

SEQUENCE LISTING

<110> Janssen Vaccines & Prevention B.V.
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 Langedijk, Johannes P.M.

<120> Trimer Stabilizing HIV Envelope Protein Mutations

<130> 0276 WO 00 ORD

<150> EP16188866.4
 <151> 2016-09-15

<160> 34

<170> PatentIn version 3.5

<210> 1
 <211> 856
 <212> PRT
 <213> HIV-1

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 <221> misc_feature
 <223> gp160 of HIV-1 isolate HXB2

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Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
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Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
 35 40 45

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

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

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

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

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

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

Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn
 645 650 655
 Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp
 660 665 670
 Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met Ile
 675 680 685
 Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Ile
 690 695 700
 Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His
 705 710 715 720
 Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu
 725 730 735
 Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser
 740 745 750
 Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr
 755 760 765
 His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile Val Glu Leu
 770 775 780
 Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp Trp Asn Leu Leu
 785 790 795 800
 Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn
 805 810 815
 Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val
 820 825 830
 Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile Pro Arg Arg Ile Arg
 835 840 845
 Gln Gly Leu Glu Arg Ile Leu Leu
 850 855

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 <212> PRT
 <213> Artificial Sequence

<220>

<223> HIV Env consensus clade C sequence

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

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

Pro Gln Glu Met Val Leu Glu Asn Val Thr Glu Asn Phe Asn Met Trp
50          55          60

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

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr
85          90          95

Leu Asn Cys Thr Asn Val Asn Val Thr Asn Thr Asn Asn Asn Asn Met
100         105         110

Lys Glu Glu Met Lys Asn Cys Ser Phe Asn Thr Thr Thr Glu Ile Arg
115         120         125

Asp Lys Lys Gln Lys Glu Tyr Ala Leu Phe Tyr Arg Leu Asp Ile Val
130         135         140

Pro Leu Asn Glu Asn Ser Ser Glu Tyr Arg Leu Ile Asn Cys Asn Thr
145         150         155         160

Ser Thr Ile Thr Gln Ala Cys Pro Lys Val Ser Phe Asp Pro Ile Pro
165         170         175

Ile His Tyr Cys Ala Pro Ala Gly Tyr Ala Ile Leu Lys Cys Asn Asn
180         185         190

Lys Thr Phe Asn Gly Thr Gly Pro Cys Asn Asn Val Ser Thr Val Gln
195         200         205

Cys Thr His Gly Ile Lys Pro Val Val Ser Thr Gln Leu Leu Leu Asn
210         215         220

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

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Asp Asn Ala Lys Thr Ile Ile Val His Leu Asn Glu Ser Val Glu Ile
245 250 255

Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Arg Ile Gly
260 265 270

Pro Gly Gln Thr Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile Arg
275 280 285

Gln Ala His Cys Asn Ile Ser Glu Ala Lys Trp Asn Lys Thr Leu Gln
290 295 300

Arg Val Lys Lys Lys Leu Lys Glu His Phe Pro Asn Lys Thr Ile Lys
305 310 315 320

Phe Ala Pro Ser Ser Gly Gly Asp Leu Glu Ile Thr Thr His Ser Phe
325 330 335

Asn Cys Arg Gly Glu Phe Phe Tyr Cys Asn Thr Ser Lys Leu Phe Asn
340 345 350

Ser Thr Tyr Asn Asn Thr Thr Ser Asn Ser Thr Ile Thr Leu Pro Cys
355 360 365

Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Arg Ala Met
370 375 380

Tyr Ala Pro Pro Ile Ala Gly Asn Ile Thr Cys Lys Ser Asn Ile Thr
385 390 395 400

Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Asn Asn Asn Asn Thr Glu
405 410 415

Thr Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu
420 425 430

Leu Tyr Lys Tyr Lys Val Val Glu Ile Lys Pro Leu Gly Ile Ala Pro
435 440 445

Thr Lys Ala Lys Arg Arg Val Val Glu Arg Glu Lys Arg Arg Ala Val
450 455 460

Gly Ile Gly Ala Val Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr
465 470 475 480

Met Gly Ala Ala Ser Ile Thr Leu Thr Val Gln Ala Arg Gln Leu Leu

485

490

495

Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Glu Ala
500 505 510

Gln Gln His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
515 520 525

Ala Arg Val Leu Ala Ile Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu
530 535 540

Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro
545 550 555 560

Trp Asn Ser Ser Trp Ser Asn Lys Ser Gln Glu Asp Ile Trp Asp Asn
565 570 575

Met Thr Trp Met Gln Trp Asp Arg Glu Ile Ser Asn Tyr Thr Asp Thr
580 585 590

Ile Tyr Arg Leu Leu Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu
595 600 605

Lys Asp Leu Leu Ala Leu Asp
610 615

<210> 3
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<223> ConC_SOSIP sequence

<400> 3

Asn Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
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Lys Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Glu Lys Glu
20 25 30

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

Pro Gln Glu Met Val Leu Glu Asn Val Thr Glu Asn Phe Asn Met Trp
50 55 60

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

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr
 85 90 95

Leu Asn Cys Thr Asn Val Asn Val Thr Asn Thr Asn Asn Asn Asn Met
 100 105 110

Lys Glu Glu Met Lys Asn Cys Ser Phe Asn Thr Thr Thr Glu Ile Arg
 115 120 125

Asp Lys Lys Gln Lys Glu Tyr Ala Leu Phe Tyr Arg Leu Asp Ile Val
 130 135 140

Pro Leu Asn Glu Asn Ser Ser Glu Tyr Arg Leu Ile Asn Cys Asn Thr
 145 150 155 160

Ser Thr Ile Thr Gln Ala Cys Pro Lys Val Ser Phe Asp Pro Ile Pro
 165 170 175

Ile His Tyr Cys Ala Pro Ala Gly Tyr Ala Ile Leu Lys Cys Asn Asn
 180 185 190

Lys Thr Phe Asn Gly Thr Gly Pro Cys Asn Asn Val Ser Thr Val Gln
 195 200 205

Cys Thr His Gly Ile Lys Pro Val Val Ser Thr Gln Leu Leu Leu Asn
 210 215 220

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

Asp Asn Ala Lys Thr Ile Ile Val His Leu Asn Glu Ser Val Glu Ile
 245 250 255

Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Arg Ile Gly
 260 265 270

Pro Gly Gln Thr Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile Arg
 275 280 285

Gln Ala His Cys Asn Ile Ser Glu Ala Lys Trp Asn Lys Thr Leu Gln
 290 295 300

Arg Val Lys Lys Lys Leu Lys Glu His Phe Pro Asn Lys Thr Ile Lys
 305 310 315 320

Phe Ala Pro Ser Ser Gly Gly Asp Leu Glu Ile Thr Thr His Ser Phe

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

Asn Met Thr Trp Met Gln Trp Asp Arg Glu Ile Ser Asn Tyr Thr Asp
 580 585 590

Thr Ile Tyr Arg Leu Leu Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn
 595 600 605

Glu Lys Asp Leu Leu Ala Leu Asp
 610 615

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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HIV Env consensus Clade B sequence

<400> 4

Ala Glu Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys
 1 5 10 15

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

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

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

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

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

Val Thr Leu Asn Cys Thr Asp Leu Asn Asn Asn Thr Thr Asn Asn Asn
 100 105 110

Ser Ser Ser Glu Lys Met Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe
 115 120 125

Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys Glu Tyr Ala Leu
 130 135 140

Phe Tyr Lys Leu Asp Val Val Pro Ile Asp Asn Asn Asn Thr Ser Tyr
 145 150 155 160

Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys

Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu
405 410 415

Leu Thr Arg Asp Gly Gly Asn Asn Asn Asn Asn Thr Thr Glu Thr Phe
420 425 430

Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr
435 440 445

Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys
450 455 460

Cys Lys Arg Arg Val Val Gln Arg Arg Arg Arg Arg Arg Ala Val Gly
465 470 475 480

Ile Gly Ala Met Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met
485 490 495

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

Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Pro Glu Ala Gln
515 520 525

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

Arg Val Leu Ala Val Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly
545 550 555 560

Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Cys Thr Ala Val Pro Trp
565 570 575

Asn Thr Ser Trp Ser Asn Lys Ser Leu Asp Glu Ile Trp Asp Asn Met
580 585 590

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

Tyr Thr Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Gln
610 615 620

Glu Leu Leu Glu Leu Asp
625 630

<210> 5
<211> 630
<212> PRT
<213> Artificial Sequence

<220>
<223> ConB_SOSIP sequence

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Ala Glu Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys
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Glu Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp
20 25 30

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

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

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

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

Val Thr Leu Asn Cys Thr Asp Leu Asn Asn Asn Thr Thr Asn Asn Asn
100 105 110

Ser Ser Ser Glu Lys Met Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe
115 120 125

Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys Glu Tyr Ala Leu
130 135 140

Phe Tyr Lys Leu Asp Val Val Pro Ile Asp Asn Asn Asn Thr Ser Tyr
145 150 155 160

Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys
165 170 175

Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe
180 185 190

Ala Ile Leu Lys Cys Asn Asp Lys Lys Phe Asn Gly Thr Gly Pro Cys
195 200 205

Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val
210 215 220

Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val
225 230 235 240

Ile	Arg	Ser	Glu	Asn	Phe	Thr	Asp	Asn	Ala	Lys	Thr	Ile	Ile	Val	Gln	
				245					250					255		
Leu	Asn	Glu	Ser	Val	Glu	Ile	Asn	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	
			260					265					270			
Arg	Lys	Ser	Ile	His	Ile	Gly	Pro	Gly	Arg	Ala	Phe	Tyr	Ala	Thr	Gly	
		275					280					285				
Asp	Ile	Ile	Gly	Asp	Ile	Arg	Gln	Ala	His	Cys	Asn	Ile	Ser	Arg	Thr	
	290					295					300					
Lys	Trp	Asn	Asn	Thr	Leu	Lys	Gln	Ile	Val	Lys	Lys	Leu	Arg	Glu	Gln	
305					310					315					320	
Phe	Gly	Asn	Lys	Thr	Ile	Val	Phe	Asn	Gln	Ser	Ser	Gly	Gly	Asp	Pro	
				325					330					335		
Glu	Ile	Val	Met	His	Ser	Phe	Asn	Cys	Gly	Gly	Glu	Phe	Phe	Tyr	Cys	
			340					345					350			
Asn	Thr	Thr	Gln	Leu	Phe	Asn	Ser	Thr	Trp	Asn	Ser	Asn	Gly	Thr	Trp	
		355					360					365				
Asn	Asn	Thr	Thr	Gly	Asn	Asp	Thr	Ile	Thr	Leu	Pro	Cys	Arg	Ile	Lys	
	370					375					380					
Gln	Ile	Ile	Asn	Met	Trp	Gln	Glu	Val	Gly	Lys	Ala	Met	Tyr	Ala	Pro	
385					390					395					400	
Pro	Ile	Arg	Gly	Gln	Ile	Arg	Cys	Ser	Ser	Asn	Ile	Thr	Gly	Leu	Leu	
				405					410					415		
Leu	Thr	Arg	Asp	Gly	Gly	Asn	Asn	Asn	Asn	Asn	Thr	Thr	Glu	Thr	Phe	
			420					425					430			
Arg	Pro	Gly	Gly	Gly	Asp	Met	Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	
		435					440					445				
Lys	Tyr	Lys	Val	Val	Lys	Ile	Glu	Pro	Leu	Gly	Val	Ala	Pro	Thr	Lys	
	450					455					460					
Cys	Lys	Arg	Arg	Val	Val	Gln	Arg	Arg	Arg	Arg	Arg	Arg	Ala	Val	Gly	
465					470					475					480	
Ile	Gly	Ala	Met	Phe	Leu	Gly	Phe	Leu	Gly	Ala	Ala	Gly	Ser	Thr	Met	
				485					490					495		

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

Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Pro Glu Ala Gln
515 520 525

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

Arg Val Leu Ala Val Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly
545 550 555 560

Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Cys Thr Ala Val Pro Trp
565 570 575

Asn Thr Ser Trp Ser Asn Lys Ser Leu Asp Glu Ile Trp Asp Asn Met
580 585 590

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

Tyr Thr Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Gln
610 615 620

Glu Leu Leu Glu Leu Asp
625 630

<210> 6
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<213> Artificial Sequence

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<223> synthetic HIV envelope protein Mos2S Env C4 fragment

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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> 7
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Met Gly Asn Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys
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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 Arg 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 Cys 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 Asn 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 Cys
 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 Cys Lys Arg Arg Val Val Glu Arg Arg Arg
465 470 475 480

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

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

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

Arg Ala Pro Glu Ala Gln Gln His Met Leu Gln Leu Thr Val Trp Gly
530 535 540

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

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

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

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

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

Gln Glu Lys
625

<211> 631
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Mos1.Env sequence

<400> 8

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

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

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

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

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

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

Val Thr Leu Asn Cys Thr Asp Asp Val Arg Asn Val Thr Asn Asn Ala
 100 105 110

Thr Asn Thr Asn Ser Ser Trp Gly Glu Pro Met Glu Lys Gly Glu Ile
 115 120 125

Lys Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asn Lys Val Gln
 130 135 140

Lys Gln Tyr Ala Leu Phe Tyr Lys Leu Asp Val Val Pro Ile Asp Asn
 145 150 155 160

Asp Ser Asn Asn Thr Asn Tyr Arg Leu Ile Ser Cys Asn Thr Ser Val
 165 170 175

Ile Thr Gln Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His
 180 185 190

Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asp Lys Lys
 195 200 205

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

His Gly Ile Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser
225 230 235 240

Leu Ala Glu Glu Glu Val Val Ile Arg Ser Glu Asn Phe Thr Asn Asn
245 250 255

Ala Lys Thr Ile Met Val Gln Leu Asn Val Ser Val Glu Ile Asn Cys
260 265 270

Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile His Ile Gly Pro Gly
275 280 285

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

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

Val Glu Lys Leu Gly Lys Gln Phe Gly Asn Asn Lys Thr Ile Val Phe
325 330 335

Asn His Ser Ser Gly Gly Asp Pro Glu Ile Val Met His Ser Phe Asn
340 345 350

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

Thr Trp Thr Trp Asn Asn Ser Thr Trp Asn Asn Thr Lys Arg Ser Asn
370 375 380

Asp Thr Glu Glu His Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile
385 390 395 400

Asn Met Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Arg
405 410 415

Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg
420 425 430

Asp Gly Gly Asn Asp Thr Ser Gly Thr Glu Ile Phe Arg Pro Gly Gly
435 440 445

Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val
450 455 460

Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg

465 470 475 480

Val Val Gln Ser Glu Lys Ser Ala Val Gly Ile Gly Ala Val Phe Leu
485 490 495

Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Met Thr
500 505 510

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

Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu
530 535 540

Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Val Leu Ala Val Glu
545 550 555 560

Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly
565 570 575

Lys Leu Ile Cys Thr Thr Thr Val Pro Trp Asn Ala Ser Trp Ser Asn
580 585 590

Lys Ser Leu Asp Lys Ile Trp Asn Asn Met Thr Trp Met Glu Trp Glu
595 600 605

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

Ser Gln Asn Gln Gln Glu Lys
625 630

```
<210> 9
<211> 630
<212> PRT
<213> Artificial Sequence
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<220>
<223> Mos2.Env sequence

<400> 9

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

Glu 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 Met Val Leu Glu 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 Arg
65 70 75 80

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

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

Val Trp Gly Ile Lys Gln Leu Gln Thr Arg Val Leu Ala Ile Glu Arg
545 550 555 560

Tyr Leu Gln Asp Gln Gln Leu Leu Gly Leu Trp Gly Cys Ser Gly Lys
565 570 575

Leu Ile Cys Thr Thr Ala Val Pro Trp Asn Thr Ser Trp Ser Asn Lys
580 585 590

Ser Gln Thr Asp Ile Trp Asp Asn Met Thr Trp Met Gln Trp Asp Lys
595 600 605

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

Gln Asn Gln Gln Glu Lys
625 630

<210> 10
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> furin cleavage site mutant sequence

<400> 10

Arg Arg Arg Arg Arg Arg
1 5

<210> 11
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> signal sequence

<400> 11

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

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

<210> 12
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> example of 8 amino acid sequence that can replace HR1 loop

<400> 12

Asn Pro Asp Trp Leu Pro Asp Met
1 5

<210> 13

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> example of 8 amino acid sequence that can replace HR1 loop

<400> 13

Gly Ser Gly Ser Gly Ser Gly Ser
1 5

<210> 14

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> example of 8 amino acid sequence that can replace HR1 loop

<400> 14

Asp Asp Val His Pro Asp Trp Asp
1 5

<210> 15

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> example of 8 amino acid sequence that can replace HR1 loop

<400> 15

Arg Asp Thr Phe Ala Leu Met Met
1 5

<210> 16

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> example of 8 amino acid sequence that can replace HR1 loop

<400> 16

Asp Glu Glu Lys Val Met Asp Phe
1 5

<210> 17
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> example of 8 amino acid sequence that can replace HR1 loop

<400> 17

Asp Glu Asp Pro His Trp Asp Pro
 1 5

<210> 18
 <211> 29
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> signal sequence

<400> 18

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

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

<210> 19
 <211> 61
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> tag sequence

<400> 19

Ala Ala Ala Leu Pro Glu Thr Gly Gly Gly Ser Asp Tyr Lys Asp Asp
 1 5 10 15

Asp Asp Lys Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 35 40 45

Gly Ser Gly Gly Gly Gly Ser His His His His His His
 50 55 60

<210> 20
 <211> 616
 <212> PRT
 <213> Artificial Sequence

<220>

<223> stabilized ConC_SOSIP Env protein (HIV160544)

<400> 20

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

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

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

Pro	Gln	Glu	Met	Val	Leu	Glu	Asn	Val	Thr	Glu	Asn	Phe	Asn	Met	Trp
	50					55					60				

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

Asp	Gln	Ser	Leu	Lys	Pro	Cys	Val	Lys	Leu	Thr	Pro	Leu	Cys	Val	Thr
				85					90					95	

Leu	Asn	Cys	Thr	Asn	Val	Asn	Val	Thr	Asn	Thr	Asn	Asn	Asn	Asn	Met
			100					105					110		

Lys	Glu	Glu	Met	Lys	Asn	Cys	Ser	Phe	Asn	Thr	Thr	Thr	Glu	Ile	Arg
		115					120						125		

Asp	Lys	Lys	Gln	Lys	Glu	Tyr	Ala	Leu	Phe	Tyr	Arg	Leu	Asp	Ile	Val
	130					135					140				

Pro	Leu	Asn	Glu	Asn	Ser	Ser	Glu	Tyr	Arg	Leu	Ile	Asn	Cys	Asn	Thr
145					150					155					160

Ser	Thr	Ile	Thr	Gln	Ile	Cys	Pro	Lys	Val	Ser	Phe	Asp	Pro	Ile	Pro
				165					170					175	

Ile	His	Tyr	Cys	Ala	Pro	Ala	Gly	Tyr	Ala	Ile	Leu	Lys	Cys	Asn	Asn
			180					185					190		

Lys	Thr	Phe	Asn	Gly	Thr	Gly	Pro	Cys	Asn	Asn	Val	Ser	Thr	Val	Gln
		195					200					205			

Cys	Thr	His	Gly	Ile	Lys	Pro	Val	Val	Ser	Thr	Gln	Leu	Leu	Leu	Asn
	210					215					220				

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

Asp Asn Ala Lys Thr Ile Ile Val His Leu Asn Glu Ser Val Glu Ile
245 250 255

Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Arg Ile Gly
260 265 270

Pro Gly Gln Thr Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile Arg
275 280 285

Gln Ala His Cys Asn Ile Ser Glu Ala Lys Trp Asn Lys Thr Leu Gln
290 295 300

Arg Val Lys Lys Lys Leu Lys Glu His Phe Pro Asn Lys Thr Ile Lys
305 310 315 320

Phe Ala Pro Ser Ser Gly Gly Asp Leu Glu Ile Thr Thr His Ser Phe
325 330 335

Asn Cys Arg Gly Glu Phe Phe Tyr Cys Asn Thr Ser Lys Leu Phe Asn
340 345 350

Ser Thr Tyr Asn Asn Thr Thr Ser Asn Ser Thr Ile Thr Leu Pro Cys
355 360 365

Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Arg Ala Met
370 375 380

Tyr Ala Pro Pro Ile Ala Gly Asn Ile Thr Cys Lys Ser Asn Ile Thr
385 390 395 400

Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Asn Asn Asn Asn Thr Glu
405 410 415

Thr Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu
420 425 430

Leu Tyr Lys Tyr Lys Val Val Glu Ile Lys Pro Leu Gly Ile Ala Pro
435 440 445

Thr Lys Cys Lys Arg Arg Val Val Glu Arg Arg Arg Arg Arg Ala
450 455 460

Val Gly Ile Gly Ala Val Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser
465 470 475 480

Thr Met Gly Ala Ala Ser Asn Thr Leu Thr Val Gln Ala Arg Gln Leu

485

490

495

Leu Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Pro Glu
500 505 510

Ala Gln Gln His Met Leu Gln Leu Thr Val Trp Gly Phe Lys Gln Leu
515 520 525

Gln Ala Arg Val Leu Ala Ile Glu Arg Tyr Leu Glu Val Gln Gln Leu
530 535 540

Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Cys Thr Ala Val
545 550 555 560

Pro Trp Asn Ser Ser Trp Ser Asn Lys Ser Gln Glu Asp Ile Trp Asp
565 570 575

Asn Met Thr Trp Met Gln Trp Asp Arg Glu Ile Ser Asn Tyr Thr Asp
580 585 590

Thr Ile Tyr Arg Leu Leu Glu Glu Ser Gln Phe Gln Gln Glu Ile Asn
595 600 605

Glu Lys Asp Leu Leu Ala Leu Asp
610 615

<210> 21
<211> 634
<212> PRT
<213> Artificial Sequence

<220>
<223> BG505_SOSIP Env protein (HIV150673)

<400> 21

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

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

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

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

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

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

Val Thr Leu Gln Cys Thr Asn Val Thr Asn Asn Ile Thr Asp Asp Met
 100 105 110

Arg Gly Glu Leu Lys Asn Cys Ser Phe Asn Met Thr Thr Glu Leu Arg
 115 120 125

Asp Lys Lys Gln Lys Val Tyr Ser Leu Phe Tyr Arg Leu Asp Val Val
 130 135 140

Gln Ile Asn Glu Asn Gln Gly Asn Arg Ser Asn Asn Ser Asn Lys Glu
 145 150 155 160

Tyr Arg Leu Ile Asn Cys Asn Thr Ser Ala Ile Thr Gln Ala Cys Pro
 165 170 175

Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly
 180 185 190

Phe Ala Ile Leu Lys Cys Lys Asp Lys Lys Phe Asn Gly Thr Gly Pro
 195 200 205

Cys Pro Ser Val Ser Thr Val Gln Cys Thr His Gly Ile Lys Pro Val
 210 215 220

Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val
 225 230 235 240

Met Ile Arg Ser Glu Asn Ile Thr Asn Asn Ala Lys Asn Ile Leu Val
 245 250 255

Gln Phe Asn Thr Pro Val Gln Ile Asn Cys Thr Arg Pro Asn Asn Asn
 260 265 270

Thr Arg Lys Ser Ile Arg Ile Gly Pro Gly Gln Ala Phe Tyr Ala Thr
 275 280 285

Gly Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Val Ser Lys
 290 295 300

Ala Thr Trp Asn Glu Thr Leu Gly Lys Val Val Lys Gln Leu Arg Lys
 305 310 315 320

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

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

Asn Val Pro Trp Asn Ser Ser Trp Ser Asn Arg Asn Leu Ser Glu Ile
580 585 590

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

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

Lys Asn Glu Gln Asp Leu Leu Ala Leu Asp
625 630

<210> 22

<211> 634

<212> PRT

<213> Artificial Sequence

<220>

<223> stabilized BG505_SOSIP Env protein (HIV170863)

<400> 22

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

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

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

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

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

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

Val Thr Leu Gln Cys Thr Asn Val Thr Asn Asn Ile Thr Asp Asp Met
100 105 110

Arg Gly Glu Leu Lys Asn Cys Ser Phe Asn Met Thr Thr Glu Leu Arg
115 120 125

Asp Lys Lys Gln Lys Val Tyr Ser Leu Phe Tyr Arg Leu Asp Val Val
130 135 140

Gln Ile Asn Glu Asn Gln Gly Asn Arg Ser Asn Asn Ser Asn Lys Glu

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

Ala Met Tyr Ala Pro Pro Ile Gln Gly Val Ile Arg Cys Val Ser Asn
 405 410 415

Ile Thr Gly Leu Ile Leu Thr Arg Asp Gly Gly Ser Thr Asn Ser Thr
 420 425 430

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

Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val
 450 455 460

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

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

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

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

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

Gln Leu Gln Ala Arg Val Leu Ala Val Glu Arg Tyr Leu Arg Val Gln
 545 550 555 560

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

Asn Val Pro Trp Asn Ser Ser Trp Ser Asn Arg Asn Leu Ser Glu Ile
 580 585 590

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

Thr Gln Ile Ile Tyr Gly Leu Leu Glu Glu Ser Gln Phe Gln Gln Glu
 610 615 620

Ile Asn Glu Gln Asp Leu Leu Ala Leu Asp
 625 630

<210> 23
 <211> 619
 <212> PRT

<213> Artificial Sequence

<220>

<223> wt C97ZA_SOSIP Env protein with L535M and Q567K (HIV150673)

<400> 23

Asn	Met	Trp	Val	Thr	Val	Tyr	Tyr	Gly	Val	Pro	Val	Trp	Thr	Asp	Ala
1				5					10					15	

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

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

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

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

Asp	Gln	Ser	Leu	Lys	Pro	Cys	Val	Lys	Leu	Thr	Pro	Leu	Cys	Val	Thr
			85						90					95	

Leu	His	Cys	Thr	Asn	Ala	Thr	Phe	Lys	Asn	Asn	Val	Thr	Asn	Asp	Met
			100					105					110		

Asn	Lys	Glu	Ile	Arg	Asn	Cys	Ser	Phe	Asn	Thr	Thr	Thr	Glu	Ile	Arg
		115				120						125			

Asp	Lys	Lys	Gln	Gln	Gly	Tyr	Ala	Leu	Phe	Tyr	Arg	Pro	Asp	Ile	Val
	130					135					140				

Leu	Leu	Lys	Glu	Asn	Arg	Asn	Asn	Ser	Asn	Asn	Ser	Glu	Tyr	Ile	Leu
145					150					155					160

Ile	Asn	Cys	Asn	Ala	Ser	Thr	Ile	Thr	Gln	Ala	Cys	Pro	Lys	Val	Asn
			165						170					175	

Phe	Asp	Pro	Ile	Pro	Ile	His	Tyr	Cys	Ala	Pro	Ala	Gly	Tyr	Ala	Ile
			180					185					190		

Leu	Lys	Cys	Asn	Asn	Lys	Thr	Phe	Ser	Gly	Lys	Gly	Pro	Cys	Asn	Asn
		195					200						205		

Val	Ser	Thr	Val	Gln	Cys	Thr	His	Gly	Ile	Lys	Pro	Val	Val	Ser	Thr
	210					215					220				

Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Lys Glu Ile Ile Ile Arg
 225 230 235 240

Ser Glu Asn Leu Thr Asp Asn Val Lys Thr Ile Ile Val His Leu Asn
 245 250 255

Lys Ser Val Glu Ile Val Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys
 260 265 270

Ser Met Arg Ile Gly Pro Gly Gln Thr Phe Tyr Ala Thr Gly Asp Ile
 275 280 285

Ile Gly Asp Ile Arg Gln Ala Tyr Cys Asn Ile Ser Gly Ser Lys Trp
 290 295 300

Asn Glu Thr Leu Lys Arg Val Lys Glu Lys Leu Gln Glu Asn Tyr Asn
 305 310 315 320

Asn Asn Lys Thr Ile Lys Phe Ala Pro Ser Ser Gly Gly Asp Leu Glu
 325 330 335

Ile Thr Thr His Ser Phe Asn Cys Arg Gly Glu Phe Phe Tyr Cys Asn
 340 345 350

Thr Thr Arg Leu Phe Asn Asn Asn Ala Thr Glu Asp Glu Thr Ile Thr
 355 360 365

Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Gly Val Gly
 370 375 380

Arg Ala Met Tyr Ala Pro Pro Ile Ala Gly Asn Ile Thr Cys Lys Ser
 385 390 395 400

Asn Ile Thr Gly Leu Leu Leu Val Arg Asp Gly Gly Glu Asp Asn Lys
 405 410 415

Thr Glu Glu Ile Phe Arg Pro Gly Gly Gly Asn Met Lys Asp Asn Trp
 420 425 430

Arg Ser Glu Leu Tyr Lys Tyr Lys Val Ile Glu Leu Lys Pro Leu Gly
 435 440 445

Ile Ala Pro Thr Gly Cys Lys Arg Arg Val Val Glu Arg Arg Arg Arg
 450 455 460

Arg Arg Ala Val Gly Ile Gly Ala Val Phe Leu Gly Phe Leu Gly Ala
 465 470 475 480

Ala Gly Ser Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val Gln Ala
485 490 495

Arg Gln Leu Leu Ser Ser Ile Val Gln Gln Gln Ser Asn Leu Leu Arg
500 505 510

Ala Pro Glu Ala Gln Gln His Met Leu Lys Leu Thr Val Trp Gly Ile
515 520 525

Lys Gln Leu Gln Thr Arg Val Leu Ala Ile Glu Arg Tyr Leu Lys Asp
530 535 540

Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Cys
545 550 555 560

Thr Asn Val Pro Trp Asn Ser Ser Trp Ser Asn Lys Ser Gln Thr Asp
565 570 575

Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile Ser Asn
580 585 590

Tyr Thr Asp Thr Ile Tyr Arg Leu Leu Glu Asp Ser Gln Thr Gln Gln
595 600 605

Glu Lys Asn Glu Lys Asp Leu Leu Ala Leu Asp
610 615

<210> 24

<211> 619

<212> PRT

<213> Artificial Sequence

<220>

<223> repaired and stabilized C97ZA_SOSIP Env protein (HIV170690)

<400> 24

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

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

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

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

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

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

Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile Ser Asn
580 585 590

Tyr Thr Asp Thr Ile Tyr Arg Leu Leu Glu Asp Ser Gln Phe Gln Gln
595 600 605

Glu Ile Asn Glu Lys Asp Leu Leu Ala Asn Asp
610 615

<210> 25

<211> 628

<212> PRT

<213> Artificial Sequence

<220>

<223> variant of repaired and stabilized Du422 construct (HIV161818)

<400> 25

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

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

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

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

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

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr
85 90 95

Leu Asn Cys Lys Asn Val Asn Ile Ser Ala Asn Ala Asn Ala Thr Ala
100 105 110

Thr Leu Asn Ser Ser Met Asn Gly Glu Ile Lys Asn Cys Ser Phe Asn
115 120 125

Thr Thr Thr Glu Leu Arg Asp Lys Lys Gln Lys Val Tyr Ala Leu Phe
130 135 140

Tyr Lys Pro Asp Val Val Pro Leu Asn Gly Gly Glu His Asn Glu Thr
145 150 155 160

Gly	Glu	Tyr	Ile	Leu	Ile	Asn	Cys	Asn	Ser	Ser	Thr	Cys	Thr	Gln	Ala	
				165					170					175		
Cys	Pro	Lys	Val	Ser	Phe	Asp	Pro	Ile	Pro	Ile	His	Tyr	Cys	Ala	Pro	
			180					185					190			
Ala	Gly	Tyr	Ala	Ile	Leu	Lys	Cys	Asn	Asn	Lys	Thr	Phe	Asn	Gly	Thr	
		195					200					205				
Gly	Pro	Cys	Asn	Asn	Val	Ser	Thr	Val	Gln	Cys	Thr	His	Gly	Ile	Lys	
	210					215					220					
Pro	Val	Val	Ser	Thr	Gln	Leu	Leu	Leu	Asn	Gly	Ser	Leu	Ala	Glu	Glu	
225					230					235					240	
Glu	Ile	Ile	Ile	Arg	Ser	Glu	Asn	Leu	Thr	Asn	Asn	Ile	Lys	Thr	Ile	
				245					250					255		
Ile	Val	His	Leu	Asn	Lys	Ser	Val	Glu	Ile	Asn	Cys	Thr	Arg	Pro	Asn	
			260					265					270			
Asn	Asn	Thr	Arg	Lys	Ser	Val	Arg	Ile	Gly	Pro	Gly	Gln	Thr	Phe	Tyr	
		275					280					285				
Ala	Thr	Gly	Glu	Ile	Ile	Gly	Asp	Ile	Arg	Glu	Ala	His	Cys	Asn	Ile	
	290					295					300					
Ser	Arg	Glu	Thr	Trp	Asn	Ser	Thr	Leu	Ile	Gln	Val	Lys	Glu	Lys	Leu	
305					310					315					320	
Arg	Glu	His	Tyr	Asn	Lys	Thr	Ile	Lys	Phe	Glu	Pro	Ser	Ser	Gly	Gly	
				325					330					335		
Asp	Leu	Glu	Val	Thr	Thr	His	Ser	Phe	Asn	Cys	Arg	Gly	Glu	Phe	Phe	
			340					345					350			
Tyr	Cys	Asn	Thr	Thr	Lys	Leu	Phe	Asn	Glu	Thr	Lys	Leu	Phe	Asn	Glu	
		355					360					365				
Ser	Glu	Tyr	Val	Asp	Asn	Lys	Thr	Ile	Ile	Leu	Pro	Cys	Arg	Ile	Lys	
	370					375					380					
Gln	Ile	Ile	Asn	Met	Trp	Gln	Glu	Val	Gly	Arg	Cys	Met	Tyr	Ala	Pro	
385					390					395					400	
Pro	Ile	Glu	Gly	Asn	Ile	Thr	Cys	Lys	Ser	Asn	Ile	Thr	Gly	Leu	Leu	
				405					410					415		

Leu Thr Arg Asp Gly Gly Glu Asn Ser Thr Glu Glu Val Phe Arg Pro
420 425 430

Gly Gly Gly Asn Met Lys Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr
435 440 445

Lys Val Val Glu Ile Lys Pro Leu Gly Val Ala Pro Thr Lys Cys Lys
450 455 460

Arg Lys Asn Val Thr Arg Arg Arg Arg Arg Ala Val Gly Leu Gly
465 470 475 480

Ala Val Leu Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Ala
485 490 495

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

Val Gln Gln Gln Ser Asn Leu Pro Arg Ala Pro Glu Ala Gln Gln His
515 520 525

Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Thr Arg Val
530 535 540

Leu Ala Ile Glu Arg Tyr Leu Lys Val Gln Gln Leu Leu Gly Leu Trp
545 550 555 560

Gly Cys Ser Gly Lys Leu Ile Cys Cys Thr Ala Val Pro Trp Asn Ser
565 570 575

Ser Trp Ser Asn Lys Ser Leu Gly Asp Ile Trp Asp Asn Met Thr Trp
580 585 590

Met Gln Trp Asp Arg Glu Ile Ser Asn Tyr Thr Asn Thr Ile Tyr Arg
595 600 605

Leu Leu Glu Asp Ser Gln Phe Gln Gln Glu Lys Asn Glu Lys Asp Leu
610 615 620

Leu Ala Asn Asp
625

<210> 26
<211> 628
<212> PRT
<213> Artificial Sequence

<220>

<223> repaired and stabilized Du422_SOSIP Env protein (HIV170859)

<400> 26

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

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

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

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

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

Asp	Gln	Ser	Leu	Lys	Pro	Cys	Val	Lys	Leu	Thr	Pro	Leu	Cys	Val	Thr
				85					90					95	

Leu	Asn	Cys	Lys	Asn	Val	Asn	Ile	Ser	Ala	Asn	Ala	Asn	Ala	Thr	Ala
			100					105					110		

Thr	Leu	Asn	Ser	Ser	Met	Asn	Gly	Glu	Ile	Lys	Asn	Cys	Ser	Phe	Asn
		115					120					125			

Thr	Thr	Thr	Glu	Leu	Arg	Asp	Lys	Lys	Gln	Lys	Val	Tyr	Ala	Leu	Phe
	130					135					140				

Tyr	Lys	Pro	Asp	Val	Val	Pro	Leu	Asn	Gly	Gly	Glu	His	Asn	Glu	Thr
145					150					155					160

Gly	Glu	Tyr	Ile	Leu	Ile	Asn	Cys	Asn	Ser	Ser	Thr	Ile	Thr	Gln	Ala
				165					170					175	

Cys	Pro	Lys	Val	Ser	Phe	Asp	Pro	Ile	Pro	Ile	His	Tyr	Cys	Ala	Pro
			180					185					190		

Ala	Gly	Tyr	Ala	Ile	Leu	Lys	Cys	Asn	Asn	Lys	Thr	Phe	Asn	Gly	Thr
		195					200					205			

Gly	Pro	Cys	Asn	Asn	Val	Ser	Thr	Val	Gln	Cys	Thr	His	Gly	Ile	Lys
	210					215					220				

Pro	Val	Val	Ser	Thr	Gln	Leu	Leu	Leu	Asn	Gly	Ser	Leu	Ala	Glu	Glu
225					230					235					240

Glu Ile Ile Ile Arg Ser Glu Asn Leu Thr Asn Asn Ile Lys Thr Ile
 245 250 255

Ile Val His Leu Asn Lys Ser Val Glu Ile Asn Cys Thr Arg Pro Asn
 260 265 270

Asn Asn Thr Arg Lys Ser Val Arg Ile Gly Pro Gly Gln Thr Phe Tyr
 275 280 285

Ala Thr Gly Glu Ile Ile Gly Asp Ile Arg Glu Ala His Cys Asn Ile
 290 295 300

Ser Arg Glu Thr Trp Asn Ser Thr Leu Ile Gln Val Lys Glu Lys Leu
 305 310 315 320

Arg Glu His Tyr Asn Lys Thr Ile Lys Phe Glu Pro Ser Ser Gly Gly
 325 330 335

Asp Leu Glu Val Thr Thr His Ser Phe Asn Cys Arg Gly Glu Phe Phe
 340 345 350

Tyr Cys Asn Thr Thr Lys Leu Phe Asn Glu Thr Lys Leu Phe Asn Glu
 355 360 365

Ser Glu Tyr Val Asp Asn Lys Thr Ile Ile Leu Pro Cys Arg Ile Lys
 370 375 380

Gln Ile Ile Asn Met Trp Gln Glu Val Gly Arg Ala Met Tyr Ala Pro
 385 390 395 400

Pro Ile Glu Gly Asn Ile Thr Cys Lys Ser Asn Ile Thr Gly Leu Leu
 405 410 415

Leu Thr Arg Asp Gly Gly Glu Asn Ser Thr Glu Glu Val Phe Arg Pro
 420 425 430

Gly Gly Gly Asn Met Lys Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr
 435 440 445

Lys Val Val Glu Ile Lys Pro Leu Gly Val Ala Pro Thr Lys Cys Lys
 450 455 460

Arg Lys Val Val Gly Arg Arg Arg Arg Arg Arg Ala Val Gly Leu Gly
 465 470 475 480

Ala Val Leu Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Ala

485

490

495

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

Val Gln Gln Gln Ser Asn Leu Pro Arg Ala Pro Glu Ala Gln Gln His
 515 520 525

Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Thr Arg Val
 530 535 540

Leu Ala Ile Glu Arg Tyr Leu Glu Val Gln Gln Leu Leu Gly Leu Trp
 545 550 555 560

Gly Cys Ser Gly Lys Leu Ile Cys Cys Thr Ala Val Pro Trp Asn Ser
 565 570 575

Ser Trp Ser Asn Lys Ser Leu Gly Asp Ile Trp Asp Asn Met Thr Trp
 580 585 590

Met Gln Trp Asp Arg Glu Ile Ser Asn Tyr Thr Asn Thr Ile Tyr Arg
 595 600 605

Leu Leu Glu Asp Ser Gln Phe Gln Gln Glu Ile Asn Glu Lys Asp Leu
 610 615 620

Leu Ala Leu Asp
 625

<210> 27
 <211> 599
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> repaired and stabilized DS_sC4_SOSIP Env protein (HIV170686)

<400> 27

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 Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys
85 90 95

Val Thr Leu Asn Cys Arg Asn Val Arg Asn Val Glu Met Lys Asn Cys
100 105 110

Ser Phe Asn Ala Thr Thr Val Val Arg Asp Arg Lys Gln Lys Val His
115 120 125

Ala Leu Phe Tyr Arg Leu Asp Ile Val Pro Leu Asp Glu Asn Asn Ser
130 135 140

Ser Tyr Arg Leu Ile Asn Cys Asn Thr Ser Ala Cys Thr Gln Ile Cys
145 150 155 160

Pro Lys Val Ser Phe Asp Pro Ile Pro Ile His Tyr Cys Ala Pro Ala
165 170 175

Gly Tyr Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly
180 185 190

Pro Cys Asn Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Lys Pro
195 200 205

Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu
210 215 220

Ile Ile Ile Arg Ser Glu Asn Leu Thr Asn Asn Ala Lys Thr Ile Ile
225 230 235 240

Val His Leu Asn Glu Thr Val Asn Ile Asn Cys Thr Arg Pro Asn Asn
245 250 255

Asn Thr Arg Lys Ser Ile Arg Ile Gly Pro Gly Gln Thr Phe Tyr Ala
260 265 270

Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Leu Ser
275 280 285

Arg Asp Gly Trp Asn Lys Thr Leu Gln Gly Val Lys Lys Lys Leu Ala
290 295 300

Glu His Phe Pro Asn Lys Thr Ile Lys Phe Ala Pro His Ser Gly Gly

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

Lys Ser Gln Thr Asp Ile Trp Asp Asn Met Thr Trp Met Gln Trp Asp
565 570 575

Lys Glu Ile Gly Asn Tyr Thr Gly Glu Ile Tyr Arg Leu Leu Glu Glu
580 585 590

Ser Gln Phe Gln Gln Glu Ile
595

<210> 28
<211> 607
<212> PRT
<213> Artificial Sequence

<220>
<223> Stabilized ConC_SOSIP.v3 Env protein (HIV170654)

<400> 28

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

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

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

Pro Gln Glu Met Val Leu Glu Asn Val Thr Glu Asn Phe Asn Met Trp
50 55 60

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

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr
85 90 95

Leu Asn Cys Thr Asn Val Asn Val Thr Glu Met Lys Asn Cys Ser Phe
100 105 110

Asn Thr Thr Thr Glu Ile Arg Asp Lys Lys Gln Lys Glu Tyr Ala Leu
115 120 125

Phe Tyr Arg Leu Asp Ile Val Pro Leu Asn Glu Asn Ser Ser Glu Tyr
130 135 140

Arg Leu Ile Asn Cys Asn Thr Ser Thr Ile Thr Gln Ile Cys Pro Lys
145 150 155 160

Val Ser Phe Asp Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Tyr

165	170	175
Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys 180 185 190		
Asn Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Lys Pro Val Val 195 200 205		
Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Ile Ile 210 215 220		
Ile Arg Ser Glu Asn Leu Thr Asn Asn Val Lys Thr Ile Ile Val His 225 230 235 240		
Leu Asn Glu Ser Val Glu Ile Val Cys Thr Arg Pro Asn Asn Asn Thr 245 250 255		
Arg Lys Ser Ile Arg Ile Gly Pro Gly Gln Thr Phe Tyr Ala Thr Gly 260 265 270		
Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile Ser Glu Ala 275 280 285		
Lys Trp Asn Lys Thr Leu Gln Arg Val Lys Lys Lys Leu Lys Glu His 290 295 300		
Phe Pro Asn Lys Thr Ile Lys Phe Gln Pro Ser Ser Gly Gly Asp Leu 305 310 315 320		
Glu Ile Thr Thr His Ser Phe Asn Cys Arg Gly Glu Phe Phe Tyr Cys 325 330 335		
Asn Thr Ser Lys Leu Phe Asn Ser Thr Tyr Asn Asn Thr Thr Ser Asn 340 345 350		
Ser Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp 355 360 365		
Gln Glu Val Gly Arg Ala Met Tyr Ala Pro Pro Ile Ala Gly Asn Ile 370 375 380		
Thr Cys Lys Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly 385 390 395 400		
Asn Asn Asn Asn Asn Thr Glu Thr Phe Arg Pro Gly Gly Gly Asp Met 405 410 415		

Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Glu Ile
420 425 430

Lys Pro Leu Gly Ile Ala Pro Thr Lys Cys Lys Arg Arg Val Val Glu
435 440 445

Arg Arg Arg Arg Arg Arg Ala Val Gly Ile Gly Ala Val Phe Leu Gly
450 455 460

Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Asn Thr Leu
465 470 475 480

Thr Val Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Ser
485 490 495

Asn Leu Leu Arg Ala Pro Glu Ala Gln Gln His Met Leu Gln Leu Thr
500 505 510

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

Tyr Leu Glu Val Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys
530 535 540

Leu Ile Cys Cys Thr Ala Val Pro Trp Asn Ser Ser Trp Ser Asn Lys
545 550 555 560

Ser Gln Glu Asp Ile Trp Asp Asn Met Thr Trp Met Gln Trp Asp Arg
565 570 575

Glu Ile Ser Asn Tyr Thr Asp Thr Ile Tyr Arg Leu Leu Glu Glu Ser
580 585 590

Gln Phe Gln Gln Glu Ile Asn Glu Lys Asp Leu Leu Ala Leu Asp
595 600 605

<210> 29

<211> 634

<212> PRT

<213> Artificial Sequence

<220>

<223> Stabilized BG505_SOSIP.v2 Env protein (HIV171814)

<400> 29

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

Asp Ala Glu Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Glu

20

25

30

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

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

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

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

Val Thr Leu Gln Cys Thr Asn Val Thr Asn Asn Ile Thr Asp Asp Met
 100 105 110

Arg Gly Glu Leu Lys Asn Cys Ser Phe Asn Met Thr Thr Glu Leu Arg
 115 120 125

Asp Lys Lys Gln Lys Val Tyr Ser Leu Phe Tyr Arg Leu Asp Val Val
 130 135 140

Gln Ile Asn Glu Asn Gln Gly Asn Arg Ser Asn Asn Ser Asn Lys Glu
 145 150 155 160

Tyr Arg Leu Ile Asn Cys Asn Thr Ser Ala Cys Thr Gln Ala Cys Pro
 165 170 175

Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly
 180 185 190

Phe Ala Ile Leu Lys Cys Lys Asp Lys Lys Phe Asn Gly Thr Gly Pro
 195 200 205

Cys Pro Ser Val Ser Thr Val Gln Cys Thr His Gly Ile Lys Pro Val
 210 215 220

Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val
 225 230 235 240

Met Ile Arg Ser Glu Asn Ile Thr Asn Asn Ala Lys Asn Ile Leu Val
 245 250 255

Gln Phe Asn Thr Pro Val Gln Ile Asn Cys Thr Arg Pro Asn Asn Asn
 260 265 270

Thr	Arg	Lys	Ser	Ile	Arg	Ile	Gly	Pro	Gly	Gln	Ala	Phe	Tyr	Ala	Thr
		275					280					285			
Gly	Asp	Ile	Ile	Gly	Asp	Ile	Arg	Gln	Ala	His	Cys	Asn	Val	Ser	Lys
	290					295					300				
Ala	Thr	Trp	Asn	Glu	Thr	Leu	Gly	Lys	Val	Val	Lys	Gln	Leu	Arg	Lys
305					310					315					320
His	Phe	Gly	Asn	Asn	Thr	Ile	Ile	Arg	Phe	Ala	Asn	Ser	Ser	Gly	Gly
			325						330					335	
Asp	Leu	Glu	Val	Thr	Thr	His	Ser	Phe	Asn	Cys	Gly	Gly	Glu	Phe	Phe
			340					345					350		
Tyr	Cys	Asn	Thr	Ser	Gly	Leu	Phe	Asn	Ser	Thr	Trp	Ile	Ser	Asn	Thr
		355					360					365			
Ser	Val	Gln	Gly	Ser	Asn	Ser	Thr	Gly	Ser	Asn	Asp	Ser	Ile	Thr	Leu
	370					375					380				
Pro	Cys	Arg	Ile	Lys	Gln	Ile	Ile	Asn	Met	Trp	Gln	Arg	Ile	Gly	Gln
385					390					395					400
Cys	Met	Tyr	Ala	Pro	Pro	Ile	Gln	Gly	Val	Ile	Arg	Cys	Val	Ser	Asn
				405					410					415	
Ile	Thr	Gly	Leu	Ile	Leu	Thr	Arg	Asp	Gly	Gly	Ser	Thr	Asn	Ser	Thr
			420					425					430		
Thr	Glu	Thr	Phe	Arg	Pro	Gly	Gly	Gly	Asp	Met	Arg	Asp	Asn	Trp	Arg
		435					440					445			
Ser	Glu	Leu	Tyr	Lys	Tyr	Lys	Val	Val	Lys	Ile	Glu	Pro	Leu	Gly	Val
	450					455					460				
Ala	Pro	Thr	Arg	Cys	Lys	Arg	Arg	Val	Val	Gly	Arg	Arg	Arg	Arg	Arg
465					470					475					480
Arg	Ala	Val	Gly	Ile	Gly	Ala	Val	Phe	Leu	Gly	Phe	Leu	Gly	Ala	Ala
				485					490					495	
Gly	Ser	Thr	Met	Gly	Ala	Ala	Ser	Asn	Thr	Leu	Thr	Val	Gln	Ala	Arg
			500					505					510		
Asn	Leu	Leu	Ser	Gly	Ile	Val	Gln	Gln	Gln	Ser	Asn	Leu	Pro	Arg	Ala
							520					525			

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

Gln Leu Gln Ala Arg Val Leu Ala Val Glu Arg Tyr Leu Glu Val Gln
545 550 555 560

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

Asn Val Pro Trp Asn Ser Ser Trp Ser Asn Arg Asn Leu Ser Glu Ile
580 585 590

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

Thr Gln Ile Ile Tyr Gly Leu Leu Glu Glu Ser Gln Phe Gln Gln Glu
610 615 620

Ile Asn Glu Val Asp Leu Leu Ala Leu Asp
625 630

<210> 30

<211> 619

<212> PRT

<213> Artificial Sequence

<220>

<223> Repaired and stabilized C97ZA_SOSIP.v2 Env protein (HIV171810)

<400> 30

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

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

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

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

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

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr
85 90 95

Leu His Cys Thr Asn Ala Thr Phe Lys Asn Asn Val Thr Asn Asp Met
 100 105 110

Asn Lys Glu Ile Arg Asn Cys Ser Phe Asn Thr Thr Thr Glu Ile Arg
 115 120 125

Asp Lys Lys Gln Lys Val Tyr Ala Leu Phe Tyr Arg Leu Asp Ile Val
 130 135 140

Gln Leu Lys Glu Asn Arg Asn Asn Ser Asn Asn Ser Glu Tyr Arg Leu
 145 150 155 160

Ile Asn Cys Asn Thr Ser Thr Cys Thr Gln Ile Cys Pro Lys Val Thr
 165 170 175

Phe Asp Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Tyr Ala Ile
 180 185 190

Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Asn Asn
 195 200 205

Val Ser Thr Val Gln Cys Thr His Gly Ile Lys Pro Val Val Ser Thr
 210 215 220

Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Lys Glu Ile Ile Ile Arg
 225 230 235 240

Ser Glu Asn Leu Thr Asp Asn Val Lys Thr Ile Ile Val His Leu Asn
 245 250 255

Lys Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys
 260 265 270

Ser Ile Arg Ile Gly Pro Gly Gln Thr Phe Tyr Ala Thr Gly Asp Ile
 275 280 285

Ile Gly Asp Ile Arg Gln Ala Tyr Cys Asn Ile Ser Gly Ser Lys Trp
 290 295 300

Asn Glu Thr Leu Lys Arg Val Lys Glu Lys Leu Arg Glu His Phe Asn
 305 310 315 320

Asn Asn Lys Thr Ile Lys Phe Ala Pro Ser Ser Gly Gly Asp Leu Glu
 325 330 335

Ile Thr Thr His Ser Phe Asn Cys Arg Gly Glu Phe Phe Tyr Cys Asn
 340 345 350

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

Glu Ile Asn Glu Val Asp Leu Leu Ala Asn Asp
610 615

<210> 31
<211> 628
<212> PRT
<213> Artificial Sequence

<220>
<223> Repaired and stabilized Du422_SOSIP.v1 Env protein (HIV171812)

<400> 31

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

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

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

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

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

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr
85 90 95

Leu Asn Cys Lys Asn Val Asn Ile Ser Ala Asn Ala Asn Ala Thr Ala
100 105 110

Thr Leu Asn Ser Ser Met Asn Gly Glu Ile Lys Asn Cys Ser Phe Asn
115 120 125

Thr Thr Thr Glu Leu Arg Asp Lys Lys Gln Lys Val Tyr Ala Leu Phe
130 135 140

Tyr Lys Pro Asp Val Val Pro Leu Asn Gly Gly Glu His Asn Glu Thr
145 150 155 160

Gly Glu Tyr Ile Leu Ile Asn Cys Asn Ser Ser Thr Cys Thr Gln Ala
165 170 175

Cys Pro Lys Val Ser Phe Asp Pro Ile Pro Ile His Tyr Cys Ala Pro
180 185 190

Ala	Gly	Tyr	Ala	Ile	Leu	Lys	Cys	Asn	Asn	Lys	Thr	Phe	Asn	Gly	Thr
	195						200					205			
Gly	Pro	Cys	Asn	Asn	Val	Ser	Thr	Val	Gln	Cys	Thr	His	Gly	Ile	Lys
	210					215					220				
Pro	Val	Val	Ser	Thr	Gln	Leu	Leu	Leu	Asn	Gly	Ser	Leu	Ala	Glu	Glu
225					230					235				240	
Glu	Ile	Ile	Ile	Arg	Ser	Glu	Asn	Leu	Thr	Asn	Asn	Ile	Lys	Thr	Ile
				245					250					255	
Ile	Val	His	Leu	Asn	Lys	Ser	Val	Glu	Ile	Asn	Cys	Thr	Arg	Pro	Asn
			260					265					270		
Asn	Asn	Thr	Arg	Lys	Ser	Val	Arg	Ile	Gly	Pro	Gly	Gln	Thr	Phe	Tyr
		275					280					285			
Ala	Thr	Gly	Glu	Ile	Ile	Gly	Asp	Ile	Arg	Glu	Ala	His	Cys	Asn	Ile
	290					295					300				
Ser	Arg	Glu	Thr	Trp	Asn	Ser	Thr	Leu	Ile	Gln	Val	Lys	Glu	Lys	Leu
305					310					315					320
Arg	Glu	His	Tyr	Asn	Lys	Thr	Ile	Lys	Phe	Glu	Pro	Ser	Ser	Gly	Gly
				325					330					335	
Asp	Leu	Glu	Val	Thr	Thr	His	Ser	Phe	Asn	Cys	Arg	Gly	Glu	Phe	Phe
			340					345					350		
Tyr	Cys	Asn	Thr	Thr	Lys	Leu	Phe	Asn	Glu	Thr	Lys	Leu	Phe	Asn	Glu
		355					360					365			
Ser	Glu	Tyr	Val	Asp	Asn	Lys	Thr	Ile	Ile	Leu	Pro	Cys	Arg	Ile	Lys
	370					375					380				
Gln	Ile	Ile	Asn	Met	Trp	Gln	Glu	Val	Gly	Arg	Cys	Met	Tyr	Ala	Pro
385					390					395					400
Pro	Ile	Glu	Gly	Asn	Ile	Thr	Cys	Lys	Ser	Asn	Ile	Thr	Gly	Leu	Leu
				405					410					415	
Leu	Thr	Arg	Asp	Gly	Gly	Glu	Asn	Ser	Thr	Glu	Glu	Val	Phe	Arg	Pro
			420					425					430		
Gly	Gly	Gly	Asn	Met	Lys	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys	Tyr
		435					440					445			

Lys Val Val Glu Ile Lys Pro Leu Gly Val Ala Pro Thr Lys Cys Lys
450 455 460

Arg Lys Val Val Gly Arg Arg Arg Arg Arg Arg Arg Ala Val Gly Leu Gly
465 470 475 480

Ala Val Leu Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Ala
485 490 495

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

Val Gln Gln Gln Ser Asn Leu Pro Arg Ala Pro Glu Ala Gln Gln His
515 520 525

Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Thr Arg Val
530 535 540

Leu Ala Ile Glu Arg Tyr Leu Glu Val Gln Gln Leu Leu Gly Leu Trp
545 550 555 560

Gly Cys Ser Gly Lys Leu Ile Cys Cys Thr Ala Val Pro Trp Asn Ser
565 570 575

Ser Trp Ser Asn Lys Ser Leu Gly Asp Ile Trp Asp Asn Met Thr Trp
580 585 590

Met Gln Trp Asp Arg Glu Ile Ser Asn Tyr Thr Asn Thr Ile Tyr Arg
595 600 605

Leu Leu Glu Asp Ser Gln Phe Gln Gln Glu Ile Asn Glu Val Asp Leu
610 615 620

Leu Ala Leu Asp
625

<210> 32
<211> 599
<212> PRT
<213> Artificial Sequence

<220>
<223> Stabilized and repaired sC4_SOSIP.v4 Env protein

<400> 32

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

Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Leu Ser
275 280 285

Arg Asp Gly Trp Asn Lys Thr Leu Gln Gly Val Lys Lys Lys Leu Ala
290 295 300

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

Asp Leu Glu Ile Thr Thr His Ser Phe Asn Cys Arg Gly Glu Phe Phe
325 330 335

Tyr Cys Asn Thr Ser Asn Leu Phe Asn Glu Ser Asn Ile Glu Arg Asn
340 345 350

Asp Ser Ile Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met
355 360 365

Trp Gln Glu Val Gly Arg Cys Met Tyr Ala Pro Pro Ile Ala Gly Asn
370 375 380

Ile Thr Cys Arg Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly
385 390 395 400

Gly Ser Asn Asn Asn Asp Thr Glu Thr Phe Arg Pro Gly Gly Gly Asp
405 410 415

Met Arg Asn Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Glu
420 425 430

Val Lys Pro Leu Gly Val Ala Pro Thr Glu Cys Lys Arg Arg Asn Val
435 440 445

Thr Arg Arg Arg Arg Arg Arg Ala Val Gly Ile Gly Ala Val Phe Leu
450 455 460

Gly Ile Leu Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Asn Thr
465 470 475 480

Leu Thr Val Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln
485 490 495

Ser Asn Leu Pro Arg Ala Pro Glu Ala Gln Gln His Met Leu Gln Leu
500 505 510

Thr Val Trp Gly Ile Lys Gln Leu Gln Thr Arg Val Leu Ala Ile Glu

515

520

525

Arg Tyr Leu Glu Asp Gln Gln Leu Leu Gly Leu Trp Gly Cys Ser Gly
 530 535 540

Lys Leu Ile Cys Cys Thr Ala Val Pro Trp Asn Thr Ser Trp Ser Asn
 545 550 555 560

Lys Ser Gln Thr Asp Ile Trp Asp Asn Met Thr Trp Met Gln Trp Asp
 565 570 575

Lys Glu Ile Gly Asn Tyr Thr Gly Glu Ile Tyr Arg Leu Leu Glu Glu
 580 585 590

Ser Gln Phe Gln Gln Glu Ile
 595

<210> 33
 <211> 29
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> signal sequence

<400> 33

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> 34
 <211> 29
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> signal sequence

<400> 34

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

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