

SEQUENCE LISTING

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<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

<220>

<221> misc_feature

<223> gp160 of HIV-1 isolate HXB2

<400> 1

Met	Arg	Val	Lys	Glu	Lys	Tyr	Gln	His	Leu	Trp	Arg	Trp	Gly	Trp	Arg
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Trp	Gly	Thr	Met	Leu	Leu	Gly	Met	Leu	Met	Ile	Cys	Ser	Ala	Thr	Glu
			20					25					30		

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

Leu Lys Cys Thr Asp Leu Lys Asn Asp Thr Asn Thr Asn Ser Ser Ser
130 135 140

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

Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Phe Phe
165 170 175

Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp Thr Thr Ser Tyr Lys
180 185 190

Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
195 200 205

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

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

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

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

Arg Ser Val Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu

275

280

285

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

Lys Arg Ile Arg Ile Gln Arg Gly Pro Gly Arg Ala Phe Val Thr Ile
 305 310 315 320

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Asn Ile Ser Arg Ala
 325 330 335

Lys Trp Asn Asn Thr Leu Lys Gln Ile Ala Ser Lys Leu Arg Glu Gln
 340 345 350

Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp
 355 360 365

Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr
 370 375 380

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

<210> 2

<211> 615

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV Env consensus clade C sequence

<400> 2

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

<220>
<223> ConC_SOSIP sequence

<400> 3

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 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

<210> 4
<211> 630
<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
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

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

<220>
<223> ConB_SOSIP sequence

<400> 5

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

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
 <211> 625
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic HIV envelope protein Mos2S Env C4 fragment

<400> 6

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> 7
 <211> 627
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DS_sC4_SOSIP_E166R sequence

<400> 7

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	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

<210> 8
<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

<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

<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
 225 230 235 240

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 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 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 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 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

<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

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 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 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				