

SEQUENCE LISTING

<110> Janssen Vaccines & Prevention B.V.
 <120> Human Immunodeficiency Virus Antigens, Vectors, Compositions, and Methods of Use Thereof
 <130> 0265 EP P01 PRI
 <160> 37
 <170> PatentIn version 3.5
 <210> 1
 <211> 500
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> moslGag mosaic antigen sequence
 <400> 1

Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp
 1 5 10 15

Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Arg Leu Lys
 20 25 30

His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
 35 40 45

Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
 50 55 60

Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn
 65 70 75 80

Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp
 85 90 95

Thr Lys Glu Ala Leu Glu Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys
 100 105 110

Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly Asn Ser Ser Gln Val
 115 120 125

Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His
 130 135 140

Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu
 145 150 155 160

Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser

165

170

175

Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly
 180 185 190

Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu
 195 200 205

Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala
 210 215 220

Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr
 225 230 235 240

Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile
 245 250 255

Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys
 260 265 270

Ile Val Arg Met Tyr Ser Pro Val Ser Ile Leu Asp Ile Arg Gln Gly
 275 280 285

Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu
 290 295 300

Arg Ala Glu Gln Ala Ser Gln Asp Val Lys Asn Trp Met Thr Glu Thr
 305 310 315 320

Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala
 325 330 335

Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly
 340 345 350

Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser
 355 360 365

Gln Val Thr Asn Ser Ala Thr Ile Met Met Gln Arg Gly Asn Phe Arg
 370 375 380

Asn Gln Arg Lys Thr Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His
 385 390 395 400

Ile Ala Lys Asn Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys
 405 410 415

Gly Lys Glu Gly His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn

420

425

430

Phe Leu Gly Lys Ile Trp Pro Ser Asn Lys Gly Arg Pro Gly Asn Phe
 435 440 445

Leu Gln Asn Arg Pro Glu Pro Thr Ala Pro Pro Glu Glu Ser Phe Arg
 450 455 460

Phe Gly Glu Glu Thr Thr Thr Pro Ser Gln Lys Gln Glu Pro Ile Asp
 465 470 475 480

Lys Glu Met Tyr Pro Leu Ala Ser Leu Lys Ser Leu Phe Gly Asn Asp
 485 490 495

Pro Ser Ser Gln
 500

<210> 2
 <211> 491
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> mos2Gag mosaic antigen sequence

<400> 2

Met Gly Ala Arg Ala Ser Ile Leu Arg Gly Gly Lys Leu Asp Lys Trp
 1 5 10 15

Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys His Tyr Met Leu Lys
 20 25 30

His Leu Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Leu Asn Pro
 35 40 45

Gly Leu Leu Glu Thr Ser Glu Gly Cys Lys Gln Ile Ile Lys Gln Leu
 50 55 60

Gln Pro Ala Leu Gln Thr Gly Thr Glu Glu Leu Arg Ser Leu Phe Asn
 65 70 75 80

Thr Val Ala Thr Leu Tyr Cys Val His Ala Glu Ile Glu Val Arg Asp
 85 90 95

Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Gln
 100 105 110

Gln Lys Thr Gln Gln Ala Lys Glu Ala Asp Gly Lys Val Ser Gln Asn
 115 120 125

Tyr	Pro	Ile	Val	Gln	Asn	Leu	Gln	Gly	Gln	Met	Val	His	Gln	Pro	Ile	130	135	140	
Ser	Pro	Arg	Thr	Leu	Asn	Ala	Trp	Val	Lys	Val	Ile	Glu	Glu	Lys	Ala	145	150	155	160
Phe	Ser	Pro	Glu	Val	Ile	Pro	Met	Phe	Thr	Ala	Leu	Ser	Glu	Gly	Ala	165	170	175	
Thr	Pro	Gln	Asp	Leu	Asn	Thr	Met	Leu	Asn	Thr	Val	Gly	Gly	His	Gln	180	185	190	
Ala	Ala	Met	Gln	Met	Leu	Lys	Asp	Thr	Ile	Asn	Glu	Glu	Ala	Ala	Glu	195	200	205	
Trp	Asp	Arg	Leu	His	Pro	Val	His	Ala	Gly	Pro	Val	Ala	Pro	Gly	Gln	210	215	220	
Met	Arg	Glu	Pro	Arg	Gly	Ser	Asp	Ile	Ala	Gly	Thr	Thr	Ser	Asn	Leu	225	230	235	240
Gln	Glu	Gln	Ile	Ala	Trp	Met	Thr	Ser	Asn	Pro	Pro	Ile	Pro	Val	Gly	245	250	255	
Asp	Ile	Tyr	Lys	Arg	Trp	Ile	Ile	Leu	Gly	Leu	Asn	Lys	Ile	Val	Arg	260	265	270	
Met	Tyr	Ser	Pro	Thr	Ser	Ile	Leu	Asp	Ile	Lys	Gln	Gly	Pro	Lys	Glu	275	280	285	
Pro	Phe	Arg	Asp	Tyr	Val	Asp	Arg	Phe	Phe	Lys	Thr	Leu	Arg	Ala	Glu	290	295	300	
Gln	Ala	Thr	Gln	Asp	Val	Lys	Asn	Trp	Met	Thr	Asp	Thr	Leu	Leu	Val	305	310	315	320
Gln	Asn	Ala	Asn	Pro	Asp	Cys	Lys	Thr	Ile	Leu	Arg	Ala	Leu	Gly	Pro	325	330	335	
Gly	Ala	Thr	Leu	Glu	Glu	Met	Met	Thr	Ala	Cys	Gln	Gly	Val	Gly	Gly	340	345	350	
Pro	Ser	His	Lys	Ala	Arg	Val	Leu	Ala	Glu	Ala	Met	Ser	Gln	Thr	Asn	355	360	365	
Ser	Thr	Ile	Leu	Met	Gln	Arg	Ser	Asn	Phe	Lys	Gly	Ser	Lys	Arg	Ile	370	375	380	

Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His Ile Ala Arg Asn Cys
385 390 395 400

Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys Gly Lys Glu Gly His
405 410 415

Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn Phe Leu Gly Lys Ile
420 425 430

Trp Pro Ser His Lys Gly Arg Pro Gly Asn Phe Leu Gln Ser Arg Pro
435 440 445

Glu Pro Thr Ala Pro Pro Ala Glu Ser Phe Arg Phe Glu Glu Thr Thr
450 455 460

Pro Ala Pro Lys Gln Glu Pro Lys Asp Arg Glu Pro Leu Thr Ser Leu
465 470 475 480

Arg Ser Leu Phe Gly Ser Asp Pro Leu Ser Gln
485 490

<210> 3
<211> 850
<212> PRT
<213> Artificial Sequence

<220>
<223> moslPol mosaic antigen sequence

<400> 3

Met Ala Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys Pro
1 5 10 15

Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu Lys
20 25 30

Ile Lys Ala Leu Thr Ala Ile Cys Glu Glu Met Glu Lys Glu Gly Lys
35 40 45

Ile Thr Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe Ala
50 55 60

Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg
65 70 75 80

Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile
85 90 95

Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu Ala

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

355

360

365

Gln Leu Thr Glu Ala Val Gln Lys Ile Ala Met Glu Ser Ile Val Ile
 370 375 380

Trp Gly Lys Thr Pro Lys Phe Arg Leu Pro Ile Gln Lys Glu Thr Trp
 385 390 395 400

Glu Thr Trp Trp Thr Asp Tyr Trp Gln Ala Thr Trp Ile Pro Glu Trp
 405 410 415

Glu Phe Val Asn Thr Pro Pro Leu Val Lys Leu Trp Tyr Gln Leu Glu
 420 425 430

Lys Asp Pro Ile Ala Gly Val Glu Thr Phe Tyr Val Ala Gly Ala Ala
 435 440 445

Asn Arg Glu Thr Lys Leu Gly Lys Ala Gly Tyr Val Thr Asp Arg Gly
 450 455 460

Arg Gln Lys Ile Val Ser Leu Thr Glu Thr Thr Asn Gln Lys Thr Ala
 465 470 475 480

Leu Gln Ala Ile Tyr Leu Ala Leu Gln Asp Ser Gly Ser Glu Val Asn
 485 490 495

Ile Val Thr Ala Ser Gln Tyr Ala Leu Gly Ile Ile Gln Ala Gln Pro
 500 505 510

Asp Lys Ser Glu Ser Glu Leu Val Asn Gln Ile Ile Glu Gln Leu Ile
 515 520 525

Lys Lys Glu Arg Val Tyr Leu Ser Trp Val Pro Ala His Lys Gly Ile
 530 535 540

Gly Gly Asn Glu Gln Val Asp Lys Leu Val Ser Ser Gly Ile Arg Lys
 545 550 555 560

Val Leu Phe Leu Asp Gly Ile Asp Lys Ala Gln Glu Glu His Glu Lys
 565 570 575

Tyr His Ser Asn Trp Arg Ala Met Ala Ser Asp Phe Asn Leu Pro Pro
 580 585 590

Val Val Ala Lys Glu Ile Val Ala Ser Cys Asp Gln Cys Gln Leu Lys
 595 600 605

Gly Glu Ala Met His Gly Gln Val Asp Cys Ser Pro Gly Ile Trp Gln

610

615

620

Leu Ala Cys Thr His Leu Glu Gly Lys Ile Ile Leu Val Ala Val His
 625 630 635 640

Val Ala Ser Gly Tyr Ile Glu Ala Glu Val Ile Pro Ala Glu Thr Gly
 645 650 655

Gln Glu Thr Ala Tyr Phe Ile Leu Lys Leu Ala Gly Arg Trp Pro Val
 660 665 670

Lys Val Ile His Thr Ala Asn Gly Ser Asn Phe Thr Ser Ala Ala Val
 675 680 685

Lys Ala Ala Cys Trp Trp Ala Gly Ile Gln Gln Glu Phe Gly Ile Pro
 690 695 700

Tyr Asn Pro Gln Ser Gln Gly Val Val Ala Ser Met Asn Lys Glu Leu
 705 710 715 720

Lys Lys Ile Ile Gly Gln Val Arg Asp Gln Ala Glu His Leu Lys Thr
 725 730 735

Ala Val Gln Met Ala Val Phe Ile His Asn Phe Lys Arg Lys Gly Gly
 740 745 750

Ile Gly Gly Tyr Ser Ala Gly Glu Arg Ile Ile Asp Ile Ile Ala Thr
 755 760 765

Asp Ile Gln Thr Lys Glu Leu Gln Lys Gln Ile Ile Lys Ile Gln Asn
 770 775 780

Phe Arg Val Tyr Tyr Arg Asp Ser Arg Asp Pro Ile Trp Lys Gly Pro
 785 790 795 800

Ala Lys Leu Leu Trp Lys Gly Glu Gly Ala Val Val Ile Gln Asp Asn
 805 810 815

Ser Asp Ile Lys Val Val Pro Arg Arg Lys Val Lys Ile Ile Lys Asp
 820 825 830

Tyr Gly Lys Gln Met Ala Gly Ala Asp Cys Val Ala Gly Arg Gln Asp
 835 840 845

Glu Asp
 850

<210> 4

<211> 850
<212> PRT
<213> Artificial Sequence

<220>
<223> mos2Pol mosaic antigen sequence

<400> 4

Met Ala Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys Pro
1 5 10 15

Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu Lys
20 25 30

Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly Lys
35 40 45

Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe Ala
50 55 60

Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg
65 70 75 80

Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile
85 90 95

Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu Ala
100 105 110

Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg Lys
115 120 125

Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile
130 135 140

Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala
145 150 155 160

Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys Gln
165 170 175

Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Ala Ala Leu Tyr Val Gly
180 185 190

Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu Arg
195 200 205

Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His Gln
210 215 220

Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	Lys	225	230	235	240
Trp	Thr	Val	Gln	Pro	Ile	Val	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr	Val	245	250	255	
Asn	Asp	Ile	Gln	Lys	Leu	Val	Gly	Lys	Leu	Asn	Trp	Ala	Ser	Gln	Ile	260	265	270	
Tyr	Ala	Gly	Ile	Lys	Val	Lys	Gln	Leu	Cys	Lys	Leu	Leu	Arg	Gly	Thr	275	280	285	
Lys	Ala	Leu	Thr	Glu	Val	Val	Pro	Leu	Thr	Glu	Glu	Ala	Glu	Leu	Glu	290	295	300	
Leu	Ala	Glu	Asn	Arg	Glu	Ile	Leu	Lys	Glu	Pro	Val	His	Gly	Val	Tyr	305	310	315	320
Tyr	Asp	Pro	Ser	Lys	Asp	Leu	Ile	Ala	Glu	Ile	Gln	Lys	Gln	Gly	Gln	325	330	335	
Gly	Gln	Trp	Thr	Tyr	Gln	Ile	Tyr	Gln	Glu	Pro	Phe	Lys	Asn	Leu	Lys	340	345	350	
Thr	Gly	Lys	Tyr	Ala	Arg	Met	Arg	Gly	Ala	His	Thr	Asn	Asp	Val	Lys	355	360	365	
Gln	Leu	Thr	Glu	Ala	Val	Gln	Lys	Ile	Ala	Thr	Glu	Ser	Ile	Val	Ile	370	375	380	
Trp	Gly	Lys	Thr	Pro	Lys	Phe	Lys	Leu	Pro	Ile	Gln	Lys	Glu	Thr	Trp	385	390	395	400
Glu	Ala	Trp	Trp	Thr	Glu	Tyr	Trp	Gln	Ala	Thr	Trp	Ile	Pro	Glu	Trp	405	410	415	
Glu	Phe	Val	Asn	Thr	Pro	Pro	Leu	Val	Lys	Leu	Trp	Tyr	Gln	Leu	Glu	420	425	430	
Lys	Glu	Pro	Ile	Val	Gly	Ala	Glu	Thr	Phe	Tyr	Val	Ala	Gly	Ala	Ala	435	440	445	
Asn	Arg	Glu	Thr	Lys	Leu	Gly	Lys	Ala	Gly	Tyr	Val	Thr	Asp	Arg	Gly	450	455	460	
Arg	Gln	Lys	Val	Val	Ser	Leu	Thr	Asp	Thr	Thr	Asn	Gln	Lys	Thr	Ala	465	470	475	480

Leu Gln Ala Ile His Leu Ala Leu Gln Asp Ser Gly Leu Glu Val Asn
 485 490 495

Ile Val Thr Ala Ser Gln Tyr Ala Leu Gly Ile Ile Gln Ala Gln Pro
 500 505 510

Asp Lys Ser Glu Ser Glu Leu Val Ser Gln Ile Ile Glu Gln Leu Ile
 515 520 525

Lys Lys Glu Lys Val Tyr Leu Ala Trp Val Pro Ala His Lys Gly Ile
 530 535 540

Gly Gly Asn Glu Gln Val Asp Lys Leu Val Ser Arg Gly Ile Arg Lys
 545 550 555 560

Val Leu Phe Leu Asp Gly Ile Asp Lys Ala Gln Glu Glu His Glu Lys
 565 570 575

Tyr His Ser Asn Trp Arg Ala Met Ala Ser Glu Phe Asn Leu Pro Pro
 580 585 590

Ile Val Ala Lys Glu Ile Val Ala Ser Cys Asp Lys Cys Gln Leu Lys
 595 600 605

Gly Glu Ala Ile His Gly Gln Val Asp Cys Ser Pro Gly Ile Trp Gln
 610 615 620

Leu Ala Cys Thr His Leu Glu Gly Lys Val Ile Leu Val Ala Val His
 625 630 635 640

Val Ala Ser Gly Tyr Ile Glu Ala Glu Val Ile Pro Ala Glu Thr Gly
 645 650 655

Gln Glu Thr Ala Tyr Phe Leu Leu Lys Leu Ala Gly Arg Trp Pro Val
 660 665 670

Lys Thr Ile His Thr Ala Asn Gly Ser Asn Phe Thr Ser Ala Thr Val
 675 680 685

Lys Ala Ala Cys Trp Trp Ala Gly Ile Lys Gln Glu Phe Gly Ile Pro
 690 695 700

Tyr Asn Pro Gln Ser Gln Gly Val Val Ala Ser Ile Asn Lys Glu Leu
 705 710 715 720

Lys Lys Ile Ile Gly Gln Val Arg Asp Gln Ala Glu His Leu Lys Thr
 725 730 735

Ala Val Gln Met Ala Val Phe Ile His Asn Phe Lys Arg Lys Gly Gly
740 745 750

Ile Gly Glu Tyr Ser Ala Gly Glu Arg Ile Val Asp Ile Ile Ala Ser
755 760 765

Asp Ile Gln Thr Lys Glu Leu Gln Lys Gln Ile Thr Lys Ile Gln Asn
770 775 780

Phe Arg Val Tyr Tyr Arg Asp Ser Arg Asp Pro Leu Trp Lys Gly Pro
785 790 795 800

Ala Lys Leu Leu Trp Lys Gly Glu Gly Ala Val Val Ile Gln Asp Asn
805 810 815

Ser Asp Ile Lys Val Val Pro Arg Arg Lys Ala Lys Ile Ile Arg Asp
820 825 830

Tyr Gly Lys Gln Met Ala Gly Asp Asp Cys Val Ala Ser Arg Gln Asp
835 840 845

Glu Asp
850

<210> 5

<211> 685

<212> PRT

<213> Artificial Sequence

<220>

<223> moslEnv mosaic antigen sequence

<400> 5

Met Arg Val Thr Gly Ile Arg Lys Asn Tyr Gln His Leu Trp Arg Trp
1 5 10 15

Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Ala Gly Lys
20 25 30

Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr
35 40 45

Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val
50 55 60

His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro
65 70 75 80

Gln Glu Val Val Leu Glu Asn Val Thr Glu Asn Phe Asn Met Trp Lys

85

90

95

Asn Asn Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp
100 105 110

Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu
115 120 125

Asn Cys Thr Asp Asp Val Arg Asn Val Thr Asn Asn Ala Thr Asn Thr
130 135 140

Asn Ser Ser Trp Gly Glu Pro Met Glu Lys Gly Glu Ile Lys Asn Cys
145 150 155 160

Ser Phe Asn Ile Thr Thr Ser Ile Arg Asn Lys Val Gln Lys Gln Tyr
165 170 175

Ala Leu Phe Tyr Lys Leu Asp Val Val Pro Ile Asp Asn Asp Ser Asn
180 185 190

Asn Thr Asn Tyr Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln
195 200 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
210 215 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asp Lys Lys Phe Asn Gly
225 230 235 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile
245 250 255

Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu
260 265 270

Glu Glu Val Val Ile Arg Ser Glu Asn Phe Thr Asn Asn Ala Lys Thr
275 280 285

Ile Met Val Gln Leu Asn Val Ser Val Glu Ile Asn Cys Thr Arg Pro
290 295 300

Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe
305 310 315 320

Tyr Thr Ala Gly Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn
325 330 335

Ile Ser Arg Ala Asn Trp Asn Asn Thr Leu Arg Gln Ile Val Glu Lys

340

345

350

Leu Gly Lys Gln Phe Gly Asn Asn Lys Thr Ile Val Phe Asn His Ser
 355 360 365

Ser Gly Gly Asp Pro Glu Ile Val Met His Ser Phe Asn Cys Gly Gly
 370 375 380

Glu Phe Phe Tyr Cys Asn Ser Thr Lys Leu Phe Asn Ser Thr Trp Thr
 385 390 395 400

Trp Asn Asn Ser Thr Trp Asn Asn Thr Lys Arg Ser Asn Asp Thr Glu
 405 410 415

Glu His Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp
 420 425 430

Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Arg Gly Gln Ile
 435 440 445

Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
 450 455 460

Asn Asp Thr Ser Gly Thr Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
 465 470 475 480

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile
 485 490 495

Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln
 500 505 510

Ser Glu Lys Ser Ala Val Gly Ile Gly Ala Val Phe Leu Gly Phe Leu
 515 520 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val
 530 535 540

Gln Ala Arg Leu Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
 545 550 555 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
 565 570 575

Gly Ile Lys Gln Leu Gln Ala Arg Val Leu Ala Val Glu Arg Tyr Leu
 580 585 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile

595

600

605

Cys Thr Thr Thr Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
610 615 620

Asp Lys Ile Trp Asn Asn Met Thr Trp Met Glu Trp Glu Arg Glu Ile
625 630 635 640

Asn Asn Tyr Thr Ser Leu Ile Tyr Thr Leu Ile Glu Glu Ser Gln Asn
645 650 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
660 665 670

Ser Leu Trp Asn Trp Phe Asp Ile Ser Asn Trp Leu Trp
675 680 685

<210> 6

<211> 684

<212> PRT

<213> Artificial Sequence

<220>

<223> mos2Env mosaic antigen sequence

<400> 6

Met Arg Val Arg Gly Ile Gln Arg Asn Trp Pro Gln Trp Trp Ile Trp
1 5 10 15

Gly Ile Leu Gly Phe Trp Met Ile Ile Ile Cys Arg Val Met Gly Asn
20 25 30

Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Lys
35 40 45

Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Glu Lys Glu Val
50 55 60

His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro
65 70 75 80

Gln Glu Met Val Leu Glu Asn Val Thr Glu Asn Phe Asn Met Trp Lys
85 90 95

Asn Asp Met Val Asp Gln Met His Glu Asp Ile Ile Arg Leu Trp Asp
100 105 110

Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu
115 120 125

Glu	Cys	Arg	Asn	Val	Arg	Asn	Val	Ser	Ser	Asn	Gly	Thr	Tyr	Asn	Ile	130	135	140
Ile	His	Asn	Glu	Thr	Tyr	Lys	Glu	Met	Lys	Asn	Cys	Ser	Phe	Asn	Ala	145	150	155
Thr	Thr	Val	Val	Glu	Asp	Arg	Lys	Gln	Lys	Val	His	Ala	Leu	Phe	Tyr	165	170	175
Arg	Leu	Asp	Ile	Val	Pro	Leu	Asp	Glu	Asn	Asn	Ser	Ser	Glu	Lys	Ser	180	185	190
Ser	Glu	Asn	Ser	Ser	Glu	Tyr	Tyr	Arg	Leu	Ile	Asn	Cys	Asn	Thr	Ser	195	200	205
Ala	Ile	Thr	Gln	Ala	Cys	Pro	Lys	Val	Ser	Phe	Asp	Pro	Ile	Pro	Ile	210	215	220
His	Tyr	Cys	Ala	Pro	Ala	Gly	Tyr	Ala	Ile	Leu	Lys	Cys	Asn	Asn	Lys	225	230	235
Thr	Phe	Asn	Gly	Thr	Gly	Pro	Cys	Asn	Asn	Val	Ser	Thr	Val	Gln	Cys	245	250	255
Thr	His	Gly	Ile	Lys	Pro	Val	Val	Ser	Thr	Gln	Leu	Leu	Leu	Asn	Gly	260	265	270
Ser	Leu	Ala	Glu	Glu	Glu	Ile	Ile	Ile	Arg	Ser	Glu	Asn	Leu	Thr	Asn	275	280	285
Asn	Ala	Lys	Thr	Ile	Ile	Val	His	Leu	Asn	Glu	Thr	Val	Asn	Ile	Thr	290	295	300
Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	Arg	Ile	Gly	Pro	305	310	315
Gly	Gln	Thr	Phe	Tyr	Ala	Thr	Gly	Asp	Ile	Ile	Gly	Asp	Ile	Arg	Gln	325	330	335
Ala	His	Cys	Asn	Leu	Ser	Arg	Asp	Gly	Trp	Asn	Lys	Thr	Leu	Gln	Gly	340	345	350
Val	Lys	Lys	Lys	Leu	Ala	Glu	His	Phe	Pro	Asn	Lys	Thr	Ile	Asn	Phe	355	360	365
Thr	Ser	Ser	Ser	Gly	Gly	Asp	Leu	Glu	Ile	Thr	Thr	His	Ser	Phe	Asn	370	375	380

Cys	Arg	Gly	Glu	Phe	Phe	Tyr	Cys	Asn	Thr	Ser	Gly	Leu	Phe	Asn	Gly	385	390	395	400
Thr	Tyr	Met	Pro	Asn	Gly	Thr	Asn	Ser	Asn	Ser	Ser	Ser	Asn	Ile	Thr	405	410		415
Leu	Pro	Cys	Arg	Ile	Lys	Gln	Ile	Ile	Asn	Met	Trp	Gln	Glu	Val	Gly	420	425		430
Arg	Ala	Met	Tyr	Ala	Pro	Pro	Ile	Ala	Gly	Asn	Ile	Thr	Cys	Arg	Ser	435	440		445
Asn	Ile	Thr	Gly	Leu	Leu	Leu	Thr	Arg	Asp	Gly	Gly	Ser	Asn	Asn	Gly	450	455		460
Val	Pro	Asn	Asp	Thr	Glu	Thr	Phe	Arg	Pro	Gly	Gly	Gly	Asp	Met	Arg	465	470	475	480
Asn	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys	Tyr	Lys	Val	Val	Glu	Val	Lys	485	490		495
Pro	Leu	Gly	Val	Ala	Pro	Thr	Glu	Ala	Lys	Arg	Arg	Val	Val	Glu	Ser	500	505		510
Glu	Lys	Ser	Ala	Val	Gly	Ile	Gly	Ala	Val	Phe	Leu	Gly	Ile	Leu	Gly	515	520		525
Ala	Ala	Gly	Ser	Thr	Met	Gly	Ala	Ala	Ser	Ile	Thr	Leu	Thr	Val	Gln	530	535		540
Ala	Arg	Gln	Leu	Leu	Ser	Gly	Ile	Val	Gln	Gln	Gln	Ser	Asn	Leu	Leu	545	550	555	560
Arg	Ala	Ile	Glu	Ala	Gln	Gln	His	Met	Leu	Gln	Leu	Thr	Val	Trp	Gly	565	570		575
Ile	Lys	Gln	Leu	Gln	Thr	Arg	Val	Leu	Ala	Ile	Glu	Arg	Tyr	Leu	Gln	580	585		590
Asp	Gln	Gln	Leu	Leu	Gly	Leu	Trp	Gly	Cys	Ser	Gly	Lys	Leu	Ile	Cys	595	600		605
Thr	Thr	Ala	Val	Pro	Trp	Asn	Thr	Ser	Trp	Ser	Asn	Lys	Ser	Gln	Thr	610	615		620
Asp	Ile	Trp	Asp	Asn	Met	Thr	Trp	Met	Gln	Trp	Asp	Lys	Glu	Ile	Gly	625	630	635	640

Asn Tyr Thr Gly Glu Ile Tyr Arg Leu Leu Glu Glu Ser Gln Asn Gln
645 650 655

Gln Glu Lys Asn Glu Lys Asp Leu Leu Ala Leu Asp Ser Trp Lys Asn
660 665 670

Leu Trp Asn Trp Phe Asp Ile Thr Asn Trp Leu Trp
675 680

<210> 7

<211> 708

<212> PRT

<213> Artificial Sequence

<220>

<223> stabilized clade C gp140 trimer: C97ZA012-gp140-foldon with
cleavage mutations

<400> 7

Met Arg Val Arg Gly Ile Gln Arg Asn Cys Gln His Leu Trp Arg Trp
1 5 10 15

Gly Thr Leu Ile Leu Gly Met Leu Met Ile Cys Ser Ala Ala Glu Asn
20 25 30

Leu Trp Val Gly Asn Met Trp Val Thr Val Tyr Tyr Gly Val Pro Val
35 40 45

Trp Thr Asp Ala Lys Thr Thr Leu Phe Cys Ala Ser Asp Thr Lys Ala
50 55 60

Tyr Asp Arg Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro
65 70 75 80

Thr Asp Pro Asn Pro Gln Glu Ile Val Leu Glu Asn Val Thr Glu Asn
85 90 95

Phe Asn Met Trp Lys Asn Asp Met Val Asp Gln Met His Glu Asp Ile
100 105 110

Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro
115 120 125

Leu Cys Val Thr Leu His Cys Thr Asn Ala Thr Phe Lys Asn Asn Val
130 135 140

Thr Asn Asp Met Asn Lys Glu Ile Arg Asn Cys Ser Phe Asn Thr Thr
145 150 155 160

Thr Glu Ile Arg Asp Lys Lys Gln Gln Gly Tyr Ala Leu Phe Tyr Arg
 165 170 175

Pro Asp Ile Val Leu Leu Lys Glu Asn Arg Asn Asn Ser Asn Asn Ser
 180 185 190

Glu Tyr Ile Leu Ile Asn Cys Asn Ala Ser Thr Ile Thr Gln Ala Cys
 195 200 205

Pro Lys Val Asn Phe Asp Pro Ile Pro Ile His Tyr Cys Ala Pro Ala
 210 215 220

Gly Tyr Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Ser Gly Lys Gly
 225 230 235 240

Pro Cys Asn Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Lys Pro
 245 250 255

Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Lys Glu
 260 265 270

Ile Ile Ile Arg Ser Glu Asn Leu Thr Asp Asn Val Lys Thr Ile Ile
 275 280 285

Val His Leu Asn Lys Ser Val Glu Ile Val Cys Thr Arg Pro Asn Asn
 290 295 300

Asn Thr Arg Lys Ser Met Arg Ile Gly Pro Gly Gln Thr Phe Tyr Ala
 305 310 315 320

Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln Ala Tyr Cys Asn Ile Ser
 325 330 335

Gly Ser Lys Trp Asn Glu Thr Leu Lys Arg Val Lys Glu Lys Leu Gln
 340 345 350

Glu Asn Tyr Asn Asn Asn Lys Thr Ile Lys Phe Ala Pro Ser Ser Gly
 355 360 365

Gly Asp Leu Glu Ile Thr Thr His Ser Phe Asn Cys Arg Gly Glu Phe
 370 375 380

Phe Tyr Cys Asn Thr Thr Arg Leu Phe Asn Asn Asn Ala Thr Glu Asp
 385 390 395 400

Glu Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp
 405 410 415

Gln Gly Val Gly Arg Ala Met Tyr Ala Pro Pro Ile Ala Gly Asn Ile
 420 425 430

Thr Cys Lys Ser Asn Ile Thr Gly Leu Leu Leu Val Arg Asp Gly Gly
 435 440 445

Glu Asp Asn Lys Thr Glu Glu Ile Phe Arg Pro Gly Gly Gly Asn Met
 450 455 460

Lys Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Ile Glu Leu
 465 470 475 480

Lys Pro Leu Gly Ile Ala Pro Thr Gly Ala Lys Glu Arg Val Val Glu
 485 490 495

Arg Glu Glu Arg Ala Val Gly Ile Gly Ala Val Phe Leu Gly Phe Leu
 500 505 510

Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Leu Thr Leu Thr Val
 515 520 525

Gln Ala Arg Gln Leu Leu Ser Ser Ile Val Gln Gln Gln Ser Asn Leu
 530 535 540

Leu Arg Ala Ile Glu Ala Gln Gln His Met Leu Gln Leu Thr Val Trp
 545 550 555 560

Gly Ile Lys Gln Leu Gln Thr Arg Val Leu Ala Ile Glu Arg Tyr Leu
 565 570 575

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
 580 585 590

Cys Thr Thr Asn Val Pro Trp Asn Ser Ser Trp Ser Asn Lys Ser Gln
 595 600 605

Thr Asp Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
 610 615 620

Ser Asn Tyr Thr Asp Thr Ile Tyr Arg Leu Leu Glu Asp Ser Gln Thr
 625 630 635 640

Gln Gln Glu Lys Asn Glu Lys Asp Leu Leu Ala Leu Asp Ser Trp Lys
 645 650 655

Asn Leu Trp Ser Trp Phe Asp Ile Ser Asn Trp Leu Trp Tyr Ile Lys
 660 665 670

Ser Arg Ile Glu Gly Arg Gly Ser Gly Gly Tyr Ile Pro Glu Ala Pro
675 680 685

Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu
690 695 700

Ser Thr Phe Leu
705

<210> 8

<211> 625

<212> PRT

<213> Artificial Sequence

<220>

<223> C4 fragment: gp120-truncated gp41 without signal peptide and
transmembrane domain

<400> 8

Met Gly Asn Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys
1 5 10 15

Asp Ala Lys Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Glu
20 25 30

Lys Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp
35 40 45

Pro Asn Pro Gln Glu Ile Val Leu Gly Asn Val Thr Glu Asn Phe Asn
50 55 60

Met Trp Lys Asn Asp Met Val Asp Gln Met His Glu Asp Ile Ile Ser
65 70 75 80

Leu Trp Asp Ala Ser Leu Glu Pro Cys Val Lys Leu Thr Pro Leu Cys
85 90 95

Val Thr Leu Asn Cys Arg Asn Val Arg Asn Val Ser Ser Asn Gly Thr
100 105 110

Tyr Asn Ile Ile His Asn Glu Thr Tyr Lys Glu Met Lys Asn Cys Ser
115 120 125

Phe Asn Ala Thr Thr Val Val Glu Asp Arg Lys Gln Lys Val His Ala
130 135 140

Leu Phe Tyr Arg Leu Asp Ile Val Pro Leu Asp Glu Asn Asn Ser Ser
145 150 155 160

Glu Lys Ser Ser Glu Asn Ser Ser Glu Tyr Tyr Arg Leu Ile Asn Cys

165

170

175

Asn Thr Ser Ala Ile Thr Gln Ala Cys Pro Lys Val Ser Phe Asp Pro
 180 185 190

Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Tyr Ala Ile Leu Lys Cys
 195 200 205

Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Asn Asn Val Ser Thr
 210 215 220

Val Gln Cys Thr His Gly Ile Lys Pro Val Val Ser Thr Gln Leu Leu
 225 230 235 240

Leu Asn Gly Ser Leu Ala Glu Glu Glu Ile Ile Ile Arg Ser Glu Asn
 245 250 255

Leu Thr Asn Asn Ala Lys Thr Ile Ile Val His Leu Asn Glu Thr Val
 260 265 270

Asn Ile Thr Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Arg
 275 280 285

Ile Gly Pro Gly Gln Thr Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp
 290 295 300

Ile Arg Gln Ala His Cys Asn Leu Ser Arg Asp Gly Trp Asn Lys Thr
 305 310 315 320

Leu Gln Gly Val Lys Lys Lys Leu Ala Glu His Phe Pro Asn Lys Thr
 325 330 335

Ile Lys Phe Ala Pro His Ser Gly Gly Asp Leu Glu Ile Thr Thr His
 340 345 350

Thr Phe Asn Cys Arg Gly Glu Phe Phe Tyr Cys Asn Thr Ser Asn Leu
 355 360 365

Phe Asn Glu Ser Asn Ile Glu Arg Asn Asp Ser Ile Ile Thr Leu Pro
 370 375 380

Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Arg Ala
 385 390 395 400

Ile Tyr Ala Pro Pro Ile Ala Gly Asn Ile Thr Cys Arg Ser Asn Ile
 405 410 415

Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Ser Asn Asn Gly Val Pro

420

425

430

Asn Asp Thr Glu Thr Phe Arg Pro Gly Gly Gly Asp Met Arg Asn Asn
 435 440 445

Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Glu Val Lys Pro Leu
 450 455 460

Gly Val Ala Pro Thr Glu Ala Lys Arg Arg Val Val Glu Arg Glu Lys
 465 470 475 480

Arg Ala Val Gly Ile Gly Ala Val Phe Leu Gly Ile Leu Gly Ala Ala
 485 490 495

Gly Ser Thr Met Gly Ala Ala Ser Ile Thr Leu Thr Val Gln Ala Arg
 500 505 510

Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala
 515 520 525

Ile Glu Ala Gln Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys
 530 535 540

Gln Leu Gln Thr Arg Val Leu Ala Ile Glu Arg Tyr Leu Gln Asp Gln
 545 550 555 560

Gln Leu Leu Gly Leu Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr
 565 570 575

Ala Val Pro Trp Asn Thr Ser Trp Ser Asn Lys Ser Gln Thr Asp Ile
 580 585 590

Trp Asp Asn Met Thr Trp Met Gln Trp Asp Lys Glu Ile Gly Asn Tyr
 595 600 605

Thr Gly Glu Ile Tyr Arg Leu Leu Glu Glu Ser Gln Asn Gln Gln Glu
 610 615 620

Lys
 625

<210> 9

<211> 29

<212> PRT

<213> Artificial Sequence

<220>

<223> signal sequence

<400> 9

Met Arg Val Arg Gly Met Leu Arg Asn Trp Gln Gln Trp Trp Ile Trp
1 5 10 15

Ser Ser Leu Gly Phe Trp Met Leu Met Ile Tyr Ser Val
20 25

<210> 10
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> signal sequence

<400> 10

Met Arg Val Thr Gly Ile Arg Lys Asn Tyr Gln His Leu Trp Arg Trp
1 5 10 15

Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala
20 25

<210> 11
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> signal sequence

<400> 11

Met Arg Val Arg Gly Ile Gln Arg Asn Trp Pro Gln Trp Trp Ile Trp
1 5 10 15

Gly Ile Leu Gly Phe Trp Met Ile Ile Ile Cys Arg Val
20 25

<210> 12
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> signal sequence

<400> 12

Met Arg Val Arg Gly Ile Gln Arg Asn Cys Gln His Leu Trp Arg Trp
1 5 10 15

Gly Thr Leu Ile Leu Gly Met Leu Met Ile Cys Ser Ala
20 25

<210> 13

<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> transmembrane domain

<400> 13

Ile Phe Ile Met Ile Val Gly Gly Leu Ile Gly Leu Arg Ile Ile Phe
1 5 10 15

Ala Val Leu Ser Ile Val
20

<210> 14
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> truncated cytoplasmic region

<400> 14

Asn Arg Val Arg Gln Gly Tyr
1 5

<210> 15
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> GCN4 trimerization domain

<400> 15

Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr
1 5 10 15

His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu Val
20 25 30

<210> 16
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> foldon trimerization domain

<400> 16

Gly Ser Gly Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr
1 5 10 15

Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu

20

25

30

<210> 17
 <211> 862
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> C4 sequence

<400> 17

Met Arg Val Arg Gly Met Leu Arg Asn Trp Gln Gln Trp Trp Ile Trp
 1 5 10 15

Ser Ser Leu Gly Phe Trp Met Leu Met Ile Tyr Ser Val Met Gly Asn
 20 25 30

Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Asp Ala Lys
 35 40 45

Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Glu Lys Glu Val
 50 55 60

His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro
 65 70 75 80

Gln Glu Ile Val Leu Gly Asn Val Thr Glu Asn Phe Asn Met Trp Lys
 85 90 95

Asn Asp Met Val Asp Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp
 100 105 110

Ala Ser Leu Glu Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu
 115 120 125

Asn Cys Arg Asn Val Arg Asn Val Ser Ser Asn Gly Thr Tyr Asn Ile
 130 135 140

Ile His Asn Glu Thr Tyr Lys Glu Met Lys Asn Cys Ser Phe Asn Ala
 145 150 155 160

Thr Thr Val Val Glu Asp Arg Lys Gln Lys Val His Ala Leu Phe Tyr
 165 170 175

Arg Leu Asp Ile Val Pro Leu Asp Glu Asn Asn Ser Ser Glu Lys Ser
 180 185 190

Ser Glu Asn Ser Ser Glu Tyr Tyr Arg Leu Ile Asn Cys Asn Thr Ser
 195 200 205

Ala	Ile	Thr	Gln	Ala	Cys	Pro	Lys	Val	Ser	Phe	Asp	Pro	Ile	Pro	Ile	210	215	220	
His	Tyr	Cys	Ala	Pro	Ala	Gly	Tyr	Ala	Ile	Leu	Lys	Cys	Asn	Asn	Lys	225	230	235	240
Thr	Phe	Asn	Gly	Thr	Gly	Pro	Cys	Asn	Asn	Val	Ser	Thr	Val	Gln	Cys	245	250	255	
Thr	His	Gly	Ile	Lys	Pro	Val	Val	Ser	Thr	Gln	Leu	Leu	Leu	Asn	Gly	260	265	270	
Ser	Leu	Ala	Glu	Glu	Glu	Ile	Ile	Ile	Arg	Ser	Glu	Asn	Leu	Thr	Asn	275	280	285	
Asn	Ala	Lys	Thr	Ile	Ile	Val	His	Leu	Asn	Glu	Thr	Val	Asn	Ile	Thr	290	295	300	
Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	Arg	Ile	Gly	Pro	305	310	315	320
Gly	Gln	Thr	Phe	Tyr	Ala	Thr	Gly	Asp	Ile	Ile	Gly	Asp	Ile	Arg	Gln	325	330	335	
Ala	His	Cys	Asn	Leu	Ser	Arg	Asp	Gly	Trp	Asn	Lys	Thr	Leu	Gln	Gly	340	345	350	
Val	Lys	Lys	Lys	Leu	Ala	Glu	His	Phe	Pro	Asn	Lys	Thr	Ile	Lys	Phe	355	360	365	
Ala	Pro	His	Ser	Gly	Gly	Asp	Leu	Glu	Ile	Thr	Thr	His	Thr	Phe	Asn	370	375	380	
Cys	Arg	Gly	Glu	Phe	Phe	Tyr	Cys	Asn	Thr	Ser	Asn	Leu	Phe	Asn	Glu	385	390	395	400
Ser	Asn	Ile	Glu	Arg	Asn	Asp	Ser	Ile	Ile	Thr	Leu	Pro	Cys	Arg	Ile	405	410	415	
Lys	Gln	Ile	Ile	Asn	Met	Trp	Gln	Glu	Val	Gly	Arg	Ala	Ile	Tyr	Ala	420	425	430	
Pro	Pro	Ile	Ala	Gly	Asn	Ile	Thr	Cys	Arg	Ser	Asn	Ile	Thr	Gly	Leu	435	440	445	
Leu	Leu	Thr	Arg	Asp	Gly	Gly	Ser	Asn	Asn	Gly	Val	Pro	Asn	Asp	Thr	450	455	460	

Glu	Thr	Phe	Arg	Pro	Gly	Gly	Gly	Asp	Met	Arg	Asn	Asn	Trp	Arg	Ser	465	470	475	480
Glu	Leu	Tyr	Lys	Tyr	Lys	Val	Val	Glu	Val	Lys	Pro	Leu	Gly	Val	Ala		485	490	495
Pro	Thr	Glu	Ala	Lys	Arg	Arg	Val	Val	Glu	Arg	Glu	Lys	Arg	Ala	Val	500		505	510
Gly	Ile	Gly	Ala	Val	Phe	Leu	Gly	Ile	Leu	Gly	Ala	Ala	Gly	Ser	Thr	515	520		525
Met	Gly	Ala	Ala	Ser	Ile	Thr	Leu	Thr	Val	Gln	Ala	Arg	Gln	Leu	Leu	530	535	540	
Ser	Gly	Ile	Val	Gln	Gln	Gln	Ser	Asn	Leu	Leu	Arg	Ala	Ile	Glu	Ala	545	550	555	560
Gln	Gln	His	Met	Leu	Gln	Leu	Thr	Val	Trp	Gly	Ile	Lys	Gln	Leu	Gln		565	570	575
Thr	Arg	Val	Leu	Ala	Ile	Glu	Arg	Tyr	Leu	Gln	Asp	Gln	Gln	Leu	Leu	580	585		590
Gly	Leu	Trp	Gly	Cys	Ser	Gly	Lys	Leu	Ile	Cys	Thr	Thr	Ala	Val	Pro	595	600		605
Trp	Asn	Thr	Ser	Trp	Ser	Asn	Lys	Ser	Gln	Thr	Asp	Ile	Trp	Asp	Asn	610	615	620	
Met	Thr	Trp	Met	Gln	Trp	Asp	Lys	Glu	Ile	Gly	Asn	Tyr	Thr	Gly	Glu	625	630	635	640
Ile	Tyr	Arg	Leu	Leu	Glu	Glu	Ser	Gln	Asn	Gln	Gln	Glu	Lys	Asn	Glu		645	650	655
Lys	Asp	Leu	Leu	Ala	Leu	Asp	Ser	Trp	Asn	Asn	Leu	Trp	Asn	Trp	Phe	660	665		670
Ser	Ile	Ser	Lys	Trp	Leu	Trp	Tyr	Ile	Lys	Ile	Phe	Ile	Met	Ile	Val	675	680	685	
Gly	Gly	Leu	Ile	Gly	Leu	Arg	Ile	Ile	Phe	Ala	Val	Leu	Ser	Ile	Val	690	695	700	
Asn	Arg	Val	Arg	Gln	Gly	Tyr	Ser	Pro	Leu	Ser	Leu	Gln	Thr	Leu	Thr	705	710	715	720

Gln Asn Pro Gly Gly Leu Asp Arg Leu Gly Arg Ile Glu Glu Glu Gly
725 730 735

Gly Glu Gln Asp Lys Asp Arg Ser Ile Arg Leu Val Asn Gly Phe Phe
740 745 750

Ala Leu Phe Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr His
755 760 765

Arg Leu Arg Asp Phe Ile Leu Ile Val Ala Arg Ala Val Glu Leu Leu
770 775 780

Gly Arg Ser Ser Leu Arg Gly Leu Gln Arg Gly Trp Glu Ile Leu Lys
785 790 795 800

Tyr Leu Gly Ser Leu Leu Gln Tyr Trp Gly Leu Glu Leu Lys Lys Ser
805 810 815

Ala Ile Asn Leu Leu Asp Thr Ile Ala Ile Ala Val Ala Glu Gly Thr
820 825 830

Asp Arg Ile Ile Glu Leu Ile Gln Arg Ile Cys Arg Ala Ile Cys Asn
835 840 845

Ile Pro Arg Arg Ile Arg Gln Gly Phe Glu Ala Ala Leu Gln
850 855 860

<210> 18
<211> 711
<212> PRT
<213> Artificial Sequence

<220>
<223> C4D7 sequence

<400> 18

Met Arg Val Arg Gly Met Leu Arg Asn Trp Gln Gln Trp Trp Ile Trp
1 5 10 15

Ser Ser Leu Gly Phe Trp Met Leu Met Ile Tyr Ser Val Met Gly Asn
20 25 30

Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Asp Ala Lys
35 40 45

Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Glu Lys Glu Val
50 55 60

His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro

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

325

330

335

Ala His Cys Asn Leu Ser Arg Asp Gly Trp Asn Lys Thr Leu Gln Gly
 340 345 350

Val Lys Lys Lys Leu Ala Glu His Phe Pro Asn Lys Thr Ile Lys Phe
 355 360 365

Ala Pro His Ser Gly Gly Asp Leu Glu Ile Thr Thr His Thr Phe Asn
 370 375 380

Cys Arg Gly Glu Phe Phe Tyr Cys Asn Thr Ser Asn Leu Phe Asn Glu
 385 390 395 400

Ser Asn Ile Glu Arg Asn Asp Ser Ile Ile Thr Leu Pro Cys Arg Ile
 405 410 415

Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Arg Ala Ile Tyr Ala
 420 425 430

Pro Pro Ile Ala Gly Asn Ile Thr Cys Arg Ser Asn Ile Thr Gly Leu
 435 440 445

Leu Leu Thr Arg Asp Gly Gly Ser Asn Asn Gly Val Pro Asn Asp Thr
 450 455 460

Glu Thr Phe Arg Pro Gly Gly Gly Asp Met Arg Asn Asn Trp Arg Ser
 465 470 475 480

Glu Leu Tyr Lys Tyr Lys Val Val Glu Val Lys Pro Leu Gly Val Ala
 485 490 495

Pro Thr Glu Ala Lys Arg Arg Val Val Glu Arg Glu Lys Arg Ala Val
 500 505 510

Gly Ile Gly Ala Val Phe Leu Gly Ile Leu Gly Ala Ala Gly Ser Thr
 515 520 525

Met Gly Ala Ala Ser Ile Thr Leu Thr Val Gln Ala Arg Gln Leu Leu
 530 535 540

Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Glu Ala
 545 550 555 560

Gln Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
 565 570 575

Thr Arg Val Leu Ala Ile Glu Arg Tyr Leu Gln Asp Gln Gln Leu Leu

580

585

590

Gly Leu Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro
 595 600 605

Trp Asn Thr Ser Trp Ser Asn Lys Ser Gln Thr Asp Ile Trp Asp Asn
 610 615 620

Met Thr Trp Met Gln Trp Asp Lys Glu Ile Gly Asn Tyr Thr Gly Glu
 625 630 635 640

Ile Tyr Arg Leu Leu Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu
 645 650 655

Lys Asp Leu Leu Ala Leu Asp Ser Trp Asn Asn Leu Trp Asn Trp Phe
 660 665 670

Ser Ile Ser Lys Trp Leu Trp Tyr Ile Lys Ile Phe Ile Met Ile Val
 675 680 685

Gly Gly Leu Ile Gly Leu Arg Ile Ile Phe Ala Val Leu Ser Ile Val
 690 695 700

Asn Arg Val Arg Gln Gly Tyr
 705 710

<210> 19

<211> 704

<212> PRT

<213> Artificial Sequence

<220>

<223> sC4 sequence

<400> 19

Met Arg Val Arg Gly Met Leu Arg Asn Trp Gln Gln Trp Trp Ile Trp
 1 5 10 15

Ser Ser Leu Gly Phe Trp Met Leu Met Ile Tyr Ser Val Met Gly Asn
 20 25 30

Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Asp Ala Lys
 35 40 45

Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Glu Lys Glu Val
 50 55 60

His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro
 65 70 75 80

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

Ala	His	Cys	Asn	Leu	Ser	Arg	Asp	Gly	Trp	Asn	Lys	Thr	Leu	Gln	Gly	340	345	350
Val	Lys	Lys	Lys	Leu	Ala	Glu	His	Phe	Pro	Asn	Lys	Thr	Ile	Lys	Phe	355	360	365
Ala	Pro	His	Ser	Gly	Gly	Asp	Leu	Glu	Ile	Thr	Thr	His	Thr	Phe	Asn	370	375	380
Cys	Arg	Gly	Glu	Phe	Phe	Tyr	Cys	Asn	Thr	Ser	Asn	Leu	Phe	Asn	Glu	385	390	395
Ser	Asn	Ile	Glu	Arg	Asn	Asp	Ser	Ile	Ile	Thr	Leu	Pro	Cys	Arg	Ile	405	410	415
Lys	Gln	Ile	Ile	Asn	Met	Trp	Gln	Glu	Val	Gly	Arg	Ala	Ile	Tyr	Ala	420	425	430
Pro	Pro	Ile	Ala	Gly	Asn	Ile	Thr	Cys	Arg	Ser	Asn	Ile	Thr	Gly	Leu	435	440	445
Leu	Leu	Thr	Arg	Asp	Gly	Gly	Ser	Asn	Asn	Gly	Val	Pro	Asn	Asp	Thr	450	455	460
Glu	Thr	Phe	Arg	Pro	Gly	Gly	Gly	Asp	Met	Arg	Asn	Asn	Trp	Arg	Ser	465	470	475
Glu	Leu	Tyr	Lys	Tyr	Lys	Val	Val	Glu	Val	Lys	Pro	Leu	Gly	Val	Ala	485	490	495
Pro	Thr	Glu	Ala	Lys	Arg	Arg	Val	Val	Glu	Arg	Glu	Glu	Arg	Ala	Val	500	505	510
Gly	Ile	Gly	Ala	Val	Phe	Leu	Gly	Ile	Leu	Gly	Ala	Ala	Gly	Ser	Thr	515	520	525
Met	Gly	Ala	Ala	Ser	Ile	Thr	Leu	Thr	Val	Gln	Ala	Arg	Gln	Leu	Leu	530	535	540
Ser	Gly	Ile	Val	Gln	Gln	Gln	Ser	Asn	Leu	Leu	Arg	Ala	Ile	Glu	Ala	545	550	555
Gln	Gln	His	Met	Leu	Gln	Leu	Thr	Val	Trp	Gly	Ile	Lys	Gln	Leu	Gln	565	570	575
Thr	Arg	Val	Leu	Ala	Ile	Glu	Arg	Tyr	Leu	Gln	Asp	Gln	Gln	Leu	Leu	580	585	590

Gly Leu Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro
595 600 605

Trp Asn Thr Ser Trp Ser Asn Lys Ser Gln Thr Asp Ile Trp Asp Asn
610 615 620

Met Thr Trp Met Gln Trp Asp Lys Glu Ile Gly Asn Tyr Thr Gly Glu
625 630 635 640

Ile Tyr Arg Leu Leu Glu Glu Ser Gln Asn Gln Gln Glu Lys Met Lys
645 650 655

Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr His Ile
660 665 670

Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu Val Gly Ser
675 680 685

Gly Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg
690 695 700

<210> 20
<211> 4050
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotide sequence encoding mos1GagPol

<400> 20
atgggagcca gagccagcgt gctgtccgga ggggagctgg accgctggga gaagatcagg 60
ctgaggcctg gagggaagaa gaagtacagg ctgaagcaca tcgtgtgggc cagcagagag 120
ctggaacggt ttgccgtgaa ccctggcctg ctggaaacca gcgagggctg taggcagatt 180
ctgggacagc tgcagcccag cctgcagaca ggcagcgagg aactgcggag cctgtacaac 240
accgtggcca ccctgtactg cgtgcaccag cggatcgaga tcaaggacac caaagaagcc 300
ctggaaaaga tcgaggaaga gcagaacaag agcaagaaga aagcccagca ggctgccgct 360
gacacaggca acagcagcca ggtgtcccag aactaccca tcgtgcagaa catccaggga 420
cagatggtgc accaggccat cagccctcgg accctgaacg cctgggtgaa ggtggtggag 480
gaaaaggcct tcagccctga ggtgatcccc atgttctctg ccctgagcga gggagccaca 540
ccccaggacc tgaacaccat gctgaacacc gtgggagggc accaggctgc catgcagatg 600
ctgaaagaga caatcaacga ggaagctgcc gagtgggaca gggtcaccc agtgcacgct 660
ggacctatcg ctctggcca gatgagagag ccagaggca gcatattgc tggcaccacc 720
tccacactgc aggaacagat cggctggatg accaacaacc ctcccatccc tgtgggagag 780

atctacaagc ggtggatcat tctgggactg aacaagatcg tgcggatgta cagccctgtg	840
agcatccttg acatcaggca gggacccaaa gagcccttca gggactacgt ggaccggttc	900
tacaagaccc tgagagccga gcaggccagc caggacgtga agaactggat gaccgagaca	960
ctgctggtgc agaacgcca ccctgactgc aagaccatcc tgaaagccct gggacctgct	1020
gccacccttg aagagatgat gacagcctgc cagggagtgg gaggacctgg ccacaaggcc	1080
aggggtgctg ccgaggccat gagccagggtg accaactctg ccaccatcat gatgcagaga	1140
ggcaacttcc ggaaccagag aaagaccgtg aagtgttca actgtggcaa agagggacac	1200
attgccaaaga actgcagggc tcccaggaag aaaggctgct ggaagtgcgg aaaagaaggc	1260
caccagatga aggactgcac cgagaggcag gccaaacttcc tgggcaagat ctggcctagc	1320
aacaagggca ggcctggcaa cttcctgcag aacagaccgc agcccaccgc tcctcccag	1380
gaaagcttcc ggtttgccga ggaaaccacc acccctagcc agaagcagga acccatcgac	1440
aaagagatgt accctctggc cagcctgaag agcctgttcg gcaacgacc cagcagccag	1500
atggctccca tcagcccaat cgagacagt cctgtgaagc tgaagcctgg catggacgga	1560
cccagggatga agcagtggcc tctgaccgag gaaaagatca aagccctgac agccatctgc	1620
gaggaaatgg aaaaagaggg caagatcacc aagatcggac ccgagaaccc ctacaacacc	1680
cctgtgttcg ccatcaagaa gaaagacagc accaagtgga ggaaactggt ggacttcaga	1740
gagctgaaca agcggaccca ggacttctgg gaggtgcagc tgggcatccc tcaccctgct	1800
ggcctgaaga aaaagaaaag cgtgaccgtg ctggctgtgg gagatgccta cttcagcgtg	1860
cctctggacg agggcttccg gaagtacaca gccttcacca tcccagcac caacaacgag	1920
acacctggca tcagatacca gtacaacgtg ctgcctcagg gctggaaagg cagccctgcc	1980
atcttccagt gcagcatgac cagaatcctg gaacccttca gagccaagaa ccctgagatc	2040
gtgatctacc agtatatggc tgccctctac gtgggcagcg acctggaaat cggacagcac	2100
agagccaaaa tcgaagaact ccgcgagcac ctgctgaagt ggggattcac caccctgac	2160
aagaagcacc agaaagagcc tcccttcctg tggatgggct acgagctgca ccctgacaag	2220
tggaccgtgc agcccatcca gctgccagag aaggactcct ggaccgtgaa cgacatccag	2280
aaactggtcg gcaagctgaa ctgggcccagc cagatctacc ctggcatcaa agtcagacag	2340
ctgtgtaagc tgctgagggg agccaaagca ctgaccgaca tcgtgcctct gacagaagaa	2400
gccgagctgg aactggccga gaacagagag atcctgaaag aaccctgca cggagtgtac	2460
tacgaccctt ccaaggacct gattgccgag atccagaaac agggacacga ccagtggacc	2520
taccagatct atcaggaacc tttcaagaac ctgaaaacag gcaagtacgc caagatgcgg	2580
acagcccaca ccaacgacgt gaagcagctg accgaagccg tgcagaaaat cgccatggaa	2640
agcatcgtga tctggggaaa gacaccaag ttcaggctgc ccatccagaa agagacatgg	2700

gaaacctggt ggaccgacta ctggcaggcc acctggattc ccgagtggga gttcgtgaac	2760
acccccacccc tgggtgaagct gtggtatcag ctggaaaagg accctatcgc tggcgtggag	2820
acattctacg tggctggagc tgccaacaga gagacaaagc tgggcaaggc tggctacgtg	2880
accgacagag gcagacagaa aatcgtgagc ctgaccgaaa ccaccaacca gaaaacagcc	2940
ctgcaggcca tctatctggc actgcaggac agcgggaagcg aggtgaacat cgtgacagcc	3000
agccagtatg ccctgggcat catccaggcc cagcctgaca agagcgagag cgagctggtg	3060
aaccagatca tcgagcagct gatcaagaaa gaacgggtgt acctgagctg ggtgccagcc	3120
cacaagggca tcggagggaa cgagcaggctg gacaagctgg tgtccagcgg aatccggaag	3180
gtgctgttcc tggacggcat cgataaagcc caggaagagc acgagaagta ccacagcaat	3240
tggagagcca tggccagcga cttcaacctg cctcccgtgg tggccaaaga aatcgtggcc	3300
agctgcgacc agtgccagct gaaaggcgag gccatgcacg gacaggtgga ctgctccct	3360
ggcatctggc agctggcatg caccacacctg gaaggcaaga tcattctggt ggccgtgcac	3420
gtggccagcg gatacatcga agccgaagtg atccctgccg agacagggca ggaaacagcc	3480
tacttcatcc tgaagctggc tggcagatgg cctgtgaagg tgatccacac agccaacggc	3540
agcaacttca cctctgctgc cgtgaaggct gcctgttggt gggctggcat tcagcaggaa	3600
tttggcatcc cctacaatcc ccagtctcag ggagtgggtg ccagcatgaa caaagagctg	3660
aagaagatca tcggacaggt cagggatcag gccgagcacc tgaaaactgc cgtccagatg	3720
gccgtgttca tccacaactt caagcggaag ggagggatcg gaggtactc tgctggcgag	3780
cggatcatcg acatcattgc caccgatatc cagaccaaag agctgcagaa acagatcatc	3840
aagatccaga acttcagggt gtactacagg gacagcaggg accccatctg gaagggacct	3900
gccaagctgc tgtggaaagg cgaaggagcc gtcgtcatcc aggacaacag cgacatcaag	3960
gtggtgccca gacggaaggt gaaaatcatc aaggactacg gcaaacagat ggctggagcc	4020
gactgtgtcg ctggcaggca ggacgaggac	4050

<210> 21

<211> 4023

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence encoding mos2GagPol

<400> 21

atgggagcca gagccagcat cctgcgagga gggaagctgg acaagtggga gaagatcagg	60
ctgaggcctg gagggaagaa acactacatg ctgaagcacc tggctctggc cagcagagag	120
ctggaacggt ttgccctcaa tcctggcctg ctggaaacca gcgagggctg caagcagatc	180
atcaagcagc tgcagcctgc cctgcagaca ggaccgagg aactgcggag cctgttcaac	240

accgtggcca	ccctgtactg	cgtgcatgcc	gagatcgaag	tgagggacac	caaagaagcc	300
ctggacaaga	tcgaggaaga	gcagaacaag	agccagcaga	aaacccagca	ggccaaagaa	360
gccgacggca	aggtctccca	gaactacccc	atcgtgcaga	acctgcaggg	acagatggtg	420
caccagccca	tcagccctcg	gacactgaat	gcctgggtga	aggtgatcga	ggaaaaggcc	480
ttcagccctg	aggtgatccc	catgttcaca	gccctgagcg	agggagccac	accccaggac	540
ctgaacacca	tgctgaacac	cgtgggaggg	caccaggctg	ccatgcagat	gctgaaggac	600
accatcaacg	aggaagctgc	cgagtgggac	aggctgcacc	ctgtgcacgc	tggacctgtg	660
gctcctggcc	agatgagaga	gcccagaggc	agcgatattg	ctggcaccac	ctccaatctg	720
caggaacaga	tcgcctggat	gaccagcaac	cctcccatcc	ctgtgggaga	catctacaag	780
cggtggatca	tcctgggact	gaacaagatc	gtgcggatgt	acagccctac	ctccatcctg	840
gacatcaagc	agggacccaa	agagcctttc	agggactacg	tggaccggtt	cttcaagacc	900
ctgagagccg	agcaggccac	ccaggacgtg	aagaactgga	tgaccgacac	cctgctggtg	960
cagaacgcca	accctgactg	caagaccatc	ctgagagccc	tgggacctgg	agccaccctg	1020
gaagagatga	tgacagcctg	ccagggagtg	ggaggaccct	ctcacaaggc	tagggtgctg	1080
gccgaggcca	tgagccagac	caacagcacc	atcctgatgc	agcggagcaa	cttcaagggc	1140
agcaagcggg	tcgtgaagtg	cttcaactgt	ggcaaagagg	gacacattgc	cagaaaactgt	1200
agggcaccca	ggaagaaagg	ctgctggaag	tgcggaaaag	aaggccacca	gatgaaggac	1260
tgcaccgaga	ggcaggccaa	cttcctgggc	aagatctggc	ctagccacaa	gggcagacct	1320
ggcaacttcc	tgacagagcag	acccgagccc	accgctcctc	cagccgagag	cttcgggttc	1380
gaggaaaacca	cccctgctcc	caagcaggaa	cctaaggaca	gagagcctct	gaccagcctg	1440
agaagcctgt	tcggcagcga	ccctctgagc	cagatggctc	ccatctcccc	tatcgagaca	1500
gtgcctgtga	agctgaagcc	tggcatggac	ggacccaagg	tgaaacagtg	gcctctgacc	1560
gaggaaaaga	tcaaagccct	ggtggagatc	tgtaccgaga	tggaaaaaga	gggcaagatc	1620
agcaagatcg	gacccgagaa	cccctacaac	acccctatct	tcgccatcaa	gaagaaagac	1680
agcaccaagt	ggaggaaact	ggtggacttc	agagagctga	acaagcggac	ccaggacttc	1740
tgggaggtgc	agctgggcat	ccctcaccct	gctggcctga	agaaaaagaa	aagcgtgacc	1800
gtgctggccg	tgggagatgc	ctacttcagc	gtgcctctgg	acgaggactt	cagaaagtac	1860
acagccttca	ccatccccag	catcaacaac	gagacacctg	gcatcagata	ccagtacaac	1920
gtgctgcctc	agggatggaa	gggctctcct	gcaatcttcc	agagcagcat	gaccaagatc	1980
ctggaaccct	tccggaagca	gaaccctgac	atcgtgatct	accagtacat	ggcagccctg	2040
tacgtcggca	gcgacctgga	aatcggacag	caccggacca	agatcgaaga	actcaggcag	2100
cacctgctgc	ggtggggatt	caccaccctc	gacaagaagc	accagaaaga	gcctcccttc	2160

ctgtggatgg gctacgagct gcacccagac aagtggaccg tgcagcccat cgtgctgcct	2220
gagaaggact cctggaccgt gaacgacatc cagaaactgg tcggcaagct gaactgggcc	2280
agccagatct acgctggcat caaagtgaag cagctgtgta agctcctgag aggcaccaaa	2340
gccctgaccg aggtggtgcc actgacagag gaagccgagc tggaaactggc cgagaacaga	2400
gagatcctga aagaacccgt gcacggagtg tactacgacc ccagcaagga cctgattgcc	2460
gagatccaga agcagggaca gggacagtgg acctaccaga tctaccagga acccttcaag	2520
aacctgaaaa caggcaagta cgccaggatg aggggagccc acaccaacga cgtcaaacag	2580
ctgaccgaag ccgtgcagaa gatcgccacc gagagcatcg tgatttgggg aaagacaccc	2640
aagttcaagc tgcccatcca gaaagagaca tgggaggcct ggtggaccga gtactggcag	2700
gccacctgga ttcccagagt ggagttcgtg aacaccccac ccctggtgaa gctgtggtat	2760
cagctggaaa aagaacccat cgtgggagcc gagacattct acgtggctgg agctgccaac	2820
agagagacaa agctgggcaa ggctggctac gtgaccgaca gaggcaggca gaaagtgggtg	2880
tccctgaccg ataccaccaa ccagaaaaca gccctgcagg ccatccacct ggctctgcag	2940
gactctggcc tggaagtgaa catcgtgaca gccagccagt atgccctggg catcattcag	3000
gcacagcctg acaagagcga gagcgagctg gtgtctcaga tcattgagca gctgatcaag	3060
aaagaaaagg tgtacctggc ctgggtgcc a gccacaagg ggatcggagg gaacgagcag	3120
gtggacaagc tgggtgtccag gggcatccgg aaggtgctgt ttctggacgg catcgacaaa	3180
gccaggaag agcacgagaa gtaccacagc aattggagag ccattggccag cgagttcaac	3240
ctgcctccca tcgtggccaa agaaatcgtg gcctcttgcg acaagtgcc gctgaaaggc	3300
gaggccattc acggacaggt ggactgcagc ccaggcatct ggcagctggc ctgcacccac	3360
ctggaaggca aggtgatcct ggtggccgtg cacgtggcct ctggatacat cgaagccgaa	3420
gtgatccctg ccgagacagg ccaggaaaca gcctacttcc tgctgaagct ggctggcagg	3480
tggcctgtga aaaccatcca cacagccaac ggcagcaact tcacctctgc caccgtgaag	3540
gctgcctgtt ggtgggctgg cattaagcag gaatttggca tcccctacaa ccctcagtct	3600
cagggagtgg tggcctccat caacaaagag ctgaagaaga tcatcggaca ggtcagggat	3660
caggccgagc atctgaaaac agccgtccag atggccgtgt tcatccacaa cttcaagcgg	3720
aagggagggg tcggagagta ctctgctggc gagaggatcg tggacattat cgccagcgat	3780
atccagacca aagaactgca gaagcagatc acaaagatcc agaacttcag ggtgtactac	3840
agggacagca gagatcccct gtggaaggga cctgccaaagc tgctgtggaa aggcgaagga	3900
gccgtcgtca tccaggacaa cagcgacatc aaggtggtgc ccagacggaa ggccaagatc	3960
atcagagact acggcaaaca gatggctggc gacgactgcg tcgcctctag gcaggacgag	4020
gac	4023

<210> 22
<211> 2055
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotide sequence encoding mos1Env

<400> 22
atgcgggtga ccggcatccg gaagaactac cagcacctgt ggcggtgggg caccatgctg 60
ctgggcatcc tgatgatttg ctctgccgcc ggaaagctgt gggtgaccgt gtactacggc 120
gtgcccgtgt ggaaagaggc caccaccacc ctgttctgcg ccagcgacgc caaggcctac 180
gacaccgagg tgcacaacgt gtggggccacc cacgcctgcg tgcccaccga cccaacccc 240
caggaagtgg tcctggaaaa cgtgaccgag aacttcaaca tgtggaagaa caacatggtg 300
gagcagatgc acgaggacat catcagcctg tgggaccaga gcctgaagcc ctgctggaag 360
ctgaccccc cgtgctgac cctgaactgc accgacgacg tgcggaacgt gaccaacaac 420
gccaccaaca ccaacagcag ctggggcgag cctatggaaa agggcgagat caagaactgc 480
agcttcaaca tcaccacctc catccggaac aaggtgcaga agcagtacgc cctgttctac 540
aagctggacg tggtgcccat cgacaacgac agcaacaaca ccaactaccg gctgatcagc 600
tgcaacacca gcgtgatcac ccaggcctgc cccaagggtgt ccttcgagcc catccccatc 660
cactactgcg ccctgcccgg cttcgccatc ctgaagtgca acgacaagaa gttcaacggc 720
accggcccct gcaccaacgt gagcaccgtg cagtgcaccc acggcatccg gcccggtggtg 780
tccaccagc tgctgctgaa cggcagcctg gccgaggaag aggtggtgat cagaagcgag 840
aatttcacca acaatgcaa gaccatcatg gtgcagctga acgtgagcgt ggagatcaac 900
tgcaaccggc ccaacaacaa cacccggaag agcatccaca tcggccctgg cagggccttc 960
tacacagccg gcgacatcat cggcgacatc cggcaggccc actgcaacat cagccggggc 1020
aactggaaca acaccctgcg gcagatcgtg gagaagctgg gcaagcagtt cggcaacaac 1080
aagaccatcg tgttcaacca cagcagcggc ggagaccccg agatcgtgat gcacagcttc 1140
aactgtggcg gcgagttctt ctactgcaac agcaccaagc tgttcaacag cacctggacc 1200
tggaacaact ccacctggaa taacaccaag cggagcaacg acaccgaaga gcacatcacc 1260
ctgcccctgcc ggatcaagca gattatcaat atgtggcagg aggtcggcaa ggccatgtac 1320
gcccctccca tccggggcca gatccggtgc agcagcaaca tcaccggcct gctgctgacc 1380
cgggacggcg gcaacgatac cagcggcacc gagatcttcc ggcctggcgg cggagatatg 1440
cgggacaact ggcggagcga gctgtacaag tacaagggtg tgaagatcga gcccctgggc 1500
gtggctccca ccaaggccaa gcggcgggtg gtgcagagcg agaagagcgc cgtgggcac 1560
ggcgccgtgt ttctgggctt cctgggagcc gccggaagca ccatgggagc cgccagcatg 1620

accctgaccg tgcaggcccc gctgctgctg tccggcatcg tgcagcagca gaacaacctg	1680
ctccggggcca tcgaggcccc gcagcacctg ctgcagctga ccggtgtggg catcaagcag	1740
ctgcaggcca ggggtgctggc cgtggagaga tacctgaagg atcagcagct cctggggatc	1800
tggggctgca gcggcaagct gatctgcacc accaccgtgc cctggaacgc cagctggtcc	1860
aacaagagcc tggacaagat ctggaacaat atgacctgga tggaatggga gcgcgagatc	1920
aacaattaca ccagcctgat ctacaccctg atcgaggaaa gccagaacca gcaggaaaag	1980
aacgagcagg aactgctgga actggacaag tgggccagcc tgtggaactg gttcgacatc	2040
agcaactggc tgtgg	2055

<210> 23
 <211> 2052
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotide sequence encoding mos2Env

<400> 23	
atgagagtgc ggggcatcca gcggaactgg ccccagtggg ggatctgggg catcctgggc	60
ttttggatga tcatcatctg ccgggtgatg ggcaacctgt gggtgaccgt gtactacggc	120
gtgcccgtgt ggaaagaggc caagaccacc ctgttctgcg ccagcgacgc caaggcctac	180
gagaaagagg tgcacaacgt gtgggccacc cacgcctgcg tgcccaccga cccaacccc	240
caggaaatgg tcctggaaaa cgtgaccgag aacttcaaca tgtggaagaa cgacatggtg	300
gaccagatgc acgaggacat catccggctg tgggaccaga gcctgaagcc ctgcgtgaag	360
ctgaccccc tgtgcgtgac cctggaatgc cggaacgtga gaaacgtgag cagcaacggc	420
acctacaaca tcatccacaa cgagacctac aaagagatga agaactgcag cttcaacgcc	480
accaccgtgg tggaggaccg gaagcagaag gtgcacgccc tgttctaccg gctggacatc	540
gtgcccctgg acgagaacaa cagcagcgag aagtccagcg agaacagctc cgagtactac	600
cggtgatca actgcaacac cagcgccatc acccaggcct gcccgaagggt gtccttcgac	660
cccatcccca tccactactg cgcccctgcc ggctacgcca tcctgaagtg caacaacaag	720
accttcaacg gcaccggccc ctgcaacaac gtgagcaccg tgcagtgcac ccacggcatc	780
aagcccgtgg tgtccacca gctgctgctg aacggcagcc tggccgagga agagatcatc	840
atccgggtccg agaacctgac caacaacgcc aagaccatca tcgtgcacct gaatgagacc	900
gtgaacatca cctgcacccg gcccacaac aacaccgga agagcatccg gatcggccct	960
ggccagacct tttagccac cggcgacatc atcggcgaca tccggcaggc cactgcaac	1020
ctgagccggg acggctggaa caagaccctg cagggcgtga agaagaagct ggccgagcac	1080
ttccccaata agaccatcaa cttcaccagc agcagcggcg gagacctgga aatcaccacc	1140

cacagcttca actgcagggg cgagttcttc tactgcaata cctccggcct gttcaatggc	1200
acctacatgc ccaacggcac caacagcaac agcagcagca acatcaccct gccctgccgg	1260
atcaagcaga tcatcaatat gtggcaggag gtcggcaggg ccatgtacgc ccctcccac	1320
gccggcaata tcacctgccg gtccaacatc accggcctgc tgctgaccag ggacggcggc	1380
agcaacaacg gcgtgcctaa cgacaccgag accttccggc ctggcggcgg agatatgcgg	1440
aacaactggc ggagcgagct gtacaagtac aaggtggtgg aggtgaagcc cctgggcgtg	1500
gctcctaccg aggccaagcg gcgggtggtg gagagcgaga agagcgccgt gggcatcggc	1560
gccgtgtttc tgggcattct gggagccgcc ggaagcacca tgggagccgc cagcatcacc	1620
ctgaccgtgc aggcccggca gctgctgtcc ggcacgtgc agcagcagag caacctgctg	1680
agagccatcg aggcccagca gcacatgctg cagctgaccg tgtggggcat caagcagctg	1740
cagacccggg tgctggccat cgagagatac ctgcaggatc agcagctcct gggcctgtgg	1800
ggctgcagcg gcaagctgat ctgcaccacc gccgtgccct ggaacaccag ctggtccaac	1860
aagagccaga ccgacatctg ggacaacatg acctggatgc agtgggacaa agagatcggc	1920
aactacaccg gcgagatcta caggctgctg gaagagagcc agaaccagca ggaaaagaac	1980
gagaaggacc tgctggccct ggacagctgg aagaacctgt ggaactggtt cgacatcacc	2040
aactggctgt gg	2052

<210> 24

<211> 829

<212> DNA

<213> Artificial Sequence

<220>

<223> CMV promoter used for expression of antigens in Ad26 vectors

<400> 24

tcaatattgg ccattagcca tattattcat tggttatata gcataaatca atattggcta	60
ttggccattg catacgttgt atccatatca taatatgtac atttatattg gctcatgtcc	120
aacattaccg ccatgttgac attgattatt gactagttat taatagtaat caattacggg	180
gtcattagtt catagcccat atatggagtt ccgcgttaca taacttacgg taaatggccc	240
gcctggctga ccgccaacg acccccggcc attgacgtca ataatgacgt atgttcccat	300
agtaacgcca atagggactt tccattgacg tcaatgggtg gagtatattac ggtaaactgc	360
ccacttggca gtacatcaag tgtatcatat gccaagtacg cccctattg acgtcaatga	420
cggtaaattg cccgcctggc attatgccca gtacatgacc ttatgggact ttcctacttg	480
gcagtacatc tacgtattag tcatcgctat taccatggtg atgcggtttt ggcagtacat	540
caatgggcgt ggatagcggg ttgactcacg gggatttcca agtctccacc ccattgacgt	600
caatgggagt ttgttttggc accaaaatca acgggacttt ccaaaatgtc gtaacaactc	660

cgccccattg acgcaaattg gcggtaggcg tgtacggtgg gaggtctata taagcagagc	720
tcgttttagtg aaccgtcaga tcgcctggag acgccatcca cgctgttttg acctccatag	780
aagacaccgg gaccgatcca gcctccgcgg ccgggaacgg tgcattgga	829

<210> 25
 <211> 2586
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotide sequence encoding C4

<400> 25	
atgagagtgc ggggcatgct gagaaactgg cagcagtggg ggatctgggc cagcctgggc	60
ttctggatgc tgatgatcta cagcgtgatg ggcaacctgt gggtcaccgt gtactacggc	120
gtgcccgtgt ggaaggacgc caagaccacc ctgttttgcg cctccgatgc caaggcctac	180
gagaaagagg tgcacaacgt ctggggccacc cagcctgtg tggccaccga cccaatccc	240
caggaaatcg tcctgggcaa cgtgaccgag aacttcaaca tgtggaagaa cgacatgggc	300
gatcagatgc acgaggacat catctccctg tgggacgcct ccctggaacc ctgcgtgaag	360
ctgaccacctc tgtgcgtgac cctgaactgc cggaacgtgc gcaacgtgtc cagcaacggc	420
acctacaaca tcatccacaa cgagacatac aaagagatga agaactgcag cttcaacgct	480
accaccgtgg tcgaggaccg gaagcagaag gtgcacgccc tgttctaccg gctggacatc	540
gtgcccctgg acgagaacaa cagcagcgag aagtcctccg agaacagctc cgagtactac	600
agactgatca actgcaacac cagcgccatc acccaggcct gcccgaaggc gtccttcgac	660
cctatcccca tccactactg cgcccctgcc ggctacgcca tcctgaagtg caacaacaag	720
accttcaatg gcaccggccc ctgcaacaat gtgtccaccg tgcagtgcac ccacggcatc	780
aagcccgtgg tgtctaccca gctgctgctg aacggcagcc tggccgagga agagatcatt	840
atcagaagcg agaacctgac caacaacgcc aaaaccatca tcgtccacct gaacgaaacc	900
gtgaacatca cctgtaccgg gcctaacaac aacacccgga agtccatccg gatcggcct	960
ggccagacct tttagccac cggcgatatt atcggcgaca tccggcaggc ccaactgcaat	1020
ctgagccggg acggctggaa caagacactg cagggcgtca agaagaagct ggccgaacac	1080
ttccctaaca agactatcaa gttagccct cactctggcg gcgacctgga aatcaccacc	1140
cacaccttca actgtcgggg cgagttcttc tactgcaata cctccaacct gttcaacgag	1200
agcaacatcg agcggaacga cagcatcatc aactgcctt gccggatcaa gcagattatc	1260
aatatgtggc aggaagtggg cagagccatc tacgcccctc caatcgccgg caacatcaca	1320
tgcgggtcca atatcaccgg cctgctgctc accagagatg gcggctccaa caatggcgtg	1380
ccaaacgaca ccgagacatt cagacccggc ggaggcgaca tgcggaacaa ttggcggagc	1440

gagctgtaca agtacaaggt ggtggaagtg aagcccctgg gcgtggcccc taccgaggcc	1500
aagagaagag tggtcgaacg cgagaagcgg gccgtgggaa tcggagccgt gtttctggga	1560
atcctgggag ccgctggctc taccatgggc gctgcctcta tcaccctgac agtgcaggcc	1620
agacagctgc tcagcggcat cgtgcagcag cagagcaacc tgctgagagc cattgaggcc	1680
cagcagcaca tgctgcagct gaccgtgtgg ggcatthaagc agctccagac acgggtgctg	1740
gccatcgaga gatacctgca ggatcagcag ctccctgggccc tgtggggctg tagcggcaag	1800
ctgatctgta ccaccgccgt gccctggaat acctcttgga gcaacaagag ccagaccgac	1860
atctgggaca acatgacctg gatgcagtgg gacaaagaaa tcggcaacta taccggcgag	1920
atctatagac tgctggaaga gtcccagaac cagcaggaaa agaacgagaa ggacctgctg	1980
gccctggatt cttggaacaa tctgtggaac tggttcagca tctccaagtg gctgtggtac	2040
atcaagatct tcatcatgat cgtgggcggc ctgatcggcc tgcggatcat ctttgccgtg	2100
ctgagcatcg tgaaccgcgt gcggcaggga tacagccctc tgagcctgca gaccctgact	2160
cagaaccctg gcggactgga cagactgggc cggattgagg aagaaggcgg cgagcaggac	2220
aaggatcgga gcatcaggct ggtcaacggc ttcttcgctc tgttttgga cgacctgcgg	2280
agcctgtgcc tggtcagcta ccacagactg cgggacttta tcctgattgt ggccagagcc	2340
gtcgaaactgc tggggagaag ctctctgaga ggccctgcagc ggggctggga gattctgaag	2400
tacctgggct ccctgctgca gtactggggc ctggaactga agaagtctgc catcaatctg	2460
ctcgacacaa tcgctattgc cgtggccgaa ggcaccgata gaatcatcga gctgatccag	2520
cggatctgcc gggccatctg caacatcccc agacggatca gacagggctt cgaggccgct	2580
ctgcag	2586

<210> 26
 <211> 2133
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotide sequence encoding C4D7

<400> 26	
atgagagtgc ggggcatgct gagaaactgg cagcagtgggt ggatctggtc cagcctgggc	60
ttctggatgc tgatgatcta cagcgtgatg ggcaacctgt gggtcaccgt gtactacggc	120
gtgcccgtgt ggaaggacgc caagaccacc ctgttttgcg cctccgatgc caaggcctac	180
gagaaagagg tgcacaacgt ctggggccacc cagcctgtg tggccaccga cccaatccc	240
caggaaatcg tcctgggcaa cgtgaccgag aacttcaaca tgtggaagaa cgacatggtc	300
gatcagatgc acgaggacat catctccctg tgggacgcct ccctggaacc ctgcgtgaag	360
ctgaccctc tgtgcgtgac cctgaactgc cggaacgtgc gcaacgtgtc cagcaacggc	420

acctacaaca	tcatccacaa	cgagacatac	aaagagatga	agaactgcag	cttcaacgct	480
accaccgtgg	tcgaggaccg	gaagcagaag	gtgcacgccc	tgttctaccg	gctggacatc	540
gtgcccctgg	acgagaacaa	cagcagcgag	aagtcctccg	agaacagctc	cgagtactac	600
agactgatca	actgcaacac	cagcgccatc	acccaggcct	gccccaaagg	gtccttcgac	660
cctatcccca	tccactactg	cgccccctgcc	ggctacgcca	tcctgaagtg	caacaacaag	720
accttcaatg	gcaccggccc	ctgcaacaat	gtgtccaccg	tgcagtgcac	ccacggcatc	780
aagcccgtgg	tgtctaccca	gctgctgctg	aacggcagcc	tggccgagga	agagatcatt	840
atcagaagcg	agaacctgac	caacaacgcc	aaaaccatca	tcgtccacct	gaacgaaacc	900
gtgaacatca	cctgtacccg	gcctaacaac	aacacccgga	agtccatccg	gatcggccct	960
ggccagacct	tttacgccac	cggcgatatt	atcggcgaca	tcgggcaggc	ccactgcaat	1020
ctgagccggg	acggctggaa	caagacactg	cagggcgctca	agaagaagct	ggccgaacac	1080
ttccctaaca	agactatcaa	gttcgcccct	cactctggcg	gcgacctgga	aatcaccacc	1140
cacaccttca	actgtcgggg	cgagttcttc	tactgcaata	cctccaacct	gttcaacgag	1200
agcaacatcg	agcggaacga	cagcatcatc	acactgcctt	gccggatcaa	gcagattatc	1260
aatatgtggc	aggaagtggg	cagagccatc	tacgcccctc	caatcgccgg	caacatcaca	1320
tgccgggtcca	atatcaccgg	cctgctgctc	accagagatg	gcgggtccaa	caatggcgctg	1380
ccaaacgaca	ccgagacatt	cagacccggc	ggaggcgaca	tgcggaacaa	ttggcggagc	1440
gagctgtaca	agtacaaggt	ggtggaagtg	aagcccctgg	gcgtggcccc	taccgaggcc	1500
aagagaagag	tggtcgaacg	cgagaagcgg	gccgtgggaa	tcggagccgt	gtttctggga	1560
atcctgggag	ccgctggctc	taccatgggc	gctgcctcta	tcaccctgac	agtgcaggcc	1620
agacagctgc	tcagcggcat	cgtgcagcag	cagagcaacc	tgctgagagc	cattgaggcc	1680
cagcagcaca	tgctgcagct	gaccgtgtgg	ggcattaagc	agctccagac	acgggtgctg	1740
gccatcgaga	gatacctgca	ggatcagcag	ctcctggggc	tgtggggctg	tagcggcaag	1800
ctgatctgta	ccaccgccgt	gccctggaat	acctcttgga	gcaacaagag	ccagaccgac	1860
atctgggaca	acatgacctg	gatgcagtgg	gacaaagaaa	tcggcaacta	taccggcgag	1920
atctatagac	tgctggaaga	gtcccagaac	cagcaggaaa	agaacgagaa	ggacctgctg	1980
gccctggatt	cttggaaaca	tctgtggaac	tggttcagca	tcaccaagtg	gctgtggtac	2040
atcaagatct	tcatcatgat	cgtgggcggc	ctgatcggcc	tgcggatcat	ctttgccgtg	2100
ctgagcatcg	tgaaccgcgt	gcggcagggc	tac			2133

<210> 27

<211> 2112

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence encoding sC4

<400> 27

atgagagtgc	ggggcatgct	gagaaactgg	cagcagtgggt	ggatctgggtc	cagcctgggc	60
ttctggatgc	tgatgatcta	cagcgtgatg	ggcaacctgt	gggtcacctg	gtactacggc	120
gtgcccgtgt	ggaaggacgc	caagaccacc	ctgtttttgcg	cctccgatgc	caaggcctac	180
gagaaagagg	tgacacaacgt	ctggggccacc	cacgcctgtg	tgccaccga	ccccaatccc	240
caggaaatcg	tcctgggcaa	cgtgaccgag	aacttcaaca	tgtggaagaa	cgacatgggtc	300
gatcagatgc	acgaggacat	catctccctg	tgggacgcct	ccctggaacc	ctgcgtgaag	360
ctgacccctc	tgtgcgtgac	cctgaactgc	cggaacgtgc	gcaacgtgtc	cagcaacggc	420
acctacaaca	tcattccaaa	cgagacatac	aaagagatga	agaactgcag	cttcaacgct	480
accaccgtgg	tcgaggaccg	gaagcagaag	gtgcacgccc	tgttctaccg	gctggacatc	540
gtgcccctgg	acgagaacaa	cagcagcgag	aagtcctccg	agaacagctc	cgagtactac	600
agactgatca	actgcaacac	cagcgccatc	accaggcct	gccccaaagg	gtccttcgac	660
cctatcccca	tccactactg	cgcccctgcc	ggctacgcca	tcctgaagtg	caacaacaag	720
accttcaatg	gcaccggccc	ctgcaacaat	gtgtccaccg	tgcagtgcac	ccacggcatc	780
aagcccgtgg	tgtctaccca	gctgctgctg	aacggcagcc	tggccgagga	agagatcatt	840
atcagaagcg	agaacctgac	caacaacgcc	aaaaccatca	tcgtccacct	gaacgaaacc	900
gtgaacatca	cctgtacccg	gcctaacaac	aacacccgga	agtccatccg	gatcggccct	960
ggccagacct	tttacgccac	cggcgatatt	atcggcgaca	tccggcaggc	ccactgcaat	1020
ctgagccggg	acggctggaa	caagacactg	cagggcgtca	agaagaagct	ggccgaacac	1080
ttccctaaca	agactatcaa	gttcgcccct	cactctggcg	gcgacctgga	aatcaccacc	1140
cacaccttca	actgtcgggg	cgagttcttc	tactgcaata	cctccaacct	gttcaacgag	1200
agcaacatcg	agcggaacga	cagcatcatc	acactgcctt	gccggatcaa	gcagattatc	1260
aatatgtggc	aggaagtggg	cagagccatc	tacgcccctc	caatcgccgg	caacatcaca	1320
tgccggtcca	atatcaccgg	cctgctgctc	accagagatg	gcggctccaa	caatggcgtg	1380
ccaaacgaca	ccgagacatt	cagacccggc	ggaggcgaca	tgcggaacaa	ttggcggagc	1440
gagctgtaca	agtacaagg	gggtggaagt	aagcccctgg	gcgtggcccc	taccgaggcc	1500
aagagaagag	tggtcgaacg	cgaggaacgg	gccgtgggaa	tcggagccgt	gtttctggga	1560
atcctgggag	ccgctggctc	taccatgggc	gctgcctcta	tcaccctgac	agtgcaggcc	1620
agacagctgc	tcagcggcat	cgtgcagcag	cagagcaacc	tgctgagagc	cattgaggcc	1680
cagcagcaca	tgctgcagct	gaccgtgtgg	ggcattaagc	agctccagac	acgggtgctg	1740
gccatcgaga	gatacctgca	ggatcagcag	ctcctggggc	tgtggggctg	tagcggcaag	1800

ctgatctgta ccaccgccgt gccctggaat acctcttgga gcaacaagag ccagaccgac 1860
atctgggaca acatgacctg gatgcagtgg gacaaagaaa tcggcaacta taccggcgag 1920
atctatagac tgctggaaga gtcccagaac cagcaggaaa agatgaagca gatcgaggac 1980
aagatcgaag agattctgag caagatctac cacatcgaga acgagatcgc ccgcatcaag 2040
aaactgatcg gcgaagtggg atccggcgct cccacaaagg ccaaaagacg ggtggtgcag 2100
cgcgagaaaac gc 2112

<210> 28
<211> 1350
<212> PRT
<213> Artificial Sequence

<220>
<223> mos1GagPol mosaic antigen sequence

<400> 28

Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp
1 5 10 15

Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Arg Leu Lys
20 25 30

His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
35 40 45

Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
50 55 60

Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn
65 70 75 80

Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp
85 90 95

Thr Lys Glu Ala Leu Glu Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys
100 105 110

Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly Asn Ser Ser Gln Val
115 120 125

Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His
130 135 140

Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu
145 150 155 160

Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser

165

170

175

Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly
 180 185 190

Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu
 195 200 205

Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala
 210 215 220

Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr
 225 230 235 240

Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile
 245 250 255

Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys
 260 265 270

Ile Val Arg Met Tyr Ser Pro Val Ser Ile Leu Asp Ile Arg Gln Gly
 275 280 285

Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu
 290 295 300

Arg Ala Glu Gln Ala Ser Gln Asp Val Lys Asn Trp Met Thr Glu Thr
 305 310 315 320

Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala
 325 330 335

Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly
 340 345 350

Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser
 355 360 365

Gln Val Thr Asn Ser Ala Thr Ile Met Met Gln Arg Gly Asn Phe Arg
 370 375 380

Asn Gln Arg Lys Thr Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His
 385 390 395 400

Ile Ala Lys Asn Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys
 405 410 415

Gly Lys Glu Gly His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn

420

425

430

Phe Leu Gly Lys Ile Trp Pro Ser Asn Lys Gly Arg Pro Gly Asn Phe
 435 440 445

Leu Gln Asn Arg Pro Glu Pro Thr Ala Pro Pro Glu Glu Ser Phe Arg
 450 455 460

Phe Gly Glu Glu Thr Thr Thr Pro Ser Gln Lys Gln Glu Pro Ile Asp
 465 470 475 480

Lys Glu Met Tyr Pro Leu Ala Ser Leu Lys Ser Leu Phe Gly Asn Asp
 485 490 495

Pro Ser Ser Gln Met Ala Pro Ile Ser Pro Ile Glu Thr Val Pro Val
 500 505 510

Lys Leu Lys Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu
 515 520 525

Thr Glu Glu Lys Ile Lys Ala Leu Thr Ala Ile Cys Glu Glu Met Glu
 530 535 540

Lys Glu Gly Lys Ile Thr Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr
 545 550 555 560

Pro Val Phe Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu
 565 570 575

Val Asp Phe Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val
 580 585 590

Gln Leu Gly Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val
 595 600 605

Thr Val Leu Ala Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu
 610 615 620

Gly Phe Arg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu
 625 630 635 640

Thr Pro Gly Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys
 645 650 655

Gly Ser Pro Ala Ile Phe Gln Cys Ser Met Thr Arg Ile Leu Glu Pro
 660 665 670

Phe Arg Ala Lys Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Ala Ala

675

680

685

Leu Tyr Val Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile
 690 695 700

Glu Glu Leu Arg Glu His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp
 705 710 715 720

Lys Lys His Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu
 725 730 735

His Pro Asp Lys Trp Thr Val Gln Pro Ile Gln Leu Pro Glu Lys Asp
 740 745 750

Ser Trp Thr Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp
 755 760 765

Ala Ser Gln Ile Tyr Pro Gly Ile Lys Val Arg Gln Leu Cys Lys Leu
 770 775 780

Leu Arg Gly Ala Lys Ala Leu Thr Asp Ile Val Pro Leu Thr Glu Glu
 785 790 795 800

Ala Glu Leu Glu Leu Ala Glu Asn Arg Glu Ile Leu Lys Glu Pro Val
 805 810 815

His Gly Val Tyr Tyr Asp Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln
 820 825 830

Lys Gln Gly His Asp Gln Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe
 835 840 845

Lys Asn Leu Lys Thr Gly Lys Tyr Ala Lys Met Arg Thr Ala His Thr
 850 855 860

Asn Asp Val Lys Gln Leu Thr Glu Ala Val Gln Lys Ile Ala Met Glu
 865 870 875 880

Ser Ile Val Ile Trp Gly Lys Thr Pro Lys Phe Arg Leu Pro Ile Gln
 885 890 895

Lys Glu Thr Trp Glu Thr Trp Trp Thr Asp Tyr Trp Gln Ala Thr Trp
 900 905 910

Ile Pro Glu Trp Glu Phe Val Asn Thr Pro Pro Leu Val Lys Leu Trp
 915 920 925

Tyr Gln Leu Glu Lys Asp Pro Ile Ala Gly Val Glu Thr Phe Tyr Val

930

935

940

Ala Gly Ala Ala Asn Arg Glu Thr Lys Leu Gly Lys Ala Gly Tyr Val
 945 950 955 960

Thr Asp Arg Gly Arg Gln Lys Ile Val Ser Leu Thr Glu Thr Thr Asn
 965 970 975

Gln Lys Thr Ala Leu Gln Ala Ile Tyr Leu Ala Leu Gln Asp Ser Gly
 980 985 990

Ser Glu Val Asn Ile Val Thr Ala Ser Gln Tyr Ala Leu Gly Ile Ile
 995 1000 1005

Gln Ala Gln Pro Asp Lys Ser Glu Ser Glu Leu Val Asn Gln Ile
 1010 1015 1020

Ile Glu Gln Leu Ile Lys Lys Glu Arg Val Tyr Leu Ser Trp Val
 1025 1030 1035

Pro Ala His Lys Gly Ile Gly Gly Asn Glu Gln Val Asp Lys Leu
 1040 1045 1050

Val Ser Ser Gly Ile Arg Lys Val Leu Phe Leu Asp Gly Ile Asp
 1055 1060 1065

Lys Ala Gln Glu Glu His Glu Lys Tyr His Ser Asn Trp Arg Ala
 1070 1075 1080

Met Ala Ser Asp Phe Asn Leu Pro Pro Val Val Ala Lys Glu Ile
 1085 1090 1095

Val Ala Ser Cys Asp Gln Cys Gln Leu Lys Gly Glu Ala Met His
 1100 1105 1110

Gly Gln Val Asp Cys Ser Pro Gly Ile Trp Gln Leu Ala Cys Thr
 1115 1120 1125

His Leu Glu Gly Lys Ile Ile Leu Val Ala Val His Val Ala Ser
 1130 1135 1140

Gly Tyr Ile Glu Ala Glu Val Ile Pro Ala Glu Thr Gly Gln Glu
 1145 1150 1155

Thr Ala Tyr Phe Ile Leu Lys Leu Ala Gly Arg Trp Pro Val Lys
 1160 1165 1170

Val Ile His Thr Ala Asn Gly Ser Asn Phe Thr Ser Ala Ala Val

His Leu Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Leu Asn Pro
 35 40 45

Gly Leu Leu Glu Thr Ser Glu Gly Cys Lys Gln Ile Ile Lys Gln Leu
 50 55 60

Gln Pro Ala Leu Gln Thr Gly Thr Glu Glu Leu Arg Ser Leu Phe Asn
 65 70 75 80

Thr Val Ala Thr Leu Tyr Cys Val His Ala Glu Ile Glu Val Arg Asp
 85 90 95

Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Gln
 100 105 110

Gln Lys Thr Gln Gln Ala Lys Glu Ala Asp Gly Lys Val Ser Gln Asn
 115 120 125

Tyr Pro Ile Val Gln Asn Leu Gln Gly Gln Met Val His Gln Pro Ile
 130 135 140

Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Ile Glu Glu Lys Ala
 145 150 155 160

Phe Ser Pro Glu Val Ile Pro Met Phe Thr Ala Leu Ser Glu Gly Ala
 165 170 175

Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln
 180 185 190

Ala Ala Met Gln Met Leu Lys Asp Thr Ile Asn Glu Glu Ala Ala Glu
 195 200 205

Trp Asp Arg Leu His Pro Val His Ala Gly Pro Val Ala Pro Gly Gln
 210 215 220

Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Asn Leu
 225 230 235 240

Gln Glu Gln Ile Ala Trp Met Thr Ser Asn Pro Pro Ile Pro Val Gly
 245 250 255

Asp Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg
 260 265 270

Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Lys Gln Gly Pro Lys Glu
 275 280 285

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

Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Ile	Phe	Ala	Ile	Lys	Lys	Lys	Asp	545	550	555	560
Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	Arg	Glu	Leu	Asn	Lys	Arg	565	570	575	
Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	Ile	Pro	His	Pro	Ala	Gly	580	585	590	
Leu	Lys	Lys	Lys	Lys	Ser	Val	Thr	Val	Leu	Ala	Val	Gly	Asp	Ala	Tyr	595	600	605	
Phe	Ser	Val	Pro	Leu	Asp	Glu	Asp	Phe	Arg	Lys	Tyr	Thr	Ala	Phe	Thr	610	615	620	
Ile	Pro	Ser	Ile	Asn	Asn	Glu	Thr	Pro	Gly	Ile	Arg	Tyr	Gln	Tyr	Asn	625	630	635	640
Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	Ala	Ile	Phe	Gln	Ser	Ser	645	650	655	
Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	Gln	Asn	Pro	Asp	Ile	Val	660	665	670	
Ile	Tyr	Gln	Tyr	Met	Ala	Ala	Leu	Tyr	Val	Gly	Ser	Asp	Leu	Glu	Ile	675	680	685	
Gly	Gln	His	Arg	Thr	Lys	Ile	Glu	Glu	Leu	Arg	Gln	His	Leu	Leu	Arg	690	695	700	
Trp	Gly	Phe	Thr	Thr	Pro	Asp	Lys	Lys	His	Gln	Lys	Glu	Pro	Pro	Phe	705	710	715	720
Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	Lys	Trp	Thr	Val	Gln	Pro	725	730	735	
Ile	Val	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr	Val	Asn	Asp	Ile	Gln	Lys	740	745	750	
Leu	Val	Gly	Lys	Leu	Asn	Trp	Ala	Ser	Gln	Ile	Tyr	Ala	Gly	Ile	Lys	755	760	765	
Val	Lys	Gln	Leu	Cys	Lys	Leu	Leu	Arg	Gly	Thr	Lys	Ala	Leu	Thr	Glu	770	775	780	
Val	Val	Pro	Leu	Thr	Glu	Glu	Ala	Glu	Leu	Glu	Leu	Ala	Glu	Asn	Arg	785	790	795	800

Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr Tyr Asp Pro Ser Lys
 805 810 815

Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Gln Gly Gln Trp Thr Tyr
 820 825 830

Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys Thr Gly Lys Tyr Ala
 835 840 845

Arg Met Arg Gly Ala His Thr Asn Asp Val Lys Gln Leu Thr Glu Ala
 850 855 860

Val Gln Lys Ile Ala Thr Glu Ser Ile Val Ile Trp Gly Lys Thr Pro
 865 870 875 880

Lys Phe Lys Leu Pro Ile Gln Lys Glu Thr Trp Glu Ala Trp Trp Thr
 885 890 895

Glu Tyr Trp Gln Ala Thr Trp Ile Pro Glu Trp Glu Phe Val Asn Thr
 900 905 910

Pro Pro Leu Val Lys Leu Trp Tyr Gln Leu Glu Lys Glu Pro Ile Val
 915 920 925

Gly Ala Glu Thr Phe Tyr Val Ala Gly Ala Ala Asn Arg Glu Thr Lys
 930 935 940

Leu Gly Lys Ala Gly Tyr Val Thr Asp Arg Gly Arg Gln Lys Val Val
 945 950 955 960

Ser Leu Thr Asp Thr Thr Asn Gln Lys Thr Ala Leu Gln Ala Ile His
 965 970 975

Leu Ala Leu Gln Asp Ser Gly Leu Glu Val Asn Ile Val Thr Ala Ser
 980 985 990

Gln Tyr Ala Leu Gly Ile Ile Gln Ala Gln Pro Asp Lys Ser Glu Ser
 995 1000 1005

Glu Leu Val Ser Gln Ile Ile Glu Gln Leu Ile Lys Lys Glu Lys
 1010 1015 1020

Val Tyr Leu Ala Trp Val Pro Ala His Lys Gly Ile Gly Gly Asn
 1025 1030 1035

Glu Gln Val Asp Lys Leu Val Ser Arg Gly Ile Arg Lys Val Leu
 1040 1045 1050

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

Leu Leu Trp Lys Gly Glu Gly Ala Val Val Ile Gln Asp Asn Ser
1295 1300 1305

Asp Ile Lys Val Val Pro Arg Arg Lys Ala Lys Ile Ile Arg Asp
1310 1315 1320

Tyr Gly Lys Gln Met Ala Gly Asp Asp Cys Val Ala Ser Arg Gln
1325 1330 1335

Asp Glu Asp
1340

<210> 30
<211> 709
<212> PRT
<213> Artificial Sequence

<220>
<223> sC1 sequence

<400> 30

Met Arg Val Arg Gly Ile Gln Arg Asn Trp Pro Gln Trp Trp Ile Trp
1 5 10 15

Gly Ile Leu Gly Phe Trp Met Ile Ile Ile Cys Arg Val Met Gly Asn
20 25 30

Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Lys
35 40 45

Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Glu Lys Glu Val
50 55 60

His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro
65 70 75 80

Gln Glu Met Val Leu Glu Asn Val Thr Glu Asn Phe Asn Met Trp Lys
85 90 95

Asn Asp Met Val Asp Gln Met His Glu Asp Ile Ile Arg Leu Trp Asp
100 105 110

Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu
115 120 125

Glu Cys Arg Asn Val Arg Asn Val Ser Ser Asn Gly Thr Tyr Asn Ile
130 135 140

Ile His Asn Glu Thr Tyr Lys Glu Met Lys Asn Cys Ser Phe Asn Ala

145					150					155					160
Thr	Thr	Val	Val	Glu	Asp	Arg	Lys	Gln	Lys	Val	His	Ala	Leu	Phe	Tyr
				165					170					175	
Arg	Leu	Asp	Ile	Val	Pro	Leu	Asp	Glu	Asn	Asn	Ser	Ser	Glu	Lys	Ser
			180					185					190		
Ser	Glu	Asn	Ser	Ser	Glu	Tyr	Tyr	Arg	Leu	Ile	Asn	Cys	Asn	Thr	Ser
		195					200					205			
Ala	Ile	Thr	Gln	Ala	Cys	Pro	Lys	Val	Ser	Phe	Asp	Pro	Ile	Pro	Ile
	210					215					220				
His	Tyr	Cys	Ala	Pro	Ala	Gly	Tyr	Ala	Ile	Leu	Lys	Cys	Asn	Asn	Lys
225					230					235					240
Thr	Phe	Asn	Gly	Thr	Gly	Pro	Cys	Asn	Asn	Val	Ser	Thr	Val	Gln	Cys
				245					250					255	
Thr	His	Gly	Ile	Lys	Pro	Val	Val	Ser	Thr	Gln	Leu	Leu	Leu	Asn	Gly
			260					265					270		
Ser	Leu	Ala	Glu	Glu	Glu	Ile	Ile	Ile	Arg	Ser	Glu	Asn	Leu	Thr	Asn
		275					280					285			
Asn	Ala	Lys	Thr	Ile	Ile	Val	His	Leu	Asn	Glu	Thr	Val	Asn	Ile	Thr
	290					295					300				
Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	Arg	Ile	Gly	Pro
305					310					315					320
Gly	Gln	Thr	Phe	Tyr	Ala	Thr	Gly	Asp	Ile	Ile	Gly	Asp	Ile	Arg	Gln
				325					330					335	
Ala	His	Cys	Asn	Leu	Ser	Arg	Asp	Gly	Trp	Asn	Lys	Thr	Leu	Gln	Gly
			340					345					350		
Val	Lys	Lys	Lys	Leu	Ala	Glu	His	Phe	Pro	Asn	Lys	Thr	Ile	Asn	Phe
		355					360					365			
Thr	Ser	Ser	Ser	Gly	Gly	Asp	Leu	Glu	Ile	Thr	Thr	His	Ser	Phe	Asn
	370					375					380				
Cys	Arg	Gly	Glu	Phe	Phe	Tyr	Cys	Asn	Thr	Ser	Gly	Leu	Phe	Asn	Gly
385					390					395					400
Thr	Tyr	Met	Pro	Asn	Gly	Thr	Asn	Ser	Asn	Ser	Ser	Ser	Asn	Ile	Thr

405

410

415

Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly
 420 425 430

Arg Ala Met Tyr Ala Pro Pro Ile Ala Gly Asn Ile Thr Cys Arg Ser
 435 440 445

Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Ser Asn Asn Gly
 450 455 460

Val Pro Asn Asp Thr Glu Thr Phe Arg Pro Gly Gly Gly Asp Met Arg
 465 470 475 480

Asn Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Glu Val Lys
 485 490 495

Pro Leu Gly Val Ala Pro Thr Glu Ala Lys Arg Arg Val Val Glu Arg
 500 505 510

Glu Glu Arg Ala Val Gly Ile Gly Ala Val Phe Leu Gly Ile Leu Gly
 515 520 525

Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Ile Thr Leu Thr Val Gln
 530 535 540

Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu
 545 550 555 560

Arg Ala Ile Glu Ala Gln Gln His Met Leu Gln Leu Thr Val Trp Gly
 565 570 575

Ile Lys Gln Leu Gln Thr Arg Val Leu Ala Ile Glu Arg Tyr Leu Gln
 580 585 590

Asp Gln Gln Leu Leu Gly Leu Trp Gly Cys Ser Gly Lys Leu Ile Cys
 595 600 605

Thr Thr Ala Val Pro Trp Asn Thr Ser Trp Ser Asn Lys Ser Gln Thr
 610 615 620

Asp Ile Trp Asp Asn Met Thr Trp Met Gln Trp Asp Lys Glu Ile Gly
 625 630 635 640

Asn Tyr Thr Gly Glu Ile Tyr Arg Leu Leu Glu Glu Ser Gln Asn Gln
 645 650 655

Gln Glu Lys Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser

660

665

670

Lys Ile Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile
 675 680 685

Gly Glu Val Gly Ser Gly Ala Pro Thr Lys Ala Lys Arg Arg Val Val
 690 695 700

Gln Arg Glu Lys Arg
 705

<210> 31

<211> 867

<212> PRT

<213> Artificial Sequence

<220>

<223> C1 sequence

<400> 31

Met Arg Val Arg Gly Ile Gln Arg Asn Trp Pro Gln Trp Trp Ile Trp
 1 5 10 15

Gly Ile Leu Gly Phe Trp Met Ile Ile Ile Cys Arg Val Met Gly Asn
 20 25 30

Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Lys
 35 40 45

Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Glu Lys Glu Val
 50 55 60

His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro
 65 70 75 80

Gln Glu Met Val Leu Glu Asn Val Thr Glu Asn Phe Asn Met Trp Lys
 85 90 95

Asn Asp Met Val Asp Gln Met His Glu Asp Ile Ile Arg Leu Trp Asp
 100 105 110

Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu
 115 120 125

Glu Cys Arg Asn Val Arg Asn Val Ser Ser Asn Gly Thr Tyr Asn Ile
 130 135 140

Ile His Asn Glu Thr Tyr Lys Glu Met Lys Asn Cys Ser Phe Asn Ala
 145 150 155 160

Thr	Thr	Val	Val	Glu	Asp	Arg	Lys	Gln	Lys	Val	His	Ala	Leu	Phe	Tyr	165	170	175
Arg	Leu	Asp	Ile	Val	Pro	Leu	Asp	Glu	Asn	Asn	Ser	Ser	Glu	Lys	Ser	180	185	190
Ser	Glu	Asn	Ser	Ser	Glu	Tyr	Tyr	Arg	Leu	Ile	Asn	Cys	Asn	Thr	Ser	195	200	205
Ala	Ile	Thr	Gln	Ala	Cys	Pro	Lys	Val	Ser	Phe	Asp	Pro	Ile	Pro	Ile	210	215	220
His	Tyr	Cys	Ala	Pro	Ala	Gly	Tyr	Ala	Ile	Leu	Lys	Cys	Asn	Asn	Lys	225	230	235
Thr	Phe	Asn	Gly	Thr	Gly	Pro	Cys	Asn	Asn	Val	Ser	Thr	Val	Gln	Cys	245	250	255
Thr	His	Gly	Ile	Lys	Pro	Val	Val	Ser	Thr	Gln	Leu	Leu	Leu	Asn	Gly	260	265	270
Ser	Leu	Ala	Glu	Glu	Glu	Ile	Ile	Ile	Arg	Ser	Glu	Asn	Leu	Thr	Asn	275	280	285
Asn	Ala	Lys	Thr	Ile	Ile	Val	His	Leu	Asn	Glu	Thr	Val	Asn	Ile	Thr	290	295	300
Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	Arg	Ile	Gly	Pro	305	310	315
Gly	Gln	Thr	Phe	Tyr	Ala	Thr	Gly	Asp	Ile	Ile	Gly	Asp	Ile	Arg	Gln	325	330	335
Ala	His	Cys	Asn	Leu	Ser	Arg	Asp	Gly	Trp	Asn	Lys	Thr	Leu	Gln	Gly	340	345	350
Val	Lys	Lys	Lys	Leu	Ala	Glu	His	Phe	Pro	Asn	Lys	Thr	Ile	Asn	Phe	355	360	365
Thr	Ser	Ser	Ser	Gly	Gly	Asp	Leu	Glu	Ile	Thr	Thr	His	Ser	Phe	Asn	370	375	380
Cys	Arg	Gly	Glu	Phe	Phe	Tyr	Cys	Asn	Thr	Ser	Gly	Leu	Phe	Asn	Gly	385	390	395
Thr	Tyr	Met	Pro	Asn	Gly	Thr	Asn	Ser	Asn	Ser	Ser	Ser	Asn	Ile	Thr	405	410	415

Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly
 420 425 430

Arg Ala Met Tyr Ala Pro Pro Ile Ala Gly Asn Ile Thr Cys Arg Ser
 435 440 445

Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Ser Asn Asn Gly
 450 455 460

Val Pro Asn Asp Thr Glu Thr Phe Arg Pro Gly Gly Gly Asp Met Arg
 465 470 475 480

Asn Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Glu Val Lys
 485 490 495

Pro Leu Gly Val Ala Pro Thr Glu Ala Lys Arg Arg Val Val Glu Arg
 500 505 510

Glu Lys Arg Ala Val Gly Ile Gly Ala Val Phe Leu Gly Ile Leu Gly
 515 520 525

Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Ile Thr Leu Thr Val Gln
 530 535 540

Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu
 545 550 555 560

Arg Ala Ile Glu Ala Gln Gln His Met Leu Gln Leu Thr Val Trp Gly
 565 570 575

Ile Lys Gln Leu Gln Thr Arg Val Leu Ala Ile Glu Arg Tyr Leu Gln
 580 585 590

Asp Gln Gln Leu Leu Gly Leu Trp Gly Cys Ser Gly Lys Leu Ile Cys
 595 600 605

Thr Thr Ala Val Pro Trp Asn Thr Ser Trp Ser Asn Lys Ser Gln Thr
 610 615 620

Asp Ile Trp Asp Asn Met Thr Trp Met Gln Trp Asp Lys Glu Ile Gly
 625 630 635 640

Asn Tyr Thr Gly Glu Ile Tyr Arg Leu Leu Glu Glu Ser Gln Asn Gln
 645 650 655

Gln Glu Lys Asn Glu Lys Asp Leu Leu Ala Leu Asp Ser Trp Lys Asn
 660 665 670

Leu Trp Asn Trp Phe Asp Ile Thr Asn Trp Leu Trp Tyr Ile Lys Ile
675 680 685

Phe Ile Met Ile Val Gly Gly Leu Ile Gly Leu Arg Ile Ile Phe Ala
690 695 700

Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser
705 710 715 720

Leu Gln Thr Leu Thr Gln Asn Pro Gly Gly Leu Asp Arg Leu Gly Arg
725 730 735

Ile Glu Glu Glu Gly Gly Glu Gln Asp Lys Asp Arg Ser Ile Arg Leu
740 745 750

Val Asn Gly Phe Phe Ala Leu Phe Trp Asp Asp Leu Arg Ser Leu Cys
755 760 765

Leu Phe Ser Tyr His Arg Leu Arg Asp Phe Ile Leu Ile Val Ala Arg
770 775 780

Ala Val Glu Leu Leu Gly Arg Ser Ser Leu Arg Gly Leu Gln Arg Gly
785 790 795 800

Trp Glu Ile Leu Lys Tyr Leu Gly Ser Leu Leu Gln Tyr Trp Gly Leu
805 810 815

Glu Leu Lys Lys Ser Ala Ile Asn Leu Leu Asp Thr Ile Ala Ile Ala
820 825 830

Val Ala Glu Gly Thr Asp Arg Ile Ile Glu Leu Ile Gln Arg Ile Cys
835 840 845

Arg Ala Ile Cys Asn Ile Pro Arg Arg Ile Arg Gln Gly Phe Glu Ala
850 855 860

Ala Leu Gln
865

<210> 32
<211> 716
<212> PRT
<213> Artificial Sequence

<220>
<223> C1D7 sequence

<400> 32

Met Arg Val Arg Gly Ile Gln Arg Asn Trp Pro Gln Trp Trp Ile Trp

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

260

265

270

Ser Leu Ala Glu Glu Glu Ile Ile Ile Arg Ser Glu Asn Leu Thr Asn
 275 280 285

Asn Ala Lys Thr Ile Ile Val His Leu Asn Glu Thr Val Asn Ile Thr
 290 295 300

Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Arg Ile Gly Pro
 305 310 315 320

Gly Gln Thr Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln
 325 330 335

Ala His Cys Asn Leu Ser Arg Asp Gly Trp Asn Lys Thr Leu Gln Gly
 340 345 350

Val Lys Lys Lys Leu Ala Glu His Phe Pro Asn Lys Thr Ile Asn Phe
 355 360 365

Thr Ser Ser Ser Gly Gly Asp Leu Glu Ile Thr Thr His Ser Phe Asn
 370 375 380

Cys Arg Gly Glu Phe Phe Tyr Cys Asn Thr Ser Gly Leu Phe Asn Gly
 385 390 395 400

Thr Tyr Met Pro Asn Gly Thr Asn Ser Asn Ser Ser Ser Asn Ile Thr
 405 410 415

Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly
 420 425 430

Arg Ala Met Tyr Ala Pro Pro Ile Ala Gly Asn Ile Thr Cys Arg Ser
 435 440 445

Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Ser Asn Asn Gly
 450 455 460

Val Pro Asn Asp Thr Glu Thr Phe Arg Pro Gly Gly Gly Asp Met Arg
 465 470 475 480

Asn Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Glu Val Lys
 485 490 495

Pro Leu Gly Val Ala Pro Thr Glu Ala Lys Arg Arg Val Val Glu Arg
 500 505 510

Glu Lys Arg Ala Val Gly Ile Gly Ala Val Phe Leu Gly Ile Leu Gly

515

520

525

Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Ile Thr Leu Thr Val Gln
 530 535 540

Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu
 545 550 555 560

Arg Ala Ile Glu Ala Gln Gln His Met Leu Gln Leu Thr Val Trp Gly
 565 570 575

Ile Lys Gln Leu Gln Thr Arg Val Leu Ala Ile Glu Arg Tyr Leu Gln
 580 585 590

Asp Gln Gln Leu Leu Gly Leu Trp Gly Cys Ser Gly Lys Leu Ile Cys
 595 600 605

Thr Thr Ala Val Pro Trp Asn Thr Ser Trp Ser Asn Lys Ser Gln Thr
 610 615 620

Asp Ile Trp Asp Asn Met Thr Trp Met Gln Trp Asp Lys Glu Ile Gly
 625 630 635 640

Asn Tyr Thr Gly Glu Ile Tyr Arg Leu Leu Glu Glu Ser Gln Asn Gln
 645 650 655

Gln Glu Lys Asn Glu Lys Asp Leu Leu Ala Leu Asp Ser Trp Lys Asn
 660 665 670

Leu Trp Asn Trp Phe Asp Ile Thr Asn Trp Leu Trp Tyr Ile Lys Ile
 675 680 685

Phe Ile Met Ile Val Gly Gly Leu Ile Gly Leu Arg Ile Ile Phe Ala
 690 695 700

Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr
 705 710 715

<210> 33

<211> 2127

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence encoding sC1

<400> 33

atgagagtgc ggggcattca gagaaactgg cccagtggt ggatctgggg catcctgggc 60

ttttggatga tcattatctg ccgcgtgatg ggcaacctgt gggtcaccgt gtactacggc 120

gtgcccgtgt	ggaaagaggc	caagaccacc	ctgttctgcg	ccagcgacgc	caaggcctac	180
gagaaagagg	tgcacaacgt	ctgggccacc	cacgcctgtg	tgcccaccga	ccccaatccc	240
caggaaatgg	tcctggaaaa	cgtgaccgag	aacttcaaca	tgtggaagaa	cgacatggtg	300
gaccagatgc	acgaggacat	catccggctg	tgggaccaga	gcctgaagcc	ctgcgtgaag	360
ctgacccctc	tgtgcgtgac	cctggaatgc	cggaacgtgc	gcaacgtgtc	cagcaacggc	420
acctacaata	tcatccacaa	cgagacatac	aaagagatga	agaactgcag	cttcaacgct	480
accaccgtgg	tcgaggaccg	gaagcagaag	gtgcacgccc	tgttttaccg	gctggacatc	540
gtgcccctgg	acgagaacaa	cagcagcgag	aagtcctccg	agaacagctc	cgagtactac	600
agactgatca	actgcaacac	cagcgccatc	accaggcct	gccccaaagg	gtccttcgac	660
cctatcccca	tccactactg	cgccccctgc	ggctacgcca	tcctgaagtg	caacaacaag	720
accttcaatg	gcaccggccc	ctgcaacaat	gtgtccaccg	tgcagtgcac	ccacggcatc	780
aagcccgtgg	tgtctaccca	gctgctgctg	aacggcagcc	tggccgagga	agagatcatc	840
atcagaagcg	agaacctgac	caacaacgcc	aagacaatca	tcgtccacct	gaacgaaacc	900
gtgaacatca	cctgtaccgg	gcctaacaac	aacacccgga	agtccatccg	gatcggccct	960
ggccagacct	tttacgccac	cggcgatatt	atcggcgaca	tccggcaggc	ccactgcaat	1020
ctgagccggg	acggctggaa	caagacactg	cagggcgctc	agaagaagct	ggccgaacac	1080
ttccccaaac	aaaccatcaa	cttcaccagc	tcctctggcg	gcgacctgga	aatcaccacc	1140
cacagcttta	actgcagagg	cgagttcttc	tactgcaata	cctccggcct	gttcaatgga	1200
acctacatgc	ccaacgggac	caacagcaac	tccagcagca	atatcaccct	gccttgccgg	1260
atcaagcaga	ttatcaatat	gtggcaggaa	gtgggcagag	ctatgtacgc	ccctccaatc	1320
gccggcaaca	tcacatgcag	aagcaacatt	accggcctgc	tgtcaccag	ggacggcggc	1380
tctaacaatg	gcgtgccaaa	cgacaccgag	acattcagac	ccggcgagg	cgacatgcgg	1440
aacaattggc	ggagcgagct	gtacaagtac	aaggtggtgg	aagtgaagcc	cctgggcgtg	1500
gcccctaccg	aagccaagag	aagagtggtc	gaacgcgagg	aacgggccgt	gggcattgga	1560
gccgtgtttc	tgggaatcct	gggagccgct	ggcagcacca	tgggcgctgc	ctctatcaca	1620
ctgacagtgc	aggccagaca	gctcctgagc	ggcatcgtgc	agcagcagag	caacctgctg	1680
agagccatcg	aggcacagca	gcacatgctg	cagctgaccg	tgtggggcat	taagcagctc	1740
cagacacggg	tgctggccat	tgagagatac	ctgcaggatc	agcagctgct	cggcctgtgg	1800
ggctgtagcg	gcaagctgat	ctgtaccacc	gccgtgcctt	ggaacacctc	ctggtccaac	1860
aagagccaga	ccgacatctg	ggacaacatg	acctggatgc	agtgggacaa	agaaatcggc	1920
aactataccg	gcgagatcta	ccgactgctg	gaagagtccc	agaaccagca	ggaaaagatg	1980
aagcagatcg	aggacaagat	cgaagagatt	ctgagcaaaa	tctaccacat	cgagaacgag	2040

atcgcccgca tcaagaaact gatcggcgaa gtgggatccg gcgctccac aaaggccaaa	2100
agacgggtgg tgcagcgga gaaacgc	2127
<210> 34	
<211> 2601	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> nucleotide sequence encoding C1	
<400> 34	
atgagagtgc ggggcattca gagaaactgg cccagtggt ggatctgggg catcctgggc	60
ttttggatga tcattatctg ccgcgtgatg ggcaacctgt gggtcaccgt gtactacggc	120
gtgccgtgt ggaaagaggc caagaccacc ctgttctgcg ccagcgacgc caaggcctac	180
gagaaagagg tgcacaacgt ctgggccacc cagcctgtg tggccaccga cccaatccc	240
caggaaatgg tcctggaaaa cgtgaccgag aacttcaaca tgtggaagaa cgacatggtg	300
gaccagatgc acgaggacat catccggctg tgggaccaga gcctgaagcc ctgcgtgaag	360
ctgaccctc tgtgcgtgac cctggaatgc cggaacgtgc gcaacgtgtc cagcaacggc	420
acctacaata tcatccacaa cgagacatac aaagagatga agaactgcag cttcaacgct	480
accaccgtgg tcgaggaccg gaagcagaag gtgcacgccc tgttttaccg gctggacatc	540
gtgcccctgg acgagaacaa cagcagcgag aagtcctccg agaacagctc cgagtactac	600
agactgatca actgcaacac cagcgccatc acccaggcct gcccgaaggt gtccttcgac	660
cctatcccca tccactactg cgcccctgcc ggctacgcca tcctgaagtg caacaacaag	720
accttcaatg gcaccggccc ctgcaacaat gtgtccaccg tgcagtgcac ccacggcatc	780
aagcccgtgg tgtctaccca gctgctgctg aacggcagcc tggccgagga agagatcatc	840
atcagaagcg agaacctgac caacaacgcc aagacaatca tcgtccacct gaacgaaacc	900
gtgaacatca cctgtaccgc gcctaacaac aacacccgga agtccatccg gatcggccct	960
ggccagacct tttagccac cggcgatatt atcggcgaca tccggcaggc cactgcaat	1020
ctgagccggg acggctggaa caagacactg cagggcgtca agaagaagct ggccgaacac	1080
ttccccaaca aaacctcaaa cttcaccagc tcctctggcg gcgacctgga aatcaccacc	1140
cacagcttta actgcagagg cgagttcttc tactgcaata cctccggcct gttcaatgga	1200
acctacatgc ccaacgggac caacagcaac tccagcagca atatcaccct gccttgccgg	1260
atcaagcaga ttatcaatat gtggcaggaa gtgggcagag ctatgtacgc ccctccaatc	1320
gccggcaaca tcacatgcag aagcaacatt accggcctgc tgctcaccag ggacggcggc	1380
tctaacaatg gcgtgccaaa cgacaccgag acattcagac ccggcgagg cgacatgcgg	1440
aacaattggc ggagcgagct gtacaagtac aaggtggtgg aagtgaagcc cctgggcgtg	1500

gccccctaccg aagccaagag aagagtggtc gaacgcgaga agcggggccgt gggcattgga	1560
gccgtgtttc tgggaatcct gggagccgct ggcagcacca tgggcgctgc ctctatcaca	1620
ctgacagtgc aggccagaca gctcctgagc ggcacgtgc agcagcagag caacctgctg	1680
agagccatcg aggcacagca gcacatgctg cagctgaccg tgtggggcat taagcagctc	1740
cagacacggg tgctggccat tgagagatac ctgcaggatc agcagctgct cggcctgtgg	1800
ggctgtagcg gcaagctgat ctgtaccacc gccgtgcctt ggaacacctc ctggtccaac	1860
aagagccaga ccgacatctg ggacaacatg acctggatgc agtgggacaa agaaatcggc	1920
aactataccg gcgagatcta ccgactgctg gaagagtccc agaaccagca ggaaaagaac	1980
gagaaggacc tgctggccct ggacagctgg aaaaatctgt ggaattggtt cgacatcacc	2040
aactggctgt ggtacatcaa gatcttcac c atgatcgtgg gcggcctgat cggcctgcgg	2100
atcatctttg ccgtgctgag catcgtgaac cgcgtgcggc agggatacag ccctctgagc	2160
ctgcagaccc tgaccagaa tccaggcgga ctggatcggc tgggccggat tgaggaagaa	2220
ggcggcgagc aggacaagga ccgcagcatc agactcgtga acggcttctt cgctctgttt	2280
tgggacgacc tgcggagcct gtgcctgttc tcctaccaca gactgcggga ctttatcctg	2340
attgtggcca gagccgtcga gctgctgggc agatcttctc tgagaggcct gcagcggggc	2400
tgggagattc tgaagtacct gggctccctg ctgcagtatt ggggcctgga actgaagaag	2460
tccgccatca atctgctcga cacaatcgct attgccgtgg ccgaaggcac cgacagaatc	2520
atcgagctga tccagcggat ctgccggggc atctgcaaca tccccagacg gatcagacag	2580
ggctttgaag ccgccctcca g	2601

<210> 35

<211> 2148

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence encoding C1D7

<400> 35

atgagagtgc ggggcattca gagaaactgg cccagtggt ggatctgggg catcctgggc	60
ttttggatga tcattatctg ccgcgtgatg ggcaacctgt gggtcaccgt gtactacggc	120
gtgcccgtgt ggaaagaggc caagaccacc ctgttctgcg ccagcgacgc caaggcctac	180
gagaaagagg tgcacaacgt ctgggccacc cacgcctgtg tgcccaccga cccaatccc	240
caggaaatgg tcctggaaaa cgtgaccgag aacttcaaca tgtggaagaa cgacatggtg	300
gaccagatgc acgaggacat catccggctg tgggaccaga gcctgaagcc ctgcgtgaag	360
ctgaccctc tgtgcgtgac cctggaatgc cggaacgtgc gcaacgtgtc cagcaacggc	420
acctacaata tcatccacaa cgagacatac aaagagatga agaactgcag cttcaacgct	480

accaccgtgg	tcgaggaccg	gaagcagaag	gtgcacgccc	tgttttaccg	gctggacatc	540
gtgcccctgg	acgagaacaa	cagcagcgag	aagtcctccg	agaacagctc	cgagtactac	600
agactgatca	actgcaacac	cagcgccatc	acccaggcct	gccccaaagg	gtccttcgac	660
cctatcccca	tccactactg	cgcccctgcc	ggctacgcca	tcctgaagtg	caacaacaag	720
accttcaatg	gcaccggccc	ctgcaacaat	gtgtccaccg	tgcagtgcac	ccacggcatc	780
aagcccgtgg	tgtctaccca	gctgctgctg	aacggcagcc	tggccgagga	agagatcatc	840
atcagaagcg	agaacctgac	caacaacgcc	aagacaatca	tcgtccacct	gaacgaaacc	900
gtgaacatca	cctgtaccgg	gcctaacaac	aacaccggga	agtccatccg	gatcggccct	960
ggccagacct	tttacgccac	cggcgatatt	atcggcgaca	tccggcaggc	ccactgcaat	1020
ctgagccggg	acggctggaa	caagacactg	cagggcgcta	agaagaagct	ggccgaacac	1080
ttccccaaca	aaaccatcaa	cttcaccagc	tcctctggcg	gcgacctgga	aatcaccacc	1140
cacagcttta	actgcagagg	cgagttcttc	tactgcaata	cctccggcct	gttcaatgga	1200
acctacatgc	ccaacgggac	caacagcaac	tccagcagca	atatcaccct	gccttgccgg	1260
atcaagcaga	ttatcaatat	gtggcaggaa	gtgggcagag	ctatgtacgc	ccctccaatc	1320
gccggcaaca	tcacatgcag	aagcaacatt	accggcctgc	tgctcaccag	ggacggcggc	1380
tctaacaatg	gcgtgccaaa	cgacaccgag	acattcagac	ccggcgagg	cgacatgcgg	1440
aacaattggc	ggagcgagct	gtacaagtac	aaggtggtgg	aagtgaagcc	cctgggcgtg	1500
gcccttaccg	aagccaagag	aagagtggtc	gaacgcgaga	agcgggccgt	gggcattgga	1560
gccgtgtttc	tgggaatcct	gggagccgct	ggcagcacca	tgggcgctgc	ctctatcaca	1620
ctgacagtgc	aggccagaca	gctcctgagc	ggcatcgtgc	agcagcagag	caacctgctg	1680
agagccatcg	aggcacagca	gcacatgctg	cagctgaccg	tgtggggcat	taagcagctc	1740
cagacacggg	tgctggccat	tgagagatac	ctgcaggatc	agcagctgct	cggcctgtgg	1800
ggctgtagcg	gcaagctgat	ctgtaccacc	gccgtgcctt	ggaacacctc	ctggtccaac	1860
aagagccaga	ccgacatctg	ggacaacatg	acctggatgc	agtgggacaa	agaaatcggc	1920
aactataccg	gcgagatcta	ccgactgctg	gaagagtccc	agaaccagca	ggaaaagaac	1980
gagaaggacc	tgctggccct	ggacagctgg	aaaaatctgt	ggaattggtt	cgacatcacc	2040
aactggctgt	ggtacatcaa	gatcttcata	atgatcgtgg	gcggcctgat	cggcctgcgg	2100
atcatctttg	ccgtgctgag	catcgtgaac	cgcgtgcggc	agggctac		2148

<210> 36

<211> 724

<212> PRT

<213> Artificial Sequence

<220>

<223> mosaic Env trimer sequence

<400> 36

Met Arg Val Arg Gly Ile Gln Arg Asn Cys Gln His Leu Trp Arg Trp
1 5 10 15

Gly Thr Leu Ile Leu Gly Met Leu Met Ile Cys Ser Ala Ala Gly Lys
20 25 30

Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr
35 40 45

Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val
50 55 60

His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro
65 70 75 80

Gln Glu Val Val Leu Glu Asn Val Thr Glu Asn Phe Asn Met Trp Lys
85 90 95

Asn Asn Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp
100 105 110

Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu
115 120 125

Asn Cys Thr Asp Asp Val Arg Asn Val Thr Asn Asn Ala Thr Asn Thr
130 135 140

Asn Ser Ser Trp Gly Glu Pro Met Glu Lys Gly Glu Ile Lys Asn Cys
145 150 155 160

Ser Phe Asn Ile Thr Thr Ser Ile Arg Asn Lys Val Gln Lys Gln Tyr
165 170 175

Ala Leu Phe Tyr Lys Leu Asp Val Val Pro Ile Asp Asn Asp Ser Asn
180 185 190

Asn Thr Asn Tyr Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln
195 200 205

Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala
210 215 220

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asp Lys Lys Phe Asn Gly
225 230 235 240

Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile

			245					250					255				
Arg	Pro	Val	Val	Ser	Thr	Gln	Leu	Leu	Leu	Asn	Gly	Ser	Leu	Ala	Glu		
			260					265					270				
Glu	Glu	Val	Val	Ile	Arg	Ser	Glu	Asn	Phe	Thr	Asn	Asn	Ala	Lys	Thr		
			275				280					285					
Ile	Met	Val	Gln	Leu	Asn	Val	Ser	Val	Glu	Ile	Asn	Cys	Thr	Arg	Pro		
			290				295					300					
Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	His	Ile	Gly	Pro	Gly	Arg	Ala	Phe		
					310					315					320		
Tyr	Thr	Ala	Gly	Asp	Ile	Ile	Gly	Asp	Ile	Arg	Gln	Ala	His	Cys	Asn		
				325					330					335			
Ile	Ser	Arg	Ala	Asn	Trp	Asn	Asn	Thr	Leu	Arg	Gln	Ile	Val	Glu	Lys		
			340					345					350				
Leu	Gly	Lys	Gln	Phe	Gly	Asn	Asn	Lys	Thr	Ile	Val	Phe	Asn	His	Ser		
			355				360					365					
Ser	Gly	Gly	Asp	Pro	Glu	Ile	Val	Met	His	Ser	Phe	Asn	Cys	Gly	Gly		
			370				375					380					
Glu	Phe	Phe	Tyr	Cys	Asn	Ser	Thr	Lys	Leu	Phe	Asn	Ser	Thr	Trp	Thr		
					390					395					400		
Trp	Asn	Asn	Ser	Thr	Trp	Asn	Asn	Thr	Lys	Arg	Ser	Asn	Asp	Thr	Glu		
				405					410					415			
Glu	His	Ile	Thr	Leu	Pro	Cys	Arg	Ile	Lys	Gln	Ile	Ile	Asn	Met	Trp		
			420					425					430				
Gln	Glu	Val	Gly	Lys	Ala	Met	Tyr	Ala	Pro	Pro	Ile	Arg	Gly	Gln	Ile		
			435				440					445					
Arg	Cys	Ser	Ser	Asn	Ile	Thr	Gly	Leu	Leu	Leu	Thr	Arg	Asp	Gly	Gly		
			450				455					460					
Asn	Asp	Thr	Ser	Gly	Thr	Glu	Ile	Phe	Arg	Pro	Gly	Gly	Gly	Asp	Met		
					470					475					480		
Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys	Tyr	Lys	Val	Val	Lys	Ile		
				485					490					495			
Glu	Pro	Leu	Gly	Val	Ala	Pro	Thr	Lys	Ala	Lys	Glu	Arg	Val	Val	Glu		

500

505

510

Arg Glu Glu Arg Ala Val Gly Ile Gly Ala Val Phe Leu Gly Phe Leu
 515 520 525

Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val
 530 535 540

Gln Ala Arg Leu Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
 545 550 555 560

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
 565 570 575

Gly Ile Lys Gln Leu Gln Ala Arg Val Leu Ala Val Glu Arg Tyr Leu
 580 585 590

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
 595 600 605

Cys Thr Thr Thr Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
 610 615 620

Asp Lys Ile Trp Asn Asn Met Thr Trp Met Glu Trp Glu Arg Glu Ile
 625 630 635 640

Asn Asn Tyr Thr Ser Leu Ile Tyr Thr Leu Ile Glu Glu Ser Gln Asn
 645 650 655

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
 660 665 670

Ser Leu Trp Asn Trp Phe Asp Ile Ser Asn Trp Leu Trp Tyr Ile Lys
 675 680 685

Ser Arg Ile Glu Gly Arg Gly Ser Gly Gly Tyr Ile Pro Glu Ala Pro
 690 695 700

Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu
 705 710 715 720

Ser Thr Phe Leu

<210> 37

<211> 28

<212> PRT

<213> Artificial Sequence

<220>

<223> Residues 655-682 of SEQ ID NO:18

<400> 37

Asn	Glu	Lys	Asp	Leu	Leu	Ala	Leu	Asp	Ser	Trp	Asn	Asn	Leu	Trp	Asn
1				5					10					15	

Trp	Phe	Ser	Ile	Ser	Lys	Trp	Leu	Trp	Tyr	Ile	Lys
			20					25			