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

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

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

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

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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 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

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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 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

<400> 5

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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

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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
```

<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 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 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
```

<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
        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