<110> NOVARTIS AG

<120> STABILIZED GP120

<130> PAT054316-WO-PCT

<140> PCT/EP2013/_____
<141> 14 JUNE 2013

<150> 61/661,050
<151> 18 JUNE 2012

<160> 23

<170> SeqWin99, version 1.02

<210> 1
<211> 1494
<212> DNA
<213> HIV-1

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gaggccacca ccaccctgtt ctgcgccagc gacgccaagg cctacgacac cgaggtgcac 180
aacgtgtggg ccacccacgc ctgcgtgccc accgacccca acccccagga gatcgtgctg 240
gagaacgtga ccgagaactt caacatgtgg aagaacaaca tggtggagca gatgcacgag 300
gacatcatca gcctgtggga ccagagcctg aagccctgcg tgaagctgac ccccctgtgc 360
gtgaccctgc actgcaccaa cctgaagaac gccaccaaca ccaagagcag caactggaag 420
gagatggacc gcggcgagat caagaactgc agcttcaagg tgaccaccag catccgcaac 480
aagatgcaga aggagtacgc cctgttctac aagctggacg tggtgcccat cgacaacgac 540
aacaccagct acaagctgat caactgcaac accagcgtga tcacccaggc ctgccccaag 600
gtgagcttcg agcccatccc catccactac tgcgcccccg ccggcttcgc catcctgaag 660
tgcaacgaca agaagttcaa cggcagcggc ccctgcacca acgtgagcac cgtgcagtgc 720
acccacggca tccgccccgt ggtgagcacc cagctgctgc tgaacggcag cctggccgag 780
gagggcgtgg tgatccgcag cgagaacttc accgacaacg ccaagaccat catcgtgcag 840
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gcccactgca acatcagcgg cgagaagtgg aacaacaccc tgaagcagat cgtgaccaag 1020
ctgcaggccc agttcggcaa caagaccatc gtgttcaagc agagcagcgg cggcgacccc 1080
gagatcgtga tgcacagctt caactgcggc ggcgagttct tctactgcaa cagcacccag 1140
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ctgccctgcc gcatcaagca gatcatcaac cgctggcagg aggtgggcaa ggccatgtac 1260
gccccccca tccgcggcca gatccgctgc agcagcaaca tcaccggcct gctgctgacc 1320
cgcgacggcg gcaaggagat cagcaacacc accgagatct tccgccccgg cggcggcgac 1380
atgcgcgaca actggcgcag cgagctgtac aagtacaagg tggtgaagat cgagcccctg 1440
ggcgtggccc ccaccaaggc caagcgccgc gtggtgcagc gcgagaagcg ctaa 1494

<210> 2
<211> 497
<212> PRT
<213> HIV-1

<220>
<221> domain
<222> 1-248, 458-497
<223> Inner Domain

<400> 2
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Ala Val Phe Val Ser Pro Ser Ala Val Glu Lys Leu Trp Val Thr Val
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Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr Thr Thr Leu Phe Cys
35 40 45

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Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val His Asn Val Trp Ala
    50                  55                  60

Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Ile Val Leu
65                  70                  75                  80

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

Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro
            100                 105                 110

Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu His Cys Thr Asn Leu
        115                 120                 125

Lys Asn Ala Thr Asn Thr Lys Ser Ser Asn Trp Lys Glu Met Asp Arg
    130                 135                 140

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

Lys Met Gln Lys Glu Tyr Ala Leu Phe Tyr Lys Leu Asp Val Val Pro
                165                 170                 175

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

Val Ile Thr Gln Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile
        195                 200                 205

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

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

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

Ser Leu Ala Glu Glu Gly Val Val Ile Arg Ser Glu Asn Phe Thr Asp
            260                 265                 270

Asn Ala Lys Thr Ile Ile Val Gln Leu Lys Glu Ser Val Glu Ile Asn
        275                 280                 285

Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly Pro
    290                 295                 300

Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln
305                 310                 315                 320

Ala His Cys Asn Ile Ser Gly Glu Lys Trp Asn Asn Thr Leu Lys Gln
                325                 330                 335

Ile Val Thr Lys Leu Gln Ala Gln Phe Gly Asn Lys Thr Ile Val Phe
            340                 345                 350

Lys Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Met His Ser Phe Asn
        355                 360                 365

Cys Gly Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser
    370                 375                 380

Thr Trp Asn Asn Thr Ile Gly Pro Asn Asn Thr Asn Gly Thr Ile Thr
385                 390                 395                 400

Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Arg Trp Gln Glu Val Gly
                405                 410                 415
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Lys Ala Met Tyr Ala Pro Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser
            420                 425                 430

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

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

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

Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys
                485                 490                 495

Arg


<210>   3
<211>   1494
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   HIV-1 gp120 V59C and S109C

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gaggccacca ccaccctgtt ctgcgccagc gacgccaagg cctacgacac cgagtgccac   180
aacgtgtggg ccacccacgc ctgcgtgccc accgacccca acccccagga gatcgtgctg   240
gagaacgtga ccgagaactt caacatgtgg aagaacaaca tggtggagca gatgcacgag   300
gacatcatca gcctgtggga ccagtgcctg aagccctgcg tgaagctgac ccccctgtgc   360
gtgaccctgc actgcaccaa cctgaagaac gccaccaaca ccaagagcag caactggaag   420
gagatggacc gcggcgagat caagaactgc agcttcaagg tgaccaccag catccgcaac   480
aagatgcaga aggagtacgc cctgttctac aagctggacg tggtgcccat cgacaacgac   540
aacaccagct acaagctgat caactgcaac accagcgtga tcacccaggc ctgccccaag   600
gtgagcttcg agcccatccc catccactac tgcgcccccg ccggcttcgc catcctgaag   660
tgcaacgaca agaagttcaa cggcagcggc ccctgcacca acgtgagcac cgtgcagtgc   720
acccacggca tccgccccgt ggtgagcacc cagctgctgc tgaacggcag cctggccgag   780
gagggcgtgg tgatccgcag cgagaacttc accgacaacg ccaagaccat catcgtgcag   840
ctgaaggaga gcgtggagat caactgcacc cgccccaaca acaacacccg caagagcatc   900
accatcggcc ccggccgcgc cttctacgcc accggcgaca tcatcggcga catccgccag   960
gcccactgca acatcagcgg cgagaagtgg aacaacaccc tgaagcagat cgtgaccaag   1020
ctgcaggccc agttcggcaa caagaccatc gtgttcaagc agagcagcgg cggcgacccc   1080
gagatcgtga tgcacagctt caactgcggc ggcgagttct tctactgcaa cagcacccag   1140
ctgttcaaca gcacctggaa caacaccatc ggccccaaca acaccaacgg caccatcacc   1200
ctgccctgcc gcatcaagca gatcatcaac cgctggcagg aggtgggcaa ggccatgtac   1260
gcccccccca tccgcggcca gatccgctgc agcagcaaca tcaccggcct gctgctgacc   1320
cgcgacggcg gcaaggagat cagcaacacc accgagatct tccgccccgg cggcggcgac   1380
atgcgcgaca actggcgcag cgagctgtac aagtacaagg tggtgaagat cgagcccctg   1440
ggcgtggccc ccaccaaggc caagcgccgc gtggtgcagc gcgagaagcg ctaa          1494

<210>   4
<211>   497
<212>   PRT
<213>   Artificial Sequence

<220>
<223>   HIV-1 gp120 V59C and S109C

<400>   4
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
1               5                   10                  15

Ala Val Phe Val Ser Pro Ser Ala Val Glu Lys Leu Trp Val Thr Val
            20                  25                  30
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Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr Thr Thr Leu Phe Cys
        35                  40                  45

Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Cys His Asn Val Trp Ala
    50                  55                  60

Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Ile Val Leu
65                  70                  75                  80

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

Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Cys Leu Lys Pro
            100                 105                 110

Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu His Cys Thr Asn Leu
        115                 120                 125

Lys Asn Ala Thr Asn Thr Lys Ser Ser Asn Trp Lys Glu Met Asp Arg
    130                 135                 140

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

Lys Met Gln Lys Glu Tyr Ala Leu Phe Tyr Lys Leu Asp Val Val Pro
                165                 170                 175

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

Val Ile Thr Gln Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile
        195                 200                 205

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

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

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

Ser Leu Ala Glu Glu Gly Val Val Ile Arg Ser Glu Asn Phe Thr Asp
            260                 265                 270

Asn Ala Lys Thr Ile Ile Val Gln Leu Lys Glu Ser Val Glu Ile Asn
        275                 280                 285

Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly Pro
    290                 295                 300

Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln
305                 310                 315                 320

Ala His Cys Asn Ile Ser Gly Glu Lys Trp Asn Asn Thr Leu Lys Gln
                325                 330                 335

Ile Val Thr Lys Leu Gln Ala Gln Phe Gly Asn Lys Thr Ile Val Phe
            340                 345                 350

Lys Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Met His Ser Phe Asn
        355                 360                 365

Cys Gly Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser
    370                 375                 380

Thr Trp Asn Asn Thr Ile Gly Pro Asn Asn Thr Asn Gly Thr Ile Thr
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385 390 395 400

Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Arg Trp Gln Glu Val Gly
405 410 415

Lys Ala Met Tyr Ala Pro Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser
420 425 430

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

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

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

Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys
485 490 495

Arg

<210> 5
<211> 1494
<212> DNA
<213> Artificial Sequence

<220>
<223> HIV-1 gp120 V95C and W465C

<400> 5
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gaggccacca ccaccctgtt ctgcgccagc gacgccaagg cctacgacac cgaggtgcac 180
aacgtgtggg ccacccacgc ctgcgtgccc accgacccca acccccagga gatcgtgctg 240
gagaacgtga ccgagaactt caacatgtgg aagaacaaca tgtgygagca gatgcacgag 300
gacatcatca gcctgtggga ccagagcctg aagccctgcg tgaagctgac ccccctgtgc 360
gtgaccctgc actgcaccaa cctgaagaac gccaccaaca ccaagagcag caactggaag 420
gagatggacc gcggcgagat caagaactgc agcttcaagg tgaccaccag catccgcaac 480
aagatgcaga aggagtacgc cctgttctac aagctggacg tggtgcccat cgacaacgac 540
aacaccagct acaagctgat caactgcaac accagcgtga tcacccaggc ctgccccaag 600
gtgagcttcg agcccatccc catccactac tgcgcccccg ccggcttcgc catcctgaag 660
tgcaacgaca agaagttcaa cggcagcggc ccctgcacca acgtgagcac cgtgcagtgc 720
acccacggca tccgccccgt ggtgagcacc cagctgctgc tgaacggcag cctggccgag 780
gagggcgtgg tgatccgcag cgagaacttc accgacaacg ccaagaccat catcgtgcag 840
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gagatcgtga tgcacagctt caactgcggc ggcgagttct tctactgcaa cagcacccag 1140
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cgcgacggcg gcaaggagat cagcaacacc accgagatct tccgccccgg cggcggcgac 1380
atgcgcgaca actgycgcag cgagctgtac aagtacaagg tggtgaagat cgagcccctg 1440
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<210> 6
<211> 497
<212> PRT
<213> Artificial Sequence

<220>
<223> HIV-1 gp120 V95C and W465C

<400> 6
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Ala Val Phe Val Ser Pro Ser Ala Val Glu Lys Leu Trp Val Thr Val
            20                  25                  30

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

Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val His Asn Val Trp Ala
    50                  55                  60

Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Ile Val Leu
65                  70                  75                  80

Glu Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asn Met Cys Glu
                85                  90                  95

Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro
            100                 105                 110

Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu His Cys Thr Asn Leu
        115                 120                 125

Lys Asn Ala Thr Asn Thr Lys Ser Ser Asn Trp Lys Glu Met Asp Arg
    130                 135                 140

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

Lys Met Gln Lys Glu Tyr Ala Leu Phe Tyr Lys Leu Asp Val Val Pro
                165                 170                 175

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

Val Ile Thr Gln Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile
        195                 200                 205

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

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

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

Ser Leu Ala Glu Glu Gly Val Val Ile Arg Ser Glu Asn Phe Thr Asp
            260                 265                 270

Asn Ala Lys Thr Ile Ile Val Gln Leu Lys Glu Ser Val Glu Ile Asn
        275                 280                 285

Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly Pro
    290                 295                 300

Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln
305                 310                 315                 320

Ala His Cys Asn Ile Ser Gly Glu Lys Trp Asn Asn Thr Leu Lys Gln
                325                 330                 335

Ile Val Thr Lys Leu Gln Ala Gln Phe Gly Asn Lys Thr Ile Val Phe
            340                 345                 350

Lys Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Met His Ser Phe Asn
        355                 360                 365
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Cys Gly Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser
    370                 375                 380

Thr Trp Asn Asn Thr Ile Gly Pro Asn Asn Thr Asn Gly Thr Ile Thr
385                 390                 395                 400

Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Arg Trp Gln Glu Val Gly
                405                 410                 415

Lys Ala Met Tyr Ala Pro Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser
            420                 425                 430

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

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

Cys Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu
465                 470                 475                 480

Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys
                485                 490                 495

Arg
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<210> 7
<211> 1494
<212> DNA
<213> Artificial Sequence

<220>
<223> HIV-1 gp120 V95C and R462C

<400> 7

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gaggccacca ccaccctgtt ctgcgccagc gacgccaagg cctacgacac cgaggtgcac   180
aacgtgtggg ccacccacgc ctgcgtgccc accgacccca acccccagga gatcgtgctg   240
gagaacgtga ccgagaactt caacatgtgg aagaacaaca tgtgygagca gatgcacgag   300
gacatcatca gcctgtggga ccagagcctg aagccctgcg tgaagctgac ccccctgtgc   360
gtgaccctgc actgcaccaa cctgaagaac gccaccaaca ccaagagcag caactggaag   420
gagatggacc gcggcgagat caagaactgc agcttcaagg tgaccaccag catccgcaac   480
aagatgcaga aggagtacgc cctgttctac aagctggacg tggtgcccat cgacaacgac   540
aacaccagct acaagctgat caactgcaac accagcgtga tcacccaggc ctgccccaag   600
gtgagcttcg agcccatccc catccactac tgcgcccccg ccggcttcgc catcctgaag   660
tgcaacgaca agaagttcaa cggcagcggc ccctgcacca acgtgagcac cgtgcagtgc   720
acccacggca tccgccccgt ggtgagcacc cagctgctgc tgaacggcag cctggccgag   780
gagggcgtgg tgatccgcag cgagaacttc accgacaacg ccaagaccat catcgtgcag   840
ctgaaggaga gcgtggagat caactgcacc cgccccaaca acaacacccg caagagcatc   900
accatcggcc ccggccgcgc cttctacgcc accggcgaca tcatcggcga catccgccag   960
gcccactgca acatcagcgg cgagaagtgg aacaacaccc tgaagcagat cgtgaccaag   1020
ctgcaggccc agttcggcaa caagaccatc gtgttcaagc agagcagcgg cggcgacccc   1080
gagatcgtga tgcacagctt caactgcggc ggcgagttct tctactgcaa cagcacccag   1140
ctgttcaaca gcacctggaa caacaccatc ggccccaaca acaccaacgg caccatcacc   1200
ctgccctgcc gcatcaagca gatcatcaac cgctggcagg aggtgggcaa ggccatgtac   1260
gccccccccca tccgcggcca gatccgctgc agcagcaaca tcaccggcct gctgctgacc   1320
cgcgacggcg gcaaggagat cagcaacacc accgagatct tccgccccgg cggcggcgac   1380
atgtcygaca actggcgcag cgagctgtac aagtacaagg tggtgaagat cgagcccctg   1440
ggcgtggccc ccaccaaggc caagcgccgc gtggtgcagc gcgagaagcg ctaa          1494
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<210> 8
<211> 497
<212> PRT
<213> Artificial Sequence

<220>

<223> HIV-1 gp120 V95C and R462C

<400> 8

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Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
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Ala Val Phe Val Ser Pro Ser Ala Val Glu Lys Leu Trp Val Thr Val
            20                  25                  30

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

Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val His Asn Val Trp Ala
    50                  55                  60

Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Ile Val Leu
65                  70                  75                  80

Glu Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asn Met Cys Glu
                85                  90                  95

Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro
            100                 105                 110

Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu His Cys Thr Asn Leu
        115                 120                 125

Lys Asn Ala Thr Asn Thr Lys Ser Ser Asn Trp Lys Glu Met Asp Arg
    130                 135                 140

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

Lys Met Gln Lys Glu Tyr Ala Leu Phe Tyr Lys Leu Asp Val Val Pro
                165                 170                 175

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

Val Ile Thr Gln Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile
        195                 200                 205

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

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

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

Ser Leu Ala Glu Glu Gly Val Val Ile Arg Ser Glu Asn Phe Thr Asp
            260                 265                 270

Asn Ala Lys Thr Ile Ile Val Gln Leu Lys Glu Ser Val Glu Ile Asn
        275                 280                 285

Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly Pro
    290                 295                 300

Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln
305                 310                 315                 320

Ala His Cys Asn Ile Ser Gly Glu Lys Trp Asn Asn Thr Leu Lys Gln
                325                 330                 335

Ile Val Thr Lys Leu Gln Ala Gln Phe Gly Asn Lys Thr Ile Val Phe
            340                 345                 350
```

```
Lys Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Met His Ser Phe Asn
        355                 360                 365

Cys Gly Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser
    370                 375                 380

Thr Trp Asn Asn Thr Ile Gly Pro Asn Asn Thr Asn Gly Thr Ile Thr
385                 390                 395                 400

Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Arg Trp Gln Glu Val Gly
                405                 410                 415

Lys Ala Met Tyr Ala Pro Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser
            420                 425                 430

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

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

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

Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys
                485                 490                 495

Arg
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<210> 9
<211> 1494
<212> DNA
<213> Artificial Sequence

<220>
<223> HIV-1 gp120 V95C and L469C

<400> 9

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tcgcccagcg ccgtggagaa gctgtgggtg accgtgtact acggcgtgcc cgtgtggaag   120
gaggccacca ccaccctgtt ctgcgccagc gacgccaagg cctacgacac cgaggtgcac   180
aacgtgtggg ccacccacgc ctgcgtgccc accgacccca acccccagga gatcgtgctg   240
gagaacgtga ccgagaactt caacatgtgg aagaacaaca tgtgygagca gatgcacgag   300
gacatcatca gcctgtggga ccagagcctg aagccctgcg tgaagctgac ccccctgtgc   360
gtgaccctgc actgcaccaa cctgaagaac gccaccaaca ccaagagcag caactggaag   420
gagatggacc gcggcgagat caagaactgc agcttcaagg tgaccaccag catccgcaac   480
aagatgcaga aggagtacgc cctgttctac aagctggacg tggtgcccat cgacaacgac   540
aacaccagct acaagctgat caactgcaac accagcgtga tcacccaggc ctgccccaag   600
gtgagcttcg agcccatccc catccactac tgcgcccccg ccggcttcgc catcctgaag   660
tgcaacgaca agaagttcaa cggcagcggc ccctgcacca acgtgagcac cgtgcagtgc   720
acccacggca tccgccccgt ggtgagcacc cagctgctgc tgaacggcag cctggccgag   780
gagggcgtgg tgatccgcag cgagaacttc accgacaacg ccaagaccat catcgtgcag   840
ctgaaggaga gcgtggagat caactgcacc cgccccaaca acaacacccg caagagcatc   900
accatcggcc ccggccgcgc cttctacgcc accggcgaca tcatcggcga catccgccag   960
gcccactgca acatcagcgg cgagaagtgg aacaacaccc tgaagcagat cgtgaccaag   1020
ctgcaggccc agttcggcaa caagaccatc gtgttcaagc agagcagcgg cggcgacccc   1080
gagatcgtga tgcacagctt caactgcggc ggcgagttct tctactgcaa cagcacccag   1140
ctgttcaaca gcacctggaa caacaccatc ggccccaaca acaccaacgg caccatcacc   1200
ctgccctgcc gcatcaagca gatcatcaac cgctggcagg aggtgggcaa ggccatgtac   1260
gccccccca tccgcggcca gatccgctgc agcagcaaca tcaccggcct gctgctgacc   1320
cgcgacggcg gcaaggagat cagcaacacc accgagatct tccgccccgg cggcggcgac   1380
atgcgcgaca actggcgcag cgagtgytac aagtacaagg tggtgaagat cgagcccctg   1440
ggcgtggccc ccaccaaggc caagcgccgc gtggtgcagc gcgagaagcg ctaa         1494
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<210> 10
<211> 497

<212> PRT
<213> Artificial Sequence

<220>
<223> HIV-1 gp120 V95C and L469C

<400> 10

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Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
1               5                  10                  15

Ala Val Phe Val Ser Pro Ser Ala Val Glu Lys Leu Trp Val Thr Val
            20                  25                  30

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

Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val His Asn Val Trp Ala
    50                  55                  60

Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Ile Val Leu
65                  70                  75                  80

Glu Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asn Met Cys Glu
                85                  90                  95

Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro
            100                 105                 110

Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu His Cys Thr Asn Leu
        115                 120                 125

Lys Asn Ala Thr Asn Thr Lys Ser Ser Asn Trp Lys Glu Met Asp Arg
    130                 135                 140

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

Lys Met Gln Lys Glu Tyr Ala Leu Phe Tyr Lys Leu Asp Val Val Pro
                165                 170                 175

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

Val Ile Thr Gln Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile
        195                 200                 205

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

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

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

Ser Leu Ala Glu Glu Gly Val Val Ile Arg Ser Glu Asn Phe Thr Asp
            260                 265                 270

Asn Ala Lys Thr Ile Ile Val Gln Leu Lys Glu Ser Val Glu Ile Asn
        275                 280                 285

Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly Pro
    290                 295                 300

Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln
305                 310                 315                 320

Ala His Cys Asn Ile Ser Gly Glu Lys Trp Asn Asn Thr Leu Lys Gln
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                325                 330                 335

Ile Val Thr Lys Leu Gln Ala Gln Phe Gly Asn Lys Thr Ile Val Phe
            340                 345                 350

Lys Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Met His Ser Phe Asn
        355                 360                 365

Cys Gly Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser
    370                 375                 380

Thr Trp Asn Asn Thr Ile Gly Pro Asn Asn Thr Asn Gly Thr Ile Thr
385                 390                 395                 400

Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Arg Trp Gln Glu Val Gly
                405                 410                 415

Lys Ala Met Tyr Ala Pro Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser
            420                 425                 430

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

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

Trp Arg Ser Glu Cys Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu
465                 470                 475                 480

Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys
                485                 490                 495

Arg
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<210> 11
<211> 1494
<212> DNA
<213> Artificial Sequence

<220>
<223> HIV-1 gp120 H99C and R462C

<400> 11

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tcgcccagcg ccgtggagaa gctgtgggtg accgtgtact acggcgtgcc cgtgtggaag   120
gaggccacca ccaccctgtt ctgcgccagc gacgccaagg cctacgacac cgaggtgcac   180
aacgtgtggg ccacccacgc ctgcgtgccc accgacccca acccccagga gatcgtgctg   240
gagaacgtga ccgagaactt caacatgtgg aagaacaaca tggtggagca gatgtgcgag   300
gacatcatca gcctgtggga ccagagcctg aagccctgcg tgaagctgac ccccctgtgc   360
gtgaccctgc actgcaccaa cctgaagaac gccaccaaca ccaagagcag caactggaag   420
gagatggacc gcggcgagat caagaactgc agcttcaagg tgaccaccag catccgcaac   480
aagatgcaga aggagtacgc cctgttctac aagctggacg tggtgcccat cgacaacgac   540
aacaccagct acaagctgat caactgcaac accagcgtga tcacccaggc ctgccccaag   600
gtgagcttcg agcccatccc catccactac tgcgcccccg ccggcttcgc catcctgaag   660
tgcaacgaca agaagttcaa cggcagcggc ccctgcacca acgtgagcac cgtgcagtgc   720
acccacggca tccgccccgt ggtgagcacc cagctgctgc tgaacggcag cctggccgag   780
gagggcgtgg tgatccgcag cgagaacttc accgacaacg ccaagaccat catcgtgcag   840
ctgaaggaga gcgtggagat caactgcacc cgccccaaca acaacacccg caagagcatc   900
accatcggcc ccggccgcgc cttctacgcc accggcgaca tcatcggcga catccgccag   960
gcccactgca acatcagcgg cgagaagtgg aacaacaccc tgaagcagat cgtgaccaag   1020
ctgcaggccc agttcggcaa caagaccatc gtgttcaagc agagcagcgg cggcgacccc   1080
gagatcgtga tgcacagctt caactgcggc ggcgagttct tctactgcaa cagcacccag   1140
ctgttcaaca gcacctggaa caacaccatc ggccccaaca acaccaacgg caccatcacc   1200
ctgccctgcc gcatcaagca gatcatcaac cgctggcagg aggtgggcaa ggccatgtac   1260
gcccccccca tccgcggcca gatccgctgc agcagcaaca tcaccggcct gctgctgacc   1320
cgcgacggcg gcaaggagat cagcaacacc accgagatct tccgccccgg cggcggcgac   1380
atgtgygaca actggcgcag cgagctgtac aagtacaagg tggtgaagat cgagcccctg   1440
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ggcgtggccc ccaccaaggc caagcgccgc gtggtgcagc gcgagaagcg ctaa 1494

<210> 12
<211> 497
<212> PRT
<213> Artificial Sequence

<220>
<223> HIV-1 gp120 H99C and R462C

<400> 12
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
1 5 10 15

Ala Val Phe Val Ser Pro Ser Ala Val Glu Lys Leu Trp Val Thr Val
20 25 30

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

Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val His Asn Val Trp Ala
50 55 60

Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Ile Val Leu
65 70 75 80

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

Gln Met Cys Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro
100 105 110

Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu His Cys Thr Asn Leu
115 120 125

Lys Asn Ala Thr Asn Thr Lys Ser Ser Asn Trp Lys Glu Met Asp Arg
130 135 140

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

Lys Met Gln Lys Glu Tyr Ala Leu Phe Tyr Lys Leu Asp Val Val Pro
165 170 175

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

Val Ile Thr Gln Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile
195 200 205

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

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

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

Ser Leu Ala Glu Glu Gly Val Val Ile Arg Ser Glu Asn Phe Thr Asp
260 265 270

Asn Ala Lys Thr Ile Ile Val Gln Leu Lys Glu Ser Val Glu Ile Asn
275 280 285

Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly Pro
290 295 300

```
Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln
305                 310                 315                 320

Ala His Cys Asn Ile Ser Gly Glu Lys Trp Asn Asn Thr Leu Lys Gln
                325                 330                 335

Ile Val Thr Lys Leu Gln Ala Gln Phe Gly Asn Lys Thr Ile Val Phe
            340                 345                 350

Lys Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Met His Ser Phe Asn
        355                 360                 365

Cys Gly Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser
    370                 375                 380

Thr Trp Asn Asn Thr Ile Gly Pro Asn Asn Thr Asn Gly Thr Ile Thr
385                 390                 395                 400

Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Arg Trp Gln Glu Val Gly
                405                 410                 415

Lys Ala Met Tyr Ala Pro Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser
            420                 425                 430

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

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

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

Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys
                485                 490                 495

Arg
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<210> 13
<211> 1494
<212> DNA
<213> Artificial Sequence

<220>
<223> HIV-1 gp120 V59C S109C and V95C W465C

<400> 13

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gaggccacca ccaccctgtt ctgcgccagc gacgccaagg cctacgacac cgagtgccac   180
aacgtgtggg ccacccacgc ctgcgtgccc accgacccca acccccagga gatcgtgctg   240
gagaacgtga ccgagaactt caacatgtgg aagaacaaca tgtgygagca gatgcacgag   300
gacatcatca gcctgtggga ccagtgcctg aagccctgcg tgaagctgac ccccctgtgc   360
gtgaccctgc actgcaccaa cctgaagaac gccaccaaca ccaagagcag caactggaag   420
gagatggacc gcggcgagat caagaactgc agcttcaagg tgaccaccag catccgcaac   480
aagatgcaga aggagtacgc cctgttctac aagctggacg tggtgcccat cgacaacgac   540
aacaccagct acaagctgat caactgcaac accagcgtga tcacccaggc ctgccccaag   600
gtgagcttcg agcccatccc catccactac tgcgcccccg ccggcttcgc catcctgaag   660
tgcaacgaca agaagttcaa cggcagcggc ccctgcacca acgtgagcac cgtgcagtgc   720
acccacggca tccgccccgt ggtgagcacc cagctgctgc tgaacggcag cctggccgag   780
gagggcgtgg tgatccgcag cgagaacttc accgacaacg ccaagaccat catcgtgcag   840
ctgaaggaga gcgtggagat caactgcacc cgccccaaca acaacacccg caagagcatc   900
accatcggcc ccggccgcgc cttctacgcc accggcgaca tcatcggcga catccgccag   960
gcccactgca acatcagcgg cgagaagtgg aacaacaccc tgaagcagat cgtgaccaag   1020
ctgcaggccc agttcggcaa caagaccatc gtgttcaagc agagcagcgg cggcgacccc   1080
gagatcgtga tgcacagctt caactgcggc ggcgagttct tctactgcaa cagcacccag   1140
ctgttcaaca gcacctggaa caacaccatc ggccccaaca acaccaacgg caccatcacc   1200
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ctgccctgcc gcatcaagca gatcatcaac cgctggcagg aggtgggcaa ggccatgtac 1260
gccccccccca tccgcggcca gatccgctgc agcagcaaca tcaccggcct gctgctgacc 1320
cgcgacggcg gcaaggagat cagcaacacc accgagatct tccgccccgg cggcggcgac 1380
atgcgcgaca actgycgcag cgagctgtac aagtacaagg tggtgaagat cgagcccctg 1440
ggcgtggccc ccaccaaggc caagcgccgc gtggtgcagc gcgagaagcg ctaa 1494

<210> 14
<211> 497
<212> PRT
<213> Artificial Sequence

<220>
<223> HIV-1 gp120 V59C S109C and V95C W465C

<400> 14
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
1 5 10 15

Ala Val Phe Val Ser Pro Ser Ala Val Glu Lys Leu Trp Val Thr Val
20 25 30

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

Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Cys His Asn Val Trp Ala
50 55 60

Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Ile Val Leu
65 70 75 80

Glu Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asn Met Cys Glu
85 90 95

Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Cys Leu Lys Pro
100 105 110

Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu His Cys Thr Asn Leu
115 120 125

Lys Asn Ala Thr Asn Thr Lys Ser Ser Asn Trp Lys Glu Met Asp Arg
130 135 140

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

Lys Met Gln Lys Glu Tyr Ala Leu Phe Tyr Lys Leu Asp Val Val Pro
165 170 175

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

Val Ile Thr Gln Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile
195 200 205

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

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

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

Ser Leu Ala Glu Glu Gly Val Val Ile Arg Ser Glu Asn Phe Thr Asp
260 265 270

Asn Ala Lys Thr Ile Ile Val Gln Leu Lys Glu Ser Val Glu Ile Asn
275 280 285

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Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly Pro
    290                 295                 300

Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln
305                 310                 315                 320

Ala His Cys Asn Ile Ser Gly Glu Lys Trp Asn Asn Thr Leu Lys Gln
                325                 330                 335

Ile Val Thr Lys Leu Gln Ala Gln Phe Gly Asn Lys Thr Ile Val Phe
            340                 345                 350

Lys Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Met His Ser Phe Asn
        355                 360                 365

Cys Gly Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser
    370                 375                 380

Thr Trp Asn Asn Thr Ile Gly Pro Asn Asn Thr Asn Gly Thr Ile Thr
385                 390                 395                 400

Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Arg Trp Gln Glu Val Gly
                405                 410                 415

Lys Ala Met Tyr Ala Pro Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser
            420                 425                 430

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

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

Cys Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu
465                 470                 475                 480

Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys
                485                 490                 495

Arg
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<210> 15
<211> 1494
<212> DNA
<213> Artificial Sequence

<220>
<223> HIV-1 gp120 V59C S109C and W90C E268C

<400> 15

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tcgcccagcg ccgtggagaa gctgtgggtg accgtgtact acggcgtgcc cgtgtggaag   120
gaggccacca ccaccctgtt ctgcgccagc gacgccaagg cctacgacac cgagtgccac   180
aacgtgtggg ccacccacgc ctgcgtgccc accgacccca acccccagga gatcgtgctg   240
gagaacgtga ccgagaactt caacatgtgy aagaacaaca tggtggagca gatgcacgag   300
gacatcatca gcctgtggga ccagtgcctg aagccctgcg tgaagctgac ccccctgtgc   360
gtgaccctgc actgcaccaa cctgaagaac gccaccaaca ccaagagcag caactggaag   420
gagatggacc gcggcgagat caagaactgc agcttcaagg tgaccaccag catccgcaac   480
aagatgcaga aggagtacgc cctgttctac aagctggacg tggtgcccat cgacaacgac   540
aacaccagct acaagctgat caactgcaac accagcgtga tcacccaggc ctgccccaag   600
gtgagcttcg agcccatccc catccactac tgcgcccccg ccggcttcgc catcctgaag   660
tgcaacgaca agaagttcaa cggcagcggc ccctgcacca acgtgagcac cgtgcagtgc   720
acccacggca tccgccccgt ggtgagcacc cagctgctgc tgaacggcag cctggccgag   780
gagggcgtgg tgatccgcag ctgyaacttc accgacaacg ccaagaccat catcgtgcag   840
ctgaaggaga gcgtggagat caactgcacc cgccccaaca acaacacccg caagagcatc   900
accatcggcc ccggccgcgc cttctacgcc accggcgaca tcatcggcga catccgccag   960
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gcccactgca acatcagcgg cgagaagtgg aacaacaccc tgaagcagat cgtgaccaag   1020
ctgcaggccc agttcggcaa caagaccatc gtgttcaagc agagcagcgg cggcgacccc   1080
gagatcgtga tgcacagctt caactgcggc ggcgagttct tctactgcaa cagcacccag   1140
ctgttcaaca gcacctggaa caacaccatc ggccccaaca acaccaacgg caccatcacc   1200
ctgccctgcc gcatcaagca gatcatcaac cgctggcagg aggtgggcaa ggccatgtac   1260
gccccccca tccgcggcca gatccgctgc agcagcaaca tcaccggcct gctgctgacc   1320
cgcgacggcg gcaaggagat cagcaacacc accgagatct tccgccccgg cggcggcgac   1380
atgcgcgaca actggcgcag cgagctgtac aagtacaagg tggtgaagat cgagcccctg   1440
ggcgtggccc ccaccaaggc caagcgccgc gtggtgcagc gcgagaagcg ctaa          1494

<210>   16
<211>   497
<212>   PRT
<213>   HIV-1 gp120 V59C S109C and W90C E268C

<400>   16
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
1               5                  10                  15

Ala Val Phe Val Ser Pro Ser Ala Val Glu Lys Leu Trp Val Thr Val
            20                  25                  30

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

Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Cys His Asn Val Trp Ala
    50                  55                  60

Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Ile Val Leu
65                  70                  75                  80

Glu Asn Val Thr Glu Asn Phe Asn Met Cys Lys Asn Asn Met Val Glu
                85                  90                  95

Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Cys Leu Lys Pro
            100                 105                 110

Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu His Cys Thr Asn Leu
        115                 120                 125

Lys Asn Ala Thr Asn Thr Lys Ser Ser Asn Trp Lys Glu Met Asp Arg
    130                 135                 140

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

Lys Met Gln Lys Glu Tyr Ala Leu Phe Tyr Lys Leu Asp Val Val Pro
                165                 170                 175

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

Val Ile Thr Gln Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile
        195                 200                 205

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

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

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

Ser Leu Ala Glu Glu Gly Val Val Ile Arg Ser Cys Asn Phe Thr Asp
            260                 265                 270

Asn Ala Lys Thr Ile Ile Val Gln Leu Lys Glu Ser Val Glu Ile Asn
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        275                 280                 285

Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly Pro
    290                 295                 300

Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln
305                 310                 315                 320

Ala His Cys Asn Ile Ser Gly Glu Lys Trp Asn Asn Thr Leu Lys Gln
                325                 330                 335

Ile Val Thr Lys Leu Gln Ala Gln Phe Gly Asn Lys Thr Ile Val Phe
            340                 345                 350

Lys Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Met His Ser Phe Asn
        355                 360                 365

Cys Gly Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser
    370                 375                 380

Thr Trp Asn Asn Thr Ile Gly Pro Asn Asn Thr Asn Gly Thr Ile Thr
385                 390                 395                 400

Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Arg Trp Gln Glu Val Gly
                405                 410                 415

Lys Ala Met Tyr Ala Pro Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser
            420                 425                 430

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

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

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

Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys
                485                 490                 495

Arg
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<210> 17
<211> 1494
<212> DNA
<213> Artificial Sequence

<220>
<223> HIV-1 gp120 V59C S109C and I103C Q413C

<400> 17

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tcgcccagcg ccgtggagaa gctgtgggtg accgtgtact acggcgtgcc cgtgtggaag   120
gaggccacca ccaccctgtt ctgcgccagc gacgccaagg cctacgacac cgagtgccac   180
aacgtgtggg ccacccacgc ctgcgtgccc accgacccca acccccagga gatcgtgctg   240
gagaacgtga ccgagaactt caacatgtgg aagaacaaca tggtggagca gatgcacgag   300
gacatctgya gcctgtggga ccagtgcctg aagccctgcg tgaagctgac ccccctgtgc   360
gtgaccctgc actgcaccaa cctgaagaac gccaccaaca ccaagagcag caactggaag   420
gagatggacc gcggcgagat caagaactgc agcttcaagg tgaccaccag catccgcaac   480
aagatgcaga aggagtacgc cctgttctac aagctggacg tggtgcccat cgacaacgac   540
aacaccagct acaagctgat caactgcaac accagcgtga tcacccaggc ctgccccaag   600
gtgagcttcg agcccatccc catccactac tgcgcccccg ccggcttcgc catcctgaag   660
tgcaacgaca agaagttcaa cggcagcggc ccctgcacca acgtgagcac cgtgcagtgc   720
acccacggca tccgccccgt ggtgagcacc cagctgctgc tgaacggcag cctggccgag   780
gagggcgtgg tgatccgcag cgagaacttc accgacaacg ccaagaccat catcgtgcag   840
ctgaaggaga gcgtggagat caactgcacc cgccccaaca acaacacccg caagagcatc   900
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accatcggcc ccggccgcgc cttctacgcc accggcgaca tcatcggcga catccgccag   960
gcccactgca acatcagcgg cgagaagtgg aacaacaccc tgaagcagat cgtgaccaag   1020
ctgcaggccc agttcggcaa caagaccatc gtgttcaagc agagcagcgg cggcgacccc   1080
gagatcgtga tgcacagctt caactgcggc ggcgagttct tctactgcaa cagcacccag   1140
ctgttcaaca gcacctggaa caacaccatc ggccccaaca acaccaacgg caccatcacc   1200
ctgccctgcc gcatcaagca gatcatcaac cgctggtgyg aggtgggcaa ggccatgtac   1260
gccccccca tccgcggcca gatccgctgc agcagcaaca tcaccggcct gctgctgacc   1320
cgcgacggcg gcaaggagat cagcaacacc accgagatct tccgccccgg cggcggcgac   1380
atgcgcgaca actggcgcag cgagctgtac aagtacaagg tggtgaagat cgagcccctg   1440
ggcgtggccc ccaccaaggc caagcgccgc gtggtgcagc gcgagaagcg ctaa          1494

<210>   18
<211>   497
<212>   PRT
<213>   HIV-1 gp120 V59C S109C and I103C Q413C

<400>   18
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
1               5                   10                  15

Ala Val Phe Val Ser Pro Ser Ala Val Glu Lys Leu Trp Val Thr Val
            20                  25                  30

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

Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Cys His Asn Val Trp Ala
    50                  55                  60

Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Ile Val Leu
65                  70                  75                  80

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

Gln Met His Glu Asp Ile Cys Ser Leu Trp Asp Gln Cys Leu Lys Pro
            100                 105                 110

Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu His Cys Thr Asn Leu
        115                 120                 125

Lys Asn Ala Thr Asn Thr Lys Ser Ser Asn Trp Lys Glu Met Asp Arg
    130                 135                 140

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

Lys Met Gln Lys Glu Tyr Ala Leu Phe Tyr Lys Leu Asp Val Val Pro
                165                 170                 175

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

Val Ile Thr Gln Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile
        195                 200                 205

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

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

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

Ser Leu Ala Glu Glu Gly Val Val Ile Arg Ser Glu Asn Phe Thr Asp
            260                 265                 270
```

```
Asn Ala Lys Thr Ile Ile Val Gln Leu Lys Glu Ser Val Glu Ile Asn
        275                 280                 285

Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly Pro
    290                 295                 300

Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln
305                 310                 315                 320

Ala His Cys Asn Ile Ser Gly Glu Lys Trp Asn Asn Thr Leu Lys Gln
                325                 330                 335

Ile Val Thr Lys Leu Gln Ala Gln Phe Gly Asn Lys Thr Ile Val Phe
            340                 345                 350

Lys Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Met His Ser Phe Asn
        355                 360                 365

Cys Gly Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser
    370                 375                 380

Thr Trp Asn Asn Thr Ile Gly Pro Asn Asn Thr Asn Gly Thr Ile Thr
385                 390                 395                 400

Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Arg Trp Cys Glu Val Gly
                405                 410                 415

Lys Ala Met Tyr Ala Pro Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser
            420                 425                 430

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

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

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

Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys
                485                 490                 495

Arg
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<210> 19
<211> 1494
<212> DNA
<213> Artificial Sequence

<220>
<223> HIV-1 gp120 V95C W465C and W90C E268C

<400> 19

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tcgcccagcg ccgtggagaa gctgtgggtg accgtgtact acggcgtgcc cgtgtggaag   120
gaggccacca ccaccctgtt ctgcgccagc gacgccaagg cctacgacac cgaggtgcac   180
aacgtgtggg ccacccacgc ctgcgtgccc accgacccca acccccagga gatcgtgctg   240
gagaacgtga ccgagaactt caacatgtgy aagaacaaca tgtgygagca gatgcacgag   300
gacatcatca gcctgtggga ccagagcctg aagccctgcg tgaagctgac ccccctgtgc   360
gtgaccctgc actgcaccaa cctgaagaac gccaccaaca ccaagagcag caactggaag   420
gagatggacc gcggcgagat caagaactgc agcttcaagg tgaccaccag catccgcaac   480
aagatgcaga aggagtacgc cctgttctac aagctggacg tggtgcccat cgacaacgac   540
aacaccagct acaagctgat caactgcaac accagcgtga tcacccaggc ctgccccaag   600
gtgagcttcg agcccatccc catccactac tgcgcccccg ccggcttcgc catcctgaag   660
tgcaacgaca agaagttcaa cggcagcggc ccctgcacca acgtgagcac cgtgcagtgc   720
acccacggca tccgccccgt ggtgagcacc cagctgctgc tgaacggcag cctggccgag   780
gagggcgtgg tgatccgcag ctgyaacttc accgacaacg ccaagaccat catcgtgcag   840
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ctgaaggaga gcgtggagat caactgcacc cgccccaaca acaacacccg caagagcatc   900
accatcggcc ccggccgcgc cttctacgcc accggcgaca tcatcggcga catccgccag   960
gcccactgca acatcagcgg cgagaagtgg aacaacaccc tgaagcagat cgtgaccaag   1020
ctgcaggccc agttcggcaa caagaccatc gtgttcaagc agagcagcgg cggcgacccc   1080
gagatcgtga tgcacagctt caactgcggc ggcgagttct tctactgcaa cagcacccag   1140
ctgttcaaca gcacctggaa caacaccatc ggccccaaca acaccaacgg caccatcacc   1200
ctgccctgcc gcatcaagca gatcatcaac cgctggcagg aggtgggcaa ggccatgtac   1260
gcccccccca tccgcggcca gatccgctgc agcagcaaca tcaccggcct gctgctgacc   1320
cgcgacggcg gcaaggagat cagcaacacc accgagatct tccgccccgg cggcggcgac   1380
atgcgcgaca actgycgcag cgagctgtac aagtacaagg tggtgaagat cgagcccctg   1440
ggcgtggccc ccaccaaggc caagcgccgc gtggtgcagc gcgagaagcg ctaa          1494

<210>   20
<211>   497
<212>   PRT
<213>   Artificial Sequence

<220>
<223>   HIV-1 gp120 V95C W465C and W90C E268C

<400>   20
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
1               5                   10                  15

Ala Val Phe Val Ser Pro Ser Ala Val Glu Lys Leu Trp Val Thr Val
            20                  25                  30

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

Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val His Asn Val Trp Ala
    50                  55                  60

Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Ile Val Leu
65                  70                  75                  80

Glu Asn Val Thr Glu Asn Phe Asn Met Cys Lys Asn Asn Met Cys Glu
                85                  90                  95

Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro
            100                 105                 110

Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu His Cys Thr Asn Leu
        115                 120                 125

Lys Asn Ala Thr Asn Thr Lys Ser Ser Asn Trp Lys Glu Met Asp Arg
    130                 135                 140

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

Lys Met Gln Lys Glu Tyr Ala Leu Phe Tyr Lys Leu Asp Val Val Pro
                165                 170                 175

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

Val Ile Thr Gln Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile
        195                 200                 205

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

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

Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly
                245                 250                 255
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Ser Leu Ala Glu Glu Gly Val Val Ile Arg Ser Cys Asn Phe Thr Asp
            260                 265                 270

Asn Ala Lys Thr Ile Ile Val Gln Leu Lys Glu Ser Val Glu Ile Asn
        275                 280                 285

Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly Pro
    290                 295                 300

Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln
305                 310                 315                 320

Ala His Cys Asn Ile Ser Gly Glu Lys Trp Asn Asn Thr Leu Lys Gln
                325                 330                 335

Ile Val Thr Lys Leu Gln Ala Gln Phe Gly Asn Lys Thr Ile Val Phe
            340                 345                 350

Lys Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Met His Ser Phe Asn
        355                 360                 365

Cys Gly Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser
    370                 375                 380

Thr Trp Asn Asn Thr Ile Gly Pro Asn Asn Thr Asn Gly Thr Ile Thr
385                 390                 395                 400

Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Arg Trp Gln Glu Val Gly
                405                 410                 415

Lys Ala Met Tyr Ala Pro Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser
            420                 425                 430

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

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

Cys Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu
465                 470                 475                 480

Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys
                485                 490                 495

Arg
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<210> 21
<211> 1494
<212> DNA
<213> Artificial Sequence

<220>
<223> HIV-1 gp120 V95C W465C and I103C Q413C

<400> 21

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tcgcccagcg ccgtggagaa gctgtgggtg accgtgtact acggcgtgcc cgtgtggaag   120
gaggccacca ccaccctgtt ctgcgccagc gacgccaagg cctacgacac cgaggtgcac   180
aacgtgtggg ccacccacgc ctgcgtgccc accgacccca acccccagga gatcgtgctg   240
gagaacgtga ccgagaactt caacatgtgg aagaacaaca tgtgygagca gatgcacgag   300
gacatctgya gcctgtggga ccagagcctg aagccctgcg tgaagctgac ccccctgtgc   360
gtgaccctgc actgcaccaa cctgaagaac gccaccaaca ccaagagcag caactggaag   420
gagatggacc gcggcgagat caagaactgc agcttcaagg tgaccaccag catccgcaac   480
aagatgcaga aggagtacgc cctgttctac aagctggacg tggtgcccat cgacaacgac   540
aacaccagct acaagctgat caactgcaac accagcgtga tcacccaggc ctgccccaag   600
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gtgagcttcg agcccatccc catccactac tgcgcccccg ccggcttcgc catcctgaag   660
tgcaacgaca agaagttcaa cggcagcggc ccctgcacca acgtgagcac cgtgcagtgc   720
acccacggca tccgccccgt ggtgagcacc cagctgctgc tgaacggcag cctggccgag   780
gagggcgtgg tgatccgcag cgagaacttc accgacaacg ccaagaccat catcgtgcag   840
ctgaaggaga gcgtggagat caactgcacc cgccccaaca acaacacccg caagagcatc   900
accatcggcc ccggccgcgc cttctacgcc accggcgaca tcatcggcga catccgccag   960
gcccactgca acatcagcgg cgagaagtgg aacaacaccc tgaagcagat cgtgaccaag   1020
ctgcaggccc agttcggcaa caagaccatc gtgttcaagc agagcagcgg cggcgacccc   1080
gagatcgtga tgcacagctt caactgcggc ggcgagttct tctactgcaa cagcacccag   1140
ctgttcaaca gcacctggaa caacaccatc ggccccaaca acaccaacgg caccatcacc   1200
ctgccctgcc gcatcaagca gatcatcaac cgctggtgyg aggtgggcaa ggccatgtac   1260
gccccccccca tccgcggcca gatccgctgc agcagcaaca tcaccggcct gctgctgacc   1320
cgcgacggcg gcaaggagat cagcaacacc accgagatct tccgccccgg cggcggcgac   1380
atgcgcgaca actgycgcag cgagctgtac aagtacaagg tggtgaagat cgagcccctg   1440
ggcgtggccc ccaccaaggc caagcgccgc gtggtgcagc gcgagaagcg ctaa          1494

<210>   22
<211>   497
<212>   PRT
<213>   Artificial Sequence

<220>
<223>   HIV-1 gp120 V95C W465C and I103C Q413C

<400>   22
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
1               5                   10                  15

Ala Val Phe Val Ser Pro Ser Ala Val Glu Lys Leu Trp Val Thr Val
            20                  25                  30

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

Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val His Asn Val Trp Ala
    50                  55                  60

Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Ile Val Leu
65                  70                  75                  80

Glu Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asn Met Cys Glu
                85                  90                  95

Gln Met His Glu Asp Ile Cys Ser Leu Trp Asp Gln Ser Leu Lys Pro
            100                 105                 110

Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu His Cys Thr Asn Leu
        115                 120                 125

Lys Asn Ala Thr Asn Thr Lys Ser Ser Asn Trp Lys Glu Met Asp Arg
    130                 135                 140

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

Lys Met Gln Lys Glu Tyr Ala Leu Phe Tyr Lys Leu Asp Val Val Pro
                165                 170                 175

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

Val Ile Thr Gln Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile
        195                 200                 205

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

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

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

Ser Leu Ala Glu Glu Gly Val Val Ile Arg Ser Glu Asn Phe Thr Asp
260 265 270

Asn Ala Lys Thr Ile Ile Val Gln Leu Lys Glu Ser Val Glu Ile Asn
275 280 285

Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly Pro
290 295 300

Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln
305 310 315 320

Ala His Cys Asn Ile Ser Gly Glu Lys Trp Asn Asn Thr Leu Lys Gln
325 330 335

Ile Val Thr Lys Leu Gln Ala Gln Phe Gly Asn Lys Thr Ile Val Phe
340 345 350

Lys Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Met His Ser Phe Asn
355 360 365

Cys Gly Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser
370 375 380

Thr Trp Asn Asn Thr Ile Gly Pro Asn Asn Thr Asn Gly Thr Ile Thr
385 390 395 400

Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Arg Trp Cys Glu Val Gly
405 410 415

Lys Ala Met Tyr Ala Pro Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser
420 425 430

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

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

Cys Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu
465 470 475 480

Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg Glu Lys
485 490 495

Arg

<210> 23
<211> 668
<212> PRT
<213> HIV-1

<400> 23
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
1 5 10 15

Ala Val Phe Val Ser Pro Ser Ala Val Glu Lys Leu Trp Val Thr Val
20 25 30

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

```
Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val His Asn Val Trp Ala
    50                  55                  60

Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Ile Val Leu
65                  70                  75                  80

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

Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro
            100                 105                 110

Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu His Cys Thr Asn Leu
        115                 120                 125

Lys Asn Ala Thr Asn Thr Lys Ser Ser Asn Trp Lys Glu Met Asp Arg
    130                 135                 140

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

Lys Met Gln Lys Glu Tyr Ala Leu Phe Tyr Lys Leu Asp Val Val Pro
                165                 170                 175

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

Val Ile Thr Gln Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile
        195                 200                 205

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

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

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

Ser Leu Ala Glu Glu Gly Val Val Ile Arg Ser Glu Asn Phe Thr Asp
            260                 265                 270

Asn Ala Lys Thr Ile Ile Val Gln Leu Lys Glu Ser Val Glu Ile Asn
        275                 280                 285

Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Ile Gly Pro
    290                 295                 300

Gly Arg Ala Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln
305                 310                 315                 320

Ala His Cys Asn Ile Ser Gly Glu Lys Trp Asn Asn Thr Leu Lys Gln
                325                 330                 335

Ile Val Thr Lys Leu Gln Ala Gln Phe Gly Asn Lys Thr Ile Val Phe
            340                 345                 350

Lys Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Met His Ser Phe Asn
        355                 360                 365

Cys Gly Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser
    370                 375                 380

Thr Trp Asn Asn Thr Ile Gly Pro Asn Asn Thr Asn Gly Thr Ile Thr
385                 390                 395                 400

Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Arg Trp Gln Glu Val Gly
                405                 410                 415
```

```
Lys Ala Met Tyr Ala Pro Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser
            420                 425                 430

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

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

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

Gly Val Ala Pro Thr Lys Ala Ile Ser Ser Val Val Gln Ser Glu Lys
                485                 490                 495

Ser Ala Val Thr Leu Gly Ala Met Phe Leu Gly Phe Leu Gly Ala Ala
            500                 505                 510

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

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

Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys
545                 550                 555                 560

Gln Leu Gln Ala Arg Val Leu Ala Val Glu Arg Tyr Leu Lys Asp Gln
                565                 570                 575

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

Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Asp Gln Ile
        595                 600                 605

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

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

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

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