt tcatgaacaa acctgaagag ccttttcagc cagttaagga agcgactcaa 720
ctcatgaatg aattgggtga ctcgcaataa 750

```

```

<210> 86
<211> 249
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> TEV protease (S219N) with amino-terminus
polyhistidine affinity tag

```

```

<400> 86
Met His His His His His His Gly Glu Ser Leu Phe Lys Gly Pro Arg
1 5 10 15
Asp Tyr Asn Pro Ile Ser Ser Thr Ile Cys His Leu Thr Asn Glu Ser
20 25 30
Asp Gly His Thr Thr Ser Leu Tyr Gly Ile Gly Phe Gly Pro Phe Ile
35 40 45
Ile Thr Asn Lys His Leu Phe Arg Arg Asn Asn Gly Thr Leu Leu Val
50 55 60
Gln Ser Leu His Gly Val Phe Lys Val Lys Asn Thr Thr Thr Leu Gln
65 70 75 80
Gln His Leu Ile Asp Gly Arg Asp Met Ile Ile Ile Arg Met Pro Lys
85 90 95
Asp Phe Pro Pro Phe Pro Gln Lys Leu Lys Phe Arg Glu Pro Gln Arg
100 105 110
Glu Glu Arg Ile Cys Leu Val Thr Thr Asn Phe Gln Thr Lys Ser Met
115 120 125
Ser Ser Met Val Ser Asp Thr Ser Cys Thr Phe Pro Ser Ser Asp Gly
130 135 140
Ile Phe Trp Lys His Trp Ile Gln Thr Lys Asp Gly Gln Cys Gly Ser
145 150 155 160
Pro Leu Val Ser Thr Arg Asp Gly Phe Ile Val Gly Ile His Ser Ala
165 170 175
Ser Asn Phe Thr Asn Thr Asn Asn Tyr Phe Thr Ser Val Pro Lys Asn
180 185 190
Phe Met Glu Leu Leu Thr Asn Gln Glu Ala Gln Gln Trp Val Ser Gly
195 200 205
Trp Arg Leu Asn Ala Asp Ser Val Leu Trp Gly Gly His Lys Val Phe
210 215 220
Met Asn Lys Pro Glu Glu Pro Phe Gln Pro Val Lys Glu Ala Thr Gln
225 230 235 240
Leu Met Asn Glu Leu Val Tyr Ser Gln
245

```

```

<210> 87
<211> 3984
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Open reading frame encoding BoNT/A-TEV

```

atgcccgttcg taaacaaca gttcaactat aagaaccag tcaacggcgt tgaacattga aatccataac 120
tataccaata tccgcaatgc gggcccaatg cagcccggtg tcttaactatg atagacataa 140
aaatttggg tgaatccgga ggcggaatgc tgaatgaagg agattttaac 180
ccaaccgctg aggtcaataa ggtcccggtg tcttaactatg atagacataa 240
gacaatgtaa aggtcaataa ggtcccggtg tcttaactatg atagacataa 300
acagatctcg gtcgcatgtt gctgaacttc atgttgcgag gcatctcggt 360
agccaactcg atcaatggtt gcaatggtt gcaatggtt gcaatggtt 420
gatggaggtt accgttcgga aatgttcaat atgttgcgag gcatctcggt 480
atccaattcg aatgttcaat atgttgcgag aatgttcaat atgttgcgag 540
ggatcgagcg agtatattcg ttttcttcca gatttccaat ttggaattga 600
gaagttcgag ttaaggcgcg ggaataatcg ggaataatcg ggaataatcg 660
ttggccatgc aactattca ttccggcgat ttccggcgat ttccggcgat 720
cgtgttttca aggtggaatc ggaacgggat ttccggcgat ttccggcgat 780
gaaagaactgc gcaatgttgc ggtcatgtat gcaaatatta ttgatatgtt 840
gaaatccctc gttatattca caataaatgc aataaatgc aataaatgc 900
taaccttcta ggtgaagcac ttccggcgat caatatatga aaaaatgtt 960
1020
atgtatataa ttcttcaatg gaaatgttca aatgttcaatg gaaatgttca 1080
ttgaatcgga aaaaatgttca gaaatgttca aatgttcaatg gaaatgttca 1140
aaagttaact acacacatca ttgattgttc aatgttcaatg gaaatgttca 1200
aaattttacc aaattttacc aaattttacc aaattttacc aaattttacc 1260
caaaaaccacaa ttatccacggta ttatccacggta ttatccacggta 1320
ttccctggcggtg gttgttggcggtg ttccctggcggtg gttgttggcggtg 1380
tataacacggc ttccctggcggtg gttgttggcggtg ttccctggcggtg 1440
ttccctggcggtg gttgttggcggtg ttccctggcggtg gttgttggcggtg 1500
aacatcggaag caatcggaag gaaatgttca ttcaaatata ttcaaatata 1560
tttaatttgc ataacggagc ttgaatgtat ttcaatgtat ttcaatgtat 1620
gttatattcg gaaatgttca ttgaatgtat ttcaatgtat ttcaatgtat 1680
caagtctcgt caagtctcgt caagtctcgt caagtctcgt caagtctcgt 1740
gtaacacattt gtaacacattt gtaacacattt gtaacacattt gtaacacattt 1800
ttccctggcggtg gttgttggcggtg ttccctggcggtg gttgttggcggtg 1860
gaaacacggc ttccctggcggtg gttgttggcggtg ttccctggcggtg 1920
gaaacacggc ttccctggcggtg gttgttggcggtg ttccctggcggtg 1980
tatccctggcggtg gttgttggcggtg ttccctggcggtg gttgttggcggtg 2040
gttccctggcggtg gttgttggcggtg ttccctggcggtg gttgttggcggtg 2100
taacgaataa taacgaataa taacgaataa taacgaataa taacgaataa 2160
2220
gaaacacggc ttccctggcggtg gttgttggcggtg ttccctggcggtg 2280
gaaacacggc ttccctggcggtg gttgttggcggtg ttccctggcggtg 2340
taatatataa taatatataa taatatataa taatatataa taatatataa 2400
2460
tatattgaatg ttgaatgttca aatgttcaatg ttgaatgttca aatgttcaatg 2520
caacacacggc taacacacggc taacacacggc taacacacggc taacacacggc 2580
2640
gctgttccacg gctgttccacg gctgttccacg gctgttccacg gctgttccacg 2700
aacatcggttc ttgaatgttca aatgttcaatg ttgaatgttca aatgttcaatg 2760
ttcgatcttca ttcgatcttca ttcgatcttca ttcgatcttca ttcgatcttca 2820
gttatcttca gtatatcttca gtatatcttca gtatatcttca gtatatcttca 2880
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3000
aatcatcttgc aatcatcttgc aatcatcttgc aatcatcttgc aatcatcttgc 3060
3120
ccggttcgaac ttacttaacaa ttacttaacaa ttacttaacaa ttacttaacaa 3180
3240
caacacacggc taacacacggc taacacacggc taacacacggc taacacacggc 3300
3360
tgatatttgc tgatatttgc tgatatttgc tgatatttgc tgatatttgc 3420
3480
cgttgaacggc cgttgaacggc cgttgaacggc cgttgaacggc cgttgaacggc 3540
3600
taacacacggc taacacacggc taacacacggc taacacacggc taacacacggc 3660
3720
gaaagaaaatg gaaagaaaatg gaaagaaaatg gaaagaaaatg gaaagaaaatg 3780
3840
ggccttcaat ggcttcaat ggcttcaat ggcttcaat ggcttcaat 3900
3960
ggccttcaat ggcttcaat ggcttcaat ggcttcaat ggcttcaat 3984

<210> 88
 <211> 1327
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> BONT/A-TEV

<400> 88
 Met Pro Phe Val Asn Lys Gln Phe Asn Tyr Lys Asp Pro Val Asn Gly
 1 5 10 15
 Val Asp Ile Ala Tyr Ile Lys Ile Pro Asn Ala Gly Gln Met Gln Pro
 20 25 30
 Val Lys Ala Phe Lys Ile His Asn Lys Ile Trp Val Ile Pro Glu Arg
 35 40 45
 Asp Thr Phe Thr Asn Pro Glu Gly Asp Leu Asn Pro Pro Pro Glu
 50 55 60
 Ala Lys Gln Val Pro Val Ser Tyr Tyr Asp Ser Thr Tyr Leu Ser Thr
 65 70 75 80
 Asp Asn Glu Lys Asp Asn Tyr Leu Lys Gly Val Thr Lys Leu Phe Glu
 85 90 95
 Arg Ile Tyr Ser Thr Asp Leu Gly Arg Met Leu Leu Thr Ser Ile Val
 100 105 110
 Arg Gly Ile Pro Phe Trp Gly Gly Ser Thr Ile Asp Thr Glu Leu Lys
 115 120 125
 Val Ile Asp Thr Asn Cys Ile Asn Val Ile Gln Pro Asp Gly Ser Tyr
 130 135 140
 Arg Ser Glu Glu Leu Asn Leu Val Ile Ile Gly Pro Ser Ala Asp Ile
 145 150 155 160
 Ile Gln Phe Glu Cys Lys Ser Phe Gly His Glu Val Leu Asn Leu Thr
 165 170 175
 Arg Asn Gly Tyr Gly Ser Thr Gln Tyr Ile Arg Phe Ser Pro Asp Phe
 180 185 190
 Thr Phe Gly Phe Glu Glu Ser Leu Glu Val Asp Thr Asn Pro Leu Leu
 195 200 205
 Gly Ala Gly Lys Phe Ala Thr Asp Pro Ala Val Thr Leu Ala His Glu
 210 215 220
 Leu Ile His Ala Gly His Arg Leu Tyr Gly Ile Ala Ile Asn Pro Asn
 225 230 235 240
 Arg Val Phe Lys Val Asn Thr Asn Ala Tyr Tyr Glu Met Ser Gly Leu
 245 250 255
 Glu Val Ser Phe Glu Glu Leu Arg Thr Phe Gly Gly His Asp Ala Lys
 260 265 270
 Phe Ile Asp Ser Leu Gln Glu Asn Glu Phe Arg Leu Tyr Tyr Tyr Asn
 275 280 285
 Lys Phe Lys Asp Ile Ala Ser Thr Leu Asn Lys Ala Lys Ser Ile Val
 290 295 300
 Gly Thr Thr Ala Ser Leu Gln Tyr Met Lys Asn Val Phe Lys Glu Lys
 305 310 315 320
 Tyr Leu Leu Ser Glu Asp Thr Ser Gly Lys Phe Ser Val Asp Lys Leu
 325 330 335
 Lys Phe Asp Lys Leu Tyr Lys Met Leu Thr Glu Ile Tyr Thr Glu Asp
 340 345 350
 Asn Phe Val Lys Phe Phe Lys Val Leu Asn Arg Lys Thr Tyr Leu Asn
 355 360 365
 Phe Asp Lys Ala Val Phe Lys Ile Asn Ile Val Pro Lys Val Asn Tyr
 370 375 380
 Thr Ile Tyr Asp Gly Phe Asn Leu Arg Asn Thr Asn Leu Ala Ala Asn
 385 390 395 400
 Phe Asn Gly Gln Asn Thr Glu Ile Asn Asn Met Asn Phe Thr Lys Leu
 405 410 415
 Lys Asn Phe Thr Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg
 420 425 430
 Gly Ile Ile Thr Ser Lys Thr Lys Ser Leu Gly Gly Gly Gly Glu Asn
 435 440 445
 Leu Tyr Phe Gln Gly Gly Gly Gly Asp Lys Gly Tyr Asn Lys Ala
 450 455 460

Leu	Asn	Asp	Leu	Cys	Ile	Lys	Val	Asn	Asn	Trp	Asp	Leu	Phe	Phe	Ser
465					470					475					480
Pro	Ser	Glu	Asp	Asn	Phe	Thr	Asn	Asp	Leu	Asn	Lys	Gly	Glu	Glu	Ile
				485					490						495
Thr	Ser	Asp	Thr	Asn	Ile	Glu	Ala	Ala	Glu	Glu	Asn	Ile	Ser	Leu	Asp
				500				505					510		
Leu	Ile	Gln	Gln	Tyr	Tyr	Leu	Thr	Phe	Asn	Phe	Asp	Asn	Glu	Pro	Glu
		515					520					525			
Asn	Ile	Ser	Ile	Glu	Asn	Leu	Ser	Ser	Asp	Ile	Ile	Gly	Gln	Leu	Glu
		530				535					540				
Leu	Met	Pro	Asn	Ile	Glu	Arg	Phe	Pro	Asn	Gly	Lys	Lys	Tyr	Glu	Leu
545					550					555					560
Asp	Lys	Tyr	Thr	Met	Phe	His	Tyr	Leu	Arg	Ala	Gln	Glu	Phe	Glu	His
				565					570					575	
Gly	Lys	Ser	Arg	Ile	Ala	Leu	Thr	Asn	Ser	Val	Asn	Glu	Ala	Leu	Leu
				580				585					590		
Asn	Pro	Ser	Arg	Val	Tyr	Thr	Phe	Ser	Ser	Asp	Tyr	Val	Lys	Lys	
				595			600					605			
Val	Asn	Lys	Ala	Thr	Glu	Ala	Ala	Met	Phe	Leu	Gly	Trp	Val	Glu	Gln
						615					620				
Leu	Val	Tyr	Asp	Phe	Thr	Asp	Glu	Thr	Ser	Glu	Val	Ser	Thr	Thr	Asp
625					630					635					640
Lys	Ile	Ala	Asp	Ile	Thr	Ile	Ile	Ile	Pro	Tyr	Ile	Gly	Pro	Ala	Leu
				645					650					655	
Asn	Ile	Gly	Asn	Met	Leu	Tyr	Lys	Asp	Phe	Val	Gly	Ala	Leu	Ile	
				660								670			
Phe	Ser	Gly	Ala	Val	Ile	Leu	Leu	Glu	Phe	Ile	Pro	Glu	Ile	Ala	Ile
				675			680					685			
Pro	Val	Leu	Gly	Thr	Phe	Ala	Leu	Val	Ser	Tyr	Ile	Ala	Asn	Lys	Val
				690			695				700				
Leu	Thr	Val	Gln	Thr	Ile	Asp	Asn	Ala	Leu	Ser	Lys	Arg	Asn	Glu	Lys
705					710					715					720
Trp	Asp	Glu	Val	Tyr	Lys	Tyr	Ile	Val	Thr	Asn	Trp	Leu	Ala	Lys	Val
				725					730					735	
Asn	Thr	Gln	Ile	Asp	Leu	Ile	Arg	Lys	Lys	Met	Lys	Glu	Ala	Leu	Glu
				740				745					750		
Asn	Gln	Ala	Glu	Ala	Thr	Lys	Ala	Ile	Ile	Asn	Tyr	Gln	Tyr	Asn	Gln
		755					760					765			
Tyr	Thr	Glu	Glu	Glu	Lys	Asn	Asn	Ile	Asn	Phe	Asn	Ile	Asp	Asp	Leu
		770				775					780				
Ser	Ser	Lys	Leu	Asn	Glu	Ser	Ile	Asn	Lys	Ala	Met	Ile	Asn	Ile	Asn
785					790					795					800
Lys	Phe	Leu	Asn	Gln	Cys	Ser	Val	Ser	Tyr	Leu	Met	Asn	Ser	Met	Ile
				805					810					815	
Pro	Tyr	Gly	Val	Lys	Arg	Leu	Glu	Asp	Phe	Asp	Ala	Ser	Leu	Lys	Asp
				820				825					830		
Ala	Leu	Leu	Lys	Tyr	Ile	Tyr	Asp	Asn	Arg	Gly	Thr	Leu	Ile	Gly	Gln
		835					840					845			
Val	Asp	Arg	Leu	Lys	Asp	Lys	Val	Asn	Asn	Thr	Leu	Ser	Thr	Asp	Ile
		850				855					860				
Pro	Phe	Gln	Leu	Ser	Lys	Tyr	Val	Asp	Asn	Gln	Arg	Leu	Leu	Ser	Thr
865					870					875					880
Phe	Thr	Glu	Tyr	Ile	Lys	Asn	Ile	Ile	Asn	Thr	Ser	Ile	Leu	Asn	Leu
				885					890					895	
Arg	Tyr	Glu	Ser	Asn	His	Leu	Ile	Asp	Leu	Ser	Arg	Tyr	Ala	Ser	Lys
				900				905					910		
Ile	Asn	Ile	Gly	Ser	Lys	Val	Asn	Phe	Asp	Pro	Ile	Asp	Lys	Asn	Gln
		915					920					925			
Ile	Gln	Leu	Phe	Asn	Leu	Glu	Ser	Ser	Lys	Ile	Glu	Val	Ile	Leu	Lys
		930				935					940				
Asn	Ala	Ile	Val	Tyr	Asn	Ser	Met	Tyr	Glu	Asn	Phe	Ser	Thr	Ser	Phe
945					950					955					960
Trp	Ile	Arg	Ile	Pro	Lys	Tyr	Phe	Asn	Ser	Ile	Ser	Leu	Asn	Asn	Glu
				965					970					975	
Tyr	Thr	Ile	Ile	Asn	Cys	Met	Glu	Asn	Asn	Ser	Gly	Trp	Lys	Val	Ser
				980				985					990		
Leu	Asn	Tyr	Gly	Glu	Ile	Ile	Trp	Thr	Leu	Gln	Asp	Thr	Gln	Glu	Ile
		995					1000						1005		

Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser Asp
 1010 1015 1020
 Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Asn
 1025 1030 1035 1040
 Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro Ile
 1045 1050 1055
 Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met Phe Lys Leu
 1060 1065 1070
 Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Lys Tyr Phe Asn
 1075 1080 1085
 Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr Asp
 1090 1095 1100
 Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr Leu
 1105 1110 1115 1120
 Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr Asp Pro Asn Lys
 1125 1130 1135
 Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met Tyr Leu Lys
 1140 1145 1150
 Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser Ser
 1155 1160 1165
 Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly Asn
 1170 1175 1180
 Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val Val
 1185 1190 1195 1200
 Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala Gly
 1205 1210 1215
 Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn Leu
 1220 1225 1230
 Ser Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly Ile Thr Asn
 1235 1240 1245
 Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly Phe
 1250 1255 1260
 Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val Ala Ser Asn
 1265 1270 1275 1280
 Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu Gly Cys Ser
 1285 1290 1295
 Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu Arg Pro Leu Lys
 1300 1305 1310
 Val Asp Lys Leu Ala Ala Ala Leu Glu His His His His His His
 1315 1320 1325

<210> 89
 <211> 1044
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Intervening sequence containing transcriptional
 and translational sites.

<400> 89
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 caccatcact gagcggccgc ataattgctta agtcgaacag attgatattg agctataagt 180
 aatcgatttg tacacggccg cataatcgaa attaatacga ctactatag gggaattgtg 240
 agcggataac aattcccat cttagtatat tagttaagta taagaaggag atataccatg 300
 ggcgaatctc tgttcaaggg tccgcgtgat tataaccga tatcttctc tatttgatcat 360
 ctgactaacg aaagcgacgg ccacacgact tctctgtacg gtatcggtt cggtcggtc 420
 atcattacca acaagcatct gttccgccgt aacaacggtt cctgctggt tcaatctctg 480
 cacggcgtct tcaaggtaaa agacaccact acgctgcagc agcacctggt cgacggccgt 540
 gacatgatca tcatccgcac gccgaaagat tttccgccgt tcccgaataa actgaagttt 600
 cgtgaaccgc aacgcgaaga acgtatttgc ctggttacca ccaacttca gacaaaagc 660
 atgtcttcta tggttaccga tacctcttgc accctcccaa gcggtgacgg tattttctgg 720
 aaacattgga ttacagacaa agatgggtcag tgcggctctc cgctggtgtc tacgcgtgac 780
 gggttcatcg ttggtatcca ttctgcttct aacttacta acactaacia ctactttact 840
 tccgttccga aaaacttcat ggagctgctg actaaccag aggccagca gtgggtgtcc 900
 gggtggcgcc tgaacgcaga ttctgtactg tggggtggtc ataaggtatt catgaacaaa 960

1020 cggagagagc cgttccagcc ggtccaaagag gcgacccagc tgaatgaacga actggtttac 1044

06 <012>

<211> 4851

AND <7T7>

<2L3> AffT17C1a1 sequence

<223> BONT/A-TEV and TEV protease variant 4 open reading frames with the intervening transcription and translation elements.

<400> 90

[illegible]

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gattctttatg acaatcagtc taattcgggt attctgaaag actttgggg ttgattaccct 3360
cagtaacgata aagttatatac ttatattatgc cgaataataa cgttgacgttc 3420
aaccaacgttg gacatccttg gacatccttg ctatagttatg cgtatagttac 3480
actaaacattt actaaacattt ctccctctat cgcgtatatac aatttatat 3540
gacctttggca acaaggacaa tatcgttacgc aataacgatac gctgtatag 3600
gtgaagataa aagaatatatg tctggcgaac aatgtctatg aggcgggcgt ggagaaat 3660
cgttccttccg ttgtaatacc ggaatgtggt aagttgggtgt gatgaaagt 3720
aaataatgacc aaggatctac caataatgc aaatgatac tgaagataa caacggcaac 3780
gacatttggt ttatcggctt ccaacattc aataatatac ggaagcttgt ggccctcaat 3840
ttgtacaacac gtcagattga gcgcagcttc ccgactttag gctgtatagtc ggaattcat 3900
ccgtttgtag aagttgggg atcaacccac atcaacccac ttgactatatac gtaattcgt 4020
gcatatgtc taagtccgaac agattgatatac gtagctatatac ttgatacggcc 4080
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aatcccgaaag attttccgac gttcccgcaa aaatggaagt ttctgtgaac gcaacgcgaa 4440
gaacgttatg gctttggtac cacaactt cagacccaaa gcatgtcttc tatgtttcc 4500
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cattctgctt ctacttcaac taacattaac aactactta ctccgcttc gaaaacattc 4680
atggaagctgc tgaataaacc agaggtccag cagttgggtc ccgtttggcg cctgaacgca 4740
gattctgtac ttgtgggttg tcataggt tcatagaa gaaactggttt acttcagta a 4851

<210> 91
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> TEV variant 7

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catcttgata acgaaagcga cggccacag acttctcgt acggtatcgg ttccggtccg 120
ttcatatata ccaacagca tctgttccgc cgtaaacaag gtaccctgtc ggttcaatc 180
ctgaacgggt tcttcaacac aataagacac actacgctgc agcagacgc ggtcgcgcgc 240
cgtgacatga tcatcaccg catgccgaa gatttccgc gtttccgca aaactgaaag 300
tttcgtgaac cgcacgcga agaatgatat tgcctgttta ccaaccaatt tcagaccaaa 360
agcatgtctt ctatgtttc cgtatcctt tgcaccttc cagcgggtga cgttatttc 420
tggaaacatt ggaatcggc caaagatgt cagtgcgct ctccgctgt gtctacgcgt 480
gacgtttca ccatctgt tctaacata ctacacata ctacacata caactatt 540
acttccgtc cgaataact catgagctg gtcataacc gcatgtgggt 600
tccggttgc gctgaacgc agattctga ctgttgggt gtcataagggt attcatgaac 660
aaaacggagg agcgttcca gccgttcaaa gagcgaccc agctgatgaa agcttggtt 720
tacttcagt aa 732

<210> 92
<211> 415
<212> DNA
<213> Artificial Sequence

<220>
<223> Intervening sequence containing transcriptional
and translational sites and T7 termination site.

<400> 92
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tgtagctggg agttcattcc gttagatgag gtttggggag aacgcccatt gccaccatc 120
caccatcact gagcggccgc ataagtctta agtcgaaacg attgatatgt agctataagt 180
aatgtataga ctgaaccag gctgtctgcca ccgcttgagca ataactagca taaccccttg 240
gggccctcaa accgggtttt tgcgtatcgt ataactcag gcatctatga 300
gtgtacacag tccgcatat cgaatratat ataggggaat tgtgagcggg 360
taacaattcc ccattctagt atattagtt agtaagaa ogagatatc catgg 415

<210> 93
<211> 4965
<212> DNA
<213> Artificial Sequence

<220>
<223> BONT/A-TEV and TEV protease variant 4 open reading
frames with the intervening transcription and
translation elements and termination site.

<400> 93

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60
tataatcaaa tccgaatg caggcccgatg aagccattaa aatccatac
120
aaatttggg tgaatccggg ggcgatacg ttcaggaac cggaagagg
180
ccaccggctg aggcctaaac ggcctccatg atagccataa ccttgatc
240
gacaatgaa aggaacaact gttaccgaac atgaccataa gttccgagc
300
acagatctcg gtcgcaatgt gctgaactct atgtgcgcg gcatccggt
360
agcaccatcg caagtgtgat gacaccaa gcatcaatgt gattcagct
420
gatggagctc accggcttaa atcgcccgag atcgcccgag cgcggatat
480
atccaatcg aatgtaaatc ttgtggcat gaagtccctg atcgcccgag
540
ggatcgagcg agtatattcg ttttttcga gatttccat ttggattga
600
ggaattgata cgaacccctc tttaggcgcg ggaataatcg gacgggagcc
660
ttggatcata aattattca gaccgggcat cgcttgatg gaattcgccat
720
cgtttttca agttgatatc gaacggctat tacgagatgt cgggttaga
780
gaaagaactc gacggttttg cggatcatgt gcaaattta ttgatagct
840
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1020
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1140
ataagtaact tgaatgcga atactgcga atacgaatc ggcggcgagc
1200
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1260
ggcctgtttg aattctata gtcctgtgtg ttatccag ttatccag
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3300
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3360

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<210> 94

<211> 2697

<212> DNA

<213> Artificial Sequence

<220> Open reading frame for NOC1LHN/A-TEV

<400> 94

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cacaacgttg aaggtatcg atgtatcg atgtatcg atgtatcg atgtatcg 1860

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<210> 95
 <211> 898
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> NocILHN/A-TEV

<400> 95

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

Asn	Phe	Val	Lys	Phe	Phe	Lys	Val	Leu	Asn	Arg	Lys	Thr	Tyr	Leu	Asn
		355					360					365			
Phe	Asp	Lys	Ala	Val	Phe	Lys	Ile	Asn	Ile	Val	Pro	Lys	Val	Asn	Tyr
	370					375					380				
Thr	Ile	Tyr	Asp	Gly	Phe	Asn	Leu	Arg	Asn	Thr	Asn	Leu	Ala	Ala	Asn
	385					390				395					400
Phe	Asn	Gly	Gln	Asn	Thr	Glu	Ile	Asn	Asn	Met	Asn	Phe	Thr	Lys	Leu
			405					410						415	
Lys	Asn	Phe	Thr	Gly	Leu	Phe	Glu	Phe	Tyr	Lys	Leu	Leu	Cys	Val	Arg
			420					425					430		
Gly	Ile	Ile	Thr	Ser	Lys	Glu	Asn	Leu	Tyr	Phe	Gln	Phe	Gly	Gly	Phe
		435					440					445			
Thr	Gly	Ala	Arg	Lys	Ser	Ala	Arg	Lys	Arg	Lys	Asn	Gln	Ala	Leu	Ala
	450					455					460				
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ala
	465				470				475						480
Leu	Asn	Asp	Leu	Cys	Ile	Lys	Val	Asn	Asn	Trp	Asp	Leu	Phe	Phe	Ser
				485					490					495	
Pro	Ser	Glu	Asp	Asn	Phe	Thr	Asn	Asp	Leu	Asn	Lys	Gly	Glu	Glu	Ile
			500					505					510		
Thr	Ser	Asp	Thr	Asn	Ile	Glu	Ala	Ala	Glu	Glu	Asn	Ile	Ser	Leu	Asp
		515					520					525			
Leu	Ile	Gln	Gln	Tyr	Tyr	Leu	Thr	Phe	Asn	Phe	Asp	Asn	Glu	Pro	Glu
	530					535					540				
Asn	Ile	Ser	Ile	Glu	Asn	Leu	Ser	Ser	Asp	Ile	Ile	Gly	Gln	Leu	Glu
	545				550				555						560
Leu	Met	Pro	Asn	Ile	Glu	Arg	Phe	Pro	Asn	Gly	Lys	Lys	Tyr	Glu	Leu
				565					570					575	
Asp	Lys	Tyr	Thr	Met	Phe	His	Tyr	Leu	Arg	Ala	Gln	Glu	Phe	Glu	His
			580					585					590		
Gly	Lys	Ser	Arg	Ile	Ala	Leu	Thr	Asn	Ser	Val	Asn	Glu	Ala	Leu	Leu
		595					600					605			
Asn	Pro	Ser	Arg	Val	Tyr	Thr	Phe	Phe	Ser	Ser	Asp	Tyr	Val	Lys	Lys
	610					615					620				
Val	Asn	Lys	Ala	Thr	Glu	Ala	Ala	Met	Phe	Leu	Gly	Trp	Val	Glu	Gln
	625				630					635					640
Leu	Val	Tyr	Asp	Phe	Thr	Asp	Glu	Thr	Ser	Glu	Val	Ser	Thr	Thr	Asp
				645					650					655	
Lys	Ile	Ala	Asp	Ile	Thr	Ile	Ile	Ile	Pro	Tyr	Ile	Gly	Pro	Ala	Leu
			660					665					670		
Asn	Ile	Gly	Asn	Met	Leu	Tyr	Lys	Asp	Asp	Phe	Val	Gly	Ala	Leu	Ile
		675					680					685			
Phe	Ser	Gly	Ala	Val	Ile	Leu	Leu	Glu	Phe	Ile	Pro	Glu	Ile	Ala	Ile
	690					695					700				
Pro	Val	Leu	Gly	Thr	Phe	Ala	Leu	Val	Ser	Tyr	Ile	Ala	Asn	Lys	Val
	705				710				715						720
Leu	Thr	Val	Gln	Thr	Ile	Asp	Asn	Ala	Leu	Ser	Lys	Arg	Asn	Glu	Lys
				725					730					735	
Trp	Asp	Glu	Val	Tyr	Lys	Tyr	Ile	Val	Thr	Asn	Trp	Leu	Ala	Lys	Val
			740					745					750		
Asn	Thr	Gln	Ile	Asp	Leu	Ile	Arg	Lys	Lys	Met	Lys	Glu	Ala	Leu	Glu
	755					760						765			
Asn	Gln	Ala	Glu	Ala	Thr	Lys	Ala	Ile	Ile	Asn	Tyr	Gln	Tyr	Asn	Gln
	770					775					780				
Tyr	Thr	Glu	Glu	Glu	Lys	Asn	Asn	Ile	Asn	Phe	Asn	Ile	Asp	Asp	Leu
	785				790					795					800
Ser	Ser	Lys	Leu	Asn	Glu	Ser	Ile	Asn	Lys	Ala	Met	Ile	Asn	Ile	Asn
				805					810					815	
Lys	Phe	Leu	Asn	Gln	Cys	Ser	Val	Ser	Tyr	Leu	Met	Asn	Ser	Met	Ile
			820					825					830		
Pro	Tyr	Gly	Val	Lys	Arg	Leu	Glu	Asp	Phe	Asp	Ala	Ser	Leu	Lys	Asp
		835					840					845			
Ala	Leu	Leu	Lys	Tyr	Ile	Tyr	Asp	Asn	Arg	Gly	Thr	Leu	Ile	Gly	Gln
	850					855					860				
Val	Asp	Arg	Leu	Lys	Asp	Lys	Val	Asn	Asn	Thr	Leu	Ser	Thr	Asp	Ile
	865				870					875					880
Pro	Phe	Gln	Leu	Ser	Lys	Tyr	Val	Asp	Asn	Gln	Arg	His	His	His	His
				885					890					895	

His H1s

<210> 96
<211> 2709
<212> DNA
<213> Artificial Sequence

<220>
<223> Open reading frame for DYNLHN/A-TEV

<400> 96
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aatccataac aagcatttga aagcccggtga cagcccggtga aagcccggtga
120
aaatttggg tgaatccggg ggcgatacg ttcaagacc cggaaaggag agatttaac
180
ccacggcccg aggtcccggtg tcttaactatg atagcataa cctgagtaac
240
gacaatgaa aggaacaata cctgaagggt gtttcgaagc gatttatacc
300
acagatcctg gtcgcatactt atgtgacgag gcatccggtt ttgggggtggt
360
agcaccatcg atacagaaat caaagtgtat gacacccaat gcatcattgt
420
gatccggtat ctcgtatca atggccttaac atggccttga atctgacggg
480
gatggggagt accggtccga aggtccctga atggccttga atctgacggg
540
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600
gaagtgtata cgaacctctt tttagggcgg ggaataatcg gacgggtgacc
660
ttggcatg aactatata tgcggggcat cgtttgtat gaaatcgccat
720
ttggcatg aactatata tgcggggcat cgtttgtat gaaatcgccat
780
gaagaactcg gacggttttg cgttcatatg aaaaattta ttgatatgtt
840
gaatttcggc tgaatatata caataaattc aagaacattg catcaacctt
900
aaaagcattg ttggatccac ggcctagctta caatatatga aaaaagtatt
960
taacctataa tgcataccga gatctacaca gaggaataat ttgtcaaat
1020
ttgaatacga aaaaacctct ttaagatcaa catcgtaccg
1140
aaagttaact acacatctta tgaatgcttt aatctgcga atagaaatc
1200
tttaacacga aatacaacac atgaacttta cttaacacga aaatrttcc
1260
aattcgtttg aattcattaa gtccttgtgt ttatcaccag caaagaaac
1320
cgtatcctcc agtatggcgg ttcccttccg atctgaaagt atctgaaagt
1440
ctcaatgata aatttataca ggtgaaacac ggtgaaacac ggtgaaacac
1500
aatttataca acaacttga gaaatgagag gaaatatact cgaataccaa
1560
gcaaggaaga aatatagttc agatcttatt caaataatat accatgacct
1620
aacgagcctg agaacatttc cataggaat ctacgctctg acatcatcgg
1680
ctgagcctga atatacctga atgtatgga caaatatacc
1740
atgttcccat atctccggcg gacgacggca agtctcgtat tgcctcgtat
1800
aattcogtaa acaagacctt tttaaatctt tgcgctgtgt acacaccttt
1860
tatgttaaaa aagtgaacaa ggcgaacggaa gtcgctgtgt tttagggatg
1920
ctgttatatg actttaacga tgaaccttct gaagtctcga ccaaccgcaa
1980
gatttatatg gatgacggat ttgtgaaaca ttgttaacat tccgtgtga
2040
gatttatatg gatgacggat ttgtgaaaca ttgttaacat tccgtgtga
2100
gaaatcggca ttccagtatc ggcgtgtgtt cctatatcgc aaaaagtgt
2160
ttgaactgtc agacgatcga caacggcttc agtaaacgtt agtaaacgtt
2220
tatataatga tatgctcgtt aaggtatgga cccagattga cctgattcgc
2280
aagaatgata aggaagcgtt ggaagaccaa aataacatca acttaacat
2340
caatatatac agtaacacaa ggaagaaaaa aataacatca acttaacat
2400
tcttcaaacg tgaatgaatc tattaacaaa gtccttgaaac
2460
caaatgtatg gacgacatcg atgaaactcg atgaaactcg atgaaactcg
2520
gaatttcgat caagccttaa agatgcccctt ctgaagatata acacgcttgag
2580
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2640
cattattgag ccttttcagc ccatcaccat 2700
caccactaa 2709

<400> 97

Met	Pro	Phe	Val	Asn	Lys	Gln	Phe	Asn	Tyr	Lys	Asp	Pro	Val	Asn	Gly
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Val	Asp	Ile	Ala	Tyr	Ile	Lys	Ile	Pro	Asn	Ala	Gly	Gln	Met	Gln	Pro
			20					25					30		
Val	Lys	Ala	Phe	Lys	Ile	His	Asn	Lys	Ile	Trp	Val	Ile	Pro	Glu	Arg
			35				40					45			
Asp	Thr	Phe	Thr	Asn	Pro	Glu	Glu	Gly	Asp	Leu	Asn	Pro	Pro	Pro	Glu
			50			55					60				
Ala	Lys	Gln	Val	Pro	Val	Ser	Tyr	Tyr	Asp	Ser	Thr	Tyr	Leu	Ser	Thr
65					70					75				80	
Asp	Asn	Glu	Lys	Asp	Asn	Tyr	Leu	Lys	Gly	Val	Thr	Lys	Leu	Phe	Glu
				85					90					95	
Arg	Ile	Tyr	Ser	Thr	Asp	Leu	Gly	Arg	Met	Leu	Leu	Thr	Ser	Ile	Val
			100					105					110		
Arg	Gly	Ile	Pro	Phe	Trp	Gly	Gly	Ser	Thr	Ile	Asp	Thr	Glu	Leu	Lys
			115				120					125			
Val	Ile	Asp	Thr	Asn	Cys	Ile	Asn	Val	Ile	Gln	Pro	Asp	Gly	Ser	Tyr
			130			135					140				
Arg	Ser	Glu	Glu	Leu	Asn	Leu	Val	Ile	Ile	Gly	Pro	Ser	Ala	Asp	Ile
145					150					155				160	
Ile	Gln	Phe	Glu	Cys	Lys	Ser	Phe	Gly	His	Glu	Val	Leu	Asn	Leu	Thr
				165					170					175	
Arg	Asn	Gly	Tyr	Gly	Ser	Thr	Gln	Tyr	Ile	Arg	Phe	Ser	Pro	Asp	Phe
			180					185					190		
Thr	Phe	Gly	Phe	Glu	Glu	Ser	Leu	Glu	Val	Asp	Thr	Asn	Pro	Leu	Leu
			195				200					205			
Gly	Ala	Gly	Lys	Phe	Ala	Thr	Asp	Pro	Ala	Val	Thr	Leu	Ala	His	Glu
			210			215					220				
Leu	Ile	His	Ala	Gly	His	Arg	Leu	Tyr	Gly	Ile	Ala	Ile	Asn	Pro	Asn
225					230					235				240	
Arg	Val	Phe	Lys	Val	Asn	Thr	Asn	Ala	Tyr	Tyr	Glu	Met	Ser	Gly	Leu
				245					250					255	
Glu	Val	Ser	Phe	Glu	Glu	Leu	Arg	Thr	Phe	Gly	Gly	His	Asp	Ala	Lys
			260					265					270		
Phe	Ile	Asp	Ser	Leu	Gln	Glu	Asn	Glu	Phe	Arg	Leu	Tyr	Tyr	Tyr	Asn
			275				280					285			
Lys	Phe	Lys	Asp	Ile	Ala	Ser	Thr	Leu	Asn	Lys	Ala	Lys	Ser	Ile	Val
			290			295					300				
Gly	Thr	Thr	Ala	Ser	Leu	Gln	Tyr	Met	Lys	Asn	Val	Phe	Lys	Glu	Lys
305					310					315				320	
Tyr	Leu	Leu	Ser	Glu	Asp	Thr	Ser	Gly	Lys	Phe	Ser	Val	Asp	Lys	Leu
				325					330					335	
Lys	Phe	Asp	Lys	Leu	Tyr	Lys	Met	Leu	Thr	Glu	Ile	Tyr	Thr	Glu	Asp
			340					345					350		
Asn	Phe	Val	Lys	Phe	Phe	Lys	Val	Leu	Asn	Arg	Lys	Thr	Tyr	Leu	Asn
			355				360					365			
Phe	Asp	Lys	Ala	Val	Phe	Lys	Ile	Asn	Ile	Val	Pro	Lys	Val	Asn	Tyr
			370			375					380				
Thr	Ile	Tyr	Asp	Gly	Phe	Asn	Leu	Arg	Asn	Thr	Asn	Leu	Ala	Ala	Asn
385					390					395				400	
Phe	Asn	Gly	Gln	Asn	Thr	Glu	Ile	Asn	Asn	Met	Asn	Phe	Thr	Lys	Leu
				405					410					415	
Lys	Asn	Phe	Thr	Gly	Leu	Phe	Glu	Phe	Tyr	Lys	Leu	Leu	Cys	Val	Arg
			420					425					430		
Gly	Ile	Ile	Thr	Ser	Lys	Glu	Asn	Leu	Tyr	Phe	Gln	Tyr	Gly	Gly	Phe
			435				440					445			
Leu	Arg	Arg	Ile	Arg	Pro	Lys	Leu	Lys	Trp	Asp	Asn	Gln	Ala	Leu	Ala
			450			455					460				
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ala
465					470					475				480	
Leu	Asn	Asp	Leu	Cys	Ile	Lys	Val	Asn	Asn	Trp	Asp	Leu	Phe	Phe	Ser
				485					490					495	
Pro	Ser	Glu	Asp	Asn	Phe	Thr	Asn	Asp	Leu	Asn	Lys	Gly	Glu	Glu	Ile
			500					505					510		
Thr	Ser	Asp	Thr	Asn	Ile	Glu	Ala	Ala	Glu	Glu	Asn	Ile	Ser	Leu	Asp
			515				520					525			
Leu	Ile	Gln	Gln	Tyr	Tyr	Leu	Thr	Phe	Asn	Phe	Asp	Asn	Glu	Pro	Glu

530 535 540
 Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln Leu Glu
 545 550 555 560
 Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr Glu Leu
 565 570 575
 Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe Glu His
 580 585 590
 Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser Val Asn Glu Ala Leu Leu
 595 600 605
 Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val Lys Lys
 610 615 620
 Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val Glu Gln
 625 630 635 640
 Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr Thr Asp
 645 650 655 660
 Lys Ile Ala Asp Ile Thr Ile Ile Ile Pro Tyr Ile Gly Pro Ala Leu
 660 665 670
 Asn Ile Gly Asn Met Leu Tyr Lys Asp Phe Val Gly Ala Leu Ile
 675 680 685
 Phe Ser Gly Ala Val Ile Leu Leu Glu Phe Ile Pro Glu Ile Ala Ile
 690 695 700
 Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn Lys Val
 705 710 715 720
 Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn Glu Lys
 725 730 735
 Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala Lys Val
 740 745 750
 Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met Lys Glu Ala Leu Glu
 755 760 765
 Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr Asn Gln
 770 775 780
 Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp Asp Leu
 785 790 795 800
 Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met Ile Asn Ile Asn
 805 810 815
 Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met Ile
 820 825 830
 Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu Lys Asp
 835 840 845
 Ala Leu Leu Lys Tyr Ile Tyr Asp Asn Arg Gly Thr Leu Ile Gly Gln
 850 855 860
 Val Asp Arg Leu Lys Asp Lys Val Asn Asn Thr Leu Ser Thr Asp Ile
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 Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Gln Arg Leu Leu Ser Thr
 885 890 895
 His His His His His
 900

<210> 98
 <211> 320
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA fragment encoding a di-chain loop region
 comprising an integrated TEV protease cleavage
 site-Galanin binding domain

<400> 98
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 ctgtacttcc agggctggac ttggaactct gctggttata tcctgggccc acatgcggtt 120
 gctcttgcgt gtggcgggtg ctctggcggt ggcggtagcg gcggtggcgg ttctgcacta 180
 gtgcttcagt gtatcaagg taacaactgg gatttattct tcagcccgag tgaagacaac 240
 ttcaccaacg acctgaacaa aggtgaagaa atcacctcag atactaacat cgaagcagcc 300
 gaagaaaaca tcagtctaga 320

<210> 99

<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Di-chain loop region comprising an integrated TEV protease cleavage site-galanin binding domain

<400> 99
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Lys Ser Glu Asn Leu Tyr Phe Glu Trp Thr Leu Asn Ser Ala Gly
20 25 30
Tyr Leu Leu Gly Pro His Ala Val Ala Leu Ala Gly Gly Gly Ser
35 40 45
Gly Gly Gly Ser Gly Gly Gly Ser Ala Leu Val Leu Glu Cys
50 55
Ile Lys Val Asn Asn Trp Asp Leu Phe Phe Ser Pro Ser Glu Asp Asn
60 65
Phe Thr Asn Asp Leu Asn Lys Gly Glu Ile Thr Ser Asp Thr Asn
70 75 80
Ile Glu Ala Ala 100
105

<210> 100
<211> 2703
<212> DNA
<213> Artificial Sequence

<220>
<223> Open reading frame for GalLHN/A-TEV

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120
tcccgaaatg agcccccgtg aagacgccag tcaacggcgt ggcatttcgc
180
tataatcaaa tcccgaaatg agcccccgtg aagacgccag tcaacggcgt ggcatttcgc
240
tcccgaaatg agcccccgtg aagacgccag tcaacggcgt ggcatttcgc
300
tataatcaaa tcccgaaatg agcccccgtg aagacgccag tcaacggcgt ggcatttcgc
360
tcccgaaatg agcccccgtg aagacgccag tcaacggcgt ggcatttcgc
420
tataatcaaa tcccgaaatg agcccccgtg aagacgccag tcaacggcgt ggcatttcgc
480
tcccgaaatg agcccccgtg aagacgccag tcaacggcgt ggcatttcgc
540
tataatcaaa tcccgaaatg agcccccgtg aagacgccag tcaacggcgt ggcatttcgc
600
tcccgaaatg agcccccgtg aagacgccag tcaacggcgt ggcatttcgc
660
tataatcaaa tcccgaaatg agcccccgtg aagacgccag tcaacggcgt ggcatttcgc
720
tcccgaaatg agcccccgtg aagacgccag tcaacggcgt ggcatttcgc
780
tataatcaaa tcccgaaatg agcccccgtg aagacgccag tcaacggcgt ggcatttcgc
840
tcccgaaatg agcccccgtg aagacgccag tcaacggcgt ggcatttcgc
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960
tcccgaaatg agcccccgtg aagacgccag tcaacggcgt ggcatttcgc
1020
tataatcaaa tcccgaaatg agcccccgtg aagacgccag tcaacggcgt ggcatttcgc
1080
tcccgaaatg agcccccgtg aagacgccag tcaacggcgt ggcatttcgc
1140
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1200
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1260
tataatcaaa tcccgaaatg agcccccgtg aagacgccag tcaacggcgt ggcatttcgc
1320
tcccgaaatg agcccccgtg aagacgccag tcaacggcgt ggcatttcgc
1380
tataatcaaa tcccgaaatg agcccccgtg aagacgccag tcaacggcgt ggcatttcgc
1440
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1500
tataatcaaa tcccgaaatg agcccccgtg aagacgccag tcaacggcgt ggcatttcgc
1560
tcccgaaatg agcccccgtg aagacgccag tcaacggcgt ggcatttcgc
1620
tataatcaaa tcccgaaatg agcccccgtg aagacgccag tcaacggcgt ggcatttcgc
1680
tcccgaaatg agcccccgtg aagacgccag tcaacggcgt ggcatttcgc
1740
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1800
tcccgaaatg agcccccgtg aagacgccag tcaacggcgt ggcatttcgc
1860
tataatcaaa tcccgaaatg agcccccgtg aagacgccag tcaacggcgt ggcatttcgc
1920
tcccgaaatg agcccccgtg aagacgccag tcaacggcgt ggcatttcgc
1980
tataatcaaa tcccgaaatg agcccccgtg aagacgccag tcaacggcgt ggcatttcgc
2040

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tataaagatg attttgtggg cgccctgac ttttcaggcg ctgtttatcct gctggaattt 2100
atcccggaaa tcgccattcc agtactcggg acctttgcgc tgggtgtccta tatcgcaaac 2160
aaagttttga ctgtccagac gatcgacaac gcgctcagta aacgtaacga aaaatgggat 2220
gaggtgtata agtatattgt taccaactgg ctgcgtaaaag taaacaccca gattgacctg 2280
attcgcaaga agatgaaaga agcgtgggaa aaccaagcag aagcgaccaa agctattatc 2340
aactatcaat ataaccagta cacagaggaa gaaaagaata acatcaactt caacatcgac 2400
gacttatctt caaagctgaa tgaatctatt aacaaagcga tgattaatat taacaagttc 2460
ttgaaccaat gtagtgtcag ctatctgatg aactcgatga tcccttacgg tgtgaaacgt 2520
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ggaactctta ttggccaagt ggatcgctta aaagataaag tcaacaacac gctgagtaca 2640
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taa 2703

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<210> 101
 <211> 900
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> GalLHN/A-TEV

<400> 101

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

Phe	Asp	Lys	Ala	Val	Phe	Lys	Ile	Asn	Ile	Val	Pro	Lys	Val	Asn	Tyr
370						375					380				
Thr	Ile	Tyr	Asp	Gly	Phe	Asn	Leu	Arg	Asn	Thr	Asn	Leu	Ala	Ala	Asn
385					390					395					400
Phe	Asn	Gly	Gln	Asn	Thr	Glu	Ile	Asn	Asn	Met	Asn	Phe	Thr	Lys	Leu
				405					410					415	
Lys	Asn	Phe	Thr	Gly	Leu	Phe	Glu	Phe	Tyr	Lys	Leu	Leu	Cys	Val	Asp
			420					425					430		
Gly	Ile	Ile	Thr	Ser	Lys	Thr	Lys	Ser	Glu	Asn	Leu	Tyr	Phe	Gln	Gly
		435					440					445			
Trp	Thr	Leu	Asn	Ser	Ala	Gly	Tyr	Leu	Leu	Gly	Pro	His	Ala	Val	Ala
450						455					460				
Leu	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly
465					470					475					480
Ser	Ala	Leu	Val	Leu	Gln	Cys	Ile	Lys	Val	Asn	Asn	Trp	Asp	Leu	Phe
				485					490					495	
Phe	Ser	Pro	Ser	Glu	Asp	Asn	Phe	Thr	Asn	Asp	Leu	Asn	Lys	Gly	Glu
			500					505					510		
Glu	Ile	Thr	Ser	Asp	Thr	Asn	Ile	Glu	Ala	Ala	Glu	Glu	Asn	Ile	Ser
		515					520					525			
Leu	Asp	Leu	Ile	Gln	Gln	Tyr	Tyr	Leu	Thr	Phe	Asn	Phe	Asp	Asn	Glu
530						535					540				
Pro	Glu	Asn	Ile	Ser	Ile	Glu	Asn	Leu	Ser	Ser	Asp	Ile	Ile	Gly	Gln
545					550					555					560
Leu	Glu	Leu	Met	Pro	Asn	Ile	Glu	Arg	Phe	Pro	Asn	Gly	Lys	Lys	Tyr
				565					570					575	
Glu	Leu	Asp	Lys	Tyr	Thr	Met	Phe	His	Tyr	Leu	Arg	Ala	Gln	Glu	Phe
			580					585					590		
Glu	His	Gly	Lys	Ser	Arg	Ile	Ala	Leu	Thr	Asn	Ser	Val	Asn	Glu	Ala
		595					600					605			
Leu	Leu	Asn	Pro	Ser	Arg	Val	Tyr	Thr	Phe	Phe	Ser	Ser	Asp	Tyr	Val
	610					615					620				
Lys	Lys	Val	Asn	Lys	Ala	Thr	Glu	Ala	Ala	Met	Phe	Leu	Gly	Trp	Val
625					630					635					640
Glu	Gln	Leu	Val	Tyr	Asp	Phe	Thr	Asp	Glu	Thr	Ser	Glu	Val	Ser	Thr
				645					650					655	
Thr	Asp	Lys	Ile	Ala	Asp	Ile	Thr	Ile	Ile	Ile	Pro	Tyr	Ile	Gly	Pro
			660					665					670		
Ala	Leu	Asn	Ile	Gly	Asn	Met	Leu	Tyr	Lys	Asp	Asp	Phe	Val	Gly	Ala
		675					680					685			
Leu	Ile	Phe	Ser	Gly	Ala	Val	Ile	Leu	Leu	Glu	Phe	Ile	Pro	Glu	Ile
	690					695					700				
Ala	Ile	Pro	Val	Leu	Gly	Thr	Phe	Ala	Leu	Val	Ser	Tyr	Ile	Ala	Asn
705					710					715					720
Lys	Val	Leu	Thr	Val	Gln	Thr	Ile	Asp	Asn	Ala	Leu	Ser	Lys	Arg	Asn
				725					730					735	
Glu	Lys	Trp	Asp	Glu	Val	Tyr	Lys	Tyr	Ile	Val	Thr	Asn	Trp	Leu	Ala
			740					745					750		
Lys	Val	Asn	Thr	Gln	Ile	Asp	Leu	Ile	Arg	Lys	Lys	Met	Lys	Glu	Ala
		755					760					765			
Leu	Glu	Asn	Gln	Ala	Glu	Ala	Thr	Lys	Ala	Ile	Ile	Asn	Tyr	Gln	Tyr
	770					775					780				
Asn	Gln	Tyr	Thr	Glu	Glu	Glu	Lys	Asn	Asn	Ile	Asn	Phe	Asn	Ile	Asp
785					790					795					800
Asp	Leu	Ser	Ser	Lys	Leu	Asn	Glu	Ser	Ile	Asn	Lys	Ala	Met	Ile	Asn
			805						810					815	
Ile	Asn	Lys	Phe	Leu	Asn	Gln	Cys	Ser	Val	Ser	Tyr	Leu	Met	Asn	Ser
			820					825					830		
Met	Ile	Pro	Tyr	Gly	Val	Lys	Arg	Leu	Glu	Asp	Phe	Asp	Ala	Ser	Leu
		835					840					845			
Lys	Asp	Ala	Leu	Leu	Lys	Tyr	Ile	Tyr	Asp	Asn	Arg	Gly	Thr	Leu	Ile
	850					855					860				
Gly	Gln	Val	Asp	Arg	Leu	Lys	Asp	Lys	Val	Asn	Thr	Leu	Ser	Thr	
865					870					875					880
Asp	Ile	Pro	Phe	Gln	Leu	Ser	Lys	Tyr	Val	Asp	Asn	Gln	Arg	His	His
				885					890					895	
His	His	His	His												
			900												

<210> 102
 <211> 314
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA fragment encoding a di-chain loop region
 comprising an integrated TEV protease cleavage
 site-Nociceptin binding domain

<400> 102
 gaattctata agctcctgtg tgtccgcggt attatcacca gcaaagaaaa cctgtacttc 60
 cagttcggcg gttttaccgg cgctcgtaaa tctgcacgta aacgcaagaa tcaggctctg 120
 gctgggtggcg gtggctctgg tgggtggcggg agcggcggtg gcggttctgc gctcaatgat 180
 ttatgcatca aggtgaacaa ctgggacttg tttttctctc catctgaaga taattttact 240
 aacgacttga acaaaggaga ggaaattact tccgatacca acatcgaagc agcgggaagag 300
 aatattagtc taga 314

<210> 103
 <211> 104
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Di-chain loop region comprising an integrated TEV
 protease cleavage site-Nociceptin binding domain

<400> 103
 Glu Phe Tyr Lys Leu Leu Cys Val Arg Gly Ile Ile Thr Ser Lys Glu
 1 5 10 15
 Asn Leu Tyr Phe Gln Phe Gly Gly Phe Thr Gly Ala Arg Lys Ser Ala
 20 25 30
 Arg Lys Arg Lys Asn Gln Ala Leu Ala Gly Gly Gly Gly Ser Gly Gly
 35 40 45
 Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Asn Asp Leu Cys Ile Lys
 50 55 60
 Val Asn Asn Trp Asp Leu Phe Phe Ser Pro Ser Glu Asp Asn Phe Thr
 65 70 75 80
 Asn Asp Leu Asn Lys Gly Glu Glu Ile Thr Ser Asp Thr Asn Ile Glu
 85 90 95
 Ala Ala Glu Glu Asn Ile Ser Leu
 100

<210> 104
 <211> 314
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA fragment encoding a di-chain loop region
 comprising an integrated TEV protease cleavage
 site-Dynorphin binding domain

<400> 104
 gaattctata agctcctgtg tgtccgtggt attatcacca gcaaagaaaa cctgtacttc 60
 cagtatggcg gtttcctgcg tcgcattcgt cctaagctta aatgggataa ccaggctctt 120
 gctgggtggcg gtggctctgg tgggtggcggg agcggcggtg gtggttctgc actcaatgat 180
 ttatgtatca aggtgaacaa ctgggacttg tttttctctc catctgaaga taattttact 240
 aacgacttga acaaaggaga ggaaattact tccgatacca acatcgaagc agcgggaagag 300
 aatattagtc taga 314

<210> 105
 <211> 104
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Di-chain loop region comprising an integrated TEV protease cleavage site-Dynorphin binding domain

<400> 105
 Glu Phe Tyr Lys Leu Leu Cys Val Arg Gly Ile Ile Thr Ser Lys Glu
 1 5 10 15
 Asn Leu Tyr Phe Gln Tyr Gly Gly Phe Leu Arg Arg Ile Arg Pro Lys
 20 25 30
 Leu Lys Trp Asp Asn Gln Ala Leu Ala Gly Gly Gly Ser Gly Gly
 35 40 45
 Gly Gly Ser Gly Gly Gly Gly Ser Ala Leu Asn Asp Leu Cys Ile Lys
 50 55 60
 Val Asn Asn Trp Asp Leu Phe Phe Ser Pro Ser Glu Asp Asn Phe Thr
 65 70 75 80
 Asn Asp Leu Asn Lys Gly Glu Glu Ile Thr Ser Asp Thr Asn Ile Glu
 85 90 95
 Ala Ala Glu Glu Asn Ile Ser Leu
 100

<210> 106
 <211> 750
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Open reading frame encoding TEV protease variant 7

<400> 106
 ccattggatgg gtggcgaatc tctgttcaag ggtccgcgtg attataaccc gatattcttct 60
 actatttgtc atctgactaa cgaaagcgac ggccacacga cttctctgta cggatctcgtt 120
 ttccgtccgt tcatcattac caacaagcat ctgttccgcc gtaacaacgg taccctgctg 180
 gttcaatctc tgcacggcgt cttcaaggta aaagacacca ctacgctgca gcagcacctg 240
 gtcgacggcc gtgacatgat catcatccgc atgccgaaag attttccgcc gttcccgcaa 300
 aaactgaagt ttccgtgaacc gcaacgcgaa gaacgtattt gcctgggttac caccaacttt 360
 cagacaaaaa gcatgtcttc tatggtttcc gatacctctt gcaccttccc aagcgggtgac 420
 ggtattttct ggaaacattg gatccagacc aaagatgggtc agtgcggctc tccgctggtg 480
 tctacgcgtg acggtttcat cgttgggtat cattctgctt ctaacttcac taactactaac 540
 aactacttta cttccgttcc gaaaaacttc atggagctgc tgactaacca agaggcccag 600
 cagtgggtgt ccggttggcg cctgaacgca gattctgtac tgtggggtgg tcataaggta 660
 ttcattgaaca aaccggagga gccgttccag ccggtcaaag aggcgaccca gctgatgaac 720
 gaactgggtt actctcagta atgaaagctt 750

<210> 107
 <211> 3791
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> ORF encoding p10-TEV variant 7 and polH-DynLHn/A-TEV

<400> 107
 agatcttatg cggccgcact cgagtcatta gtggtgatgg tgatgggtggg ttgacagaag 60
 tctctgatta tcaacatact tgcacagttg gaacgggatg tctgttgaca gagtgttgtt 120
 taccttatct ttcagacggt caacttggcc aatgagcgtt cccctgttat cgtagatgta 180
 cttagaagg gcgtctttca gcgaggcgct gaagtccttc agtctcttta caccatatgg 240
 gatcattgag ttcattcaagt atgatacact gcattgggtg aggaacttgt taatgtttat 300
 cattgccttg tttatgctct cgttgagttt actagagagg tcgtcaatgt tgaagtgtat 360
 gttgttcttt tctcctcgg tgtactgggt gtactgatag ttaatgatgg cctttgtcgc 420
 ttacgcctgg ttctccagcg cctccttcat ctttttctg atgaggctga tttgggtgtt 480
 gaccttagcg agccagttag tcacgatgta ttgtacact tcatccact tctcgtttct 540
 ttttgacaga gcattatcga ttgtttggac agtgaggacc ttgttagcaa tgtagctgac 600
 caaagcgaag gtaccaagaa caggaatagc gatctctggg atgaactcca acaaatcac 660
 tgctcccag aaaatcaacg caccgacgaa gtcgtccttg tacagcatat tgccgatgtt 720
 aagagcaggt ccaatgtagg gtatgatgat agtgatgtct gcgatcttgt ccgtagtcga 780

[illegible]