UPVG0053WO2_ST25

SEQUENCE LISTING

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<120> DNA ANTIBODY CONSTRUCTS AND METHOD OF USING SAME

<130> UPVG0053 WO2

<150> PCT/US13/075137
<151> 2013-12-13

<160> 78

<170> PatentIn version 3.5

<210> 1
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence of HIV-1 Env-4E10 Ig

<400> 1

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Arg
20 25 30

Pro Gly Ser Ser Val Thr Val Ser Cys Lys Ala Ser Gly Gly Ser Phe
35 40 45

Ser Thr Tyr Ala Leu Ser Trp Val Arg Gln Ala Pro Gly Arg Gly Leu
50 55 60

Glu Trp Met Gly Gly Val Ile Pro Leu Leu Thr Ile Thr Asn Tyr Ala
65 70 75 80

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Pro Arg Phe Gln Gly Arg Ile Thr Ile Thr Ala Asp Arg Ser Thr Ser
                85                  90                  95

Thr Ala Tyr Leu Glu Leu Asn Ser Leu Arg Pro Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Arg Glu Gly Thr Thr Gly Trp Gly Trp Leu Gly Lys
        115                 120                 125

Pro Ile Gly Ala Phe Ala His Trp Gly Gln Gly Thr Leu Val Thr Val
    130                 135                 140

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
145                 150                 155                 160

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
                165                 170                 175

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
            180                 185                 190

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
        195                 200                 205

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
    210                 215                 220

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
225                 230                 235                 240

Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
                245                 250                 255

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
            260                 265                 270
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Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
        275                 280                 285

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
    290                 295                 300

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
305                 310                 315                 320

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
                325                 330                 335

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
            340                 345                 350

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
        355                 360                 365

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
    370                 375                 380

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
385                 390                 395                 400

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
                405                 410                 415

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
            420                 425                 430

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
        435                 440                 445

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
    450                 455                 460
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Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Arg Gly Arg Lys
465                 470                 475                 480


Arg Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala
                485                 490                 495


Gly Asp Val Glu Glu Asn Pro Gly Pro Met Val Leu Gln Thr Gln Val
            500                 505                 510


Phe Ile Ser Leu Leu Leu Trp Ile Ser Gly Ala Tyr Gly Glu Ile Val
        515                 520                 525


Leu Thr Gln Ser Pro Gly Thr Gln Ser Leu Ser Pro Gly Glu Arg Ala
    530                 535                 540


Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Asn Asn Lys Leu Ala
545                 550                 555                 560


Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly
                565                 570                 575


Ala Ser Ser Arg Pro Ser Gly Val Ala Asp Arg Phe Ser Gly Ser Gly
            580                 585                 590


Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp
        595                 600                 605


Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Gln Ser Leu Ser Thr Phe
    610                 615                 620


Gly Gln Gly Thr Lys Val Glu Lys Arg Thr Val Ala Ala Pro Ser Val
625                 630                 635                 640


Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser
                645                 650                 655
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Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln
            660                 665                 670

Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val
        675                 680                 685

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu
    690                 695                 700

Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu
705                 710                 715                 720

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
                725                 730                 735

Gly Glu
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<210> 2
<211> 768
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence of HIV-1 Env-PG9 Ig

<400> 2

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Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1               5                   10                  15

Thr His Ala Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Phe Leu
            20                  25                  30

Arg Gly Val Gln Cys Gln Arg Leu Val Glu Ser Gly Gly Gly Val Val
        35                  40                  45

Gln Pro Gly Ser Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asp
```

```
    50                  55                  60

Phe Ser Arg Gln Gly Met His Trp Val Arg Gln Ala Pro Gly Gln Gly
65                  70                  75                  80

Leu Glu Trp Val Ala Phe Ile Lys Tyr Asp Gly Ser Glu Lys Tyr His
                85                  90                  95

Ala Asp Ser Val Trp Gly Arg Leu Ser Ile Ser Arg Asp Asn Ser Lys
            100                 105                 110

Asp Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala
        115                 120                 125

Thr Tyr Phe Cys Val Arg Glu Ala Gly Gly Pro Asp Tyr Arg Asn Gly
    130                 135                 140

Tyr Asn Tyr Tyr Asp Phe Tyr Asp Gly Tyr Tyr Asn Tyr His Tyr Met
145                 150                 155                 160

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
                165                 170                 175

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
            180                 185                 190

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
        195                 200                 205

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
    210                 215                 220

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
225                 230                 235                 240

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
```

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                245                 250                 255

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
            260                 265                 270

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
        275                 280                 285

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
    290                 295                 300

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
305                 310                 315                 320

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
                325                 330                 335

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
            340                 345                 350

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
        355                 360                 365

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
    370                 375                 380

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
385                 390                 395                 400

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
                405                 410                 415

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
            420                 425                 430

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
```

```
        435                 440                 445

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
    450                 455                 460

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
465                 470                 475                 480

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
                485                 490                 495

Leu Ser Leu Ser Pro Gly Lys Arg Gly Arg Lys Arg Arg Ser Gly Ser
            500                 505                 510

Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu
        515                 520                 525

Asn Pro Gly Pro Met Ala Trp Thr Pro Leu Phe Leu Phe Leu Leu Thr
    530                 535                 540

Cys Cys Pro Gly Gly Ser Asn Ser Gln Ser Ala Leu Thr Gln Pro Ala
545                 550                 555                 560

Ser Val Ser Gly Ser Pro Gly Gln Ser Ile Thr Ile Ser Cys Asn Gly
                565                 570                 575

Thr Ser Asn Asp Val Gly Gly Tyr Glu Ser Val Ser Trp Tyr Gln Gln
            580                 585                 590

His Pro Gly Lys Ala Pro Lys Val Val Ile Tyr Asp Val Ser Lys Arg
        595                 600                 605

Pro Ser Gly Val Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr
    610                 615                 620

Ala Ser Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Gly Asp Tyr
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625 630 635 640

Tyr Cys Lys Ser Leu Thr Ser Thr Arg Arg Arg Val Phe Gly Thr Gly
645 650 655

Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
660 665 670

Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
675 680 685

Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp
690 695 700

Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro
705 710 715 720

Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu
725 730 735

Thr Pro Glu Gln Trp Lys Ser His Lys Ser Tyr Ser Cys Gln Val Thr
740 745 750

His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
755 760 765

<210> 3
<211> 792
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic Acid Sequence Encoding the Heavy Chain (VH-CH1) of HIV-1 Env Fab

<400> 3
aagcttgccg ccaccatgga gactgataca ctgctgctgt gggtgctgct gctgtgggtg 60

ccagggtcaa ccggagatgg ggctcaggtc agctggtcc agagcggcgg acagatgaag 120

aaacccggcg agagcatgag gatctcctgc agagcatctg gatacgagtt catcgactgt 180

accctgaact ggattaggct ggctcctgga aagagaccag agtggatggg gtggctgaaa 240

ccacgagggg gagcagtgaa ttacgcccgg cccctgcagg gacgagtgac catgaccagg 300

gacgtgtaca gcgataccgc cttcctggag ctgcggtccc tgacagtgga cgatactgct 360

gtctacttct gcacacgcgg aaagaactgt gactataatt gggattttga acactggggc 420

cggggaacac ccgtgatcgt cagctccccc agtactaagg gaccttcagt gtttccactg 480

gccccctcta gtaaatccac ctctggaggg acagccgctc tgggatgcct ggtgaaagat 540

tatttccccg aacctgtgac cgtcagttgg aactcagggg ctctgacttc tggcgtgcac 600

acctttcctg cagtcctgca gtcaagcggg ctgtacagtc tgtcctctgt ggtcactgtg 660

cctagttcaa gcctgggcac tcagacctat atttgtaacg tgaatcataa gccatccaat 720

acaaaagtgg acaaaaaagc cgaacccaaa tcctgttacc cttatgatgt gcccgactac 780

gcctgactcg ag 792

<210> 4
<211> 756
<212> DNA
<213> Artificial Sequence

<220>
<223> Light Chain (VL-CL) of HIV-1 Env Fab

<400> 4
aagcttgccg ccaccatgga aaccgataca ctgctgctgt gggtgctgct gctgtgggtg 60

ccaggaagta ccggggatgg ggctcaggtc cagattgtgc tgactcagtc ccctgggacc 120

ctgtctctga gtccaggcga gacagctatc atttcatgcc gaactagcca gtacggcagc 180

ctggcttggt atcagcagcg accaggacag gcaccacgac tggtcatcta ctcaggcagc 240

acaagggccg ctggcatccc cgacaggttc tccggcagca ggtgggggcc tgattacaac 300

ctgactatct ctaatctgga gagtggggac tttggcgtgt actattgcca gcagtatgag 360

ttcttcggcc agggaactaa ggtgcaggtg gacatcaaaa gaaccgtggc agccccatcc 420

gtcttcattt ttccccttc tgatgagcag ctgaagtcag gcaccgccag cgtggtctgt 480

ctgctgaaca atttctaccc ccgggaagcc aaggtgcagt ggaaagtgga caacgctctg 540

cagagtggaa attcacagga gagcgtgacc gaacaggact ccaaggattc tacatatagt 600

ctgagcagca ccctgaccct gagtaaagca gattacgaga agcacaaagt gtatgcctgt 660

gaagtcacac atcagggcct gaggagcccc gtgactaaaa gtttcaaccg aggagagtgc 720

tacccttatg atgtgcccga ctacgcctaa ctcgag 756

<210> 5
<211> 731
<212> PRT
<213> Artificial Sequence

<220>
<223> VRC01 IgG

<400> 5

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1 5 10 15

His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Gln Met Lys Lys Pro
20 25 30

Gly Glu Ser Met Arg Ile Ser Cys Arg Ala Ser Gly Tyr Glu Phe Ile
35 40 45

Asp Cys Thr Leu Asn Trp Ile Arg Leu Ala Pro Gly Lys Arg Pro Glu
50 55 60

Trp Met Gly Trp Leu Lys Pro Arg Gly Gly Ala Val Asn Tyr Ala Arg
65 70 75 80

Pro Leu Gln Gly Arg Val Thr Met Thr Arg Asp Val Tyr Ser Asp Thr
85 90 95

```
Ala Phe Leu Glu Leu Arg Ser Leu Thr Val Asp Asp Thr Ala Val Tyr
            100                 105                 110

Phe Cys Thr Arg Gly Lys Asn Cys Asp Tyr Asn Trp Asp Phe Glu His
        115                 120                 125

Trp Gly Arg Gly Thr Pro Val Ile Val Ser Ser Pro Ser Thr Lys Gly
    130                 135                 140

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
145                 150                 155                 160

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
                165                 170                 175

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
            180                 185                 190

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
        195                 200                 205

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

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Ala Glu Pro Lys
225                 230                 235                 240

Ser Cys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
                245                 250                 255

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
            260                 265                 270

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
        275                 280                 285
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```
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
    290                 295                 300

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
305                 310                 315                 320

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
                325                 330                 335

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
            340                 345                 350

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
        355                 360                 365

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
    370                 375                 380

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
385                 390                 395                 400

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
                405                 410                 415

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
            420                 425                 430

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
        435                 440                 445

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
    450                 455                 460

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Arg Gly Arg Lys Arg Arg
465                 470                 475                 480
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```
Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp
                485                 490                 495

Val Glu Glu Asn Pro Gly Pro Met Asp Trp Thr Trp Ile Leu Phe Leu
            500                 505                 510

Val Ala Ala Ala Thr Arg Val His Ser Glu Ile Val Leu Thr Gln Ser
        515                 520                 525

Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Thr Ala Ile Ile Ser Cys
    530                 535                 540

Arg Thr Ser Gln Tyr Gly Ser Leu Ala Trp Tyr Gln Gln Arg Pro Gly
545                 550                 555                 560

Gln Ala Pro Arg Leu Val Ile Tyr Ser Gly Ser Thr Arg Ala Ala Gly
                565                 570                 575

Ile Pro Asp Arg Phe Ser Gly Ser Arg Trp Gly Pro Asp Tyr Asn Leu
            580                 585                 590

Thr Ile Ser Asn Leu Glu Ser Gly Asp Phe Gly Val Tyr Tyr Cys Gln
        595                 600                 605

Gln Tyr Glu Phe Phe Gly Gln Gly Thr Lys Val Gln Val Asp Ile Lys
    610                 615                 620

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
625                 630                 635                 640

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
                645                 650                 655

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
            660                 665                 670
```

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
675 680 685

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
690 695 700

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Arg Ser
705 710 715 720

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
725 730

<210> 6
<211> 819
<212> DNA
<213> Artificial Sequence

<220>
<223> Optimized Nucleic Acid Sequence Encoding IgG Heavy Chain

<400> 6
ggatccgcca ccatggaaac cgacactctg ctgctgtggg tgctgctgct gtgggtgccc 60

ggctcaacag gcgacggcgc tcaggtccag ctggtccagt ctggagctgt gatcaagacc 120

cctggcagct ccgtcaaaat ttcttgcaga gcaagtggct acaacttccg ggactatagc 180

atccactggg tgcggctgat tcctgataag ggatttgagt ggatcggctg gatcaagcca 240

ctgtggggcg ctgtgtccta cgcaaggcag ctgcaggggc gcgtctccat gacacgacag 300

ctgtctcagg acccagacga tcccgattgg ggggtggcct acatggagtt cagtggactg 360

actcccgcag acaccgccga atatttttgc gtgcggagag gctcctgcga ctactgtggg 420

gatttcccat ggcagtattg gtgtcaggga actgtggtcg tggtctctag tgcatcaacc 480

aagggcccca gcgtgtttcc tctggcccca tcaagcaaaa gtacatcagg aggaactgca 540

gctctgggat gtctggtgaa ggattacttc cccgagcctg tgaccgtcag ctggaactcc 600

ggagcactga cctccggagt gcacacattt cccgctgtcc tgcagtcctc tgggctgtac 660

tctctgagtt cagtggtcac agtgcctagc tcctctctgg gcacccagac atatatctgc 720

aacgtcaatc ataagccaag taatactaaa gtggacaaga aagtcgaacc caaatcatgt 780

tacccctatg acgtgcctga ttatgcttga taactcgag 819

<210> 7
<211> 753
<212> DNA
<213> Artificial Sequence

<220>
<223> Optimized Nucleic Acid Sequence Encoding IgG Light Chain

<400> 7
ggatccgcca ccatggagac tgatacactg ctgctgtggg tgctgctgct gtgggtgcct 60

ggctcaaccg gcgacggggc tcaggtccag attgtgctga cccagagccc tggcatcctg 120

tcactgagcc caggagagac cgcaacactg ttctgcaagg cctcccaggg cgggaacgct 180

atgacatggt accagaaacg gagaggacag gtgccccgac tgctgatcta tgacacttca 240

aggcgagcaa gcggagtgcc tgatcgattt gtcggcagcg gctctgggac agacttcttt 300

ctgactatta ataagctgga cagagaggat ttcgctgtgt actattgcca gcagtttgaa 360

ttctttggac tgggcagcga gctggaagtg cacaggaccg tcgccgctcc aagtgtgttc 420

atttttcccc ctagcgatga gcagctgaaa tccgggacag cctctgtggt ctgtctgctg 480

aacaatttct acccccgcga agcaaaggtg cagtggaaag tcgacaacgc cctgcagagt 540

ggcaattcac aggagagcgt gaccgaacag gactccaagg attctacata tagtctgagc 600

tccactctga ccctgtctaa agctgattac gagaagcaca aagtgtatgc atgcgaagtc 660

actcatcagg gcctgtctag tcctgtgacc aagagcttta accgagggga gtgttaccca 720

tatgacgtcc ccgattacgc ctgataactc gag 753

<210> 8
<211> 18
<212> PRT
<213> Artificial Sequence

<220>

<223> IgE1 Signal Peptide of VRC-1 IgG

<400> 8

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Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1               5                   10                  15


His Ser
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<210> 9
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable Heavy Region of VRC01 IgG

<400> 9

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Gln Val Gln Leu Val Gln Ser Gly Gly Gln Met Lys Lys Pro Gly Glu
1               5                   10                  15


Ser Met Arg Ile Ser Cys Arg Ala Ser Gly Tyr Glu Phe Ile Asp Cys
            20                  25                  30


Thr Leu Asn Trp Ile Arg Leu Ala Pro Gly Lys Arg Pro Glu Trp Met
        35                  40                  45


Gly Trp Leu Lys Pro Arg Gly Gly Ala Val Asn Tyr Ala Arg Pro Leu
    50                  55                  60


Gln Gly Arg Val Thr Met Thr Arg Asp Val Tyr Ser Asp Thr Ala Phe
65                  70                  75                  80


Leu Glu Leu Arg Ser Leu Thr Val Asp Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95


Thr Arg Gly Lys Asn Cys Asp Tyr Asn Trp Asp Phe Glu His Trp Gly
            100                 105                 110
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Arg Gly Thr Pro Val Ile Val Ser Ser Pro Ser Thr Lys Gly
        115   120   125

<210> 10
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> Constant Heavy region 1 (CH1) of VRC01 IgG

<400> 10

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
1   5   10   15

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

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
        35   40   45

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
    50   55   60

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
65   70   75   80

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Ala Glu Pro Lys
                85   90   95

Ser Cys

<210> 11
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Hinge Region of VRC01 IgG

<400> 11

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1   5   10   15

<210> 12
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Constant Heavy Region 2 (CH2) of VRC01 IgG

<400> 12

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
1   5   10   15

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            20   25   30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
        35   40   45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    50   55   60

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65   70   75   80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                85   90   95

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
            100   105   110

<210> 13
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Constant Heavy Region 3 (CH3) of VRC01 IgG

<400> 13

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
1 5 10 15

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
20 25 30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

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

<220>
<223> Furin Cleavage Site of VRC01 IgG

<400> 14

Arg Gly Arg Lys Arg Arg Ser
1 5

<210> 15
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> GSG Linker and P2A Peptide of VRC01 IgG

<400> 15

Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val
1 5 10 15

Glu Glu Asn Pro Gly Pro
20

<210> 16
<211> 104
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable Light Region (VL) of VRC01 IgG

<400> 16

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Thr Ala Ile Ile Ser Cys Arg Thr Ser Gln Tyr Gly Ser Leu Ala
20 25 30

Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Val Ile Tyr Ser
35 40 45

Gly Ser Thr Arg Ala Ala Gly Ile Pro Asp Arg Phe Ser Gly Ser Arg
50 55 60

```
Trp Gly Pro Asp Tyr Asn Leu Thr Ile Ser Asn Leu Glu Ser Gly Asp
65                  70                  75                  80


Phe Gly Val Tyr Tyr Cys Gln Gln Tyr Glu Phe Phe Gly Gln Gly Thr
                85                  90                  95


Lys Val Gln Val Asp Ile Lys Arg
            100
```

<210> 17
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Constant Light Region (CL, kappa) of VRC01 IgG

<400> 17

```
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1               5                   10                  15


Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
            20                  25                  30


Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
        35                  40                  45


Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
    50                  55                  60


Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65                  70                  75                  80


His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Arg Ser Pro
                85                  90                  95


Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
            100                 105
```

<210> 18
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IgG Heavy Chain Signal Peptide of HIV-1 Env-PG9 Ig

<400> 18

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala

<210> 19
<211> 154
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable Heavy Region of HIV-1 Env-PG9 Ig

<400> 19

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

Gln Cys Gln Arg Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly
20 25 30

Ser Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser Arg
35 40 45

Gln Gly Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp
50 55 60

Val Ala Phe Ile Lys Tyr Asp Gly Ser Glu Lys Tyr His Ala Asp Ser
65 70 75 80

```
Val Trp Gly Arg Leu Ser Ile Ser Arg Asp Asn Ser Lys Asp Thr Leu
                85                  90                  95


Tyr Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Thr Tyr Phe
            100                 105                 110


Cys Val Arg Glu Ala Gly Gly Pro Asp Tyr Arg Asn Gly Tyr Asn Tyr
        115                 120                 125


Tyr Asp Phe Tyr Asp Gly Tyr Tyr Asn Tyr His Tyr Met Asp Val Trp
    130                 135                 140


Gly Lys Gly Thr Thr Val Thr Val Ser Ser
145                 150


<210>  20
<211>  98
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Constant Heavy region 1 (CH1) of HIV-1 Env-PG9 Ig

<400>  20

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1               5                   10                  15


Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30


Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45


Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60
```

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val

<210> 21
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Hinge Region of HIV-1 Env-PG9 Ig

<400> 21

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15

<210> 22
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Constant Heavy Region 2 (CH2) of HIV-1 Env-PG9 Ig

<400> 22

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
1 5 10 15

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
100 105 110

<210> 23
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Constant Heavy Region 3 (CH3) of HIV-1 Env-PG9 Ig

<400> 23

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
1 5 10 15

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
20 25 30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 24
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Furin Cleavage Site of HIV-1 Env-PG9 Ig

<400> 24

Arg Gly Arg Lys Arg Arg Ser
1 5

<210> 25
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> GSG Linker and P2A Peptide of HIV-1 Env-PG9 Ig

<400> 25

Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val
1 5 10 15

Glu Glu Asn Pro Gly Pro
20

<210> 26
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Human Lamba Light Chain Signal Peptide of HIV-1 Env-PG9 Ig

<400> 26

Met Ala Trp Thr Pro Leu Phe Leu Phe Leu Leu Thr Cys Cys Pro Gly
1 5 10 15

Gly Ser Asn Ser
20

<210> 27
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable Light Region (VL) of HIV-1 Env-PG9 Ig

<400> 27

Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

Ser Ile Thr Ile Ser Cys Asn Gly Thr Ser Asn Asp Val Gly Gly Tyr
20 25 30

Glu Ser Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Val
35 40 45

Val Ile Tyr Asp Val Ser Lys Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Gly Asp Tyr Tyr Cys Lys Ser Leu Thr Ser Thr
85 90 95

Arg Arg Arg Val Phe Gly Thr Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 28
<211> 106

<212> PRT
<213> Artificial Sequence

<220>
<223> Constant Light Region (CL, lamba) of HIV-1 Env-PG9 Ig

<400> 28

Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
1 5 10 15

Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
20 25 30

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

Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
50 55 60

Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
65 70 75 80

Ser His Lys Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val
85 90 95

Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
100 105

<210> 29
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IgG Heavy Chain Signal Peptide of HIV-1 Env-4E10 Ig

<400> 29

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala

<210> 30
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable Heavy Region of HIV-1 Env-4E10 Ig

<400> 30

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Arg Pro Gly Ser
1 5 10 15

Ser Val Thr Val Ser Cys Lys Ala Ser Gly Gly Ser Phe Ser Thr Tyr
20 25 30

Ala Leu Ser Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Met
35 40 45

Gly Gly Val Ile Pro Leu Leu Thr Ile Thr Asn Tyr Ala Pro Arg Phe
50 55 60

Gln Gly Arg Ile Thr Ile Thr Ala Asp Arg Ser Thr Ser Thr Ala Tyr
65 70 75 80

Leu Glu Leu Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Gly Thr Thr Gly Trp Gly Trp Leu Gly Lys Pro Ile Gly
100 105 110

Ala Phe Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 31
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> Constant Heavy region 1 (CH1) of HIV-1 Env-4E10 Ig

<400> 31

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val

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

<220>
<223> Hinge Region of HIV-1 Env-4E10 Ig

<400> 32

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15

<210> 33
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Constant Heavy Region 2 (CH2) of HIV-1 Env-4E10 Ig

<400> 33

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
1 5 10 15

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
100 105 110

<210> 34
<211> 107
<212> PRT
<213> Artificial Sequence

<220>

<223> Constant Heavy Region 3 (CH3) of HIV-1 Env-4E10 Ig

<400> 34

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
1 5 10 15

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
20 25 30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 35
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Furin Cleavage Site of HIV-1 Env-4E10 Ig

<400> 35

Arg Gly Arg Lys Arg Arg Ser
1 5

<210> 36
<211> 22

<212> PRT
<213> Artificial Sequence

<220>
<223> GSG Linker and P2A Peptide of HIV-1 Env-4E10 Ig

<400> 36

Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val
1 5 10 15

Glu Glu Asn Pro Gly Pro
20

<210> 37
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Human Kappa Light Chain Signal Peptide of HIV-1 Env-4E10 Ig

<400> 37

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

Gly Ala Tyr Gly
20

<210> 38
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Variable Light Region (VL) of HIV-1 Env-4E10 Ig

<400> 38

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Gln Ser Leu Ser Pro Gly
1 5 10 15

```
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Asn Asn
            20                  25                  30

Lys Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45

Ile Tyr Gly Ala Ser Ser Arg Pro Ser Gly Val Ala Asp Arg Phe Ser
    50                  55                  60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Gln Ser Leu
                85                  90                  95

Ser Thr Phe Gly Gln Gly Thr Lys Val Glu
            100                 105
```

<210> 39
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Constant Light Region (CL, kappa) of HIV-1 Env-4E10 Ig

<400> 39

```
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
1               5                   10                  15

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
            20                  25                  30

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
        35                  40                  45

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
    50                  55                  60
```

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
65 70 75 80

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
85 90 95

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
100 105

<210> 40
<211> 744
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic Acid Sequence Encoding the VH-CH1 of anti-Her-2 Fab

<400> 40
ggatccgcca ccatggactg gacatggatt ctgtttctgg tcgccgccgc tacaagagtg 60

cattccgaag tgcagctggt cgagagtgga gggggactgg tgcagcccgg cggatctctg 120

cgactgagtt gcgccgcttc aggcttcacc tttacagact acaccatgga ttgggtgaga 180

caggcacctg gcaagggact ggagtgggtg gctgatgtca acccaaatag tgggggctca 240

atctacaacc agaggttcaa gggcaggttc accctgagcg tggacaggtc caaaaacact 300

ctgtatctgc agatgaattc tctgcgggct gaagataccg cagtctacta ttgcgcccgc 360

aatctgggcc caagcttcta ctttgactat tgggggcagg gcacactggt gactgtcagc 420

tccgcttcta caaagggacc aagcgtgttc ccactggcac cctctagtaa atccacctct 480

ggagggacag cagccctggg ctgtctggtg aaagactatt tccccgagcc tgtgactgtc 540

agctggaact ccggagcact gactagcgga gtgcacacct ttccagccgt cctgcagtca 600

agcggcctgt actccctgtc ctctgtggtc acagtgccta gttcaagcct gggaactcag 660

acctatattt gtaatgtgaa ccataaacca agcaatacaa aggtggacaa gaaggtggaa 720

ccaaaatcct gctgataact cgag 744

<210> 41
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence of the VH-CH1 of anti-Her-2 Fab

<400> 41

```
Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1               5                   10                  15


His Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
            20                  25                  30


Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr
        35                  40                  45


Asp Tyr Thr Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
    50                  55                  60


Trp Val Ala Asp Val Asn Pro Asn Ser Gly Gly Ser Ile Tyr Asn Gln
65                  70                  75                  80


Arg Phe Lys Gly Arg Phe Thr Leu Ser Val Asp Arg Ser Lys Asn Thr
                85                  90                  95


Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
            100                 105                 110


Tyr Cys Ala Arg Asn Leu Gly Pro Ser Phe Tyr Phe Asp Tyr Trp Gly
        115                 120                 125


Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140
```

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

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

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
225 230 235 240

<210> 42
<211> 720
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic Acid Sequence Encoding the VL-CL of anti-Her-2 Fab

<400> 42
ggatccgcca ccatggattg gacttggatt ctgttcctgg tcgccgccgc tacccgcgtg 60

cattccgata ttcagatgac tcagagcccc tcctcactgt cagccagcgt gggcgaccga 120

gtcaccatca catgcaaagc ttctcaggat gtgagtattg gggtcgcatg gtaccagcag 180

aagccaggca aagcacccaa gctgctgatc tattccgcct cttacaggta tacaggagtg 240

cccagcagat tcagtggctc aggaagcggg actgacttta ctctgaccat cagctccctg 300

cagcctgagg atttcgctac ctactattgc cagcagtact atatctaccc atataccttt 360

ggccagggaa caaaagtgga gatcaagcgg accgtggccg ctccctccgt cttcattttt 420

ccccttctg acgaacagct gaagagcgga acagcaagcg tggtctgtct gctgaacaat 480

ttctaccctc gcgaggccaa agtgcagtgg aaggtcgata acgctctgca gtccgggaat 540

tctcaggaga gtgtgactga acaggactca aaagatagca cctattccct gtctagtaca 600

ctgactctga gcaaggcaga ctacgaaaag cacaaagtgt atgcctgtga ggtcacccac 660

caggggctgt caagtcccgt caccaagtcc ttcaatagag gcgaatgctg ataactcgag 720

<210> 43
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence of the VL-CL of anti-Her-2 Fab

<400> 43

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1 5 10 15

His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
20 25 30

Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Ser
35 40 45

Ile Gly Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
50 55 60

Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro Ser Arg Phe
65 70 75 80

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
85 90 95

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Ile Tyr
100 105 110

```
Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val
        115                 120                 125


Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
    130                 135                 140


Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
145                 150                 155                 160


Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
                165                 170                 175


Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
            180                 185                 190


Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
        195                 200                 205


Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
    210                 215                 220


Lys Ser Phe Asn Arg Gly Glu Cys
225                 230


<210>  44
<211>  2241
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Nucleic Acid Sequence Encoding anti-DENV Human IgG

<400>  44
ggatccgcca ccatggactg gacttggagg attctgtttc tggtcgccgc cgctactggg       60

actcacgctc aggcacatct ggtcgaatct ggaggaggag tggtccagcc tggccgatcc      120

ctgcgactgt cttgcgcagc tagcgccttc aacttcagca caaacgcaat gcactgggtg      180

cgacaggcac caggcaaggg actggagtgg gtcgctgtga tctcatacga cggaagccat      240
```

aagtactatg cagattctgt gaaaggccgg ttcaccattt ccagggacaa ttctaagaac 300

accctgtatc tgcagatgaa tagcctgcgc gcagccgata ccgcagtgta ctattgcgca 360

actgtcggcg tgctgacctg gccagtgaac gccgaatact ttcaccattg gggacagggc 420

agtctggtct cagtgagctc cgcaagtact aagggaccat cagtgttccc actggcaccc 480

tctagtaaat ctactagtgg cgggaccgct gcactgggat gtctggtgaa ggactatttc 540

cccgagcctg tcaccgtgag ctggaattcc ggagccctga caagcggcgt ccacactttt 600

cccgctgtgc tgcagtcaag cggactgtac tccctgtcct ctgtggtcac tgtgcctagt 660

tcaagcctgg gcactcagac ctatatctgc aatgtgaacc acaagccctc taacaccaaa 720

gtcgacaaga aagtggaacc taagagctgt gataaaacac atacttgccc accttgtcca 780

gcaccagagc tgctgggagg accaagcgtg ttcctgtttc cacccaagcc taaagacaca 840

ctgatgatta gccggacacc tgaagtcact tgcgtggtcg tggacgtgtc ccacgaggac 900

cccgaagtca agtttaattg gtacgtggat ggcgtcgagg tgcataacgc caagaccaaa 960

ccccgggagg aacagtacaa tagcacatat agagtcgtgt ccgtcctgac tgtgctgcat 1020

caggattggc tgaatgggaa ggagtataag tgcaaagtgt ctaacaaggc tctgcctgca 1080

ccaatcgaga aaaccattag caaggctaaa ggccagccta gggaaccaca ggtgtacaca 1140

ctgcctccaa gtcgcgacga gctgaccaag aatcaggtct ccctgacatg tctggtgaaa 1200

ggcttctatc catcagatat cgccgtggag tgggaaagca acgggcagcc cgaaaacaat 1260

tacaagacca cacccctgt gctggactct gatggcagtt tctttctgta ttctaagctg 1320

accgtggaca aaagtagatg gcagcagggg aatgtctttt catgtagcgt gatgcacgag 1380

gccctgcaca accattacac acagaagtcc ctgtctctga gtcccggaaa gaggggccgc 1440

aaacggagat cagggagcgg agctactaat ttcagcctgc tgaaacaggc aggggatgtg 1500

gaggaaaacc ccggacctat ggcttggacc ccactgttcc tgtttctgct gacatgctgt 1560

cccgggggca gcaattctca gagtgtcctg acacagccac catcagtgag cggagcacca 1620

ggacagaggg tgaccatctc ctgcacaggc agcagcagca acattggcgc cgggtacgac 1680

gtgcattggt atcagcagct gcccggcacc gctcctaagc tgctgatctg tggcaacaat 1740

aaccgcccat ctggggtgcc cgatcgattc tccggctcta aaagtgggac ttcagccagc 1800

ctggctatta ccggcctgca ggccgaggac gaagctgatt actattgcca gagctacgac 1860

tcaagcctga ccggagtcgt gttcggagga ggaaccaagc tgacagtcct gggacagcct 1920

aaagccgctc caagcgtgac actgtttcct ccatcctctg aggaactgca ggcaaacaag 1980

gccaccctgg tgtgcctgat ttccgacttc taccccgggg cagtcactgt ggcttggaag 2040

gcagatagtt cacctgtcaa agccggagtg gagactacca caccatcaaa gcagagcaat 2100

aacaaatacg cagccagctc ctatctgtcc ctgacccctg agcagtggaa gtctcacaaa 2160

tcctattctt gccaggtcac tcacgaagga agcactgtgg agaaaactgt cgcaccaacc 2220

gaatgtagtt gataactcga g 2241

<210> 45
<211> 739
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence of anti-DENV Human IgG

<400> 45

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Gln Ala His Leu Val Glu Ser Gly Gly Gly Val Val Gln
20 25 30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Ala Phe Asn Phe
35 40 45

Ser Thr Asn Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

```
Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser His Lys Tyr Tyr Ala
65                  70                  75                  80


Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
                85                  90                  95


Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Ala Asp Thr Ala Val
            100                 105                 110


Tyr Tyr Cys Ala Thr Val Gly Val Leu Thr Trp Pro Val Asn Ala Glu
        115                 120                 125


Tyr Phe His His Trp Gly Gln Gly Ser Leu Val Ser Val Ser Ser Ala
    130                 135                 140


Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
145                 150                 155                 160


Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
                165                 170                 175


Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
            180                 185                 190


Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
        195                 200                 205


Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
    210                 215                 220


Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
225                 230                 235                 240


Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
                245                 250                 255
```

```
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
            260                 265                 270

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
        275                 280                 285

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
    290                 295                 300

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
305                 310                 315                 320

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
                325                 330                 335

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
            340                 345                 350

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
        355                 360                 365

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
    370                 375                 380

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
385                 390                 395                 400

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
                405                 410                 415

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
            420                 425                 430

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
        435                 440                 445
```

```
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
    450                 455                 460

Lys Ser Leu Ser Leu Ser Pro Gly Lys Arg Gly Arg Lys Arg Arg Ser
465                 470                 475                 480

Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val
                485                 490                 495

Glu Glu Asn Pro Gly Pro Met Ala Trp Thr Pro Leu Phe Leu Phe Leu
            500                 505                 510

Leu Thr Cys Cys Pro Gly Gly Ser Asn Ser Gln Ser Val Leu Thr Gln
        515                 520                 525

Pro Pro Ser Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys
    530                 535                 540

Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val His Trp Tyr
545                 550                 555                 560

Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Cys Gly Asn Asn
                565                 570                 575

Asn Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
            580                 585                 590

Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala
        595                 600                 605

Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser Leu Thr Gly Val Val Phe
    610                 615                 620

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala Ala Pro
625                 630                 635                 640
```

Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys
645 650 655

Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr
660 665 670

Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr
675 680 685

Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr
690 695 700

Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Lys Ser Tyr Ser Cys
705 710 715 720

Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr
725 730 735

Glu Cys Ser

<210> 46
<211> 265
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG Heavy Chain

<400> 46

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Asp Gly Ala Gln Val Gln Leu Val Gln Ser Gly Ala
20 25 30

Val Ile Lys Thr Pro Gly Ser Ser Val Lys Ile Ser Cys Arg Ala Ser
35 40 45

```
Gly Tyr Asn Phe Arg Asp Tyr Ser Ile His Trp Val Arg Leu Ile Pro
    50                  55                  60

Asp Lys Gly Phe Glu Trp Ile Gly Trp Ile Lys Pro Leu Trp Gly Ala
65                  70                  75                  80

Val Ser Tyr Ala Arg Gln Leu Gln Gly Arg Val Ser Met Thr Arg Gln
                85                  90                  95

Leu Ser Gln Asp Pro Asp Asp Pro Asp Trp Gly Val Ala Tyr Met Glu
            100                 105                 110

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

Arg Gly Ser Cys Asp Tyr Cys Gly Asp Phe Pro Trp Gln Tyr Trp Cys
    130                 135                 140

Gln Gly Thr Val Val Val Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
145                 150                 155                 160

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
                165                 170                 175

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
            180                 185                 190

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
        195                 200                 205

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
    210                 215                 220

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
225                 230                 235                 240
```

```
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
                245                 250                 255


Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
            260                 265


<210>  47
<211>  243
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  IgG Light Chain

<400>  47

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1               5                   10                  15


Gly Ser Thr Gly Asp Gly Ala Gln Val Gln Ile Val Leu Thr Gln Ser
            20                  25                  30


Pro Gly Ile Leu Ser Leu Ser Pro Gly Glu Thr Ala Thr Leu Phe Cys
        35                  40                  45


Lys Ala Ser Gln Gly Gly Asn Ala Met Thr Trp Tyr Gln Lys Arg Arg
    50                  55                  60


Gly Gln Val Pro Arg Leu Leu Ile Tyr Asp Thr Ser Arg Arg Ala Ser
65                  70                  75                  80


Gly Val Pro Asp Arg Phe Val Gly Ser Gly Ser Gly Thr Asp Phe Phe
                85                  90                  95


Leu Thr Ile Asn Lys Leu Asp Arg Glu Asp Phe Ala Val Tyr Tyr Cys
            100                 105                 110
```

```
Gln Gln Phe Glu Phe Phe Gly Leu Gly Ser Glu Leu Glu Val His Arg
        115                 120                 125


Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
    130                 135                 140


Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145                 150                 155                 160


Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
                165                 170                 175


Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
            180                 185                 190


Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
        195                 200                 205


His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
    210                 215                 220


Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Tyr Pro Tyr Asp Val Pro
225                 230                 235                 240


Asp Tyr Ala
```

<210> 48
<211> 256
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence of the Heavy Chain (VH-CH1) of HIV-1 Env Fab

<400> 48

```
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1               5                   10                  15
```

```
Gly Ser Thr Gly Asp Gly Ala Gln Val Gln Leu Val Gln Ser Gly Gly
            20                  25                  30

Gln Met Lys Lys Pro Gly Glu Ser Met Arg Ile Ser Cys Arg Ala Ser
        35                  40                  45

Gly Tyr Glu Phe Ile Asp Cys Thr Leu Asn Trp Ile Arg Leu Ala Pro
    50                  55                  60

Gly Lys Arg Pro Glu Trp Met Gly Trp Leu Lys Pro Arg Gly Gly Ala
65                  70                  75                  80

Val Asn Tyr Ala Arg Pro Leu Gln Gly Arg Val Thr Met Thr Arg Asp
                85                  90                  95

Val Tyr Ser Asp Thr Ala Phe Leu Glu Leu Arg Ser Leu Thr Val Asp
            100                 105                 110

Asp Thr Ala Val Tyr Phe Cys Thr Arg Gly Lys Asn Cys Asp Tyr Asn
        115                 120                 125

Trp Asp Phe Glu His Trp Gly Arg Gly Thr Pro Val Ile Val Ser Ser
    130                 135                 140

Pro Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
145                 150                 155                 160

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
                165                 170                 175

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
            180                 185                 190

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
        195                 200                 205
```

```
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
    210                 215                 220


Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
225                 230                 235                 240


Lys Ala Glu Pro Lys Ser Cys Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
                245                 250                 255


<210>  49
<211>  244
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Amino Acid Sequence of the Light Chain (VL-CL) of HIV-1 Env Fab

<400>  49

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1               5                   10                  15


Gly Ser Thr Gly Asp Gly Ala Gln Val Gln Ile Val Leu Thr Gln Ser
            20                  25                  30


Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Thr Ala Ile Ile Ser Cys
        35                  40                  45


Arg Thr Ser Gln Tyr Gly Ser Leu Ala Trp Tyr Gln Gln Arg Pro Gly
    50                  55                  60


Gln Ala Pro Arg Leu Val Ile Tyr Ser Gly Ser Thr Arg Ala Ala Gly
65                  70                  75                  80


Ile Pro Asp Arg Phe Ser Gly Ser Arg Trp Gly Pro Asp Tyr Asn Leu
                85                  90                  95
```

```
Thr Ile Ser Asn Leu Glu Ser Gly Asp Phe Gly Val Tyr Tyr Cys Gln
            100                 105                 110

Gln Tyr Glu Phe Phe Gly Gln Gly Thr Lys Val Gln Val Asp Ile Lys
        115                 120                 125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
    130                 135                 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145                 150                 155                 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
                165                 170                 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
            180                 185                 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
        195                 200                 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Arg Ser
    210                 215                 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Tyr Pro Tyr Asp Val
225                 230                 235                 240

Pro Asp Tyr Ala
```

<210> 50
<211> 1536
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic Acid Sequence Encoding HIV-1 PG9 Fab

<400> 50

ggatccgcca ccatggcaag acccctgtgc accctgctgc tgctgatggc aaccctggcc 60

ggagccctgg cacagagcgc cctgacccag cccgcaagcg tctccggctc accaggccag 120

agcatcacta ttagttgcaa cgggactagc aacgacgtgg gaggctatga gagtgtcagc 180

tggtaccagc agcatcccgg aaaagcacca aaagtggtca tctacgatgt cagtaaaagg 240

ccaagtgggg tctcaaatag gttctcaggg agtaaatctg ggaatacagc atctctgacc 300

atctccggac tgggcgcaga agatgaaggc gactactatt gcaaaagcct gacctcaacc 360

agacggcgag tctttgggac aggcaccaag ctgacagtcc tgacagtcgc tgcccctcc 420

gtcttcattt ttccaccttc agatgagcag ctgaaatctg gcactgcatc tgtggtctgc 480

ctgctgaaca acttctatcc acgagaggcc aaggtgcagt ggaaagtgga taacgcactg 540

cagtccggca atagtcagga aagcgtgact gagcaggatt ccaaggacag tacctatagc 600

ctgtccagta cactgaccct gtccaaggct gactacgaaa aacataaggt gtatgcatgt 660

gaagtgactc accagggact gaggtcacca gtcactaagt cttttaacag gggagagtgc 720

ggcgggggag gatctggagg cggcggctct ggagggggag gctcaggggg cggaggaagc 780

ggcggaggag ggtccggagg aggaggcagt cagagactgg tcgaaagcgg gggaggagtg 840

gtgcagcctg ggtcctcact gagactgtca tgcgctgcca gtggctttga tttttcacga 900

cagggaatgc attgggtcag gcaggcaccc ggacagggcc tggaatgggt cgccttcatt 960

aagtacgacg gaagcgagaa gtaccatgcc gactcagtgt ggggaaggct gagcatctca 1020

agggacaact caaaggacac cctgtacctg cagatgaata gcctgagagt ggaagatacc 1080

gctacttatt tctgcgtgcg agaggccgga gggccagatt accggaacgg gtacaattac 1140

tatgatttct acgacggcta ctacaattac cattatatgg atgtctgggg caaaggaact 1200

acagtcaccg tgagctccgc aagtactaag ggaccttccg tgtttcctct ggctcccagt 1260

tccaaaagta catccggagg aacagccgct ctgggatgtc tggtcaagga ctattttccc 1320

gagcccgtga ctgtctcctg gaacagcggg gctctgacaa gcggggtgca cacctttcct 1380

gccgtgctgc agtccagtgg gctgtacagt ctgtctagtg tcgtcactgt gccaagctca 1440

agtctgggga cccagacata catttgtaat gtgaaccata aaccctcaaa caccaaagtg 1500

gacaagaaag tggaacctaa aagctgataa ctcgag 1536

<210> 51
<211> 504
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence of HIV-1 PG9 Fab

<400> 51

Met Ala Arg Pro Leu Cys Thr Leu Leu Leu Leu Met Ala Thr Leu Ala
1 5 10 15

Gly Ala Leu Ala Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly
20 25 30

Ser Pro Gly Gln Ser Ile Thr Ile Ser Cys Asn Gly Thr Ser Asn Asp
35 40 45

Val Gly Gly Tyr Glu Ser Val Ser Trp Tyr Gln Gln His Pro Gly Lys
50 55 60

Ala Pro Lys Val Val Ile Tyr Asp Val Ser Lys Arg Pro Ser Gly Val
65 70 75 80

Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr
85 90 95

Ile Ser Gly Leu Gly Ala Glu Asp Glu Gly Asp Tyr Tyr Cys Lys Ser
100 105 110

Leu Thr Ser Thr Arg Arg Arg Val Phe Gly Thr Gly Thr Lys Leu Thr
115 120 125

```
Val Leu Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
    130                 135                 140

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
145                 150                 155                 160

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
                165                 170                 175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
            180                 185                 190

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
        195                 200                 205

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Arg
    210                 215                 220

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Gly Gly Gly Gly
225                 230                 235                 240

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                245                 250                 255

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Arg Leu Val Glu Ser
            260                 265                 270

Gly Gly Gly Val Val Gln Pro Gly Ser Ser Leu Arg Leu Ser Cys Ala
        275                 280                 285

Ala Ser Gly Phe Asp Phe Ser Arg Gln Gly Met His Trp Val Arg Gln
    290                 295                 300

Ala Pro Gly Gln Gly Leu Glu Trp Val Ala Phe Ile Lys Tyr Asp Gly
305                 310                 315                 320
```

```
Ser Glu Lys Tyr His Ala Asp Ser Val Trp Gly Arg Leu Ser Ile Ser
                325                 330                 335

Arg Asp Asn Ser Lys Asp Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
            340                 345                 350

Val Glu Asp Thr Ala Thr Tyr Phe Cys Val Arg Glu Ala Gly Gly Pro
        355                 360                 365

Asp Tyr Arg Asn Gly Tyr Asn Tyr Tyr Asp Phe Tyr Asp Gly Tyr Tyr
    370                 375                 380

Asn Tyr His Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val
385                 390                 395                 400

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
                405                 410                 415

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
            420                 425                 430

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
        435                 440                 445

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
    450                 455                 460

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
465                 470                 475                 480

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
                485                 490                 495

Asp Lys Lys Val Glu Pro Lys Ser
            500
```

<210> 52
<211> 1503
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic Acid Sequence Encoding HIV-1 4E10 Fab

<400> 52
ggatccgcca ccatggcaag acctctgtgc actctgctgc tgctgatggc tactctggcc 60

ggggctctgg ctgagattgt cctgacccag tcccctggca ctcagtcact gtcccccggc 120

gagcgcgcaa ctctgtcctg cagagcaagc cagtccgtcg ggaacaacaa gctggcatgg 180

taccagcagc gcccaggaca ggcacccagg ctgctgatct acggagcaag ctcccggcct 240

agcggagtcg ctgatagatt ctccggaagc ggctccggga ccgatttcac tctgaccatc 300

tccaggctgg aacctgagga ttttgccgtg tattactgtc agcagtacgg gcagagcctg 360

tcaactttcg gccagggaac taaagtcgaa aagagaaccg tggccgcacc aagcgtcttt 420

atttttcccc ctagcgatga acagctgaaa tccgggactg cttccgtggt ctgcctgctg 480

aataacttct atccaagaga ggcaaaggtg cagtggaaag tggacaacgc cctgcagagc 540

ggaaactcac aggaatctgt gacagagcag gactccaagg atagcacata cagtctgtcc 600

tcaactctga ccctgtccaa agctgactat gagaagcata aagtctacgc atgtgaggtg 660

acccaccagg gactgaggtc ccccgtcact aagtccttca atagaggcga gtgcgggggc 720

gggggcagtg gcggaggggg aagtgggggc ggagggagtg gcggcggcgg gagtggcggc 780

ggcggctcag ggggcggcgg ctcccaggtc cagctggtcc agagcggagc cgaggtcaag 840

agaccaggct cttcagtcac cgtgagctgc aaagccagcg gaggctcctt tagcacttac 900

gccctgtcat gggtgcggca ggccccaggc cgaggcctgg agtggatggg cggcgtgatc 960

cccctgctga ccattactaa ctatgccccc agatttggag gccggatcac catcacagct 1020

gacagatcca catccacagc ttacctggag ctgaacagtc tgaggcccga ggacactgca 1080

gtctactact gtgcacgaga aggcaccact ggatgggggt ggctggggaa gcccatcggg 1140

gcttttgcac attggggcgg agggacactg gtgactgtga gctctgccag cactaaaggg 1200

cccagtgtct tccctctggc cccaagttcc aagagtacat caggggggcac cgccgcactg 1260

gggtgtctgg tgaaggatta cttcccagag cccgtgacag tcagttggaa cagcggcgct 1320

ctgaccagtg gggtgcacac tttcccagcc gtgctgcaga gttcagggct gtactccctg 1380

tcctcagtgg tgactgtgcc ctcaagcagt ctggggactc agacttacat ttgtaatgtg 1440

aaccataaac cctcaaatac taaagtggac aaaaaagtgg aaccaaagag ctgataactc 1500

gag 1503

<210> 53
<211> 493
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence of HIV-1 4E10 Fab

<400> 53

Met Ala Arg Pro Leu Cys Thr Leu Leu Leu Leu Met Ala Thr Leu Ala
1 5 10 15

Gly Ala Leu Ala Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Gln Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
35 40 45

Val Gly Asn Asn Lys Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln Ala
50 55 60

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Pro Ser Gly Val Ala
65 70 75 80

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
85 90 95

```
Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
            100                 105                 110

Gly Gln Ser Leu Ser Thr Phe Gly Gln Gly Thr Lys Val Glu Lys Arg
        115                 120                 125

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
    130                 135                 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145                 150                 155                 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
                165                 170                 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
            180                 185                 190

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
        195                 200                 205

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Arg Ser Pro
    210                 215                 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Gly Gly Gly Gly Ser Gly
225                 230                 235                 240

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
                245                 250                 255

Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly
            260                 265                 270

Ala Glu Val Lys Arg Pro Gly Ser Ser Val Thr Val Ser Cys Lys Ala
        275                 280                 285
```

```
Ser Gly Gly Ser Phe Ser Thr Tyr Ala Leu Ser Trp Val Arg Gln Ala
    290                 295                 300

Pro Gly Arg Gly Leu Glu Trp Met Gly Gly Val Ile Pro Leu Leu Thr
305                 310                 315                 320

Ile Thr Asn Tyr Ala Pro Arg Phe Gly Gly Arg Ile Thr Ile Thr Ala
                325                 330                 335

Asp Arg Ser Thr Ser Thr Ala Tyr Leu Glu Leu Asn Ser Leu Arg Pro
            340                 345                 350

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Gly Thr Thr Gly Trp
        355                 360                 365

Gly Trp Leu Gly Lys Pro Ile Gly Ala Phe Ala His Trp Gly Gly Gly
    370                 375                 380

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
385                 390                 395                 400

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
                405                 410                 415

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
            420                 425                 430

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
        435                 440                 445

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
    450                 455                 460

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
465                 470                 475                 480
```

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
485 490

<210> 54
<211> 1446
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic Acid Sequence Encoding the HIV-1 VRC01 IgG1 Heavy Chain (VH/CH1/Hinge/CH2/CH3)

<400> 54
ggatccgcca ccatggattg gacatggatt ctgttcctgg tcgccgccgc aactagagtg 60

cattcacagg tgcagctggt gcagtcaggc gggcagatga agaaacccgg cgagagtatg 120

cgaatctcat gccgggctag cgggtacgaa ttcatcgact gtaccctgaa ctggattaga 180

ctggcacctg ggaagaggcc agagtggatg ggatggctga aacctagagg cggggcagtg 240

aattacgcca gaccactgca gggcagggtc actatgaccc gcgacgtgta ttctgatacc 300

gcattcctgg agctgcgaag tctgacagtc gacgatactg ccgtgtactt ctgcacacgg 360

ggcaagaact gtgactataa ttgggatttt gaacactggg gcaggggggac acctgtcatt 420

gtgagctccc caagtactaa gggaccctca gtgtttcccc tggccccttc tagtaaaagt 480

acctcaggag gcacagccgc tctgggatgc ctggtgaagg attacttccc tgagccagtc 540

accgtgagtt ggaactcagg cgccctgaca agcggggtcc atacttttcc agctgtgctg 600

cagtcaagcg ggctgtactc cctgtcctct gtggtcacag tgcccagttc aagcctggga 660

acacagactt atatctgtaa cgtcaatcac aagcctagca atactaaagt ggacaagaaa 720

gccgagccta agagctgcga accaaagtcc tgtgataaaa cccatacatg ccctccctgt 780

ccagctcctg aactgctggg cggcccatcc gtgttcctgt ttccacccaa gcccaaagac 840

accctgatga ttagcaggac tcctgaggtc acctgcgtgg tcgtggacgt gtcccacgag 900

gaccccgaag tcaagtttaa ctggtacgtg gatggcgtcg aagtgcataa tgccaagaca 960

aaaccccggg aggaacagta caactctacc tatagagtcg tgagtgtcct gacagtgctg 1020

caccaggact ggctgaacgg gaaggagtat aagtgcaaag tgtctaataa ggccctgcca 1080

gctcccatcg agaaaacaat ttccaaggca aaaggccagc caagggaacc ccaggtgtac 1140

actctgcctc catcccgcga cgagctgact aagaaccagg tctctctgac ctgtctggtg 1200

aaaggattct atccaagcga tatcgccgtg gagtgggaat ccaatggcca gcccgagaac 1260

aattacaaga ccacaccccc tgtgctggac agcgatggct ccttctttct gtattcaaag 1320

ctgaccgtgg ataaaagccg ctggcagcag gggaacgtct ttagctgctc cgtgatgcac 1380

gaagctctgc acaatcatta cacccagaag tctctgagtc tgtcacctgg caagtgataa 1440

ctcgag 1446

<210> 55
<211> 474
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence of the HIV-1 VRC01 IgG1 Heavy Chain (VH/CH1/CH2/CH3)

<400> 55

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1 5 10 15

His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Gln Met Lys Lys Pro
20 25 30

Gly Glu Ser Met Arg Ile Ser Cys Arg Ala Ser Gly Tyr Glu Phe Ile
35 40 45

Asp Cys Thr Leu Asn Trp Ile Arg Leu Ala Pro Gly Lys Arg Pro Glu
50 55 60

Trp Met Gly Trp Leu Lys Pro Arg Gly Gly Ala Val Asn Tyr Ala Arg
65 70 75 80

```
Pro Leu Gln Gly Arg Val Thr Met Thr Arg Asp Val Tyr Ser Asp Thr
                85                  90                  95

Ala Phe Leu Glu Leu Arg Ser Leu Thr Val Asp Asp Thr Ala Val Tyr
            100                 105                 110

Phe Cys Thr Arg Gly Lys Asn Cys Asp Tyr Asn Trp Asp Phe Glu His
        115                 120                 125

Trp Gly Arg Gly Thr Pro Val Ile Val Ser Ser Pro Ser Thr Lys Gly
    130                 135                 140

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
145                 150                 155                 160

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
                165                 170                 175

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
            180                 185                 190

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
        195                 200                 205

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

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Ala Glu Pro Lys
225                 230                 235                 240

Ser Cys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
                245                 250                 255

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
            260                 265                 270
```

```
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
        275                 280                 285

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
    290                 295                 300

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
305                 310                 315                 320

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
                325                 330                 335

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
            340                 345                 350

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
        355                 360                 365

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
    370                 375                 380

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
385                 390                 395                 400

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
                405                 410                 415

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
            420                 425                 430

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
        435                 440                 445

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
    450                 455                 460
```

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470

<210> 56
<211> 708
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic Acid Sequence Encoding the HIV-1 VRC01 IgG Light Chain (VL/CL)

<400> 56
ggatccgcca ccatggattg gacttggatt ctgttcctgg tggcagccgc taccagagtc 60

cattccgaaa ttgtgctgac ccagtctccc ggaacactgt ctctgagtcc tggcgagaca 120

gccatcattt cctgtaggac ttctcagtac gggagtctgg catggtatca gcagcgacca 180

ggacaggctc ctcgactggt catctactca ggaagcactc gggcagccgg cattcccgac 240

cgattctccg ggtctcggtg gggacctgat tacaacctga ccatctcaaa tctggaaagc 300

ggagactttg gcgtgtacta ttgccagcag tatgagttct ttgggcaggg aaccaaggtc 360

caggtggaca tcaaacgcac agtcgctgca ccaagcgtgt tcatctttcc accctcagat 420

gaacagctga agtccggcac cgcctctgtg gtgtgcctgc tgaacaattt ctacccccgg 480

gaggcaaagg tccagtggaa agtggacaac gccctgcagt ctggcaatag tcaggagtca 540

gtgactgaac aggacagcaa ggattccacc tattctctgt cctctactct gaccctgagc 600

aaagctgatt acgagaagca caaagtgtat gcatgtgagg tcacccacca gggactgcgg 660

tcacccgtca ccaagagctt caatcgcgga gagtgttgat aactcgag 708

<210> 57
<211> 228
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence of the HIV-1 VRC01 IgG Light Chain (VL/CL)

<400> 57

```
Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1               5                  10                  15

His Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser
            20                  25                  30

Pro Gly Glu Thr Ala Ile Ile Ser Cys Arg Thr Ser Gln Tyr Gly Ser
        35                  40                  45

Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Val Ile
    50                  55                  60

Tyr Ser Gly Ser Thr Arg Ala Ala Gly Ile Pro Asp Arg Phe Ser Gly
65                  70                  75                  80

Ser Arg Trp Gly Pro Asp Tyr Asn Leu Thr Ile Ser Asn Leu Glu Ser
                85                  90                  95

Gly Asp Phe Gly Val Tyr Tyr Cys Gln Gln Tyr Glu Phe Phe Gly Gln
            100                 105                 110

Gly Thr Lys Val Gln Val Asp Ile Lys Arg Thr Val Ala Ala Pro Ser
        115                 120                 125

Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala
    130                 135                 140

Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
145                 150                 155                 160

Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser
                165                 170                 175

Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr
            180                 185                 190
```

Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys
195 200 205

Glu Val Thr His Gln Gly Leu Arg Ser Pro Val Thr Lys Ser Phe Asn
210 215 220

Arg Gly Glu Cys
225

<210> 58
<211> 744
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic Acid Sequence Encoding the Heavy Chain (VH-CH1) of the CHIKV-Env-Fab

<400> 58
ggatccgcca ccatggattg gacatggagg attctgtttc tggtcgccgc cgctactgga 60

actcacgctc aggtgcagct ggtgcagtca gggtccgaac tgaagaaacc aggggcatct 120

gtgaaggtca gttgcaaagc ctcaggctac accctgacac ggtatgccat gacttgggtg 180

cgccaggctc ctggacaggg actggagtgg atgggctgga tcaacactta caccggaaat 240

ccaacttatg tgcaggggtt caccggccga ttcgtgtttt ctctggacac ttccgtctct 300

accgcctttc tgcacattac aagtctgaag gcagaggaca ctgccgtgta cttctgcgct 360

agggaaggcg gagcaagagg ctttgattat tggggccagg gaaccctggt gacagtcagc 420

tccgccagca caaagggacc ctccgtgttc ccactggctc cctctagtaa aagtacatca 480

gggggcactg ccgctctggg atgtctggtc aaagattact tccccgaacc tgtgaccgtc 540

agctggaact ccggagctct gaccagcggg gtgcatacat ttcccgcagt cctgcagtca 600

agcggactgt actccctgtc ctctgtggtc acagtgccta gttcaagcct ggggacacag 660

acttatatct gtaatgtgaa ccataagcca agcaacacca aagtggacaa aaaagtggaa 720

cctaagagct gctgataact cgag 744

<210> 59
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence of the Heavy Chain (VH-CH1) of the CHIKV-Env-Fab

<400> 59

```
Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1               5                  10                  15


Thr His Ala Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys
            20                  25                  30


Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Leu
        35                  40                  45


Thr Arg Tyr Ala Met Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
    50                  55                  60


Glu Trp Met Gly Trp Ile Asn Thr Tyr Thr Gly Asn Pro Thr Tyr Val
65                  70                  75                  80


Gln Gly Phe Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser
                85                  90                  95


Thr Ala Phe Leu His Ile Thr Ser Leu Lys Ala Glu Asp Thr Ala Val
            100                 105                 110


Tyr Phe Cys Ala Arg Glu Gly Gly Ala Arg Gly Phe Asp Tyr Trp Gly
        115                 120                 125


Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140
```

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

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

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
225 230 235 240

<210> 60
<211> 738
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic Acid Sequence Encoding the Light Chain (VL-CL) of the CHIKV-Env-Fab

<400> 60
ggatccgcca ccatggcatg gaccccactg ttcctgttcc tgctgacttg ttgtcctggc 60

gggagcaatt cacagagcgt cctgacccag ccccttctg tgtccggagc accaggacag 120

cgagtcacaa tctcttgcac tggaagctcc tctaacattg gggccagcca cgacgtgcat 180

tggtaccagc agctgccagg gaccgctccc acactgctga tctatgtgaa ctctaatagg 240

cctagtggcg tcccagatag attttcaggg agcaagtccg gcacctctgc tagtctggca 300

attacaggac tgcaggctga ggacgaagca gattactatt gccagagtta cgactcaaac 360

ctgtcaggca gcgcagtgtt cggaggagga actaagctga ccgtcctggg acagcccaaa 420

gccgctcctt ctgtgaccct gtttcccccct agttcagagg aactgcaggc caacaaggct 480

actctggtgt gtctgatctc cgacttctac cctggagcag tgaccgtcgc atggaaggcc 540

gatagctccc cagtgaaagc tggggtcgag accacaactc ccagcaagca gtccaacaac 600

aagtacgcag cctctagtta tctgtcactg acacctgaac agtggaagag ccacaaatcc 660

tattcttgcc aagtgactca tgagggcagt accgtggaaa agacagtcgc cccaactgag 720

tgttcctgat aactcgag 738

<210> 61
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence of the Light Chain (VL-CL) of the CHIKV-Env-Fab

<400> 61

Met Ala Trp Thr Pro Leu Phe Leu Phe Leu Leu Thr Cys Cys Pro Gly
1 5 10 15

Gly Ser Asn Ser Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly
20 25 30

Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn
35 40 45

Ile Gly Ala Ser His Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr
50 55 60

Ala Pro Thr Leu Leu Ile Tyr Val Asn Ser Asn Arg Pro Ser Gly Val
65 70 75 80

Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala
85 90 95

```
Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser
            100                 105                 110


Tyr Asp Ser Asn Leu Ser Gly Ser Ala Val Phe Gly Gly Gly Thr Lys
        115                 120                 125


Leu Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe
    130                 135                 140


Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys
145                 150                 155                 160


Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala
                165                 170                 175


Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys
            180                 185                 190


Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro
        195                 200                 205


Glu Gln Trp Lys Ser His Lys Ser Tyr Ser Cys Gln Val Thr His Glu
    210                 215                 220


Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
225                 230                 235


<210>  62
<211>  2238
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Nucleic Acid Sequence Encoding HIV-1 Env-4E10 Ig

<400>  62
ggatccgcca ccatggattg gacatggagg attctgtttc tggtcgccgc cgctacagga       60
```

actcacgccc aggtgcagct ggtgcagtca ggagccgaag tgaagcgacc aggcagctcc 120

gtcactgtgt cctgcaaagc atctggcgga tcattcagca cctacgccct gagctgggtg 180

agacaggctc ctggacgagg actggaatgg atgggaggcg tcatcccact gctgacaatt 240

actaactacg ccccccgatt tcagggcagg atcaccatta cagcagaccg ctccacttct 300

accgcctatc tggagctgaa tagcctgaga ccagaagata ccgcagtgta ctattgcgcc 360

cgggagggaa ccacaggatg gggatggctg ggaaagccca tcggggcttt cgcacactgg 420

ggccagggaa ccctggtcac agtgtctagt gccagcacaa agggcccctc cgtgtttccc 480

ctggctcctt caagcaaaag tacttcagga gggaccgccg ctctgggatg tctggtgaag 540

gactacttcc ctgagccagt caccgtgtcc tggaactctg gcgctctgac ctccggagtg 600

catacatttc ccgcagtcct gcagtcctct gggctgtact ctctgagttc agtggtcact 660

gtgcctagct cctctctggg cacacagact tatatctgca acgtgaatca caagccctcc 720

aataccaaag tcgacaagaa agtggaacct aagtcttgtg ataaaaccca tacatgccca 780

ccttgtccag cacctgagct gctgggcgga ccttccgtgt tcctgtttcc acccaagcca 840

aaagacacac tgatgattag ccggacacct gaagtgactt gtgtggtcgt ggacgtcagc 900

cacgaggacc ccgaagtgaa gttcaactgg tacgtggatg gcgtcgaggt gcataatgcc 960

aagaccaaac ccagggagga acagtacaac tctacttata gggtcgtgag tgtcctgacc 1020

gtgctgcacc aggactggct gaacgggaag gagtataagt gcaaagtgtc caataaggcc 1080

ctgccagctc ccatcgagaa aacaatttct aaggctaaag gccagccacg cgaaccccag 1140

gtgtacactc tgcctcccag cagggacgag ctgaccaaga accaggtgag tctgacatgt 1200

ctggtcaaag gcttctatcc aagcgatatc gccgtggagt gggaatccaa tggacagccc 1260

gaaaacaatt acaagactac ccccccctgtg ctggacagtg atggatcatt ctttctgtat 1320

tccaagctga ccgtggacaa atctcgctgg cagcagggga acgtctttag ctgctccgtg 1380

atgcacgagg ccctgcacaa tcattacaca cagaagtctc tgagtctgtc accaggcaag 1440

cggggacgca aaaggagaag cgggtccggc gctactaact tcagcctgct gaaacaggca 1500

ggggatgtgg aggaaaatcc tggcccaatg gtcctgcaga cccaggtgtt tatctcactg 1560

ctgctgtgga ttagcggggc ttatggcgaa atcgtgctga ctcagagccc cggaacccag 1620

tctctgagtc ctggggagcg cgctacactg agctgtcgag catcacagag cgtggggaac 1680

aataagctgg catggtacca gcagaggcct ggccaggctc caagactgct gatctatggc 1740

gcaagttcac ggcctagcgg agtggcagac cgcttctccg gatctgggag tggcaccgat 1800

tttactctga ccattagcag gctggagcca gaagacttcg ctgtgtacta ttgccagcag 1860

tacggccagt cactgagcac atttggacag gggactaagg tcgaaaaaag aaccgtggca 1920

gccccaagtg tcttcatttt tccaccctca gacgagcagc tgaagagtgg aacagcctca 1980

gtcgtgtgtc tgctgaacaa tttctacccc agggaggcca aggtccagtg gaaagtggat 2040

aacgctctgc agagcggcaa ttcccaggag tctgtgacag aacaggacag taaggattca 2100

acttatagcc tgagctccac actgactctg tccaaagcag attacgagaa gcacaaagtg 2160

tatgcctgcg aagtcaccca tcagggactg tctagtcctg tgacaaagtc ttttaacaga 2220

ggggagtgat aactcgag 2238

<210> 63
<211> 2328
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic Acid Sequence Encoding HIV-1 Env-PG9 Ig

<400> 63
ggatccgcca ccatggactg gacttggagg attctgtttc tggtcgccgc cgcaactgga 60

actcacgctg aatttggact gtcatgggtc tttctggtgg cctttctgcg aggggtccag 120

tgccagaggc tggtggagtc cggaggagga gtggtccagc caggcagctc cctgcgactg 180

agttgtgccg cttcagggtt cgacttttct agacagggca tgcactgggt gcggcaggca 240

ccaggacagg gactggagtg ggtggctttc atcaagtacg acggaagtga aaaatatcat 300

gccgattcag tgtgggggcg gctgtcaatt agccgcgaca actccaagga taccctgtac 360

ctgcagatga attctctgag ggtcgaggac acagctactt atttctgcgt gagggaagca 420

ggcggacctg attacagaaa cgggtataat tactatgact tttacgatgg ctactataac 480

taccactata tggacgtgtg gggcaaggga accacagtca cagtgtctag tgcatcaact 540

aaaggcccaa gcgtgtttcc cctggcccct tcaagcaagt ccacttctgg aggaaccgca 600

gcactgggat gtctggtgaa ggattacttc cctgagccag tcaccgtgag ttggaactca 660

ggcgccctga ctagcggagt ccataccttt cctgctgtgc tgcagtcctc tgggctgtac 720

agcctgagtt cagtggtcac agtgccaagc tcctctctgg gcacccagac atatatctgc 780

aacgtgaatc acaagcctag caatactaag gtcgacaaaa gagtggaacc aaagagctgt 840

gataaaactc atacctgccc accttgtcca gcacctgagc tgctgggagg gccttccgtg 900

ttcctgtttc cacccaagcc aaaagacacc ctgatgatta gccggacacc agaagtcact 960

tgcgtggtcg tggacgtgag ccacgaggac cccgaagtca agtttaactg gtacgtggat 1020

ggcgtcgagg tgcataatgc taagacaaaa ccacgggagg aacagtacaa ctccacatat 1080

cgcgtcgtgt ctgtcctgac tgtgctgcac caggactggc tgaacggcaa ggagtataag 1140

tgcaaagtgt ccaataaggc actgccagcc cccatcgaga aaaccatttc taaggccaaa 1200

ggccagccac gagaacccca ggtgtacaca ctgcctccaa gtagggacga gctgactaag 1260

aaccaggtct ctctgacctg tctggtgaaa ggcttctatc cctctgatat cgctgtggag 1320

tgggaaagta atggacagcc tgaaaacaat tacaagacta ccccccctgt gctggacagc 1380

gatggcagct tcttcctgta tagcaagctg accgtggaca aatccagatg gcagcagggg 1440

aacgtcttta gttgctcagt gatgcacgag gcactgcaca atcattacac ccagaaaagc 1500

ctgtccctgt ctcctggcaa gaggggaaga aaaaggagaa gtgggtcagg cgcaacaaac 1560

ttcagcctgc tgaagcaggc cggagatgtg gaggaaaatc ctgggccaat ggcttggacc 1620

cccctgttcc tgtttctgct gacatgctgt cctggcggaa gcaactccca gtctgcactg 1680

acacagccag caagtgtgtc agggagccca ggacagagca tcaccatttc ctgtaacggc 1740

acaagcaatg acgtcggggg ctacgagtcc gtgtcttggt atcagcagca tcctggaaag 1800

gccccaaaag tcgtgatcta cgatgtcagc aaacgcccct ctggggtgag taaccgattc 1860

agtggatcaa agagcgggaa taccgcttct ctgacaatta gtggcctgca ggcagaggac 1920

gaaggagatt actattgcaa atcactgaca agcactcggc gccgagtctt cggaaccggg 1980

acaaagctga ctgtgctggg ccagcccaaa gctgcaccta gcgtgaccct gtttccaccc 2040

agttcagagg aactgcaggc taataaggca acactggtgt gtctgatctc cgacttctac 2100

cctggcgctg tcactgtggc ctggaaggct gatagctccc cagtcaaagc aggagtggaa 2160

acaactaccc cctccaagca gtctaacaac aagtacgccg cttctagtta tctgtcactg 2220

actcccgagc agtggaagag ccacaaatcc tattcttgcc aggtgaccca tgagggctcc 2280

actgtcgaaa agaccgtggc ccctacagag tgttcttgat aactcgag 2328

<210> 64
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic Acid Sequence Encoding VRC01 IgG

<400> 64
ggatccgcca ccatggattg gacatggatt ctgttcctgg tcgccgccgc aactagagtg 60

cattcacagg tgcagctggt gcagtcaggc gggcagatga agaaacccgg cgagagtatg 120

cgaatctcat gccgggctag cgggtacgaa ttcatcgact gtaccctgaa ctggattaga 180

ctggcacctg ggaagaggcc agagtggatg ggatggctga aacctagagg cggggcagtg 240

aattacgcca gaccactgca gggcagggtc actatgaccc gcgacgtgta ttctgatacc 300

gcattcctgg agctgcgaag tctgacagtc gacgatactg ccgtgtactt ctgcacacgg 360

ggcaagaact gtgactataa ttgggatttt gaacactggg gcaaggggac acctgtcatt 420

gtgagctccc caagtactaa gggaccctca gtgtttcccc tggccccttc tagtaaaagt 480

acctcaggag gcacagccgc tctgggatgc ctggtgaagg attacttccc tgagccagtc 540

accgtgagtt ggaactcagg cgccctgaca agcggggtcc atactttcc agctgtgctg 600

cagtcaagcg ggctgtactc cctgtcctct gtggtcacag tgcccagttc aagcctggga 660

acacagactt atatctgtaa cgtcaatcac aagcctagca atactaaagt ggacaagaaa 720

gccgagccta agagctgcga accaaagtcc tgtgataaaa cccatacatg ccctccctgt 780

ccagctcctg aactgctggg cggcccatcc gtgttcctgt ttccacccaa gcccaaagac 840

accctgatga ttagcaggac tcctgaggtc acctgcgtgg tcgtggacgt gtcccacgag 900

gaccccgaag tcaagtttaa ctggtacgtg gatggcgtcg aagtgcataa tgccaagaca 960

aaaccccggg aggaacagta caactctacc tatagagtcg tgagtgtcct gacagtgctg 1020

caccaggact ggctgaacgg gaaggagtat aagtgcaaag tgtctaataa ggccctgcca 1080

gctcccatcg agaaaacaat ttccaaggca aaaggccagc caagggaacc ccaggtgtac 1140

actctgcctc catcccgcga cgagctgact aagaaccagg tctctctgac ctgtctggtg 1200

aaaggattct atccaagcga tatcgccgtg gagtgggaat ccaatggcca gcccgagaac 1260

aattacaaga ccacaccccc tgtgctggac agcgatggct ccttctttct gtattcaaag 1320

ctgaccgtgg ataaaagccg ctggcagcag gggaacgtct ttagctgctc cgtgatgcac 1380

gaagctctgc acaatcatta cacccagaag tctctgagtc tgtcacctgg caagagggga 1440

cgaaaacgga gaagcggcag cggagctaca aacttcagcc tgctgaaaca ggcaggcgac 1500

gtggaggaaa atcctgggcc aatggattgg acttggattc tgttcctggt ggcagccgct 1560

accagagtcc attccgaaat tgtgctgacc cagtctcccg gaacactgtc tctgagtcct 1620

ggcgagacag ccatcatttc ctgtaggact tctcagtacg ggagtctggc atggtatcag 1680

cagcgaccag gacaggctcc tcgactggtc atctactcag gaagcactcg ggcagccggc 1740

attcccgacc gattctccgg gtctcggtgg ggacctgatt acaacctgac catctcaaat 1800

ctggaaagcg gagactttgg cgtgtactat tgccagcagt atgagttctt tgggcaggga 1860

accaaggtcc aggtggacat caaacgcaca gtcgctgcac caagcgtgtt catctttcca 1920

ccctcagatg aacagctgaa gtccggcacc gcctctgtgg tgtgcctgct gaacaatttc 1980

taccccgggg aggcaaaggt ccagtggaaa gtggacaacg ccctgcagtc tggcaatagt 2040

caggagtcag tgactgaaca ggacagcaag gattccacct attctctgtc ctctactctg 2100

accctgagca aagctgatta cgagaagcac aaagtgtatg catgtgaggt cacccaccag 2160

ggactgcggt cacccgtcac caagagcttc aatcgcggag agtgttgata actcgag 2217

<210> 65
<211> 2223
<212> DNA
<213> Artificial Sequence

<220>
<223> CHIKV snapi nucleic acid sequence

<400> 65
ggatccgcca ccatggactg gacttggatt ctgtttctgg tcgccgccgc tacccgagtg 60

cattcacagg tgcagctgca gcagcctggg gccgctctgg tgaagccagg agctagcgca 120

atgatgtcct gcaaagcctc tggctacact ttcacctcct attggatcac ctgggtgaag 180

cagcgacctg gacagggact ggagtggatc ggcgacatct acccaggcac cgggagaaca 240

atctacaagg aaaaattcaa gacaaaagcc acactgactg tggacaccag ctcctctaca 300

gcttttatgc agctgaacag cctgacttcc gaggatagcg ccgtgtacta ttgcgcaaga 360

ggatacggct ctccttacta tgccctggac tattgggggc agggaactag cgtcaccgtg 420

agttcagcat ctaccaaggg accaagcgtg ttcccactgg cacctagctc caaatccact 480

tctggcggga ccgccgctct gggatgtctg gtgaaggatt acttccctga gccagtcaca 540

gtgagttgga actcaggggc tctgaccagc ggagtccaca catttcctgc agtgctgcag 600

tctagtggac tgtactccct gtcaagcgtg gtcactgtcc catcctctag tctgggcacc 660

cagacatata tctgcaacgt gaatcacaag ccatccaata ccaaagtcga taagaaagtg 720

gagcccaagt cttgtgacaa aactcatacc tgccctccct gtccagcacc tgaactgctg 780

ggaggcccaa gcgtgttcct gtttccaccc aagcctaaag acaccctgat gattagcagg 840

acaccagagg tcacttgcgt ggtcgtggac gtgagccacg aagaccccga ggtcaagttc 900

aactggtacg tggatggcgt cgaagtgcat aatgccaaga caaaaccccg ggaggaacag 960

tacaactcaa cctatcgggt cgtgagcgtc ctgacagtgc tgcaccagga ctggctgaac 1020

ggaaaggagt acaagtgcaa agtgtctaat aaggccctgc cagctcccat cgaaaaaacc 1080

attagcaagg ctaaaggcca gccaagagag ccccaggtgt acacactgcc tccatcaagg 1140

gacgaactga caaagaacca ggtcagcctg acttgtctgg tgaaaggctt ctatcccagc 1200

gatatcgcag tggaatggga gtccaatggg cagcctgaga acaattacaa gaccacaccc 1260

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cggtggcagc agggaaacgt ctttagttgc tcagtgatgc acgaagccct gcacaatcat 1380

tacactcaga agagcctgtc cctgtctccc ggaaagaggg gccgcaaacg gagaagtggc 1440

tcaggggcaa ccaacttctc tctgctgaaa caggccggcg atgtggagga aaatcctggg 1500

ccaatggact ggacatggat tctgttcctg gtggcagccg ctacaagggt ccattccgac 1560

attgtgctga ctcagtctcc tgcaagtctg gccgtgtctc agggacagcg agcaaccatc 1620

agttgtaagg ctagccagtc cgtcgactac gatggggaca gttacgtgaa ctggtatcag 1680

cagaagcctg gacagtcccc aaaactgctg atctatgatg ctagtaatct ggagtcaggc 1740

attcccgcac gattctctgg aagtggctca gggacagact tcaccctgaa cattcaccct 1800

gtcgaggaag aggacgtggc tacctactat tgccaggaaa gcaatgagga cccccgcact 1860

ttcgggggag gcaccaagct ggagatcaaa cgaactgtcg cagcccccag cgtgttcatc 1920

tttccaccct cagacgaaca gctgaagagc ggaaccgcat ccgtggtgtg cctgctgaac 1980

aacttctacc cccgcgaggc caaggtccag tggaaagtgg ataacgctct gcagtcaggc 2040

aatagccagg aatccgtgac tgagcaggat tctaaggaca gtacctattc actgtcaagc 2100

acactgactc tgagcaaagc agactacgaa aagcataaag tgtatgcctg cgaagtcacc 2160

caccaggggc tgaggtctcc agtcactaag tctttcaaca gaggggaatg ctgataactc 2220

gag 2223

<210> 66
<211> 733
<212> PRT

<213> Artificial Sequence

<220>
<223> CHIKV-snapi amino acid sequence

<400> 66

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Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1               5                   10                  15


His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Ala Leu Val Lys Pro
            20                  25                  30


Gly Ala Ser Ala Met Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
        35                  40                  45


Ser Tyr Trp Ile Thr Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu
    50                  55                  60


Trp Ile Gly Asp Ile Tyr Pro Gly Thr Gly Arg Thr Ile Tyr Lys Glu
65                  70                  75                  80


Lys Phe Lys Thr Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser Thr
                85                  90                  95


Ala Phe Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr
            100                 105                 110


Tyr Cys Ala Arg Gly Tyr Gly Ser Pro Tyr Tyr Ala Leu Asp Tyr Trp
        115                 120                 125


Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
    130                 135                 140


Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
145                 150                 155                 160


Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
```

```
                165                 170                 175

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
            180                 185                 190

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
        195                 200                 205

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

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
225                 230                 235                 240

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
                245                 250                 255

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            260                 265                 270

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        275                 280                 285

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    290                 295                 300

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
305                 310                 315                 320

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                325                 330                 335

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            340                 345                 350

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
```

```
        355                 360                 365

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

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
385                 390                 395                 400

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                405                 410                 415

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            420                 425                 430

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        435                 440                 445

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    450                 455                 460

Ser Pro Gly Lys Arg Gly Arg Lys Arg Arg Ser Gly Ser Gly Ala Thr
465                 470                 475                 480

Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly
                485                 490                 495

Pro Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg
            500                 505                 510

Val His Ser Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val
        515                 520                 525

Ser Gln Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val
    530                 535                 540

Asp Tyr Asp Gly Asp Ser Tyr Val Asn Trp Tyr Gln Gln Lys Pro Gly
```

```
545                 550                 555                 560

Gln Ser Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Ser Gly
                565                 570                 575

Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
            580                 585                 590

Asn Ile His Pro Val Glu Glu Glu Asp Val Ala Thr Tyr Tyr Cys Gln
        595                 600                 605

Glu Ser Asn Glu Asp Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu
    610                 615                 620

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
625                 630                 635                 640

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
                645                 650                 655

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
            660                 665                 670

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
        675                 680                 685

Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
    690                 695                 700

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
705                 710                 715                 720

Arg Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
                725                 730
```

<210> 67

<211> 2241
<212> DNA
<213> Artificial Sequence

<220>
<223> DVSF-1 WT nucleic acid sequence

<400> 67
ggatccgcca ccatggactg gacttggagg attctgtttc tggtcgccgc cgctactggg 60

actcacgctc aggcacatct ggtcgaatct ggaggaggag tggtccagcc tggccgatcc 120

ctgcgactgt cttgcgcagc tagcgccttc aacttcagca caaacgcaat gcactgggtg 180

cgacaggcac caggcaaggg actggagtgg gtcgctgtga tctcatacga cggaagccat 240

aagtactatg cagattctgt gaaaggccgg ttcaccattt ccagggacaa ttctaagaac 300

accctgtatc tgcagatgaa tagcctgcgc gcagccgata ccgcagtgta ctattgcgca 360

actgtcggcg tgctgacctg gccagtgaac gccgaatact ttcaccattg gggacagggc 420

agtctggtct cagtgagctc cgcaagtact aagggaccat cagtgttccc actggcaccc 480

tctagtaaat ctactagtgg cgggaccgct gcactgggat gtctggtgaa ggactatttc 540

cccgagcctg tcaccgtgag ctggaattcc ggagccctga caagcggcgt ccacactttt 600

cccgctgtgc tgcagtcaag cggactgtac tccctgtcct ctgtggtcac tgtgcctagt 660

tcaagcctgg gcactcagac ctatatctgc aatgtgaacc acaagccctc taacaccaaa 720

gtcgacaaga aagtggaacc taagagctgt gataaaacac atacttgccc accttgtcca 780

gcaccagagc tgctgggagg accaagcgtg ttcctgtttc cacccaagcc taaagacaca 840

ctgatgatta gccggacacc tgaagtcact tgcgtggtcg tggacgtgtc ccacgaggac 900

cccgaagtca agtttaattg gtacgtggat ggcgtcgagg tgcataacgc caagaccaaa 960

ccccgggagg aacagtacaa tagcacatat agagtcgtgt ccgtcctgac tgtgctgcat 1020

caggattggc tgaatgggaa ggagtataag tgcaaagtgt ctaacaaggc tctgcctgca 1080

ccaatcgaga aaaccattag caaggctaaa ggccagccta gggaaccaca ggtgtacaca 1140

ctgcctccaa gtcgcgacga gctgaccaag aatcaggtct ccctgacatg tctggtgaaa 1200

ggcttctatc catcagatat cgccgtggag tgggaaagca acgggcagcc cgaaaacaat 1260

tacaagacca cacccctgt gctggactct gatggcagtt tctttctgta ttctaagctg 1320

accgtggaca aaagtagatg gcagcagggg aatgtctttt catgtagcgt gatgcacgag 1380

gccctgcaca accattacac acagaagtcc ctgtctctga gtcccggaaa gaggggccgc 1440

aaacggagat cagggagcgg agctactaat ttcagcctgc tgaaacaggc aggggatgtg 1500

gaggaaaacc ccggacctat ggcttggacc ccactgttcc tgtttctgct gacatgctgt 1560

cccgggggca gcaattctca gagtgtcctg acacagccac catcagtgag cggagcacca 1620

ggacagaggg tgaccatctc ctgcacaggc agcagcagca acattggcgc cgggtacgac 1680

gtgcattggt atcagcagct gcccggcacc gctcctaagc tgctgatctg tggcaacaat 1740

aaccgcccat ctggggtgcc cgatcgattc tccggctcta aaagtgggac ttcagccagc 1800

ctggctatta ccggcctgca ggccgaggac gaagctgatt actattgcca gagctacgac 1860

tcaagcctga ccggagtcgt gttcggagga ggaaccaagc tgacagtcct gggacagcct 1920

aaagccgctc caagcgtgac actgtttcct ccatcctctg aggaactgca ggcaaacaag 1980

gccaccctgg tgtgcctgat ttccgacttc taccccgggg cagtcactgt ggcttggaag 2040

gcagatagtt cacctgtcaa agccggagtg gagactacca caccatcaaa gcagagcaat 2100

aacaaatacg cagccagctc ctatctgtcc ctgacccctg agcagtggaa gtctcacaaa 2160

tcctattctt gccaggtcac tcacgaagga agcactgtgg agaaaactgt cgcaccaacc 2220

gaatgtagtt gataactcga g 2241

<210> 68
<211> 739
<212> PRT
<213> Artificial Sequence

<220>
<223> DVSF-1 WT amino acid sequence

<400> 68

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly

```
1               5                   10                  15

Thr His Ala Gln Ala His Leu Val Glu Ser Gly Gly Gly Val Val Gln
            20                  25                  30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Ala Phe Asn Phe
        35                  40                  45

Ser Thr Asn Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60

Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser His Lys Tyr Tyr Ala
65                  70                  75                  80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
                85                  90                  95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Ala Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Thr Val Gly Val Leu Thr Trp Pro Val Asn Ala Glu
        115                 120                 125

Tyr Phe His His Trp Gly Gln Gly Ser Leu Val Ser Val Ser Ser Ala
    130                 135                 140

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
145                 150                 155                 160

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
                165                 170                 175

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
            180                 185                 190

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
```

```
        195                 200                 205

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
    210                 215                 220

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
225                 230                 235                 240

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
                245                 250                 255

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
            260                 265                 270

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
        275                 280                 285

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
    290                 295                 300

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
305                 310                 315                 320

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
                325                 330                 335

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
            340                 345                 350

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
        355                 360                 365

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
    370                 375                 380

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
```

```
385                 390                 395                 400

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
                405                 410                 415

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
            420                 425                 430

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
        435                 440                 445

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
    450                 455                 460

Lys Ser Leu Ser Leu Ser Pro Gly Lys Arg Gly Arg Lys Arg Arg Ser
465                 470                 475                 480

Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val
                485                 490                 495

Glu Glu Asn Pro Gly Pro Met Ala Trp Thr Pro Leu Phe Leu Phe Leu
            500                 505                 510

Leu Thr Cys Cys Pro Gly Gly Ser Asn Ser Gln Ser Val Leu Thr Gln
        515                 520                 525

Pro Pro Ser Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys
    530                 535                 540

Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val His Trp Tyr
545                 550                 555                 560

Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Cys Gly Asn Asn
                565                 570                 575

Asn Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
```

580 585 590

Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala
595 600 605

Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser Leu Thr Gly Val Val Phe
610 615 620

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala Ala Pro
625 630 635 640

Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys
645 650 655

Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr
660 665 670

Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr
675 680 685

Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr
690 695 700

Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Lys Ser Tyr Ser Cys
705 710 715 720

Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr
725 730 735

Glu Cys Ser

<210> 69
<211> 2241
<212> DNA
<213> Artificial Sequence

<220>
<223> DVSF-1 LALA nucleic acid sequence

<400> 69
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actcacgctc aggcacatct ggtcgaatct ggaggaggag tggtccagcc tggccgatcc 120

ctgcgactgt cttgcgcagc tagcgccttc aacttcagca caaacgcaat gcactgggtg 180

cgacaggcac caggcaaggg actggagtgg gtcgctgtga tctcatacga cggaagccat 240

aagtactatg cagattctgt gaaaggccgg ttcaccattt ccagggacaa ttctaagaac 300

accctgtatc tgcagatgaa tagcctgcgc gcagccgata ccgcagtgta ctattgcgca 360

actgtcggcg tgctgacctg gccagtgaac gccgaatact ttcaccattg gggacagggc 420

agtctggtct cagtgagctc cgcaagtact aagggaccat cagtgttccc actggcaccc 480

tctagtaaat ctactagtgg cgggaccgct gcactgggat gtctggtgaa ggactatttc 540

cccgagcctg tcaccgtgag ctggaattcc ggagccctga caagcggcgt ccacactttt 600

cccgctgtgc tgcagtcaag cggactgtac tccctgtcct ctgtggtcac tgtgcctagt 660

tcaagcctgg gcactcagac ctatatctgc aatgtgaacc acaagccctc taacaccaaa 720

gtcgacaaga aagtggaacc taagagctgt gataaaacac atacttgccc accttgtcca 780

gcaccagagg cagctggagg accaagcgtg ttcctgtttc cacccaagcc taaagacaca 840

ctgatgatta gccggacacc tgaagtcact tgcgtggtcg tggacgtgtc ccacgaggac 900

cccgaagtca agtttaattg gtacgtggat ggcgtcgagg tgcataacgc caagaccaaa 960

ccccgggagg aacagtacaa tagcacatat agagtcgtgt ccgtcctgac tgtgctgcat 1020

caggattggc tgaatgggaa ggagtataag tgcaaagtgt ctaacaaggc tctgcctgca 1080

ccaatcgaga aaaccattag caaggctaaa ggccagccta gggaaccaca ggtgtacaca 1140

ctgcctccaa gtcgcgacga gctgaccaag aatcaggtct ccctgacatg tctggtgaaa 1200

ggcttctatc catcagatat cgccgtggag tgggaaagca acgggcagcc cgaaaacaat 1260

tacaagacca cacccctgt gctggactct gatggcagtt tctttctgta ttctaagctg 1320

accgtggaca aaagtagatg gcagcagggg aatgtctttt catgtagcgt gatgcacgag 1380

gccctgcaca accattacac acagaagtcc ctgtctctga gtcccggaaa gaggggccgc 1440

aaacggagat cagggagcgg agctactaat ttcagcctgc tgaaacaggc aggggatgtg 1500

gaggaaaacc ccggacctat ggcttggacc ccactgttcc tgtttctgct gacatgctgt 1560

cccgggggca gcaattctca gagtgtcctg acacagccac catcagtgag cggagcacca 1620

ggacagaggg tgaccatctc ctgcacaggc agcagcagca acattggcgc cgggtacgac 1680

gtgcattggt atcagcagct gcccggcacc gctcctaagc tgctgatctg tggcaacaat 1740

aaccgcccat ctggggtgcc cgatcgattc tccggctcta aaagtgggac ttcagccagc 1800

ctggctatta ccggcctgca ggccgaggac gaagctgatt actattgcca gagctacgac 1860

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aaagccgctc caagcgtgac actgtttcct ccatcctctg aggaactgca ggcaaacaag 1980

gccaccctgg tgtgcctgat ttccgacttc taccccgggg cagtcactgt ggcttggaag 2040

gcagatagtt cacctgtcaa agccggagtg gagactacca caccatcaaa gcagagcaat 2100

aacaaatacg cagccagctc ctatctgtcc ctgacccctg agcagtggaa gtctcacaaa 2160

tcctattctt gccaggtcac tcacgaagga agcactgtgg agaaaactgt cgcaccaacc 2220

gaatgtagtt gataactcga g 2241

<210> 70
<211> 739
<212> PRT
<213> Artificial Sequence

<220>
<223> DVSF-1 LALA amino acid sequence

<400> 70

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Gln Ala His Leu Val Glu Ser Gly Gly Gly Val Val Gln

```
            20                  25                  30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Ala Phe Asn Phe
        35                  40                  45

Ser Thr Asn Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60

Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser His Lys Tyr Tyr Ala
65                  70                  75                  80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
                85                  90                  95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Ala Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Thr Val Gly Val Leu Thr Trp Pro Val Asn Ala Glu
        115                 120                 125

Tyr Phe His His Trp Gly Gln Gly Ser Leu Val Ser Val Ser Ser Ala
    130                 135                 140

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
145                 150                 155                 160

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
                165                 170                 175

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
            180                 185                 190

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
        195                 200                 205

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
```

```
    210                 215                 220

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
225                 230                 235                 240

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
                245                 250                 255

Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
            260                 265                 270

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
        275                 280                 285

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
    290                 295                 300

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
305                 310                 315                 320

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
                325                 330                 335

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
            340                 345                 350

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
        355                 360                 365

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
    370                 375                 380

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
385                 390                 395                 400

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
```

```
                405                 410                 415

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
            420                 425                 430

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
        435                 440                 445

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
    450                 455                 460

Lys Ser Leu Ser Leu Ser Pro Gly Lys Arg Gly Arg Lys Arg Arg Ser
465                 470                 475                 480

Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val
                485                 490                 495

Glu Glu Asn Pro Gly Pro Met Ala Trp Thr Pro Leu Phe Leu Phe Leu
            500                 505                 510

Leu Thr Cys Cys Pro Gly Gly Ser Asn Ser Gln Ser Val Leu Thr Gln
        515                 520                 525

Pro Pro Ser Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys
    530                 535                 540

Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val His Trp Tyr
545                 550                 555                 560

Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Cys Gly Asn Asn
                565                 570                 575

Asn Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
            580                 585                 590

Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala
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595 600 605

Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser Leu Thr Gly Val Val Phe
610 615 620

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala Ala Pro
625 630 635 640

Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys
645 650 655

Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr
660 665 670

Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr
675 680 685

Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr
690 695 700

Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Lys Ser Tyr Ser Cys
705 710 715 720

Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr
725 730 735

Glu Cys Ser

<210> 71
<211> 2241
<212> DNA
<213> Artificial Sequence

<220>
<223> DVSF-2 WT nucleic acid sequence

<400> 71

ggatccgcca ccatggactg gacatggaga atcctgttcc tggtcgccgc cgcaaccggg 60

acacacgccg aagtgcagct ggtggaatct ggaggggggat gggtgcagcc aggagggtcc 120

ctgcgactgt cttgcgccgc tagtggcttc acttttttcca gatacgacat gcactgggtc 180

aggcaggtga ccggaaaggg cctggaatgg gtgagcgcaa tcaccacagc cggagacaca 240

tactatcccg attctgtgaa gggccggttc accattagtc gggagaacgc caaaagctcc 300

ctgtatctgc agatgaacaa tctgagagct ggcgacaccg cactgtacta ttgcgctagg 360

ggccccccta cagattgctc tagtggacga tgtctgggag tcggagtggg actggaccca 420

tgggggcagg gaacactggt cactgtgtca agcgcctcca caaagggacc ctctgtgttc 480

cctctggctc catcctctaa aagtacttca ggaggaaccg cagcactggg atgtctggtg 540

aaggattact tcccagagcc cgtcaccgtg agctggaact ccggagctct gactagcggc 600

gtccatacct ttcctgcagt gctgcagagt tcaggcctgt acagcctgag ctccgtggtc 660

accgtgccat ctagttcact ggggacccag acatatatct gcaacgtgaa tcacaagcca 720

tctaatacaa aagtcgacaa gaaagtggaa cccaagagtt gtgataaaac tcatacctgc 780

ccaccatgtc ctgcaccaga gctgctggga ggaccatccg tgttcctgtt tcctccaaag 840

cccaaagaca cactgatgat tagcaggaca cccgaagtca cttgcgtggt cgtggacgtg 900

agccacgagg accccgaagt caagtttaac tggtacgtgg atggcgtcga ggtgcataat 960

gccaagacca aaccccggga ggaacagtac aacagtacct atagagtcgt gtcagtcctg 1020

acagtgctgc accaggactg gctgaacggg aaagagtata agtgcaaagt gtccaataag 1080

gcactgcccg cccctatcga gaaaaccatt tctaaggcca aaggacagcc ccgagaacct 1140

caggtgtaca cactgccccc tagccgcgac gagctgacaa agaaccaggt ctccctgact 1200

tgtctggtga aagggttcta tccttcagat atcgccgtgg agtgggaaag caatggacag 1260

ccagaaaaca attacaagac taccccaccc gtgctggact ctgatggcag tttctttctg 1320

tatagcaagc tgaccgtgga caaatcccgc tggcagcagg ggaacgtctt tagctgctcc 1380

gtgatgcatg aggccctgca caatcattac actcagaagt ctctgagtct gtcacctgga 1440

aagaggggac gaaaacgaag aagcggctcc ggagcaacca acttcagcct gctgaaacag 1500

gccggggatg tggaggaaaa tccaggaccc atggcatgga ctcctctgtt cctgtttctg 1560

ctgacctgct gtccaggcgg gagcaacagc tcctacgagg tgacccagcc tccatctgtc 1620

agtgtgtcac ccggccagac cgcttcaatc acatgtagcg gggacaagct gggaaagaaa 1680

tacacaagtt ggtatcagca gaaaccagga cagtcacccc tgctggtcat ctaccaggat 1740

actaagcgcc ctagcggcat tccagaacgg ttcagcggct ccaactctgg gaatacagct 1800

actctgacca tctccggcac ccaggccatg gacgaggctg attactattg ccaggcatgg 1860

gattctacaa ctcacgtcat tttcggaggc gggaccaagc tgacagtgct ggggcagccc 1920

aaagctgcac ctagcgtcac cctgtttccc ccttctagtg aggaactgca ggctaataag 1980

gcaacactgg tgtgtctgat ttccgacttc tacccaggag cagtcactgt ggcatggaag 2040

gctgattcaa gccccgtcaa agccggagtg gaaaccacaa ctccttcaaa gcagagcaac 2100

aacaagtacg ccgcttcctc ttatctgtcc ctgactcccg agcagtggaa gtctcacaaa 2160

agttattcat gccaggtgac ccatgagggc tccactgtcg aaaagaccgt ggcccctaca 2220

gagtgttctt gataactcga g 2241

<210> 72
<211> 739
<212> PRT
<213> Artificial Sequence

<220>
<223> DVSF-2 WT amino acid sequence

<400> 72

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Trp Val Gln
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe

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        35                  40                  45

Ser Arg Tyr Asp Met His Trp Val Arg Gln Val Thr Gly Lys Gly Leu
    50                  55                  60

Glu Trp Val Ser Ala Ile Thr Thr Ala Gly Asp Thr Tyr Tyr Pro Asp
65                  70                  75                  80

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Ser Ser
                85                  90                  95

Leu Tyr Leu Gln Met Asn Asn Leu Arg Ala Gly Asp Thr Ala Leu Tyr
            100                 105                 110

Tyr Cys Ala Arg Gly Pro Pro Thr Asp Cys Ser Ser Gly Arg Cys Leu
        115                 120                 125

Gly Val Gly Val Gly Leu Asp Pro Trp Gly Gln Gly Thr Leu Val Thr
    130                 135                 140

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
145                 150                 155                 160

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
                165                 170                 175

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
            180                 185                 190

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
        195                 200                 205

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
    210                 215                 220

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
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225                 230                 235                 240

Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
                245                 250                 255

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
            260                 265                 270

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
        275                 280                 285

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
    290                 295                 300

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
305                 310                 315                 320

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
                325                 330                 335

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
            340                 345                 350

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

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
    370                 375                 380

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
385                 390                 395                 400

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
                405                 410                 415

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
```

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            420                 425                 430

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
        435                 440                 445

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
    450                 455                 460

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Arg Gly Arg
465                 470                 475                 480

Lys Arg Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln
                485                 490                 495

Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Trp Thr Pro Leu
            500                 505                 510

Phe Leu Phe Leu Leu Thr Cys Cys Pro Gly Gly Ser Asn Ser Ser Tyr
        515                 520                 525

Glu Val Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln Thr Ala
    530                 535                 540

Ser Ile Thr Cys Ser Gly Asp Lys Leu Gly Lys Lys Tyr Thr Ser Trp
545                 550                 555                 560

Tyr Gln Gln Lys Pro Gly Gln Ser Pro Leu Leu Val Ile Tyr Gln Asp
                565                 570                 575

Thr Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser
            580                 585                 590

Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met Asp Glu
        595                 600                 605

Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Ser Thr Thr His Val Ile Phe
```

610 615 620

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala Ala Pro
625 630 635 640

Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys
645 650 655

Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr
660 665 670

Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr
675 680 685

Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr
690 695 700

Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Lys Ser Tyr Ser Cys
705 710 715 720

Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr
725 730 735

Glu Cys Ser

<210> 73
<211> 2241
<212> DNA
<213> Artificial Sequence

<220>
<223> DVSF-2 LALA nucleic acid sequence

<400> 73
ggatccgcca ccatggactg gacatggaga atcctgttcc tggtcgccgc cgctactggg 60

actcacgccg aagtgcagct ggtcgagagt ggaggggggat gggtgcagcc cggcggcagc 120

ctgaggctgt cttgcgccgc tagtggcttc acttttttcta gatacgacat gcactgggtc 180

cggcaggtga ccgggaaggg actggaatgg gtgagcgcca tcaccacagc aggggacaca 240

tactatcccg attctgtgaa gggcaggttc accattagta gggagaacgc aaaaagctcc 300

ctgtatctgc agatgaacaa tctgagagcc ggcgacaccg ctctgtacta ttgcgccagg 360

ggccctccca cagattgctc tagtggacgc tgtctgggag tcggagtggg actggaccca 420

tggggacagg ggacactggt caccgtgagc agcgcctcca ctaagggacc aagcgtgttc 480

cctctggcac catcctctaa aagtacttca gggggcaccg cagccctggg atgtctggtg 540

aaggattact tcccagagcc cgtcacagtg agctggaact ccggggccct gacttccgga 600

gtccacacct ttcctgctgt gctgcagagt tcaggcctgt actctctgag ctccgtggtc 660

acagtgccat ctagttcact gggaacccag acatatatct gcaacgtgaa tcacaagcca 720

agtaatacta aagtcgacaa gaaagtggaa cccaagtctt gtgataaaac tcatacctgc 780

ccaccctgtc ctgcaccaga ggctgcagga gggccatccg tgttcctgtt tcctccaaag 840

cccaaagaca ccctgatgat tagccggaca cccgaagtca cttgcgtggt cgtggacgtg 900

tcccacgagg accccgaagt caagtttaac tggtacgtgg atggcgtcga ggtgcataat 960

gccaagacaa aacccaggga ggaacagtac aacagtacct atagagtcgt gtcagtcctg 1020

acagtgctgc accaggactg gctgaacgga aaggagtata agtgcaaagt gtctaataag 1080

gctctgcccg cacctatcga gaaaaccatt agcaaggcca aagggcagcc ccgagaacct 1140

caggtgtaca cactgccccc ttcccgcgac gagctgacaa agaaccaggt ctctctgact 1200

tgtctggtga aaggattcta tccttcagat atcgccgtgg agtgggaaag caatgggcag 1260

ccagaaaaca attacaagac taccccaccc gtgctggact ctgatggcag tttctttctg 1320

tatagcaagc tgaccgtgga caaatcccgc tggcagcagg gaaacgtctt tagctgctcc 1380

gtgatgcatg aggccctgca caatcattac acccagaagt ctctgagtct gtcacctggg 1440

aagcgaggac gaaaaaggag aagcggctcc ggagctacaa acttctccct gctgaaacag 1500

gcaggagatg tggaggaaaa tccagggccc atggcctgga ctcctctgtt cctgtttctg 1560

ctgacctgct gtccaggcgg aagcaacagc tcctacgagg tgacccagcc tccaagcgtg 1620

agcgtgagcc caggccagac cgcttcaatc acatgtagcg gagacaagct ggggaagaaa 1680

tacactagtt ggtatcagca gaaaccaggg cagtcacccc tgctggtcat ctaccaggat 1740

accaagcgcc ctagcggcat tccagaacga ttcagcggct ccaactctgg aaatacagcc 1800

actctgacca tcagcggcac ccaggcaatg gacgaggccg attactattg ccaggcttgg 1860

gattccacaa ctcacgtcat tttcgggggc ggaaccaagc tgacagtgct gggacagccc 1920

aaagccgctc cttccgtcac cctgtttccc ccttctagtg aggaactgca ggccaataag 1980

gccaccctgg tgtgcctgat tagcgacttc taccccggag ctgtcactgt ggcatggaag 2040

gccgattcaa gccccgtcaa agcaggggtg gaaaccacaa ctccttcaaa gcagagcaac 2100

aacaagtacg cagcctcctc ttatctgtcc ctgaccccctg agcagtggaa gtctcataaa 2160

agttattcat gtcaggtcac ccatgagggc agcacagtgg aaaaaaccgt ggcaccaaca 2220

gaatgtagct gataactcga g 2241

<210> 74
<211> 739
<212> PRT
<213> Artificial Sequence

<220>
<223> DVSF-2 LALA amino acid sequence

<400> 74

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Trp Val Gln
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Arg Tyr Asp Met His Trp Val Arg Gln Val Thr Gly Lys Gly Leu

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    50                  55                  60

Glu Trp Val Ser Ala Ile Thr Thr Ala Gly Asp Thr Tyr Tyr Pro Asp
65                  70                  75                  80

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Ser Ser
                85                  90                  95

Leu Tyr Leu Gln Met Asn Asn Leu Arg Ala Gly Asp Thr Ala Leu Tyr
            100                 105                 110

Tyr Cys Ala Arg Gly Pro Pro Thr Asp Cys Ser Ser Gly Arg Cys Leu
        115                 120                 125

Gly Val Gly Val Gly Leu Asp Pro Trp Gly Gln Gly Thr Leu Val Thr
    130                 135                 140

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
145                 150                 155                 160

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
                165                 170                 175

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
            180                 185                 190

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
        195                 200                 205

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
    210                 215                 220

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
225                 230                 235                 240

Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
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                245                 250                 255

Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu
            260                 265                 270

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
        275                 280                 285

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
    290                 295                 300

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
305                 310                 315                 320

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
                325                 330                 335

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
            340                 345                 350

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

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
    370                 375                 380

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
385                 390                 395                 400

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
                405                 410                 415

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
            420                 425                 430

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
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        435                 440                 445

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
    450                 455                 460

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Arg Gly Arg
465                 470                 475                 480

Lys Arg Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln
                485                 490                 495

Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Trp Thr Pro Leu
            500                 505                 510

Phe Leu Phe Leu Leu Thr Cys Cys Pro Gly Gly Ser Asn Ser Ser Tyr
        515                 520                 525

Glu Val Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln Thr Ala
    530                 535                 540

Ser Ile Thr Cys Ser Gly Asp Lys Leu Gly Lys Lys Tyr Thr Ser Trp
545                 550                 555                 560

Tyr Gln Gln Lys Pro Gly Gln Ser Pro Leu Leu Val Ile Tyr Gln Asp
                565                 570                 575

Thr Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser
            580                 585                 590

Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met Asp Glu
        595                 600                 605

Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Ser Thr Thr His Val Ile Phe
    610                 615                 620

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala Ala Pro
```

625 630 635 640

Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys
645 650 655

Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr
660 665 670

Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr
675 680 685

Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr
690 695 700

Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Lys Ser Tyr Ser Cys
705 710 715 720

Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr
725 730 735

Glu Cys Ser

<210> 75
<211> 2229
<212> DNA
<213> Artificial Sequence

<220>
<223> DVSF-3 WT nucleic acid sequence

<400> 75
ggatccgcca ccatggactg gacatggaga atcctgttcc tggtcgccgc cgcaaccggg 60

acacacgccg aagtgcagct ggtggaatca gggggagggc tggtgcagcc tggaagaagt 120

ctgaggctgt catgcgccgc tagcggcttc acctttgacg attacgccat gttctgggtg 180

aggcaggctc caggcaaggg actggaatgg atcagcggca tttcctggaa ctctgcaact 240

atcgggtatg ccgactccgt gaaaggacgg tttaccattt caagagacaa cgccaagaaa 300

agcctggatc tgcagatgaa ttccctgcgg cccgacgata ccgctctgta ctattgcgca 360

aagggaggac ctagaggcct gcagctgctg agctcctggg tggactactg gggacagggc 420

actctggtca ccgtgtctag tgcttccaca aagggacctt ctgtgttccc actggcaccc 480

tcaagcaaat caacaagcgg aggaactgca gcactgggat gtctggtgaa ggattatttc 540

cccgagcctg tcaccgtgag ttggaactca ggagcactga cttccggagt ccacaccttt 600

ccagcagtgc tgcagtcctc tggactgtac agcctgagtt cagtggtcac agtgcctagc 660

tcctctctgg gcacacagac ttatatctgc aacgtgaatc acaagcctag caatactaaa 720

gtcgacaaga aagtggaacc aaagtcctgt gataaaaccc atacatgccc accttgtcca 780

gcaccagagc tgctgggggg accaagcgtg ttcctgtttc cacccaagcc caaagacaca 840

ctgatgattt ctcggacccc tgaagtcaca tgtgtggtcg tggacgtgag ccacgaggac 900

cccgaagtca agttcaactg gtacgtggat ggcgtcgagg tgcataatgc taagaccaaa 960

ccccgagagg aacagtacaa cagcacttat cgggtcgtgt ccgtcctgac cgtgctgcac 1020

caggactggc tgaacgggaa ggagtataag tgcaaagtgt ccaataaggc cctgcctgct 1080

ccaatcgaga aaacaatttc taaggcaaaa ggacagcctc gcgaaccaca ggtgtacact 1140

ctgcctccat cccgagacga gctgaccaag aaccaggtct ctctgacatg tctggtgaaa 1200

ggcttctatc caagtgatat cgctgtggag tgggaaagca atgggcagcc cgaaaacaat 1260

tacaagacca cacccctgt gctggacagc gatggctcct tctttctgta ttctaagctg 1320

accgtggata aaagtagatg gcagcagggg aacgtctttt cctgctctgt gatgcatgag 1380

gccctgcaca atcattacac acagaagagt ctgtcactga gcccagggaa gcgaggacgg 1440

aaacggagat ccgggtctgg agcaaccaac ttctccctgc tgaaacaggc aggcgacgtg 1500

gaggaaaatc caggacctat ggtcctgcag acccaggtgt ttatctctct gctgctgtgg 1560

attagtggcg cctacgggga tatccagatg acacagtccc ccagttcact gagtgcctca 1620

gtcggcgaca gggtgactat cacctgtcgc gctagccagg atattaggcg ctacctgaac 1680

tggtatcagc agcgaccagg acgagtgcct cagctgctga tctacactac ctccaccctg 1740

cagtctggag tcccaagtag gttcagcggc tccgggtctg tgacagactt tacactgact 1800

attagctccc tgcagcccga agatttcggc acttactatt gccagcagag ttattcacca 1860

ccccacacat ttggacaggg cactaagctg gaaatcaaaa ctgtcgctgc accctcagtg 1920

ttcatttttc ctccatctga cgagcagctg aagtcaggca ccgccagcgt cgtgtgtctg 1980

ctgaacaatt tctaccctcg cgaggctaag gtccagtgga aagtggataa cgcactgcag 2040

tctgggaata gtcaggagtc agtgacagaa caggacagca aggattccac ttattctctg 2100

tctagtaccc tgacactgag caaagccgac tacgagaagc acaaagtcta tgcttgcgaa 2160

gtgacccatc aggggctgag aagtcccgtg acaaagagct tcaacagggg agagtgttga 2220

taactcgag 2229

<210> 76
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> DVSF-3 WT amino acid sequence

<400> 76

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
20 25 30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Asp Asp Tyr Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Ile Ser Gly Ile Ser Trp Asn Ser Ala Thr Ile Gly Tyr Ala

```
65                  70                  75                  80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys
                85                  90                  95

Ser Leu Asp Leu Gln Met Asn Ser Leu Arg Pro Asp Asp Thr Ala Leu
            100                 105                 110

Tyr Tyr Cys Ala Lys Gly Gly Pro Arg Gly Leu Gln Leu Leu Ser Ser
        115                 120                 125

Trp Val Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala
    130                 135                 140

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
145                 150                 155                 160

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
                165                 170                 175

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
            180                 185                 190

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
        195                 200                 205

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
    210                 215                 220

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
225                 230                 235                 240

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
                245                 250                 255

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
```

```
            260                 265                 270

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
        275                 280                 285

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
    290                 295                 300

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
305                 310                 315                 320

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
                325                 330                 335

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
            340                 345                 350

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
        355                 360                 365

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
    370                 375                 380

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
385                 390                 395                 400

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
                405                 410                 415

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
            420                 425                 430

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
        435                 440                 445

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
```

```
    450                 455                 460

Lys Ser Leu Ser Leu Ser Pro Gly Lys Arg Gly Arg Lys Arg Arg Ser
465                 470                 475                 480

Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val
                485                 490                 495

Glu Glu Asn Pro Gly Pro Met Val Leu Gln Thr Gln Val Phe Ile Ser
            500                 505                 510

Leu Leu Leu Trp Ile Ser Gly Ala Tyr Gly Asp Ile Gln Met Thr Gln
        515                 520                 525

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
    530                 535                 540

Cys Arg Ala Ser Gln Asp Ile Arg Arg Tyr Leu Asn Trp Tyr Gln Gln
545                 550                 555                 560

Arg Pro Gly Arg Val Pro Gln Leu Leu Ile Tyr Thr Thr Ser Thr Leu
                565                 570                 575

Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Val Thr Asp
            580                 585                 590

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

Tyr Cys Gln Gln Ser Tyr Ser Pro Pro His Thr Phe Gly Gln Gly Thr
    610                 615                 620

Lys Leu Glu Ile Lys Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
625                 630                 635                 640

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
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645 650 655

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
660 665 670

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
675 680 685

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
690 695 700

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
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Gly Leu Arg Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
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ctgcggctgt catgcgccgc tagcggcttc acctttgacg attacgcaat gttctgggtg 180

aggcaggcac caggcaaggg actggaatgg atcagcggca tttcctggaa ctctgctacc 240

atcggatatg cagacagcgt gaaagggagg tttacaattt ctagagacaa cgccaagaaa 300

agtctggatc tgcagatgaa ttcactgcgc cccgacgata ccgccctgta ctattgcgct 360

aagggcggac ccaggggcct gcagctgctg agctcctggg tggactactg ggggcagggc 420

actctggtca ccgtgtctag tgcctccaca aagggcccta gcgtgttccc actggctccc 480

tcaagcaaat caacaagcgg gggcactgca gccctgggat gtctggtgaa ggattatttc 540

cccgagcctg tcaccgtgag ttggaactca ggggctctga ctagcggcgt ccacaccttt 600

cccgcagtgc tgcagtcctc tggcctgtac agcctgagtt cagtggtcac tgtccctagc 660

tcctctctgg gaacacagac ttatatctgc aacgtgaatc acaagccttc caataccaaa 720

gtcgacaaga aagtggaacc aaagtcttgt gataaaaccc atacatgccc tccctgtcca 780

gcaccagagg ctgcaggagg gccaagcgtg ttcctgtttc cacccaagcc caaagacaca 840

ctgatgatta gccggacccc tgaagtcaca tgcgtggtcg tggacgtgag ccacgaggac 900

cccgaagtca agtttaactg gtacgtggat ggcgtcgagg tgcataatgc taagaccaaa 960

ccccgagagg aacagtacaa cagtacttat agggtcgtgt cagtcctgac cgtgctgcac 1020

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gccctgcaca atcattacac acagaagagt ctgtcactga gcccaggaaa gcgagggagg 1440

aaaaggagat ccggatctgg ggctactaac ttctccctgc tgaagcaggc aggcgacgtg 1500

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ctgaacaatt tctaccctag agaagccaag gtccagtgga aagtggataa cgctctgcag 2040

tctgggaata gtcaggagtc agtgacagaa caggacagca aggattccac ttattctctg 2100

tctagtaccc tgacactgag caaagcagac tacgagaagc ataaagtgta tgcctgcgaa 2160

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taactcgag 2229

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<212> PRT
<213> Artificial Sequence

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<400> 78

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Thr His Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
20 25 30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Asp Asp Tyr Ala Met Phe Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Ile Ser Gly Ile Ser Trp Asn Ser Ala Thr Ile Gly Tyr Ala
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys
85 90 95

Ser Leu Asp Leu Gln Met Asn Ser Leu Arg Pro Asp Asp Thr Ala Leu

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            100                 105                 110

Tyr Tyr Cys Ala Lys Gly Gly Pro Arg Gly Leu Gln Leu Leu Ser Ser
        115                 120                 125

Trp Val Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala
    130                 135                 140

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
145                 150                 155                 160

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
                165                 170                 175

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
            180                 185                 190

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
        195                 200                 205

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
    210                 215                 220

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
225                 230                 235                 240

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
                245                 250                 255

Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
            260                 265                 270

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
        275                 280                 285

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
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    290                 295                 300

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
305                 310                 315                 320

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
                325                 330                 335

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
            340                 345                 350

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
        355                 360                 365

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
    370                 375                 380

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
385                 390                 395                 400

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
                405                 410                 415

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
            420                 425                 430

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
        435                 440                 445

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
    450                 455                 460

Lys Ser Leu Ser Leu Ser Pro Gly Lys Arg Gly Arg Lys Arg Arg Ser
465                 470                 475                 480

Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val
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                485                 490                 495

Glu Glu Asn Pro Gly Pro Met Val Leu Gln Thr Gln Val Phe Ile Ser
            500                 505                 510

Leu Leu Leu Trp Ile Ser Gly Ala Tyr Gly Asp Ile Gln Met Thr Gln
        515                 520                 525

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
    530                 535                 540

Cys Arg Ala Ser Gln Asp Ile Arg Arg Tyr Leu Asn Trp Tyr Gln Gln
545                 550                 555                 560

Arg Pro Gly Arg Val Pro Gln Leu Leu Ile Tyr Thr Thr Ser Thr Leu
                565                 570                 575

Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Val Thr Asp
            580                 585                 590

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

Tyr Cys Gln Gln Ser Tyr Ser Pro Pro His Thr Phe Gly Gln Gly Thr
    610                 615                 620

Lys Leu Glu Ile Lys Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
625                 630                 635                 640

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                645                 650                 655

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
            660                 665                 670

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
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675 680 685

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
690 695 700

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
705 710 715 720

Gly Leu Arg Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
725 730 735