Sequence listing

<110> Roche Diagnostics GmbH
F. Hoffmann-La Roche AG

<120> A soluble complex comprising a retroviral surface glycoprotein

<130> 19290WO-WN

<140>
<141>

<150> EP01115225.3
<151> 2001-06-22

<150> EP01120939.2
<151> 2001-08-31

<160> 10

<170> PatentIn Ver. 2.1

<210> 1
<211> 147
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:correponds to positions 535 to 681 of envelope protein of HIV-1

<400> 1

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Met Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln
  1               5                  10                  15

Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu
             20                  25                  30

Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala
         35                  40                  45

Val Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys
     50                  55                  60

Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp
 65                  70                  75                  80

Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu
                 85                  90                  95

Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile
            100                 105                 110

Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu
        115                 120                 125
```

Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp
130 135 140

Leu Trp Tyr
145

<210> 2
<211> 143
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:corresponds to positions 534 to 676 of envelope protein of HIV-2

<400> 2
Leu Thr Val Ser Ala Gln Ser Arg Thr Leu Leu Ala Gly Ile Val Gln
1 5 10 15

Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg Gln Gln Glu Leu Leu
20 25 30

Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln Ala Arg Val Thr Ala
35 40 45

Ile Glu Lys Tyr Leu Gln Asp Gln Ala Arg Leu Asn Ser Trp Gly Cys
50 55 60

Ala Phe Arg Gln Val Cys His Thr Thr Val Pro Trp Val Asn Asp Ser
65 70 75 80

Leu Ala Pro Asp Trp Asp Asn Met Thr Trp Gln Glu Trp Glu Lys Gln
85 90 95

Val Arg Tyr Leu Glu Ala Asn Ile Ser Lys Ser Leu Glu Gln Ala Gln
100 105 110

Ile Gln Gln Glu Lys Asn Met Tyr Glu Leu Gln Lys Leu Asn Ser Trp
115 120 125

Asp Ile Phe Gly Asn Trp Phe Asp Leu Thr Ser Trp Val Lys Tyr
130 135 140

<210> 3
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer1

<400> 3
gcgggtgttc cgggtatccc accgaattc 29

<210> 4
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer2

<400> 4
gaattcggtg ggatacccgg aacacccgc 29

<210> 5
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer3

<400> 5
cgggatccgg tggcggttca ggcggtggct ctggtggcgg tacgctgacg gtacaggcca 60
g 61

<210> 6
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer4

<400> 6
ccgctcgagg taccacagcc aatttgttat 30

<210> 7
<211> 1269
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence::coding for a
FkpA-gp41 fusion protein

<400> 7
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gatcagaaat cagcttatgc actgggtgct tcgctgggtc gttacatgga aaactctctt 120
aaagaacaag aaaaactggg catcaaactg ataaagatc agctgatcgc tggtgttcag 180
gatgcatttg ctgataagag caaactctcc gaccaagaga tcgaacagac tctgcaagca 240
ttcgaagctc gcgtgaagtc ttctgctcag gcgaagatgg aaaaagacgc ggctgataac 300
gaagcaaaag gtaaagagta ccgcgagaaa tttgccaaag agaaaggtgt gaaaacctct 360
tcaactggtc tggtttatca ggtagtagaa gccggtaaag gcgaagcacc gaaagacagc 420
gatactgttg tagtgaacta caaaggtacg ctgatcgacg gtaaagagtt cgacaactct 480

tacacccgtg gtgaaccgct ctctttccgt ctggacggtg ttatcccggg ttggacagaa
540
ggtctgaaga acatcaagaa aggcggtaag atcaaactgg ttattccacc agaactggct 600
tacggcaaag cgggtgttcc gggtatccca ccgaattcta ccctggtgtt tgacgtagag 660
ctgctggatg tgaaaccagc gccgaaggct gatgcaaagc cggaagctga tgcgaaagcc 720
gcagattctg ctaaaaaagg tggcggttcc ggcggtggct ctggtggcgg atccggtggc 780
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gctgtgcctt ggaatgctag ttggagtaat aaatctctgg aacagatttg gaataacatg
1080
acctggatgg agtgggacag agaaattaac aattacacaa gcttaataca ttccttaatt
1140
gaagaatcgc aaaaccagca agaaaagaat gaacaagaat tattggaatt agataaatgg
1200
gcaagtttgt ggaattggtt taacataaca aattggctgt ggtacctcga gcaccaccac
1260
caccaccac
1269

<210> 8
<211> 1026
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:coding for a
SlyD-gp41 fusion protein

<400> 8
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gtgttggttg atgagtctcc ggtgagtgcg ccgctggact acctgcatgg tcacggttcc 120
ctgatctctg gcctggaaac ggcgctggaa ggtcatgaag ttggcgacaa atttgatgtc 180
gctgttggcg cgaacgacgc ttacggtcag tacgacgaaa acctggtgca acgtgttcct 240
aaagacgtat ttatgggcgt tgatgaactg caggtaggta tgcgtttcct ggctgaaacc 300
gaccagggtc cggtaccggt tgaaatcact gcggttgaag acgatcacgt cgtggttgat 360
ggtaaccaca tgctggccgg tcagaacctg aaattcaacg ttgaagttgt ggcgattcgc 420
gaagcgactg aagaagaact ggctcatggt cacgttcacg gcgcgcacga tcaccaccac 480
gatcacgacc acgacggtgg cggttccggc ggtggctctg gtggcggatc cggtggcggt 540
tccggcggtg gctctggtgg cggtacgctg acggtacagg ccagacaatt attgtctggt 600
atagtgcagc agcagaacaa tgagctgagg gctattgagg cgcaacagca tctggagcaa 660
ctcacagtct ggggcaccaa gcagctccag gcaagagaac tggctgtgga aagataccta 720
aaggatcaac agctcctggg gatttggggt tgctctggaa aactcatttg caccactgct 780
gtgccttgga atgctagttg gagtaataaa tctctggaac agatttggaa taacatgacc 840
tggatggagt gggacagaga aattaacaat tacacaagct taatacattc cttaattgaa 900
gaatcgcaaa accagcaaga aaagaatgaa caagaattat tggaattaga taaatgggca 960
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caccac
1026

<210> 9

<211> 688
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:FkpAFkpAgp36 (3mut) fusion protein

<400> 9

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Met Ala Glu Ala Ala Lys Pro Ala Thr Thr Ala Asp Ser Lys Ala Ala
 1               5                  10                  15

Phe Lys Asn Asp Asp Gln Lys Ser Ala Tyr Ala Leu Gly Ala Ser Leu
            20                  25                  30

Gly Arg Tyr Met Glu Asn Ser Leu Lys Glu Gln Glu Lys Leu Gly Ile
        35                  40                  45

Lys Leu Asp Lys Asp Gln Leu Ile Ala Gly Val Gln Asp Ala Phe Ala
    50                  55                  60

Asp Lys Ser Lys Leu Ser Asp Gln Glu Ile Glu Gln Thr Leu Gln Ala
65                  70                  75                  80

Phe Glu Ala Arg Val Lys Ser Ser Ala Gln Ala Lys Met Glu Lys Asp
                85                  90                  95

Ala Ala Asp Asn Glu Ala Lys Gly Lys Glu Tyr Arg Glu Lys Phe Ala
            100                 105                 110

Lys Glu Lys Gly Val Lys Thr Ser Ser Thr Gly Leu Val Tyr Gln Val
        115                 120                 125

Val Glu Ala Gly Lys Gly Glu Ala Pro Lys Asp Ser Asp Thr Val Val
    130                 135                 140

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

Tyr Thr Arg Gly Glu Pro Leu Ser Phe Arg Leu Asp Gly Val Ile Pro
                165                 170                 175

Gly Trp Thr Glu Gly Leu Lys Asn Ile Lys Lys Gly Gly Lys Ile Lys
            180                 185                 190

Leu Val Ile Pro Pro Glu Leu Ala Tyr Gly Lys Ala Gly Val Pro Gly
        195                 200                 205

Ile Pro Pro Asn Ser Thr Leu Val Phe Asp Val Glu Leu Leu Asp Val
    210                 215                 220

Lys Pro Ala Pro Lys Ala Asp Ala Lys Pro Glu Ala Asp Ala Lys Ala
225                 230                 235                 240

Ala Asp Ser Ala Lys Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
                245                 250                 255
```

```
Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ala Glu Ala
            260                 265                 270

Ala Lys Pro Ala Thr Thr Ala Asp Ser Lys Ala Ala Phe Lys Asn Asp
        275                 280                 285

Asp Gln Lys Ser Ala Tyr Ala Leu Gly Ala Ser Leu Gly Arg Tyr Met
    290                 295                 300

Glu Asn Ser Leu Lys Glu Gln Glu Lys Leu Gly Ile Lys Leu Asp Lys
305                 310                 315                 320

Asp Gln Leu Ile Ala Gly Val Gln Asp Ala Phe Ala Asp Lys Ser Lys
                325                 330                 335

Leu Ser Asp Gln Glu Ile Glu Gln Thr Leu Gln Ala Phe Glu Ala Arg
            340                 345                 350

Val Lys Ser Ser Ala Gln Ala Lys Met Glu Lys Asp Ala Ala Asp Asn
        355                 360                 365

Glu Ala Lys Gly Lys Glu Tyr Arg Glu Lys Phe Ala Lys Glu Lys Gly
    370                 375                 380

Val Lys Thr Ser Ser Thr Gly Leu Val Tyr Gln Val Val Glu Ala Gly
385                 390                 395                 400

Lys Gly Glu Ala Pro Lys Asp Ser Asp Thr Val Val Val Asn Tyr Lys
                405                 410                 415

Gly Thr Leu Ile Asp Gly Lys Glu Phe Asp Asn Ser Tyr Thr Arg Gly
            420                 425                 430

Glu Pro Leu Ser Phe Arg Leu Asp Gly Val Ile Pro Gly Trp Thr Glu
        435                 440                 445

Gly Leu Lys Asn Ile Lys Lys Gly Gly Lys Ile Lys Leu Val Ile Pro
    450                 455                 460

Pro Glu Leu Ala Tyr Gly Lys Ala Gly Val Pro Gly Ile Pro Pro Asn
465                 470                 475                 480

Ser Thr Leu Val Phe Asp Val Glu Leu Leu Asp Val Lys Pro Ala Pro
                485                 490                 495

Lys Ala Asp Ala Lys Pro Glu Ala Asp Ala Lys Ala Ala Asp Ser Ala
            500                 505                 510

Lys Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
        515                 520                 525

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

Arg Thr Leu Leu Ala Gly Ile Val Gln Gln Gln Gln Gln Glu Leu Asp
```

```
545                 550                 555                 560

Val Val Lys Arg Gln Gln Glu Leu Glu Arg Leu Thr Val Trp Gly Thr
                565                 570                 575

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

Gln Ala Arg Leu Asn Ser Trp Gly Cys Ala Phe Arg Gln Val Cys His
        595                 600                 605

Thr Thr Val Pro Trp Val Asn Asp Ser Leu Ala Pro Asp Trp Asp Asn
    610                 615                 620

Met Thr Trp Gln Glu Trp Glu Lys Gln Val Arg Tyr Leu Glu Ala Asn
625                 630                 635                 640

Ile Ser Lys Ser Leu Glu Gln Ala Gln Ile Gln Gln Glu Lys Asn Met
                645                 650                 655

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

Asp Leu Thr Ser Trp Val Lys Tyr Leu Glu His His His His His His
        675                 680                 685
```

<210> 10
<211> 385
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:FkpA-gp21
fusion protein

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<400> 10
Met Ala Glu Ala Ala Lys Pro Ala Thr Thr Ala Asp Ser Lys Ala Ala
  1               5                  10                  15

Phe Lys Asn Asp Asp Gln Lys Ser Ala Tyr Ala Leu Gly Ala Ser Leu
             20                  25                  30

Gly Arg Tyr Met Glu Asn Ser Leu Lys Glu Gln Glu Lys Leu Gly Ile
         35                  40                  45

Lys Leu Asp Lys Asp Gln Leu Ile Ala Gly Val Gln Asp Ala Phe Ala
     50                  55                  60

Asp Lys Ser Lys Leu Ser Asp Gln Glu Ile Glu Gln Thr Leu Gln Ala
 65                  70                  75                  80

Phe Glu Ala Arg Val Lys Ser Ser Ala Gln Ala Lys Met Glu Lys Asp
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```
                    85                  90                  95

Ala Ala Asp Asn Glu Ala Lys Gly Lys Glu Tyr Arg Glu Lys Phe Ala
            100                 105                 110

Lys Glu Lys Gly Val Lys Thr Ser Ser Thr Gly Leu Val Tyr Gln Val
        115                 120                 125

Val Glu Ala Gly Lys Gly Glu Ala Pro Lys Asp Ser Asp Thr Val Val
    130                 135                 140

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

Tyr Thr Arg Gly Glu Pro Leu Ser Phe Arg Leu Asp Gly Val Ile Pro
                165                 170                 175

Gly Trp Thr Glu Gly Leu Lys Asn Ile Lys Lys Gly Gly Lys Ile Lys
            180                 185                 190

Leu Val Ile Pro Pro Glu Leu Ala Tyr Gly Lys Ala Gly Val Pro Gly
        195                 200                 205

Ile Pro Pro Asn Ser Thr Leu Val Phe Asp Val Glu Leu Leu Asp Val
    210                 215                 220

Lys Pro Ala Pro Lys Ala Asp Ala Lys Pro Glu Ala Asp Ala Lys Ala
225                 230                 235                 240

Ala Asp Ser Ala Lys Lys Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
                245                 250                 255

Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Leu Ala
            260                 265                 270

Ser Gly Lys Ser Leu Leu His Glu Val Asp Lys Asp Ile Ser Gln Leu
        275                 280                 285

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

Tyr Ala Ala Gln Asn Arg Arg Gly Leu Asp Leu Leu Phe Trp Glu Gln
305                 310                 315                 320

Gly Gly Leu Cys Lys Ala Leu Gln Glu Gln Cys Cys Phe Leu Asn Ile
                325                 330                 335

Thr Asn Ser His Val Ser Ile Leu Gln Glu Arg Pro Pro Leu Glu Asn
            340                 345                 350

Arg Val Leu Thr Gly Trp Gly Leu Asn Trp Asp Leu Gly Leu Ser Gln
        355                 360                 365

Trp Ala Arg Glu Ala Leu Gln Thr Gly Leu Glu His His His His His
    370                 375                 380
```

His
385