Genphar.740.ST25.txt
SEQUENCE LISTING

<110> Wang, Danher

<120> GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS

<130> 22488-740

<150> US 09/585,599
<151> 2000-06-02

<150> PCT/US01/18238
<151> 2001-06-04

<150> US 10/003,035
<151> 2001-11-01

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<170> PatentIn version 3.1

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<223> Modified IL-2

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tcaaagcatc atctcaacac taacttga 508

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<212> DNA

<213> Artificial sequence

<220>

<223> Modified Env

<400> 16

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gagagagaca gagacagatc cattcgatta gtgaacggat ccttagcact tatctggtaa 2280

<210> 17

<211> 1496

<212> DNA

<213> Artificial sequence

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<223> Full length Gag

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tatgggcaag cagggagcta gaacgactac aaccatccct tcagacagga tcagaagaac 180

ttagatcatt atataataca gtagcaaccc tctattgtgt gcatcaaagg atagagataa 240

aagacaccaa ggaagcttta gacaagatag aggaagagca aaacaaaagt aagaaaaaag 300

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gggtaaaagt agtagaagag aaggctttca gcccagaagt aatacccatg ttttcagcat 480

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ctatcccagt aggagaaatt tataaaagat ggataatcct gggattaaat aaaatagtaa 780

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<210> 18

<211> 492

<212> PRT

<213> Human immunodeficiency virus type 1

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

Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn Thr Val Ala Thr
50 55 60

Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp Thr Lys Glu Ala
65 70 75 80

Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys Lys Lys Ala Gln
85 90 95

Gln Ala Ala Ala Asp Thr Gly His Ser Ser Gln Val Ser Gln Asn Tyr
100 105 110

Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His Gln Ala Ile Ser
115 120 125

Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu Glu Lys Ala Phe
130 135 140

Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala Thr
145 150 155 160

Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln Ala
165 170 175

Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Glu Trp
180 185 190

Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln Met
195 200 205

Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu Gln
210 215 220

Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly Glu
225 230 235 240

Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg Met
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Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu Pro
260 265 270

Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu Gln
275 280 285

Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val Gln
290 295 300

Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala
305 310 315 320

Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly Pro
325 330 335

Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser Gln Val Thr Asn
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Thr Ala Thr Ile Met Met Gln Arg Gly Asn Phe Arg Asn Gln Arg Lys
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Met Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His Thr Ala Arg Asn
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Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys Gly Lys Glu Gly
385 390 395 400

His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn Phe Leu Gly Lys
405 410 415

Ile Trp Pro Ser Tyr Lys Gly Arg Pro Gly Asn Phe Leu Gln Ser Arg
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Pro Glu Pro Thr Ala Pro Pro Phe Leu Gln Ser Arg Pro Glu Pro Thr
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Ala Pro Pro Glu Glu Ser Phe Arg Ser Gly Val Glu Thr Thr Thr Pro
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<212> DNA

<213> Artificial sequence

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<223> Modified Env from HIV strain pNL4-3

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<212> DNA

<213> Artificial sequence

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<223> Modified Env/Tat/Rev from pNL4-3

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<211> 3417
<212> DNA
<213> Artificial sequence

<220>

<223> Modified Env/Tat/Rev/Nef from strain BH10

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gcggagacag cgacgaagac ctcctcaagg cagtcagact catcaagttt ctctatcaaa 300

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<211> 2950
<212> DNA
<213> Artificial sequence

<220>

<223> Modified Env/Nef from strain BH10

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acagtctatt atggggtacc tgtgtggaag gaagcaacca ccactctatt ttgtgcatca 180

gatgctaaag catatgatac agaggtacat aatgtttggg ccacacatgc ctgtgtaccc 240

acagacccca acccacaaga agtagtattg gtaaatgtga cagaaaattt taacatgtgg 300

aaaaatgaca tggtagaaca gatgcatgag gatataatca gtttatggga tcaaagccta 360

aagccatgtg taaaattaac cccactctgt gttagtttaa agtgcactga tttgaagaat 420

gatactaata ccaatagtag tagcgggaga atgataatgg agaaaggaga gataaaaaac 480

tgctctttca atatcagcac aagcataaga ggtaaggtgc agaaagaata tgcatttttt 540

tataaacttg atataatacc aatagataat gatactacca gctatacgtt gacaagttgt 600

aacacctcag tcattacaca ggcctgtcca aaggtatcct ttgagccaat tcccatacat 660

tattgtgccc cggctggttt tgcgattcta aaatgtaata ataagacgtt caatggaaca 720

ggaccatgta caaatgtcag cacagtacaa tgtacacatg gaattaggcc agtagtatca 780

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tttgttacaa taggaaaaat aggaaatatg agacaagcac attgtaacat tagtagagca 1020

aaatggaata acactttaaa acagatagat agcaaattaa gagaacaatt tggaaataat 1080

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gacaattgga gaagtgaatt atataaatat aaagtagtaa aaattgaacc attaggagta 1500

gcacccacca aggcaaagag aagagtggtg cagactagtg cagtgggaat aggagctttg 1560

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<211> 2747
<212> DNA
<213> Artificial sequence

<220>
<223> Modified Env/Tat from strain BH10

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gaagcatcca ggaagtcagc ctaaaactgc ttgtaccaat tgctattgta aaaagtgttg 180
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ctgtagtgaa tagagttagg cagggatatt caccattatc gtttcagacc cacctcccaa 2640

tcccgagggg acccgacagg cccgaaggaa tagaagaaga aggtggagag agagacagag 2700

acagatccat tcgattagtg aacggatcct tagcacttat ctggtaa 2747

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<211> 2583

<212> DNA

<213> Artificial sequence

<220>

<223> Modified Env

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acagtctatt atggggtacc tgtgtggaag gaagcaacca ccactctatt ttgtgcatca 180

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aagccatgtg taaaattaac cccactctgt gttagtttaa agtgcactga tttgaagaat 420

gatactaata ccaatagtag tagcgggaga atgataatgg agaaaggaga gataaaaaac 480

tgctctttca atatcagcac aagcataaga ggtaaggtgc agaaagaata tgcatttttt 540

tataaacttg atataatacc aatagataat gatactacca gctatacgtt gacaagttgt 600

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tattgtgccc cggctggttt tgcgattcta aaatgtaata ataagacgtt caatggaaca 720

ggaccatgta caaatgtcag cacagtacaa tgtacacatg gaattaggcc agtagtatca 780

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acaagaccca acaacaatac aagaaaaagt atccgtatcc agagaggacc agggagagca 960

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aaatggaata acactttaaa acagatagat agcaaattaa gagaacaatt tggaaataat 1080

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ggtggagaga gagacagaga cagatccatt cgattagtga acggatcctt agcacttatc 2280

tgggacgatc tgcggagcct gtgcctcttc agctaccacc gcttgagaga cttactcttg 2340

attgtaacga ggattgtgga acttctggga cgcaggggt gggaagccct caaatattgg 2400

tggaatctcc tacagtattg gagtcaggag ctaaagaata gtgctgttag cttgctcaat 2460

gccacagcta tagcagtagc tgaggggaca gatagggtta tagaagtagt acaaggagct 2520

tatagagcta ttcgccacat acctagaaga ataagacagg gcttggaaag gattttgcta 2580

taa 2583

<210> 25

<211> 108

<212> DNA

<213> Human immunodeficiency virus type 1

<400> 25
tgtacaagac ccaacaacaa tacaagaaaa agtatccgta tccagagagg accagggaga 60

gcatttgtta caataggaaa aataggaaat atgagacaag cacattgt 108

<210> 26

<211> 105

<212> DNA

<213> Human immunodeficiency virus type 1

<400> 26
tgtaccagac ctaacaacaa tacaagaaaa agtgtacgta taggaccagg acaaacattc 60

tatgcaacag gtgatataat aggggatata agacaagcac attgt 105

<210> 27

<211> 105

<212> DNA

<213> Human immunodeficiency virus type 1

<400> 27
tgtacgagac ccaacaataa tacaagaaaa agtataagga taggaccagg acaagcattc 60

tatgcaacag gagaaataat aggagatata agacaagcac attgt 105

<210> 28

<211> 102

<212> DNA

<213> Human immunodeficiency virus type 1

<400> 28
tgcacaaggc cctacaacaa tataagacaa aggaccccca taggactagg gcaagcactc 60

tatacaacaa gaagaataga agatataaga agagcacatt gt 102

<210> 29

<211> 105

<212> DNA

<213> Human immunodeficiency virus type 1

<400> 29
tgtaccagac cctccaccaa tacaagaaca agtatacgta taggaccagg acaagtattc 60

tatagaacag gagacataac aggagatata agaaaagcat attgt 105

<210> 30

<211> 105

<212> DNA

<213> Human immunodeficiency virus type 1

<400> 30
tgtacaagac ccaacaacaa tacaagaaaa agaatatctt taggaccagg acgagtattt 60

tatacagcag gagaaataat aggagacatc agaaaggcac attgt 105

<210> 31

<211> 105

<212> DNA

<213> Human immunodeficiency virus type 1

<400> 31
tgtaccagac ctaataacaa tacaagaaaa agtataactt ttgcaccagg acaagcgctc 60

tatgcaacag gtgaaataat aggagatata agacaagcac attgt 105

<210> 32

<211> 2562

<212> DNA

<213> Artificial sequence

<220>

<223> Env with multi-clade V3 loops

<400> 32

atgagagtga aggagaaata tcagcacttg tggagatggg ggtggagatg gggcaccatg 60

ctccttggga tgttgatgat ctgtagtgct acagaaaaat tgtgggtcac agtctattat 120

ggggtacctg tgtggaagga agcaaccacc actctatttt gtgcatcaga tgctaaagca 180

tatgatacag aggtacataa tgtttgggcc acacatgcct gtgtacccac agaccccaac 240

ccacaagaag tagtattggt aaatgtgaca gaaaatttta acatgtggaa aaatgacatg 300

gtagaacaga tgcatgagga tataatcagt ttatgggatc aaagcctaaa gccatgtgta 360

aaattaaccc cactctgtgt tggagctggt agttgtaaca cctcagtcat tacacaggcc 420

tgtccaaagg tatcctttga gccaattccc atacattatt gtgccccggc tggttttgcg 480

attctaaaat gtaataataa gacgttcaat ggaacaggac catgtacaaa tgtcagcaca 540

gtacaatgta cacatggaat taggccagta gtatcaactc aactgctgtt aaatggcagt 600

ctggcagaag aagaggtagt aattagatct gccaatttca cagacaatgc taaaaccata 660

atagtacagc tgaaccaatc tgtagaaatt aattgtacaa gacccaacaa caatacaaga 720

aaaagtatcc gtatccagag aggaccaggg agagcatttg ttacaatagg aaaaatagga 780

aatatgagac aagcacattg tctcgggtgt accagaccta acaacaatac aagaaaaagt 840

gtacgtatag gaccaggaca aacattctat gcaacaggtg atataatagg ggatataaga 900

caagcacatt gttgtacgag acccaacaat aatacaagaa aaagtataag gataggacca 960

ggacaagcat tctatgcaac aggagaaata ataggagata taagacaagc acattgttgc 1020

acaaggccct acaacaatat aagacaaagg acccccatag gactagggca agcactctat 1080

acaacaagaa gaatagaaga tataagaaga gcacattgtt gtaccagacc ctccaccaat 1140

acaagaacaa gtatacgtat aggaccagga caagtattct atagaacagg agacataaca 1200

ggagatataa gaaaagcata ttgtggatcc tgtacaagac ccaacaacaa tacaagaaaa 1260

agaatatctt taggaccagg acgagtattt tatacagcag gagaaataat aggagacatc 1320

agaaaggcac attgttgtac cagacctaat aacaatacaa gaaaaagtat aacttttgca 1380

ccaggacaag cgctctatgc aacaggtgaa ataataggag atataagaca agcacattgt 1440

ctcgggaaca ttagtagagc aaaatggaat aacactttaa aacagataga tagcaaatta 1500

agagaacaat ttggaaataa taaaacaata atctttaagc agtcctcagg aggggaccca 1560

gaaattgtaa cgcacagttt taattgtgga ggggaatttt tctactgtaa ttcaacacaa 1620

ctgtttaata gtacttggtt taatagtact tggagtacta aagggtcaaa taacactgaa 1680

ggaagtgaca caatcaccct cccatgcaga ataaaacaaa ttataaacat gtggcaggaa 1740

gtaggaaaag caatgtatgc ccctcccatc agtggacaaa ttagatgttc atcaaatatt 1800

acagggctgc tattaacaag agatggtggt aatagcaaca atgagtccga gatcttcaga 1860

cctggaggag gagatatgag ggacaattgg agaagtgaat tatataaata taaagtagta 1920

aaaattgaac cattaggagt agcacccacc aaggcaaaga gaagagtggt gcagactagt 1980

gcagtgggaa taggagcttt gttccttggg ttcttgggag cagcaggaag cactatgggc 2040

gcagcgtcaa tgacgctgac ggtacaggcc agacaattat tgtctggtat agtgcagcag 2100

cagaacaatt tgctgagggc tattgaggcg caacagcatc tgttgcaact cacagtctgg 2160

ggcatcaagc agctccaggc aagaatcctg gctgtggaaa gatacctaaa ggatcaacag 2220

ctcctgggga tttggggttg ctctggaaaa ctcatttgca ccactgctgt gccttggaat 2280

gctagttgga gtaataaatc tctggaacag atttggaata acatgacctg gatggagtgg 2340

gacagagaaa ttaacaatta cacaagctta atacactcct taattgaaga atcgcaaaac 2400

cagcaagaaa agaatgaaca agaattattg gaattagata aatgggcaag tttgtggaat 2460

tggtttaaca taacaaattg gctgtggtat ataaaatcgt ggctgctgct gctcctgctc 2520

tccctctccc tcctccaggc cacggatttc atgtccctgt ga 2562

<210> 33

<211> 853

<212> PRT

<213> Artificial sequence

<220>

<223> Modified Env with multi-clade V3 loops

<400> 33

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

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

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

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

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

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

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

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

Ala Gly Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
130 135 140

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
145 150 155 160

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
165 170 175

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
180 185 190

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
195 200 205

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
210 215 220

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
225 230 235 240

Lys Ser Ile Arg Ile Gln Arg Gly Pro Gly Arg Ala Phe Val Thr Ile
245 250 255

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Leu Gly Cys Thr Arg
260 265 270

Pro Asn Asn Asn Thr Arg Lys Ser Val Arg Ile Gly Pro Gly Gln Thr
275 280 285

Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys
290 295 300

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

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

Ala His Cys Cys Thr Arg Pro Tyr Asn Asn Ile Arg Gln Arg Thr Pro
340 345 350

Ile Gly Leu Gly Gln Ala Leu Tyr Thr Thr Arg Arg Ile Glu Asp Ile
355 360 365

Arg Arg Ala His Cys Cys Thr Arg Pro Ser Thr Asn Thr Arg Thr Ser
370 375 380

Ile Arg Ile Gly Pro Gly Gln Val Phe Tyr Arg Thr Gly Asp Ile Thr
385 390 395 400

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

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

Ala Gly Glu Ile Ile Gly Asp Ile Arg Lys Ala His Cys Cys Thr Arg
435 440 445

Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Phe Ala Pro Gly Gln Ala
450 455 460

Leu Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys
465 470 475 480

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

Asp Ser Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe
500 505 510

Lys Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn
515 520 525

Cys Gly Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser
530 535 540

Thr Trp Phe Asn Ser Thr Trp Ser Thr Lys Gly Ser Asn Asn Thr Glu
545 550 555 560

Gly Ser Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn
565 570 575

Met Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly
580 585 590

Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp
595 600 605

Gly Gly Asn Ser Asn Asn Glu Ser Glu Ile Phe Arg Pro Gly Gly Gly
610 615 620

Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val
625 630 635 640

Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val
645 650 655

Val Gln Thr Ser Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
660 665 670

Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val
675 680 685

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
690 695 700

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
705 710 715 720

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr Leu
725 730 735

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
740 745 750

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
755 760 765

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
770 775 780

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
785 790 795 800

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
805 810 815

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys

820 825 830

Ser Trp Leu Leu Leu Leu Leu Leu Ser Leu Ser Leu Leu Gln Ala Thr
835 840 845

Asp Phe Met Ser Leu
850

<210> 34

<211> 1092

<212> DNA

<213> Human immunodeficiency virus type 1

<400> 34
atgggtgcga gagcgtcagt attaagcggg ggagaattag atcgatggga aaaaattcgg 60
ttaaggccag ggggaaagaa aaaatataaa ttaaaacata tagtatgggc aagcagggag 120
ctagaacgat tcgcagttaa tcctggcctg ttagaaacat cagaaggctg tagacaaata 180
ctgggacagc tacaaccatc ccttcagaca ggatcagaag aacttagatc attatataat 240
acagtagcaa ccctctattg tgtgcatcaa aggatagaga taaaagacac caaggaagct 300
ttagacaaga tagaggaaga gcaaaacaaa agtaagaaaa aagcacagca agcagcagct 360
gacacaggac acagcagtca ggtcagccaa aattacccta tagtgcagaa catccagggg 420
caaatggtac atcaggccat atcacctaga actttaaatg catgggtaaa agtagtagaa 480
gagaaggctt tcagcccaga agtaataccc atgttttcag cattatcaga aggagccacc 540
ccacaagatt taaacaccat gctaaacaca gtgggggggac atcaagcagc catgcaaatg 600
ttaaaagaga ccatcaatga ggaagctgca gaatgggata gagtacatcc agtgcatgca 660
gggcctattg caccaggcca gatgagagaa ccaaggggaa gtgacatagc aggaactact 720
agtacccttc aggaacaaat aggatggatg acaaataatc cacctatccc agtaggagaa 780
atttataaaa gatggataat cctgggatta aataaaatag taagaatgta tagccctacc 840
agcattctgg acataagaca aggaccaaaa gaacctttta gagactatgt agaccggttc 900
tataaaactc taagagccga gcaagcttca caggaggtaa aaaattggat gacagaaacc 960
ttgttggtcc aaaatgcgaa cccagattgt aagactattt taaaagcatt gggaccagcg 1020
gctacactag aagaaatgat gacagcatgt cagggagtag gaggacccgg ccataaggca 1080
agagttttgt aa 1092

<210> 35

<211> 1179

<212> DNA

<213> Human immunodeficiency virus type 1

<400> 35

atgagagtga aggagaaata tcagcacttg tggagatggg ggtggagatg gggcaccatg 60

ctccttggga tgttgatgat ctgtagtgct ggtgcgagag cgtcagtatt aagcggggga 120

gaattagatc gatgggaaaa aattcggtta aggccagggg gaaagaaaaa atataaatta 180

aaacatatag tatgggcaag cagggagcta gaacgattcg cagttaatcc tggcctgtta 240

gaaacatcag aaggctgtag acaaatactg ggacagctac aaccatccct tcagacagga 300

tcagaagaac ttagatcatt atataataca gtagcaaccc tctattgtgt gcatcaaagg 360

atagagataa aagacaccaa ggaagcttta gacaagatag aggaagagca aaacaaaagt 420

aagaaaaaag cacagcaagc agcagctgac acaggacaca gcagtcaggt cagccaaaat 480

taccctatag tgcagaacat ccaggggcaa atggtacatc aggccatatc acctagaact 540

ttaaatgcat gggtaaaagt agtagaagag aaggctttca gcccagaagt aatacccatg 600

ttttcagcat tatcagaagg agccacccca caagatttaa acaccatgct aaacacagtg 660

gggggacatc aagcagccat gcaaatgtta aaagagacca tcaatgagga agctgcagaa 720

tgggatagag tacatccagt gcatgcaggg cctattgcac caggccagat gagagaacca 780

aggggaagtg acatagcagg aactactagt acccttcagg aacaaatagg atggatgaca 840

aataatccac ctatcccagt aggagaaatt tataaaagat ggataatcct gggattaaat 900

aaaatagtaa gaatgtatag ccctaccagc attctggaca taagacaagg accaaaagaa 960

ccttttagag actatgtaga ccggttctat aaaactctaa gagccgagca agcttcacag 1020

gaggtaaaaa attggatgac agaaaccttg ttggtccaaa atgcgaaccc agattgtaag 1080

actattttaa aagcattggg accagcggct acactagaag aaatgatgac agcatgtcag 1140

ggagtaggag gacccggcca taaggcaaga gttttgtaa 1179

<210> 36

<211> 1308

<212> DNA

<213> Human immunodeficiency virus type 1

<400> 36

atgagagtga aggagaaata tcagcacttg tggagatggg ggtggagatg gggcaccatg 60

ctccttggga tgttgatgat ctgtagtgct ggtgcgagag cgtcagtatt aagcggggga 120

gaattagatc gatgggaaaa aattcggtta aggccagggg gaaagaaaaa atataaatta 180

aaacatatag tatgggcaag cagggagcta gaacgattcg cagttaatcc tggcctgtta 240

gaaacatcag aaggctgtag acaaatactg ggacagctac aaccatccct tcagacagga 300

tcagaagaac ttagatcatt atataatаca gtagcaaccc tctattgtgt gcatcaaagg 360

atagagataa aagacaccaa ggaagcttta gacaagatag aggaagagca aaacaaaagt 420

aagaaaaaag cacagcaagc agcagctgac acaggacaca gcagtcaggt cagccaaaat 480

taccctatag tgcagaacat ccaggggcaa atggtacatc aggccatatc acctagaact 540

ttaaatgcat gggtaaaagt agtagaagag aaggctttca gcccagaagt aatacccatg 600

ttttcagcat tatcagaagg agccacccca caagatttaa acaccatgct aaacacagtg 660

gggggacatc aagcagccat gcaaatgtta aaagagacca tcaatgagga agctgcagaa 720

tgggatagag tacatccagt gcatgcaggg cctattgcac caggccagat gagagaacca 780

aggggaagtg acatagcagg aactactagt acccttcagg aacaaatagg atggatgaca 840

aataatccac ctatcccagt aggagaaatt tataaaagat ggataatcct gggattaaat 900

aaaatagtaa gaatgtatag ccctaccagc attctggaca taagacaagg accaaaagaa 960

ccttttagag actatgtaga ccggttctat aaaactctaa gagccgagca agcttcacag 1020

gaggtaaaaa attggatgac agaaaccttg ttggtccaaa atgcgaaccc agattgtaag 1080

actattttaa aagcattggg accagcggct acactagaag aaatgatgac agcatgtcag 1140

ggagtaggag gacccggcca taaggcaaga gttttgttat tcataatgat agtaggaggc 1200

ttggtaggtt taagaatagt ttttgctgta ctttctgtag tgaatagagt taggcaggga 1260

tattcaccat atcgtttca gacccacctc ccaatcccga ggggataa 1308

<210> 37

<211> 363

<212> PRT

<213> Human immunodeficiency virus type 1

<400> 37

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly
        275                 280                 285
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Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu
290 295 300

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

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

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

Val Gly Gly Pro Gly His Lys Ala Arg Val Leu
355 360

<210> 38

<211> 410

<212> PRT

<213> Human immunodeficiency virus type 1

<400> 38

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

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Gly Ala
20 25 30

Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp Glu Lys Ile
35 40 45

Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys His Ile Val
50 55 60

Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro Gly Leu Leu
65 70 75 80

Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu Gln Pro Ser
85 90 95

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

Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp Thr Lys Glu
115 120 125

Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys Lys Lys Ala
130 135 140

Gln Gln Ala Ala Ala Asp Thr Gly His Ser Ser Gln Val Ser Gln Asn
145 150 155 160

Tyr Pro Gln Gln Ala Ala Ala Asp Thr Gly His Ser Ser Gln Val Ser
165 170 175

Gln Asn Tyr Pro Gln Gln Ala Ala Ala Asp Thr Gly His Ser Ser Gln
180 185 190

Val Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val
195 200 205

His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val
210 215 220

Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu
225 230 235 240

Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val
245 250 255

Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu
260 265 270

Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile
275 280 285

Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr
290 295 300

Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro
305 310 315 320

Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn
325 330 335

Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln
340 345 350

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

Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Thr Ile Leu Lys Ala Leu

370 375 380

Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val
385 390 395 400

Gly Gly Pro Gly His Lys Ala Arg Val Leu
405 410

<210> 39

<211> 453

<212> PRT

<213> Human immunodeficiency virus type 1

<400> 39

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

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Gly Ala
20 25 30

Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp Glu Lys Ile
35 40 45

Arg Leu Arg Pro Gly Gly Leu Ser Gly Gly Glu Leu Asp Arg Trp Glu
50 55 60

Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys His
65 70 75 80

Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro Gly
85 90 95

Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu Gln
100 105 110

Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn Thr
115 120 125

Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp Thr
130 135 140

Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys Lys
145 150 155 160

Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Ser Gln Val Ser
165 170 175

Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His Gln
180 185 190

Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu Glu
195 200 205

Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu
210 215 220

Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly
225 230 235 240

His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala
245 250 255

Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro
260 265 270

Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser
275 280 285

Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro
290 295 300

Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile
305 310 315 320

Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro
325 330 335

Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg
340 345 350

Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu
355 360 365

Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu
370 375 380

Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val
385 390 395 400

Gly Gly Pro Gly His Lys Ala Arg Val Leu Leu Phe Ile Met Ile Val
405 410 415

Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Val Val
420 425 430

Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His Leu
435 440 445

Pro Ile Pro Arg Gly
450

<210> 40

<211> 399

<212> DNA

<213> Human immunodeficiency virus type 1

<400> 40
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ttaaggccag ggggaaagaa aaaatataaa ttaaaacata tagtatgggc aagcagggag 120

ctagaacgat tcgcagttaa tcctggcctg ttagaaacat cagaaggctg tagacaaata 180

ctgggacagc tacaaccatc ccttcagaca ggatcagaag aacttagatc attatataat 240

acagtagcaa ccctctattg tgtgcatcaa aggatagaga taaaagacac caaggaagct 300

ttagacaaga tagaggaaga gcaaaacaaa agtaagaaaa aagcacagca agcagcagct 360

gacacaggac acagcagtca ggtcagccaa aattactaa 399

<210> 41

<211> 486

<212> DNA

<213> Human immunodeficiency virus type 1

<400> 41
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ctccttggga tgttgatgat ctgtagtgct ggtgcgagag cgtcagtatt aagcgggga 120

gaattagatc gatgggaaaa aattcggtta aggccagggg gaaagaaaaa atataaatta 180

aaacatatag tatgggcaag cagggagcta gaacgattcg cagttaatcc tggcctgtta 240

gaaacatcag aaggctgtag acaaatactg ggacagctac aaccatccct tcagacagga 300

tcagaagaac ttagatcatt atataataca gtagcaaccc tctattgtgt gcatcaaagg 360

atagagataa aagacaccaa ggaagcttta gacaagatag aggaagagca aaacaaaagt 420

aagaaaaaag cacagcaagc agcagctgac acaggacaca gcagtcaggt cagccaaaat 480

tactaa 486

<210> 42

<211> 615

<212> DNA

<213> Human immunodeficiency virus type 1

<400> 42

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gaattagatc gatgggaaaa aattcggtta aggccagggg gaaagaaaaa atataaatta 180

aaacatatag tatgggcaag cagggagcta gaacgattcg cagttaatcc tggcctgtta 240

gaaacatcag aaggctgtag acaaatactg ggacagctac aaccatccct tcagacagga 300

tcagaagaac ttagatcatt atataataca gtagcaaccc tctattgtgt gcatcaaagg 360

atagagataa aagacaccaa ggaagcttta gacaagatag aggaagagca aaacaaaagt 420

aagaaaaaag cacagcaagc agcagctgac acaggacaca gcagtcaggt cagccaaaat 480

tacttattca taatgatagt aggaggcttg gtaggtttaa gaatagtttt tgctgtactt 540

tctgtagtga atagagttag gcagggatat tcaccattat cgtttcagac ccacctccca 600

atcccgaggg gataa 615

<210> 43

<211> 132

<212> PRT

<213> Human immunodeficiency virus type 1

<400> 43

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

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

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

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

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

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

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

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

Ser Gln Asn Tyr
130

<210> 44

<211> 179

<212> PRT

<213> Human immunodeficiency virus type 1

<400> 44

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

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Gly Ala
20 25 30

Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp Glu Lys Ile
35 40 45

Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys His Ile Val
50 55 60

Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro Gly Leu Leu
65 70 75 80

Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu Gln Pro Ser
85 90 95

Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Gly Gln Leu Gln
100 105 110

Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn Thr
115 120 125

Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp Thr
130 135 140

Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys Lys
145 150 155 160

Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Ser Gln Val Ser
165 170 175

Gln Asn Tyr

<210> 45

<211> 186

<212> PRT

<213> Human immunodeficiency virus type 1

<400> 45

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

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Gly Ala
20 25 30

Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp Glu Lys Ile
35 40 45

Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys His Ile Val
50 55 60

Trp Ala Ser Arg Glu Leu Glu Arg Gly Gln Leu Gln Pro Ser Leu Gln
65 70 75 80

Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn Thr Val Ala Thr Leu
85 90 95

Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp Thr Lys Glu Ala Leu
100 105 110

Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys Lys Lys Ala Gln Gln

115 120 125

Ala Ala Ala Asp Thr Gly His Ser Ser Gln Val Ser Gln Asn Tyr Leu
130 135 140

Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala
145 150 155 160

Val Leu Ser Val Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser
165 170 175

Phe Gln Thr His Leu Pro Ile Pro Arg Gly
180 185

<210> 46

<211> 699

<212> DNA

<213> Human immunodeficiency virus type 1

<400> 46
atgcctatag tgcagaacat ccaggggcaa atggtacatc aggccatatc acctagaact 60

ttaaatgcat gggtaaaagt agtagaagag aaggctttca gcccagaagt aatacccatg 120

ttttcagcat tatcagaagg agccacccca caagatttaa acaccatgct aaacacagtg 180

gggggacatc aagcagccat gcaaatgtta aaagagacca tcaatgagga agctgcagaa 240

tgggatagag tacatccagt gcatgcaggg cctattgcac caggccagat gagagaacca 300

aggggaagtg acatagcagg aactactagt acccttcagg aacaaatagg atggatgaca 360

aataatccac ctatcccagt aggagaaatt tataaaagat ggataatcct gggattaaat 420

aaaatagtaa gaatgtatag ccctaccagc attctggaca taagacaagg accaaaagaa 480

ccttttagag actatgtaga ccggttctat aaaactctaa gagccgagca agcttcacag 540

gaggtaaaaa attggatgac agaaaccttg ttggtccaaa atgcgaaccc agattgtaag 600

actattttaa aagcattggg accagcggct acactagaag aaatgatgac agcatgtcag 660

ggagtaggag gacccggcca taaggcaaga gttttgtaa 699

<210> 47

<211> 786

<212> DNA

<213> Human immunodeficiency virus type 1

<400> 47
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gtacatcagg ccatatcacc tagaacttta aatgcatggg taaaagtagt agaagagaag 180
gctttcagcc cagaagtaat acccatgttt tcagcattat cagaaggagc caccccacaa 240
gatttaaaca ccatgctaaa cacagtgggg ggacatcaag cagccatgca aatgttaaaa 300
gagaccatca atgaggaagc tgcagaatgg gatagagtac atccagtgca tgcagggcct 360
attgcaccag gccagatgag agaaccaagg ggaagtgaca tagcaggaac tactagtacc 420
cttcaggaac aaataggatg gatgacaaat aatccaccta tcccagtagg agaaatttat 480
aaaagatgga taatcctggg attaaataaa atagtaagaa tgtatagccc taccagcatt 540
ctggacataa gacaaggacc aaaagaacct tttagagact atgtagaccg gttctataaa 600
actctaagag ccgagcaagc ttcacaggag gtaaaaaatt ggatgacaga aaccttgttg 660
gtccaaaatg cgaacccaga ttgtaagact attttaaaag cattgggacc agcggctaca 720
ctagaagaaa tgatgacagc atgtcaggga gtaggaggac ccggccataa ggcaagagtt 780
ttgtaa 786

<210> 48
<211> 915
<212> DNA
<213> Human immunodeficiency virus type 1

<400> 48
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ctccttggga tgttgatgat ctgtagtgct cctatagtgc agaacatcca ggggcaaatg 120
gtacatcagg ccatatcacc tagaacttta aatgcatggg taaaagtagt agaagagaag 180
gctttcagcc cagaagtaat acccatgttt tcagcattat cagaaggagc caccccacaa 240
gatttaaaca ccatgctaaa cacagtgggg ggacatcaag cagccatgca aatgttaaaa 300
gagaccatca atgaggaagc tgcagaatgg gatagagtac atccagtgca tgcagggcct 360
attgcaccag gccagatgag agaaccaagg ggaagtgaca tagcaggaac tactagtacc 420
cttcaggaac aaataggatg gatgacaaat aatccaccta tcccagtagg agaaatttat 480
aaaagatgga taatcctggg attaaataaa atagtaagaa tgtatagccc taccagcatt 540
ctggacataa gacaaggacc aaaagaacct tttagagact atgtagaccg gttctataaa 600

actctaagag ccgagcaagc ttcacaggag gtaaaaaatt ggatgacaga aaccttgttg 660

gtccaaaatg cgaacccaga ttgtaagact attttaaaag cattgggacc agcggctaca 720

ctagaagaaa tgatgacagc atgtcaggga gtaggaggac ccggccataa ggcaagagtt 780

ttgttattca taatgatagt aggaggcttg gtaggtttaa gaatagtttt tgctgtactt 840

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atcccgaggg gataa 915

<210> 49

<211> 232

<212> PRT

<213> Human immunodeficiency virus type 1

<400> 49

Met Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His Gln Ala Ile
1 5 10 15

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

Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala
35 40 45

Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln
50 55 60

Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Glu
65 70 75 80

Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln
85 90 95

Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu
100 105 110

Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly
115 120 125

Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg
130 135 140

Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu
145 150 155 160

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

Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val
            180                 185                 190

Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro
        195                 200                 205

Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly
    210                 215                 220

Pro Gly His Lys Ala Arg Val Leu
225                 230
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<210> 50

<211> 261

<212> PRT

<213> Human immunodeficiency virus type 1

<400> 50

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

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Pro Ile
            20                  25                  30

Val Gln Asn Ile Gln Gly Gln Met Val His Gln Ala Ile Ser Pro Arg
        35                  40                  45

Thr Leu Asn Ala Trp Val Lys Val Val Glu Glu Lys Ala Phe Ser Pro
    50                  55                  60

Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln
65                  70                  75                  80

Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln Ala Ala Met
                85                  90                  95

Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Glu Trp Asp Arg
            100                 105                 110

Val His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln Met Arg Glu
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115 120 125

Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu Gln Glu Gln
130 135 140

Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly Glu Ile Tyr
145 150 155 160

Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg Met Tyr Ser
165 170 175

Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg
180 185 190

Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu Gln Ala Ser
195 200 205

Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val Gln Asn Ala
210 215 220

Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala Ala Thr
225 230 235 240

Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly Pro Gly His
245 250 255

Lys Ala Arg Val Leu
260

<210> 51

<211> 286

<212> PRT

<213> Human immunodeficiency virus type 1

<400> 51

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

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Pro Ile
20 25 30

Val Gln Asn Ile Gln Gly Gln Met Val His Gln Ala Ile Ser Pro Arg
35 40 45

Thr Leu Asn Ala Trp Val Lys Val Val Glu Glu Lys Ala Phe Ser Pro
50 55 60

Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln
65 70 75 80

Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln Ala Ala Met
85 90 95

Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Arg Glu Pro Arg
100 105 110

Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly
115 120 125

Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg
130 135 140

Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg Met Tyr Ser Pro Thr
145 150 155 160

Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr
165 170 175

Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu Gln Ala Ser Gln Glu
180 185 190

Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val Gln Asn Ala Asn Pro
195 200 205

Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu
210 215 220

Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly Pro Gly His Lys Ala
225 230 235 240

Arg Val Leu Leu Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg
245 250 255

Ile Val Phe Ala Val Leu Ser Val Val Asn Arg Val Arg Gln Gly Tyr
260 265 270

Ser Pro Leu Ser Phe Gln Thr His Leu Pro Ile Pro Arg Gly
275 280 285

<210> 52

<211> 3839

<212> DNA

<213> Artificial sequence

<220>

<223> Modified Env/Tat

<400> 52

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ggcgttactc gacagaggag agcaagaaat ggagccagta gatcctagac tagagccctg 120

gaagcatcca ggaagtcagc ctaaaactgc ttgtaccaat tgctattgta aaaagtgttg 180

ctttcattgc caagtttgtt tcataacaaa agccttaggc atctcctatg gcaggaagaa 240

gcggagacag cgacgaagac ctcctcaagg cagtcagact catcaagttt ctctatcaaa 300

gcagtaagta gtacatgtaa tgcaacctat acaaatagca atagtagcat tagtagtagc 360

aataataata gcaatagttg tgtggtccat agtaatcata gaatatagga aaatattaag 420

acaaagaaaa atagacaggt taattgatag actaatagaa agagcagaag acagtggcaa 480

tgagagtgaa ggagaaatat cagcacttgt ggagatgggg gtggagatgg ggcaccatgc 540

tccttgggat gttgatgatc tgtagtgcta cagaaaaatt gtgggtcaca gtctattatg 600

gggtacctgt gtggaaggaa gcaaccacca ctctattttg tgcatcagat gctaaagcat 660

atgatacaga ggtacataat gtttgggcca cacatgcctg tgtacccaca gaccccaacc 720

cacaagaagt agtattggta aatgtgacag aaaattttaa catgtggaaa aatgacatgg 780

tagaacagat gcatgaggat ataatcagtt tatgggatca aagcctaaag ccatgtgtaa 840

aattaacccc actctgtgtt ggagctggta gttgtaacac ctcagtcatt acacaggcct 900

gtccaaaggt atcctttgag ccaattccca tacattattg tgccccggct ggttttgcga 960

ttctaaaatg taataataag acgttcaatg gaacaggacc atgtacaaat gtcagcacag 1020

tacaatgtac acatggaatt aggccagtag tatcaactca actgctgtta aatggcagtc 1080

tggcagaaga agaggtagta attagatctg ccaatttcac agacaatgct aaaaccataa 1140

tagtacagct gaaccaatct gtagaaatta attgtacaag acccaacaac aatacaagaa 1200

aaagtatccg tatccagaga ggaccaggga gagcatttgt tacaatagga aaaataggaa 1260

atatgagaca agcacattgt ctcgggtgta ccagacctaa caacaataca agaaaaagtg 1320

tacgtatagg accaggacaa acattctatg caacaggtga tataataggg gatataagac 1380

aagcacattg ttgtacgaga cccaacaata atacaagaaa aagtataagg ataggaccag 1440

gacaagcatt ctatgcaaca ggagaaataa taggagatat aagacaagca cattgttgca 1500

caaggcccta caacaatata agacaaagga cccccatagg actagggcaa gcactctata 1560

caacaagaag aatagaagat ataagaagag cacattgttg taccagaccc tccaccaata 1620
caagaacaag tatacgtata ggaccaggac aagtattcta tagaacagga gacataacag 1680
gagatataag aaaagcatat tgtggatcct gtacaagacc caacaacaat acaagaaaaa 1740
gaatatcttt aggaccagga cgagtatttt atacagcagg agaaataata ggagacatca 1800
gaaaggcaca ttgttgtacc agacctaata acaatacaag aaaaagtata acttttgcac 1860
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ccaacaataa tacaagaaaa agtataagga taggaccagg acaagcattc tatgcaacag 2100
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tccttgggtt cttgggagca gcaggaagca ctatgggcgc agcgtcaatg acgctgacgg 3180
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tggaacagat ttggaataac atgacctgga tggagtggga cagagaaatt aacaattaca 3480

caagcttaat acactcctta attgaagaat cgcaaaacca gcaagaaaag aatgaacaag 3540

aattattgga attagataaa tgggcaagtt tgtggaattg gtttaacata acaaattggc 3600

tgtggtatat aaaattattc ataatgatag taggaggctt ggtaggttta agaatagttt 3660

ttgctgtact ttctgtagtg aatagagtta ggcagggata ttcaccatta tcgtttcaga 3720

cccacctccc aatcccgagg ggacccgaca ggcccgaagg aatagaagaa gaaggtggag 3780

agagagacag agacagatcc attcgattag tgaacggatc cttagcactt atctggtaa 3839

<210> 53

<211> 1101

<212> PRT

<213> Artificial sequence

<220>

<223> Modified Env/Tat

<400> 53

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
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Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
20 25 30

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

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

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

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

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

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

Ala Gly Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
130 135 140

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
145 150 155 160

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
165 170 175

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
180 185 190

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
195 200 205

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
210 215 220

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
225 230 235 240

Lys Ser Ile Arg Ile Gln Arg Gly Pro Gly Arg Ala Phe Val Thr Ile
245 250 255

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Leu Gly Cys Thr Arg
260 265 270

Pro Asn Asn Asn Thr Arg Lys Ser Val Arg Ile Gly Pro Gly Gln Thr
275 280 285

Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys
290 295 300

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

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

Ala His Cys Cys Thr Arg Pro Tyr Asn Asn Ile Arg Gln Arg Thr Pro
340 345 350

Ile Gly Leu Gly Gln Ala Leu Tyr Thr Thr Arg Arg Ile Glu Asp Ile
355 360 365

Arg Arg Ala His Cys Cys Thr Arg Pro Ser Thr Asn Thr Arg Thr Ser
370 375 380

Ile Arg Ile Gly Pro Gly Gln Val Phe Tyr Arg Thr Gly Asp Ile Thr
385 390 395 400

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

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

Ala Gly Glu Ile Ile Gly Asp Ile Arg Lys Ala His Cys Cys Thr Arg
435 440 445

Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Phe Ala Pro Gly Gln Ala
450 455 460

Leu Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys
465 470 475 480

Leu Gly Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Val Arg Ile
485 490 495

Gly Pro Gly Gln Thr Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile
500 505 510

Arg Gln Ala His Cys Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser
515 520 525

Ile Arg Ile Gly Pro Gly Gln Ala Phe Tyr Ala Thr Gly Glu Ile Ile
530 535 540

Gly Asp Ile Arg Gln Ala His Cys Cys Thr Arg Pro Tyr Asn Asn Ile
545 550 555 560

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

Arg Ile Glu Asp Ile Arg Arg Ala His Cys Cys Thr Arg Pro Ser Thr
580 585 590

Asn Thr Arg Thr Ser Ile Arg Ile Gly Pro Gly Gln Val Phe Tyr Arg
595 600 605

Thr Gly Asp Ile Thr Gly Asp Ile Arg Lys Ala Tyr Cys Gly Ser Cys
610 615 620

Thr Arg Pro Asn Asn Asn Thr Arg Lys Arg Ile Ser Leu Gly Pro Gly
625 630 635 640

Arg Val Phe Tyr Thr Ala Gly Glu Ile Ile Gly Asp Ile Arg Lys Ala
645 650 655

His Cys Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Phe
660 665 670

Ala Pro Gly Gln Ala Leu Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile
675 680 685

Arg Gln Ala His Cys Leu Gly Asn Ile Ser Arg Ala Lys Trp Asn Asn
690 695 700

Thr Leu Lys Gln Ile Asp Ser Lys Leu Arg Glu Gln Phe Gly Asn Asn
705 710 715 720

Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp Pro Glu Ile Val
725 730 735

Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asn Ser Thr
740 745 750

Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp Ser Thr Lys Gly
755 760 765

Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu Pro Cys Arg Ile
770 775 780

Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys Ala Met Tyr Ala
785 790 795 800

Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu
805 810 815

Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu Ser Glu Ile Phe
820 825 830

Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr
835 840 845

Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys
850 855 860

Ala Lys Arg Arg Val Val Gln Thr Ser Ala Val Gly Ile Gly Ala Leu
865 870 875 880

Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser

885 890 895

Met Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln
900 905 910

Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu
915 920 925

Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala
930 935 940

Val Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys
945 950 955 960

Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp
965 970 975

Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu
980 985 990

Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile
995 1000 1005

Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu
1010 1015 1020

Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe Asn Ile Thr
1025 1030 1035

Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met Ile Val Gly Gly
1040 1045 1050

Leu Val Gly Leu Arg Ile Val Phe Ala Thr His Leu Pro Ile Pro
1055 1060 1065

Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu Gly Gly Glu
1070 1075 1080

Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser Leu Ala
1085 1090 1095

Leu Ile Trp
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<210> 54

<211> 4040

<212> DNA

<213> Artificial sequence

<220>

<223> Modified Env/Tat/Rev

<400> 54

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gaagcatcca ggaagtcagc ctaaaactgc ttgtaccaat tgctattgta aaaagtgttg 180

ctttcattgc caagtttgtt tcataacaaa agccttaggc atctcctatg gcaggaagaa 240

gcggagacag cgacgaagac ctcctcaagg cagtcagact catcaagttt ctctatcaaa 300

gcagtaagta gtacatgtaa tgcaacctat acaaatagca atagtagcat tagtagtagc 360

aataataata gcaatagttg tgtggtccat agtaatcata gaatatagga aaatattaag 420

acaaagaaaa atagacaggt taattgatag actaatagaa agagcagaag acagtggcaa 480

tgagagtgaa ggagaaatat cagcacttgt ggagatgggg gtggagatgg ggcaccatgc 540

tccttgggat gttgatgatc tgtagtgcta cagaaaaatt gtgggtcaca gtctattatg 600

gggtacctgt gtggaaggaa gcaaccacca ctctattttg tgcatcagat gctaaagcat 660

atgatacaga ggtacataat gtttgggcca cacatgcctg tgtacccaca gaccccaacc 720

cacaagaagt agtattggta aatgtgacag aaaattttaa catgtggaaa aatgacatgg 780

tagaacagat gcatgaggat ataatcagtt tatgggatca aagcctaaag ccatgtgtaa 840

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gtccaaaggt atcctttgag ccaattccca tacattattg tgccccggct ggttttgcga 960

ttctaaaatg taataataag acgttcaatg gaacaggacc atgtacaaat gtcagcacag 1020

tacaatgtac acatggaatt aggccagtag tatcaactca actgctgtta aatggcagtc 1080

tggcagaaga agaggtagta attagatctg ccaatttcac agacaatgct aaaaccataa 1140

tagtacagct gaaccaatct gtagaaatta attgtacaag acccaacaac aatacaagaa 1200

aaagtatccg tatccagaga ggaccaggga gagcatttgt tacaatagga aaaataggaa 1260

atatgagaca agcacattgt ctcgggtgta ccagacctaa caacaataca agaaaaagtg 1320

tacgtatagg accaggacaa acattctatg caacaggtga tataataggg gatataagac 1380

aagcacattg ttgtacgaga cccaacaata atacaagaaa aagtataagg ataggaccag 1440

gacaagcatt ctatgcaaca ggagaaataa taggagatat aagacaagca cattgttgca 1500

caaggcccta caacaatata agacaaagga cccccatagg actagggcaa gcactctata 1560

caacaagaag aatagaagat ataagaagag cacattgttg taccagaccc tccaccaata 1620

caagaacaag tatacgtata ggaccaggac aagtattcta tagaacagga gacataacag 1680

gagatataag aaaagcatat tgtggatcct gtacaagacc caacaacaat acaagaaaaa 1740

gaatatcttt aggaccagga cgagtatttt atacagcagg agaaataata ggagacatca 1800

gaaaggcaca ttgttgtacc agacctaata acaatacaag aaaaagtata acttttgcac 1860

caggacaagc gctctatgca acaggtgaaa taataggaga tataagacaa gcacattgtc 1920

tcgggtgtac cagacctaac aacaatacaa gaaaaagtgt acgtatagga ccaggacaaa 1980

cattctatgc aacaggtgat ataatagggg atataagaca agcacattgt tgtacgagac 2040

ccaacaataa tacaagaaaa agtataagga taggaccagg acaagcattc tatgcaacag 2100

gagaaataat aggagatata agacaagcac attgttgcac aaggccctac aacaatataa 2160

gacaaaggac ccccatagga ctagggcaag cactctatac aacaagaaga atagaagata 2220

taagaagagc acattgttgt accagaccct ccaccaatac aagaacaagt atacgtatag 2280

gaccaggaca agtattctat agaacaggag acataacagg agatataaga aaagcatatt 2340

gtggatcctg tacaagaccc aacaacaata caagaaaaag aatatcttta ggaccaggac 2400

gagtatttta tacagcagga gaaataatag gagacatcag aaaggcacat tgttgtacca 2460

gacctaataa caatacaaga aaaagtataa cttttgcacc aggacaagcg ctctatgcaa 2520

caggtgaaat aataggagat ataagacaag cacattgtct cgggaacatt agtagagcaa 2580

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aaacaataat ctttaagcag tcctcaggag gggacccaga aattgtaacg cacagtttta 2700

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atagtacttg gagtactaaa gggtcaaata acactgaagg aagtgacaca atcaccctcc 2820

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acaattggag aagtgaatta tataaatata aagtagtaaa aattgaacca ttaggagtag 3060

cacccaccaa ggcaaagaga agagtggtgc agactagtgc agtgggaata ggagctttgt 3120

tccttgggtt cttgggagca gcaggaagca ctatgggctg cacgtcaatg acgctgacgg 3180

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ctggaaaact catttgcacc actgctgtgc cttggaatgc tagttggagt aataaatctc 3420

tggaacagat ttggaataac atgacctgga tggagtggga cagagaaatt aacaattaca 3480

caagcttaat acactcctta attgaagaat cgcaaaacca gcaagaaaag aatgaacaag 3540

aattattgga attagataaa tgggcaagtt tgtggaattg gtttaacata acaaattggc 3600

tgtggtatat aaaattattc ataatgatag taggaggctt ggtaggttta agaatagttt 3660

ttgctgtact ttctatagtg aatagagtta ggcagggata ttcaccatta tcgtttcaga 3720

cccacctccc aatcccgagg ggacccgaca ggcccgaagg aatagaagaa gaaggtggag 3780

agagagacag agacagatcc attcgattag tgaacggatc cttagcactt atctgggacg 3840

atctgcggag cctgtgcctc ttcagctacc accgcttgag agacttactc ttgattgtaa 3900

cgaggattgt ggaacttctg ggacgcaggg ggtgggaagc cctcaaatat tggtggaatc 3960

tcctacagta ttggagtcag gaactaaaga atagtgctgt taacttgctc aatgccacag 4020

ccatagcagt agctgagtaa 4040

<210> 55

<211> 1186

<212> PRT

<213> Artificial sequence

<220>

<223> Modified Env/Tat/Rev

<400> 55

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

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

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

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

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

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp

100 105 110

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

Ala Gly Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
130 135 140

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
145 150 155 160

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
165 170 175

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
180 185 190

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
195 200 205

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
210 215 220

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
225 230 235 240

Lys Ser Ile Arg Ile Gln Arg Gly Pro Gly Arg Ala Phe Val Thr Ile
245 250 255

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Leu Gly Cys Thr Arg
260 265 270

Pro Asn Asn Asn Thr Arg Lys Ser Val Arg Ile Gly Pro Gly Gln Thr
275 280 285

Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys
290 295 300

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

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

Ala His Cys Cys Thr Arg Pro Tyr Asn Asn Ile Arg Gln Arg Thr Pro
340 345 350

Ile Gly Leu Gly Gln Ala Leu Tyr Thr Thr Arg Arg Ile Glu Asp Ile
355 360 365

Arg Arg Ala His Cys Cys Thr Arg Pro Ser Thr Asn Thr Arg Thr Ser
370 375 380

Ile Arg Ile Gly Pro Gly Gln Val Phe Tyr Arg Thr Gly Asp Ile Thr
385 390 395 400

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

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

Ala Gly Glu Ile Ile Gly Asp Ile Arg Lys Ala His Cys Cys Thr Arg
435 440 445

Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Phe Ala Pro Gly Gln Ala
450 455 460

Leu Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys
465 470 475 480

Leu Gly Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Val Arg Ile
485 490 495

Gly Pro Gly Gln Thr Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile
500 505 510

Arg Gln Ala His Cys Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser
515 520 525

Ile Arg Ile Gly Pro Gly Gln Ala Phe Tyr Ala Thr Gly Glu Ile Ile
530 535 540

Gly Asp Ile Arg Gln Ala His Cys Cys Thr Arg Pro Tyr Asn Asn Ile
545 550 555 560

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

Arg Ile Glu Asp Ile Arg Arg Ala His Cys Cys Thr Arg Pro Ser Thr
580 585 590

Asn Thr Arg Thr Ser Ile Arg Ile Gly Pro Gly Gln Val Phe Tyr Arg
595 600 605

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Thr Gly Asp Ile Thr Gly Asp Ile Arg Lys Ala Tyr Cys Gly Ser Cys
    610                 615                 620

Thr Arg Pro Asn Asn Asn Thr Arg Lys Arg Ile Ser Leu Gly Pro Gly
625                 630                 635                 640

Arg Val Phe Tyr Thr Ala Gly Glu Ile Ile Gly Asp Ile Arg Lys Ala
                645                 650                 655

His Cys Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Phe
            660                 665                 670

Ala Pro Gly Gln Ala Leu Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile
        675                 680                 685

Arg Gln Ala His Cys Leu Gly Asn Ile Ser Arg Ala Lys Trp Asn Asn
    690                 695                 700

Thr Leu Lys Gln Ile Asp Ser Lys Leu Arg Glu Gln Phe Gly Asn Asn
705                 710                 715                 720

Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp Pro Glu Ile Val
                725                 730                 735

Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asn Ser Thr
            740                 745                 750

Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp Ser Thr Lys Gly
        755                 760                 765

Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu Pro Cys Arg Ile
    770                 775                 780

Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys Ala Met Tyr Ala
785                 790                 795                 800

Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu
                805                 810                 815

Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu Ser Glu Ile Phe
            820                 825                 830

Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr
        835                 840                 845

Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys
    850                 855                 860
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Ala Lys Arg Arg Val Val Gln Thr Ser Ala Val Gly Ile Gly Ala Leu
865 870 875 880

Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Cys Thr Ser
885 890 895

Met Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser Asp Ile Val Gln
900 905 910

Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu
915 920 925

Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala
930 935 940

Val Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys
945 950 955 960

Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp
965 970 975

Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu
980 985 990

Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile
995 1000 1005

Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu
1010 1015 1020

Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe Asn Ile Thr
1025 1030 1035

Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met Ile Val Gly Gly
1040 1045 1050

Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Ile Val Asn
1055 1060 1065

Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His Leu
1070 1075 1080

Pro Ile Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu
1085 1090 1095

Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly

1100 1105 1110

Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe
1115 1120 1125

Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile
1130 1135 1140

Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp
1145 1150 1155

Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
1160 1165 1170

Val Asn Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu
1175 1180 1185

<210> 56

<211> 507

<212> DNA

<213> Human immunodeficiency virus type 1

<400> 56
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agaagagagc ttcaggtctg gggtagagac aacaactccc cctcagaagc aggagccgat 180

agacaaggaa ctgtatcctt taacttccct cagatcactc tttggcaacg acccctcgtc 240

acaataaaga taggggggca actaaaggaa gctctattag atacaggagc agatgataca 300

gtattagaag aaatgagttt gccaggaaga tggaaaccaa aaatgatagg gggaattgga 360

ggttttatca aagtaagaca gtatgatcag atactcatag aaatctgtgg acataaagct 420

ataggtacag tattagtagg acctacacct gtcaacataa ttggaagaaa tctgttgact 480

cagattggtt gcactttaaa ttttaa 507

<210> 57

<211> 168

<212> PRT

<213> Human immunodeficiency virus type 1

<400> 57

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Phe Ser Ser Glu Gln Thr Arg Ala Asn Ser Pro Thr Ile Ser Ser Glu
20 25 30

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

Arg Asp Asn Asn Ser Pro Ser Glu Ala Gly Ala Asp Arg Gln Gly Thr
50 55 60

Val Ser Phe Asn Phe Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val
65 70 75 80

Thr Ile Lys Ile Gly Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly
85 90 95

Ala Asp Asp Thr Val Leu Glu Glu Met Ser Leu Pro Gly Arg Trp Lys
100 105 110

Pro Lys Met Ile Gly Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr
115 120 125

Asp Gln Ile Leu Ile Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val
130 135 140

Leu Val Gly Pro Thr Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr
145 150 155 160

Gln Ile Gly Cys Thr Leu Asn Phe
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<210> 58

<211> 1800

<212> DNA

<213> Artificial sequence

<220>

<223> Gag-PI

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ctagaacgat tcgcagttaa tcctggcctg ttagaaacat cagaaggctg tagacaaata 180

ctgggacagc tacaaccatc ccttcagaca ggatcagaag aacttagatc attatataat 240

acagtagcaa ccctctattg tgtgcatcaa aggatagaga taaaagacac caaggaagct 300

ttagacaaga tagaggaaga gcaaaacaaa agtaagaaaa aagcacagca agcagcagct 360

gacacaggac acagcagtca ggtcagccaa aattacccta tagtgcagaa catccagggg 420

caaatggtac atcaggccat atcacctaga actttaaatg catgggtaaa agtagtagaa 480

gagaaggctt tcagcccaga agtaataccc atgttttcag cattatcaga aggagccacc 540

ccacaagatt taaacaccat gctaaacaca gtgggggggac atcaagcagc catgcaaatg 600

ttaaaagaga ccatcaatga ggaagctgca gaatgggata gagtacatcc agtgcatgca 660

gggcctattg caccaggcca gatgagagaa ccaaggggaa gtgacatagc aggaactact 720

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atttataaaa gatggataat cctgggatta ataaaaatag taagaatgta tagccctacc 840

agcattctgg acataagaca aggaccaaaa gaacctttta gagactatgt agaccggttc 900

tataaaactc taagagccga gcaagcttca caggaggtaa aaaattggat gacagaaacc 960

ttgttggtcc aaaatgcgaa cccagattgt aagactattt taaaagcatt gggaccagcg 1020

gctacactag aagaaatgat gacagcatgt cagggagtag gaggacccgg ccataaggca 1080

agagttttgg ctgaagcaat gagccaagta acaaatacag ctaccataat gatgcagaga 1140

ggcaatttta ggaaccaaag aaagatggtt aagtgtttca attgtggcaa agaagggcac 1200

acagccagaa attgcagggc ccctaggaaa aagggctgtt ggaaatgtgg aaaggaagga 1260

caccaaatga aagattgtac tgagagacag gctaatttct ttagggaaga tctggccttc 1320

ctacaaggga aggccaggga attttcttca gagcagacca gagccaacag ccccaccatt 1380

tcttcagagc agaccagagc caacagcccc accagaagag agcttcaggt ctggggtaga 1440

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cctcagatca ctctttggca acgacccctc gtcacaataa agataggggg gcaactaaag 1560

gaagctctat tagatacagg agcagatgat acagtattag aagaaatgag tttgccagga 1620

agatggaaac caaaaatgat agggggaatt ggaggtttta tcaaagtaag acagtatgat 1680

cagatactca tagaaatctg tggacataaa gctataggta cagtattagt aggacctaca 1740

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<210> 59

<211> 599

<212> PRT

<213> Artificial sequence

<220>

<223> Gag-PI

<400> 59

Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp
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Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys
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His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
35 40 45

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Phe Phe Arg Glu Asp Leu Ala Phe Leu Gln Gly Lys Ala Arg Glu Phe
435 440 445

Ser Ser Glu Gln Thr Arg Ala Asn Ser Pro Thr Ile Ser Ser Glu Gln
450 455 460

Thr Arg Ala Asn Ser Pro Thr Arg Arg Glu Leu Gln Val Trp Gly Arg
465 470 475 480

Asp Asn Asn Ser Pro Ser Glu Ala Gly Ala Asp Arg Gln Gly Thr Val
485 490 495

Ser Phe Asn Phe Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr
500 505 510

Ile Lys Ile Gly Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala
515 520 525

Asp Asp Thr Val Leu Glu Glu Met Ser Leu Pro Gly Arg Trp Lys Pro
530 535 540

Lys Met Ile Gly Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp
545 550 555 560

Gln Ile Leu Ile Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu
565 570 575

Val Gly Pro Thr Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln
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Ile Gly Cys Thr Leu Asn Phe
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ctgctgcag 9

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<212> DNA

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<223> DNA encoding gp120 signal peptide

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ctccttggga tgttgatgat ctgtagtgct 90

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<211> 129

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<213> Artificial sequence

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<223> DNA encoding gp41 transmembrane domain

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gtagtgaata gagttaggca gggatattca ccattatcgt ttcagaccca cctcccaatc 120

ccgagggga 129