

B67428PC-sequence listing
SEQUENCE LISTING

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 <120> Animal model for the evaluation of the efficacy of an HIV vaccine
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 <170> PatentIn version 3.5
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B67428PC-sequence listing

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B67428PC-sequence listing

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B67428PC-sequence listing

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 1 5

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B67428PC-sequence listing

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B67428PC-sequence listing

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B67428PC-sequence listing

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B67428PC-sequence listing

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B67428PC-sequence listing

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B67428PC-sequence listing

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1

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B67428PC-sequence listing

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B67428PC-sequence listing

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B67428PC-sequence listing

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B67428PC-sequence listing

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B67428PC-sequence listing

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Leu Asp Xaa Xaa Glu Asn Leu Trp Val Leu Asp Xaa Xaa Glu Asn Leu
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Trp Val

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<213> Human immunodeficiency virus

<400> 54

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 Ser
115 120 125

Leu Lys Cys Thr Asp Leu Lys Asn Asp Thr Asn Thr Asn Ser Ser Ser
130 135 140

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

B67428PC-sequence listing.

Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Phe Phe
165 170 175

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

Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
195 200 205

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

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

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

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

Arg Ser Val Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
275 280 285

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

Lys Arg Ile Arg Ile Gln Arg Gly Pro Gly Arg Ala Phe Val Thr Ile
305 310 315 320

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Asn Ile Ser Arg Ala
325 330 335

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

Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp
355 360 365

Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr
370 375 380

Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp
385 390 395 400

Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu
405 410 415

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

B67428PC-sequence listing

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

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

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

Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val
485 490 495

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

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

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

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

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

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

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

Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn
610 615 620

His Thr Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser
625 630 635 640

Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn
645 650 655

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

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

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

B67428PC-sequence listing

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

Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu
725 730 735

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

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

His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile Val Glu Leu
770 775 780

Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp Trp Asn Leu Leu
785 790 795 800

Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu Asn
805 810 815

Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu Val
820 825 830

Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile Pro Arg Arg Ile Arg
835 840 845

Gln Gly Leu Glu Arg Ile Leu Leu
850 855

<210> 55
<211> 511
<212> PRT
<213> Human immunodeficiency virus

<400> 55

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

B67428PC-sequence listing

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 Ser
 115 120 125
 Leu Lys Cys Thr Asp Leu Lys Asn Asp Thr Asn Thr Asn Ser Ser Ser
 130 135 140
 Gly Arg Met Ile Met Glu Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn
 145 150 155 160
 Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Phe Phe
 165 170 175
 Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp Thr Thr Ser Tyr Lys
 180 185 190
 Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
 195 200 205
 Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
 210 215 220
 Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
 225 230 235 240
 Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
 245 250 255
 Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
 260 265 270
 Arg Ser Val Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
 275 280 285
 Asn Thr Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
 290 295 300
 Lys Arg Ile Arg Ile Gln Arg Gly Pro Gly Arg Ala Phe Val Thr Ile
 305 310 315 320
 Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Asn Ile Ser Arg Ala
 325 330 335
 Lys Trp Asn Asn Thr Leu Lys Gln Ile Ala Ser Lys Leu Arg Glu Gln
 340 345 350

B67428PC-sequence listing

Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp
355 360 365

Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr
370 375 380

Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp
385 390 395 400

Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu
405 410 415

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

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

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

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

Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val
485 490 495

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

<210> 56
<211> 345
<212> PRT
<213> Human immunodeficiency virus

<400> 56

Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu Gly Ala Ala Gly
1 5 10 15

Ser Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val Gln Ala Arg Gln
20 25 30

Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile
35 40 45

Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln
50 55 60

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

B67428PC-sequence listing

Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala
 85 90 95
 Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp
 100 105 110
 Asn His Thr Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr
 115 120 125
 Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys
 130 135 140
 Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn
 145 150 155 160
 Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met
 165 170 175
 Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser
 180 185 190
 Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr
 195 200 205
 His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu
 210 215 220
 Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly
 225 230 235 240
 Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser
 245 250 255
 Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile Val Glu
 260 265 270
 Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp Trp Asn Leu
 275 280 285
 Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Val Ser Leu Leu
 290 295 300
 Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Val Ile Glu
 305 310 315 320
 Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile Pro Arg Arg Ile
 325 330 335
 Arg Gln Gly Leu Glu Arg Ile Leu Leu
 340 345

B67428PC-sequence listing

<210> 57
 <211> 842
 <212> PRT
 <213> Human immunodeficiency virus

<400> 57

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

Gly Ile Leu Phe Leu Gly Ile Leu Ile Ile Cys Ser Asn Ala Asp Lys
 20 25 30

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

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

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

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

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

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

Asn Cys Thr Asp Tyr Lys Gly Thr Asn Ser Thr Asn Asn Ala Thr Ser
 130 135 140

Thr Val Val Ser Pro Ala Glu Ile Lys Asn Cys Ser Phe Asn Ile Thr
 145 150 155 160

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

Leu Asp Val Leu Pro Leu Asn Gly Glu Gly Asn Asn Ser Ser Thr Glu
 180 185 190

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

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

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

Cys Lys Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Lys Pro Val

B67428PC-sequence listing

245

250

255

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

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

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

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

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

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

His Phe Lys Asn Gly Thr Ile Thr Phe Lys Pro Pro Asn Pro Gly Gly
355 360 365

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

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

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

Val Gly Lys Ala Ile Tyr Ala Pro Pro Ile Ala Gly Ser Ile Asn Cys
420 425 430

Ser Ser Asn Ile Thr Gly Met Ile Leu Thr Arg Asp Gly Gly Asn Asn
435 440 445

Thr His Asn Glu Thr 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 Gln Ile Glu Pro Leu
465 470 475 480

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

Arg Ala Val Gly Leu Gly Ala Val Phe Phe Gly Phe Leu Gly Ala Ala
500 505 510

Gly Ser Thr Met Gly Ala Ala Ser Ile Thr Leu Thr Val Gln Ala Arg

B67428PC-sequence listing

515

520

525

Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Ser 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 Arg Ala Arg Ile 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

Asn Val Pro Trp Asn Ser Ser Trp Ser Asn Lys Ser Trp Glu Glu Ile
595 600 605

Trp Asn Asn Met Thr Trp Met Glu Trp Glu Lys Glu Ile Gly Asn Tyr
610 615 620

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

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

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

Met Ile Ile Gly Gly Leu Ile Gly Leu Arg Ile Ala Phe Ala Val Leu
675 680 685

Ser Val Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln
690 695 700

Thr Leu Ile Pro Thr Ser Arg Gly Ala Asp Arg Pro Glu Gly Ile Glu
705 710 715 720

Glu Glu Gly Gly Glu Gln Asp Lys Asn Arg Ser Val Arg Leu Val Ser
725 730 735

Gly Phe Leu Ala Leu Ala Trp Asp Asp Leu Arg Asn Leu Cys Leu Phe
740 745 750

Ser Tyr Arg Gln Leu Arg Asn Leu Ile Leu Ile Val Thr Arg Ile Leu
755 760 765

Glu Arg Gly Leu Arg Gly Gly Trp Glu Ala Leu Lys Tyr Leu Trp Asn
770 775 780

Leu Val Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Ile Ser Leu
seite 25

B67428PC-sequence listing

785 790 795 800

Leu Asn Thr Thr Ala Ile Ala Val Ala Gly Gly Thr Asp Arg Ile Ile
805 810 815

Glu Ile Gly Gln Arg Ala Phe Arg Ala Leu Leu His Ile Pro Arg Arg
820 825 830

Ile Arg Gln Gly Leu Glu Arg Ala Leu Leu
835 840

<210> 58
<211> 497
<212> PRT
<213> Human immunodeficiency virus

<400> 58

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

Gly Ile Leu Phe Leu Gly Ile Leu Ile Ile Cys Ser Asn Ala Asp Lys
20 25 30

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

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

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

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

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

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

Asn Cys Thr Asp Tyr Lys Gly Thr Asn Ser Thr Asn Asn Ala Thr Ser
130 135 140

Thr Val Val Ser Pro Ala Glu Ile Lys Asn Cys Ser Phe Asn Ile Thr
145 150 155 160

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

Leu Asp Val Leu Pro Leu Asn Gly Glu Gly Asn Asn Ser Ser Thr Glu
180 185 190

B67428PC-sequence listing

Tyr Arg Leu Ile Asn Cys Asn Thr Ser Thr Ile Thr Gln Thr Cys Pro
 195 200 205
 Lys Val Thr Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly
 210 215 220
 Phe Ala Ile Leu Lys Cys Lys Asp Lys Arg Phe Asn Gly Thr Gly Pro
 225 230 235 240
 Cys Lys Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Lys Pro Val
 245 250 255
 Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Ile
 260 265 270
 Ile Ile Arg Ser Glu Asn Ile Thr Asp Asn Thr Lys Asn Ile Ile Val
 275 280 285
 Gln Leu Asn Glu Thr Val Gln Ile Asn Cys Thr Arg Pro Asn Asn Asn
 290 295 300
 Thr Arg Lys Ser Ile His Met Gly Pro Gly Lys Ala Phe Tyr Thr Thr
 305 310 315 320
 Gly Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile Ser Gly
 325 330 335
 Glu Lys Trp Asn Met Thr Leu Ser Arg Val Lys Glu Lys Leu Lys Glu
 340 345 350
 His Phe Lys Asn Gly Thr Ile Thr Phe Lys Pro Pro Asn Pro Gly Gly
 355 360 365
 Asp Pro Glu Ile Leu Thr His Met Phe Asn Cys Ala Gly Glu Phe Phe
 370 375 380
 Tyr Cys Asn Thr Thr Lys Leu Phe Asn Glu Thr Gly Glu Asn Gly Thr
 385 390 395 400
 Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Lys
 405 410 415
 Val Gly Lys Ala Ile Tyr Ala Pro Pro Ile Ala Gly Ser Ile Asn Cys
 420 425 430
 Ser Ser Asn Ile Thr Gly Met Ile Leu Thr Arg Asp Gly Gly Asn Asn
 435 440 445
 Thr His Asn Glu Thr Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn
 450 455 460

B67428PC-sequence listing

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

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

Arg

<210> 59
<211> 345
<212> PRT
<213> Human immunodeficiency virus

<400> 59

Ala Val Gly Leu Gly Ala Val Phe Phe Gly Phe Leu Gly Ala Ala Gly
1 5 10 15

Ser Thr Met Gly Ala Ala Ser Ile Thr Leu Thr Val Gln Ala Arg Gln
20 25 30

Leu Leu Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile
35 40 45

Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln
50 55 60

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

Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Asn
85 90 95

Val Pro Trp Asn Ser Ser Trp Ser Asn Lys Ser Trp Glu Glu Ile Trp
100 105 110

Asn Asn Met Thr Trp Met Glu Trp Glu Lys Glu Ile Gly Asn Tyr Ser
115 120 125

Asp Thr Ile Tyr Lys Leu Ile Glu Glu Ser Gln Thr Gln Gln Glu Lys
130 135 140

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

Trp Phe Asp Ile Thr Lys Trp Leu Trp Tyr Ile Lys Ile Phe Ile Met
165 170 175

Ile Ile Gly Gly Leu Ile Gly Leu Arg Ile Ala Phe Ala Val Leu Ser
180 185 190

B67428PC-sequence listing

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Val Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr
    195                200                205

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

Glu Gly Gly Glu Gln Asp Lys Asn Arg Ser Val Arg Leu Val Ser Gly
    225                230                235                240

Phe Leu Ala Leu Ala Trp Asp Asp Leu Arg Asn Leu Cys Leu Phe Ser
    245                250                255

Tyr Arg Gln Leu Arg Asn Leu Ile Leu Ile Val Thr Arg Ile Leu Glu
    260                265                270

Arg Gly Leu Arg Gly Gly Trp Glu Ala Leu Lys Tyr Leu Trp Asn Leu
    275                280                285

Val Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala Ile Ser Leu Leu
    290                295                300

Asn Thr Thr Ala Ile Ala Val Ala Gly Gly Thr Asp Arg Ile Ile Glu
    305                310                315                320

Ile Gly Gln Arg Ala Phe Arg Ala Leu Leu His Ile Pro Arg Arg Ile
    325                330                335

Arg Gln Gly Leu Glu Arg Ala Leu Leu
    340                345

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<210> 60
<211> 825
<212> PRT
<213> Human immunodeficiency virus

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<222> (18)..(18)
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B67428PC-sequence listing

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<222> (638)..(669)
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<222> (696)..(696)
<223> unknown

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<222> (774)..(774)
<223> unknown

<400> 60

Met Lys Ala Lys Gly Met Gln Arg Asn Tyr Gln His Leu Trp Arg Trp
1 5 10 15

B67428PC-sequence listing

Gly Xaa Met Leu Phe Trp Xaa Ile Ile Met Cys Lys Ala Ala Glu Asn
 20 25 30
 Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Arg Asp Ala Glu
 35 40 45
 Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Lys Glu Val
 50 55 60
 His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro
 65 70 75 80
 Gln Glu Ile Ala Leu Glu Asn Val Thr Glu Lys Phe Asp Met Trp Lys
 85 90 95
 Asn Asn Met Val Glu Gln Met Gln Thr Asp Ile Ile Ser Leu Trp Asp
 100 105 110
 Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu
 115 120 125
 Asn Cys Ala Glu Pro Asn Ser Thr Ser Ser Asn Asn Asn Ser Val Asn
 130 135 140
 Ser Asn Ser Ser Asp Ser Val Phe Glu Glu Met Lys Asn Cys Thr Phe
 145 150 155 160
 Asn Met Thr Thr Glu Leu Arg Asp Lys Arg Lys Thr Val His Ser Leu
 165 170 175
 Phe Tyr Lys Leu Asp Ile Val Ser Thr Gly Ser Asn Gly Ser Gly Gln
 180 185 190
 Tyr Arg Leu Ile Asn Cys Asn Thr Ser Ala Met Thr Gln Ala Cys Pro
 195 200 205
 Lys Val Thr Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly
 210 215 220
 Phe Ala Ile Leu Lys Cys Lys Asp Thr Asn Phe Thr Gly Thr Gly Pro
 225 230 235 240
 Cys Lys Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Lys Pro Val
 245 250 255
 Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Lys Glu Val
 260 265 270
 Met Xaa Arg Ser Glu Asn Ile Thr Asp Asn Gly Lys Xaa Ile Ile Val
 275 280 285

B67428PC-sequence listing

Gln Leu Thr Glu Pro Val Asn Ile Thr Cys Ile Arg Pro Gly Asn Asn
 290 295 300
 Thr Arg Thr Ser Ile Arg Ile Gly Pro Gly Gln Thr Phe Tyr Ala Thr
 305 310 315 320
 Xaa Asp Val Ile Gly Asp Ile Arg Lys Ala Tyr Cys Xaa Val Ser Arg
 325 330 335
 Ala Ala Trp Xaa Ser Thr Leu Gln Lys Ile Ser Thr Gln Leu Arg Lys
 340 345 350
 Tyr Phe Asn Asn Lys Thr Ile Xaa Phe Lys Asn Ser Ser Gly Gly Asp
 355 360 365
 Leu Glu Val Thr Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr
 370 375 380
 Cys Asn Thr Thr Asp Leu Phe Asn Ser Thr Trp Asp Gly Xaa Gly Thr
 385 390 395 400
 Xaa Thr Xaa Ile Thr Xaa Ala Asn Gly Thr Ile Thr Leu Pro Cys Arg
 405 410 415
 Ile Lys Gln Ile Ile Asn Met Trp Gln Arg Val Gly Gln Ala Met Tyr
 420 425 430
 Ala Pro Pro Ile Lys Gly Ser Ile Arg Cys Glu Ser Asn Ile Thr Gly
 435 440 445
 Leu Xaa Leu Thr Arg Asp Gly Gly Gly Gly Thr Asn Xaa Xaa Xaa Glu
 450 455 460
 Thr Phe Arg Pro Ile Gly Gly Asn Met Arg Asp Asn Trp Arg Ser Glu
 465 470 475 480
 Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Ile Gly Val Ala Pro
 485 490 495
 Thr Arg Ala Lys Arg Arg Val Val Glu Arg Glu Lys Arg Ala Ile Gly
 500 505 510
 Leu Gly Ala Ala Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met
 515 520 525
 Gly Ala Ala Ser Met Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser
 530 535 540
 Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Glu Ala Gln
 545 550 555 560

B67428PC-sequence listing

Gln His Leu Leu Lys₅₆₅ Leu Thr Val Trp Gly₅₇₀ Ile Lys Gln Leu Gln Ala₅₇₅

Arg Val Leu Ala₅₈₀ Val Glu Arg Tyr Leu₅₈₅ Lys Asp Gln Gln Leu₅₉₀ Leu Gly

Ile Trp Gly₅₉₅ Cys Ser Gly Lys Leu₆₀₀ Ile Cys Thr Thr Asn₆₀₅ Val Pro Trp

Asn Ser₆₁₀ Ser Trp Ser Asn Lys₆₁₅ Ser Gln Ser Glu Ile₆₂₀ Trp Asp Asn Met

Thr Trp Met Gln Trp Asp₆₃₀ Lys Glu Val Ile Asn₆₃₅ Tyr Thr Xaa Ile Ile₆₄₀

Tyr Asp Leu Ile Glu₆₄₅ Lys Ser Gln Asn Gln₆₅₀ Gln Glu Lys Asn Glu₆₅₅ Gln

Asp Leu Leu Ala₆₆₀ Leu Asp Lys Trp Ala₆₆₅ Ser Leu Trp Xaa Trp₆₇₀ Phe Asp

Ile Ser Asn Trp Leu Trp Tyr Ile₆₈₀ Lys Ile Phe Ile Ile₆₈₅ Ile Val Gly

Ser Leu₆₉₀ Ile Gly Leu Arg Ile₆₉₅ Xaa Phe Ala Val Leu₇₀₀ Tyr Ile Ile Asn

Arg Ala Arg Gln Gly Tyr₇₁₀ Ser Pro Leu Ser Leu₇₁₅ Gln Thr Leu Thr Pro₇₂₀

His Pro Glu Gly Pro₇₂₅ Asp Arg Pro Gly Arg₇₃₀ Ile Lys Glu Glu Gly₇₃₅ Gly

Glu Gln Gly Arg₇₄₀ Asp Arg Ser Ile Arg₇₄₅ Leu Val Ser Gly Phe₇₅₀ Leu Ala

Leu Ala Trp₇₅₅ Asp Asp Leu Arg Ser₇₆₀ Leu Cys Leu Phe Ser₇₆₅ Tyr His Arg

Leu Arg Asp Phe Ile Xaa Ile₇₇₅ Ala Ala Arg Thr Val₇₈₀ Glu Leu Leu Gly

Arg Ser Ser Leu Lys Gly₇₉₀ Leu Arg Leu Gly Trp₇₉₅ Glu Gly Leu Lys Tyr₈₀₀

Leu Gly Asn Leu Leu₈₀₅ Gly Tyr Trp Gly Gln₈₁₀ Glu Leu Lys Ser Ser₈₁₅ Ala

Ile Asn Leu Ile₈₂₀ Asp Thr Ile Ala Ile₈₂₅

B67428PC-sequence listing

<210> 61
 <211> 509
 <212> PRT
 <213> Human immunodeficiency virus

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B67428PC-sequence listing

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 <222> (461)..(463)
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<400> 61

Met Lys Ala Lys Gly Met Gln Arg Asn Tyr Gln His Leu Trp Arg Trp
 1 5 10 15

Gly Xaa Met Leu Phe Trp Xaa Ile Ile Met Cys Lys Ala Ala Glu Asn
 20 25 30

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

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

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

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

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

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

Asn Cys Ala Glu Pro Asn Ser Thr Ser Ser Asn Asn Asn Ser Val Asn
 130 135 140

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

Asn Met Thr Thr Glu Leu Arg Asp Lys Arg Lys Thr Val His Ser Leu
 165 170 175

Phe Tyr Lys Leu Asp Ile Val Ser Thr Gly Ser Asn Gly Ser Gly Gln
 180 185 190

Tyr Arg Leu Ile Asn Cys Asn Thr Ser Ala Met Thr Gln Ala Cys Pro
 195 200 205

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

B67428PC-sequence listing

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

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

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

Met Xaa Arg Ser Glu Asn Ile Thr Asp Asn Gly Lys Xaa Ile Ile Val
 275 280 285

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

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

Xaa Asp Val Ile Gly Asp Ile Arg Lys Ala Tyr Cys Xaa Val Ser Arg
 325 330 335

Ala Ala Trp Xaa Ser Thr Leu Gln Lys Ile Ser Thr Gln Leu Arg Lys
 340 345 350

Tyr Phe Asn Asn Lys Thr Ile Xaa Phe Lys Asn Ser Ser Gly Gly Asp
 355 360 365

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

Cys Asn Thr Thr Asp Leu Phe Asn Ser Thr Trp Asp Gly Xaa Gly Thr
 385 390 395 400

Xaa Thr Xaa Ile Thr Xaa Ala Asn Gly Thr Ile Thr Leu Pro Cys Arg
 405 410 415

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

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

Leu Xaa Leu Thr Arg Asp Gly Gly Gly Gly Thr Asn Xaa Xaa Xaa Glu
 450 455 460

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

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

B67428PC-sequence listing

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

<210> 62
<211> 352
<212> PRT
<213> Human immunodeficiency virus

<220>
<221> MISC_FEATURE
<222> (129)..(129)
<223> unknown

<220>
<221> MISC_FEATURE
<222> (160)..(160)
<223> unknown

<220>
<221> MISC_FEATURE
<222> (187)..(187)
<223> unknown

<220>
<221> MISC_FEATURE
<222> (265)..(265)
<223> unknown

<220>
<221> MISC_FEATURE
<222> (324)..(324)
<223> unknown

<220>
<221> MISC_FEATURE
<222> (347)..(347)
<223> unknown

<400> 62

Ala Ile Gly Leu Gly Ala Ala Phe Leu Gly Phe Leu Gly Ala Ala Gly
1 5 10 15

Ser Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val Gln Ala Arg Gln
20 25 30

Leu Leu Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile
35 40 45

Glu Ala Gln Gln His Leu Leu Lys Leu Thr Val Trp Gly Ile Lys Gln
50 55 60

Leu Gln Ala Arg Val Leu Ala Val Glu Arg Tyr Leu Lys Asp Gln Gln
65 70 75 80

Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Asn
85 90 95

Val Pro Trp Asn Ser Ser Trp Ser Asn Lys Ser Gln Ser Glu Ile Trp
100 105 110

B67428PC-sequence listing

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Asp Asn Met Thr Trp Met Gln Trp Asp Lys Glu Val Ile Asn Tyr Thr
    115          120          125

Xaa Ile Ile Tyr Asp Leu Ile Glu Lys Ser Gln Asn Gln Gln Glu Lys
    130          135          140

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

Trp Phe Asp Ile Ser Asn Trp Leu Trp Tyr Ile Lys Ile Phe Ile Ile
    165          170          175

Ile Val Gly Ser Leu Ile Gly Leu Arg Ile Xaa Phe Ala Val Leu Tyr
    180          185          190

Ile Ile Asn Arg Ala Arg Gln Gly Tyr Ser Pro Leu Ser Leu Gln Thr
    195          200          205

Leu Thr Pro His Pro Glu Gly Pro Asp Arg Pro Gly Arg Ile Lys Glu
    210          215          220

Glu Gly Gly Glu Gln Gly Arg Asp Arg Ser Ile Arg Leu Val Ser Gly
    225          230          235          240

Phe Leu Ala Leu Ala Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser
    245          250          255

Tyr His Arg Leu Arg Asp Phe Ile Xaa Ile Ala Ala Arg Thr Val Glu
    260          265          270

Leu Leu Gly Arg Ser Ser Leu Lys Gly Leu Arg Leu Gly Trp Glu Gly
    275          280          285

Leu Lys Tyr Leu Gly Asn Leu Leu Gly Tyr Trp Gly Gln Glu Leu Lys
    290          295          300

Ser Ser Ala Ile Asn Leu Ile Asp Thr Ile Ala Ile Ala Val Ala Arg
    305          310          315          320

Trp Thr Asp Xaa Val Ile Glu Ile Gly Gln Arg Leu Cys Arg Ala Ile
    325          330          335

Arg Asn Ile Pro Arg Arg Ile Arg Gln Gly Xaa Glu Lys Ala Leu Gln
    340          345          350

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<210> 63
<211> 878
<212> PRT
<213> Human immunodeficiency virus
<400> 63

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B67428PC-sequence listing

Met Arg Val Arg Gly Ile Pro Arg Asn Trp Gln Gln Trp Trp Ile Trp
 1 5 10 15
 Ile Ile Leu Gly Phe Trp Met Leu Leu Ile Cys Asn Val Gly Gly Asn
 20 25 30
 Ser Trp Val Thr Ile Tyr Tyr Gly Val Pro Val Trp Arg Glu Ala Lys
 35 40 45
 Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala His Glu Thr Glu Val
 50 55 60
 His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro
 65 70 75 80
 Gln Glu Ile Glu Leu Glu Asn Val Thr Glu Asn Phe Asn Met Trp Lys
 85 90 95
 Asn Asp Met Val Asp Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp
 100 105 110
 Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu
 115 120 125
 Asn Cys Thr Asn Ala Thr Arg Pro Val Thr Arg Thr Asn Thr Thr Ala
 130 135 140
 Thr Gly Thr Asn Asn Thr Val Thr Asn Cys Ser Gly Ser Ala Ser Thr
 145 150 155 160
 Asn Asn Thr Cys Met Glu Asn Ile Glu Gly Met Lys Asn Cys Ser Phe
 165 170 175
 Asn Ile Thr Thr Glu Leu Arg Asp Lys Lys Lys Lys Glu Tyr Ala Leu
 180 185 190
 Phe Tyr Arg Leu Asp Ile Val Pro Leu Asn Glu Thr Arg Asp Asn Ser
 195 200 205
 Ser Tyr Arg Leu Ile Asn Cys Asn Thr Ser Thr Ile Thr Gln Ala Cys
 210 215 220
 Pro Lys Val Ser Phe Asp Pro Ile Pro Ile His Tyr Cys Ala Pro Ala
 225 230 235 240
 Gly Tyr Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Ser Gly Thr Gly
 245 250 255
 Pro Cys Asn Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Met Pro
 260 265 270

B67428PC-sequence listing

Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Met
 275 280 285
 Val Ile Ile Arg Ser Asp Asn Met Thr Asn Ala Ala Thr Thr Ile Ile
 290 295 300
 Val His Leu Lys Asp Pro Val Glu Ile Val Cys Thr Arg Pro Asn Asn
 305 310 315 320
 Thr Thr Arg Arg Glu Val Gly Ile Gly Pro Gly Gln Thr Phe Tyr Thr
 325 330 335
 Thr Gly Gln Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile Thr
 340 345 350
 Gly Lys Glu Trp Asn Lys Thr Leu Arg Gln Val Gly Ala Glu Leu Glu
 355 360 365
 Lys His Phe Pro Asn Lys Thr Ile Gln Phe Lys Pro His Ser Gly Gly
 370 375 380
 Asp Leu Glu Ile Thr Thr His Ser Phe Thr Cys Ser Gly Glu Phe Phe
 385 390 395 400
 Tyr Cys Asn Thr Ser Lys Leu Phe Asn Ile Ser Met Ser Asn Leu Thr
 405 410 415
 Tyr Asn Asn Thr Asp Asn Thr Asp Asn Pro Thr Gln Ile Thr Leu Pro
 420 425 430
 Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Arg Ala
 435 440 445
 Ile Tyr Ala Pro Pro Ile Ala Gly Asn Ile Thr Cys Lys Ser Asn Ile
 450 455 460
 Thr Gly Leu Leu Leu Thr Trp Asp Gly Gly Ser Gly Glu Asn Asn Thr
 465 470 475 480
 Glu Thr Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser
 485 490 495
 Glu Leu Tyr Lys Tyr Lys Val Val Glu Ile Lys Pro Leu Gly Ile Ala
 500 505 510
 Pro Thr Glu Ala Lys Arg Arg Val Val Glu Arg Glu Lys Arg Ala Ile
 515 520 525
 Gly Ile Gly Ala Val Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr
 530 535 540

B67428PC-sequence listing

Met Gly Ala Ala Ser Ile Thr Leu Thr Val Gln Ala Arg Gln Leu Leu
 545 550 555 560
 Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Glu Ala
 565 570 575
 Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
 580 585 590
 Ala Arg Val Leu Ala Ile Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu
 595 600 605
 Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ser Val Pro
 610 615 620
 Trp Asn Ser Ser Trp Ser Asn Lys Thr Leu Gly Glu Ile Trp Asn Asn
 625 630 635 640
 Met Thr Trp Met Glu Trp Asp Lys Glu Ile Ser Asn Tyr Thr His Thr
 645 650 655
 Ile Tyr Gln Leu Leu Glu Glu Ser Gln Ile Gln Gln Glu Gln Asn Glu
 660 665 670
 Lys Glu Leu Leu Ala Leu Asp Ser Trp Lys Asn Leu Trp Asn Trp Phe
 675 680 685
 Asp Ile Ser Asn Trp Leu Trp Tyr Ile Lys Ile Phe Ile Met Ile Val
 690 695 700
 Gly Gly Leu Ile Gly Leu Arg Ile Val Phe Ala Val Leu Ser Ile Val
 705 710 715 720
 Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr Leu Thr
 725 730 735
 Pro Ser Pro Arg Glu Pro Asp Arg Leu Arg Gly Ile Glu Glu Glu Gly
 740 745 750
 Gly Glu Gln Asp Lys Gly Arg Ser Ile Arg Leu Val Gln Gly Phe Leu
 755 760 765
 Ala Leu Ala Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr His
 770 775 780
 Arg Leu Arg Asp Phe Ile Ser Ile Ala Ala Arg Val Val Glu Val Leu
 785 790 795 800
 Gly His Ser Ser Leu Arg Gly Leu Gln Arg Gly Trp Glu Ala Leu Lys
 805 810 815

B67428PC-sequence listing

Tyr Leu Lys Ser Leu Val Gln Tyr Trp Gly Leu Glu Leu Lys Lys Ser
820 825 830

Ala Val Ser Leu Leu Asp Thr Leu Ala Ile Ala Val Gly Glu Gly Thr
835 840 845

Asp Arg Ile Ile Glu Leu Ile Gln Gly Ile Cys Arg Ala Ile Arg Asn
850 855 860

Ile Pro Arg Arg Ile Arg Gln Gly Phe Glu Ala Ala Leu Leu
865 870 875

<210> 64
<211> 526
<212> PRT
<213> Human immunodeficiency virus

<400> 64

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

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

Ser Trp Val Thr Ile Tyr Tyr Gly Val Pro Val Trp Arg Glu Ala Lys
35 40 45

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

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

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

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

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

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

Thr Gly Thr Asn Asn Thr Val Thr Asn Cys Ser Gly Ser Ala Ser Thr
145 150 155 160

Asn Asn Thr Cys Met Glu Asn Ile Glu Gly Met Lys Asn Cys Ser Phe
165 170 175

B67428PC-sequence listing

Asn Ile Thr Thr Glu Leu Arg Asp Lys Lys Lys Lys Glu Tyr Ala Leu
 180 185 190
 Phe Tyr Arg Leu Asp Ile Val Pro Leu Asn Glu Thr Arg Asp Asn Ser
 195 200 205
 Ser Tyr Arg Leu Ile Asn Cys Asn Thr Ser Thr Ile Thr Gln Ala Cys
 210 215 220
 Pro Lys Val Ser Phe Asp Pro Ile Pro Ile His Tyr Cys Ala Pro Ala
 225 230 235 240
 Gly Tyr Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Ser Gly Thr Gly
 245 250 255
 Pro Cys Asn Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Met Pro
 260 265 270
 Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Met
 275 280 285
 Val Ile Ile Arg Ser Asp Asn Met Thr Asn Ala Ala Thr Thr Ile Ile
 290 295 300
 Val His Leu Lys Asp Pro Val Glu Ile Val Cys Thr Arg Pro Asn Asn
 305 310 315 320
 Thr Thr Arg Arg Glu Val Gly Ile Gly Pro Gly Gln Thr Phe Tyr Thr
 325 330 335
 Thr Gly Gln Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile Thr
 340 345 350
 Gly Lys Glu Trp Asn Lys Thr Leu Arg Gln Val Gly Ala Glu Leu Glu
 355 360 365
 Lys His Phe Pro Asn Lys Thr Ile Gln Phe Lys Pro His Ser Gly Gly
 370 375 380
 Asp Leu Glu Ile Thr Thr His Ser Phe Thr Cys Ser Gly Glu Phe Phe
 385 390 395 400
 Tyr Cys Asn Thr Ser Lys Leu Phe Asn Ile Ser Met Ser Asn Leu Thr
 405 410 415
 Tyr Asn Asn Thr Asp Asn Thr Asp Asn Pro Thr Gln Ile Thr Leu Pro
 420 425 430
 Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Arg Ala
 435 440 445

B67428PC-sequence listing

Ile Tyr Ala Pro Pro Ile Ala Gly Asn Ile Thr Cys Lys Ser Asn Ile
450 455 460

Thr Gly Leu Leu Leu Thr Trp Asp Gly Gly Ser Gly Glu Asn Asn Thr
465 470 475 480

Glu Thr Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser
485 490 495

Glu Leu Tyr Lys Tyr Lys Val Val Glu Ile Lys Pro Leu Gly Ile Ala
500 505 510

Pro Thr Glu Ala Lys Arg Arg Val Val Glu Arg Glu Lys Arg
515 520 525

<210> 65
<211> 352
<212> PRT
<213> Human immunodeficiency virus
<400> 65

Ala Ile Gly Ile Gly Ala Val Phe Leu Gly Phe Leu Gly Ala Ala Gly
1 5 10 15

Ser Thr Met Gly Ala Ala Ser Ile Thr Leu Thr Val Gln Ala Arg Gln
20 25 30

Leu Leu Ser Gly Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile
35 40 45

Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln
50 55 60

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

Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ser
85 90 95

Val Pro Trp Asn Ser Ser Trp Ser Asn Lys Thr Leu Gly Glu Ile Trp
100 105 110

Asn Asn Met Thr Trp Met Glu Trp Asp Lys Glu Ile Ser Asn Tyr Thr
115 120 125

His Thr Ile Tyr Gln Leu Leu Glu Glu Ser Gln Ile Gln Gln Glu Gln
130 135 140

Asn Glu Lys Glu Leu Leu Ala Leu Asp Ser Trp Lys Asn Leu Trp Asn
145 150 155 160

Trp Phe Asp Ile Ser Asn Trp Leu Trp Tyr Ile Lys Ile Phe Ile Met
Seite 44

B67428PC-sequence listing

165

170

175

Ile Val Gly Gly Leu Ile Gly Leu Arg Ile Val Phe Ala Val Leu Ser
180 185 190

Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr
195 200 205

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

Glu Gly Gly Glu Gln Asp Lys Gly Arg Ser Ile Arg Leu Val Gln Gly
225 230 235 240

Phe Leu Ala Leu Ala Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser
245 250 255

Tyr His Arg Leu Arg Asp Phe Ile Ser Ile Ala Ala Arg Val Val Glu
260 265 270

Val Leu Gly His Ser Ser Leu Arg Gly Leu Gln Arg Gly Trp Glu Ala
275 280 285

Leu Lys Tyr Leu Lys Ser Leu Val Gln Tyr Trp Gly Leu Glu Leu Lys
290 295 300

Lys Ser Ala Val Ser Leu Leu Asp Thr Leu Ala Ile Ala Val Gly Glu
305 310 315 320

Gly Thr Asp Arg Ile Ile Glu Leu Ile Gln Gly Ile Cys Arg Ala Ile
325 330 335

Arg Asn Ile Pro Arg Arg Ile Arg Gln Gly Phe Glu Ala Ala Leu Leu
340 345 350

<210> 66
<211> 58
<212> DNA
<213> Artificial Sequence

<220>
<223> gp41(160) Reverse for subtype A (rare variant)

<220>
<221> misc_feature
<222> (48)..(48)
<223> n is a, c, g, or t

<400> 66
atagcggccg cctagtgggtg gtgatgggtg ttagtagcaaag cyctttcngc gccctgtc

58

<210> 67
<211> 58
<212> DNA

B67428PC-sequence listing

<213> Artificial Sequence

<220>
<223> gp41(160) Reverse for C subtype

<400> 67
atagcggccg cctagtgggtg gtgatgggtg tgtwgcaaag ctgcttcaaa gccctgtc 58

<210> 68
<211> 58
<212> DNA
<213> Artificial Sequence

<220>
<223> gp41(160) Reverse for G subtype

<220>
<221> misc_feature
<222> (48)..(48)
<223> n is a, c, g, or t

<400> 68
atagcggccg cctagtgggtg gtgatgggtg tgtagcaaag cyctttcnaa gccttgtc 58

<210> 69
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward gp120 Const1 for B subtype

<400> 69
aattctagac gctrcagaam aattgtgggt cac 33

<210> 70
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward gp120 Const1 for C subtype

<400> 70
aattctagac gtrrtgggra acttgtgggt cac 33

<210> 71
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward gp120 Const1 for G subtype

<400> 71
aattctagac gcctcarata acttgtgggt cacag 35

<210> 72
<211> 5
<212> PRT
<213> Artificial Sequence

B67428PC-sequence listing

<220>
<223> minimal translation of V1 forward for subtypes A,G B,C,F1,H

<400> 72

Leu Cys Val Thr Leu
1 5

<210> 73
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> minimal translation of V2 forward for all subtypes

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Y or F

<400> 73

Asn Cys Ser Xaa
1

<210> 74
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> minimal translation of V3 forward for A, B, G subtypes

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> K or Q or E

<400> 74

Xaa Ile Asn Cys
1

<210> 75
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> minimal translation of V3 forward for subtype D

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> T or P or A

<400> 75

Xaa Ile Asn Cys
1

B67428PC-sequence listing

<210> 76
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> minimal translation of V4 forward for all subtypes
 <400> 76

Glu Phe Phe Tyr Cys
 1 5

<210> 77
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> minimal translation of V5 forward
 <400> 77

Thr Arg Asp Gly
 1

<210> 78
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> minimal translation of Forward gp120 Const1 for A subtype

<220>
 <221> MISC_FEATURE
 <222> (3)..(3)
 <223> T or A

<220>
 <221> MISC_FEATURE
 <222> (4)..(4)
 <223> T or A

<400> 78

Leu Asp Xaa Xaa Glu Asn Leu Trp Val Leu Asp
 1 5 10