SEQUENCE LISTING

<110> Janssen Vaccines & Prevention B.V.
Bavarian Nordic A/S

<120> POXVIRUS VECTORS ENCODING HIV ANTIGENS, AND METHODS OF USE THEREOF

<130> 688097-331WO
0291 WO 00 ORD
BN96PCT

<150> US 62/520,079
<151> 2017-06-15

<160> 46

<170> PatentIn version 3.5

<210> 1
<211> 500
<212> PRT
<213> Artificial Sequence

<220>
<223> mos1Gag mosaic antigen sequence

<400> 1

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

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

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

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

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

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

Thr Lys Glu Ala Leu Glu Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys

```
            100                 105                 110

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Lys Glu Gly His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn
            420                 425                 430

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

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

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

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

Pro Ser Ser Gln
            500
```

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

<220>
<223> mos2Gag mosaic antigen sequence

<400> 2

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


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


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


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


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


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


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


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


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


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


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


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


Ala Ala Met Gln Met Leu Lys Asp Thr Ile Asn Glu Glu Ala Ala Glu
```

```
        195                 200                 205

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

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

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

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

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

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

Gln Ala Thr Gln Asp Val Lys Asn Trp Met Thr Asp Thr Leu Leu Val
305                 310                 315                 320

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

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

Pro Ser His Lys Ala Arg Val Leu Ala Glu Ala Met Ser Gln Thr Asn
        355                 360                 365

Ser Thr Ile Leu Met Gln Arg Ser Asn Phe Lys Gly Ser Lys Arg Ile
    370                 375                 380

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

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

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

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

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

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

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

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

<220>
<223> mos1Pol mosaic antigen sequence

<400> 3

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys
225                 230                 235                 240

Trp Thr Val Gln Pro Ile Gln Leu Pro Glu Lys Asp Ser Trp Thr Val
                245                 250                 255

Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile
            260                 265                 270

Tyr Pro Gly Ile Lys Val Arg Gln Leu Cys Lys Leu Leu Arg Gly Ala
        275                 280                 285

Lys Ala Leu Thr Asp Ile Val Pro Leu Thr Glu Glu Ala Glu Leu Glu
    290                 295                 300

Leu Ala Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr
```

```
305                 310                 315                 320

Tyr Asp Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly His
                325                 330                 335

Asp Gln Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys
            340                 345                 350

Thr Gly Lys Tyr Ala Lys Met Arg Thr Ala His Thr Asn Asp Val Lys
        355                 360                 365

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ala Val Gln Met Ala Val Phe Ile His Asn Phe Lys Arg Lys Gly Gly
```

740 745 750

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

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

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

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

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

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

Glu Asp
850

<210> 4
<211> 850
<212> PRT
<213> Artificial Sequence

<220>
<223> mos2Pol mosaic antigen sequence

<400> 4

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

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

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

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

```
    50                  55                  60

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

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

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

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

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

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

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

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

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

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

Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys
225                 230                 235                 240

Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr Val
                245                 250                 255

Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile
            260                 265                 270
```

```
Tyr Ala Gly Ile Lys Val Lys Gln Leu Cys Lys Leu Leu Arg Gly Thr
        275                 280                 285

Lys Ala Leu Thr Glu Val Val Pro Leu Thr Glu Glu Ala Glu Leu Glu
    290                 295                 300

Leu Ala Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr
305                 310                 315                 320

Tyr Asp Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Gln
                325                 330                 335

Gly Gln Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys
            340                 345                 350

Thr Gly Lys Tyr Ala Arg Met Arg Gly Ala His Thr Asn Asp Val Lys
        355                 360                 365

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

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

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

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

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

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

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

Leu Gln Ala Ile His Leu Ala Leu Gln Asp Ser Gly Leu Glu Val Asn
```

```
                485                 490                 495

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

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

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

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

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

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

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

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

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

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

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

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

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

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


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


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


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


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


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


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


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


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


Glu Asp
    850
```

<210> 5
<211> 685
<212> PRT
<213> Artificial Sequence

<220>
<223> mos1Env mosaic antigen sequence

<400> 5

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asp Lys Lys Phe Asn Gly
```

```
225                 230                 235                 240

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
```

660 665 670

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

<210> 6
<211> 684
<212> PRT
<213> Artificial Sequence

<220>
<223> mos2Env mosaic antigen sequence

<400> 6

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

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

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

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

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

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

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

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

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

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

```
145                 150                 155                 160

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

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

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

Ala Ile Thr Gln Ala Cys Pro Lys Val Ser Phe Asp Pro Ile Pro Ile
    210                 215                 220

His Tyr Cys Ala Pro Ala Gly Tyr Ala Ile Leu Lys Cys Asn Asn Lys
225                 230                 235                 240

Thr Phe Asn Gly Thr Gly Pro Cys Asn Asn Val Ser Thr Val Gln Cys
                245                 250                 255

Thr His Gly Ile Lys Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly
            260                 265                 270

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ile Lys Gln Leu Gln Thr Arg Val Leu Ala Ile Glu Arg Tyr Leu Gln
```

```
            580                 585                 590

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

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

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

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

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

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

<210> 7
<211> 708
<212> PRT
<213> Artificial Sequence

<220>
<223> stabilized clade C gp140 trimer: C97ZA012-gp140-foldon with cleavage mutations

<400> 7

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Thr Phe Leu
705
```

<210> 8
<211> 625
<212> PRT
<213> Artificial Sequence

<220>
<223> C4 fragment: gp120-truncated gp41 without signal peptide and transmembrane domain

<400> 8

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


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


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


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


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


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


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


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


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


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


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

```
                165                 170                 175

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Trp Asp Asn Met Thr Trp Met Gln Trp Asp Lys Glu Ile Gly Asn Tyr
```

595 600 605

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

Lys
625

<210> 9
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> signal sequence

<400> 9

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

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

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

<220>
<223> signal sequence

<400> 10

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

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

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

<220>
<223> signal sequence

<400> 11

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

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

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

<220>
<223> signal sequence

<400> 12

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

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

<210> 13
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> transmembrane domain

<400> 13

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

Ala Val Leu Ser Ile Val
20

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

<220>
<223> truncated cytoplasmic region

<400> 14

Asn Arg Val Arg Gln Gly Tyr
1 5

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

<220>
<223> GCN4 trimerization domain

<400> 15

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

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

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

<220>
<223> foldon trimerization domain

<400> 16

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

Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu
20 25 30

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

<220>
<223> C4 sequence

<400> 17

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

```
1               5                   10                  15

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

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

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

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

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

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

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

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

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

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

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

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

Ala Ile Thr Gln Ala Cys Pro Lys Val Ser Phe Asp Pro Ile Pro Ile
    210                 215                 220
```

```
His Tyr Cys Ala Pro Ala Gly Tyr Ala Ile Leu Lys Cys Asn Asn Lys
225                 230                 235                 240

Thr Phe Asn Gly Thr Gly Pro Cys Asn Asn Val Ser Thr Val Gln Cys
                245                 250                 255

Thr His Gly Ile Lys Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly
            260                 265                 270

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

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

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

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

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

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

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

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

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

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

Pro Pro Ile Ala Gly Asn Ile Thr Cys Arg Ser Asn Ile Thr Gly Leu
```

```
        435                 440                 445

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 18

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

<220>
<223> C4D7 sequence

<400> 18

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

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

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

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

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

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

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

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

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

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

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

Arg Leu Asp Ile Val Pro Leu Asp Glu Asn Asn Ser Ser Glu Lys Ser

```
            180                 185                 190

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

Ala Ile Thr Gln Ala Cys Pro Lys Val Ser Phe Asp Pro Ile Pro Ile
    210                 215                 220

His Tyr Cys Ala Pro Ala Gly Tyr Ala Ile Leu Lys Cys Asn Asn Lys
225                 230                 235                 240

Thr Phe Asn Gly Thr Gly Pro Cys Asn Asn Val Ser Thr Val Gln Cys
                245                 250                 255

Thr His Gly Ile Lys Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly
            260                 265                 270

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Trp Asn Thr Ser Trp Ser Asn Lys Ser Gln Thr Asp Ile Trp Asp Asn
```

610 615 620

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

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

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

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

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

Asn Arg Val Arg Gln Gly Tyr
705 710

<210> 19
<211> 704
<212> PRT
<213> Artificial Sequence

<220>
<223> sC4 sequence

<400> 19

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

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

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

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

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

```
65                  70                  75                  80

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

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

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

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

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

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

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

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

Ala Ile Thr Gln Ala Cys Pro Lys Val Ser Phe Asp Pro Ile Pro Ile
    210                 215                 220

His Tyr Cys Ala Pro Ala Gly Tyr Ala Ile Leu Lys Cys Asn Asn Lys
225                 230                 235                 240

Thr Phe Asn Gly Thr Gly Pro Cys Asn Asn Val Ser Thr Val Gln Cys
                245                 250                 255

Thr His Gly Ile Lys Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly
            260                 265                 270

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Thr Glu Ala Lys Arg Arg Val Val Glu Arg Glu Glu Arg Ala Val
```

```
            500                 505                 510

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

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

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

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

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

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

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

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

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

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

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

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

<210> 20
<211> 4050
<212> DNA

<213> Artificial Sequence

<220>
<223> nucleotide sequence encoding mos1GagPol

<400> 20
atgggagcca gagccagcgt gctgtccgga ggggagctgg accgctggga gaagatcagg 60

ctgaggcctg gagggaagaa gaagtacagg ctgaagcaca tcgtgtgggc cagcagagag 120

ctggaacggt ttgccgtgaa ccctggcctg ctggaaacca gcgagggctg taggcagatt 180

ctgggacagc tgcagcccag cctgcagaca ggcagcgagg aactgcggag cctgtacaac 240

accgtggcca ccctgtactg cgtgcaccag cggatcgaga tcaaggacac caaagaagcc 300

ctggaaaaga tcgaggaaga gcagaacaag agcaagaaga aagcccagca ggctgccgct 360

gacacaggca acagcagcca ggtgtcccag aactacccca tcgtgcagaa catccaggga 420

cagatggtgc accaggccat cagccctcgg accctgaacg cctgggtgaa ggtggtggag 480

gaaaaggcct tcagccctga ggtgatcccc atgttctctg ccctgagcga gggagccaca 540

ccccaggacc tgaacaccat gctgaacacc gtgggagggc accaggctgc catgcagatg 600

ctgaaagaga caatcaacga ggaagctgcc gagtgggaca gggtccaccc agtgcacgct 660

ggacctatcg ctcctggcca gatgagagag cccagaggca gcgatattgc tggcaccacc 720

tccacactgc aggaacagat cggctggatg accaacaacc ctcccatccc tgtgggagag 780

atctacaagc ggtggatcat tctgggactg aacaagatcg tgcggatgta cagccctgtg 840

agcatcctgg acatcaggca gggacccaaa gagcccttca gggactacgt ggaccggttc 900

tacaagaccc tgagagccga gcaggccagc caggacgtga agaactggat gaccgagaca 960

ctgctggtgc agaacgccaa ccctgactgc aagaccatcc tgaaagccct gggacctgct 1020

gccaccctgg aagagatgat gacagcctgc cagggagtgg gaggacctgg ccacaaggcc 1080

agggtgctgg ccgaggccat gagccaggtg accaactctg ccaccatcat gatgcagaga 1140

ggcaacttcc ggaaccagag aaagaccgtg aagtgcttca actgtggcaa agagggacac 1200

attgccaaga actgcagggc tcccaggaag aaaggctgct ggaagtgcgg aaaagaaggc 1260

caccagatga aggactgcac cgagaggcag gccaacttcc tgggcaagat ctggcctagc 1320

aacaagggca ggcctggcaa cttcctgcag aacagacccg agcccaccgc tcctcccgag 1380

gaaagcttcc ggtttggcga ggaaaccacc acccctagcc agaagcagga acccatcgac 1440

aaagagatgt accctctggc cagcctgaag agcctgttcg gcaacgaccc cagcagccag 1500

atggctccca tcagcccaat cgagacagtg cctgtgaagc tgaagcctgg catggacgga 1560

cccagggtga agcagtggcc tctgaccgag gaaaagatca aagccctgac agccatctgc 1620

gaggaaatgg aaaaagaggg caagatcacc aagatcggac ccgagaaccc ctacaacacc 1680

cctgtgttcg ccatcaagaa gaaagacagc accaagtgga ggaaactggt ggacttcaga 1740

gagctgaaca agcggaccca ggacttctgg gaggtgcagc tgggcatccc tcaccctgct 1800

ggcctgaaga aaaagaaaag cgtgaccgtg ctggctgtgg gagatgccta cttcagcgtg 1860

cctctggacg agggcttccg gaagtacaca gccttcacca tccccagcac caacaacgag 1920

acacctggca tcagatacca gtacaacgtg ctgcctcagg gctggaaagg cagccctgcc 1980

atcttccagt gcagcatgac cagaatcctg gaacccttca gagccaagaa ccctgagatc 2040

gtgatctacc agtatatggc tgccctctac gtgggcagcg acctggaaat cggacagcac 2100

agagccaaaa tcgaagaact ccgcgagcac ctgctgaagt ggggattcac cacccctgac 2160

aagaagcacc agaaagagcc tcccttcctg tggatgggct acgagctgca ccctgacaag 2220

tggaccgtgc agcccatcca gctgccagag aaggactcct ggaccgtgaa cgacatccag 2280

aaactggtcg gcaagctgaa ctgggccagc cagatctacc ctggcatcaa agtcagacag 2340

ctgtgtaagc tgctgagggg agccaaagca ctgaccgaca tcgtgcctct gacagaagaa 2400

gccgagctgg aactggccga gaacagagag atcctgaaag aacccgtgca cggagtgtac 2460

tacgacccct ccaaggacct gattgccgag atccagaaac agggacacga ccagtggacc 2520

taccagatct atcaggaacc tttcaagaac ctgaaaacag gcaagtacgc caagatgcgg 2580

acagcccaca ccaacgacgt gaagcagctg accgaagccg tgcagaaaat cgccatggaa 2640

agcatcgtga tctggggaaa gacacccaag ttcaggctgc ccatccagaa agagacatgg 2700

gaaacctggt ggaccgacta ctggcaggcc acctggattc ccgagtggga gttcgtgaac 2760

accccacccc tggtgaagct gtggtatcag ctggaaaagg accctatcgc tggcgtggag 2820

acattctacg tggctggagc tgccaacaga gagacaaagc tgggcaaggc tggctacgtg 2880

accgacagag gcagacagaa aatcgtgagc ctgaccgaaa ccaccaacca gaaaacagcc 2940

ctgcaggcca tctatctggc actgcaggac agcggaagcg aggtgaacat cgtgacagcc 3000

agccagtatg ccctgggcat catccaggcc cagcctgaca agagcgagag cgagctggtg 3060

aaccagatca tcgagcagct gatcaagaaa gaacgggtgt acctgagctg ggtgccagcc 3120

cacaagggca tcggagggaa cgagcaggtg gacaagctgg tgtccagcgg aatccggaag 3180

gtgctgttcc tggacggcat cgataaagcc caggaagagc acgagaagta ccacagcaat 3240

tggagagcca tggccagcga cttcaacctg cctcccgtgg tggccaaaga aatcgtggcc 3300

agctgcgacc agtgccagct gaaaggcgag gccatgcacg gacaggtgga ctgctccct 3360

ggcatctggc agctggcatg cacccacctg gaaggcaaga tcattctggt ggccgtgcac 3420

gtggccagcg gatacatcga agccgaagtg atccctgccg agacagggca ggaaacagcc 3480

tacttcatcc tgaagctggc tggcagatgg cctgtgaagg tgatccacac agccaacggc 3540

agcaacttca cctctgctgc cgtgaaggct gcctgttggt gggctggcat tcagcaggaa 3600

tttggcatcc cctacaatcc ccagtctcag ggagtggtgg ccagcatgaa caaagagctg 3660

aagaagatca tcggacaggt cagggatcag gccgagcacc tgaaaactgc cgtccagatg 3720

gccgtgttca tccacaactt caagcggaag ggagggatcg gagggtactc tgctggcgag 3780

cggatcatcg acatcattgc caccgatatc cagaccaaag agctgcagaa acagatcatc 3840

aagatccaga acttcagggt gtactacagg gacagcaggg accccatctg gaagggacct 3900

gccaagctgc tgtggaaagg cgaaggagcc gtcgtcatcc aggacaacag cgacatcaag 3960

gtggtgccca gacggaaggt gaaaatcatc aaggactacg gcaaacagat ggctggagcc 4020

gactgtgtcg ctggcaggca ggacgaggac 4050

<210> 21
<211> 4023
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotide sequence encoding mos2GagPol

<400> 21
atgggagcca gagccagcat cctgcgagga gggaagctgg acaagtggga gaagatcagg 60

ctgaggcctg gagggaagaa acactacatg ctgaagcacc tggtctgggc cagcagagag 120

ctggaacggt ttgccctcaa tcctggcctg ctggaaacca gcgagggctg caagcagatc 180

atcaagcagc tgcagcctgc cctgcagaca ggcaccgagg aactgcggag cctgttcaac 240

accgtggcca ccctgtactg cgtgcatgcc gagatcgaag tgagggacac caaagaagcc 300

ctggacaaga tcgaggaaga gcagaacaag agccagcaga aaacccagca ggccaaagaa 360

gccgacggca aggtctccca gaactacccc atcgtgcaga acctgcaggg acagatggtg 420

caccagccca tcagccctcg gacactgaat gcctgggtga aggtgatcga ggaaaaggcc 480

ttcagccctg aggtgatccc catgttcaca gccctgagcg agggagccac accccaggac 540

ctgaacacca tgctgaacac cgtgggaggg caccaggctg ccatgcagat gctgaaggac 600

accatcaacg aggaagctgc cgagtgggac aggctgcacc ctgtgcacgc tggacctgtg 660

gctcctggcc agatgagaga gcccagaggc agcgatattg ctggcaccac ctccaatctg 720

caggaacaga tcgcctggat gaccagcaac cctcccatcc ctgtgggaga catctacaag 780

cggtggatca tcctgggact gaacaagatc gtgcggatgt acagccctac ctccatcctg 840

gacatcaagc agggacccaa agagcctttc agggactacg tggaccggtt cttcaagacc 900

ctgagagccg agcaggccac ccaggacgtg aagaactgga tgaccgacac cctgctggtg 960

cagaacgcca accctgactg caagaccatc ctgagagccc tgggacctgg agccaccctg 1020

gaagagatga tgacagcctg ccagggagtg ggaggaccct ctcacaaggc tagggtgctg 1080

gccgaggcca tgagccagac caacagcacc atcctgatgc agcggagcaa cttcaagggc 1140

agcaagcgga tcgtgaagtg cttcaactgt ggcaaagagg gacacattgc cagaaactgt 1200

agggcaccca ggaagaaagg ctgctggaag tgcggaaaag aaggccacca gatgaaggac 1260

tgcaccgaga ggcaggccaa cttcctgggc aagatctggc ctagccacaa gggcagacct 1320

ggcaacttcc tgcagagcag acccgagccc accgctcctc cagccgagag cttccggttc 1380

gaggaaacca cccctgctcc caagcaggaa cctaaggaca gagagcctct gaccagcctg 1440

agaagcctgt tcggcagcga ccctctgagc cagatggctc ccatctcccc tatcgagaca 1500

gtgcctgtga agctgaagcc tggcatggac ggacccaagg tgaaacagtg gcctctgacc 1560

gaggaaaaga tcaaagccct ggtggagatc tgtaccgaga tggaaaaaga gggcaagatc 1620

agcaagatcg gacccgagaa cccctacaac acccctatct tcgccatcaa gaagaaagac 1680

agcaccaagt ggaggaaact ggtggacttc agagagctga acaagcggac ccaggacttc 1740

tgggaggtgc agctgggcat ccctcaccct gctggcctga agaaaaagaa aagcgtgacc 1800

gtgctggccg tgggagatgc ctacttcagc gtgcctctgg acgaggactt cagaaagtac 1860

acagccttca ccatccccag catcaacaac gagacacctg gcatcagata ccagtacaac 1920

gtgctgcctc agggatggaa gggctctcct gcaatcttcc agagcagcat gaccaagatc 1980

ctggaaccct tccggaagca gaaccctgac atcgtgatct accagtacat ggcagccctg 2040

tacgtcggca gcgacctgga aatcggacag caccggacca agatcgaaga actcaggcag 2100

cacctgctgc ggtggggatt caccacccct gacaagaagc accagaaaga gcctcccttc 2160

ctgtggatgg gctacgagct gcacccagac aagtggaccg tgcagcccat cgtgctgcct 2220

gagaaggact cctggaccgt gaacgacatc cagaaactgg tcggcaagct gaactgggcc 2280

agccagatct acgctggcat caaagtgaag cagctgtgta agctcctgag aggcaccaaa 2340

gccctgaccg aggtggtgcc actgacagag gaagccgagc tggaactggc cgagaacaga 2400

gagatcctga aagaacccgt gcacggagtg tactacgacc ccagcaagga cctgattgcc 2460

gagatccaga agcagggaca gggacagtgg acctaccaga tctaccagga acccttcaag 2520

aacctgaaaa caggcaagta cgccaggatg aggggagccc acaccaacga cgtcaaacag 2580

ctgaccgaag ccgtgcagaa gatcgccacc gagagcatcg tgatttgggg aaagacaccc 2640

aagttcaagc tgcccatcca gaaagagaca tgggaggcct ggtggaccga gtactggcag 2700

gccacctgga ttcccgagtg ggagttcgtg aacaccccac ccctggtgaa gctgtggtat 2760

cagctggaaa aagaacccat cgtgggagcc gagacattct acgtggctgg agctgccaac 2820

agagagacaa agctgggcaa ggctggctac gtgaccgaca gaggcaggca gaaagtggtg 2880

tccctgaccg ataccaccaa ccagaaaaca gccctgcagg ccatccacct ggctctgcag 2940

gactctggcc tggaagtgaa catcgtgaca gccagccagt atgccctggg catcattcag 3000

gcacagcctg acaagagcga gagcgagctg gtgtctcaga tcattgagca gctgatcaag 3060

aaagaaaagg tgtacctggc ctgggtgcca gcccacaagg ggatcggagg gaacgagcag 3120

gtggacaagc tggtgtccag gggcatccgg aaggtgctgt ttctggacgg catcgacaaa 3180

gcccaggaag agcacgagaa gtaccacagc aattggagag ccatggccag cgagttcaac 3240

ctgcctccca tcgtggccaa agaaatcgtg gcctcttgcg acaagtgcca gctgaaaggc 3300

gaggccattc acggacaggt ggactgcagc ccaggcatct ggcagctggc ctgcacccac 3360

ctggaaggca aggtgatcct ggtggccgtg cacgtggcct ctggatacat cgaagccgaa 3420

gtgatccctg ccgagacagg ccaggaaaca gcctacttcc tgctgaagct ggctggcagg 3480

tggcctgtga aaaccatcca cacagccaac ggcagcaact tcacctctgc caccgtgaag 3540

gctgcctgtt ggtgggctgg cattaagcag gaatttggca tcccctacaa ccctcagtct 3600

cagggagtgg tggcctccat caacaaagag ctgaagaaga tcatcggaca ggtcagggat 3660

caggccgagc atctgaaaac agccgtccag atggccgtgt tcatccacaa cttcaagcgg 3720

aagggaggga tcggagagta ctctgctggc gagaggatcg tggacattat cgccagcgat 3780

atccagacca aagaactgca gaagcagatc acaaagatcc agaacttcag ggtgtactac 3840

agggacagca gagatcccct gtggaaggga cctgccaagc tgctgtggaa aggcgaagga 3900

gccgtcgtca tccaggacaa cagcgacatc aaggtggtgc ccagacggaa ggccaagatc 3960

atcagagact acggcaaaca gatggctggc gacgactgcg tcgcctctag gcaggacgag 4020

gac 4023

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

<220>
<223> nucleotide sequence encoding mos1Env

<400> 22
atgcgggtga ccggcatccg gaagaactac cagcacctgt ggcggtgggg caccatgctg 60

ctgggcatcc tgatgatttg ctctgccgcc ggaaagctgt gggtgaccgt gtactacggc 120

gtgcccgtgt ggaaagaggc caccaccacc ctgttctgcg ccagcgacgc caaggcctac 180

gacaccgagg tgcacaacgt gtgggccacc cacgcctgcg tgcccaccga ccccaacccc 240

caggaagtgg tcctggaaaa cgtgaccgag aacttcaaca tgtggaagaa caacatggtg 300

gagcagatgc acgaggacat catcagcctg tgggaccaga gcctgaagcc ctgcgtgaag 360

ctgacccccc tgtgcgtgac cctgaactgc accgacgacg tgcggaacgt gaccaacaac 420

gccaccaaca ccaacagcag ctggggcgag cctatggaaa agggcgagat caagaactgc 480

agcttcaaca tcaccacctc catccggaac aaggtgcaga agcagtacgc cctgttctac 540

aagctggacg tggtgcccat cgacaacgac agcaacaaca ccaactaccg gctgatcagc 600

tgcaacacca gcgtgatcac ccaggcctgc cccaaggtgt ccttcgagcc catccccatc 660

cactactgcg cccctgccgg cttcgccatc ctgaagtgca acgacaagaa gttcaacggc 720

accggcccct gcaccaacgt gagcaccgtg cagtgcaccc acggcatccg gcccgtggtg 780

tccacccagc tgctgctgaa cggcagcctg gccgaggaag aggtggtgat cagaagcgag 840

aatttcacca acaatgccaa gaccatcatg gtgcagctga acgtgagcgt ggagatcaac 900

tgcacccggc ccaacaacaa cacccggaag agcatccaca tcggccctgg cagggccttc 960

tacacagccg gcgacatcat cggcgacatc cggcaggccc actgcaacat cagccgggcc 1020

aactggaaca acaccctgcg gcagatcgtg gagaagctgg gcaagcagtt cggcaacaac 1080

aagaccatcg tgttcaacca cagcagcggc ggagaccccg agatcgtgat gcacagcttc 1140

aactgtggcg gcgagttctt ctactgcaac agcaccaagc tgttcaacag cacctggacc 1200

tggaacaact ccacctggaa taacaccaag cggagcaacg acaccgaaga gcacatcacc 1260

ctgccctgcc ggatcaagca gattatcaat atgtggcagg aggtcggcaa ggccatgtac 1320

gcccctccca tccggggcca gatccggtgc agcagcaaca tcaccggcct gctgctgacc 1380

cgggacggcg gcaacgatac cagcggcacc gagatcttcc ggcctggcgg cggagatatg 1440

cgggacaact ggcggagcga gctgtacaag tacaaggtgg tgaagatcga gcccctgggc 1500

gtggctccca ccaaggccaa gcggcgggtg gtgcagagcg agaagagcgc cgtgggcatc 1560

ggcgccgtgt ttctgggctt cctgggagcc gccggaagca ccatgggagc cgccagcatg 1620

accctgaccg tgcaggcccg gctgctgctg tccggcatcg tgcagcagca gaacaacctg 1680

ctccgggcca tcgaggccca gcagcacctg ctgcagctga ccgtgtgggg catcaagcag 1740

ctgcaggcca gggtgctggc cgtggagaga tacctgaagg atcagcagct cctggggatc 1800

tggggctgca gcggcaagct gatctgcacc accaccgtgc cctggaacgc cagctggtcc 1860

aacaagagcc tggacaagat ctggaacaat atgacctgga tggaatggga gcgcgagatc 1920

aacaattaca ccagcctgat ctacaccctg atcgaggaaa gccagaacca gcaggaaaag 1980

aacgagcagg aactgctgga actggacaag tgggccagcc tgtggaactg gttcgacatc 2040

agcaactggc tgtgg 2055

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

<220>
<223> nucleotide sequence encoding mos2Env

<400> 23

atgagagtgc ggggcatcca gcggaactgg ccccagtggt ggatctgggg catcctgggc 60

ttttggatga tcatcatctg ccgggtgatg ggcaacctgt gggtgaccgt gtactacggc 120

gtgcccgtgt ggaaagaggc caagaccacc ctgttctgcg ccagcgacgc caaggcctac 180

gagaaagagg tgcacaacgt gtgggccacc cacgcctgcg tgcccaccga ccccaacccc 240

caggaaatgg tcctggaaaa cgtgaccgag aacttcaaca tgtggaagaa cgacatggtg 300

gaccagatgc acgaggacat catccggctg tgggaccaga gcctgaagcc ctgcgtgaag 360

ctgacccccc tgtgcgtgac cctggaatgc cggaacgtga gaaacgtgag cagcaacggc 420

acctacaaca tcatccacaa cgagacctac aaagagatga agaactgcag cttcaacgcc 480

accaccgtgg tggaggaccg gaagcagaag gtgcacgccc tgttctaccg gctggacatc 540

gtgcccctgg acgagaacaa cagcagcgag aagtccagcg agaacagctc cgagtactac 600

cggctgatca actgcaacac cagcgccatc acccaggcct gccccaaggt gtccttcgac 660

cccatcccca tccactactg cgcccctgcc ggctacgcca tcctgaagtg caacaacaag 720

accttcaacg gcaccggccc ctgcaacaac gtgagcaccg tgcagtgcac ccacggcatc 780

aagcccgtgg tgtccaccca gctgctgctg aacggcagcc tggccgagga agagatcatc 840

atccggtccg agaacctgac caacaacgcc aagaccatca tcgtgcacct gaatgagacc 900

gtgaacatca cctgcacccg gcccaacaac aacacccgga agagcatccg gatcggccct 960

ggccagacct tttacgccac cggcgacatc atcggcgaca tccggcaggc ccactgcaac 1020

ctgagccggg acggctggaa caagaccctg cagggcgtga agaagaagct ggccgagcac 1080

ttccccaata agaccatcaa cttcaccagc agcagcggcg gagacctgga aatcaccacc 1140

cacagcttca actgcagggg cgagttcttc tactgcaata cctccggcct gttcaatggc 1200

acctacatgc ccaacggcac caacagcaac agcagcagca acatcaccct gccctgccgg 1260

atcaagcaga tcatcaatat gtggcaggag gtcggcaggg ccatgtacgc ccctcccatc 1320

gccggcaata tcacctgccg gtccaacatc accggcctgc tgctgaccag ggacggcggc 1380

agcaacaacg gcgtgcctaa cgacaccgag accttccggc ctggcggcgg agatatgcgg 1440

aacaactggc ggagcgagct gtacaagtac aaggtggtgg aggtgaagcc cctgggcgtg 1500

gctcctaccg aggccaagcg gcgggtggtg gagagcgaga agagcgccgt gggcatcggc 1560

gccgtgtttc tgggcattct gggagccgcc ggaagcacca tgggagccgc cagcatcacc 1620

ctgaccgtgc aggcccggca gctgctgtcc ggcatcgtgc agcagcagag caacctgctg 1680

agagccatcg aggcccagca gcacatgctg cagctgaccg tgtggggcat caagcagctg 1740

cagacccggg tgctggccat cgagagatac ctgcaggatc agcagctcct gggcctgtgg 1800

ggctgcagcg gcaagctgat ctgcaccacc gccgtgccct ggaacaccag ctggtccaac 1860

aagagccaga ccgacatctg ggacaacatg acctggatgc agtgggacaa agagatcggc 1920

aactacaccg gcgagatcta caggctgctg gaagagagcc agaaccagca ggaaaagaac 1980

gagaaggacc tgctggccct ggacagctgg aagaacctgt ggaactggtt cgacatcacc 2040

aactggctgt gg 2052

<210> 24
<211> 829
<212> DNA
<213> Artificial Sequence

<220>
<223> CMV promoter used for expression of antigens in Ad26 vectors

<400> 24
tcaatattgg ccattagcca tattattcat tggttatata gcataaatca atattggcta 60

ttggccattg catacgttgt atccatatca taatatgtac atttatattg gctcatgtcc 120

aacattaccg ccatgttgac attgattatt gactagttat taatagtaat caattacggg 180

gtcattagtt catagcccat atatggagtt ccgcgttaca taacttacgg taaatggccc 240

gcctggctga ccgcccaacg acccccgccc attgacgtca ataatgacgt atgttcccat 300

agtaacgcca atagggactt tccattgacg tcaatgggtg gagtatttac ggtaaactgc 360

ccacttggca gtacatcaag tgtatcatat gccaagtacg ccccctattg acgtcaatga 420

cggtaaatgg cccgcctggc attatgccca gtacatgacc ttatgggact ttcctacttg 480

gcagtacatc tacgtattag tcatcgctat taccatggtg atgcggtttt ggcagtacat 540

caatgggcgt ggatagcggt ttgactcacg gggatttcca agtctccacc ccattgacgt 600

caatgggagt ttgttttggc accaaaatca acgggacttt ccaaaatgtc gtaacaactc 660

cgccccattg acgcaaatgg gcggtaggcg tgtacggtgg gaggtctata taagcagagc 720

tcgtttagtg aaccgtcaga tcgcctggag acgccatcca cgctgttttg acctccatag 780

aagacaccgg gaccgatcca gcctccgcgg ccgggaacgg tgcattgga 829

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

<220>
<223> nucleotide sequence encoding c4

<400> 25
atgagagtgc ggggcatgct gagaaactgg cagcagtggt ggatctggtc cagcctgggc 60

ttctggatgc tgatgatcta cagcgtgatg ggcaacctgt gggtcaccgt gtactacggc 120

gtgcccgtgt ggaaggacgc caagaccacc ctgttttgcg cctccgatgc caaggcctac 180

gagaaagagg tgcacaacgt ctgggccacc cacgcctgtg tgcccaccga ccccaatccc 240

caggaaatcg tcctgggcaa cgtgaccgag aacttcaaca tgtggaagaa cgacatggtc 300

gatcagatgc acgaggacat catctccctg tgggacgcct ccctggaacc ctgcgtgaag 360

ctgacccctc tgtgcgtgac cctgaactgc cggaacgtgc gcaacgtgtc cagcaacggc 420

acctacaaca tcatccacaa cgagacatac aaagagatga agaactgcag cttcaacgct 480

accaccgtgg tcgaggaccg gaagcagaag gtgcacgccc tgttctaccg gctggacatc 540

gtgcccctgg acgagaacaa cagcagcgag aagtcctccg agaacagctc cgagtactac 600

agactgatca actgcaacac cagcgccatc acccaggcct gccccaaggt gtccttcgac 660

cctatcccca tccactactg cgcccctgcc ggctacgcca tcctgaagtg caacaacaag 720

accttcaatg gcaccggccc ctgcaacaat gtgtccaccg tgcagtgcac ccacggcatc 780

aagcccgtgg tgtctaccca gctgctgctg aacggcagcc tggccgagga agagatcatt 840

atcagaagcg agaacctgac caacaacgcc aaaaccatca tcgtccacct gaacgaaacc 900

gtgaacatca cctgtacccg gcctaacaac aacacccgga agtccatccg gatcggccct 960

ggccagacct tttacgccac cggcgatatt atcggcgaca tccggcaggc ccactgcaat 1020

ctgagccggg acggctggaa caagacactg cagggcgtca agaagaagct ggccgaacac 1080

ttccctaaca agactatcaa gttcgccccc cactctggcg gcgacctgga aatcaccacc 1140

cacaccttca actgtcgggg cgagttcttc tactgcaata cctccaacct gttcaacgag 1200

agcaacatcg agcggaacga cagcatcatc acactgcctt gccggatcaa gcagattatc 1260

aatatgtggc aggaagtggg cagagccatc tacgcccctc caatcgccgg caacatcaca 1320

tgccggtcca atatcaccgg cctgctgctc accagagatg gcggctccaa caatggcgtg 1380

ccaaacgaca ccgagacatt cagacccggc ggaggcgaca tgcggaacaa ttggcggagc 1440

gagctgtaca agtacaaggt ggtggaagtg aagcccctgg gcgtggcccc taccgaggcc 1500

aagagaagag tggtcgaacg cgagaagcgg gccgtgggaa tcggagccgt gtttctggga 1560

atcctgggag ccgctggctc taccatgggc gctgcctcta tcaccctgac agtgcaggcc 1620

agacagctgc tcagcggcat cgtgcagcag cagagcaacc tgctgagagc cattgaggcc 1680

cagcagcaca tgctgcagct gaccgtgtgg ggcattaagc agctccagac acgggtgctg 1740

gccatcgaga gatacctgca ggatcagcag ctcctgggcc tgtggggctg tagcggcaag 1800

ctgatctgta ccaccgccgt gccctggaat acctcttgga gcaacaagag ccagaccgac 1860

atctgggaca acatgacctg gatgcagtgg gacaaagaaa tcggcaacta taccggcgag 1920

atctatagac tgctggaaga gtcccagaac cagcaggaaa agaacgagaa ggacctgctg 1980

gccctggatt cttggaacaa tctgtggaac tggttcagca tctccaagtg gctgtggtac 2040

atcaagatct tcatcatgat cgtgggcggc ctgatcggcc tgcggatcat ctttgccgtg 2100

ctgagcatcg tgaaccgcgt gcggcaggga tacagccctc tgagcctgca gaccctgact 2160

cagaaccctg gcggactgga cagactgggc cggattgagg aagaaggcgg cgagcaggac 2220

aaggatcgga gcatcaggct ggtcaacggc ttcttcgctc tgttttggga cgacctgcgg 2280

agcctgtgcc tgttcagcta ccacagactg cgggacttta tcctgattgt ggccagagcc 2340

gtcgaactgc tggggagaag ctctctgaga ggcctgcagc ggggctggga gattctgaag 2400

tacctgggct ccctgctgca gtactggggc ctggaactga agaagtctgc catcaatctg 2460

ctcgacacaa tcgctattgc cgtggccgaa ggcaccgata gaatcatcga gctgatccag 2520

cggatctgcc gggccatctg caacatcccc agacggatca gacagggctt cgaggccgct 2580

ctgcag 2586

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

<220>
<223> nucleotide sequence encoding C4D7

<400> 26

atgagagtgc ggggcatgct gagaaactgg cagcagtggt ggatctggtc agcctgggc 60

ttctggatgc tgatgatcta cagcgtgatg ggcaacctgt gggtcaccgt gtactacggc 120

gtgcccgtgt ggaaggacgc caagaccacc ctgttttgcg cctccgatgc caaggcctac 180

gagaaagagg tgcacaacgt ctgggccacc cacgcctgtg tgcccaccga ccccaatccc 240

caggaaatcg tcctgggcaa cgtgaccgag aacttcaaca tgtggaagaa cgacatggtc 300

gatcagatgc acgaggacat catctccctg tgggacgcct ccctggaacc ctgcgtgaag 360

ctgacccctc tgtgcgtgac cctgaactgc cggaacgtgc gcaacgtgtc cagcaacggc 420

acctacaaca tcatccacaa cgagacatac aaagagatga agaactgcag cttcaacgct 480

accaccgtgg tcgaggaccg gaagcagaag gtgcacgccc tgttctaccg gctggacatc 540

gtgcccctgg acgagaacaa cagcagcgag aagtcctccg agaacagctc cgagtactac 600

agactgatca actgcaacac cagcgccatc acccaggcct gccccaaggt gtccttcgac 660

cctatcccca tccactactg cgcccctgcc ggctacgcca tcctgaagtg caacaacaag 720

accttcaatg gcaccggccc ctgcaacaat gtgtccaccg tgcagtgcac ccacggcatc 780

aagcccgtgg tgtctaccca gctgctgctg aacggcagcc tggccgagga agagatcatt 840

atcagaagcg agaacctgac caacaacgcc aaaaccatca tcgtccacct gaacgaaacc 900

gtgaacatca cctgtacccg gcctaacaac aacacccgga agtccatccg gatcggccct 960

ggccagacct tttacgccac cggcgatatt atcggcgaca tccggcaggc ccactgcaat 1020

ctgagccggg acggctggaa caagacactg cagggcgtca agaagaagct ggccgaacac 1080

ttccctaaca agactatcaa gttcgcccct cactctggcg gcgacctgga aatcaccacc 1140

cacaccttca actgtcgggg cgagttcttc tactgcaata cctccaacct gttcaacgag 1200

agcaacatcg agcggaacga cagcatcatc acactgcctt gccggatcaa gcagattatc 1260

aatatgtggc aggaagtggg cagagccatc tacgcccctc caatcgccgg caacatcaca 1320

tgccggtcca atatcaccgg cctgctgctc accagagatg gcggctccaa caatggcgtg 1380

ccaaacgaca ccgagacatt cagacccggc ggaggcgaca tgcggaacaa ttggcggagc 1440

gagctgtaca agtacaaggt ggtggaagtg aagcccctgg gcgtggcccc taccgaggcc 1500

aagagaagag tggtcgaacg cgagaagcgg gccgtgggaa tcggagccgt gtttctggga 1560

atcctgggag ccgctggctc taccatgggc gctgcctcta tcaccctgac agtgcaggcc 1620

agacagctgc tcagcggcat cgtgcagcag cagagcaacc tgctgagagc cattgaggcc 1680

cagcagcaca tgctgcagct gaccgtgtgg ggcattaagc agctccagac acgggtgctg 1740

gccatcgaga gatacctgca ggatcagcag ctcctgggcc tgtggggctg tagcggcaag 1800

ctgatctgta ccaccgccgt gccctggaat acctcttgga gcaacaagag ccagaccgac 1860

atctgggaca acatgacctg gatgcagtgg gacaaagaaa tcggcaacta taccggcgag 1920

atctatagac tgctggaaga gtcccagaac cagcaggaaa agaacgagaa ggacctgctg 1980

gccctggatt cttggaacaa tctgtggaac tggttcagca tctccaagtg gctgtggtac 2040

atcaagatct tcatcatgat cgtgggcggc ctgatcggcc tgcggatcat ctttgccgtg 2100

ctgagcatcg tgaaccgcgt gcggcagggc tac 2133

<210> 27
<211> 2112
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotide sequence encoding sC4

<400> 27
atgagagtgc ggggcatgct gagaaactgg cagcagtggt ggatctggtc cagcctgggc 60

ttctggatgc tgatgatcta cagcgtgatg ggcaacctgt gggtcaccgt gtactacggc 120

gtgcccgtgt ggaaggacgc caagaccacc ctgttttgcg cctccgatgc caaggcctac 180

gagaaagagg tgcacaacgt ctgggccacc cacgcctgtg tgcccaccga ccccaatccc 240

caggaaatcg tcctgggcaa cgtgaccgag aacttcaaca tgtggaagaa cgacatggtc 300

gatcagatgc acgaggacat catctccctg tgggacgcct ccctggaacc ctgcgtgaag 360

ctgacccctc tgtgcgtgac cctgaactgc cggaacgtgc gcaacgtgtc cagcaacggc 420

acctacaaca tcatccacaa cgagacatac aaagagatga agaactgcag cttcaacgct 480

accaccgtgg tcgaggaccg gaagcagaag gtgcacgccc tgttctaccg gctggacatc 540

gtgcccctgg acgagaacaa cagcagcgag aagtcctccg agaacagctc cgagtactac 600

agactgatca actgcaacac cagcgccatc acccaggcct gccccaaggt gtccttcgac 660

cctatcccca tccactactg cgcccctgcc ggctacgcca tcctgaagtg caacaacaag 720

accttcaatg gcaccggccc ctgcaacaat gtgtccaccg tgcagtgcac ccacggcatc 780

aagcccgtgg tgtctaccca gctgctgctg aacggcagcc tggccgagga agagatcatt 840

atcagaagcg agaacctgac caacaacgcc aaaaccatca tcgtccacct gaacgaaacc 900

gtgaacatca cctgtacccg gcctaacaac aacacccgga agtccatccg gatcggccct 960

ggccagacct tttacgccac cggcgatatt atcggcgaca tccggcaggc ccactgcaat 1020

ctgagccggg acggctggaa caagacactg cagggcgtca agaagaagct ggccgaacac 1080

ttccctaaca agactatcaa gttcgcccct cactctggcg gcgacctgga aatcaccacc 1140

cacaccttca actgtcgggg cgagttcttc tactgcaata cctccaacct gttcaacgag 1200

agcaacatcg agcggaacga cagcatcatc acactgcctt gccggatcaa gcagattatc 1260

aatatgtggc aggaagtggg cagagccatc tacgcccctc caatcgccgg caacatcaca 1320

tgccggtcca atatcaccgg cctgctgctc accagagatg gcggctccaa caatggcgtg 1380

ccaaacgaca ccgagacatt cagacccggc ggaggcgaca tgcggaacaa ttggcggagc 1440

gagctgtaca agtacaaggt ggtggaagtg aagcccctgg gcgtggcccc taccgaggcc 1500

aagagaagag tggtcgaacg cgaggaacgg gccgtgggaa tcggagccgt gtttctggga 1560

atcctgggag ccgctggctc taccatgggc gctgcctcta tcaccctgac agtgcaggcc 1620

agacagctgc tcagcggcat cgtgcagcag cagagcaacc tgctgagagc cattgaggcc 1680

cagcagcaca tgctgcagct gaccgtgtgg ggcattaagc agctccagac acgggtgctg 1740

gccatcgaga gatacctgca ggatcagcag ctcctgggcc tgtggggctg tagcggcaag 1800

ctgatctgta ccaccgccgt gccctggaat acctcttgga gcaacaagag ccagaccgac 1860

atctgggaca acatgacctg gatgcagtgg gacaaagaaa tcggcaacta taccggcgag 1920

atctatagac tgctggaaga gtcccagaac cagcaggaaa agatgaagca gatcgaggac 1980

aagatcgaag agattctgag caagatctac cacatcgaga acgagatcgc ccgcatcaag 2040

aaactgatcg gcgaagtggg atccggcgct cccacaaagg ccaaaagacg ggtggtgcag 2100

cgcgagaaac gc 2112

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

<220>
<223> mos1GagPol mosaic antigen sequence

<400> 28

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

```
            420                 425                 430

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Phe Arg Ala Lys Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Ala Ala
        675                 680                 685

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

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

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

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

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

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

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

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

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

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

Lys Asn Leu Lys Thr Gly Lys Tyr Ala Lys Met Arg Thr Ala His Thr
```

```
    850                 855                 860

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

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

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

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

Tyr Gln Leu Glu Lys Asp Pro Ile Ala Gly Val Glu Thr Phe Tyr Val
    930                 935                 940

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Val Ile  His Thr Ala Asn Gly  Ser Asn Phe Thr Ser  Ala Ala Val
    1175                1180                1185

Lys Ala  Ala Cys Trp Trp Ala  Gly Ile Gln Gln Glu  Phe Gly Ile
    1190                1195                1200

Pro Tyr  Asn Pro Gln Ser Gln  Gly Val Val Ala Ser  Met Asn Lys
    1205                1210                1215

Glu Leu  Lys Lys Ile Ile Gly  Gln Val Arg Asp Gln  Ala Glu His
    1220                1225                1230

Leu Lys  Thr Ala Val Gln Met  Ala Val Phe Ile His  Asn Phe Lys
    1235                1240                1245

Arg Lys  Gly Gly Ile Gly Gly  Tyr Ser Ala Gly Glu  Arg Ile Ile
    1250                1255                1260

Asp Ile  Ile Ala Thr Asp Ile  Gln Thr Lys Glu Leu  Gln Lys Gln
```

1265 1270 1275

Ile Ile Lys Ile Gln Asn Phe Arg Val Tyr Tyr Arg Asp Ser Arg
1280 1285 1290

Asp Pro Ile Trp Lys Gly Pro Ala Lys Leu Leu Trp Lys Gly Glu
1295 1300 1305

Gly Ala Val Val Ile Gln Asp Asn Ser Asp Ile Lys Val Val Pro
1310 1315 1320

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

Gly Ala Asp Cys Val Ala Gly Arg Gln Asp Glu Asp
1340 1345 1350

<210> 29
<211> 1341
<212> PRT
<213> Artificial Sequence

<220>
<223> mos2GagPol mosaic antigen sequence

<400> 29

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

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

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

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

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

Thr Val Ala Thr Leu Tyr Cys Val His Ala Glu Ile Glu Val Arg Asp

```
               85                  90                  95

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

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

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

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

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

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

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

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

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

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

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

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

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

```
Gln Ala Thr Gln Asp Val Lys Asn Trp Met Thr Asp Thr Leu Leu Val
305                 310                 315                 320

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

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

Pro Ser His Lys Ala Arg Val Leu Ala Glu Ala Met Ser Gln Thr Asn
        355                 360                 365

Ser Thr Ile Leu Met Gln Arg Ser Asn Phe Lys Gly Ser Lys Arg Ile
    370                 375                 380

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

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

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

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

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

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

Arg Ser Leu Phe Gly Ser Asp Pro Leu Ser Gln Met Ala Pro Ile Ser
                485                 490                 495

Pro Ile Glu Thr Val Pro Val Lys Leu Lys Pro Gly Met Asp Gly Pro
            500                 505                 510

Lys Val Lys Gln Trp Pro Leu Thr Glu Glu Lys Ile Lys Ala Leu Val
```

```
        515                 520                 525

Glu Ile Cys Thr Glu Met Glu Lys Glu Gly Lys Ile Ser Lys Ile Gly
    530                 535                 540

Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe Ala Ile Lys Lys Lys Asp
545                 550                 555                 560

Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg Glu Leu Asn Lys Arg
                565                 570                 575

Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile Pro His Pro Ala Gly
            580                 585                 590

Leu Lys Lys Lys Lys Ser Val Thr Val Leu Ala Val Gly Asp Ala Tyr
        595                 600                 605

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

Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile Arg Tyr Gln Tyr Asn
625                 630                 635                 640

Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe Gln Ser Ser
                645                 650                 655

Met Thr Lys Ile Leu Glu Pro Phe Arg Lys Gln Asn Pro Asp Ile Val
            660                 665                 670

Ile Tyr Gln Tyr Met Ala Ala Leu Tyr Val Gly Ser Asp Leu Glu Ile
        675                 680                 685

Gly Gln His Arg Thr Lys Ile Glu Glu Leu Arg Gln His Leu Leu Arg
    690                 695                 700

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

Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys Trp Thr Val Gln Pro
                725                 730                 735
```

```
Ile Val Leu Pro Glu Lys Asp Ser Trp Thr Val Asn Asp Ile Gln Lys
            740                 745                 750

Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile Tyr Ala Gly Ile Lys
        755                 760                 765

Val Lys Gln Leu Cys Lys Leu Leu Arg Gly Thr Lys Ala Leu Thr Glu
    770                 775                 780

Val Val Pro Leu Thr Glu Glu Ala Glu Leu Glu Leu Ala Glu Asn Arg
785                 790                 795                 800

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

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

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

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

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

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

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

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

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

Leu Gly Lys Ala Gly Tyr Val Thr Asp Arg Gly Arg Gln Lys Val Val
```

```
945                 950                 955                 960

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

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

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

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

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

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

Phe Leu  Asp Gly Ile Asp Lys  Ala Gln Glu Glu His  Glu Lys Tyr
    1055                1060                1065

His Ser  Asn Trp Arg Ala Met  Ala Ser Glu Phe Asn  Leu Pro Pro
    1070                1075                1080

Ile Val  Ala Lys Glu Ile Val  Ala Ser Cys Asp Lys  Cys Gln Leu
    1085                1090                1095

Lys Gly  Glu Ala Ile His Gly  Gln Val Asp Cys Ser  Pro Gly Ile
    1100                1105                1110

Trp Gln  Leu Ala Cys Thr His  Leu Glu Gly Lys Val  Ile Leu Val
    1115                1120                1125

Ala Val  His Val Ala Ser Gly  Tyr Ile Glu Ala Glu  Val Ile Pro
    1130                1135                1140

Ala Glu  Thr Gly Gln Glu Thr  Ala Tyr Phe Leu Leu  Lys Leu Ala
    1145                1150                1155
```

```
Gly Arg  Trp Pro Val Lys Thr  Ile His Thr Ala Asn  Gly Ser Asn
    1160                1165                1170

Phe Thr  Ser Ala Thr Val Lys  Ala Ala Cys Trp Trp  Ala Gly Ile
    1175                1180                1185

Lys Gln  Glu Phe Gly Ile Pro  Tyr Asn Pro Gln Ser  Gln Gly Val
    1190                1195                1200

Val Ala  Ser Ile Asn Lys Glu  Leu Lys Lys Ile Ile  Gly Gln Val
    1205                1210                1215

Arg Asp  Gln Ala Glu His Leu  Lys Thr Ala Val Gln  Met Ala Val
    1220                1225                1230

Phe Ile  His Asn Phe Lys Arg  Lys Gly Gly Ile Gly  Glu Tyr Ser
    1235                1240                1245

Ala Gly  Glu Arg Ile Val Asp  Ile Ile Ala Ser Asp  Ile Gln Thr
    1250                1255                1260

Lys Glu  Leu Gln Lys Gln Ile  Thr Lys Ile Gln Asn  Phe Arg Val
    1265                1270                1275

Tyr Tyr  Arg Asp Ser Arg Asp  Pro Leu Trp Lys Gly  Pro Ala Lys
    1280                1285                1290

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

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

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

Asp Glu  Asp
    1340
```

<210> 30

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

<220>
<223> sc1 sequence

<400> 30

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

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

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

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

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

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

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

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

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

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

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

Arg Leu Asp Ile Val Pro Leu Asp Glu Asn Asn Ser Ser Glu Lys Ser

```
            180                 185                 190

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

Ala Ile Thr Gln Ala Cys Pro Lys Val Ser Phe Asp Pro Ile Pro Ile
    210                 215                 220

His Tyr Cys Ala Pro Ala Gly Tyr Ala Ile Leu Lys Cys Asn Asn Lys
225                 230                 235                 240

Thr Phe Asn Gly Thr Gly Pro Cys Asn Asn Val Ser Thr Val Gln Cys
                245                 250                 255

Thr His Gly Ile Lys Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly
            260                 265                 270

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Thr Thr Ala Val Pro Trp Asn Thr Ser Trp Ser Asn Lys Ser Gln Thr
```

610 615 620

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

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

Gln Glu Lys Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser
660 665 670

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

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

Gln Arg Glu Lys Arg
705

<210> 31
<211> 867
<212> PRT
<213> Artificial Sequence

<220>
<223> C1 sequence

<400> 31

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

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

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

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

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

```
65                  70                  75                  80

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

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

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

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

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

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

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

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

Ala Ile Thr Gln Ala Cys Pro Lys Val Ser Phe Asp Pro Ile Pro Ile
    210                 215                 220

His Tyr Cys Ala Pro Ala Gly Tyr Ala Ile Leu Lys Cys Asn Asn Lys
225                 230                 235                 240

Thr Phe Asn Gly Thr Gly Pro Cys Asn Asn Val Ser Thr Val Gln Cys
                245                 250                 255

Thr His Gly Ile Lys Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly
            260                 265                 270

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

```
            500                 505                 510

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ala Leu Gln
865
```

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

<220>
<223> C1D7 sequence

<400> 32

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

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

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

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

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

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

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

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

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

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

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

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

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

Ala Ile Thr Gln Ala Cys Pro Lys Val Ser Phe Asp Pro Ile Pro Ile
    210                 215                 220

His Tyr Cys Ala Pro Ala Gly Tyr Ala Ile Leu Lys Cys Asn Asn Lys
```

```
225                 230                 235                 240

Thr Phe Asn Gly Thr Gly Pro Cys Asn Asn Val Ser Thr Val Gln Cys
                245                 250                 255

Thr His Gly Ile Lys Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly
            260                 265                 270

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gln Glu Lys Asn Glu Lys Asp Leu Leu Ala Leu Asp Ser Trp Lys Asn
```

660 665 670

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

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

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

<210> 33
<211> 2127
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotide sequence encoding sC1

<400> 33
atgagagtgc ggggcattca gagaaactgg ccccagtggt ggatctgggg catcctgggc 60

ttttggatga tcattatctg ccgcgtgatg ggcaacctgt gggtcaccgt gtactacggc 120

gtgcccgtgt ggaaagaggc caagaccacc ctgttctgcg ccagcgacgc caaggcctac 180

gagaaagagg tgcacaacgt ctgggccacc cacgcctgtg tgcccaccga ccccaatccc 240

caggaaatgg tcctggaaaa cgtgaccgag aacttcaaca tgtggaagaa cgacatggtg 300

gaccagatgc acgaggacat catccggctg tgggaccaga gcctgaagcc ctgcgtgaag 360

ctgacccctc tgtgcgtgac cctggaatgc cggaacgtgc gcaacgtgtc cagcaacggc 420

acctacaata tcatccacaa cgagacatac aaagagatga agaactgcag cttcaacgct 480

accaccgtgg tcgaggaccg gaagcagaag gtgcacgccc tgttttaccg gctggacatc 540

gtgcccctgg acgagaacaa cagcagcgag aagtcctccg agaacagctc cgagtactac 600

agactgatca actgcaacac cagcgccatc acccaggcct gccccaaggt gtccttcgac 660

cctatcccca tccactactg cgcccctgcc ggctacgcca tcctgaagtg caacaacaag 720

accttcaatg gcaccggccc ctgcaacaat gtgtccaccg tgcagtgcac ccacggcatc 780

aagcccgtgg tgtctaccca gctgctgctg aacggcagcc tggccgagga agagatcatc 840

atcagaagcg agaacctgac caacaacgcc aagacaatca tcgtccacct gaacgaaacc 900

gtgaacatca cctgtacccg gcctaacaac aacacccgga agtccatccg gatcggccct 960

ggccagacct tttacgccac cggcgatatt atcggcgaca tccggcaggc ccactgcaat 1020

ctgagccggg acggctggaa caagacactg cagggcgtca agaagaagct ggccgaacac 1080

ttccccaaca aaaccatcaa cttcaccagc tcctctggcg gcgacctgga aatcaccacc 1140

cacagcttta actgcagagg cgagttcttc tactgcaata cctccggcct gttcaatgga 1200

acctacatgc ccaacgggac caacagcaac tccagcagca atatcaccct gccttgccgg 1260

atcaagcaga ttatcaatat gtggcaggaa gtgggcagag ctatgtacgc ccctccaatc 1320

gccggcaaca tcacatgcag aagcaacatt accggcctgc tgctcaccag ggacggcggc 1380

tctaacaatg gcgtgccaaa cgacaccgag acattcagac ccggcggagg cgacatgcgg 1440

aacaattggc ggagcgagct gtacaagtac aaggtggtgg aagtgaagcc cctgggcgtg 1500

gcccctaccg aagccaagag aagagtggtc gaacgcgagg aacgggccgt gggcattgga 1560

gccgtgtttc tgggaatcct gggagccgct ggcagcacca tgggcgctgc ctctatcaca 1620

ctgacagtgc aggccagaca gctcctgagc ggcatcgtgc agcagcagag caacctgctg 1680

agagccatcg aggcacagca gcacatgctg cagctgaccg tgtggggcat taagcagctc 1740

cagacacggg tgctggccat tgagagatac ctgcaggatc agcagctgct cggcctgtgg 1800

ggctgtagcg gcaagctgat ctgtaccacc gccgtgcctt ggaacacctc ctggtccaac 1860

aagagccaga ccgacatctg ggacaacatg acctggatgc agtgggacaa agaaatcggc 1920

aactataccg gcgagatcta ccgactgctg gaagagtccc agaaccagca ggaaaagatg 1980

aagcagatcg aggacaagat cgaagagatt ctgagcaaaa tctaccacat cgagaacgag 2040

atcgcccgca tcaagaaact gatcggcgaa gtgggatccg gcgctcccac aaaggccaaa 2100

agacgggtgg tgcagcgcga gaaacgc 2127

<210> 34
<211> 2601
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotide sequence encoding C1

<400> 34
atgagagtgc ggggcattca gagaaactgg ccccagtggt ggatctgggg catcctgggc 60

ttttggatga tcattatctg ccgcgtgatg ggcaacctgt gggtcaccgt gtactacggc 120

gtgcccgtgt ggaaagaggc caagaccacc ctgttctgcg ccagcgacgc caaggcctac 180

gagaaagagg tgcacaacgt ctgggccacc cacgcctgtg tgcccaccga ccccaatccc 240

caggaaatgg tcctggaaaa cgtgaccgag aacttcaaca tgtggaagaa cgacatggtg 300

gaccagatgc acgaggacat catccggctg tgggaccaga gcctgaagcc ctgcgtgaag 360

ctgacccctc tgtgcgtgac cctggaatgc cggaacgtgc gcaacgtgtc cagcaacggc 420

acctacaata tcatccacaa cgagacatac aaagagatga agaactgcag cttcaacgct 480

accaccgtgg tcgaggaccg gaagcagaag gtgcacgccc tgttttaccg gctggacatc 540

gtgcccctgg acgagaacaa cagcagcgag aagtcctccg agaacagctc cgagtactac 600

agactgatca actgcaacac cagcgccatc acccaggcct gccccaaggt gtccttcgac 660

cctatcccca tccactactg cgcccctgcc ggctacgcca tcctgaagtg caacaacaag 720

accttcaatg gcaccggccc ctgcaacaat gtgtccaccg tgcagtgcac ccacggcatc 780

aagcccgtgg tgtctaccca gctgctgctg aacggcagcc tggccgagga agagatcatc 840

atcagaagcg agaacctgac caacaacgcc aagacaatca tcgtccacct gaacgaaacc 900

gtgaacatca cctgtacccg gcctaacaac aacacccgga agtccatccg gatcggccct 960

ggccagacct tttacgccac cggcgatatt atcggcgaca tccggcaggc ccactgcaat 1020

ctgagccggg acggctggaa caagacactg cagggcgtca agaagaagct ggccgaacac 1080

ttccccaaca aaaccatcaa cttcaccagc tcctctggcg gcgacctgga aatcaccacc 1140

cacagcttta actgcagagg cgagttcttc tactgcaata cctccggcct gttcaatgga 1200

acctacatgc ccaacgggac caacagcaac tccagcagca atatcaccct gccttgccgg 1260

atcaagcaga ttatcaatat gtggcaggaa gtgggcagag ctatgtacgc ccctccaatc 1320

gccggcaaca tcacatgcag aagcaacatt accggcctgc tgctcaccag ggacggcggc 1380

tctaacaatg gcgtgccaaa cgacaccgag acattcagac ccggcggagg cgacatgcgg 1440

aacaattggc ggagcgagct gtacaagtac aaggtggtgg aagtgaagcc cctgggcgtg 1500

gcccctaccg aagccaagag aagagtggtc gaacgcgaga agcgggccgt gggcattgga 1560

gccgtgtttc tgggaatcct gggagccgct ggcagcacca tgggcgctgc ctctatcaca 1620

ctgacagtgc aggccagaca gctcctgagc ggcatcgtgc agcagcagag caacctgctg 1680

agagccatcg aggcacagca gcacatgctg cagctgaccg tgtggggcat taagcagctc 1740

cagacacggg tgctggccat tgagagatac ctgcaggatc agcagctgct cggcctgtgg 1800

ggctgtagcg gcaagctgat ctgtaccacc gccgtgcctt ggaacacctc ctggtccaac 1860

aagagccaga ccgacatctg ggacaacatg acctggatgc agtgggacaa agaaatcggc 1920

aactataccg gcgagatcta ccgactgctg gaagagtccc agaaccagca ggaaaagaac 1980

gagaaggacc tgctggccct ggacagctgg aaaaatctgt ggaattggtt cgacatcacc 2040

aactggctgt ggtacatcaa gatcttcatc atgatcgtgg gcggcctgat cggcctgcgg 2100

atcatctttg ccgtgctgag catcgtgaac cgcgtgcggc agggatacag ccctctgagc 2160

ctgcagaccc tgacccagaa tccaggcgga ctggatcggc tgggccggat tgaggaagaa 2220

ggcggcgagc aggacaagga ccgcagcatc agactcgtga acggcttctt cgctctgttt 2280

tgggacgacc tgcggagcct gtgcctgttc tcctaccaca gactgcggga ctttatcctg 2340

attgtggcca gagccgtcga gctgctgggc agatcttctc tgagaggcct gcagcggggc 2400

tgggagattc tgaagtacct gggctccctg ctgcagtatt ggggcctgga actgaagaag 2460

tccgccatca atctgctcga cacaatcgct attgccgtgg ccgaaggcac cgacagaatc 2520

atcgagctga tccagcggat ctgccgggcc atctgcaaca tccccagacg gatcagacag 2580

ggctttgaag ccgccctcca g 2601

<210> 35
<211> 2148
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotide sequence encoding C1D7

<400> 35
atgagagtgc ggggcattca gagaaactgg ccccagtggt ggatctgggg catcctgggc 60

ttttggatga tcattatctg ccgcgtgatg ggcaacctgt gggtcaccgt gtactacggc 120

gtgcccgtgt ggaaagaggc caagaccacc ctgttctgcg ccagcgacgc caaggcctac 180

gagaaagagg tgcacaacgt ctgggccacc cacgcctgtg tgcccaccga ccccaatccc 240

caggaaatgg tcctggaaaa cgtgaccgag aacttcaaca tgtggaagaa cgacatggtg 300

gaccagatgc acgaggacat catccggctg tgggaccaga gcctgaagcc ctgcgtgaag 360

ctgacccctc tgtgcgtgac cctggaatgc cggaacgtgc gcaacgtgtc cagcaacggc 420

acctacaata tcatccacaa cgagacatac aaagagatga agaactgcag cttcaacgct 480

accaccgtgg tcgaggaccg gaagcagaag gtgcacgccc tgttttaccg gctggacatc 540

gtgcccctgg acgagaacaa cagcagcgag aagtcctccg agaacagctc cgagtactac 600

agactgatca actgcaacac cagcgccatc acccaggcct gccccaaggt gtccttcgac 660

cctatcccca tccactactg cgcccctgcc ggctacgcca tcctgaagtg caacaacaag 720

accttcaatg gcaccggccc ctgcaacaat gtgtccaccg tgcagtgcac ccacggcatc 780

aagcccgtgg tgtctaccca gctgctgctg aacggcagcc tggccgagga agagatcatc 840

atcagaagcg agaacctgac caacaacgcc aagacaatca tcgtccacct gaacgaaacc 900

gtgaacatca cctgtacccg gcctaacaac aacacccgga agtccatccg gatcggccct 960

ggccagacct tttacgccac cggcgatatt atcggcgaca tccggcaggc ccactgcaat 1020

ctgagccggg acggctggaa caagacactg cagggcgtca agaagaagct ggccgaacac 1080

ttccccaaca aaaccatcaa cttcaccagc tcctctggcg gcgacctgga aatcaccacc 1140

cacagcttta actgcagagg cgagttcttc tactgcaata cctccggcct gttcaatgga 1200

acctacatgc ccaacgggac caacagcaac tccagcagca atatcaccct gccttgccgg 1260

atcaagcaga ttatcaatat gtggcaggaa gtgggcagag ctatgtacgc ccctccaatc 1320

gccggcaaca tcacatgcag aagcaacatt accggcctgc tgctcaccag ggacggcggc 1380

tctaacaatg gcgtgccaaa cgacaccgag acattcagac ccggcggagg cgacatgcgg 1440

aacaattggc ggagcgagct gtacaagtac aaggtggtgg aagtgaagcc cctgggcgtg 1500

gcccctaccg aagccaagag aagagtggtc gaacgcgaga agcgggccgt gggcattgga 1560

gccgtgtttc tgggaatcct gggagccgct ggcagcacca tgggcgctgc ctctatcaca 1620

ctgacagtgc aggccagaca gctcctgagc ggcatcgtgc agcagcagag caacctgctg 1680

agagccatcg aggcacagca gcacatgctg cagctgaccg tgtggggcat taagcagctc 1740

cagacacggg tgctggccat tgagagatac ctgcaggatc agcagctgct cggcctgtgg 1800

ggctgtagcg gcaagctgat ctgtaccacc gccgtgcctt ggaacacctc ctggtccaac 1860

aagagccaga ccgacatctg ggacaacatg acctggatgc agtgggacaa agaaatcggc 1920

aactataccg gcgagatcta ccgactgctg gaagagtccc agaaccagca ggaaaagaac 1980

gagaaggacc tgctggccct ggacagctgg aaaaatctgt ggaattggtt cgacatcacc 2040

aactggctgt ggtacatcaa gatcttcatc atgatcgtgg gcggcctgat cggcctgcgg 2100

atcatctttg ccgtgctgag catcgtgaac cgcgtgcggc agggctac 2148

<210> 36
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> mosaic Env trimer sequence

<400> 36

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

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

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

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

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

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

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

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

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

Asn Ser Ser Trp Gly Glu Pro Met Glu Lys Gly Glu Ile Lys Asn Cys

```
145                 150                 155                 160

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Ile Lys Gln Leu Gln Ala Arg Val Leu Ala Val Glu Arg Tyr Leu
```

580 585 590

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

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

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

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

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

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

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

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

Ser Thr Phe Leu

<210> 37
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Residues 655-682 of SEQ ID NO:18

<400> 37

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

Trp Phe Ser Ile Ser Lys Trp Leu Trp Tyr Ile Lys

20 25

<210> 38
<211> 4056
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotide sequence of Mos1Gag-Pol antigen

<400> 38
atgggagcta gagccagtgt gctgagcggc ggagagctgg atagatggga gaaaattcgg 60

ctgcggccag gcggcaaaaa gaagtatcgc ctgaaacata ttgtgtgggc ctctcgcgag 120

ctggaaagat ttgctgtgaa tcctggactg ctcgagacat ctgaaggctg ccgccagatc 180

ctcggtcaac tgcagccatc tctgcagacc ggctcagaag agctgagatc tctgtataat 240

actgtcgcca cactctattg cgtccaccag cgcattgaaa tcaaagatac aaaggaggct 300

ctggagaaga tagaagagga acagaataag tctaaaaaga aggctcagca ggccgctgcc 360

gataccggca acagctctca ggtctcacaa aattacccta tcgttcagaa tattcaaggt 420

caaatggtcc atcaggctat cagccctcgc acactgaatg cttgggtgaa agtggtcgag 480

gaaaaagcct ttagtccaga ggttatacct atgtttagcg cactgtctga aggagccact 540

cctcaggacc tcaataccat gctgaatact gtcggaggcc atcaggccgc tatgcaaatg 600

ctgaaagaaa ccattaacga ggaagccgcc gaatgggatc gagtgcatcc agtccatgca 660

ggaccaatcg ctccaggcca gatgagagaa cctcgaggct ctgatatcgc cggaaccaca 720

agcacactgc aggaacagat tggatggatg acaaacaatc ctcctatccc tgtcggcgag 780

atctataaga gatggattat cctcggcctc aacaagattg tcagaatgta ttcacctgtg 840

tccattctgg atatccgcca aggacctaaa gagccattcc gcgattacgt cgaccgcttt 900

tacaaaaccc tgagagctga gcaggcatct caggatgtca aaaattggat gacagaaact 960

ctcctggtcc agaacgctaa tcctgattgc aagacaattc tgaaggctct gggaccagcc 1020

gccactctcg aggaaatgat gaccgcttgt cagggagtcg gaggacctgg acacaaggca 1080

agagtgctcg ctgaagccat gtctcaggtc acaaacagcg ccacaattat gatgcagcgc 1140

ggtaacttca gaaaccagcg gaaaaccgtc aagtgtttta attgcggtaa agagggccat 1200

attgccaaaa attgcagagc tcctcggaaa aagggctgct ggaaatgtgg aaaagaaggt 1260

catcaaatga aggattgcac agaacgccag gccaatttcc ttgggaagat ttggccttcc 1320

aacaaaggcc gaccaggaaa ctttctgcag aatcggcctg agcctaccgc tccacctgaa 1380

gagagcttta gattcggcga ggaaacaacc acaccatctc agaaacaaga gcctattgat 1440

aaggaaatgt atcctctggc ttctctgaag tctctgttcg gcaatgatcc tagctcacaa 1500

atggctccca ttagtcctat tgaaacagtg cctgtgaaac tgaaacctgg aatggacggt 1560

cctagagtca agcagtggcc tctcacagaa gagaagatta aggcactcac cgctatttgc 1620

gaagagatgg agaaagaagg caagattaca aagattggac ctgagaatcc atacaataca 1680

cctgtctttg ccatcaaaaa gaaagattct accaaatggc gcaagctcgt ggatttcaga 1740

gaactcaaca aacgcacaca ggatttttgg gaggtccagc tcggaattcc tcatccagcc 1800

ggactgaaaa agaagaagtc cgtcacagtc ctggcagtcg gcgacgccta tttctccgtg 1860

cctctcgatg aaggttttag gaagtatacc gcctttacaa ttccatccac aaacaacgaa 1920

acaccaggca tccggtacca gtataatgtc ctgccacaag gatggaaggg atctcctgcc 1980

atctttcagt gttccatgac acggatcctt gaacctttca gagccaagaa tccagagatt 2040

gtgatctatc aatacatggc cgcactctat gtcggatctg acctcgagat tggacagcac 2100

cgcgccaaga tcgaagagct gagagaacat ctgctgaaat ggggctttac aacaccagat 2160

aagaaacatc agaaagaacc tccttttctt tggatgggat atgaactgca tcccgacaaa 2220

tggacagtcc agcctatcca gctgccagag aaggatagct ggaccgttaa tgatattcag 2280

aagctcgttg gtaaactgaa ttgggccagt caaatctatc ctggaatcaa agtccgacag 2340

ctgtgcaagc tgctcagagg cgccaaggct ctcaccgata ttgtgcctct gaccgaagag 2400

gctgaactgg agctggccga gaatagagaa atcctcaagg agcctgtcca cggcgtctac 2460

tacgatcctt ctaaagacct gatcgctgaa atccaaaagc aaggacatga tcaatggaca 2520

tatcagatct accaggagcc ttttaagaat cttaagaccg gcaagtatgc caaaatgcgc 2580

accgctcata caaatgacgt gaaacagctc accgaggctg tccagaaaat tgctatggaa 2640

tctatcgtca tttggggcaa aacacctaaa ttccggcttc ctattcagaa agaaacctgg 2700

gagacatggt ggacagatta ctggcaagct acatggatcc ctgaatggga atttgtgaat 2760

acacctcctc tcgtcaaact gtggtaccag ttggagaagg atccaatcgc cggcgtggaa 2820

acattctatg tggcaggcgc cgctaacaga gaaactaagc tcggcaaggc cggatatgtg 2880

acagacagag gtagacagaa gattgtatct ctgacagaga caacaaatca gaaaaccgct 2940

ctccaggcta tctacctcgc actgcaggat tccggcagcg aagtgaatat tgtgaccgcc 3000

tctcagtatg cactcggaat tattcaggca cagcctgata agtccgagtc cgagctggtc 3060

aatcagatca tcgaacagct gattaagaag gaaagagtct acctgtcttg ggtgccagca 3120

cacaagggaa tcggcggcaa tgaacaggtg gacaaacttg tgtcctccgg tattagaaag 3180

gtcctgttcc tcgatggaat tgacaaggct caggaagaac acgagaaata tcactccaac 3240

tggagagcta tggcctccga tttcaatctg ccacctgttg tggctaagga aattgtcgct 3300

tcctgcgatc agtgtcaact caaaggcgaa gctatgcatg gacaggtcga ctgttctcct 3360

ggaatatggc aactcgcttg tacacacctc gaaggcaaaa tcatcctcgt ggctgtccat 3420

gtggcctccg gctatattga agccgaagtg attcctgctg aaaccggcca ggaaaccgct 3480

tactttattc tgaaactcgc tggacggtgg cctgtgaaag tgattcatac cgccaatggc 3540

tccaacttca ccagcgccgc tgtgaaagcc gcttgctggt gggccggaat ccagcaggag 3600

ttcggaatac cgtataaccc tcagtcacaa ggagtggtcg cctctatgaa caaggaattg 3660

aagaaaatca taggtcaagt ccgagaccaa gccgaacacc tcaagaccgc tgtccagatg 3720

gcagtcttta tccacaattt caagcgcaaa ggcggcattg gcggctacag tgccggcgag 3780

agaattatcg acataatcgc cacagacatt cagacaaagg agctccagaa gcagataatc 3840

aagatacaga atttccgcgt gtactaccgc gactctagag accctatatg gaagggtcca 3900

gctaagctct tgtggaaggg cgaaggcgct gtggtcattc aggacaattc cgatatcaag 3960

gtcgttcctc ggcggaaagt caagatcatt aaggattatg gtaaacaaat ggccggagct 4020

gattgcgtgg caggccggca ggacgaagat tgataa 4056

<210> 39
<211> 2061
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotide sequence of Mos1Env antigen

<400> 39
atgcgcgtga ccggcatcag gaaaaactat cagcatctgt ggagatgggg tacaatgctc 60

ctcggaattc tcatgatctg tagcgccgct ggcaaactgt gggttacagt ctattatggc 120

gttccagtgt ggaaagaagc tacaacaaca ctgttctgtg cctccgatgc caaggcctat 180

gatacagaag tgcataacgt ctgggctaca catgcttgtg tgcctaccga tcctaatcct 240

caggaggtcg tcctcgaaaa cgtcacagaa aactttaata tgtggaaaaa caatatggtc 300

gaacagatgc acgaagatat catttctctg tgggatcaga gtctcaagcc ttgtgtgaaa 360

ctgacacctc tgtgcgtcac actcaattgc acagatgatg tccggaacgt cacaaacaat 420

gctacaaata ccaactcctc ctggggtgaa cctatggaaa aaggcgaaat caaaaattgt 480

tcctttaata tcacaaccag catccgcaac aaagtccaga aacagtatgc tctcttttac 540

aaactcgacg tcgtgcctat cgataatgac tccaacaata caaattaccg cctcatctcc 600

tgtaacacct ccgtgattac tcaggcctgt cctaaagtct cttttgagcc tatcccaatt 660

cactattgtg cacctgctgg atttgccatc ctcaagtgta atgacaagaa gtttaacggt 720

accggtcctt gtaccaacgt gtccacagtg cagtgtacac acggaattag acctgtggtg 780

tctactcagc tgctcctgaa tggctctctg gccgaagagg aagtcgtgat tcggagcgag 840

aactttacaa ataacgctaa aacaatcatg gtccagctca atgtctccgt cgagattaac 900

tgtaccagac ctaacaataa cactcgcaag tccatccaca ttggaccagg acgcgccttt 960

tacaccgctg gtgacattat cggagatatc aggcaggcac actgtaatat ctctcgcgcc 1020

aactggaaca acactctcag acagattgtc gagaagctcg gtaaacagtt tggtaacaac 1080

aaaacaatcg tctttaatca cagctctggc ggcgatcctg agatcgtcat gcattccttc 1140

aattgcggag gggagttctt ttattgcaac tctaccaagc tctttaactc cacatggact 1200

tggaataaca gcacatggaa caataccaaa cgctccaacg atacagagga acacatcact 1260

ttgccatgca gaatcaagca aatcattaac atgtggcaag aggtgggtaa agccatgtat 1320

gctcctccta tcagaggaca gatcagatgc agctccaaca ttacaggcct gctcctgaca 1380

agagatggcg gaaacgacac ctccggaaca gagatcttca gaccaggcgg aggagacatg 1440

agagacaact ggagaagcga actctataag tataaggtcg tcaagattga gccacttgga 1500

gtggctccca caaaggccaa gagacgcgtg gtgcagtccg aaaagtccgc cgtcggaatt 1560

ggagctgtgt ttctcggatt tctgggagct gccggctcta ccatgggagc agcctccatg 1620

acactgacag tccaggctag actgctgctg agtggcattg tccagcaaca gaacaatctc 1680

ctgagagcca ttgaagctca gcaacatctc ctccagctca cagtctgggg catcaaacag 1740

ctccaggcaa gagtgctcgc cgtcgagcgg tacctgaaag accagcaact cctcggcatt 1800

tggggctgtt ccggaaaact gatctgcacc acaacagttc cctggaatgc ctcttggagc 1860

aacaaatctc tcgataagat ttggaataac atgacttgga tggagtggga aagagaaatc 1920

aacaactaca cctctctcat ctacacactc atcgaagagt ctcaaaatca gcaagaaaag 1980

aatgaacagg agctcctcga gctggataag tgggcttctc tctggaattg gttcgatatc 2040

tctaactggc tctggtgata a 2061

<210> 40
<211> 4029
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotide sequence of Mos2 Gag-Pol antigen

<400> 40
atgggcgcca gagcctctat cctgcgcgga ggcaaactgg ataagtggga aaagattaga 60

ctccgacctg gcggtaaaaa gcattatatg ctcaaacacc tcgtctgggc tagcagagaa 120

ctcgagagat tcgctctgaa ccctggtctc ctggaaacat ccgaagggtg taaacagatt 180

atcaaacagc tccagcctgc actccagact ggaacagagg aacttcgctc tctgtttaat 240

accgtggcta cactgtattg tgtgcacgct gaaatcgaag tccgcgacac aaaagaagct 300

ctcgacaaaa ttgaggaaga gcagaacaaa tctcagcaga agacacagca ggctaaggaa 360

gccgacggaa aagtgagcca gaattatccc attgtccaaa atctccaagg acagatggtg 420

catcagccaa tctctccaag aacactcaac gcctgggtca aggtcataga agagaaggca 480

ttctcacctg aagtcattcc aatgttcacc gctctgtccg aaggcgcaac accacaggat 540

ctgaacacta tgctcaatac cgtcggcgga caccaggcag caatgcagat gctcaaggat 600

acaatcaatg aagaggcagc tgagtgggat agactccatc ctgtgcatgc cggtccagtc 660

gcacctggac agatgcgcga gcctagaggc tccgacattg ctggcacaac cagtaacctc 720

caggagcaga tcgcttggat gacttccaat ccacctattc cagtcggaga tatctacaaa 780

cgctggatca ttctcggtct gaacaaaatc gtgcggatgt actctcctac cagcatcctc 840

gatattaagc aaggtccaaa agaacctttt cgagactatg tcgacagatt ctttaaaaca 900

ctgcgcgcag aacaggctac acaggacgtg aagaactgga tgactgatac actcctcgtg 960

cagaatgcaa atccagactg taaaacaatc ctgagagctc tcggtccagg cgctacactg 1020

gaagagatga tgactgcatg tcaaggtgtc ggtggaccta gccacaaagc tcgcgtgctg 1080

gcagaggcta tgtcacagac caattccaca atcctcatgc aacgctccaa tttcaaaggc 1140

tccaagcgca ttgtcaaatg ctttaactgt ggcaaagaag gacatatcgc tcggaattgc 1200

cgcgcaccac gcaagaaagg atgttggaag tgcggcaagg aaggacatca gatgaaagac 1260

tgtactgaga gacaagctaa ttttctcggc aaaatctggc catctcacaa aggacgacct 1320

ggaaatttcc tgcagtctcg gccagaacct acagctcctc ctgccgagtc cttcagattc 1380

gaagagacta caccagctcc taaacaggaa cctaaggata gagaacctct gacctctctg 1440

cgcagcctgt ttggctccga tcctctgtcc cagatggcac caatttctcc aatcgaaacc 1500

gttcctgtca agctcaagcc aggcatggat ggaccaaaag tcaaacaatg gccactcact 1560

gaggagaaaa tcaaggctct ggtcgaaatc tgcacagaaa tggaaaagga aggaaagatt 1620

tccaaaatcg gaccagaaaa tccttacaac acacctatct ttgctattaa gaagaaggac 1680

tccacaaagt ggcgaaagct ggtcgacttt cgcgagctga acaagagaac tcaggacttc 1740

tgggaagtgc aactcggtat tccacatcct gcaggactca agaaaaagaa atctgtcact 1800

gtgctcgccg tcggtgacgc ttacttttct gtgccactgg atgaagattt tcgcaagtac 1860

accgcattca caatcccttc cattaacaat gagacacctg gtattcgcta tcagtacaat 1920

gtgcttcctc aaggctggaa aggtagtcct gctattttcc agtcctctat gacaaagatt 1980

cttgagcctt ttcgcaaaca gaatcctgat atcgtcatct accagtatat ggcagctctg 2040

tacgtcggct ctgatctgga aatcggccag catagaacta agattgagga actccgacag 2100

cacctgctcc gctggggttt tactactcct gacaagaagc accagaagga accaccattc 2160

ctctggatgg gttacgaact tcatcctgat aagtggactg tgcagccaat tgtcctgcct 2220

gaaaaggatt cttggacagt caatgacatc cagaaactcg tcggaaaact caactgggct 2280

tctcagatct atgccggcat taaggtcaag cagctctgca aactcctgag aggcacaaag 2340

gcactgacag aagtggttcc tctcactgaa gaagcagaac tcgaactcgc tgagaaccgc 2400

gaaattctca aagaaccagt gcatggtgtc tattatgatc caagcaaaga tctcattgca 2460

gagattcaga aacaaggcca aggccagtgg acttaccaaa tctatcagga acctttcaaa 2520

aatctcaaga caggcaaata cgctcggatg cgaggcgctc acaccaatga tgtcaagcaa 2580

ctcacagagg cagtgcagaa gattgccaca gagtctattg tgatctgggg aaagactcca 2640

aagtttaagc ttccaatcca aaaggagact tgggaagctt ggtggactga atattggcag 2700

gcaacttgga ttccagagtg ggagtttgtc aatactccac cactcgtgaa gctctggtat 2760

cagctcgaga aagagcctat cgtcggcgcc gaaacctttt atgtcgctgg tgccgcaaac 2820

cgcgagacaa aactcggaaa agcaggatac gtcaccgata gaggacggca gaaggtcgtc 2880

agcctgaccg acactactaa ccagaagact gcacttcagg caattcatct ggctctccag 2940

gatagcggtc tggaagtcaa tatcgtcacc gctagtcagt acgctctggg tattatccag 3000

gctcagccag acaaaagcga atccgaactc gtgtctcaga ttattgagca gctcatcaag 3060

aaagagaaag tctatctcgc ctgggttccg gctcacaaag gcattggtgg aaatgagcaa 3120

gtcgataagc tcgtcagcag aggaatcagg aaagtcctct tcctggacgg tatcgataag 3180

gcacaggagg aacatgagaa gtaccacagt aactggcgcg ccatggcttc tgagtttaac 3240

ctgcctccaa tcgtcgccaa agagatcgtg gcaagctgtg acaaatgtca gctgaaagga 3300

gaggcaatcc atggccaggt tgactgctca ccaggaattt ggcagctcgc ctgcactcat 3360

ctggaaggaa aagtgattct ggtcgctgtg catgtcgcta gtggctacat cgaggctgag 3420

gtcatacctg cagagacagg acaggagact gcttattttc tgctcaagct cgccggaaga 3480

tggccagtca agaccattca caccgctaac ggctctaatt tcacaagcgc cacagtcaaa 3540

gcagcatgtt ggtgggctgg tatcaaacag gaattcggca ttccttataa tccacagtct 3600

caaggcgtcg tggctagtat caacaaagaa ctcaaaaaga tcattggcca agtcagagac 3660

caggctgagc atctcaaaac tgcagtgcaa atggctgtgt ttattcataa ctttaagaga 3720

aaaggtggca tcggcgagta cagcgctggc gagcgcatcg tggatattat tgcttcagat 3780

atacagacta aggaactgca gaaacaaatt accaagatcc agaactttag agtctactac 3840

agagattctc gagatcctct ctggaaagga ccagcaaaac ttctgtggaa aggagaaggt 3900

gcagtcgtga tccaggataa ctctgacatc aaagtggtgc ctcggagaaa ggccaaaatc 3960

attagagatt acggaaagca gatggcaggc gatgattgtg tcgctagtag acaggatgag 4020

gattgataa 4029

<210> 41
<211> 2139
<212> DNA

<213> Artificial Sequence

<220>
<223> nucleotide sequence of Env Mos2-C4D7 antigen

<400> 41
atgcgagtca gaggtatgct gagaaattgg cagcagtggt ggatttggtc agcctcgga 60

ttctggatgc tgatgatcta cagcgtcatg ggtaatctct gggtcacagt gtattacgga 120

gttcctgtct ggaaggacgc caagactaca ctcttttgcg cctctgacgc caaagcttac 180

gaaaaggaag tccacaatgt gtgggcaact catgcctgtg ttcctacaga tccaaatcca 240

caggagatcg tgctcggcaa tgtcaccgag aatttcaaca tgtggaagaa tgatatggtg 300

gatcaaatgc atgaggacat catttccctc tgggacgcct ctctggaacc atgtgtcaag 360

ctcactccac tgtgtgtgac cctcaactgc agaaacgtgc gcaacgtgtc ctccaatggc 420

acatacaata tcattcataa tgagacttat aaggaaatga agaattgctc tttcaatgcc 480

accacagtcg tcgaggatcg caaacagaaa gtccatgctc tgttttaccg gctggatatc 540

gttcctctcg atgagaacaa ttcctccgag aagtcctctg agaactctag cgagtactac 600

aggctcatta attgtaatac ctctgccatc acacaggctt gtccaaaggt ctccttcgat 660

cctattccta tccattactg tgctcctgcc ggatacgcta ttctcaaatg taacaacaag 720

acattcaatg gtactggtcc atgcaacaat gtgtctaccg tccagtgcac tcatggtatt 780

aagcctgtcg tcagtacaca gctcctgctc aatggatctc tcgctgagga agaaatcatt 840

atcagaagtg aaaacctcac taacaacgcc aaaaccatta ttgtccatct gaacgagaca 900

gtcaatatca catgcacacg acctaataac aataccagaa agtctatcag aatcggacct 960

ggccagacat tctatgccac aggcgatatc attggtgaca ttagacaggc tcattgcaat 1020

ctgtccagag atggttggaa taagacactc caaggtgtca agaagaaact cgccgaacac 1080

tttcctaaca agaccattaa gtttgcccct cactcaggcg gtgacctcga gattacaaca 1140

cacaccttta actgtagagg cgaattcttc tactgtaaca caagcaacct cttcaacgag 1200

agcaacatcg agcggaacga cagcatcatt acacttccat gtcgcatcaa gcagatcatt 1260

aatatgtggc aggaagtcgg acgcgctatc tacgctccac ctattgccgg aaacatcaca 1320

tgtcggagca atattaccgg actcctgctc acacgcgacg gtggctctaa caatggcgtg 1380

ccaaatgata ccgaaacctt tagacctggt ggaggcgaca tgcgcaacaa ttggcgctct 1440

gaactgtaca agtacaaagt cgtcgaagtc aaacctctcg gagtcgctcc taccgaggct 1500

aaacgcagag tggtggaacg cgagaagcgg gctgtcggta tcggtgcagt gttcctaggc 1560

atcctcggcg cagccggcag cacaatgggc gctgcttcta ttacactcac tgtgcaggcc 1620

agacagctcc tgagcggaat tgtgcagcag caatcaaatc tgctgcgcgc tatcgaagca 1680

cagcagcata tgctccaact gactgtttgg ggtattaagc aactgcagac tagagtcctg 1740

gccattgaac ggtatctcca ggatcagcag ctgctcggac tctggggatg ctctggcaag 1800

ctcatctgta caacagctgt gccttggaac acttcctggt ctaacaagtc tcagaccgat 1860

atttgggata atatgacatg gatgcagtgg gataaggaaa tcggtaatta tacaggcgag 1920

atctaccgac tgctcgagga atctcagaat caacaggaga agaacgaaaa ggatctcctg 1980

gctctcgact cctggaacaa tctgtggaac tggtttagca tttccaagtg gctgtggtac 2040

atcaagatct tcatcatgat cgtgggcggc ctgatcggcc tgcggatcat ctttgccgtg 2100

ctgagcatcg tgaaccgcgt gcggcagggc tactgataa 2139

<210> 42
<211> 124
<212> DNA
<213> Artificial Sequence

<220>
<223> Pr13.5 Long Promoter Sequence

<400> 42
taaaaataga aactataatc atataatagt gtaggttggt agtattgctc ttgtgactag 60

agactttagt taaggtactg taaaaataga aactataatc atataatagt gtaggttggt 120

agta 124

<210> 43
<211> 227
<212> DNA
<213> Artificial Sequence

<220>
<223> PrHyb Promoter Sequence

<400> 43
gttttgaaaa ttttttttata ataaatatcc ggtaaaaatt gaaaaactat tctaatttat 60

tgcacggtcc ggtaaaaatt gaaaaactat tctaatttat tgcacggtcc ggtaaaaatt 120

gaaaaactat tctaatttat tgcacggtcc ggtaaaaatt gaaaaactat tctaatttat 180

tgcacggtcc ggtaaaaatt gaaaaactat tctaatttat tgcacgg 227

<210> 44
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Env peptide

<400> 44

Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr Ala Gly Asp Ile
1 5 10 15

<210> 45
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Gag peptide

<400> 45

Ala Met Gln Met Leu Lys Glu Thr Ile
1 5

<210> 46
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Pol peptide

<400> 46

Tyr Tyr Asp Pro Ser Lys Asp Leu Ile
1 5