

206108_0033_30wo_606194_seqlisting
SEQUENCE LISTING

<110> WEINER, David
MUTHUMANI, Karupiah
Flingai, Seleeke
SARDESAI, Niranjan
Elliott, Sarah
Yan, Jian
Patel, Ami

<120> DNA ANTIBODY CONSTRUCTS AND METHOD OF USING SAME

<130> 206108-0033-30-WO.606194

<150> US 62/311,316
<151> 2016-03-21

<150> US 62/396,750
<151> 2016-09-19

<150> US 62/417,093
<151> 2016-11-03

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<151> 2016-08-17

<150> US 62/429,454
<151> 2016-12-02

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<151> 2016-12-02

<160> 171

<170> PatentIn version 3.5

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

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

<400> 1

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Arg Gly Arg Lys
465 470 475 480

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

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

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

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

Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Asn Asn Lys Leu Ala
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545 206108_0033_30wo_606194_seqlisting 550 555 560

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

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

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

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

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

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser
645 650 655

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln
660 665 670

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

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

Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu
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Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
725 730 735

Gly Glu

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

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

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

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

Gln Pro Gly Ser Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asp
50 55 60

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

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

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

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

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

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

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

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

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

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

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

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
245 250 255

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu

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260
 Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
 275 280 285
 Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 290 295 300
 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 305 310 315 320
 Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 325 330 335
 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
 340 345 350
 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 355 360 365
 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
 370 375 380
 Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 385 390 395 400
 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
 405 410 415
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 420 425 430
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 435 440 445
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 450 455 460
 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
 465 470 475 480
 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 485 490 495
 Leu Ser Leu Ser Pro Gly Lys Arg Gly Arg Lys Arg Arg Ser Gly Ser
 500 505 510

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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 ccagggtcaa ccggagatgg ggctcaggtc cagctggtcc agagcggcgg acagatgaag 120
 aaacccggcg agagcatgag gatctcctgc agagcatctg gatacgagtt catcgactgt 180
 accctgaact ggattaggct ggctcctgga aagagaccag agtggatggg gtggctgaaa 240
 ccacgagggg gagcagtga ttacgcccgg cccctgcagg gacgagtga catgaccagg 300
 gacgtgtaca gcgataccgc cttcctggag ctgcgggtccc tgacagtgga cgatactgct 360
 gtctacttct gcacacgcgg aaagaactgt gactataatt gggattttga acactggggc 420
 cggggaacac ccgtgatcgt cagctcccc agtactaagg gaccttcagt gtttccactg 480
 gccccctcta gtaaattccac ctctggaggg acagccgctc tgggatgcct ggtgaaagat 540
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 acctttcctg cagtcctgca gtcaagcggg ctgtacagtc tgtcctctgt ggtcactgtg 660
 cctagttcaa gcctggggcac tcagacctat atttgtaacg tgaatcataa gccatccaat 720
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 <211> 756
 <212> DNA
 <213> Artificial Sequence

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

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 ccaggaagta ccgggggatgg ggctcaggtc cagattgtgc tgactcagtc ccctgggacc 120
 ctgtctctga gtccaggcga gacagctatc atttcatgcc gaactagcca gtacggcagc 180
 ctggcttggg atcagcagcg accaggacag gcaccacgac tggatcatcta ctcaggcagc 240
 acaagggccg ctggcatccc cgacagggtc tccggcagca ggtggggggc tgattacaac 300
 ctgactatct ctaatctgga gagtggggac tttggcgtgt actattgcca gcagtatgag 360
 ttcttcggcc agggaaactaa ggtgcagggtg gacatcaaaa gaaccgtggc agcccatcc 420

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gtcttcattt ttcccccttc tgatgagcag ctgaagtcag gcaccgccag cgtggtctgt	480
ctgctgaaca atttctaccc ccgggaagcc aagggtgcagt ggaaagtgga caacgctctg	540
cagagtggaa attcacagga gagcgtgacc gaacaggact ccaaggattc tacatatagt	600
ctgagcagca ccctgaccct gagtaaagca gattacgaga agcacaaagt gtatgcctgt	660
gaagtcacac atcagggcct gaggagcccc gtgactaaaa gtttcaaccg aggagagtgc	720
tacccttatg atgtgcccga ctacgcctaa ctcgag	756

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

<220>
 <223> VRC01 IgG

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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cctggcagct ccgtcaaaat ttcttgacaga gcaagtggct acaacttccg ggactatagc 180
atccactggg tgctggctgat tcctgataag ggattttgagt ggatcggctg gatcaagcca 240
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ctgtctcagg acccagacga tcccgaattgg ggggtggcct acatggagtt cagtggactg 360
actcccgag acaccgccga atatttttgc gtgcggagag gctcctgcga ctactgtggg 420
gatttcccat ggcagtattg gtgtcagggg actgtggtcg tgggtctctag tgcataaacc 480
aagggcccca gcgtgtttcc tctggcccca tcaagcaaaa gtacatcagg aggaactgca 540
gctctgggat gtctggtgaa ggattacttc cccgagcctg tgaccgtcag ctggaactcc 600
ggagcactga cctccggagt gcacacattt cccgctgtcc tgcagtcctc tgggctgtac 660
tctctgagtt cagtgggtcac agtccttagc tctctcttgg gcacccagac atatatctgc 720
aacgtcaatc ataagccaag taatactaaa gtggacaaga aagtcgaacc caaatcatgt 780
taccctatg acgtgcctga ttatgcttga taactcgag 819

<210> 7
<211> 753
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<223> Optimized Nucleic Acid Sequence Encoding IgG Light Chain

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tactgagcc caggagagac cgcaacactg ttctgcaagg cctcccaggg cgggaacgct      180
atgacatggt accagaaacg gagaggacag gtgccccgac tgctgatcta tgacacttca      240
aggcgagcaa gcggagtgcc tgatcgattt gtcggcagcg gctctgggac agacttcttt      300
ctgactatta ataagctgga cagagaggat ttgctgtgtg actattgcca gcagtttgaa      360
ttctttggac tgggcagcga gctggaagtg cacaggaccg tcgccgctcc aagtgtgttc      420
atTTTTCCCC ctagcgatga gcagctgaaa tccgggacag cctctgtggt ctgtctgctg      480
aacaatttct acccccgcga agcaaagggtg cagtggaaag tcgacaacgc cctgcagagt      540
ggcaattcac aggagagcgt gaccgaacag gactccaagg attctacata tagtctgagc      600
tccactctga ccctgtctaa agctgattac gagaagcaca aagtgtatgc atgcgaagtc      660
actcatcagg gcctgtctag tcctgtgacc aagagcttta accgagggga gtgttaccca      720
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<211> 18
<212> PRT
<213> Artificial Sequence

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<220>
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His Ser

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

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

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<400> 9
Gln Val Gln Leu Val Gln Ser Gly Gly Gln Met Lys Lys Pro Gly Glu
1           5           10           15

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

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

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

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

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

Thr Arg Gly Lys Asn Cys Asp Tyr Asn Trp Asp Phe Glu His Trp Gly
100 105 110

Arg Gly Thr Pro Val Ile Val Ser Ser Pro Ser Thr Lys Gly
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<210> 10

<211> 98

<212> PRT

<213> Artificial Sequence

<220>

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

<400> 10

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

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

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

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

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

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

Ser Cys

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

<220>
 <223> Hinge Region of VRC01 IgG

<400> 11

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

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

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

<400> 12

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

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

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

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

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

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

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

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

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

<400> 13

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

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

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

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

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

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

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

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

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

<400> 14

Arg Gly Arg Lys Arg Arg Ser
1 5

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

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

<400> 15

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

Glu Glu Asn Pro Gly Pro
20

<210> 16
<211> 104
<212> PRT

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<213> Artificial Sequence

<220>

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

<400> 16

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

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

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

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

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

Lys Val Gln Val Asp Ile Lys Arg
100

<210> 17

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

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

<400> 17

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

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

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

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

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

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

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

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

<220>
<223> Human IgG Heavy Chain Signal Peptide of HIV-1 Env-PG9 Ig
<400> 18

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

Thr His Ala

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

<220>
<223> Variable Heavy Region of HIV-1 Env-PG9 Ig
<400> 19

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

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

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

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

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

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

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

206108_0033_30wo_606194_seqlisting

100 105 110

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

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

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

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

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

<400> 20

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

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

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

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

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

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

Arg Val

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

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

<400> 21

206108_0033_30wo_606194_seqlisting

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

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

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

<400> 22

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

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

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

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

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

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

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

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

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

<400> 23

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

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

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

206108_0033_30wo_606194_seqlisting

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

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

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

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

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

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

<400> 24

Arg Gly Arg Lys Arg Arg Ser
1 5

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

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

<400> 25

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

Glu Glu Asn Pro Gly Pro
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<210> 26
<211> 20
<212> PRT
<213> Artificial Sequence

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

<400> 26

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

206108_0033_30wo_606194_seqlisting

Gly Ser Asn Ser
20

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

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

<400> 27

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

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

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

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

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

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

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

<210> 28
<211> 106
<212> PRT
<213> Artificial Sequence

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

<400> 28

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

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

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

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

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

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

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

<210> 29

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

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

<400> 29

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

Thr His Ala

<210> 30

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

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

<400> 30

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

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

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

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

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

206108_0033_30wo_606194_seqlisting

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

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

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

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

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

<400> 31

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

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

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

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

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

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

Lys Val

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

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

<400> 32

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
Page 24

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1 5 10 15

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

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

<400> 33

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

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

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

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

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

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

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

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

<220>
 <223> Constant Heavy Region 3 (CH3) of HIV-1 Env-4E10 Ig

<400> 34

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

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

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

206108_0033_30wo_606194_seqlisting

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

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

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

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

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

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

<400> 35

Arg Gly Arg Lys Arg Arg Ser
1 5

<210> 36
<211> 22
<212> PRT
<213> Artificial Sequence

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

<400> 36

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

Glu Glu Asn Pro Gly Pro
20

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

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

<400> 37

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

Gly Ala Tyr Gly

20

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

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

<400> 38

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

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

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

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

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

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

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

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

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

<400> 39

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

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

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

206108_0033_30wo_606194_seqlisting
 Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
 50 55 60

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

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

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

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

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

<400> 40
 ggatccgccca ccatggactg gacatggatt ctgtttctgg tgcgccccgc tacaagagtg 60
 cattccgaag tgcagctggt cgagagtgga gggggactgg tgcagcccgg cggatctctg 120
 cgactgagtt gcgccgcttc aggccttcacc ttacagact acaccatgga ttgggtgaga 180
 caggcacctg gcaagggact ggagtgggtg gctgatgtca acccaaatag tgggggtca 240
 atctacaacc agagggttcaa gggcaggttc accctgagcg tggacaggtc caaaaacact 300
 ctgtatctgc agatgaattc tctgcgggct gaagataccg cagtctacta ttgcgccccg 360
 aatctgggcc caagcttcta ctttgactat tgggggcagg gcacactggt gactgtcagc 420
 tccgcttcta caaagggacc aagcgtgttc cactggcac cctctagtaa atccacctct 480
 ggagggacag cagccctggg ctgtctggtg aaagactatt tccccgagcc tgtgactgtc 540
 agctggaact ccggagcact gactagcgga gtgcacacct ttccagccgt cctgcagtca 600
 agcggcctgt actccctgtc ctctgtggtc acagtgccta gttcaagcct gggaactcag 660
 acctatattt gtaatgtgaa ccataaacca agcaatacaa aggtggacaa gaaggtggaa 720
 ccaaaatcct gctgataact cgag 744

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

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

<400> 41

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
 Page 28

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```

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

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

206108_0033_30wo_606194_seqlisting

<220>

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

<400> 42

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ggatccgccca ccatggattg gacttggatt ctgttcctgg tcgccgccgc taccgcgctg      60
cattccgata ttcagatgac tcagagcccc tcctcactgt cagccagcgt gggcgaccga      120
gtcaccatca catgcaaagc ttctcaggat gtgagtattg gggtcgcatg gtaccagcag      180
aagccaggca aagcacccaa gctgctgac tattccgcct cttacaggta tacaggagt      240
cccagcagat tcagtggctc aggaagcggg actgacttta ctctgaccat cagctccctg      300
cagcctgagg atttcgctac ctactattgc cagcagtact atatctaccc atataccttt      360
ggccagggaa caaaagtgga gatcaagcgg accgtggccg ctccctccgt cttcatTTTT      420
cccccttctg acgaacagct gaagagcggg acagcaagcg tggctctgtc gctgaacaat      480
ttctaccctc gcgaggccaa agtgcagtgg aaggctgata acgctctgca gtccgggaat      540
tctcaggaga gtgtgactga acaggactca aaagatagca cctattccct gtctagtaca      600
ctgactctga gcaaggcaga ctacgaaaag cacaaagtgt atgcctgtga ggtcacccac      660
caggggctgt caagtcccgt caccaagtcc ttcaatagag gcgaatgctg ataactcgag      720

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<210> 43

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

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

<400> 43

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys Ser Phe Asn Arg Gly Glu Cys
225 230

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

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

<400> 44
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actcacgctc aggcacatct ggtcgaatct ggaggaggag tggccagcc tggccgatcc 120
ctgcgactgt cttgcgcagc tagcgccttc aacttcagca caaacgcaat gcactgggtg 180
cgacaggcac caggcaaggg actggagtgg gtcgctgtga tctcatagca cggaagccat 240
aagtactatg cagattctgt gaaaggccgg ttcaccattt ccagggacaa ttctaagaac 300
accctgtatc tgcagatgaa tagcctgcgc gcagccgata ccgcagtgtg ctattgcgca 360
actgtcggcg tgctgacctg gccagtgaac gccgaatact ttcaccattg gggacagggc 420
agtctggtct cagtgcgtc cgcaagtact aaggggacat cagtgttccc actggcacc 480
tctagtaaat ctactagtgg cgggaccgct gcactgggat gtctggtgaa ggactatttc 540

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720
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780
gcaccagagc tgcctgggagg accaagcgtg ttccctgttc cacccaagcc taagaacaca
840
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ccaatcagga aaaccattag caaggctaaa ggcagacctg gggaaccaca ggtgtacaca
1140
ctgcccctcaa gtcgcgaacga gctgaaccaag aatcaggtct ccttgacatg tctgtgtgaaa
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gcagatagtt caccgttcaa agccggagt gagaactaca caccatcaaa gcagagcaat
2100
aaacaaatac cagccacgtc ctatctgtcc ctgaacccctg agcagtggaa gttctcacaaa
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2241

<210> 45
<211> 739
<212> PRT

<213> Artificial Sequence

<220>

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

<400> 45

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

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

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

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

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

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

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

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

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

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

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

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

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

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

206108-0033-30WO-606194-seq1isting
Ile Cys Asn Val Asn His 230
Lys Pro Ser Asn Thr Lys Val Asp Lys 240

Val Glu Pro Lys Ser Cys Asp Lys Thr His 245
Lys Thr Cys Pro Pro Cys Pro 250
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys 260
265
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val 275
280
285

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

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu 305
310
315
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His 325
330
335

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys 340
345
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln 355
360
365

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu 370
375
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro 385
390
395
400

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn 405
410
415
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu 420
425
430
435

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val 440
445
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln 450
455
460

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

206108_0033_30wo_606194_seqlisting

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

206108_0033_30wo_606194_seqlisting

Glu Cys Ser

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

<220>
 <223> IgG Heavy Chain

<400> 46

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

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

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

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

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

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

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

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

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

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

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

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

206108_0033_30wo_606194_seqlisting

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

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

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

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

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
260 265

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

<220>
<223> IgG Light Chain

<400> 47

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

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

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

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

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

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

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

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

206108_0033_30wo_606194_seqlisting

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

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

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

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

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

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

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

Asp Tyr Ala

<210> 48

<211> 256

<212> PRT

<213> Artificial Sequence

<220>

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

<400> 48

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

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

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

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

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

Val Asn Tyr Ala Arg Pro Leu Gln Gly Arg Val Thr Met Thr Arg Asp
Page 38

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85 90 95

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

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

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

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

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

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

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

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

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

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

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

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

<400> 49

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

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

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

206108_0033_30wo_606194_seqlisting

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

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

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

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

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

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

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

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

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

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

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

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

Pro Asp Tyr Ala

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

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

<400> 50

206108_0033_30WO_606194_seq11.sting
 60 ggatccgcca ccatggccaag acccctgtgc tgcctgctgc aaccctggcc
 120 ggagcccttg cacagagcgc cctgacccaag ccgcgaagcg tctccggctc accagggcag
 180 agcatcacta ttagttgcaa cgggactagc aacgacgttg gaggtctatga gagtgtcagc
 240 tggtaaccag agcatcccg aaaagcacc aaagtgttca tctacgagt cagtaaaaag
 300 ccaagtgggg tctcaaatag gtctcaggg agtaaatctg ggaatatagc atctctgacc
 360 atctccggac tgggcgcaga agatgaagc gactactatt gcaaaagcct gacctcaacc
 420 agacggcgag tcttgggac aggcaccaag ctgacagtcg tgacagtcgc tgcctccctc
 480 gtcttcattt tccaccctc agatgagcag ctgaatctg gcactgcatc tgtgtctgc
 540 ctgctgaaca acttctacc acgagagcc aggttcagc gaaagtga taacgcactg
 600 cagttccgca atagtcaagg aagcgttgat gagcaggat ccaaggacag tactatagc
 660 ctgtccagta cactgacct gtccaagct gactaagct aacataaggt gtatgcatgt
 720 gaagtgaac accaaggact gaggccaaca gtcactaagt ctttaacag gggagagtgc
 780 ggcgggggag gattctggag cggcggctct ggagggggag gctcaggggg cggagggaagc
 840 ggcgggaggg ggtccggagg aggagcagt cagagactgg tcgaaagcgg gggaggagtg
 900 gtgcagccctg ggtctccact gactgtca tgcgttgcca gtgctttga ttttcaaga
 960 cagggaatgc attgggtcag gcaggcacc ggacagggcc tggaatgggt cgccttcatt
 1020 aagtaacgag gaagcgagaa gtaccatgcc gactcagtgt gggaaggt gagcatctca
 1080 agggacaact caaaggacac cctgtacctg cagatgaata gcctgagagt ggaagatacc
 1140 gtaacttatt tctgcgtgcg agagccgga gggccagatt accggaacgg gtacaattac
 1200 tatgatttct acgacggcta ctacaattac cattatatg atgtcttggg caaaggaaact
 1260 aacgtcaccc tgaactccgc aagtaataag ggaccttcg tgttccctc ggctccagt
 1320 tccaagaata catccggagc aacagccgct ctgggatgtc tggtaagga ctattttccc
 1380 gagcccgta ctgtctctcg gaacagcggg gctctgacaa gcggggtgca cactttcct
 1440 gccgtctgc agttccagttg gctgtacagt ctgtctagtg tgcgtcactgt gccaaagctca
 1500 agtctggga ccagacata cattgtaat gtgaacata aacctcaaa caccaagtg
 1536 gacaagaaag tggaaacctaa aagctgataa ctcgag

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

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

<400> 51

206108_0033_30wo_606194_seqlisting

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

206108_0033_30wo_606194_seqlisting

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Asp Lys Lys Val Glu Pro Lys Ser
500

206108_0033_30wo_606194_seqlisting

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

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

<400> 52
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gagcgcgcaa ctctgtcctg cagagcaagc cagtccgtcg ggaacaacaa gctggcatgg      180
taccagcagc gcccaggaca ggcacctcag ctgctgatct acggagcaag ctccccggcct      240
agcggagtcg ctgatatgatt ctccggaagc ggctccggga ccgatttcac tctgaccatc      300
tccaggctgg aacctgagga ttttgccgtg tattactgtc agcagtacgg gcagagcctg      360
tcaactttcg gccagggaac taaagtcgaa aagagaaccg tggccgcacc aagcgtcttt      420
atTTTTcccc ctgacgatga acagctgaaa tccgggactg cttccgtggg ctgcctgctg      480
aataacttct atccaagaga ggcaaagggt cagtggaaag tggacaacgc cctgcagagc      540
ggaaactcac aggaatctgt gacagagcag gactccaagg atagcacata cagtctgtcc      600
tcaactctga ccctgtccaa agctgactat gagaagcata aagtctacgc atgtgaggtg      660
accaccagg gactgaggtc ccccgctact aagtccttca atagaggcga gtgcggggggc      720
gggggcagtg gcggaggggg aagtgggggc ggagggagtg gcggcgccgg gagtggcggc      780
ggcggctcag ggggcggcgg ctcccaggtc cagctggtcc agagcggagc cgagggtcaag      840
agaccaggct cttcagtcac cgtgagctgc aaagccagcg gaggtctcct tagcacttac      900
gccctgtcat ggggtcggca ggccccaggc cgaggcctgg agtggatggg cggcgtgatc      960
cccctgctga ccattactaa ctatgccctt agatttggag gccggatcac catcacagct     1020
gacagatcca catccacagc ttacctggag ctgaacagtc tgaggccccga ggacactgca     1080
gtctactact gtgcacgaga aggcaccact ggatgggggt ggctggggaa gcccatcggg     1140
gcttttgcac attggggcgg agggacactg gtgactgtga gctctgccag cactaaaggg     1200
cccagtgtct tccctctggc cccaagttcc aagagtacat cagggggcac cgccgcactg     1260
gggtgtcttg tgaaggatta cttcccagag cccgtgacag tcagttggaa cagcggcgct     1320
ctgaccagtg ggggtcacac tttcccagcc gtgctgcaga gttcagggtg gtactccctg     1380
tcctcagtg tgactgtgcc ctcaagcagt ctggggactc agacttacat ttgtaatgtg     1440
aaccataaac cctcaaatac taaagtggac aaaaaagtg aaccaaagag ctgataactc     1500
gag                                                                1503

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206108_0033_30wo_606194_seqlisting

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

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

<400> 53

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

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

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

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

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

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

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

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

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

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

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

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

206108_0033_30wo_606194_seqlisting

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 54

<211> 1446

<212> DNA

<213> Artificial Sequence

<220>

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

<400> 54

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ggatccgccca ccatggattg gacatggatt ctgttcctgg tcgccgccgc aactagagtg      60
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cgaatctcat gccgggctag cgggtacgaa ttcacgact gtaccctgaa ctggattaga      180
ctggcacctg ggaagaggcc agagtggatg ggatggctga aacctagagg cggggcagtg      240
aattacgccca gaccactgca gggcaggggc actatgaccc gcgacgtgta ttctgatacc      300
gcattccttg agctgcgaag tctgacagtc gacgatactg cctgtgactt ctgcacacgg      360
ggcaagaact gtgactataa ttgggatttt gaacactggg gcagggggac acctgtcatt      420
gtgagctccc caagtactaa gggaccctca gtgtttcccc tggccccttc tagtaaaagt      480
acctcaggag gcacagccgc tctgggatgc ctggtgaagg attacttccc tgagccagtc      540
accgtgagtt ggaactcagg cggcctgaca agcgggggtcc atacttttcc agctgtgctg      600
cagtcaagcg ggctgtactc cctgtcctct gtggtcacag tgcccagttc aagcctggga      660
acacagactt atatctgtaa cgtcaatcac aagcctagca atactaaagt ggacaagaaa      720
gccgagccta agagctgcga accaaagtcc tgtgataaaa ccatacatg ccctccctgt      780
ccagctcctg aactgctggg cggcccatcc gtgttcctgt ttccacccaa gcccgaagac      840
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gaccccgaa tcaagtttaa ctggtacgtg gatggcgtcg aagtgcataa tgccaagaca      960
aaaccccggg aggaacagta caactctacc tatagagtcg tgagtgtcct gacagtgtctg     1020
caccaggact ggctgaacgg gaaggagtat aagtgcaaag tgtctaataa ggccctgccca     1080
gctcccatcg agaaaacaat ttccaaggca aaaggccagc caagggaacc ccaggtgtac     1140
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aaaggattct atccaagcga tatcgccgtg gagtgggaat ccaatggcca gcccgagaac     1260
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ctcgag	1446

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

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

<400> 55

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

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

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

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

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

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

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

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

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

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

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

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe

180 185 190

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

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

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

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

<210> 56

<211> 708

<212> DNA

<213> Artificial Sequence

<220>

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

<400> 56

ggatccgccca ccatggattg gacttggatt ctgttcctgg tggcagccgc taccagagtc	60
cattccgaaa ttgtgctgac ccagtctccc ggaacactgt ctctgagtcc tggcgagaca	120
gccatcattt cctgtaggac ttctcagtac gggagtctgg catggtatca gcagcgacca	180
ggacaggctc ctcgactggg catctactca ggaagcactc gggcagccgg cattcccgac	240
cgattctccg ggtctcgggtg gggacctgat tacaacctga ccattctaaa tctggaaagc	300
ggagactttg gcgtgtacta ttgccagcag tatgagttct ttgggcaggg aaccaaggtc	360
caggtggaca tcaaacgcac agtcgctgca ccaagcgtgt tcattctttcc accctcagat	420
gaacagctga agtccggcac cgctctgtg gtgtgcctgc tgaacaattt ctacccccgg	480
gaggcaaagg tccagtggaa agtggacaac gccctgcagt ctggcaatag tcaggagtca	540
gtgactgaac aggacagcaa ggattccacc tattctctgt cctctactct gaccctgagc	600
aaagctgatt acgagaagca caaagtgtat gcatgtgagg tcaccaccca gggactgcgg	660
tcacccgtca ccaagagctt caatcgcgga gagtgttgat aactcgag	708

<210> 57

<211> 228

<212> PRT

<213> Artificial Sequence

<220>

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

<400> 57

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Arg Gly Glu Cys
225

<210> 58

<211> 744

<212> DNA

<213> Artificial Sequence

<220>

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

206108_0033_30wo_606194_seqlisting

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<400> 58
ggatccgccca ccatggattg gacatggagg attctgtttc tggtcgccgc cgctactgga      60
actcacgctc aggtgcagct ggtgcagtca ggggccgaac tgaagaaacc aggggcatct      120
gtgaaggcca gttgcaaagc ctgaggctac accctgacac ggtatgccat gacttgggtg      180
cgccaggctc ctggacaggg actggagtgg atgggctgga tcaacactta caccggaaat      240
ccaacttatg tgcagggggt caccggccga ttcgtgtttt ctctggacac ttccgtctct      300
accgcctttc tgcacattac aagtctgaag gcagaggaca ctgccgtgta cttctgcgct      360
aggggaaggcg gagcaagagg ctttgattat tggggccagg gaaccctggg gacagtcagc      420
tccgccagca caaagggaac ctccgtgttc cactggctc cctctagtaa aagtacatca      480
gggggcactg ccgctctggg atgtctggtc aaagattact tccccgaacc tgtgaccgtc      540
agctggaact ccggagctct gaccagcggg gtgcatacat tccccgcagt cctgcagtca      600
agcggactgt actccctgtc ctctgtggtc acagtgccta gttcaagcct ggggacacag      660
acttatatct gtaatgtgaa ccataagcca agcaacacca aagtggacaa aaaagtggaa      720
cctaagagct gctgataact cgag                                     744

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

```

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

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<400> 59
Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1          5          10          15

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<400> 60
ggatccgccca ccatggcatg gacccactg ttctgttcc tgctgacttg ttgtcctggc 60
gggagcaatt cacagagcgt cctgacccag ccccttctg tgtccggagc accaggacag 120
cgagtcacaa tctcttgac tggaagctcc tctaacattg gggccagcca cgacgtgcat 180
tggtaccagc agctgccagg gaccgctccc aactgctga tctatgtgaa ctctaattagg 240
cctagtggcg tcccagatag attttcaggg agcaagtccg gcacctctgc tagtctggca 300
attacaggac tgcaggctga ggacgaagca gattactatt gccagagtta cgactcaaac 360
ctgtcaggca ggcagtggt cggaggagga actaagctga ccgtcctggg acagcccaaa 420
gccgctcctt ctgtgacct gtttccccct agttcagagg aactgcaggc caacaaggct 480
actctggtgt gtctgatctc cgacttctac cctggagcag tgaccgtcgc atggaaggcc 540

206108_0033_30wo_606194_seqlisting

gatagctccc cagtgaagc tggggtcgag accacaactc ccagcaagca gtccaacaac	600
aagtacgcag cctctagtta tctgtcactg acacctgaac agtggaagag ccacaaatcc	660
tattcttgcc aagtgactca tgagggcagt accgtggaaa agacagtcgc cccaactgag	720
tgttcctgat aactcgag	738

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

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

<400> 61

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

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

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

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

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

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

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

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

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

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

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

206108_0033_30wo_606194_seqlisting

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

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

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

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

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

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

<400> 62
ggatccgccca ccatggattg gacatggagg attctgtttc tggtcgccgc cgctacagga 60
actcacgccc aggtgcagct ggtgcagtca ggagccgaag tgaagcgacc aggcagctcc 120
gtcactgtgt cctgcaaagc atctggcgga tcattcagca cctacgccct gagctgggtg 180
agacaggctc ctggacgagg actggaatgg atgggaggcg tcatcccact gctgacaatt 240
actaactacg ccccccgatt tcagggcagg atcaccatta cagcagaccg ctccacttct 300
accgcctatc tggagctgaa tagcctgaga ccagaagata ccgcagtgtg ctattgcgcc 360
cgggagggaa ccacaggatg gggatggctg ggaaagccca tcggggcctt cgcacactgg 420
ggccagggaa ccctggtcac agtgtctagt gccagcaca agggcccctc cgtgtttccc 480
ctggctcctt caagcaaaag tacttcagga gggaccgccg ctctgggatg tctggtgaag 540
gactacttcc ctgagccagt caccgtgtcc tggaactctg gcgctctgac ctccggagtg 600
catacatttc ccgcagtcct gcagtcctct gggctgtact ctctgagttc agtggtcact 660
gtgcctagct cctctctggg cacacagact tatacttgca acgtgaatca caagccctcc 720
aataccaaag tcgacaagaa agtggaaact aagtcttgtg ataaaacca tacatgcccc 780
ccttgtccag cacctgagct gctgggcgga ccttcctgtg tcctgtttcc acccaagcca 840
aaagacacac tgatgattag ccggacacct gaagtgaact gtgtggtcgt ggacgtcagc 900
cacgaggacc ccgaagtga gttcaactgg tacgtggatg gcgtcgaggt gcataatgcc 960
aagaccaaac ccagggagga acagtacaac tctacttata gggtcgtgag tgtcctgacc 1020
gtgctgcacc aggactggct gaacgggaag gagtataagt gcaaagtgtc caataaggcc 1080

ctgccagctc ccatcgagaa aacaattct aaggttaag gccagccacg cgaaccacag
gtgtacactc tgcctccag caggagccag ctgaaccaaga accaggtgag tctgacatgt
ctgtccaag gcttctatcc aagcgatatc gccgttgagt gggaatccaa tggacagccc
gaaacaatt acaagactac cccccctgt ctgacagtg atgatatcatt ctttctgtat
tccaagctga ccgttgacaa atctcgcttg cagcagggga acgtcttttag ctgctccgtg
atgcacgag ccttcacaa tcatcacaa cagaagcttc tgaatctgtc accagggcaag
cggggacga aaaggagaag cgggtccgac gctaactc tcagcctgtc gaaaacagga
ggggatgtg aggaataacc tggcccaatg gtccctgaga ccaggtgtt tatctcactg
ctgctgtgga tagcgggggc ttatggcgaa atcgtctga ctacagggccc cggaaaccag
tctctgagtc ctggggagcg cgtacactg agctgtcgag catcacagag cgtggggaa
aatagcttg catgtacca gcagagcct gccaggtc caagactgtc gatctatg
gcaagttcac ggcctagcgg agtggcagac cgttctcg gatctgggag tggcacccgat
ttacttga ccattagcag gctggagcca gaagacttcg ctgtgtacta ttgccagcag
tacggccagt cactgagcac attggacag gggaactaagg tcgaaaaaag aaccgttgga
gcccccaagt tcttcatitt tccacctca gagagcagc tgaagagtgg aacagctca
gtcgtgtgtc tgcgtgaacaa ttctacccc agggagcca agtccagt gaaagtgtgat
aacgtcttc agagcggcaa tcccaggag tctgtgacag aacagagcag taaggttca
actatagcc tgaagctcac actgacttc tccaaagcag attacgagaa gcacaagaagt
tatgccttcg aagtccacca tcagggactg tctagttcctg tgaacaaagtc ttttaacaga
ggggagtgt aactcgag

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

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

>400> 63
ggatccgcca ccatggaactg gacttgagg attctgttcc tgttcgccc cgaactgga
actcacgctg aatttgacct gtcatgggtc ttctgtgtgg ccttcttcg aggggtccag
tgcagaggc tgggtgagtc cggagggaga gtgtccagc caggcagctc cctgcgactg
agttgtgccg ctcaagggtt cgactttct agacagggca tgcacttggt gcgcagggca
ccaggacagg gactggagt gggtgcttc atcaagtacg acggaagtga aaaaatatcat
gccgattcac tgtggggggc gctgtcaatt agccgcgaca actccaagga taccctgtac
ctgcagatga attctctgag ggtcgaagac acagctactt atttctgcgt gagggaaagca

ggcggaacctg attacagaaa cgggtataat tactatgact ttacgatgg ctactataac
480
taccataata tggacgtgtg gggcaaggga accaagtca cagtgtctag tgcatacaat
540
aaaggcccaa gctgtgttcc cctggccctt tcaagcaagt ccacttctgg aggaaaccga
600
gcactgggat gtcctgtgtaa ggaltaactc cctgaaccag tcaccgtgag ttgaaactca
660
ggcgccctga ctacgggagt ccatacctt cctgctgtgc tgcagtcttc tggcgtgtac
720
agcctgagtt cagtgtcac agtgccaagc tcctctctgg gcaaccagac atatatactgc
780
aacgtgaatc acaagcctag caatactaag gtcgaacaaa gagtggaaac aaagagctgt
840
gatataaact atacctgccc acctgtcca gcaacctgagc tgcctggaggg gcccttccgtg
900
ttcctgtttc cacccaagcc aaaaagacac cttgatatta gccggaacac agaatctact
960
tgcgtgtctg tggacgtgag ccacgagggac ccgaagtca agtttaactg gtaactgtgat
1020
ggcgtcggag tgcataatgc taagacaaaa ccacgggaggg aacagtacaa ctccacatat
1080
cgcgtcgtgt cttgtcctgac tgtcctgac caggaactgg tgaaccggcaa ggaatataag
1140
tgcaaatgtt ccaataaaggc actgccagcc cccatcgaga aaaccatttc taaggccaaa
1200
ggccaggcac gagaacccca ggtgtacaca cttgcccaa gtagggcaga gctgaactaag
1260
aaccaagtct ctcgtgaccg tctgtgtgaaa ggtctctatc cctctgatat cgcgtgtgag
1320
tgggaagta atggaagccc tgaataaat tactaagacta cccccctgt gctggacagc
1380
gattggcagc tcttccgtta tagcaagctg accgttgaca aatccagatg gcagcagggg
1440
aacgtcttta gttgctcagt gatgcacgag gcactgcaca atcatatac ccagaaaaagc
1500
ctgttccctgt ctcctgtcaa gagggtgaag aaaaaggaga gttgggtcagg cgaacaaaac
1560
ttcagcctgc tgaagcaggc cggagatgtg gaggaatac cttgggccaat ggccttggacc
1620
ccccctgtcc tgttcttctg gatctgtgt cctggcgga gcaactccca gttctgcactg
1680
acacagccag caagtgtgtc aggtgagcccc ggaacagaga tcaccatttc ctgtaaaggc
1740
acaagccaatg acgtcggggg ctacgagttcc gttgtcttgg atcagcagca tccgtgaaaag
1800
gccccaaaag tctgtgatctc cgatgtcagc aaacgcccc cttgggtgtgag taaccgattc
1860
agttgatcaa agagcgggaa taaccttct ctgaacaatta gtgcccctga ggcagaggaac
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1980
acaagcctga ctgtgtcgtgg ccagcccaa gctgcaccta gcgtgacct gtttcccaac
2040
agttcagagg aactgcaggc taataaggca acactgtgtg gttctgattc cgaacttctac
2100
cctgtgcgtg tcactgtgtg cttgaaagct gatagctccc cagtccaagc aggtgtgga
2160
acaactaccc cctccaagca gtctaaacac aagtaaccgg cttctagtta tctgttcatg
2220
actcccgagc agtggaaagag ccacaaatcc tattcttgc aggtgaacca tgaaggctcc
2280

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

<220>
<223> Nucleic Acid Sequence Encoding VR01 IgG

<400> 64
ggatccgccca ccatgggatg gacatggatt ctgttccctg tcgccgccgc aactagatg
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cattcacagg tgcagcttgt gcagtcaggc gggcagatga agaaaccggc cgaagatagt
120
cgaaatctcat gccgggctcag cgggtacgaa ttcatcgact gtaccctga cgtgattaga
180
ctggcaccttg ggaagaggcc agagtggatg gattgctga aacctagagg cggggcagtg
240
aatatacgcca gaccactgca gggcaggttc actatgacc gccgacgtgta ttctgatacc
300
gcatctcttg agctgcgaag tctgacagtc gacgatctg ccgtgtactt ctgcacacgg
360
ggcaagaact gtgaactataa ttgggatttt gaacactggg gcagggggac acctgtcat
420
gtgagctccc caagtactaa gggaccctca gtgtttcccc tggccccctt tagtaaaagt
480
acctcaggag gacacagccg tctgggatgc ctggtgaagg attaattccc tgaaggcagt
540
accgtgatgt ggaactcagg cgccctgaca agcgggtccc atactttcc agctgtgtctg
600
cagtcagaagc ggtgtgactc cctgtccctt gtgtgtcaca gtgttcacag tgcaccagt
660
acacagactt atatctgtaa cgtcaatcac aagcctagca atactaaagt ggacaagaaa
720
gccgagctta agagctgcca accaaagtcc tgtgatataa cccatacatg ccttccctgt
780
ccagctcttg aactgctggg cggccccatc gtgttccctg ttccaccca aa gcccaagac
840
accctgatga ttagcaggac tccctgagtc acctgcgttg tcgttgacgt gtccccagag
900
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960
aaaaacccggg aggaacagtta caactctaac tataagatcg tgaagtgtcc tgcagtgctg
1020
caccaaggact ggtctgaacgg gaagagtata agtgcacaag tgtctaataa ggtccctgcca
1080
gtctcccatc agaaaaaacaat ttccaaggca aaaggccaag caaggggaaac ccagggtta
1140
actctgcttc catcccgcca cgaagctgact aagaaaccag tcttcttgac ctgtcttggtg
1200
aaaggtctt atccaagcga tatccgcttg gagtggggaat ccaatggcca gcccgagaa
1260
aatatacaga ccaacacccc tgtgtctgga cagcgtatgct ccttcttctt gtattcaaga
1320
ctgaaccgttg ataaaaagccg ctggcagcag gggaaagctt ttagctgttc cgtgatgcca
1380
gaagctcttc acaatcataa caccagaag tctcttgatc tgtcaccttg caagagggga
1440
cgaaaaacga gaagcggcca cggagctaca aacttcagcc tgcctgaaca gccagggcga
1500
gtggaggaagaa atccctgggcc aatggatgg acttgatc tgttccctgt ggcagccgct
1560

1620 accagagttcc attccgaaat tgtgctgacc cagtctcccg gaacactgtc tctgagttcct
1680 ggcgagacag ccatcatctc ctgtaggact tctcagtagc ggagttctggc atgttatcag
1740 cagcgaccag gacaggtctcc tgcactgttc atctactcag gaagcactcg ggcagccggc
1800 attcccgacc gattcctccgg gtctcgttgg ggaacctgatt acaacctgac catctcaaat
1860 ctgaaagcg gagactttgg cgttactat tgcagcaggt atgattctt tgggcaggga
1920 accaagttcc agtgtgacat caaacgcaca gtgcgtggcac caagcgtgtt catctttcca
1980 cctcagatg aacagctgaa gtccggcac gccctctgtgg tgtgccctgtt gaacaatttc
2040 taaccccgga aggcaaaagt ccagtggaaa gtggacaag cctgcagtc tggcaatagt
2100 cagagttcag tgactgaaac ggaagcgaag gattccacct attctctgtc ctctacttg
2160 accctgagca aagctgatta cgaagaagcac aaagtgtatg catgtgaggt caccaccag
2217 ggcactgcgt caccgtcac caagagcttc aatcgcggag agtgttgata actcgag

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

<220>
<223> CHIKV snap! nucleic acid sequence

<400> 65
ggtaccgcca ccatggactg gacttgatt ctgtttctgg tcgcccgcgc tacccgagtg
60 catcacagg tgcagctgca gcagcctggg gccgctctgg tgaagccagg agctagcgca
120 atgattgtcct gcaaaagctc tggctacact ttcaacctct attgatcac ctgggtgaa
180 cagcgacctg gacagggact ggagttggatc ggcgacatct acccagggcac cgggagaaca
240 atctacaagg aaaaaattcaa gacaaaaagcc acactgactg tggacaaccag ctctctaca
300 gcttttatgc agctgaaacag cctgacttcc gaggatagcg ccgtgtacta ttgcgcaaga
360 ggtatacggt ctcttacta tgccttgga tacttggggc agggaactag cgtcaaccgtg
420 agttcagcat ctaccaaagg accaagcgtg ttcccactgg cacttagctc caaatccact
480 tctggcggga ccgctgctct gggatgtctg gtgaaggatt acttccctga gccagttaca
540 gtgagttgga actcaggggc tctgaccagc ggagttccaca catcttctgc agttctgca
600 tctagtggac tgtactcctt gtcaagcgtg gtcaactgtcc catctcttag tctgggcac
660 cagacatata tctgcaacgt gaatcacaa ccatccaata ccaagtcga taagaaagt
720 gagcccaagt ctgttgacaa aactcatacc tgccttccct gtccagcacc tgaactgtcg
780 ggaagcccaa gctgttctt gtttccacc aagccctaaag acaaccttgat gattagcagg
840 acaaccagag tcaacttgct ggtctgctgt ggtcgttggaac gttaggccag aagccccga
900

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960 aactgggtacg tggatggcgt cgaagtgcct aatgccaaaga caaaaccccg ggagggaacag

1020 tacaaatcaa cctatcgggt cgtgagcgtc ctgacagtg c tgacaccagg ctggtctgaac

1080 ggaaggagt acaagtgc aa agtctaat aaggccctgc cagctcccat cgaaaaaaac

1140 attagcaagg ctaaggcca gccaaagag gccaggtgt acacactgcc tccatcaagg

1200 gacgaactga caaagaacca ggtcagcctg acttgcttg tgaaagcctt ctatcccagc

1260 gatatacgag tggaaatggga gtccaatgg cagcctgaga acaattacaa gaccacaccc

1320 cctgtctg agcagcgtgg gtccctctt ctgtattca agctgacagt gataaatct

1380 cgtgtgcagc agggaaacgt cttagttgc tcagtgtgc acgaagccct gcacaatcat

1440 tacactcaga agagcctgtc cctgtctccc ggaagagggg gccgcacaacg gagaagtggc

1500 tcaggggcaa ccaactctc tctgtctgaaa caggccggcg atgtggaggga aatctctggg

1560 ccaatggact ggacatggat tctgttcttg gtgacagccg ctacaagggt ccatccgac

1620 attgtctga ctacgtccc tgcaagtctg gccgtgtctc agggacagcg agcaaacatc

1680 agttgtaagg ctagccagtc cgtccgactac gatggggaca gttaagtga ctgttatcag

1740 cagaagccctg gacagctccc aaaaactctg atctatgatg ctagttaatct ggagtcaagg

1800 attcccgcac gattctcttg aagtgtctca ggacacagact tcaacctga catccaccc

1860 gtcgagggaag agtagctggc tactactat tgcaggaaga gcaatgagga cccccgcact

1920 ttcgggggag gccacaaagt ggagatcaaa cgaactgtcg cagccccccag cgtgttcatc

1980 tttccacct cagacgaaca gctgaagagc ggaacccgat ccgtgtgttg cctgctgaac

2040 aacttctacc cccgcgaggc caaggtccag tggaaagtgg ataacgctct gcagtcaagg

2100 aatagccagg aatccgtgac tgagcagbat tctaaggca gtacctatc actgtcaagc

2160 acaactgactc tgagcaaaag agactacgaa aagcataaag tgtatgacct cgaagtcaac

2220 caccaggggc tgaggctccc agtcaactaag tctttcaaca gaggggaaatg ctgataactc

2223 gag

<210> 66
<211> 2241
<212> DNA
<213> Artificial Sequence

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

<400> 66

ggatccgccca ccatggactg gacttggagg attctgttc tgtcgcgccg cgtactggg

120 actcaagctc aggcacatct ggtcgaatct ggaggaggag tgtccagcc tggccgattcc

180 ctgcgactgt ctgctgcagc tagcgccttc aacttcagca caaaagcaat gcacttgggtg

240 cgcacagggcac caggcaaggg actggagtgg gtccgtgtga tctcatatcga cggaaagccat

300 aagtactatg cagatcttct gaaaggccgg ttcaaccattt ccaggggacaa ttctaagaaac
360 accctgtatc tgcagatgtaa tagccctgcgc gcagccgata ccgcagtgta ctattgcga
420 actgtcgcg tgcctgaacc gccagtgaac gccgaatact ttcaaccattg gggaacagggc
480 agtctgtct cagtgaactc cgaagtact aagggaacct cagtgttccc actggcacc
540 tctagttaat ctactagtgg cgggaacct gcactgggat gttctgtgaa ggaactattc
600 ccggagccctg tcaaccgtgag ctggaattcc ggagccctga caagcggcgt ccacacttt
660 ccgcctgtgc tgcagttcaag cggactgtac tccctgtcct ctgtgttcaac tgttcctagt
720 tcaagccctg gcactcagac ctatatctgc aatgtgaacc acaagccctc taacaccaaa
780 gttcgaacaa aagtggaaac taagagctgt gataaaacac atacttgcac accttgtcca
840 gcaaccagag tgcctgggagg accaagcgtg ttccctgttc cacccaagcc taagacacaa
900 ctgatatata gccggacacc tgaagttcaat tgcgtgtgtc tggacgtgtc ccaacgaggac
960 ccgaagtca agtttaattg gtactgtgat ggcttgcagg tgcataacgc caagaccaaa
1020 cccggggagg aacagtacaa tagcacatat agagtctgtt cgttcctgac tgtgtctgcat
1080 caggatttgc tgaattggaa ggaattataa tgaaaagtgt ctaacaaggc tctgtcctga
1140 ccaatcgaga aaaccattag caagccta aa ggccagccta gggaaccaca ggtgtatacaca
1200 ctgcccctca gttgcgaaga gctgaacca g aatcaggtct ccttgacatg tctgtgtgaaa
1260 ggtcttctac catcagatat cgcctgtgag tgggaagca acgggcagcc cgaaaaacaa
1320 taacaagacca caccctctgt gctggacct gatggcagtt tcttctgtta ttctaagctg
1380 accgttgaca aaagtatgat gcagcagggg aatgtctttt catgtagcgt gatgcacgag
1440 gtcctgacaa accattacac acagaagtcc ctgtctctga gtcccgggaa gaggggccgc
1500 aaacgagat caggggcgg agctaatat ttacgacctg tgaacaaggc aggggatgtg
1560 gtaggaaaaa ccggaacct gcttggat ccaactgtcc tgttctgtc gacatgtctg
1620 cccggggggc gcaatttca gattgtcctg acacagccac catcagtgtag cggagcaca
1680 ggacagaggg tgaacctctc ctgcacagbc agcagcagca acattgtgcgc cgggtatacga
1740 gtgcatgtgt atcagagctt gcccggaacc gctcctaagc tgcctgatac tggcaacaat
1800 aaccgcccat ctgggtgtcc cgtatcgttc tccgtctcta aaagtgggac ttcaagccagc
1860 ctgtctata ccgttccc gcgcagcc aggcaggaac gaagtgttat actatlgcac gagtatacga
1920 tcaagccctg acgttgcgt gttcggagga ggaaaccaagc tgaacagttct gggaacagcct
1980 aagccgcctc caagcgtgac actgtttctt ccatctctctg aggaacttgc ggcaaaaacaag
2040 gccacccctg tgtgtccctt atttccgtat ttccctccgggg cagtcaactgt ggttggagag
2100 gtcagatagt ttctcctt caccgttcaaa agcccgagtg gagactacca caccatcaaa gcagagccaat

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tcctattctt gccagggtcac tcacgaagga agcactgtgg agaaaactgt cgcaccaacc 2220
gaatgtagtt gataactcga g 2241

<210> 67
<211> 739
<212> PRT
<213> Artificial Sequence

<220>
<223> DVSF-1 WT amino acid sequence
<400> 67

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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435

440

445

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Glu Cys Ser

<210> 68
<211> 2241
<212> DNA
<213> Artificial Sequence

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

<400> 68
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actcacgctc aggcacatct ggtcgaatct ggaggaggag tggccagcc tggccgatcc 120
ctgcgactgt cttgcgcagc tagcgccttc aacttcagca caaacgcaat gcactgggtg 180
cgacaggcac caggcaaggg actggagtgg gtcgctgtga tctcatagca cggaagccat 240
aagtactatg cagattctgt gaaaggccgg ttcaccattt ccaggggaaa ttctaagaac 300
accctgtatc tgcagatgaa tagcctgcgc gcagccgata ccgcagtgtg ctattgcgca 360
actgtcggcg tgctgacctg gccagtgaac gccgaatact ttcaccattg gggacagggc 420
agtctgggtc cagtgcgctc cgcaagtact aagggaacct cagtgttccc actggcacc 480
tctagtaaat ctactagtgg cgggaccgct gcactgggat gtctgggtgaa ggactatttc 540
cccagacctg tcaccgtgag ctggaattcc ggagccctga caagcggcgt ccacactttt 600
cccgtgtgct tgcagtcaag cggactgtac tccctgtcct ctgtgggtcac tgtgcctagt 660
tcaagcctgg gcactcagac ctatatctgc aatgtgaacc acaagccctc taacacaaaa 720
gtcgacaaga aagtgggaacc taagagctgt gataaaacac atacttgccc accttgacca 780
gcaccagagg cagctggagg accaagcgtg ttctgttttc caccgaagcc taaagacaca 840
ctgatgatta gccggacacc tgaagtcact tgcgtgggtc tggacgtgtc ccacgaggac 900
cccgaagtca agtttaattg gtacgtggat ggcgtcgagg tgcataacgc caagacaaaa 960
ccccgggagg aacagtacaa tagcacatat agagtcgtgt ccgtcctgac tgtgctgcat 1020
caggattggc tgaatgggaa ggagtataag tgcaaagtgt ctaacaaggc tctgcctgca 1080
ccaatcgaga aaaccattag caaggctaaa ggccagccta gggaaccaca ggtgtacaca 1140

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ctgcctccaa gtcgcgacga gctgaccaag aatcaggtct ccctgacatg tctggtgaaa	1200
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tacaagacca caccctgtgt gctggactct gatggcagtt tctttctgta ttctaagctg	1320
accgtggaca aaagtagatg gcagcagggg aatgtctttt catgtagcgt gatgcacgag	1380
gccctgcaca accattacac acagaagtcc ctgtctctga gtcccggaaa gaggggccgc	1440
aaacggagat cagggagcgg agctactaat ttcagcctgc tgaaacaggc aggggatgtg	1500
gaggaaaacc ccggacctat ggcttggacc ccactgttcc tgtttctgct gacatgctgt	1560
ccggggggca gcaattctca gagtgtcctg acacagccac catcagttag cgagcacca	1620
ggacagaggg tgaccatctc ctgcacaggc agcagcagca acattggcgc cgggtacgac	1680
gtgcattggt atcagcagct gcccggcacc gctcctaagc tgctgatctg tggcaacaat	1740
aaccgcccac ctggggtgcc cgatcgattc tccggctcta aaagtgggac ttcagccagc	1800
ctggctatta ccggcctgca ggccgaggac gaagctgatt actattgcca gagctacgac	1860
tcaagcctga ccggagtcgt gttcggagga ggaaccaagc tgacagtcct gggacagcct	1920
aaagccgctc caagcgtgac actgtttcct ccctcctctg aggaactgca ggcaaacaag	1980
gccaccctgg tgtgcctgat ttccgacttc taccggggg cagtcactgt ggcttggag	2040
gcagatagtt cacctgtcaa agccggagtg gagactacca caccatcaaa gcagagcaat	2100
aacaaatacg cagccagctc ctatctgtcc ctgaccctg agcagtggaa gtctcacaaa	2160
tcctattctt gccaggtcac tcacgaagga agcactgtgg agaaaactgt cgcaccaacc	2220
gaatgtagtt gataactcga g	2241

<210> 69
 <211> 739
 <212> PRT
 <213> Artificial Sequence

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

<400> 69

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

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

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

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

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Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser His Lys Tyr Tyr Ala
 65 70 75 80
 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
 85 90 95
 Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Ala Asp Thr Ala Val
 100 105 110
 Tyr Tyr Cys Ala Thr Val Gly Val Leu Thr Trp Pro Val Asn Ala Glu
 115 120 125
 Tyr Phe His His Trp Gly Gln Gly Ser Leu Val Ser Val Ser Ser Ala
 130 135 140
 Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
 145 150 155 160
 Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
 165 170 175
 Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
 180 185 190
 Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
 195 200 205
 Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
 210 215 220
 Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
 225 230 235 240
 Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 245 250 255
 Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 260 265 270
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 275 280 285
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 290 295 300
 Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu

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305 310 315 320

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Glu Cys Ser

<210> 70

<211> 2241

<212> DNA

<213> Artificial Sequence

<220>

<223> DVSF-2 WT nucleic acid sequence

<400> 70

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acacacgccg aagtgcagct ggtggaatct ggagggggat ggggtgcagcc aggaggggtcc 120

ctgcgactgt cttgcgccgc tagtggcttc actttttcca gatacgacat gcactggggtc 180

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aggcaggtga	ccggaaaggg	cctggaatgg	gtgagcgcaa	tcaccacagc	cggagacaca	240
tactatcccc	attctgtgaa	gggccgggttc	accattagtc	gggagaacgc	caaaagctcc	300
ctgtatctgc	agatgaacaa	tctgagagct	ggcgacaccg	cactgtacta	ttgcgctagg	360
ggcccccccta	cagattgctc	tagtggacga	tgtctgggag	tcggagtggg	actggaccca	420
tgggggcagg	gaacactggt	cactgtgtca	agcgccctcca	caaagggacc	ctctgtgttc	480
cctctggctc	catcctctaa	aagtacttca	ggaggaaccg	cagcactggg	atgtctggtg	540
aaggattact	tcccagagcc	cgtcaccgtg	agctggaact	ccggagctct	gactagcggc	600
gtccatacct	ttcctgcagt	gctgcagagt	tcaggcctgt	acagcctgag	ctccgtggtc	660
accgtgccat	ctagtctact	ggggacccag	acatatactt	gcaacgtgaa	tcacaagcca	720
tctaatacaa	aagtcgacaa	gaaagtggaa	cccaagagtt	gtgataaaaac	tcatacctgc	780
ccaccatgtc	ctgcaccaga	gctgctggga	ggaccatccg	tgttcctgtt	tcctccaaag	840
cccaaagaca	cactgatgat	tagcaggaca	cccgaagtca	cttgctgggt	cgtggacgtg	900
agccacgagg	accccgaagt	caagtttaac	tggtacgtgg	atggcgctga	ggtgcataat	960
gccaagacca	aaccccgga	ggaacagtac	aacagtacct	atagagtcgt	gtcagtcctg	1020
acagtgcctg	accaggactg	gctgaacggg	aaagagtata	agtgcaaagt	gtccaataag	1080
gcactgcccc	cccctatcga	gaaaaccatt	tctaaggcca	aaggacagcc	ccgagaacct	1140
caggtgtaca	cactgcccc	tagccgcgac	gagctgacaa	agaaccaggt	ctccctgact	1200
tgtctggtga	aaggggttcta	tccttcagat	atcgccgtgg	agtgggaaag	caatggacag	1260
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gcaacactgg	tgtgtctgat	ttccgacttc	taccagagg	cagtcactgt	ggcatggaag	2040
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gagtgttctt gataactcga g 2241

<210> 71
<211> 739
<212> PRT
<213> Artificial Sequence

<220>
<223> DVSF-2 WT amino acid sequence

<400> 71

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

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

Ser Arg Tyr Asp Met His Trp Val Arg Gln Val Thr Gly Lys Gly Leu
50 55 60

Glu Trp Val Ser Ala Ile Thr Thr Ala Gly Asp Thr Tyr Tyr Pro Asp
65 70 75 80

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

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

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

Gly Val Gly Val Gly Leu Asp Pro Trp Gly Gln Gly Thr Leu Val Thr
130 135 140

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
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 450 455 460
 His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Arg Gly Arg
 465 470 475 480
 Lys Arg Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln
 485 490 495
 Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Trp Thr Pro Leu
 500 505 510
 Phe Leu Phe Leu Leu Thr Cys Cys Pro Gly Gly Ser Asn Ser Ser Tyr
 515 520 525
 Glu Val Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln Thr Ala
 530 535 540
 Ser Ile Thr Cys Ser Gly Asp Lys Leu Gly Lys Lys Tyr Thr Ser Trp
 545 550 555 560
 Tyr Gln Gln Lys Pro Gly Gln Ser Pro Leu Leu Val Ile Tyr Gln Asp
 565 570 575
 Thr Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser
 580 585 590
 Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met Asp Glu
 595 600 605
 Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Ser Thr Thr His Val Ile Phe
 610 615 620
 Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala Ala Pro
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 Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys
 645 650 655
 Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr
 660 665 670
 Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr
 675 680 685

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

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

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

Glu Cys Ser

<210> 72
<211> 2241
<212> DNA
<213> Artificial Sequence

<220>
<223> DVSF-2 LALA nucleic acid sequence

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ctgaggctgt cttgcgccgc tagtggcttc actttttcta gatacgacat gcactgggtc 180
cggcaggtga ccgggaaggg actggaatgg gtgagcgcca tcaccacagc aggggacaca 240
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ctgtatctgc agatgaacaa tctgagagcc ggcgacaccg ctctgtacta ttgcgccagg 360
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<210> 73

<211> 739

<212> PRT

<213> Artificial Sequence

<220>

<223> DVSF-2 LALA amino acid sequence

<400> 73

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

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

Ser Arg Tyr Asp Met His Trp Val Arg Gln Val Thr Gly Lys Gly Leu

50 206108_0033_30wo_606194_seqlisting 55 60

Glu Trp Val Ser Ala Ile Thr Thr Ala Gly Asp Thr Tyr Tyr Pro Asp
65 70 75 80

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

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

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

Gly Val Gly Val Gly Leu Asp Pro Trp Gly Gln Gly Thr Leu Val Thr
130 135 140

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

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

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

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

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

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

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

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

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

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

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Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
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Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
325 330 335

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

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

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

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

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

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

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

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

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Arg Gly Arg
465 470 475 480

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

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

Phe Leu Phe Leu Leu Thr Cys Cys Pro Gly Gly Ser Asn Ser Ser Tyr
515 520 525

Glu Val Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln Thr Ala
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Ser Ile Thr Cys Ser Gly Asp Lys Leu Gly Lys Lys Tyr Thr Ser Trp
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Tyr Gln Gln Lys Pro Gly Gln Ser Pro Leu Leu Val Ile Tyr Gln Asp
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Thr Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser
580 585 590

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

Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Ser Thr Thr His Val Ile Phe
610 615 620

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

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

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

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

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

Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Lys Ser Tyr Ser Cys
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Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr
725 730 735

Glu Cys Ser

<210> 74

<211> 2229

<212> DNA

<213> Artificial Sequence

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<223> DVSF-3 WT nucleic acid sequence

<400> 74

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2040

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gtgacccatc aggggctgag aagtcccgtg acaaagagct tcaacagggg agagtgttga	2220
taactcgag	2229

<210> 75
 <211> 735
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DVSF-3 WT amino acid sequence

<400> 75

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 1 5 10 15

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

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

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

Glu Trp Ile Ser Gly Ile Ser Trp Asn Ser Ala Thr Ile Gly Tyr Ala
 65 70 75 80

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

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

Tyr Tyr Cys Ala Lys Gly Gly Pro Arg Gly Leu Gln Leu Leu Ser Ser
 115 120 125

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Glu Glu Asn Pro Gly Pro Met Val Leu Gln Thr Gln Val Phe Ile Ser
500 505 510

Leu Leu Leu Trp Ile Ser Gly Ala Tyr Gly Asp Ile Gln Met Thr Gln
515 520 525

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
530 535 540

Cys Arg Ala Ser Gln Asp Ile Arg Arg Tyr Leu Asn Trp Tyr Gln Gln
545 550 555 560

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

Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Val Thr Asp
580 585 590

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

Tyr Cys Gln Gln Ser Tyr Ser Pro Pro His Thr Phe Gly Gln Gly Thr
610 615 620

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

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

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
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Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
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690 695 700

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

Gly Leu Arg Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
725 730 735

<210> 76

<211> 2229

<212> DNA

<213> Artificial Sequence

<220>

<223> DVSF-3 LALA nucleic acid sequence

<400> 76

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cccgaagtca agtttaactg gtacgtggat ggcgtcgagg tgcataatgc taagacaaaa      960
ccccgagagg aacagtacaa cagtacttat agggctcgtgt cagtcctgac cgtgctgcac     1020
caggactggc tgaacgggaa ggagtataag tgcaaagtgt ccaataaggc actgcctgcc     1080
ccaatcgaga aaactatttc taaggctaaa ggccagccta gagaaccaca ggtgtacacc     1140
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accgtggata aatcccgtctg gcagcagggg aacgtctttt cctgctctgt gatgcatgag	1380
gccctgcaca atcattacac acagaagagt ctgtcactga gcccaggaaa gcgagggagg	1440
aaaaggagat ccggatctgg ggctactaac ttctccctgc tgaagcaggc aggcgacgtg	1500
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ctgaacaatt tctaccctag agaagccaag gtccagtggg aagtggataa cgctctgcag	2040
tctgggaata gtcaggagtc agtgacagaa caggacagca aggattccac ttattctctg	2100
tctagtaccc tgacactgag caaagcagac tacgagaagc ataaagtgtg tgcctgcgaa	2160
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taactcgag	2229

<210> 77
 <211> 735
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DSVF-3 LALA amino acid sequence

<400> 77

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

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

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

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

206108_0033_30wo_606194_seqlisting

Glu Trp Ile Ser Gly Ile Ser Trp Asn Ser Ala Thr Ile Gly Tyr Ala
 65 70 75 80
 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys
 85 90 95
 Ser Leu Asp Leu Gln Met Asn Ser Leu Arg Pro Asp Asp Thr Ala Leu
 100 105 110
 Tyr Tyr Cys Ala Lys Gly Gly Pro Arg Gly Leu Gln Leu Leu Ser Ser
 115 120 125
 Trp Val Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala
 130 135 140
 Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
 145 150 155 160
 Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
 165 170 175
 Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
 180 185 190
 Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
 195 200 205
 Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
 210 215 220
 Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
 225 230 235 240
 Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 245 250 255
 Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 260 265 270
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 275 280 285
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 290 295 300
 Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 305 310 315 320

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

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

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

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

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

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

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

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

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

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

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

Glu Glu Asn Pro Gly Pro Met Val Leu Gln Thr Gln Val Phe Ile Ser
500 505 510

Leu Leu Leu Trp Ile Ser Gly Ala Tyr Gly Asp Ile Gln Met Thr Gln
515 520 525

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
530 535 540

Cys Arg Ala Ser Gln Asp Ile Arg Arg Tyr Leu Asn Trp Tyr Gln Gln
545 550 555 560

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

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Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Val Thr Asp
580 585 590

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

Tyr Cys Gln Gln Ser Tyr Ser Pro Pro His Thr Phe Gly Gln Gly Thr
610 615 620

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

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

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

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

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

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

Gly Leu Arg Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
725 730 735

<210> 78

<211> 2217

<212> DNA

<213> Artificial Sequence

<220>

<223> Anti-PSMA nucleic acid sequence

<400> 78

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ctgaaaatct catgcaaagg aagtgggtac tcattcacta gcaactggat tggatgggtg 180

cggcagatgc caggcaaggg actggagtgg atgggaatca tctaccccg ggactccgat 240

acacgctata gtccttcatt tcagggccag gtgacaatct ctgccgacaa aagcatttcc 300

actgcttatc tgcagtggag ctccctgaag gcttccgata ccgcaatgta ctattgcgcc 360

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 480 agtggcggaa ccgcccgtct gggtgtctg gtgaaggatt acttccctga gccagtcaaca
 540 gttgtccctgga actctggcgc tctgaccagc ggagttcaca catttccgc agtgcctgca
 600 agttcagccc tgtaccctct gagctccgtg gtccagttcc cttctagtct actgggaaact
 660 cagaccctata tctgcacaagt gaatcacaaa ccttccaata ctaaggtcga caagaaagt
 720 gaaaccaaaat ctgtgtataa gacacatact tgccttccct gttccagcacc tgaagctgctg
 780 ggccggcccaa gcgtgttccct gtttccaccc aagcccaag ataccctgat gattagcagg
 840 acacagaaag tcaactgctg ggtcgtgtgac gtgttcccaag aggaaccccg agttcaagttc
 900 aactgtgtacg tggaccgctg cgaagtgtcat aatgtctaaga ccaaaaccaag agaggaacag
 960 taacaactcaa cctatcgggt cgtgagcgtc ctgacagtgc tgcaccagga ctgctgtaac
 1020 ggaaggagt ataatgtcaca agtgtctaac aagccctgc cagctcccat cgaagaagact
 1080 attagcaagg ctaaaaggca gccacgcgaa cccaggtgtt acaccctgccc tccatcagga
 1140 gatgagctga caaaaaaacc ggtctctctg acttgtcttg tgaagggat ctatccctct
 1200 gacatcgcag tggagtgtgga aagtaatggc cagccttgaa acaattacaa gaccacaccc
 1260 cctgtgtcgg acagtgtatgg atcatcttt ctgtatagta aactgaccgt gataaagta
 1320 agatgvcagc aggggaacgt ctttcatgc agcgtgtatgc atgagggccct gcacaatcat
 1380 tacaccagga agtccctgtc tctgagttcc ttgcaaacggg gacgcagaag gagatcagga
 1440 agcggggtcta caaaccttct cctgctgaag caggcagggg acgtggagga aaatcctggc
 1500 ccaatgtctc tgcagagacca gttgtttatc tccctgctgc tgtgtatttc tggggcatata
 1560 ggccgcccact agctgacaca gtctcccgag tccctgtccg catctgtcgg cgaaccgagt
 1620 accatcatat gtagggccag ccaggtatat tctagtctc tgcacatggt ccagcagaag
 1680 cctgggaaag caccaaaagt gctgtatat gatgtctcaa gccctggaatc cggagtgcct
 1740 agccggttct cctgatatcgg aagtgtgaca gactttactc tgaccatata cagccctgca
 1800 cctgaggtat tgcgcacata ctattgtccag cagttcaata gttatccact gaatttttga
 1860 gggggccaaca aagtggaaat caagcgaact gtcgcagccc cttagcgtgtt catttttcca
 1920 ccttccgagt agcagctgaa gagcggcacc gcttccgtgg tgtgcccgtc gaaacaactc
 1980 tacccacgcg aggtccaaagt ccaagtggaa gtgtgacaag cttctgagtc tggaaatagt
 2040 caggagtcat tgaactgaaca ggacagcaaa gattccaact attctctgtc ctctacactg
 2100 actctgagca aggcagacta cgaagaagca aggtgtatg cctgagaaat caccaccaag
 2160 gggtctgttctt caccagtcaac taaatctttc aatcggggag aatgttgtata acttcgag
 2217

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<210> 79

<211> 731

<212> PRT

<213> Artificial Sequence

<220>

<223> Anti-PSMA amino acid sequence

<400> 79

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

Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe
35 40 45

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

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

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

Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met
100 105 110

Tyr Tyr Cys Ala Arg Gln Thr Gly Phe Leu Trp Ser Ser Asp Leu Trp
115 120 125

Gly Arg Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
130 135 140

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

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

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

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

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
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210 206108_0033_30wo_606194_seqlisting 215 220

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

206108_0033_30wo_606194_seqlisting

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

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

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

Ser Gly Ala Tyr Gly Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu
515 520 525

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

Asp Ile Ser Ser Ala Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala
545 550 555 560

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

Ser Arg Phe Ser Gly Tyr Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
580 585 590

Asn Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Phe
595 600 605

Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
610 615 620

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

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

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

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

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

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

206108_0033_30wo_606194_seqlisting

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

<210> 80
<211> 733
<212> PRT
<213> Artificial Sequence

<220>
<223> CHIKV-snapi amino acid sequence

<400> 80

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1 5 10 15

His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Ala Leu Val Lys Pro
20 25 30

Gly Ala Ser Ala Met Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
35 40 45

Ser Tyr Trp Ile Thr Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu
50 55 60

Trp Ile Gly Asp Ile Tyr Pro Gly Thr Gly Arg Thr Ile Tyr Lys Glu
65 70 75 80

Lys Phe Lys Thr Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser Thr
85 90 95

Ala Phe Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr
100 105 110

Tyr Cys Ala Arg Gly Tyr Gly Ser Pro Tyr Tyr Ala Leu Asp Tyr Trp
115 120 125

Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
130 135 140

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
145 150 155 160

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
165 170 175

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
180 185 190

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Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
195 200 205

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
210 215 220

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
225 230 235 240

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
245 250 255

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
260 265 270

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
275 280 285

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
290 295 300

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
305 310 315 320

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
325 330 335

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
340 345 350

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
355 360 365

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
370 375 380

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
385 390 395 400

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
405 410 415

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
420 425 430

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
435 440 445

206108_0033_30wo_606194_seqlisting

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
450 455 460

Ser Pro Gly Lys Arg Gly Arg Lys Arg Arg Ser Gly Ser Gly Ala Thr
465 470 475 480

Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly
485 490 495

Pro Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg
500 505 510

Val His Ser Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val
515 520 525

Ser Gln Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val
530 535 540

Asp Tyr Asp Gly Asp Ser Tyr Val Asn Trp Tyr Gln Gln Lys Pro Gly
545 550 555 560

Gln Ser Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Ser Gly
565 570 575

Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
580 585 590

Asn Ile His Pro Val Glu Glu Glu Asp Val Ala Thr Tyr Tyr Cys Gln
595 600 605

Glu Ser Asn Glu Asp Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu
610 615 620

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
625 630 635 640

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
645 650 655

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
660 665 670

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
675 680 685

Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
690 695 700

206108_0033_30wo_606194_seqlisting

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
705 710 715 720

Arg Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
725 730

<210> 81
<211> 457
<212> PRT
<213> Artificial Sequence

<220>
<223> CHIKV E1 consensus

<400> 81

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1 5 10 15

His Ser Tyr Glu His Val Thr Val Ile Pro Asn Thr Val Gly Val Pro
20 25 30

Tyr Lys Thr Leu Val Asn Arg Pro Gly Tyr Ser Pro Met Val Leu Glu
35 40 45

Met Glu Leu Leu Ser Val Thr Leu Glu Pro Thr Leu Ser Leu Asp Tyr
50 55 60

Ile Thr Cys Glu Tyr Lys Thr Val Ile Pro Ser Pro Tyr Val Lys Cys
65 70 75 80

Cys Gly Thr Ala Glu Cys Lys Asp Lys Asn Leu Pro Asp Tyr Ser Cys
85 90 95

Lys Val Phe Thr Gly Val Tyr Pro Phe Met Trp Gly Gly Ala Tyr Cys
100 105 110

Phe Cys Asp Ala Glu Asn Thr Gln Leu Ser Glu Ala His Val Glu Lys
115 120 125

Ser Glu Ser Cys Lys Thr Glu Phe Ala Ser Ala Tyr Arg Ala His Thr
130 135 140

Ala Ser Ala Ser Ala Lys Leu Arg Val Leu Tyr Gln Gly Asn Asn Ile
145 150 155 160

Thr Val Thr Ala Tyr Ala Asn Gly Asp His Ala Val Thr Val Lys Asp
165 170 175

206108_0033_30wo_606194_seqlisting

Ala Lys Phe Ile Val Gly Pro Met Ser Ser Ala Trp Thr Pro Phe Asp
180 185 190

Asn Lys Ile Val Val Tyr Lys Gly Asp Val Tyr Asn Met Asp Tyr Pro
195 200 205

Pro Phe Gly Ala Gly Arg Pro Gly Gln Phe Gly Asp Ile Gln Ser Arg
210 215 220

Thr Pro Glu Ser Lys Asp Val Tyr Ala Asn Thr Gln Leu Val Leu Gln
225 230 235 240

Arg Pro Ala Val Gly Thr Val His Val Pro Tyr Ser Gln Ala Pro Ser
245 250 255

Gly Phe Lys Tyr Trp Leu Lys Glu Arg Gly Ala Ser Leu Gln His Thr
260 265 270

Ala Pro Phe Gly Cys Gln Ile Ala Thr Asn Pro Val Arg Ala Val Asn
275 280 285

Cys Ala Val Gly Asn Met Pro Ile Ser Ile Asp Ile Pro Glu Ala Ala
290 295 300

Phe Thr Arg Val Val Asp Ala Pro Ser Leu Thr Asp Met Ser Cys Glu
305 310 315 320

Val Pro Ala Cys Thr His Ser Ser Asp Phe Gly Gly Val Ala Ile Ile
325 330 335

Lys Tyr Ala Ala Ser Lys Lys Gly Lys Cys Ala Val His Ser Met Thr
340 345 350

Asn Ala Val Thr Ile Arg Glu Ala Glu Ile Glu Val Glu Gly Asn Ser
355 360 365

Gln Leu Gln Ile Ser Phe Ser Thr Ala Leu Ala Ser Ala Glu Phe Arg
370 375 380

Val Gln Val Cys Ser Thr Gln Val His Cys Ala Ala Glu Cys His Pro
385 390 395 400

Pro Lys Asp His Ile Val Asn Tyr Pro Ala Ser His Thr Thr Leu Gly
405 410 415

Val Gln Asp Ile Ser Ala Thr Ala Met Ser Trp Val Gln Lys Ile Thr
420 425 430

206108_0033_30wo_606194_seqlisting

Gly Gly Val Gly Leu Val Val Ala Val Ala Ala Leu Ile Leu Ile Val
435 440 445

Val Leu Cys Val Ser Phe Ser Arg His
450 455

<210> 82
<211> 441
<212> PRT
<213> Artificial Sequence

<220>
<223> CHIKV E2 consensus

<400> 82

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1 5 10 15

His Ser Ser Thr Lys Asp Asn Phe Asn Val Tyr Lys Ala Thr Arg Pro
20 25 30

Tyr Leu Ala His Cys Pro Asp Cys Gly Glu Gly His Ser Cys His Ser
35 40 45

Pro Val Ala Leu Glu Arg Ile Arg Asn Glu Ala Thr Asp Gly Thr Leu
50 55 60

Lys Ile Gln Val Ser Leu Gln Ile Gly Ile Lys Thr Asp Asp Ser His
65 70 75 80

Asp Trp Thr Lys Leu Arg Tyr Met Asp Asn His Met Pro Ala Asp Ala
85 90 95

Glu Arg Ala Gly Leu Phe Val Arg Thr Ser Ala Pro Cys Thr Ile Thr
100 105 110

Gly Thr Met Gly His Phe Ile Leu Ala Arg Cys Pro Lys Gly Glu Thr
115 120 125

Leu Thr Val Gly Phe Thr Asp Ser Arg Lys Ile Ser His Ser Cys Thr
130 135 140

His Pro Phe His His Asp Pro Pro Val Ile Gly Arg Glu Lys Phe His
145 150 155 160

Ser Arg Pro Gln His Gly Lys Glu Leu Pro Cys Ser Thr Tyr Val Gln
165 170 175

206108_0033_30wo_606194_seqlisting

Ser Thr Ala Ala Thr Thr Glu Glu Ile Glu Val His Met Pro Pro Asp
180 185 190

Thr Pro Asp Arg Thr Leu Met Ser Gln Gln Ser Gly Asn Val Lys Ile
195 200 205

Thr Val Asn Gly Gln Thr Val Arg Tyr Lys Cys Asn Cys Gly Gly Ser
210 215 220

Asn Glu Gly Leu Thr Thr Thr Asp Lys Val Ile Asn Asn Cys Lys Val
225 230 235 240

Asp Gln Cys His Ala Ala Val Thr Asn His Lys Lys Trp Gln Tyr Asn
245 250 255

Ser Pro Leu Val Pro Arg Asn Ala Glu Leu Gly Asp Arg Lys Gly Lys
260 265 270

Ile His Ile Pro Phe Pro Leu Ala Asn Val Thr Cys Arg Val Pro Lys
275 280 285

Ala Arg Asn Pro Thr Val Thr Tyr Gly Lys Asn Gln Val Ile Met Leu
290 295 300

Leu Tyr Pro Asp His Pro Thr Leu Leu Ser Tyr Arg Asn Met Gly Glu
305 310 315 320

Glu Pro Asn Tyr Gln Glu Glu Trp Val Met His Lys Lys Glu Val Val
325 330 335

Leu Thr Val Pro Thr Glu Gly Leu Glu Val Thr Trp Gly Asn Asn Glu
340 345 350

Pro Tyr Lys Tyr Trp Pro Gln Leu Ser Thr Asn Gly Thr Ala His Gly
355 360 365

His Pro His Glu Ile Ile Leu Tyr Tyr Tyr Glu Leu Tyr Pro Thr Met
370 375 380

Thr Val Val Val Val Ser Val Ala Thr Phe Ile Leu Leu Ser Met Val
385 390 395 400

Gly Met Ala Ala Gly Met Cys Met Cys Ala Arg Arg Arg Cys Ile Thr
405 410 415

Pro Tyr Glu Leu Thr Pro Gly Ala Thr Val Pro Phe Leu Leu Ser Leu
420 425 430

206108_0033_30wo_606194_seqlisting

Ile Cys Cys Ile Arg Thr Ala Lys Ala
435 440

<210> 83
<211> 279
<212> PRT
<213> Artificial Sequence

<220>
<223> CHIKV capsid consensus

<400> 83

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1 5 10 15

His Ser Met Glu Phe Ile Pro Thr Gln Thr Phe Tyr Asn Arg Arg Tyr
20 25 30

Gln Pro Arg Pro Trp Thr Pro Arg Pro Thr Ile Gln Val Ile Arg Pro
35 40 45

Arg Pro Arg Pro Gln Arg Gln Ala Gly Gln Leu Ala Gln Leu Ile Ser
50 55 60

Ala Val Asn Lys Leu Thr Met Arg Ala Val Pro Gln Gln Lys Pro Arg
65 70 75 80

Arg Asn Arg Lys Asn Lys Lys Gln Lys Gln Lys Gln Ala Pro Gln
85 90 95

Asn Asn Thr Asn Gln Lys Lys Gln Pro Pro Lys Lys Lys Pro Ala Gln
100 105 110

Lys Lys Lys Lys Pro Gly Arg Arg Glu Arg Met Cys Met Lys Ile Glu
115 120 125

Asn Asp Cys Ile Phe Glu Val Lys His Glu Gly Lys Val Thr Gly Tyr
130 135 140

Ala Cys Leu Val Gly Asp Lys Val Met Lys Pro Ala His Val Lys Gly
145 150 155 160

Thr Ile Asp Asn Ala Asp Leu Ala Lys Leu Ala Phe Lys Arg Ser Ser
165 170 175

Lys Tyr Asp Leu Glu Cys Ala Gln Ile Pro Val His Met Lys Ser Asp
180 185 190

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Ala Ser Lys Phe Thr His Glu Lys Pro Glu Gly Tyr Tyr Asn Trp His
195 200 205

His Gly Ala Val Gln Tyr Ser Gly Gly Arg Phe Thr Ile Pro Thr Gly
210 215 220

Ala Gly Lys Pro Gly Asp Ser Gly Arg Pro Ile Phe Asp Asn Lys Gly
225 230 235 240

Arg Val Val Ala Ile Val Leu Gly Gly Ala Asn Glu Gly Ala Arg Thr
245 250 255

Ala Leu Ser Val Val Thr Trp Asn Lys Asp Ile Val Thr Lys Ile Thr
260 265 270

Pro Glu Gly Ala Glu Glu Trp
275

<210> 84
<211> 439
<212> PRT
<213> Artificial Sequence

<220>
<223> CHIKV E1 consensus

<400> 84

Tyr Glu His Val Thr Val Ile Pro Asn Thr Val Gly Val Pro Tyr Lys
1 5 10 15

Thr Leu Val Asn Arg Pro Gly Tyr Ser Pro Met Val Leu Glu Met Glu
20 25 30

Leu Leu Ser Val Thr Leu Glu Pro Thr Leu Ser Leu Asp Tyr Ile Thr
35 40 45

Cys Glu Tyr Lys Thr Val Ile Pro Ser Pro Tyr Val Lys Cys Cys Gly
50 55 60

Thr Ala Glu Cys Lys Asp Lys Asn Leu Pro Asp Tyr Ser Cys Lys Val
65 70 75 80

Phe Thr Gly Val Tyr Pro Phe Met Trp Gly Gly Ala Tyr Cys Phe Cys
85 90 95

Asp Ala Glu Asn Thr Gln Leu Ser Glu Ala His Val Glu Lys Ser Glu
100 105 110

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Ser Cys Lys Thr Glu Phe Ala Ser Ala Tyr Arg Ala His Thr Ala Ser
115 120 125

Ala Ser Ala Lys Leu Arg Val Leu Tyr Gln Gly Asn Asn Ile Thr Val
130 135 140

Thr Ala Tyr Ala Asn Gly Asp His Ala Val Thr Val Lys Asp Ala Lys
145 150 155 160

Phe Ile Val Gly Pro Met Ser Ser Ala Trp Thr Pro Phe Asp Asn Lys
165 170 175

Ile Val Val Tyr Lys Gly Asp Val Tyr Asn Met Asp Tyr Pro Pro Phe
180 185 190

Gly Ala Gly Arg Pro Gly Gln Phe Gly Asp Ile Gln Ser Arg Thr Pro
195 200 205

Glu Ser Lys Asp Val Tyr Ala Asn Thr Gln Leu Val Leu Gln Arg Pro
210 215 220

Ala Val Gly Thr Val His Val Pro Tyr Ser Gln Ala Pro Ser Gly Phe
225 230 235 240

Lys Tyr Trp Leu Lys Glu Arg Gly Ala Ser Leu Gln His Thr Ala Pro
245 250 255

Phe Gly Cys Gln Ile Ala Thr Asn Pro Val Arg Ala Val Asn Cys Ala
260 265 270

Val Gly Asn Met Pro Ile Ser Ile Asp Ile Pro Glu Ala Ala Phe Thr
275 280 285

Arg Val Val Asp Ala Pro Ser Leu Thr Asp Met Ser Cys Glu Val Pro
290 295 300

Ala Cys Thr His Ser Ser Asp Phe Gly Gly Val Ala Ile Ile Lys Tyr
305 310 315 320

Ala Ala Ser Lys Lys Gly Lys Cys Ala Val His Ser Met Thr Asn Ala
325 330 335

Val Thr Ile Arg Glu Ala Glu Ile Glu Val Glu Gly Asn Ser Gln Leu
340 345 350

Gln Ile Ser Phe Ser Thr Ala Leu Ala Ser Ala Glu Phe Arg Val Gln
355 360 365

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Val Cys Ser Thr Gln Val His Cys Ala Ala Glu Cys His Pro Pro Lys
370 375 380

Asp His Ile Val Asn Tyr Pro Ala Ser His Thr Thr Leu Gly Val Gln
385 390 395 400

Asp Ile Ser Ala Thr Ala Met Ser Trp Val Gln Lys Ile Thr Gly Gly
405 410 415

Val Gly Leu Val Val Ala Val Ala Ala Leu Ile Leu Ile Val Val Leu
420 425 430

Cys Val Ser Phe Ser Arg His
435

<210> 85
<211> 423
<212> PRT
<213> Artificial Sequence

<220>
<223> CHIKV E2 consensus

<400> 85

Ser Thr Lys Asp Asn Phe Asn Val Tyr Lys Ala Thr Arg Pro Tyr Leu
1 5 10 15

Ala His Cys Pro Asp Cys Gly Glu Gly His Ser Cys His Ser Pro Val
20 25 30

Ala Leu Glu Arg Ile Arg Asn Glu Ala Thr Asp Gly Thr Leu Lys Ile
35 40 45

Gln Val Ser Leu Gln Ile Gly Ile Lys Thr Asp Asp Ser His Asp Trp
50 55 60

Thr Lys Leu Arg Tyr Met Asp Asn His Met Pro Ala Asp Ala Glu Arg
65 70 75 80

Ala Gly Leu Phe Val Arg Thr Ser Ala Pro Cys Thr Ile Thr Gly Thr
85 90 95

Met Gly His Phe Ile Leu Ala Arg Cys Pro Lys Gly Glu Thr Leu Thr
100 105 110

Val Gly Phe Thr Asp Ser Arg Lys Ile Ser His Ser Cys Thr His Pro
115 120 125

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Phe His His Asp Pro Pro Val Ile Gly Arg Glu Lys Phe His Ser Arg
130 135 140

Pro Gln His Gly Lys Glu Leu Pro Cys Ser Thr Tyr Val Gln Ser Thr
145 150 155 160

Ala Ala Thr Thr Glu Glu Ile Glu Val His Met Pro Pro Asp Thr Pro
165 170 175

Asp Arg Thr Leu Met Ser Gln Gln Ser Gly Asn Val Lys Ile Thr Val
180 185 190

Asn Gly Gln Thr Val Arg Tyr Lys Cys Asn Cys Gly Gly Ser Asn Glu
195 200 205

Gly Leu Thr Thr Thr Asp Lys Val Ile Asn Asn Cys Lys Val Asp Gln
210 215 220

Cys His Ala Ala Val Thr Asn His Lys Lys Trp Gln Tyr Asn Ser Pro
225 230 235 240

Leu Val Pro Arg Asn Ala Glu Leu Gly Asp Arg Lys Gly Lys Ile His
245 250 255

Ile Pro Phe Pro Leu Ala Asn Val Thr Cys Arg Val Pro Lys Ala Arg
260 265 270

Asn Pro Thr Val Thr Tyr Gly Lys Asn Gln Val Ile Met Leu Leu Tyr
275 280 285

Pro Asp His Pro Thr Leu Leu Ser Tyr Arg Asn Met Gly Glu Glu Pro
290 295 300

Asn Tyr Gln Glu Glu Trp Val Met His Lys Lys Glu Val Val Leu Thr
305 310 315 320

Val Pro Thr Glu Gly Leu Glu Val Thr Trp Gly Asn Asn Glu Pro Tyr
325 330 335

Lys Tyr Trp Pro Gln Leu Ser Thr Asn Gly Thr Ala His Gly His Pro
340 345 350

His Glu Ile Ile Leu Tyr Tyr Tyr Glu Leu Tyr Pro Thr Met Thr Val
355 360 365

Val Val Val Ser Val Ala Thr Phe Ile Leu Leu Ser Met Val Gly Met
370 375 380

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Ala Ala Gly Met Cys Met Cys Ala Arg Arg Arg Cys Ile Thr Pro Tyr
385 390 395 400

Glu Leu Thr Pro Gly Ala Thr Val Pro Phe Leu Leu Ser Leu Ile Cys
405 410 415

Cys Ile Arg Thr Ala Lys Ala
420

<210> 86

<211> 261

<212> PRT

<213> Artificial Sequence

<220>

<223> CHIKV capsid consensus

<400> 86

Met Glu Phe Ile Pro Thr Gln Thr Phe Tyr Asn Arg Arg Tyr Gln Pro
1 5 10 15

Arg Pro Trp Thr Pro Arg Pro Thr Ile Gln Val Ile Arg Pro Arg Pro
20 25 30

Arg Pro Gln Arg Gln Ala Gly Gln Leu Ala Gln Leu Ile Ser Ala Val
35 40 45

Asn Lys Leu Thr Met Arg Ala Val Pro Gln Gln Lys Pro Arg Arg Asn
50 55 60

Arg Lys Asn Lys Lys Gln Lys Gln Lys Gln Gln Ala Pro Gln Asn Asn
65 70 75 80

Thr Asn Gln Lys Lys Gln Pro Pro Lys Lys Lys Pro Ala Gln Lys Lys
85 90 95

Lys Lys Pro Gly Arg Arg Glu Arg Met Cys Met Lys Ile Glu Asn Asp
100 105 110

Cys Ile Phe Glu Val Lys His Glu Gly Lys Val Thr Gly Tyr Ala Cys
115 120 125

Leu Val Gly Asp Lys Val Met Lys Pro Ala His Val Lys Gly Thr Ile
130 135 140

Asp Asn Ala Asp Leu Ala Lys Leu Ala Phe Lys Arg Ser Ser Lys Tyr
145 150 155 160

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Asp Leu Glu Cys Ala Gln Ile Pro Val His Met Lys Ser Asp Ala Ser
165 170 175

Lys Phe Thr His Glu Lys Pro Glu Gly Tyr Tyr Asn Trp His His Gly
180 185 190

Ala Val Gln Tyr Ser Gly Gly Arg Phe Thr Ile Pro Thr Gly Ala Gly
195 200 205

Lys Pro Gly Asp Ser Gly Arg Pro Ile Phe Asp Asn Lys Gly Arg Val
210 215 220

Val Ala Ile Val Leu Gly Gly Ala Asn Glu Gly Ala Arg Thr Ala Leu
225 230 235 240

Ser Val Val Thr Trp Asn Lys Asp Ile Val Thr Lys Ile Thr Pro Glu
245 250 255

Gly Ala Glu Glu Trp
260

<210> 87
<211> 998
<212> PRT
<213> Artificial Sequence

<220>
<223> CHIKV Env consensus

<400> 87

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1 5 10 15

His Ser Ser Leu Ala Ile Pro Val Met Cys Leu Leu Ala Asn Thr Thr
20 25 30

Phe Pro Cys Ser Gln Pro Pro Cys Thr Pro Cys Cys Tyr Glu Lys Glu
35 40 45

Pro Glu Glu Thr Leu Arg Met Leu Glu Asp Asn Val Met Arg Pro Gly
50 55 60

Tyr Tyr Gln Leu Leu Gln Ala Ser Leu Thr Cys Ser Pro His Arg Gln
65 70 75 80

Arg Arg Arg Gly Arg Lys Arg Arg Ser Ala Thr Met Asp Trp Thr Trp
85 90 95

Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val His Ser Ser Thr Lys
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100                               105                               110
Asp Asn Phe Asn Val Tyr Lys Ala Thr Arg Pro Tyr Leu Ala His Cys
115                               120                               125
Pro Asp Cys Gly Glu Gly His Ser Cys His Ser Pro Val Ala Leu Glu
130                               135                               140
Arg Ile Arg Asn Glu Ala Thr Asp Gly Thr Leu Lys Ile Gln Val Ser
145                               150                               155                               160
Leu Gln Ile Gly Ile Lys Thr Asp Asp Ser His Asp Trp Thr Lys Leu
165                               170                               175
Arg Tyr Met Asp Asn His Met Pro Ala Asp Ala Glu Arg Ala Gly Leu
180                               185                               190
Phe Val Arg Thr Ser Ala Pro Cys Thr Ile Thr Gly Thr Met Gly His
195                               200                               205
Phe Ile Leu Ala Arg Cys Pro Lys Gly Glu Thr Leu Thr Val Gly Phe
210                               215                               220
Thr Asp Ser Arg Lys Ile Ser His Ser Cys Thr His Pro Phe His His
225                               230                               235                               240
Asp Pro Pro Val Ile Gly Arg Glu Lys Phe His Ser Arg Pro Gln His
245                               250                               255
Gly Lys Glu Leu Pro Cys Ser Thr Tyr Val Gln Ser Thr Ala Ala Thr
260                               265                               270
Thr Glu Glu Ile Glu Val His Met Pro Pro Asp Thr Pro Asp Arg Thr
275                               280                               285
Leu Met Ser Gln Gln Ser Gly Asn Val Lys Ile Thr Val Asn Gly Gln
290                               295                               300
Thr Val Arg Tyr Lys Cys Asn Cys Gly Gly Ser Asn Glu Gly Leu Thr
305                               310                               315                               320
Thr Thr Asp Lys Val Ile Asn Asn Cys Lys Val Asp Gln Cys His Ala
325                               330                               335
Ala Val Thr Asn His Lys Lys Trp Gln Tyr Asn Ser Pro Leu Val Pro
340                               345                               350

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206108_0033_30wo_606194_seqlisting

Arg Asn Ala Glu Leu Gly Asp Arg Lys Gly Lys Ile His Ile Pro Phe
355 360 365

Pro Leu Ala Asn Val Thr Cys Arg Val Pro Lys Ala Arg Asn Pro Thr
370 375 380

Val Thr Tyr Gly Lys Asn Gln Val Ile Met Leu Leu Tyr Pro Asp His
385 390 395 400

Pro Thr Leu Leu Ser Tyr Arg Asn Met Gly Glu Glu Pro Asn Tyr Gln
405 410 415

Glu Glu Trp Val Met His Lys Lys Glu Val Val Leu Thr Val Pro Thr
420 425 430

Glu Gly Leu Glu Val Thr Trp Gly Asn Asn Glu Pro Tyr Lys Tyr Trp
435 440 445

Pro Gln Leu Ser Thr Asn Gly Thr Ala His Gly His Pro His Glu Ile
450 455 460

Ile Leu Tyr Tyr Tyr Glu Leu Tyr Pro Thr Met Thr Val Val Val Val
465 470 475 480

Ser Val Ala Thr Phe Ile Leu Leu Ser Met Val Gly Met Ala Ala Gly
485 490 495

Met Cys Met Cys Ala Arg Arg Arg Cys Ile Thr Pro Tyr Glu Leu Thr
500 505 510

Pro Gly Ala Thr Val Pro Phe Leu Leu Ser Leu Ile Cys Cys Ile Arg
515 520 525

Thr Ala Lys Ala Arg Gly Arg Lys Arg Arg Ser Ala Thr Met Asp Trp
530 535 540

Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val His Ser Tyr
545 550 555 560

Glu His Val Thr Val Ile Pro Asn Thr Val Gly Val Pro Tyr Lys Thr
565 570 575

Leu Val Asn Arg Pro Gly Tyr Ser Pro Met Val Leu Glu Met Glu Leu
580 585 590

Leu Ser Val Thr Leu Glu Pro Thr Leu Ser Leu Asp Tyr Ile Thr Cys
595 600 605

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Glu Tyr Lys Thr Val Ile Pro Ser Pro Tyr Val Lys Cys Cys Gly Thr
610 615 620

Ala Glu Cys Lys Asp Lys Asn Leu Pro Asp Tyr Ser Cys Lys Val Phe
625 630 635 640

Thr Gly Val Tyr Pro Phe Met Trp Gly Gly Ala Tyr Cys Phe Cys Asp
645 650 655

Ala Glu Asn Thr Gln Leu Ser Glu Ala His Val Glu Lys Ser Glu Ser
660 665 670

Cys Lys Thr Glu Phe Ala Ser Ala Tyr Arg Ala His Thr Ala Ser Ala
675 680 685

Ser Ala Lys Leu Arg Val Leu Tyr Gln Gly Asn Asn Ile Thr Val Thr
690 695 700

Ala Tyr Ala Asn Gly Asp His Ala Val Thr Val Lys Asp Ala Lys Phe
705 710 715 720

Ile Val Gly Pro Met Ser Ser Ala Trp Thr Pro Phe Asp Asn Lys Ile
725 730 735

Val Val Tyr Lys Gly Asp Val Tyr Asn Met Asp Tyr Pro Pro Phe Gly
740 745 750

Ala Gly Arg Pro Gly Gln Phe Gly Asp Ile Gln Ser Arg Thr Pro Glu
755 760 765

Ser Lys Asp Val Tyr Ala Asn Thr Gln Leu Val Leu Gln Arg Pro Ala
770 775 780

Val Gly Thr Val His Val Pro Tyr Ser Gln Ala Pro Ser Gly Phe Lys
785 790 795 800

Tyr Trp Leu Lys Glu Arg Gly Ala Ser Leu Gln His Thr Ala Pro Phe
805 810 815

Gly Cys Gln Ile Ala Thr Asn Pro Val Arg Ala Val Asn Cys Ala Val
820 825 830

Gly Asn Met Pro Ile Ser Ile Asp Ile Pro Glu Ala Ala Phe Thr Arg
835 840 845

Val Val Asp Ala Pro Ser Leu Thr Asp Met Ser Cys Glu Val Pro Ala
850 855 860

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Cys Thr His Ser Ser Asp Phe Gly Gly Val Ala Ile Ile Lys Tyr Ala
865 870 875 880

Ala Ser Lys Lys Gly Lys Cys Ala Val His Ser Met Thr Asn Ala Val
885 890 895

Thr Ile Arg Glu Ala Glu Ile Glu Val Glu Gly Asn Ser Gln Leu Gln
900 905 910

Ile Ser Phe Ser Thr Ala Leu Ala Ser Ala Glu Phe Arg Val Gln Val
915 920 925

Cys Ser Thr Gln Val His Cys Ala Ala Glu Cys His Pro Pro Lys Asp
930 935 940

His Ile Val Asn Tyr Pro Ala Ser His Thr Thr Leu Gly Val Gln Asp
945 950 955 960

Ile Ser Ala Thr Ala Met Ser Trp Val Gln Lys Ile Thr Gly Gly Val
965 970 975

Gly Leu Val Val Ala Val Ala Ala Leu Ile Leu Ile Val Val Leu Cys
980 985 990

Val Ser Phe Ser Arg His
995

<210> 88
<211> 980
<212> PRT
<213> Artificial Sequence

<220>
<223> CHIKV Env consensus

<400> 88

Ser Leu Ala Ile Pro Val Met Cys Leu Leu Ala Asn Thr Thr Phe Pro
1 5 10 15

Cys Ser Gln Pro Pro Cys Thr Pro Cys Cys Tyr Glu Lys Glu Pro Glu
20 25 30

Glu Thr Leu Arg Met Leu Glu Asp Asn Val Met Arg Pro Gly Tyr Tyr
35 40 45

Gln Leu Leu Gln Ala Ser Leu Thr Cys Ser Pro His Arg Gln Arg Arg
50 55 60

206108_0033_30wo_606194_seqlisting

Arg Gly Arg Lys Arg Arg Ser Ala Thr Met Asp Trp Thr Trp Ile Leu
65 70 75 80

Phe Leu Val Ala Ala Ala Thr Arg Val His Ser Ser Thr Lys Asp Asn
85 90 95

Phe Asn Val Tyr Lys Ala Thr Arg Pro Tyr Leu Ala His Cys Pro Asp
100 105 110

Cys Gly Glu Gly His Ser Cys His Ser Pro Val Ala Leu Glu Arg Ile
115 120 125

Arg Asn Glu Ala Thr Asp Gly Thr Leu Lys Ile Gln Val Ser Leu Gln
130 135 140

Ile Gly Ile Lys Thr Asp Asp Ser His Asp Trp Thr Lys Leu Arg Tyr
145 150 155 160

Met Asp Asn His Met Pro Ala Asp Ala Glu Arg Ala Gly Leu Phe Val
165 170 175

Arg Thr Ser Ala Pro Cys Thr Ile Thr Gly Thr Met Gly His Phe Ile
180 185 190

Leu Ala Arg Cys Pro Lys Gly Glu Thr Leu Thr Val Gly Phe Thr Asp
195 200 205

Ser Arg Lys Ile Ser His Ser Cys Thr His Pro Phe His His Asp Pro
210 215 220

Pro Val Ile Gly Arg Glu Lys Phe His Ser Arg Pro Gln His Gly Lys
225 230 235 240

Glu Leu Pro Cys Ser Thr Tyr Val Gln Ser Thr Ala Ala Thr Thr Glu
245 250 255

Glu Ile Glu Val His Met Pro Pro Asp Thr Pro Asp Arg Thr Leu Met
260 265 270

Ser Gln Gln Ser Gly Asn Val Lys Ile Thr Val Asn Gly Gln Thr Val
275 280 285

Arg Tyr Lys Cys Asn Cys Gly Gly Ser Asn Glu Gly Leu Thr Thr Thr
290 295 300

Asp Lys Val Ile Asn Asn Cys Lys Val Asp Gln Cys His Ala Ala Val
305 310 315 320

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Thr Asn His Lys Lys Trp Gln Tyr Asn Ser Pro Leu Val Pro Arg Asn
325 330 335

Ala Glu Leu Gly Asp Arg Lys Gly Lys Ile His Ile Pro Phe Pro Leu
340 345 350

Ala Asn Val Thr Cys Arg Val Pro Lys Ala Arg Asn Pro Thr Val Thr
355 360 365

Tyr Gly Lys Asn Gln Val Ile Met Leu Leu Tyr Pro Asp His Pro Thr
370 375 380

Leu Leu Ser Tyr Arg Asn Met Gly Glu Glu Pro Asn Tyr Gln Glu Glu
385 390 395 400

Trp Val Met His Lys Lys Glu Val Val Leu Thr Val Pro Thr Glu Gly
405 410 415

Leu Glu Val Thr Trp Gly Asn Asn Glu Pro Tyr Lys Tyr Trp Pro Gln
420 425 430

Leu Ser Thr Asn Gly Thr Ala His Gly His Pro His Glu Ile Ile Leu
435 440 445

Tyr Tyr Tyr Glu Leu Tyr Pro Thr Met Thr Val Val Val Val Ser Val
450 455 460

Ala Thr Phe Ile Leu Leu Ser Met Val Gly Met Ala Ala Gly Met Cys
465 470 475 480

Met Cys Ala Arg Arg Arg Cys Ile Thr Pro Tyr Glu Leu Thr Pro Gly
485 490 495

Ala Thr Val Pro Phe Leu Leu Ser Leu Ile Cys Cys Ile Arg Thr Ala
500 505 510

Lys Ala Arg Gly Arg Lys Arg Arg Ser Ala Thr Met Asp Trp Thr Trp
515 520 525

Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val His Ser Tyr Glu His
530 535 540

Val Thr Val Ile Pro Asn Thr Val Gly Val Pro Tyr Lys Thr Leu Val
545 550 555 560

Asn Arg Pro Gly Tyr Ser Pro Met Val Leu Glu Met Glu Leu Leu Ser

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565 570 575

Val Thr Leu Glu Pro Thr Leu Ser Leu Asp Tyr Ile Thr Cys Glu Tyr
580 585 590

Lys Thr Val Ile Pro Ser Pro Tyr Val Lys Cys Cys Gly Thr Ala Glu
595 600 605

Cys Lys Asp Lys Asn Leu Pro Asp Tyr Ser Cys Lys Val Phe Thr Gly
610 615 620

Val Tyr Pro Phe Met Trp Gly Gly Ala Tyr Cys Phe Cys Asp Ala Glu
625 630 635 640

Asn Thr Gln Leu Ser Glu Ala His Val Glu Lys Ser Glu Ser Cys Lys
645 650 655

Thr Glu Phe Ala Ser Ala Tyr Arg Ala His Thr Ala Ser Ala Ser Ala
660 665 670

Lys Leu Arg Val Leu Tyr Gln Gly Asn Asn Ile Thr Val Thr Ala Tyr
675 680 685

Ala Asn Gly Asp His Ala Val Thr Val Lys Asp Ala Lys Phe Ile Val
690 695 700

Gly Pro Met Ser Ser Ala Trp Thr Pro Phe Asp Asn Lys Ile Val Val
705 710 715 720

Tyr Lys Gly Asp Val Tyr Asn Met Asp Tyr Pro Pro Phe Gly Ala Gly
725 730 735

Arg Pro Gly Gln Phe Gly Asp Ile Gln Ser Arg Thr Pro Glu Ser Lys
740 745 750

Asp Val Tyr Ala Asn Thr Gln Leu Val Leu Gln Arg Pro Ala Val Gly
755 760 765

Thr Val His Val Pro Tyr Ser Gln Ala Pro Ser Gly Phe Lys Tyr Trp
770 775 780

Leu Lys Glu Arg Gly Ala Ser Leu Gln His Thr Ala Pro Phe Gly Cys
785 790 795 800

Gln Ile Ala Thr Asn Pro Val Arg Ala Val Asn Cys Ala Val Gly Asn
805 810 815

206108_0033_30wo_606194_seqlisting

Met Pro Ile Ser Ile Asp Ile Pro Glu Ala Ala Phe Thr Arg Val Val
820 825 830

Asp Ala Pro Ser Leu Thr Asp Met Ser Cys Glu Val Pro Ala Cys Thr
835 840 845

His Ser Ser Asp Phe Gly Gly Val Ala Ile Ile Lys Tyr Ala Ala Ser
850 855 860

Lys Lys Gly Lys Cys Ala Val His Ser Met Thr Asn Ala Val Thr Ile
865 870 875 880

Arg Glu Ala Glu Ile Glu Val Glu Gly Asn Ser Gln Leu Gln Ile Ser
885 890 895

Phe Ser Thr Ala Leu Ala Ser Ala Glu Phe Arg Val Gln Val Cys Ser
900 905 910

Thr Gln Val His Cys Ala Ala Glu Cys His Pro Pro Lys Asp His Ile
915 920 925

Val Asn Tyr Pro Ala Ser His Thr Thr Leu Gly Val Gln Asp Ile Ser
930 935 940

Ala Thr Ala Met Ser Trp Val Gln Lys Ile Thr Gly Gly Val Gly Leu
945 950 955 960

Val Val Ala Val Ala Ala Leu Ile Leu Ile Val Val Leu Cys Val Ser
965 970 975

Phe Ser Arg His
980

<210> 89
<211> 1374
<212> DNA
<213> Artificial Sequence

<220>
<223> CHIKV E1 consensus

<400> 89
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ggctacagcc ccatgggtgct ggaaatggaa ctgctgtccg tgaccctgga acccaccctg 180
agcctggact acatcacctg cgagtacaag acagtgatcc ccagccccta cgtgaagtgc 240
tgcggcaccg ccgagtgcaa ggacaagaac ctgcccgact acagctgcaa ggtgttcacc 300

ggcggtgtacc ccttcattgt gggcggagcc tactgtctct ggcagcggcga gaaacaccag
420 cttgtccgag cccaagtgtga gaagagcgaag agctgtcaaga ccgagttcgc cagcgccctac
480 cgggcccaca cagccagcgc cagcgccaag ctgctgggtgc tgtaccagg ccaacaacatc
540 accgtgaccg cctacgcgca cggcgaccac gccgtgacag tgaaggacgc caagtctatc
600 gttggccccca ttgagcagcgc ctggaccccc ttgcacaaca agatcgttgt gtaacaagggc
660 gacgtgtaca acatgtgacta ccccccttc ggagccggca gacccggcca gttcggcgga
720 atccagagcc ggacccccga gagcaaggac gttgtaccga ataccagct ggtgtgtcag
780 agacccgcgc ttgggtcacctg gcaagtgtct tactagccagg ccccaagcgg cttcaagta
840 ttgtctgaag agaggggcgc cagccttgca caccgcgcc ccttcggctg ccagatcgc
900 accaacccgc ttgcgggcct gaattgtgct gttggcaaca ttgcccatag catcgacatc
960 ccgagggccg ccttcaccag gttgtgtgac gcccccagc ttgaccgacat gactgtcgag
1020 gttgccgcct gacccccag cagcgtactt ggcggcgtg ccatcatcaa gtaagccgc
1080 agcaagaag gcaagtgcgc cgtgcacagc atgaaccaat ccgtgacat ccgggaaggc
1140 gagatcgagg ttggaaggca cagccagctg cagatcagct tcagcaccgc cttggccag
1200 gccgagttcc ggtgtcaggt ctgcagcacc caggttgacct gttgcggccga gttgtcaccc
1260 cccaaggacc acatctgtgaa ctacccgcgc agccaccaca ccttgggcgt gcaaggacatc
1320 agcgcaccgc ccatgagctg gttgcagaag atcacaggcg gctgtcgccct ggtgtgtggc
1374 gttggccgcc ttgatccctgat cgtgtgtcgt tgcgttgact tcagccggca ctga

<210> 90
<211> 1326
<212> DNA
<213> Artificial Sequence
<220>
<223> CHIKV E2 consensus

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aaggaacaat tcaacgtgtta caaggccacc cggccctaac ttgcccactg ccccgattg
120
ggcgaggggc acagctgtcca cagccccgtg gcccctggaac ggtatccgga cgaaggccacc
180
gacggcacc ttgaagatcca ggtgtccctg cagatctgca tcaagaccga cgcacagccac
240
gacttgacca agctgtcgtta catggacaac cacatgcccc ccgacgcgga gagagccggc
300
ctgttcttc ggaccagcgc cccctgcacc atcacccgca ccatgggcca cttcatctg
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gtccgtgtcc ccaaggcga gacactgga ccactgacc gttggcttca ccgacagcgc gaagatcagc
420
cacttctga cccaacctt ccaaccagac cccccgtga tggccggga gaagtctcac
480
agcagggccc agcacggcga agagctgccc tgcaagcacc tgcaagcacc caccgccc
540

600 acaaccgagg aaatcgaagt gcacatgccc ccgatatacc ccgaccggac cctgatgagc
660 cagcagagcg gcaacagtga gatacccggt aacggccaaga cctgtcggta caagtgcaca
720 tgcggcgcca gcaacgagg cctgaacca accgaacaagg tgatacaaca ctgcaagggtg
780 gaccagtgc accgcgcctg gaccaaacac aagaagtggc agtaacaacg cccctctgtg
840 ccccggaatg ccgagcctgg ggaaccgaag ggaagatcc acatccctt cccctctggc
900 aacgtgacct gccgggtgc caaggccgg aaccccaag tgacctagc caagaaccag
960 gtgatcatgc tgcgtatacc gaaaccaacc acctctgtt cctaaccgaa catgggcgag
1020 gaaaccaact aaccaagga gtgtgtcatg cacaagaag aagtgtgtgt gaccgtcccc
1080 accgagggcc tgaagtgaac ctggggcaac aacgagccct acaagtactg gcccagctg
1140 tccaaccaag gcaaccgcca cggccaacc cagagatca tcctgtacta ctacgagctg
1200 taccatacca tgaccgttgt gtgtgtgtcc gtggccaact ttatccctgt gttccatgtc
1260 ggcattggcc ctgcatgtg catgtgcgc aggagcgct gtatacccc ctacgagctg
1320 acaacctggc ccaaccgtcc ctctctgt tccctgact gctgcatccg gaccgccaag
1326 gacctga

<210> 91
<211> 840
<212> DNA
<213> Artificial Sequence
<220>
<223> CHIKV capsid consensus

<400> 91
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gactggacct ggattctgtt cctgggtggca gccgctaccc gagtccattc ccagtctgtg	1560
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ggcgtggaaa ctaccacacc cagcaagcag tccaacaaca agtacgctgc aagttcatat	2100
ctgtccctga ccccgagca gtggaagtct cacaatctt atagtggcca ggtgacccat	2160
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<210> 99

<211> 2220

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic Acid Sequence encoding CHIKV3-IgG

<400> 99

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tctctgacat gcaccgtgag cggcgacagt atcagctcct actcatggag ctggattcgg	180
cagccccctg gcaaaggact ggagtggatc ggctacattc actatacagg aagcactaac	240
tataatccat cactgaagag ccgcctgacc atcagtgtgg acgcctcaaa aaaccagttc	300
tcctgaagc tgtctagtgt cactgccgct gacaccgccg tgtactattg cgcacgggat	360
tggggcggat actcaagctc ctggacatat gggatggacg tgtgggggca gggcaccaca	420
gtcacagtgt ctagtgcaag cactaaaggc ccctccgtgt ttccactggc cccctcaagc	480

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600 cctgtcacccg tgttccctggaa cttggagcc ctgaattccg gggtccatac ctttcccgct
660 gtgctgcagt cctctgggct gtacttcttg agttcagttg tcacagttgcc tagcttctct
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1560 aatcccgccc ctatggatg gaacttgatt ctgttccctg tcgctgcagc cacttgcgtg
1620 catccgaca ttcatgtgac ccagtctccc agttcacga gcgccttccgt cggagatcga
1680 gtgacaatca ctgttagggc aagccagggg atttcaaca gtcttggccctg gtaaccaagcag
1740 aagcccgaaa aagcttccaa gctgtctgtg tatgtctgcaa gcagaactgga atccgggtg
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1980 ccttcattct gacgaagctt gaagagtggg accgcttcag tgggtgtgct gctgaacaac
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2100 tccagggagt ctgttgaccga acaggacagt aaagattcaa catatagcct gtcttagtact
2160 ctgaacccga gcaaggctga ctacggagag cacaagtggt atgcattgca agtgacccac
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<210> 100
<211> 2208
<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic Acid Sequence encoding CHIKV4-IgG

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cagacacctg agaagcggct ggaatgggtg gcctacatca gcaacggcgg aatttcaaca	240
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ctgtacctgc agatgtcccg gctgaagtct gaagacacag caatctacta ttgcgtccgc	360
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gtgctgattc agtctccagc cattatgtct gctagtctgg gcgagcgcgt cactatgacc	1620
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<210> 101
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> ZIKV-3F12E9-VH

<400> 101

Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Ala Leu Ile Leu Lys Gly
1 5 10 15

Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys
20 25 30

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Arg Tyr Gly Met Ser Trp Gly Arg Gln Thr Pro Asp Lys Arg Leu
50 55 60

Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Thr Tyr Thr Tyr Tyr Pro
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
85 90 95

Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met
100 105 110

Tyr Tyr Cys Ala Arg Ser Trp Phe Ala Tyr Trp Gly Arg Gly Thr Leu
115 120 125

Val Thr Val Ser Ala
130

206108_0033_30wo_606194_seqlisting

<210> 102
 <211> 132
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ZIKV-3F12E9-VL

<400> 102

Met Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg
 1 5 10 15

Glu Thr Asn Gly Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser
 20 25 30

Val Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser
 35 40 45

Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg
 50 55 60

Pro Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp
 65 70 75 80

Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe
 85 90 95

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr
 100 105 110

Cys Trp Gln Gly Thr His Phe Pro His Thr Phe Gly Gly Gly Thr Lys
 115 120 125

Leu Glu Ile Lys
 130

<210> 103
 <211> 134
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ZIKV-8A9F9-VH

<400> 103

Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Ile Leu Lys Gly
 1 5 10 15

Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys
 20 25 30

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Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ser Pro Glu Lys Arg Leu
50 55 60

Glu Trp Val Ala Glu Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Pro
65 70 75 80

Asp Thr Val Thr Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
85 90 95

Thr Leu Tyr Leu Glu Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met
100 105 110

Tyr Tyr Cys Ala Ser Asp Gly Tyr Tyr Ser His Trp Gly Gln Gly Thr
115 120 125

Ser Val Thr Val Ser Ser
130

<210> 104
<211> 131
<212> PRT
<213> Artificial Sequence

<220>
<223> ZIKV-8A9F9-VL

<400> 104

Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
1 5 10 15

Ser Arg Ser Asp Val Val Met Thr Gln Ile Pro Leu Ser Leu Pro Val
20 25 30

Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
35 40 45

Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro
50 55 60

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
65 70 75 80

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
85 90 95

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Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
100 105 110

Phe Gln Ser Thr His Val Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
115 120 125

Glu Ile Lys
130

<210> 105
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> ZIKV-8D10F4-VH

<400> 105

Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Ile Leu Lys Gly
1 5 10 15

Val Lys Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys
20 25 30

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ser Pro Glu Lys Arg Leu
50 55 60

Glu Trp Val Ala Glu Ile Ser Ser Gly Gly Ser Tyr Ile Tyr Tyr Pro
65 70 75 80

Asp Thr

<210> 106
<211> 131
<212> PRT
<213> Artificial Sequence

<220>
<223> ZIKV-8D10F4-VL

<400> 106

Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
1 5 10 15

Ser Ser Ser Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val
20 25 30

206108_0033_30wo_606194_seqlisting

Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
35 40 45

Val His Ser Asn Gly Asn Thr Tyr Phe His Trp Tyr Leu Gln Lys Pro
50 55 60

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
65 70 75 80

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
85 90 95

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Leu Tyr Phe Cys
100 105 110

Ser Gln Ser Thr His Val Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
115 120 125

Glu Ile Lys
130

<210> 107
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> ZIKV-IC2A6-VH

<400> 107

Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Ile Leu Lys Gly
1 5 10 15

Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys
20 25 30

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ser Pro Glu Lys Arg Leu
50 55 60

Glu Trp Val Ala Glu Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Pro
65 70 75 80

Asp Thr Val Thr Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
85 90 95

206108_0033_30wo_606194_seqlisting

Thr Leu Tyr Leu Glu Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met
100 105 110

Tyr Tyr Cys Ala Ser Asp Gly Tyr Tyr Ser His Trp Gly Gln Gly Thr
115 120 125

Ser Val Thr Val Ser Ser
130

<210> 108
<211> 131
<212> PRT
<213> Artificial Sequence

<220>
<223> ZIKV-IC2A6-VH

<400> 108

Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
1 5 10 15

Ser Ser Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val
20 25 30

Cys Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
35 40 45

Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro
50 55 60

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
65 70 75 80

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
85 90 95

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
100 105 110

Phe Gln Ser Thr His Val Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
115 120 125

Glu Ile Lys
130

<210> 109
<211> 146
<212> PRT
<213> Artificial Sequence

206108_0033_30wo_606194_seqlisting

<220>

<223> ZIKV-ID4G7-VH

<400> 109

Met Ala Trp Val Trp Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
1 5 10 15

Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
20 25 30

Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu
50 55 60

Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala
65 70 75 80

Asp Asp Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
85 90 95

Thr Ala Tyr Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr
100 105 110

Tyr Phe Cys Ala Arg Glu Ile Ser Lys Ile Tyr Tyr Tyr Gly Ser Ser
115 120 125

Tyr Glu Asn Gly Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val
130 135 140

Ser Ser
145

<210> 110

<211> 131

<212> PRT

<213> Artificial Sequence

<220>

<223> ZIKV-ID4G7-VL

<400> 110

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Asn Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala
20 25 30

206108_0033_30wo_606194_seqlisting

Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser
35 40 45

Val Asp Ser Phe Gly Asn Ser Phe Met His Trp Phe Gln Gln Lys Pro
50 55 60

Gly Gln Pro Pro Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu Ser
65 70 75 80

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr
85 90 95

Leu Thr Ile Asp Pro Val Glu Ala Asp Asp Ala Ala Thr Tyr Tyr Cys
100 105 110

Gln Gln Asn Asn Glu Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu
115 120 125

Glu Ile Lys
130

<210> 111

<211> 728

<212> PRT

<213> Artificial Sequence

<220>

<223> Human anti-Zika (3F12E9)-IgG4: Human IgG heavy signal
peptide-VH-CH1-Hinge Region-CH2-CH3-custom Furin cleavage
site-'GSG' Linker and P2A Peptide-human kappa light chain signal
peptide-VL-CL (kappa)

<400> 111

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys
20 25 30

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Arg Tyr Gly Met Ser Trp Gly Arg Gln Thr Pro Asp Lys Arg Leu
50 55 60

Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Thr Tyr Thr Tyr Tyr Pro
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
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85

90

95

Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met
 100 105 110

Tyr Tyr Cys Ala Arg Ser Trp Phe Ala Tyr Trp Gly Arg Gly Thr Leu
 115 120 125

Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 130 135 140

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
 145 150 155 160

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 165 170 175

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 180 185 190

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 195 200 205

Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
 210 215 220

Thr Lys Val Asp Lys Arg Val Ser Pro Asn Met Val Pro His Ala His
 225 230 235 240

His Ala Gln Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe
 245 250 255

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 260 265 270

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
 275 280 285

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 290 295 300

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 305 310 315 320

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 325 330 335

206108_0033_30wo_606194_seqlisting

Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
340 345 350

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
355 360 365

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
370 375 380

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
385 390 395 400

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
405 410 415

Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
420 425 430

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
435 440 445

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Arg Gly Arg Lys
450 455 460

Arg Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala
465 470 475 480

Gly Asp Val Glu Glu Asn Pro Gly Pro Met Val Leu Gln Thr Gln Val
485 490 495

Phe Ile Ser Leu Leu Leu Trp Ile Ser Gly Ala Tyr Gly Asp Val Val
500 505 510

Met Thr Gln Thr Pro Leu Thr Leu Ser Val Thr Ile Gly Gln Pro Ala
515 520 525

Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys
530 535 540

Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser Pro Lys Arg
545 550 555 560

Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro Asp Arg Phe
565 570 575

Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val
580 585 590

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Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Trp Gln Gly Thr His Phe
595 600 605

Pro His Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val
610 615 620

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
625 630 635 640

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
645 650 655

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
660 665 670

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
675 680 685

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
690 695 700

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
705 710 715 720

Lys Ser Phe Asn Arg Gly Glu Cys
725

<210> 112

<211> 731

<212> PRT

<213> Artificial Sequence

<220>

<223> Human IgG heavy signal peptide-VH-CH1-Hinge Region-CH2-CH3-custom
Furin cleavage site-'GSG' Linker and P2A Peptide-human kappa
light chain signal peptide-VL-CL (kappa)

<400> 112

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys
20 25 30

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Arg Tyr Gly Met Ser Trp Gly Arg Gln Thr Pro Asp Lys Arg Leu
50 55 60

206108_0033_30wo_606194_seqlisting

Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Thr Tyr Thr Tyr Tyr Pro
 65 70 75 80
 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
 85 90 95
 Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met
 100 105 110
 Tyr Tyr Cys Ala Arg Ser Trp Phe Ala Tyr Trp Gly Arg Gly Thr Leu
 115 120 125
 Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 130 135 140
 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 145 150 155 160
 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 165 170 175
 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 180 185 190
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 195 200 205
 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 210 215 220
 Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
 225 230 235 240
 Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
 245 250 255
 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 260 265 270
 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
 275 280 285
 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 290 295 300
 Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
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206108_0033_30wo_606194_seqlisting
 305 310 315 320
 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 325 330 335
 Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
 340 345 350
 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
 355 360 365
 Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
 370 375 380
 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 385 390 395 400
 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
 405 410 415
 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
 420 425 430
 Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
 435 440 445
 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Arg
 450 455 460
 Gly Arg Lys Arg Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu
 465 470 475 480
 Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Val Leu Gln
 485 490 495
 Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser Gly Ala Tyr Gly
 500 505 510
 Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Val Thr Ile Gly
 515 520 525
 Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
 530 535 540
 Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser
 545 550 555 560

206108_0033_30wo_606194_seqlisting

Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
565 570 575

Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
580 585 590

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Trp Gln Gly
595 600 605

Thr His Phe Pro His Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
610 615 620

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
625 630 635 640

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Phe
645 650 655

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
660 665 670

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
675 680 685

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
690 695 700

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
705 710 715 720

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
725 730

<210> 113

<211> 729

<212> PRT

<213> Artificial Sequence

<220>

<223> Human IgG heavy signal peptide-VH-CH1-Hinge Region-CH2-CH3-custom
Furin cleavage site-'GSG' Linker and P2A Peptide-human kappa
light chain signal peptide-VL-CL (kappa)

<400> 113

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys
20 25 30

206108_0033_30wo_606194_seqlisting

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ser Pro Glu Lys Arg Leu
50 55 60

Glu Trp Val Ala Glu Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Pro
65 70 75 80

Asp Thr Val Thr Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
85 90 95

Thr Leu Tyr Leu Glu Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met
100 105 110

Tyr Tyr Cys Ala Ser Asp Gly Tyr Tyr Ser His Trp Gly Gln Gly Thr
115 120 125

Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
130 135 140

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
145 150 155 160

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
165 170 175

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
180 185 190

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
195 200 205

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
210 215 220

Asn Thr Lys Val Asp Lys Arg Val Ser Pro Asn Met Val Pro His Ala
225 230 235 240

His His Ala Gln Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
245 250 255

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
260 265 270

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
275 280 285

206108_0033_30wo_606194_seqlisting

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
 290 295 300
 Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
 305 310 315 320
 Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 325 330 335
 Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
 340 345 350
 Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
 355 360 365
 Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 370 375 380
 Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
 385 390 395 400
 Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
 405 410 415
 Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
 420 425 430
 Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
 435 440 445
 His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Arg Gly Arg
 450 455 460
 Lys Arg Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln
 465 470 475 480
 Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Val Leu Gln Thr Gln
 485 490 495
 Val Phe Ile Ser Leu Leu Leu Trp Ile Ser Gly Ala Tyr Gly Asp Val
 500 505 510
 Val Met Thr Gln Ile Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln
 515 520 525
 Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly
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530 206108_0033_30wo_606194_seqlisting
535 540

Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys
545 550 555 560

Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg
565 570 575

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg
580 585 590

Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Phe Gln Ser Thr His
595 600 605

Val Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr
610 615 620

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
625 630 635 640

Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
645 650 655

Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
660 665 670

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
675 680 685

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
690 695 700

Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
705 710 715 720

Thr Lys Ser Phe Asn Arg Gly Glu Cys
725

<210> 114
<211> 732
<212> PRT
<213> Artificial Sequence

<220>
<223> Human anti-Zika (8A9F9)-IgG1: Human IgG heavy signal
peptide-VH-CH1-Hinge Region-CH2-CH3-custom Furin cleavage
site-'GSG' Linker and P2A Peptide-human kappa light chain signal
peptide-VL-CL (kappa)

<400> 114

206108_0033_30wo_606194_seqlisting

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys
20 25 30

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ser Pro Glu Lys Arg Leu
50 55 60

Glu Trp Val Ala Glu Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Pro
65 70 75 80

Asp Thr Val Thr Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
85 90 95

Thr Leu Tyr Leu Glu Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met
100 105 110

Tyr Tyr Cys Ala Ser Asp Gly Tyr Tyr Ser His Trp Gly Gln Gly Thr
115 120 125

Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
130 135 140

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
145 150 155 160

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
165 170 175

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
180 185 190

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
195 200 205

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
210 215 220

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
225 230 235 240

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
245 250 255

206108_0033_30wo_606194_seqlisting

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
260 265 270

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
275 280 285

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
290 295 300

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
305 310 315 320

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
325 330 335

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
340 345 350

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
355 360 365

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
370 375 380

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
385 390 395 400

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
405 410 415

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
420 425 430

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
435 440 445

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455 460

Arg Gly Arg Lys Arg Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu
465 470 475 480

Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Val Leu
485 490 495

Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser Gly Ala Tyr

206108_0033_30wo_606194_seqlisting
500 505 510

Gly Asp Val Val Met Thr Gln Ile Pro Leu Ser Leu Pro Val Ser Leu
515 520 525

Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His
530 535 540

Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln
545 550 555 560

Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val
565 570 575

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
580 585 590

Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Phe Gln
595 600 605

Ser Thr His Val Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
610 615 620

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
625 630 635 640

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
645 650 655

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
660 665 670

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
675 680 685

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
690 695 700

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
705 710 715 720

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
725 730

<210> 115
<211> 728
<212> PRT
<213> Artificial Sequence

206108_0033_30wo_606194_seqlisting

<220>

<223> Human anti-Zika (8D10F4)-IgG4: Human IgG heavy signal
peptide-VH-CH1-Hinge Region-CH2-CH3-custom Furin cleavage
site-'GSG' Linker and P2A Peptide-human kappa light chain signal
peptide-VL-CL (kappa)

<400> 115

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys
20 25 30

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ser Pro Glu Lys Arg Leu
50 55 60

Glu Trp Val Ala Glu Ile Ser Ser Gly Gly Ser Tyr Ile Tyr Tyr Pro
65 70 75 80

Asp Thr Val Thr Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
85 90 95

Thr Leu Tyr Leu Glu Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met
100 105 110

Tyr Tyr Cys Ala Ser Asp Gly Tyr Tyr Ser His Trp Gly Gln Gly Thr
115 120 125

Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
130 135 140

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
145 150 155 160

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
165 170 175

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
180 185 190

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
195 200 205

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
210 215 220

206108_0033_30wo_606194_seqlisting

Asn Thr Lys Val Asp Lys Arg Val Ser Pro Asn Met Val Pro His Ala
 225 230 235 240
 His His Ala Gln Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
 245 250 255
 Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 260 265 270
 Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
 275 280 285
 Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
 290 295 300
 Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
 305 310 315 320
 Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 325 330 335
 Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
 340 345 350
 Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
 355 360 365
 Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 370 375 380
 Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
 385 390 395 400
 Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
 405 410 415
 Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
 420 425 430
 Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
 435 440 445
 His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Arg Gly Arg
 450 455 460
 Lys Arg Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln

206108_0033_30wo_606194_seqlisting

465 470 475 480

Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Val Leu Gln Thr Gln
485 490 495

Val Phe Ile Ser Leu Leu Leu Trp Ile Ser Gly Ala Tyr Gly Asp Val
500 505 510

Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln
515 520 525

Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly
530 535 540

Asn Thr Tyr Phe His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys
545 550 555 560

Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg
565 570 575

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg
580 585 590

Val Glu Ala Glu Asp Leu Gly Leu Tyr Phe Cys Ser Gln Ser Thr His
595 600 605

Val Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Thr Val
610 615 620

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
625 630 635 640

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
645 650 655

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
660 665 670

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
675 680 685

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
690 695 700

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
705 710 715 720

206108_0033_30wo_606194_seqlisting
 Lys Ser Phe Asn Arg Gly Glu Cys
 725

<210> 116
 <211> 732
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human anti-Zika (8D10F4)-IgG1: Human IgG heavy signal
 peptide-VH-CH1-Hinge Region-CH2-CH3-custom Furin cleavage
 site-'GSG' Linker and P2A Peptide-human kappa light chain signal
 peptide-VL-CL (kappa)

<400> 116

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
 1 5 10 15

Thr His Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys
 20 25 30

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 35 40 45

Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ser Pro Glu Lys Arg Leu
 50 55 60

Glu Trp Val Ala Glu Ile Ser Ser Gly Gly Ser Tyr Ile Tyr Tyr Pro
 65 70 75 80

Asp Thr Val Thr Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
 85 90 95

Thr Leu Tyr Leu Glu Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met
 100 105 110

Tyr Tyr Cys Ala Ser Asp Gly Tyr Tyr Ser His Trp Gly Gln Gly Thr
 115 120 125

Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
 130 135 140

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
 145 150 155 160

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
 165 170 175

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
 180 185 190

206108_0033_30wo_606194_seqlisting

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
195 200 205

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
210 215 220

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
225 230 235 240

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
245 250 255

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
260 265 270

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
275 280 285

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
290 295 300

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
305 310 315 320

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
325 330 335

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
340 345 350

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
355 360 365

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
370 375 380

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
385 390 395 400

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
405 410 415

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
420 425 430

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala

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435
 440
 445
 Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 450 455 460
 Arg Gly Arg Lys Arg Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu
 465 470 475 480
 Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Val Leu
 485 490 495
 Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser Gly Ala Tyr
 500 505 510
 Gly Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Leu
 515 520 525
 Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His
 530 535 540
 Ser Asn Gly Asn Thr Tyr Phe His Trp Tyr Leu Gln Lys Pro Gly Gln
 545 550 555 560
 Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val
 565 570 575
 Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
 580 585 590
 Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Leu Tyr Phe Cys Ser Gln
 595 600 605
 Ser Thr His Val Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
 610 615 620
 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
 625 630 635 640
 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
 645 650 655
 Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
 660 665 670
 Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
 675 680 685

206108_0033_30wo_606194_seqlisting
 Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
 690 695 700

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
 705 710 715 720

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 725 730

<210> 117
 <211> 740
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human anti-zika (1D4G7)-IgG4: Human IgG heavy signal
 peptide-VH-CH1-Hinge Region-CH2-CH3-custom Furin cleavage
 site-'GSG' Linker and P2A Peptide-human kappa light chain signal
 peptide-VL-CL (kappa)

<400> 117

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
 1 5 10 15

Thr His Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
 20 25 30

Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45

Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu
 50 55 60

Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala
 65 70 75 80

Asp Asp Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
 85 90 95

Thr Ala Tyr Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr
 100 105 110

Tyr Phe Cys Ala Arg Glu Ile Ser Lys Ile Tyr Tyr Tyr Gly Ser Ser
 115 120 125

Tyr Glu Asn Gly Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val
 130 135 140

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys
 145 150 155 160

206108_0033_30wo_606194_seqlisting

Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys
165 170 175

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
180 185 190

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
195 200 205

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
210 215 220

Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val
225 230 235 240

Asp Lys Arg Val Ser Pro Asn Met Val Pro His Ala His His Ala Gln
245 250 255

Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
260 265 270

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
275 280 285

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
290 295 300

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
305 310 315 320

Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
325 330 335

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
340 345 350

Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
355 360 365

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
370 375 380

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
385 390 395 400

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn

206108_0033_30wo_606194_seqlisting

405

410

415

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 420 425 430

Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val
 435 440 445

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 450 455 460

Lys Ser Leu Ser Leu Ser Leu Gly Lys Arg Gly Arg Lys Arg Arg Ser
 465 470 475 480

Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val
 485 490 495

Glu Glu Asn Pro Gly Pro Met Val Leu Gln Thr Gln Val Phe Ile Ser
 500 505 510

Leu Leu Leu Trp Ile Ser Gly Ala Tyr Gly Asn Ile Val Leu Thr Gln
 515 520 525

Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser
 530 535 540

Cys Arg Ala Ser Glu Ser Val Asp Ser Phe Gly Asn Ser Phe Met His
 545 550 555 560

Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Leu
 565 570 575

Ala Ser Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly
 580 585 590

Ser Arg Thr Asp Phe Thr Leu Thr Ile Asp Pro Val Glu Ala Asp Asp
 595 600 605

Ala Ala Thr Tyr Tyr Cys Gln Gln Asn Asn Glu Tyr Pro Tyr Thr Phe
 610 615 620

Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro Ser
 625 630 635 640

Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala
 645 650 655

206108_0033_30wo_606194_seqlisting

Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
660 665 670

Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser
675 680 685

Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr
690 695 700

Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys
705 710 715 720

Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
725 730 735

Arg Gly Glu Cys
740

<210> 118
<211> 743
<212> PRT
<213> Artificial Sequence

<220>
<223> Human anti-Zika (1D4G7)-IgG1: Human IgG heavy signal
peptide-VH-CH1-Hinge Region-CH2-CH3-custom Furin cleavage
site-'GSG' Linker and P2A Peptide-human kappa light chain signal
peptide-VL-CL (kappa)

<400> 118

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
20 25 30

Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu
50 55 60

Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala
65 70 75 80

Asp Asp Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
85 90 95

Thr Ala Tyr Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr
100 105 110

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Tyr Phe Cys Ala Arg Glu Ile Ser Lys Ile Tyr Tyr Tyr Gly Ser Ser
115 120 125

Tyr Glu Asn Gly Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val
130 135 140

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
145 150 155 160

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
165 170 175

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
180 185 190

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
195 200 205

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
210 215 220

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
225 230 235 240

Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
245 250 255

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
260 265 270

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
275 280 285

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
290 295 300

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
305 310 315 320

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
325 330 335

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
340 345 350

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
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355
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 370 375 380
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 385 390 395 400
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 405 410 415
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 420 425 430
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 435 440 445
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 450 455 460
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Arg Gly Arg Lys
 465 470 475 480
 Arg Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala
 485 490 495
 Gly Asp Val Glu Glu Asn Pro Gly Pro Met Val Leu Gln Thr Gln Val
 500 505 510
 Phe Ile Ser Leu Leu Leu Trp Ile Ser Gly Ala Tyr Gly Asn Ile Val
 515 520 525
 Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala
 530 535 540
 Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Ser Phe Gly Asn Ser
 545 550 555 560
 Phe Met His Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu
 565 570 575
 Ile Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser
 580 585 590
 Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asp Pro Val Glu
 595 600 605

206108_0033_30wo_606194_seqlisting

Ala Asp Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Asn Asn Glu Tyr Pro
610 615 620

Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala
625 630 635 640

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
645 650 655

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
660 665 670

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
675 680 685

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
690 695 700

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
705 710 715 720

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
725 730 735

Ser Phe Asn Arg Gly Glu Cys
740

<210> 119
<211> 732
<212> PRT
<213> Artificial Sequence

<220>
<223> Human anti-Zika (8A9F9)-IgG1: Human IgG heavy signal peptide-VH-CH1-Hinge Region-CH2 (with LALA variant at 4th and 5th residue)-CH3-custom Furin cleavage site-'GSG' Linker and P2A Peptide-human kappa light chain signal peptide-VL-CL (kappa)

<400> 119

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys
20 25 30

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ser Pro Glu Lys Arg Leu
50 55 60

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Glu Trp Val Ala Glu Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Pro
 65 70 75 80
 Asp Thr Val Thr Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
 85 90 95
 Thr Leu Tyr Leu Glu Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met
 100 105 110
 Tyr Tyr Cys Ala Ser Asp Gly Tyr Tyr Ser His Trp Gly Gln Gly Thr
 115 120 125
 Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
 130 135 140
 Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
 145 150 155 160
 Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
 165 170 175
 Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
 180 185 190
 Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
 195 200 205
 Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
 210 215 220
 Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
 225 230 235 240
 His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
 245 250 255
 Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 260 265 270
 Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
 275 280 285
 Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 290 295 300
 Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
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206108_0033_30wo_606194_seqlisting
 305 310 315 320
 Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 325 330 335
 Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
 340 345 350
 Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 355 360 365
 Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
 370 375 380
 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 385 390 395 400
 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 405 410 415
 Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 420 425 430
 Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 435 440 445
 Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 450 455 460
 Arg Gly Arg Lys Arg Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu
 465 470 475 480
 Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Val Leu
 485 490 495
 Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser Gly Ala Tyr
 500 505 510
 Gly Asp Val Val Met Thr Gln Ile Pro Leu Ser Leu Pro Val Ser Leu
 515 520 525
 Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His
 530 535 540
 Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln
 545 550 555 560

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Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val
565 570 575

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
580 585 590

Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Phe Gln
595 600 605

Ser Thr His Val Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
610 615 620

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
625 630 635 640

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
645 650 655

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
660 665 670

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
675 680 685

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
690 695 700

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
705 710 715 720

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
725 730

<210> 120

<211> 731

<212> PRT

<213> Artificial Sequence

<220>

<223> Human anti-Zika (3F12E9)-IgG1: Human IgG heavy signal peptide-VH-CH1-Hinge Region-CH2 (with LALA variant at 4th and 5th residue)-CH3-custom Furin cleavage site-'GSG' Linker and P2A Peptide-human kappa light chain signal peptide-VL-CL (kappa)

<400> 120

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys
20 25 30

206108_0033_30wo_606194_seqlisting

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Arg Tyr Gly Met Ser Trp Gly Arg Gln Thr Pro Asp Lys Arg Leu
50 55 60

Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Thr Tyr Thr Tyr Tyr Pro
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
85 90 95

Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met
100 105 110

Tyr Tyr Cys Ala Arg Ser Trp Phe Ala Tyr Trp Gly Arg Gly Thr Leu
115 120 125

Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
130 135 140

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
145 150 155 160

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
165 170 175

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
180 185 190

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
195 200 205

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
210 215 220

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
225 230 235 240

Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
245 250 255

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
260 265 270

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu

275 206108_0033_30wo_606194_seqlisting 280 285

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
290 295 300

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
305 310 315 320

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
325 330 335

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
340 345 350

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
355 360 365

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
370 375 380

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
385 390 395 400

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
405 410 415

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
420 425 430

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
435 440 445

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Arg
450 455 460

Gly Arg Lys Arg Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu
465 470 475 480

Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Val Leu Gln
485 490 495

Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser Gly Ala Tyr Gly
500 505 510

Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Val Thr Ile Gly
515 520 525

206108_0033_30wo_606194_seqlisting

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
530 535 540

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser
545 550 555 560

Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
565 570 575

Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
580 585 590

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Trp Gln Gly
595 600 605

Thr His Phe Pro His Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
610 615 620

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
625 630 635 640

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
645 650 655

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
660 665 670

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
675 680 685

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
690 695 700

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
705 710 715 720

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
725 730

<210> 121

<211> 780

<212> PRT

<213> Artificial Sequence

<220>

<223> Human anti-Zika (IC2A6)-IgG4: Human IgG heavy signal
peptide-VH-CH1-Hinge Region-CH2-CH3-custom Furin cleavage
site-'GSG' Linker and P2A Peptide-human kappa light chain signal
peptide-VL-CL (kappa)

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<400> 121

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys
20 25 30

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ser Pro Glu Lys Arg Leu
50 55 60

Glu Trp Val Ala Glu Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Pro
65 70 75 80

Asp Thr Val Thr Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
85 90 95

Thr Leu Tyr Leu Glu Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met
100 105 110

Tyr Tyr Cys Ala Ser Asp Gly Tyr Tyr Ser His Trp Gly Gln Gly Thr
115 120 125

Ser Val Thr Val Ser Ser Val Thr Gly Arg Phe Thr Ile Ser Arg Asp
130 135 140

Asn Ala Lys Asn Thr Leu Tyr Leu Glu Met Ser Ser Leu Arg Ser Glu
145 150 155 160

Asp Thr Ala Met Tyr Tyr Cys Ala Ser Asp Gly Tyr Tyr Ser His Trp
165 170 175

Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
180 185 190

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr
195 200 205

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
210 215 220

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
225 230 235 240

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
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245 250 255

Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp
260 265 270

His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Ser Pro Asn Met
275 280 285

Val Pro His Ala His His Ala Gln Ala Pro Glu Phe Leu Gly Gly Pro
290 295 300

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
305 310 315 320

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp
325 330 335

Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
340 345 350

Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val
355 360 365

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
370 375 380

Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys
385 390 395 400

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
405 410 415

Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
420 425 430

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
435 440 445

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
450 455 460

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys
465 470 475 480

Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu
485 490 495

206108_0033_30wo_606194_seqlisting

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
500 505 510

Lys Arg Gly Arg Lys Arg Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser
515 520 525

Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Val
530 535 540

Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser Gly Ala
545 550 555 560

Tyr Gly Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Cys
565 570 575

Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val
580 585 590

His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly
595 600 605

Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly
610 615 620

Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
625 630 635 640

Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Phe
645 650 655

Gln Ser Thr His Val Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu
660 665 670

Ile Lys Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
675 680 685

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
690 695 700

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
705 710 715 720

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
725 730 735

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
740 745 750

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Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
755 760 765

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
770 775 780

<210> 122

<211> 784

<212> PRT

<213> Artificial Sequence

<220>

<223> Human anti-Zika (IC2A6)-IgG1: Human IgG heavy signal
peptide-VH-CH1-Hinge Region-CH2-CH3-custom Furin cleavage
site-'GSG' Linker and P2A Peptide-human kappa light chain signal
peptide-VL-CL (kappa)

<400> 122

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys
20 25 30

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ser Pro Glu Lys Arg Leu
50 55 60

Glu Trp Val Ala Glu Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Pro
65 70 75 80

Asp Thr Val Thr Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
85 90 95

Thr Leu Tyr Leu Glu Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met
100 105 110

Tyr Tyr Cys Ala Ser Asp Gly Tyr Tyr Ser His Trp Gly Gln Gly Thr
115 120 125

Ser Val Thr Val Ser Ser Val Thr Gly Arg Phe Thr Ile Ser Arg Asp
130 135 140

Asn Ala Lys Asn Thr Leu Tyr Leu Glu Met Ser Ser Leu Arg Ser Glu
145 150 155 160

Asp Thr Ala Met Tyr Tyr Cys Ala Ser Asp Gly Tyr Tyr Ser His Trp
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206108_0033_30wo_606194_seqlisting
165 170 175

Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
180 185 190

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
195 200 205

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
210 215 220

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
225 230 235 240

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
245 250 255

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
260 265 270

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
275 280 285

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
290 295 300

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
305 310 315 320

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
325 330 335

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
340 345 350

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
355 360 365

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
370 375 380

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
385 390 395 400

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
405 410 415

206108_0033_30wo_606194_seqlisting

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
420 425 430

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
435 440 445

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
450 455 460

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
465 470 475 480

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
485 490 495

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
500 505 510

Ser Pro Gly Lys Arg Gly Arg Lys Arg Arg Ser Gly Ser Gly Ala Thr
515 520 525

Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly
530 535 540

Pro Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile
545 550 555 560

Ser Gly Ala Tyr Gly Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu
565 570 575

Pro Val Cys Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln
580 585 590

Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln
595 600 605

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg
610 615 620

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
625 630 635 640

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr
645 650 655

Phe Cys Phe Gln Ser Thr His Val Pro Pro Thr Phe Gly Gly Gly Thr
660 665 670

206108_0033_30wo_606194_seqlisting

Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe
675 680 685

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
690 695 700

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
705 710 715 720

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln
725 730 735

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
740 745 750

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
755 760 765

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
770 775 780

<210> 123

<211> 702

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus Zika IgE Leader-prME

<400> 123

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1 5 10 15

His Ser Gly Ile Ile Gly Leu Leu Leu Thr Thr Ala Met Ala Ala Glu
20 25 30

Ile Thr Arg Arg Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Asn Asp
35 40 45

Ala Gly Glu Ala Ile Ser Phe Pro Thr Thr Leu Gly Met Asn Lys Cys
50 55 60

Tyr Ile Gln Ile Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser
65 70 75 80

Tyr Glu Cys Pro Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp
85 90 95

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Cys Trp Cys Asn Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His
100 105 110

His Lys Lys Gly Glu Ala Arg Arg Ser Arg Arg Ala Val Thr Leu Pro
115 120 125

Ser His Ser Thr Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu
130 135 140

Ser Arg Glu Tyr Thr Lys His Leu Ile Arg Val Glu Asn Trp Ile Phe
145 150 155 160

Arg Asn Pro Gly Phe Ala Leu Ala Ala Ala Ala Ile Ala Trp Leu Leu
165 170 175

Gly Ser Ser Thr Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu
180 185 190

Ile Ala Pro Ala Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp
195 200 205

Phe Val Glu Gly Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu
210 215 220

His Gly Gly Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp
225 230 235 240

Ile Glu Leu Val Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser
245 250 255

Tyr Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys
260 265 270

Pro Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr
275 280 285

Val Cys Lys Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly
290 295 300

Leu Phe Gly Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Thr Cys Ser
305 310 315 320

Lys Lys Met Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg
325 330 335

Ile Met Leu Ser Val His Gly Ser Gln His Ser Gly Met Ile Val Asn
340 345 350

206108_0033_30wo_606194_seqlisting

Asp Ile Gly His Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Val Thr
355 360 365

Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu
370 375 380

Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr
385 390 395 400

Tyr Leu Thr Met Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe
405 410 415

His Asp Ile Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro
420 425 430

His Trp Asn Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala
435 440 445

Lys Arg Gln Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His
450 455 460

Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly
465 470 475 480

Arg Leu Phe Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu
485 490 495

Arg Leu Lys Gly Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe
500 505 510

Thr Lys Val Pro Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val
515 520 525

Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys Val Pro Ala Gln Met Ala
530 535 540

Val Asp Met Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn
545 550 555 560

Pro Val Ile Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu
565 570 575

Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Asp Lys
580 585 590

Lys Ile Thr His His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala
595 600 605

206108_0033_30wo_606194_seqlisting

Phe Glu Ala Thr Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp
610 615 620

Thr Ala Trp Asp Phe Gly Ser Val Gly Gly Val Phe Asn Ser Leu Gly
625 630 635 640

Lys Gly Ile His Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly
645 650 655

Gly Met Ser Trp Phe Ser Gln Ile Leu Ile Gly Thr Leu Leu Val Trp
660 665 670

Leu Gly Leu Asn Thr Lys Asn Gly Ser Ile Ser Leu Thr Cys Leu Ala
675 680 685

Leu Gly Gly Val Met Ile Phe Leu Ser Thr Ala Val Ser Ala
690 695 700

<210> 124
<211> 2112
<212> DNA
<213> Artificial Sequence

<220>
<223> consensus Zika IgE Leader-prME (construct 1)

<400> 124
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tatatgtacc tggaccgggc tgatgccggc aaggccatca gctttgccac cactctgggc 180
gtgaataagt gccacgtgca gatcatggac ctgggccaca tgtgcatgac caccatgtcc 240
tacgagtgtc caatgctgga cgagggcgtg gagcccgacg atgtggattg ctggtgtaac 300
accacatcta catgggtggt gtatggcacc tgtcaccaca agaagggaga ggcacggcgc 360
agcaggagag cagtgcact gccctctcac agcaccagga agctgcagac aagaagccag 420
acctggctgg agtcccggga gtatacaaag cacctgatca aggtggagaa ctggatcttt 480
cgcaatccag gattcgcact ggtggcagtg gcaatcgcac ggctgctggg cagctccacc 540
tcccagaaag tgatctacct ggtcatgac ctgctgatcg cccctgccta ttccatcagg 600
tgcatcggcg tgtctaata agacttcgtg gagggcatgt ctggcggcac ctgggtggat 660
gtggtgctgg agcacggcgg atgcgtgaca gtgatggccc aggacaagcc aaccgtggat 720
atcgagctgg tgaccacaac cgtgagcaac atggccgagg tgaggtccta ctgctatgag 780
gcctccatct ctgacatggc cagcgattcc agatgtccca cccagggcga ggcctacctg 840

206108_0033_30wo_606194_seqlisting

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aatggatgtg gcctgttttg caagggctct ctggtgacat gcgccaagtt cacctgttct	960
aagaagatga ccggcaagag catccagccc gagaacctgg agtacaggat catgctgagc	1020
gtgcacggca gccagcactc cggcatgaca gtgaacgaca tcggctatga gaccgatgag	1080
aatagggcca aggtggaggt gacacctaac agcccaagag ccgaggccac cctgggcggc	1140
tttggctccc tgggactgga ctgcgagcct agaacaggcc tggacttctc cgatctgtac	1200
tatctgacca tgaacaataa gcactggctg gtgcacaagg agtggtttca cgacatccca	1260
ctgccatggc acgcaggagc agatacagga accccacact ggaacaataa ggaggccctg	1320
gtggagttca aggatgcccc cgccaagcgc cagacagtgg tgggtgctggg cagccaggag	1380
ggagcagtgc acaccgccct ggagggcgcc ctggaggccg agatggacgg cgccaagggc	1440
aagctgtttt ccggccacct gaagtgccgg ctgaagatgg ataagctgcg cctgaagggc	1500
gtgtcttaca gcctgtgcac agccgccttc accttcacca aggtgcctgc cgagaccctg	1560
cacggcacag tgaccgtgga ggtgcagtat gccggcacag acggcccctg taagatccct	1620
gtgcagatgg ccgtggatat gcagacactg acccctgtgg gccggctgat caccgcaaat	1680
ccagtgatca cagagtccac cgagaactct aagatgatgc tggagctgga ccctcccttc	1740
ggcgacagct acatcgtgat cggcgtgggc gacaagaaga tcacacacca ctggcaccgc	1800
tccggctcta caatcggcaa ggccttcgag gcaaccgtgc ggggcgccaa gaggatggcc	1860
gtgctgggcg acaccgcatg ggattttggc tccgtgggcg gcgtgttcaa ctctctgggc	1920
aagggcatcc accagatctt cggcgccgcc ttttaagtctc tgttcggcgg aatgtcttgg	1980
ttcagccaga tcctgatcgg cacactgctg gtgtggctgg gcctgaacac caagaatggc	2040
agcatctctc tgacttgtct ggccctggga ggcgtgatga ttttctgtc cactgccgtg	2100
tctgcctgat aa	2112

<210> 125
 <211> 702
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus Zika IgE Leader-prME (construct 1)

<400> 125

Met	Asp	Trp	Thr	Trp	Ile	Leu	Phe	Leu	Val	Ala	Ala	Ala	Thr	Arg	Val
1				5					10					15	

His	Ser	Gly	Ile	Ile	Gly	Leu	Leu	Leu	Thr	Thr	Ala	Met	Ala	Ala	Glu
			20					25					30		

206108_0033_30wo_606194_seqlisting

Ile Thr Arg Arg Gly Ser Ala Tyr Tyr Met Tyr Leu Asp Arg Ser Asp
35 40 45

Ala Gly Lys Ala Ile Ser Phe Ala Thr Thr Leu Gly Val Asn Lys Cys
50 55 60

His Val Gln Ile Met Asp Leu Gly His Met Cys Asp Ala Thr Met Ser
65 70 75 80

Tyr Glu Cys Pro Met Leu Asp Glu Gly Val Glu Pro Asp Asp Val Asp
85 90 95

Cys Trp Cys Asn Thr Thr Ser Thr Trp Val Val Tyr Gly Thr Cys His
100 105 110

His Lys Lys Gly Glu Ala Arg Arg Ser Arg Arg Ala Val Thr Leu Pro
115 120 125

Ser His Ser Thr Arg Lys Leu Gln Thr Arg Ser Gln Thr Trp Leu Glu
130 135 140

Ser Arg Glu Tyr Thr Lys His Leu Ile Lys Val Glu Asn Trp Ile Phe
145 150 155 160

Arg Asn Pro Gly Phe Ala Leu Val Ala Val Ala Ile Ala Trp Leu Leu
165 170 175

Gly Ser Ser Thr Ser Gln Lys Val Ile Tyr Leu Val Met Ile Leu Leu
180 185 190

Ile Ala Pro Ala Tyr Ser Ile Arg Cys Ile Gly Val Ser Asn Arg Asp
195 200 205

Phe Val Glu Gly Met Ser Gly Gly Thr Trp Val Asp Val Val Leu Glu
210 215 220

His Gly Gly Cys Val Thr Val Met Ala Gln Asp Lys Pro Thr Val Asp
225 230 235 240

Ile Glu Leu Val Thr Thr Thr Val Ser Asn Met Ala Glu Val Arg Ser
245 250 255

Tyr Cys Tyr Glu Ala Ser Ile Ser Asp Met Ala Ser Asp Ser Arg Cys
260 265 270

Pro Thr Gln Gly Glu Ala Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr
275 280 285

206108_0033_30wo_606194_seqlisting

Val Cys Lys Arg Thr Leu Val Asp Arg Gly Trp Gly Asn Gly Cys Gly
290 295 300

Leu Phe Gly Lys Gly Ser Leu Val Thr Cys Ala Lys Phe Thr Cys Ser
305 310 315 320

Lys Lys Met Thr Gly Lys Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg
325 330 335

Ile Met Leu Ser Val His Gly Ser Gln His Ser Gly Met Thr Val Asn
340 345 350

Asp Ile Gly Tyr Glu Thr Asp Glu Asn Arg Ala Lys Val Glu Val Thr
355 360 365

Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu Gly Gly Phe Gly Ser Leu
370 375 380

Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu Asp Phe Ser Asp Leu Tyr
385 390 395 400

Tyr Leu Thr Met Asn Asn Lys His Trp Leu Val His Lys Glu Trp Phe
405 410 415

His Asp Ile Pro Leu Pro Trp His Ala Gly Ala Asp Thr Gly Thr Pro
420 425 430

His Trp Asn Asn Lys Glu Ala Leu Val Glu Phe Lys Asp Ala His Ala
435 440 445

Lys Arg Gln Thr Val Val Val Leu Gly Ser Gln Glu Gly Ala Val His
450 455 460

Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu Met Asp Gly Ala Lys Gly
465 470 475 480

Lys Leu Phe Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu
485 490 495

Arg Leu Lys Gly Val Ser Tyr Ser Leu Cys Thr Ala Ala Phe Thr Phe
500 505 510

Thr Lys Val Pro Ala Glu Thr Leu His Gly Thr Val Thr Val Glu Val
515 520 525

Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys Ile Pro Val Gln Met Ala
530 535 540

206108_0033_30wo_606194_seqlisting

Val Asp Met Gln Thr Leu Thr Pro Val Gly Arg Leu Ile Thr Ala Asn
545 550 555 560

Pro Val Ile Thr Glu Ser Thr Glu Asn Ser Lys Met Met Leu Glu Leu
565 570 575

Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val Ile Gly Val Gly Asp Lys
580 585 590

Lys Ile Thr His His Trp His Arg Ser Gly Ser Thr Ile Gly Lys Ala
595 600 605

Phe Glu Ala Thr Val Arg Gly Ala Lys Arg Met Ala Val Leu Gly Asp
610 615 620

Thr Ala Trp Asp Phe Gly Ser Val Gly Gly Val Phe Asn Ser Leu Gly
625 630 635 640

Lys Gly Ile His Gln Ile Phe Gly Ala Ala Phe Lys Ser Leu Phe Gly
645 650 655

Gly Met Ser Trp Phe Ser Gln Ile Leu Ile Gly Thr Leu Leu Val Trp
660 665 670

Leu Gly Leu Asn Thr Lys Asn Gly Ser Ile Ser Leu Thr Cys Leu Ala
675 680 685

Leu Gly Gly Val Met Ile Phe Leu Ser Thr Ala Val Ser Ala
690 695 700

<210> 126

<211> 1119

<212> DNA

<213> Artificial Sequence

<220>

<223> consensus Zika IgE Leader-NS1

<400> 126

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tgcagcgtgg acttcagcaa gaaggagacc cgctgcggaa caggcgtgtt cgtgtacaac 120

gacgtggagg cttggagaga ccggtacaag taccaccccg atagccctag aagactggcc 180

gcagccgtga aacaggcttg ggaagagggg atttgcggca tcagcagcgt gtcccggatg 240

gagaacatca tgtggaagag cgtggagggc gagctgaacg ctatcctgga ggagaacggc 300

gtgcagctga cagtggctcg gggatcagtg aagaacccca tgtggagagg ccctcagagg 360

206108_0033_30wo_606194_seqlisting

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ctgccagtgc cagtgaacga actgcctcac ggttggaagg cttggggcaa gagctacttc 420
gtgagggccg ccaagaccaa caacagcttc gtggtggacg gcgataccct caaggagtgt 480
cctctgaagc accgggcttg gaacagcttc ctggtggaag accacggctt tggcgtgttc 540
cacacaagcg tctggctgaa ggtccgcgaa gactacagcc tggagtgcga tccagcagtg 600
atcggcacag cctgaaggga aaaagaggcc gctcacagcg acctgggcta ttggatcgag 660
agcgagaaga acgacacttg gaggtgaag cgggcccacc tgatcgagat gaagacttgc 720
gagtggccca agagccacac tctgtggaca gacggcgtgg aagagagcga cctgatcatc 780
cctaagagcc tggccggacc tctgtctcat cacaacacca gggagggcta cagaaccag 840
gtgaagggac cttggcacag cgaagagctg gagatccgct tcgaggagtg tccaggaacc 900
aaggtgcacg tggaggagac ttgcggaacc agaggcccta gcctgagaag cacaacagcc 960
agcggacgcg tgatcgagga gtggtgttgt agggagtgc ccatgcctcc tctgagcttc 1020
agggccaagg acggttgttg gtacggcatg gagatcaggc ccagaaagga gccagagagc 1080
aacctcgtgc ggtctatggt gacagccgga agctgataa 1119

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<210> 127

<211> 371

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus Zika IgE Leader-NS1

<400> 127

```

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1           5           10          15

```

```

His Ser Val Gly Cys Ser Val Asp Phe Ser Lys Lys Glu Thr Arg Cys
          20          25          30

```

```

Gly Thr Gly Val Phe Val Tyr Asn Asp Val Glu Ala Trp Arg Asp Arg
          35          40          45

```

```

Tyr Lys Tyr His Pro Asp Ser Pro Arg Arg Leu Ala Ala Ala Val Lys
          50          55          60

```

```

Gln Ala Trp Glu Glu Gly Ile Cys Gly Ile Ser Ser Val Ser Arg Met
65          70          75          80

```

```

Glu Asn Ile Met Trp Lys Ser Val Glu Gly Glu Leu Asn Ala Ile Leu
          85          90          95

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```

Glu Glu Asn Gly Val Gln Leu Thr Val Val Val Gly Ser Val Lys Asn
          100          105          110

```

206108_0033_30wo_606194_seqlisting

Pro Met Trp Arg Gly Pro Gln Arg Leu Pro Val Pro Val Asn Glu Leu
115 120 125

Pro His Gly Trp Lys Ala Trp Gly Lys Ser Tyr Phe Val Arg Ala Ala
130 135 140

Lys Thr Asn Asn Ser Phe Val Val Asp Gly Asp Thr Leu Lys Glu Cys
145 150 155 160

Pro Leu Lys His Arg Ala Trp Asn Ser Phe Leu Val Glu Asp His Gly
165 170 175

Phe Gly Val Phe His Thr Ser Val Trp Leu Lys Val Arg Glu Asp Tyr
180 185 190

Ser Leu Glu Cys Asp Pro Ala Val Ile Gly Thr Ala Val Lys Gly Lys
195 200 205

Glu Ala Ala His Ser Asp Leu Gly Tyr Trp Ile Glu Ser Glu Lys Asn
210 215 220

Asp Thr Trp Arg Leu Lys Arg Ala His Leu Ile Glu Met Lys Thr Cys
225 230 235 240

Glu Trp Pro Lys Ser His Thr Leu Trp Thr Asp Gly Val Glu Glu Ser
245 250 255

Asp Leu Ile Ile Pro Lys Ser Leu Ala Gly Pro Leu Ser His His Asn
260 265 270

Thr Arg Glu Gly Tyr Arg Thr Gln Val Lys Gly Pro Trp His Ser Glu
275 280 285

Glu Leu Glu Ile Arg Phe Glu Glu Cys Pro Gly Thr Lys Val His Val
290 295 300

Glu Glu Thr Cys Gly Thr Arg Gly Pro Ser Leu Arg Ser Thr Thr Ala
305 310 315 320

Ser Gly Arg Val Ile Glu Glu Trp Cys Cys Arg Glu Cys Thr Met Pro
325 330 335

Pro Leu Ser Phe Arg Ala Lys Asp Gly Cys Trp Tyr Gly Met Glu Ile
340 345 350

Arg Pro Arg Lys Glu Pro Glu Ser Asn Leu Val Arg Ser Met Val Thr
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355 206108_0033_30wo_606194_seqlisting 360 365

Ala Gly Ser
370

<210> 128
<211> 438
<212> DNA
<213> Artificial Sequence

<220>
<223> consensus Zika IgE Leader-capsid

<400> 128
atggactgga cttggatcct gtttctggtg gccgccgcca caagagtgca tagcaagaac 60
cccaagaaga agagcggcgg cttcaggatc gtgaacatgc tgaagcgggg cgtggctaga 120
gtgaaccctc tgggaggcgg actgaagaga ctgccagcag gactgctcct gggacacgga 180
cctattcgca tgggtgctggc catcctggct ttcctgaggt tcaccgccat caagcccagc 240
ctgggactga tcaaccgctg gggttcagtc ggcaagaagg aggccatgga gatcatcaag 300
aagttcaaga aggacctggc cgccatgctg aggatcatca acgcccggaa ggagcggaag 360
agaagaggag ccgacaccag catcggcatc atcggactgc tgctgacaac cgccatggct 420
gccgagatct gatgatga 438

<210> 129
<211> 143
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus Zika IgE Leader-capsid

<400> 129

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1 5 10 15

His Ser Lys Asn Pro Lys Lys Lys Ser Gly Gly Phe Arg Ile Val Asn
20 25 30

Met Leu Lys Arg Gly Val Ala Arg Val Asn Pro Leu Gly Gly Gly Leu
35 40 45

Lys Arg Leu Pro Ala Gly Leu Leu Leu Gly His Gly Pro Ile Arg Met
50 55 60

Val Leu Ala Ile Leu Ala Phe Leu Arg Phe Thr Ala Ile Lys Pro Ser
65 70 75 80

206108_0033_30wo_606194_seqlisting

Leu Gly Leu Ile Asn Arg Trp Gly Ser Val Gly Lys Lys Glu Ala Met
85 90 95

Glu Ile Ile Lys Lys Phe Lys Lys Asp Leu Ala Ala Met Leu Arg Ile
100 105 110

Ile Asn Ala Arg Lys Glu Arg Lys Arg Arg Gly Ala Asp Thr Ser Ile
115 120 125

Gly Ile Ile Gly Leu Leu Leu Thr Thr Ala Met Ala Ala Glu Ile
130 135 140

<210> 130
<211> 2130
<212> DNA
<213> Artificial Sequence

<220>
<223> Zika IgE Leader-prME MR766

<400> 130
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gacacctcta tcggcatcgt gggactgctg ctgaccacag ccatggccgc cgaaattacc 120
aggaggggca gcgcctacta catgtacctg gacagaagcg acgccggaaa agccatcagc 180
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tgcgacgcca caatgagcta cgagtgcctt atgctggacg agggagtggg accagacgac 300
gtcgactgtt ggtgcaacac cacctccact tgggtcgtgt acggcacttg ccaccacaag 360
aagggcgagg ccagaagaag cagaagagcc gtgaccctgc ctagccacag caccagaaag 420
ctgcagacca ggagccagac ttggctggaa agccgcgagt acaccaagca cctgatcaag 480
gtggagaatt ggatcttccg gaaccccggc ttcacactgg tggccgtggc aatcgcttgg 540
ctgctgggat ctagcaccag ccagaaagtg atctacctgg tcatgatcct gctgatcgcc 600
ccagcctaca gcatccgctg tatcggagtg agcaaccggg acttcgtgga gggaaatgagc 660
ggaggaactt ggggtggacgt ggtgctggaa cacggagggt gcgtgacagt gatggctcag 720
gacaagccca ccgtggatat cgagctggtg accaccaccg tgtccaacat ggccgaagtg 780
cgcagctact gctacgaggc cagtatctcc gacatggcca gcgatagccg ctgtcctaca 840
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gtggatagag gctggggaaa cggttgcgga ctgttcggaa agggcagcct cgtgacttgc 960
gccaaattca cttgcagcaa gaagatgacc ggcaagtcta tccagcccga gaacctggag 1020
taccggatca tgctgagcgt gcacggaagc cagcacagcg gcatgatcgt gaacgacgag 1080
ggatacgaga ccgacgagaa cagggccaag gtggaagtga cccctaacag ccctagagcc 1140

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gaagccacac tgggaggatt tggcagcctg ggactggatt gcgagcctag aacaggcctg	1200
gacttcagcg acctgtacta cctgaccatg aacaacaagc attggctggt gcacaaggag	1260
tggttccacg acatccctct gccttggcac gcaggagccg atacaggcac acctcattgg	1320
aacaacaagg aggccctggt ggagttcaag gacgctcacg ccaagagaca gacagtgggtg	1380
gtgctgggaa gccaggaagg agcagtgcac acagccctgg caggagctct ggaagcagaa	1440
atggacggcg ctaagggcag actgttcagc ggacacctca agtgccggct gaagatggac	1500
aagctgcggc tgaagggcgt gtcttacagc ctctgcaccg cagccttcac cttcaccaag	1560
gtgccagcag agacactgca cggaacagtg accgtggaag tgcagtacgc cggaacagac	1620
ggaccttgca aagtgccagc ccagatggca gtggacatgc agacactgac cccagtggga	1680
aggctgatca ccgctaacc cgtcatcacc gagagcaccg agaacagcaa gatgatgctg	1740
gagctggacc ccccttcgg cgatagctac atcgtgatcg gcgtgggcca caagaagatc	1800
accaccatt ggcacagaag cggcagcaca atcggcaagg ctttcgaggc caccgtgaga	1860
ggagctaaga gaatggcgt gctgggagac accgcttggg attttggcag cgtgggagga	1920
gtgttcaaca gcctgggcaa gggcatccac cagatcttcg gagccgcctt caagagcctg	1980
ttcggcggca tgtcttggtt cagccagatc ctgatcgga cactcctcgt ctggctggga	2040
ctgaacacca agaacggcag catcagcctg acttgtctgg ccctgggagg cgtgatgatc	2100
ttcctgagca ccgccgtgtc cgcttgataa	2130

<210> 131
 <211> 708
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Zika IgE Leader-prME MR766

<400> 131

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
 1 5 10 15

His Ser Gly Ala Asp Thr Ser Ile Gly Ile Val Gly Leu Leu Leu Thr
 20 25 30

Thr Ala Met Ala Ala Glu Ile Thr Arg Arg Gly Ser Ala Tyr Tyr Met
 35 40 45

Tyr Leu Asp Arg Ser Asp Ala Gly Lys Ala Ile Ser Phe Ala Thr Thr
 50 55 60

Leu Gly Val Asn Lys Cys His Val Gln Ile Met Asp Leu Gly His Met
 65 70 75 80

206108_0033_30wo_606194_seqlisting

Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro Met Leu Asp Glu Gly Val
 85 90 95
 Glu Pro Asp Asp Val Asp Cys Trp Cys Asn Thr Thr Ser Thr Trp Val
 100 105 110
 Val Tyr Gly Thr Cys His His Lys Lys Gly Glu Ala Arg Arg Ser Arg
 115 120 125
 Arg Ala Val Thr Leu Pro Ser His Ser Thr Arg Lys Leu Gln Thr Arg
 130 135 140
 Ser Gln Thr Trp Leu Glu Ser Arg Glu Tyr Thr Lys His Leu Ile Lys
 145 150 155 160
 Val Glu Asn Trp Ile Phe Arg Asn Pro Gly Phe Thr Leu Val Ala Val
 165 170 175
 Ala Ile Ala Trp Leu Leu Gly Ser Ser Thr Ser Gln Lys Val Ile Tyr
 180 185 190
 Leu Val Met Ile Leu Leu Ile Ala Pro Ala Tyr Ser Ile Arg Cys Ile
 195 200 205
 Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr Trp
 210 215 220
 Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr Val Met Ala Gln
 225 230 235 240
 Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr Thr Val Ser Asn
 245 250 255
 Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp Met
 260 265 270
 Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp Lys
 275 280 285
 Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg Gly
 290 295 300
 Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr Cys
 305 310 315 320
 Ala Lys Phe Thr Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln Pro
 Page 185

325 330 335

Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser
565 570 575

206108_0033_30wo_606194_seqlisting

Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val
580 585 590

Ile Gly Val Gly Asp Lys Lys Ile Thr His His Trp His Arg Ser Gly
595 600 605

Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg Gly Ala Lys Arg
610 615 620

Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly
625 630 635 640

Val Phe Asn Ser Leu Gly Lys Gly Ile His Gln Ile Phe Gly Ala Ala
645 650 655

Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser Gln Ile Leu Ile
660 665 670

Gly Thr Leu Leu Val Trp Leu Gly Leu Asn Thr Lys Asn Gly Ser Ile
675 680 685

Ser Leu Thr Cys Leu Ala Leu Gly Gly Val Met Ile Phe Leu Ser Thr
690 695 700

Ala Val Ser Ala
705

<210> 132
<211> 2130
<212> DNA
<213> Artificial Sequence

<220>
<223> Zika IgE Leader-prME Brazil

<400> 132
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gacacatcag tgggcatcgt gggactgctg ctgacaacag ctatggccgc cgaagtgacc 120
agaagaggca gcgcctacta catgtacctg gaccggaacg acgccggaga ggccattagc 180
tttctacca ccctgggcat gaacaagtgc tacatccaga tcatggacct gggccacatg 240
tgcgacgcta caatgagcta cgagtgcccc atgctggacg aaggagtgga gccagacgac 300
gtggattggt ggtgcaacac cacctccact tgggtcgtgt acggcacctg tcaccacaaa 360
aagggcgaag ccaggagaag cagaagagcc gtgaccctgc ctagccactc taccaggaag 420
ctgcagacca ggagccagac ttggctggag agcagggagt acaccaagca cctgatccgc 480
gtggagaatt ggatcttcag aaaccccggc ttcgccctgg cagccgcagc aattgcttgg 540

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600 ctgctgggat ctaggcaccag ccagaaggtc atctaaccttg tcatgatcct gctgatcgcc

660 cccgcttaaca gcatccgcttg tatcggcgttg tccaacaggg acttcgttggg gggcatagagc

720 ggaaggaaactt ggggtggagctt ggtgcctggaa caggaggtt gttgtgaccgt gatgtgctcag

780 gacaagcccta ccgttggaaat cgaagctgttg accacaaccg tgtccaacat ggcctgaggtc

840 cgcagctatat gctacagaggc cagcatcagc gatataggcca gcgatatagcag gttgtcccaacc

900 cagggttgaaag cttaaccctgga caagcagagc gacacccagt acgtgttcgaa gcgagcactg

960 gttgatagag gcttggggaaaa cgttgcggc ctgttttgca agggaaagcct ggtgaccctg

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1080 tacggatca tgcctgagcgt gcaaggatct cagcatagcg gaatgatcgt gaaacgacacc

1140 ggccaagagaa ccgaagcaaaa cagggcccaag gtggaataca cccccaactc tccatagacc

1200 gagggcccaac tgggaaggtt tggaaacctg ggccttgat gcgagcctag aacaggccctg

1260 gacttcagcg acctgtacta cctgaccatg aacaacaagc attgcttgtt gcacaagga

1320 tggttccagc acatccctct gaccttggcac gcaggagcag atacaggaaac ccccatctg

1380 aacaacaagg aggcctctgtt ggaattcaag gacgctcacg ccaagagaca gacagtgttg

1440 gtgcttgggaa gccaggaaag agcagtgcac acagctcttg caggagctct ggaagccgaa

1500 atggaagga ccaaggcag acttctcc ggacaacctc agtgcggct gaagatgagc

1560 aagctgcgc tgaaggcgt gctttatagc ctctgcacag ccgctttcac cttcaaccaag

1620 atcccgag agaaccttgc cggaaacagt accgttgaa gtcagtacgc cggaaacagac

1680 ggaaaccttga agtgtgccag tcagatggca gtggacatgc agaacctgac cccagtggga

1740 agactgatca ccgttaaccc cgtcatcac gagagcaccg agaacagcaa gatgatgtg

1800 gagcttgacc ccccttcgg cgatagctac atcgtgatcg gctgtgggagga gaaaaagatc

1860 acccaactt ggcaagga cggcagagca atcgcaagg ccttgagc caccgtgaga

1920 ggagcccaaga gaatggccgt gctgggagat accgcttggg atttcggcag cgtgggaggc

1980 gccctgaaaca gcttgggcaa ggcatccac cagatcttcg gagccgacct caagagccctg

2040 ttcggcgga tgtcttgtt cagccagatc ctgatcgga cactgctcat gtgcttgggc

2100 ctgaaacacca agaaaggcag catcagccctg atgtgtcttg ctctggggag cgtgctgatac

2130 ttcctgagca ccgctgtgtc cgcttgataa

<210> 133
 <211> 708
 <212> PRT
 <213> Artificial Sequence

<220> Zika Ige Leader-prme Brazil

206108_0033_30wo_606194_seqlisting

<400> 133

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
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His Ser Gly Ala Asp Thr Ser Val Gly Ile Val Gly Leu Leu Leu Thr
20 25 30

Thr Ala Met Ala Ala Glu Val Thr Arg Arg Gly Ser Ala Tyr Tyr Met
35 40 45

Tyr Leu Asp Arg Asn Asp Ala Gly Glu Ala Ile Ser Phe Pro Thr Thr
50 55 60

Leu Gly Met Asn Lys Cys Tyr Ile Gln Ile Met Asp Leu Gly His Met
65 70 75 80

Cys Asp Ala Thr Met Ser Tyr Glu Cys Pro Met Leu Asp Glu Gly Val
85 90 95

Glu Pro Asp Asp Val Asp Cys Trp Cys Asn Thr Thr Ser Thr Trp Val
100 105 110

Val Tyr Gly Thr Cys His His Lys Lys Gly Glu Ala Arg Arg Ser Arg
115 120 125

Arg Ala Val Thr Leu Pro Ser His Ser Thr Arg Lys Leu Gln Thr Arg
130 135 140

Ser Gln Thr Trp Leu Glu Ser Arg Glu Tyr Thr Lys His Leu Ile Arg
145 150 155 160

Val Glu Asn Trp Ile Phe Arg Asn Pro Gly Phe Ala Leu Ala Ala Ala
165 170 175

Ala Ile Ala Trp Leu Leu Gly Ser Ser Thr Ser Gln Lys Val Ile Tyr
180 185 190

Leu Val Met Ile Leu Leu Ile Ala Pro Ala Tyr Ser Ile Arg Cys Ile
195 200 205

Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser Gly Gly Thr Trp
210 215 220

Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr Val Met Ala Gln
225 230 235 240

Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr Thr Val Ser Asn
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245 250 255

Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser Ile Ser Asp Met
260 265 270

Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala Tyr Leu Asp Lys
275 280 285

Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu Val Asp Arg Gly
290 295 300

Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Leu Val Thr Cys
305 310 315 320

Ala Lys Phe Ala Cys Ser Lys Lys Met Thr Gly Lys Ser Ile Gln Pro
325 330 335

Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His Gly Ser Gln His
340 345 350

Ser Gly Met Ile Val Asn Asp Thr Gly His Glu Thr Asp Glu Asn Arg
355 360 365

Ala Lys Val Glu Ile Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu
370 375 380

Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu
385 390 395 400

Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp Leu
405 410 415

Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro Trp His Ala Gly
420 425 430

Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val Glu
435 440 445

Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val Val Leu Gly Ser
450 455 460

Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu
465 470 475 480

Met Asp Gly Ala Lys Gly Arg Leu Ser Ser Gly His Leu Lys Cys Arg
485 490 495

206108_0033_30wo_606194_seqlisting

Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu Cys
500 505 510

Thr Ala Ala Phe Thr Phe Thr Lys Ile Pro Ala Glu Thr Leu His Gly
515 520 525

Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys
530 535 540

Val Pro Ala Gln Met Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly
545 550 555 560

Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser
565 570 575

Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val
580 585 590

Ile Gly Val Gly Glu Lys Lys Ile Thr His His Trp His Arg Ser Gly
595 600 605

Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg Gly Ala Lys Arg
610 615 620

Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly
625 630 635 640

Ala Leu Asn Ser Leu Gly Lys Gly Ile His Gln Ile Phe Gly Ala Ala
645 650 655

Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser Gln Ile Leu Ile
660 665 670

Gly Thr Leu Leu Met Trp Leu Gly Leu Asn Thr Lys Asn Gly Ser Ile
675 680 685

Ser Leu Met Cys Leu Ala Leu Gly Gly Val Leu Ile Phe Leu Ser Thr
690 695 700

Ala Val Ser Ala
705

<210> 134
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> IgE leader

206108_0033_30wo_606194_seqlisting

<400> 134

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
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His Ser

<210> 135

<211> 732

<212> PRT

<213> Artificial Sequence

<220>

<223> DMAb-2G4

<400> 135

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Met Gln
20 25 30

Pro Gly Gly Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Thr Phe
35 40 45

Ser Asn Tyr Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu
50 55 60

Glu Trp Val Ala Glu Ile Arg Leu Lys Ser Asn Asn Tyr Ala Thr His
65 70 75 80

Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
85 90 95

Lys Arg Ser Val Tyr Leu Gln Met Asn Thr Leu Arg Ala Glu Asp Thr
100 105 110

Gly Ile Tyr Tyr Cys Thr Arg Gly Asn Gly Asn Tyr Arg Ala Met Asp
115 120 125

Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys
130 135 140

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145 150 155 160

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
165 170 175

206108_0033_30wo_606194_seqlisting

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
180 185 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
195 200 205

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
210 215 220

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
225 230 235 240

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
245 250 255

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
260 265 270

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
275 280 285

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
290 295 300

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305 310 315 320

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
325 330 335

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
340 345 350

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
355 360 365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
370 375 380

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385 390 395 400

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
405 410 415

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys

206108_0033_30wo_606194_seqlisting

420 425 430
 Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
 435 440 445
 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 450 455 460
 Ser Leu Ser Pro Gly Lys Arg Gly Arg Lys Arg Arg Ser Gly Ser Gly
 465 470 475 480
 Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn
 485 490 495
 Pro Gly Pro Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu
 500 505 510
 Trp Ile Ser Gly Ala Tyr Gly Asp Ile Gln Met Thr Gln Ser Pro Ala
 515 520 525
 Ser Leu Ser Val Ser Val Gly Glu Thr Val Ser Ile Thr Cys Arg Ala
 530 535 540
 Ser Glu Asn Ile Tyr Ser Ser Leu Ala Trp Tyr Gln Gln Lys Gln Gly
 545 550 555 560
 Lys Ser Pro Gln Leu Leu Val Tyr Ser Ala Thr Ile Leu Ala Asp Gly
 565 570 575
 Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Ser Leu
 580 585 590
 Lys Ile Asn Ser Leu Gln Ser Glu Asp Phe Gly Thr Tyr Tyr Cys Gln
 595 600 605
 His Phe Trp Gly Thr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu
 610 615 620
 Ile Lys Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
 625 630 635 640
 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
 645 650 655
 Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
 660 665 670

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Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
675 680 685

Ser Thr Tyr Ser Leu Ser Asn Thr Leu Thr Leu Ser Lys Ala Asp Tyr
690 695 700

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
705 710 715 720

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
725 730

<210> 136
<211> 2202
<212> DNA
<213> Artificial Sequence

<220>
<223> PGX9226, DMAB-2G4

<400> 136

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tgcgtggcat ctggcttcac ctttagtaac tactggatga attgggtccg ccagtcacct	180
gagaaggac tggaatgggt ggctgagatc cgactgaaaa gcaacaatta cgccaccac	240
tatgctgagt cagtgaaggg gcgattcaca attagcaggg acgattctaa aagaagtgtg	300
tatctgcaga tgaacactct gagagccgaa gacaccggaa tctactattg cacacggggc	360
aacggaaatt accgcgctat ggattattgg gggcagggca cttccgtcac cgtgagctcc	420
gcaagcacia agggaccctc cgtgtttccc ctggcccctt ctagtaaaag cacctccgga	480
ggaacagcag ctctgggatg tctggtgaag gactacttcc ctgagccagt caccgtgtca	540
tggaacagcg gagccctgac ctctggggtc catacatttc ctgctgtgct gcagtcaagc	600
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cctagcgtgt tcctgtttcc acccaagcca aaagacacac tgatgatttc ccgcactcct	840
gaggtcacct gtgtggtcgt ggacgtgtct cagcaggacc ccgaagtcaa gttcaactgg	900
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tctacctata gggctgtgag tgcctgaca gtgctgcacc aggactggct gaacggcaag	1020
gagtataagt gcaaagtgag caataaggct ctgccagcac ccacgaaaa aactatttcc	1080
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ctggactccg atgggtctttt ctttctgtat agtaagctga cctgggataa atcacggtgg	1320
cagcagggca acgtcttttc ttgcagtgtg atgcatgaag ccctgcacaa tcattacaca	1380
cagaagtcac tgagcctgtc cccaggcaag cgaggacgaa aaaggagatc tggagtgagg	1440
gctactaact tcagcctgct gaaacaggca ggcgacgtgg aggaaaatcc tggaccaatg	1500
gtcctgcaga cccagggtgtt tatctcactg ctgctgtgga ttagcggggc ttacggcgat	1560
attcagatga cacagtcccc agcatcactg agcgtctccg tgggagaaac agtgtccatc	1620
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gattttggga cttactattg ccagcacttc tggggcacac catacacttt tggcggaggg	1860
actaagctgg agatcaaaac cgtcgcagcc ccctctgtgt tcatttttcc acccagtgac	1920
gaacagctga agagtggcac cgcctcagtc gtgtgtctgc tgaacaattt ctaccctaga	1980
gaggcaaagg tccagtggaa agtgataac gccctgcaga gcggcaattc ccaggaatct	2040
gtgactgagc aggacagtaa ggattcaacc tatagcctgt ccaacaccct gacactgagc	2100
aaagctgact acgaaaagca caaagtctat gcatgagagg tgacacatca gggactgagt	2160
tcaccagtga ctaagtcctt taatcggggg gagtgttgat aa	2202

<210> 137
 <211> 711
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DMab-4G7

<400> 137

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Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Ser	Ser	Phe	Thr	Gly	Phe
		20					25					30			

Ser	Met	Asn	Trp	Val	Lys	Gln	Ser	Asn	Gly	Lys	Ser	Leu	Glu	Trp	Ile
	35					40					45				

Gly	Asn	Ile	Asp	Thr	Tyr	Tyr	Gly	Gly	Thr	Thr	Tyr	Asn	Gln	Lys	Phe
50					55					60					

206108_0033_30wo_606194_seqlisting

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80
 Met Gln Leu Lys Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Ser Ala Tyr Tyr Gly Ser Thr Phe Ala Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
 115 120 125
 Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
 130 135 140
 Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
 145 150 155 160
 Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
 165 170 175
 Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
 180 185 190
 Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
 195 200 205
 Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
 210 215 220
 Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
 225 230 235 240
 Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 245 250 255
 Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 260 265 270
 Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 275 280 285
 Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 290 295 300
 Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 305 310 315 320

206108_0033_30wo_606194_seqlisting

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
340 345 350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

Lys Arg Gly Arg Lys Arg Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser
450 455 460

Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Val
465 470 475 480

Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser Gly Ala
485 490 495

Tyr Gly Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser
500 505 510

Val Gly Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Tyr
515 520 525

Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu
530 535 540

Leu Val Tyr Asn Ala Lys Thr Leu Ile Glu Gly Val Pro Ser Arg Phe
545 550 555 560

Ser Gly Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Asn Ser Leu
565 570 575

206108_0033_30wo_606194_seqlisting

Gln Pro Glu Asp Phe Gly Ser Tyr Phe Cys Gln His His Phe Gly Thr
580 585 590

Pro Phe Thr Phe Gly Ser Gly Thr Glu Leu Glu Ile Lys Thr Val Ala
595 600 605

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
610 615 620

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
625 630 635 640

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
645 650 655

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
660 665 670

Ser Asn Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
675 680 685

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
690 695 700

Ser Phe Asn Arg Gly Glu Cys
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<210> 138
<211> 2196
<212> DNA
<213> Artificial Sequence

<220>
<223> pGX9229, DMAB-4G7

<400> 138
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tgcaaggcat caggaagctc cttcacaggg tttagcatga actgggtgaa acagagcaat 180
gggaagtccc tggagtggat cggcaacatt gacacctact atggcggaac cacatacaat 240
cagaagttca aaggcaaggc tacactgact gtggacaaat ctagttcaac cgcataatg 300
cagctgaaga gcctgacatc cgaggattct gcagtgtact attgcgctag atcagcatac 360
tatggcagca ctttcgccta ctggggccag ggaaccctgg tcacagttag ctccgcctcc 420
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600 tcaggcgcac tgactcttgg agtcccaacc ttccctgccc tgctgcagtc aagcggccctg

660 tacaggccctgt cctctgttgt caccgtgccca agttcaagcc tgggaaccca gacatatatc

720 tgcacagtga atcaccaaac ctctaataca aaggtcgaca agaaagtga acctaaagc

780 tgtgataga ctcataacct cccaccttgt ccagcaacctg agctgctggg agggccctcc

840 gtgttccctgt ttccacccaa accaaagac acactgatga ttagcagaac cctgaagtc

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1140 aaggacagc caagagaacc ccaggtgtac actctgctc catctcggga cgagctgacc

1200 aaaaaccagg tcagttcgac atgtcttgtg aaggattct atccaagcga tatcgcagtg

1260 gagtgggaat ccaatgggca gcccgaaac aattaacaga ctacccccct tgtgcttgga

1320 agcgatggca gcttctctct gtattccaaa ctgaagttgg ataagtctcg gtggcagcag

1380 gggaaagctt ttagctcttc cgtgatgcac gaggccctgc acaatcata cactcagaag

1440 tctctgagtc tgtcaccaag caaacgagga cgaagagga gaagcggtc cggagcaacc

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1560 cagacacagg tgttatctc actgcctgctg tggattagcg ggccctacgg cgatatcag

1620 atgactcaga gccccgcata tctgagttgcc tcagtcggcg agacagtga taccacctgt

1680 cgcgcagtg aaaaactata ctcatatctg gcttgtaac agcagaaca ggggaagagc

1740 cccagctgc tgtctataa tgcataaac ctgatcgag gagtgccttc ccgattcagc

1800 ggtagcggtt ctggcacaca gtttagccctg aagattaac cctgcagcc agaggaactc

1860 ggtagctact ttgtccagca ccatttcgga actccctca ccttggcag cgggacagag

1920 ctggaatca aaaactgtgc agccccaggt gtgttcatit ttccacccctc agacgaacag

1980 ctgaagctctg ggaccgcccag tgtcgttgtt ctgctgaaca atttttacc tgggaggtt

2040 aaggtccagt ggaaggtgga taacgcactg cagtcctgga atagtcaagg gtcaagtga

2100 gaaacagaca gcaaaagatc cacttatagt ctgtcaaca cactgacct gtctaagcc

2160 gactacgaga aacaagaagt ctatgcttgc gaagtgaact atcaggggct gtccctcct

2196 gtgaccaga gcttcaatcg cggcgagtgt tgataa

<210>
139
<211>
733
<212>
PRT
<213>

Artificial Sequence

206108_0033_30wo_606194_seqlisting

<220>

<223> DMAB4

<400> 139

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
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Thr His Ala Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Lys
20 25 30

Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Leu Ser Gly Phe Ser Leu
35 40 45

Ser Thr Ser Gly Val Gly Val Gly Trp Phe Arg Gln Pro Ser Gly Lys
50 55 60

Gly Leu Glu Trp Leu Ala Leu Ile Trp Trp Asp Asp Asp Lys Tyr Tyr
65 70 75 80

Asn Pro Ser Leu Lys Ser Gln Leu Ser Ile Ser Lys Asp Phe Ser Arg
85 90 95

Asn Gln Val Phe Leu Lys Ile Ser Asn Val Asp Ile Ala Asp Thr Ala
100 105 110

Thr Tyr Tyr Cys Ala Arg Arg Asp Pro Phe Gly Tyr Asp Asn Ala Met
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Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
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Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
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Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
180 185 190

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
195 200 205

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
210 215 220

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
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Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser
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Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser
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Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser
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Asn Pro Gly Pro Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu
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Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Leu Thr Cys Lys
530 535 540

Ala Ser Gln Asn Val Gly Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro
545 550 555 560

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Ser Ala Ser Asn Arg Tyr Thr
565 570 575

Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
580 585 590

Leu Thr Ile Ser Asn Met Gln Ser Glu Asp Leu Ala Asp Tyr Phe Cys
595 600 605

Gln Gln Tyr Ser Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu
610 615 620

Glu Ile Lys Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
625 630 635 640

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
645 650 655

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
660 665 670

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
675 680 685

Asp Ser Thr Tyr Ser Leu Ser Asn Thr Leu Thr Leu Ser Lys Ala Asp
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Arg Ser Tyr Asp Met His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu
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Glu Trp Val Ser Ala Ile Gly Thr Ala Gly Asp Thr Tyr Tyr Pro Gly
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Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn Ser
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Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
100 105 110

Tyr Cys Ala Arg Val Arg Phe Gly Asp Thr Ala Val Asp Tyr Trp Gly
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115

120

125

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Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
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165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
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Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245 250 255

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260 265 270

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His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
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Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
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Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
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Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
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Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
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Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
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His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
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Pro Gly Lys Arg Gly Arg Lys Arg Arg Ser Gly Ser Gly Ala Thr Asn
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Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro
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Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
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Gly Ala Tyr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
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Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser
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Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
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Ser Leu Gln Pro Glu Asp Phe Ala Ile Tyr Tyr Cys Gln Gln Ser Tyr
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Ile Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Thr
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Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
660 665 670

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
675 680 685

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
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Arg Ser Asn Tyr Leu Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ser Leu Ile Tyr Ser Gly Gly Leu Thr Ala Tyr Ala Asp
65 70 75 80

Ser Val Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
85 90 95

Leu Tyr Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Leu Tyr
100 105 110

Tyr Cys Ala Arg Val Ala Ser Ser Ala Gly Thr Phe Tyr Tyr Gly Met
115 120 125

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
130 135 140

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145 150 155 160

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
165 170 175

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
180 185 190

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
195 200 205

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
210 215 220

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
225 230 235 240

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
245 250 255

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
260 265 270

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305 310 315 320

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
325 330 335

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340 345 350

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355 360 365

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
370 375 380

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385 390 395 400

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
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420 425 430

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
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Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
450 455 460

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465 470 475 480

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Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val
595 600 605

Gly Val Tyr Tyr Cys Met Gln Ala Leu Gln Thr Pro Ser Trp Thr Phe
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Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Val Ala Ala Pro Ser Val
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Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val
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Gly Ser Asp Thr Val Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
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Gln Arg Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Asn
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Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
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His Tyr Tyr Thr Tyr Met Asp Val Trp Gly Gln Gly Thr Leu Val Thr
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210 215 220

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
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Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
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Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
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Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
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Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
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Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
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Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
325 330 335

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
340 345 350

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
355 360 365

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
370 375 380

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
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 Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
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 His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Arg Gly Arg
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 Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Val Leu Gln Thr Gln
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 Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Ser Asn His Leu Val
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675 680 685

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Asn
690 695 700

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
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Pro Gly Gly Ser Leu Arg Leu Ser Cys Glu Val Ser Gly Leu Thr Phe
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Ser Asn Phe Gly Met Gln Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ala Phe Ile Arg Phe Asp Gly Ser Asn Lys Tyr Tyr Ala
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
85 90 95

Thr Val Tyr Leu Gln Met Gly Ser Leu Arg Ala Glu Asp Thr Ala Val
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Tyr Phe Cys Gly Arg Val Leu Tyr Gly Ala Ala Ala Asp Phe Trp Gly
115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
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165 170 175

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180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

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210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
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Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
675 680 685

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Asn Thr Leu Thr Leu Ser Lys
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Thr Glu Gly Asn Ile Ala Ala Met Ile Val Asn Lys Thr Val His Lys
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180 185 190

Ser Thr Asn Lys Tyr Trp Thr Ser Ser Asn Gly Thr Gln Thr Asn Asp
195 200 205

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210 215 220

Thr Cys Ala Pro Ser Lys Ile Pro Leu Pro Leu Pro Thr Ala Arg Pro
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Glu Val Lys Leu Thr Ser Thr Ser Thr Asp Ala Thr Lys Leu Asn Thr
245 250 255

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260 265 270

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Gly Leu Ser Ser Thr Met Pro Pro Thr Pro Ser Pro Gln Pro Ser Thr
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Pro Gln Gln Glu Gly Asn Asn Thr Asn His Ser Gln Gly Ala Val Thr
305 310 315 320

Glu Pro Gly Lys Thr Asn Thr Thr Ala Gln Pro Ser Met Pro Pro His
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Asn Thr Thr Ala Ile Ser Thr Asn Asn Thr Ser Lys His Asn Phe Ser

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 385 390 395 400
 Ser Pro Thr Thr Thr Val Pro Asn Thr Thr Asn Lys His Ser Thr Ser
 405 410 415
 Pro Ser Pro Thr Pro Asn Pro Thr Ala Gln His Leu Val Tyr Phe Arg
 420 425 430
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 Arg Leu Ala Asn Gln Thr Ala Lys Ser Leu Glu Leu Leu Leu Arg Val
 565 570 575
 Thr Thr Glu Glu Arg Thr Phe Ser Leu Ile Asn Arg His Ala Ile Asp
 580 585 590

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Phe Leu Leu Ala Arg Trp Gly Gly Thr Cys Lys Val Leu Gly Pro Asp
595 600 605

Cys Cys Ile Gly Ile Glu Asp Leu Ser Arg Asn Ile Ser Glu Gln Ile
610 615 620

Asp Gln Ile Lys Lys Asp Glu Gln Lys Glu Gly Thr Gly Trp Gly Leu
625 630 635 640

Gly Gly Lys Trp Trp Thr Ser Asp Trp Gly Val Leu Thr Asn Leu Gly
645 650 655

Ile Leu Leu Leu Leu Ser Ile Ala Val Leu Ile Ala Leu Ser Cys Ile
660 665 670

Cys Arg Ile Phe Thr Lys Tyr Ile Gly
675 680

<210> 151
<211> 2067
<212> DNA
<213> Artificial Sequence

<220>
<223> Marburg GP2 Consensus

<400> 151
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aagaccctgc caatcctgga gatcgcttcc aacgaccagc cccagaatgt ggatagcgtg 120
tgctccggca ccctgcagaa gacagaggac gtgcacctga tgggcttcac actgtctggc 180
cagaaggtgg ccgatagccc cctggaggcc tctaagaggt gggccttttag aaccggcgtg 240
ccccctaaga acgtggagta caccgagggc gaggaggcca agacatgcta taatatcagc 300
gtgaccgacc cttctggcaa gagcctgctg ctggaccac ccacaaacgt gcgcgattac 360
cctaagtgtg agaccatcca ccacatccag ggccagaatc cacacgcaca gggaatcgcc 420
ctgcacctgt ggggcgcctt ctttctgtac gataggatcg cctccaccac aatgtataga 480
ggcaaggtgt tcacagaggg caacatcgcc gccatgatcg tgaataagac cgtgcacaag 540
atgatctttt ccaggcaggg ccagggttac agacacatga acctgacatc taccaataag 600
tattggacca gctccaacgg cacacagacc aatgacaccg gctgcttcgg cactgtcgag 660
gagtacaact ccaccaagaa tcagacatgt gccccttcta agaccctcc accccctcca 720
acagcaaggc cagagatcaa gcctacaagc accccaacag acgccaccag actgaacacc 780
acaaacccca attccgacga tgaggatctg accacaagcg gctccggctc tggagagcag 840
gagccttata ccacatccga cgccgtgacc aagcagggcc tgtctagcac catgccccct 900

206108-0033-30WO-606194-seq1isting
 960 acacattccc cacagccagg aacactcag caggcgcgca acaataccaa ccaattcag
 1020 gagcccca cagagcttga taaccaaat accacagccc agccaccat gccaaagccac
 1080 aataccaacaa ccatcagcac caacaataca tccaagcaca acctgtccac cctgtctgag
 1140 cctccacaga atacaaccaa cccaatacc cagagcatgg tgacagagaa cgaagaagacc
 1200 agcgcccttc ccaagggccac cctgccacc acagagaaac ccaaacga gaagtctaac
 1260 aacaatacaa agagccctac aaccttgag ccaacaaga caaatggcca ctccacagc
 1320 cctctctca cactaaatc caacaaccag cactgatc actttaagg aaagcggtcc
 1380 atcctgtgc gcgaggcgga catgttcccc ttcttgatg gcctgataa cgccccatc
 1440 gacttcgac ctgtgccaa taccaagaca atcttgacg agagctctc tagcggagca
 1500 agcgccgag aggatcagca cgctctctt aacatcagcc tgaccctgtc ctaccitcca
 1560 cacaccctcg agaatacagc ctattctgc gagaacgaga atgactgcga tgcagagctg
 1620 cggatctgtt ctgttcagga ggagcatctg gcagcaggac tgagctggat tcccctgttc
 1680 ggaccagaa tcgaggagct gtataccgc gccctgata agaacagaa caacctgtgtg
 1740 tgcaggctgc ggcgccttgc aatcagaca gccaagtctc tgagcctgtc gctgcgggtg
 1800 acaaccgag agcgacatt cagcctgatc aaccggcacg ccaticgact tctgttgacc
 1860 cgtctgggcg gcacatgcga gttccttggc ccaagactgt gtatcggcat cgaagatctg
 1920 tctaggaaac tcagcgagca gatcgaccag atcaagaag atgagcagaa ggagggaaac
 1980 ggatgggac tgggcggcaa gtgttgaca agcatggg gcgtctgac caacctgggc
 2040 atcctgtgc tgcgtctat cgccgtgtg atcgccctga gctgcatctg tagaatctt
 2067 accaagtata tcgctgata actcgag

<210> 152
 <211> 681
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Marburg GP2 Consensus
 <400> 152

1 Met Arg Thr Thr Cys Phe Phe Ile Ser Leu Ile Leu Ile Gly Ile
 5
 10
 15

Lys Thr Leu Pro Ile Leu Glu Ile Ala Ser Asn Asp Glu Pro Glu Asn
 20
 25
 30

Val Asp Ser Val Cys Ser Gly Thr Leu Glu Lys Thr Glu Asp Val His
 35
 40
 45

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Leu Met Gly Phe Thr Leu Ser Gly Gln Lys Val Ala Asp Ser Pro Leu
50 55 60

Glu Ala Ser Lys Arg Trp Ala Phe Arg Thr Gly Val Pro Pro Lys Asn
65 70 75 80

Val Glu Tyr Thr Glu Gly Glu Glu Ala Lys Thr Cys Tyr Asn Ile Ser
85 90 95

Val Thr Asp Pro Ser Gly Lys Ser Leu Leu Leu Asp Pro Pro Thr Asn
100 105 110

Val Arg Asp Tyr Pro Lys Cys Lys Thr Ile His His Ile Gln Gly Gln
115 120 125

Asn Pro His Ala Gln Gly Ile Ala Leu His Leu Trp Gly Ala Phe Phe
130 135 140

Leu Tyr Asp Arg Ile Ala Ser Thr Thr Met Tyr Arg Gly Lys Val Phe
145 150 155 160

Thr Glu Gly Asn Ile Ala Ala Met Ile Val Asn Lys Thr Val His Lys
165 170 175

Met Ile Phe Ser Arg Gln Gly Gln Gly Tyr Arg His Met Asn Leu Thr
180 185 190

Ser Thr Asn Lys Tyr Trp Thr Ser Ser Asn Gly Thr Gln Thr Asn Asp
195 200 205

Thr Gly Cys Phe Gly Thr Leu Gln Glu Tyr Asn Ser Thr Lys Asn Gln
210 215 220

Thr Cys Ala Pro Ser Lys Thr Pro Pro Pro Pro Pro Thr Ala Arg Pro
225 230 235 240

Glu Ile Lys Pro Thr Ser Thr Pro Thr Asp Ala Thr Arg Leu Asn Thr
245 250 255

Thr Asn Pro Asn Ser Asp Asp Glu Asp Leu Thr Thr Ser Gly Ser Gly
260 265 270

Ser Gly Glu Gln Glu Pro Tyr Thr Thr Ser Asp Ala Val Thr Lys Gln
275 280 285

Gly Leu Ser Ser Thr Met Pro Pro Thr Pro Ser Pro Gln Pro Gly Thr
290 295 300

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Pro Gln Gln Gly Gly Asn Asn Thr Asn His Ser Gln Asp Ala Thr Thr
305 310 315 320

Glu Leu Asp Asn Thr Asn Thr Thr Ala Gln Pro Pro Met Pro Ser His
325 330 335

Asn Thr Thr Thr Ile Ser Thr Asn Asn Thr Ser Lys His Asn Leu Ser
340 345 350

Thr Leu Ser Glu Pro Pro Gln Asn Thr Thr Asn Pro Asn Thr Gln Ser
355 360 365

Met Val Thr Glu Asn Glu Lys Thr Ser Ala Pro Pro Lys Ala Thr Leu
370 375 380

Pro Pro Thr Glu Asn Pro Thr Thr Glu Lys Ser Thr Asn Asn Thr Lys
385 390 395 400

Ser Pro Thr Thr Leu Glu Pro Asn Lys Thr Asn Gly His Phe Thr Ser
405 410 415

Pro Ser Ser Thr Pro Asn Ser Thr Thr Gln His Leu Ile Tyr Phe Arg
420 425 430

Arg Lys Arg Ser Ile Leu Trp Arg Glu Gly Asp Met Phe Pro Phe Leu
435 440 445

Asp Gly Leu Ile Asn Ala Pro Ile Asp Phe Asp Pro Val Pro Asn Thr
450 455 460

Lys Thr Ile Phe Asp Glu Ser Ser Ser Ser Gly Ala Ser Ala Glu Glu
465 470 475 480

Asp Gln His Ala Ser Ser Asn Ile Ser Leu Thr Leu Ser Tyr Leu Pro
485 490 495

His Thr Ser Glu Asn Thr Ala Tyr Ser Gly Glu Asn Glu Asn Asp Cys
500 505 510

Asp Ala Glu Leu Arg Ile Trp Ser Val Gln Glu Asp Asp Leu Ala Ala
515 520 525

Gly Leu Ser Trp Ile Pro Leu Phe Gly Pro Gly Ile Glu Gly Leu Tyr
530 535 540

Thr Ala Gly Leu Ile Lys Asn Gln Asn Asn Leu Val Cys Arg Leu Arg
545 550 555 560

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Arg Leu Ala Asn Gln Thr Ala Lys Ser Leu Glu Leu Leu Leu Arg Val
565 570 575

Thr Thr Glu Glu Arg Thr Phe Ser Leu Ile Asn Arg His Ala Ile Asp
580 585 590

Phe Leu Leu Thr Arg Trp Gly Gly Thr Cys Lys Val Leu Gly Pro Asp
595 600 605

Cys Cys Ile Gly Ile Glu Asp Leu Ser Arg Asn Ile Ser Glu Gln Ile
610 615 620

Asp Gln Ile Lys Lys Asp Glu Gln Lys Glu Gly Thr Gly Trp Gly Leu
625 630 635 640

Gly Gly Lys Trp Trp Thr Ser Asp Trp Gly Val Leu Thr Asn Leu Gly
645 650 655

Ile Leu Leu Leu Leu Ser Ile Ala Val Leu Ile Ala Leu Ser Cys Ile
660 665 670

Cys Arg Ile Phe Thr Lys Tyr Ile Gly
675 680

<210> 153
<211> 2067
<212> DNA
<213> Artificial Sequence

<220>
<223> Marburg GP3 Consensus

<400> 153
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aagaccctgc cagtgcctga gatcgccctc aactctcagc cccaggacgt ggatagcgtg 120
tgctctggca ccctgcagaa gacagaggac gtgcacctga tgggcttcac actgtccggc 180
cagaaggtgg ccgattcccc tctggaggcc tctaagaggt gggccttttag aaccggcgtg 240
ccccctaaga acgtggagta caccgagggc gaggaggcca agacatgcta taatatctcc 300
gtgaccgacc caagcggcaa gtccctgctg ctggaccac cctctaacat cagggattac 360
cccaagtgtg agaccgtgca ccacatccag ggccagaatc ctcacgcaca gggaatcgcc 420
ctgcacctgt ggggcgcctt ctttctgtac gatcgggtgg ccagcaccac aatgtatcgc 480
ggcaaggtgt tcacagaggg caacatcgcc gccatgatcg tgaataagac cgtgcaccgg 540
atgatctttt ctcgccaggg ccagggtac aggcacatga acctgaccag cacaataag 600

206108_0033_30WO-606194-seq11.sting

660 tattggacaa gctcccaacga gacccagaga aatgacacag gctgctttgg catccttgca

720 gagtataact ccaaccaacaa tcagacatgt cctccaagcc tgaagccccc ttccctgccc

780 accgtgacac catctatcca cagcaccacac acacagatca ataccgccaa gagcggcaca

840 atgaacccct ctagcgacga tgaaggacct atgatacgcg gctccggctc tggagagcag

900 ggaaccacaca ccacactgaa tgtgttgacc gagcagaagc agtcccttac catcctgtcc

960 aacaccatctc tgcaccctgag cacatccca gacgagcaga actctaccaa tcccagccgg

1020 cagcgagtga ccgagcacaa cggcacagac cccaaccac agcctggcac cctgctgaa

1080 aatacaata ccacacctac ctacaacaca ctgaagtata atctgagcac accatccca

1140 cccaacgga acatcacaaa caatgatacc cagagagagc tggccgagtc cgaagcagacc

1200 aacgcccagc tgaatatccac actggatcca acagagaac ccaaccacag ccagatatcc

1260 aacttacca caatatcat catgaccaa tcgcacata cctctaagca cccaacaat

1320 agtcccccctg attctagccc aaccacagc cctccaact acttcaggaa gaagagagagc

1380 atcttttga aggaaggcga catctcccc ttcttgatg gccctgatcag caccgagatc

1440 gacttcgatc caatcccca caccgagaca atcttcgacg agtctccca ctttaacacc

1500 tccaataatg aggagcagca cacacccct aacatcagcc tgaaccttcc ctactttcc

1560 gacaagaatg gcgataccgc ctatagcggc gagaacgaga atgactcgga tgcgagctg

1620 cggatcttga gcgtgcagga ggacgatctg gcagcagagc tgtctctgat tccctcttc

1680 ggccttgca tcgagggcct gtataccgc gccctgatca agaaccagaa caacctgtg

1740 tgcgccttga ggagactggc caatcacaca gccaaagacc tggagctgct gctgagggtg

1800 accacagagg agagaacct ctccctgatc aaccggcacg ccactgactt tctcttgacc

1860 cgcctgggcg gcacatgcaa ggtgctggga ccagactgct gtatcggcat cgaagatctg

1920 tctaagaata tcagcgacga gatcgacaag atcaggaagg atgagcagaa ggagagagacc

1980 ggatggggac tgggcggcaa gtgttgaca agcatgtggg gcgtgctgac caacctgggc

2040 atcctgctgc tgccttccat cggcgtgctg atcgccctgt ctgcatctg tagaatcttc

2067 accaagtaca tcggctgata actcgag

1 Met Lys Thr Ile Tyr Phe Leu Ile Ser Leu Ile Leu Ile Gln Ser Ile
5
10
15

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Lys Thr Leu Pro Val Leu Glu Ile Ala Ser Asn Ser Gln Pro Gln Asp
 20 25 30
 Val Asp Ser Val Cys Ser Gly Thr Leu Gln Lys Thr Glu Asp Val His
 35 40 45
 Leu Met Gly Phe Thr Leu Ser Gly Gln Lys Val Ala Asp Ser Pro Leu
 50 55 60
 Glu Ala Ser Lys Arg Trp Ala Phe Arg Thr Gly Val Pro Pro Lys Asn
 65 70 75 80
 Val Glu Tyr Thr Glu Gly Glu Glu Ala Lys Thr Cys Tyr Asn Ile Ser
 85 90 95
 Val Thr Asp Pro Ser Gly Lys Ser Leu Leu Leu Asp Pro Pro Ser Asn
 100 105 110
 Ile Arg Asp Tyr Pro Lys Cys Lys Thr Val His His Ile Gln Gly Gln
 115 120 125
 Asn Pro His Ala Gln Gly Ile Ala Leu His Leu Trp Gly Ala Phe Phe
 130 135 140
 Leu Tyr Asp Arg Val Ala Ser Thr Thr Met Tyr Arg Gly Lys Val Phe
 145 150 155 160
 Thr Glu Gly Asn Ile Ala Ala Met Ile Val Asn Lys Thr Val His Arg
 165 170 175
 Met Ile Phe Ser Arg Gln Gly Gln Gly Tyr Arg His Met Asn Leu Thr
 180 185 190
 Ser Thr Asn Lys Tyr Trp Thr Ser Ser Asn Glu Thr Gln Arg Asn Asp
 195 200 205
 Thr Gly Cys Phe Gly Ile Leu Gln Glu Tyr Asn Ser Thr Asn Asn Gln
 210 215 220
 Thr Cys Pro Pro Ser Leu Lys Pro Pro Ser Leu Pro Thr Val Thr Pro
 225 230 235 240
 Ser Ile His Ser Thr Asn Thr Gln Ile Asn Thr Ala Lys Ser Gly Thr
 245 250 255
 Met Asn Pro Ser Ser Asp Asp Glu Asp Leu Met Ile Ser Gly Ser Gly
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260
 Ser Gly Glu Gln Gly Pro His Thr Thr Leu Asn Val Val Thr Glu Gln
 275 280 285
 Lys Gln Ser Ser Thr Ile Leu Ser Thr Pro Ser Leu His Leu Ser Thr
 290 300
 Ser Gln His Glu Gln Asn Ser Thr Asn Pro Ser Arg His Ala Val Thr
 305 310 315 320
 Glu His Asn Gly Thr Asp Pro Thr Thr Gln Pro Ala Thr Leu Leu Asn
 325 330 335
 Asn Thr Asn Thr Thr Pro Thr Tyr Asn Thr Leu Lys Tyr Asn Leu Ser
 340 345 350
 Thr Pro Ser Pro Pro Thr Arg Asn Ile Thr Asn Asn Asp Thr Gln Arg
 355 360 365
 Glu Leu Ala Glu Ser Glu Gln Thr Asn Ala Gln Leu Asn Thr Thr Leu
 370 375 380
 Asp Pro Thr Glu Asn Pro Thr Thr Gly Gln Asp Thr Asn Ser Thr Thr
 385 390 395 400
 Asn Ile Ile Met Thr Thr Ser Asp Ile Thr Ser Lys His Pro Thr Asn
 405 410 415
 Ser Ser Pro Asp Ser Ser Pro Thr Thr Arg Pro Pro Ile Tyr Phe Arg
 420 425 430
 Lys Lys Arg Ser Ile Phe Trp Lys Glu Gly Asp Ile Phe Pro Phe Leu
 435 440 445
 Asp Gly Leu Ile Ser Thr Glu Ile Asp Phe Asp Pro Ile Pro Asn Thr
 450 455 460
 Glu Thr Ile Phe Asp Glu Ser Pro Ser Phe Asn Thr Ser Thr Asn Glu
 465 470 475 480
 Glu Gln His Thr Pro Pro Asn Ile Ser Leu Thr Phe Ser Tyr Phe Pro
 485 490 495
 Asp Lys Asn Gly Asp Thr Ala Tyr Ser Gly Glu Asn Glu Asn Asp Cys
 500 505 510

206108_0033_30wo_606194_seqlisting

Asp Ala Glu Leu Arg Ile Trp Ser Val Gln Glu Asp Asp Leu Ala Ala
515 520 525

Gly Leu Ser Trp Ile Pro Phe Phe Gly Pro Gly Ile Glu Gly Leu Tyr
530 535 540

Thr Ala Gly Leu Ile Lys Asn Gln Asn Asn Leu Val Cys Arg Leu Arg
545 550 555 560

Arg Leu Ala Asn Gln Thr Ala Lys Ser Leu Glu Leu Leu Leu Arg Val
565 570 575

Thr Thr Glu Glu Arg Thr Phe Ser Leu Ile Asn Arg His Ala Ile Asp
580 585 590

Phe Leu Leu Thr Arg Trp Gly Gly Thr Cys Lys Val Leu Gly Pro Asp
595 600 605

Cys Cys Ile Gly Ile Glu Asp Leu Ser Lys Asn Ile Ser Glu Gln Ile
610 615 620

Asp Lys Ile Arg Lys Asp Glu Gln Lys Glu Glu Thr Gly Trp Gly Leu
625 630 635 640

Gly Gly Lys Trp Trp Thr Ser Asp Trp Gly Val Leu Thr Asn Leu Gly
645 650 655

Ile Leu Leu Leu Leu Ser Ile Ala Val Leu Ile Ala Leu Ser Cys Ile
660 665 670

Cys Arg Ile Phe Thr Lys Tyr Ile Gly
675 680

<210> 155

<211> 735

<212> PRT

<213> Artificial Sequence

<220>

<223> Influenza A DMAB

<400> 155

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys
20 25 30

Pro Ser Gln Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val
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35

40

45

Ser Ser Asn Asn Ala Val Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg
50 55 60

Gly Leu Glu Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn
65 70 75 80

Asp Tyr Ala Glu Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr
85 90 95

Ser Lys Asn Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp
100 105 110

Thr Ala Val Tyr Tyr Cys Ala Arg Ser Gly His Ile Thr Val Phe Gly
115 120 125

Val Asn Val Asp Ala Phe Asp Met Trp Gly Gln Gly Thr Thr Val Thr
130 135 140

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
145 150 155 160

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
165 170 175

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
180 185 190

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
195 200 205

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
210 215 220

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
225 230 235 240

Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
245 250 255

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
260 265 270

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
275 280 285

206108_0033_30wo_606194_seqlisting

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
290 295 300

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
305 310 315 320

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
325 330 335

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
340 345 350

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
355 360 365

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
370 375 380

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
385 390 395 400

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
405 410 415

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
420 425 430

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
435 440 445

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
450 455 460

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Arg Gly Arg
465 470 475 480

Lys Arg Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln
485 490 495

Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Val Leu Gln Thr Gln
500 505 510

Val Phe Ile Ser Leu Leu Leu Trp Ile Ser Gly Ala Tyr Gly Asp Ile
515 520 525

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
530 535 540

206108_0033_30wo_606194_seqlisting

Val Thr Ile Thr Cys Arg Thr Ser Gln Ser Leu Ser Ser Tyr Leu His
545 550 555 560

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
565 570 575

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
580 585 590

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
595 600 605

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Arg Thr Phe Gly Gln Gly Thr
610 615 620

Lys Val Glu Ile Lys Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
625 630 635 640

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
645 650 655

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
660 665 670

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
675 680 685

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Asn Thr Leu Thr Leu Ser Lys
690 695 700

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
705 710 715 720

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
725 730 735

<210> 156

<211> 745

<212> PRT

<213> Artificial Sequence

<220>

<223> Influenza B DMAB

<400> 156

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

206108_0033_30wo_606194_seqlisting

Thr His Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Phe
35 40 45

Leu Asn Ala Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Gly Arg Ile Lys Ser Asn Thr Asp Gly Gly Thr Thr Asp
65 70 75 80

Tyr Ala Ala Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
85 90 95

Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Thr Glu Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Thr Thr Asp Gly Pro Tyr Ser Asp Asp Phe Arg
115 120 125

Ser Gly Tyr Ala Ala Arg Tyr Arg Tyr Phe Gly Met Asp Val Trp Gly
130 135 140

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
145 150 155 160

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
165 170 175

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
180 185 190

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
195 200 205

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
210 215 220

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
225 230 235 240

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
245 250 255

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
260 265 270

206108_0033_30wo_606194_seqlisting

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
275 280 285

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
290 295 300

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
305 310 315 320

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
325 330 335

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
340 345 350

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
355 360 365

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
370 375 380

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
385 390 395 400

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
405 410 415

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
420 425 430

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
435 440 445

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
450 455 460

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
465 470 475 480

Pro Gly Lys Arg Gly Arg Lys Arg Arg Ser Gly Ser Gly Ala Thr Asn
485 490 495

Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro
500 505 510

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
515 520 525

206108_0033_30wo_606194_seqlisting

Gly Ala Tyr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser
530 535 540

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp
545 550 555 560

Ile Ser Thr Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
565 570 575

Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser
580 585 590

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
595 600 605

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn
610 615 620

Ser Phe Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Thr
625 630 635 640

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
645 650 655

Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
660 665 670

Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
675 680 685

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
690 695 700

Ser Leu Ser Asn Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
705 710 715 720

Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
725 730 735

Thr Lys Ser Phe Asn Arg Gly Glu Cys
740 745

<210> 157
<211> 736
<212> PRT
<213> Artificial Sequence

206108_0033_30wo_606194_seqlisting

<220>

<223> Influenza A DmAb

<400> 157

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Glu Val Gln Leu Val Glu Ser Gly Pro Gly Leu Val Lys
20 25 30

Pro Ser Asp Ile Leu Ser Leu Thr Cys Ala Val Ser Gly Tyr Ser Ile
35 40 45

Ser Ser Asn Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly
50 55 60

Leu Glu Trp Ile Gly Ser Ile Tyr His Ser Gly Ser Thr Tyr Tyr Lys
65 70 75 80

Pro Ser Leu Glu Ser Arg Leu Gly Ile Ser Val Asp Thr Ser Lys Asn
85 90 95

Gln Phe Ser Leu Lys Leu Ser Phe Val Ser Ala Ala Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg His Val Arg Ser Gly Tyr Pro Asp Thr Ala Tyr
115 120 125

Tyr Phe Asp Lys Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala
130 135 140

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
145 150 155 160

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
165 170 175

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
180 185 190

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
195 200 205

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
210 215 220

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
225 230 235 240

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Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
245 250 255

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
260 265 270

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
275 280 285

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
290 295 300

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
305 310 315 320

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
325 330 335

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
340 345 350

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
355 360 365

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
370 375 380

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
385 390 395 400

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
405 410 415

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
420 425 430

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
435 440 445

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
450 455 460

Lys Ser Leu Ser Leu Ser Pro Gly Lys Arg Gly Arg Lys Arg Arg Ser
465 470 475 480

Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val
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485

490

495

Glu Glu Asn Pro Gly Pro Met Val Leu Gln Thr Gln Val Phe Ile Ser
500 505 510

Leu Leu Leu Trp Ile Ser Gly Ala Tyr Gly Ser Tyr Val Leu Thr Gln
515 520 525

Pro Pro Ser Val Ser Val Ala Pro Gly Glu Thr Ala Arg Ile Ser Cys
530 535 540

Gly Gly Asn Asn Ile Gly Thr Lys Val Leu His Trp Tyr Gln Gln Thr
545 550 555 560

Pro Gly Gln Ala Pro Val Leu Val Val Tyr Asp Asp Ser Asp Arg Pro
565 570 575

Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala
580 585 590

Thr Leu Thr Ile Ser Arg Val Glu Val Gly Asp Glu Ala Asp Tyr Tyr
595 600 605

Cys Gln Val Trp Asp Ile Ser Thr Asp Gln Ala Val Phe Gly Gly Gly
610 615 620

Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
625 630 635 640

Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
645 650 655

Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp
660 665 670

Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro
675 680 685

Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu
690 695 700

Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr
705 710 715 720

His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
725 730 735

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<210> 158
 <211> 744
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Influenza A DMAB

<400> 158

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
 1 5 10 15

Thr His Ala Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
 20 25 30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 35 40 45

Ser Thr Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 50 55 60

Glu Trp Val Ala Val Ile Ser Tyr Asp Ala Asn Tyr Lys Tyr Tyr Ala
 65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
 85 90 95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
 100 105 110

Tyr Tyr Cys Ala Lys Asp Ser Gln Leu Arg Ser Leu Leu Tyr Phe Glu
 115 120 125

Trp Leu Ser Gln Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 130 135 140

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
 145 150 155 160

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
 165 170 175

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
 180 185 190

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
 195 200 205

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
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210 206108_0033_30wo_606194_seqlisting 215 220

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
225 230 235 240

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
245 250 255

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
260 265 270

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
275 280 285

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
290 295 300

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
305 310 315 320

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
325 330 335

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
340 345 350

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
355 360 365

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
370 375 380

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
385 390 395 400

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
405 410 415

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
420 425 430

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
435 440 445

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
450 455 460

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Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Arg Gly
 465 470 475 480
 Arg Lys Arg Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys
 485 490 495
 Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Val Leu Gln Thr
 500 505 510
 Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser Gly Ala Tyr Gly Asp
 515 520 525
 Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu
 530 535 540
 Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Thr Phe Asn Tyr
 545 550 555 560
 Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys
 565 570 575
 Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg
 580 585 590
 Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
 595 600 605
 Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln His Tyr Arg
 610 615 620
 Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Val
 625 630 635 640
 Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
 645 650 655
 Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
 660 665 670
 Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
 675 680 685
 Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
 690 695 700
 Leu Ser Asn Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
 705 710 715 720

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Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
725 730 735

Lys Ser Phe Asn Arg Gly Glu Cys
740

<210> 159
<211> 477
<212> PRT
<213> Artificial Sequence

<220>
<223> Influenza A DMAB

<400> 159

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys
20 25 30

Pro Ser Gln Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val
35 40 45

Ser Ser Asn Asn Ala Val Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg
50 55 60

Gly Leu Glu Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn
65 70 75 80

Asp Tyr Ala Glu Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr
85 90 95

Ser Lys Asn Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp
100 105 110

Thr Ala Val Tyr Tyr Cys Ala Arg Ser Gly His Ile Thr Val Phe Gly
115 120 125

Val Asn Val Asp Ala Phe Asp Met Trp Gly Gln Gly Thr Thr Val Thr
130 135 140

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
145 150 155 160

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
165 170 175

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Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
180 185 190

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
195 200 205

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
210 215 220

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
225 230 235 240

Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
245 250 255

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
260 265 270

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
275 280 285

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
290 295 300

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
305 310 315 320

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
325 330 335

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
340 345 350

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
355 360 365

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
370 375 380

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
385 390 395 400

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
405 410 415

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
420 425 430

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Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
435 440 445

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
450 455 460

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 160
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> Influenza A DMAB

<400> 160

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

Gly Ala Tyr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln Ser
35 40 45

Leu Ser Ser Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
50 55 60

Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Arg
100 105 110

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Val Ala Ala Pro
115 120 125

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
130 135 140

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
145 150 155 160

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Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
165 170 175

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Asn
180 185 190

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
195 200 205

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
210 215 220

Asn Arg Gly Glu Cys
225

<210> 161
<211> 477
<212> PRT
<213> Artificial Sequence

<220>
<223> Influenza A DMAB

<400> 161

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys
20 25 30

Pro Ser Gln Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val
35 40 45

Ser Ser Asn Asn Ala Val Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg
50 55 60

Gly Leu Glu Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn
65 70 75 80

Asp Tyr Ala Glu Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr
85 90 95

Ser Lys Asn Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp
100 105 110

Thr Ala Val Tyr Tyr Cys Ala Arg Ser Gly His Ile Thr Val Phe Gly
115 120 125

Val Asn Val Asp Ala Phe Asp Met Trp Gly Gln Gly Thr Thr Val Thr
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130 206108_0033_30wo_606194_seqlisting
135 140

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
145 150 155 160

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
165 170 175

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
180 185 190

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
195 200 205

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
210 215 220

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
225 230 235 240

Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
245 250 255

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
260 265 270

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
275 280 285

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
290 295 300

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
305 310 315 320

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
325 330 335

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
340 345 350

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
355 360 365

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
370 375 380

206108_0033_30wo_606194_seqlisting

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
385 390 395 400

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
405 410 415

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
420 425 430

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
435 440 445

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
450 455 460

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 162
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> Influenza A DMAB

<400> 162

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

Gly Ala Tyr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln Ser
35 40 45

Leu Ser Ser Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
50 55 60

Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Arg
100 105 110

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Val Ala Ala Pro
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115 206108_0033_30wo_606194_seqlisting 120 125

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
130 135 140

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
145 150 155 160

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
165 170 175

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Asn
180 185 190

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
195 200 205

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
210 215 220

Asn Arg Gly Glu Cys
225

<210> 163
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Influenza A DMAB

<400> 163
atggattgga cttggaggat tctgtttctg gtcgccgccg ctactggaac tcacgctcag 60
gtgcagctgc agcagtctgg acccgactg gtgaagcctt cacagactct gacgctgacc 120
tgcgccatct ccggcgactc tgtgagctcc aacaatgctg tctggaactg gattagacag 180
tccccatctc gggggctgga atggctggga cgaacatact ataggagcaa atggtacaat 240
gactatgctg agagtgtgaa gtcacgaatc acaattaacc cagatactag caagaatcag 300
ttctccctgc agctgaactc tgtgacaccc gaggatactg cagtctacta ttgcgcacgc 360
tccggacaca tcaccgtgtt cggagtcaat gtggacgcct ttgatatgtg gggacagggg 420
accacagtca cagtgtctag tgcaagtact aaaggcccat cagtgtttcc cctggccccc 480
tcaagcaaga gtacctcagg cggaacagcc gctctgggat gtctggtgaa ggactacttc 540
cctgagccag tcaccgtgag ctggaactcc ggagctctga ccagcggggg gcatacat 600
cctgcagtcc tgcagtcctc tggcctgtac agcctgagtt cagtggtcac cgtgccaagc 660
tcctctctgg gaacacagac ttatatctgc aacgtgaatc acaaaccatc caatacaaag 720

780 gtcgacaaga aagtggaaac caaatcttgt gataagacc ataatgccc tccctgtcca
840 gcaacctgagc tgcctggcgg cccatccgtg ttccctgttc caccacaagcc taagaacaca
900 ctgatgatita gccggactcc cgaagtgaac tgcgttgttcg tgagcgttag ccaagagga
960 ccgaagtga agttcaactg gtacgttgat ggcgtcgaag tgcatatgc caagaccaaa
1020 cctaggggag aacagtacaag aggtcgtgtc aggtcgtgtc cgttcctgac cgttcctgac
1080 caggttggc tgaacgggaa ggaatatag tgcaagtgt ccaacaaggc cctgccagct
1140 ccatcgaga agaccatttc taaggccaaa ggcagccac gggaaccca ggtgtacaca
1200 ctgcccaca gccgcgacga gctgaacca aaccagtgga gctgacatg tctgttcaag
1260 ggtattctat ctagtgtat cgtgtgtgag tgggaatcta atgggagcc agaaaaaat
1320 tacaagacta cccctccgt gctggacttc gatggaagt tcttctgtta ttcaaaactg
1380 accgtggaca agagccgtg gcagcagggg aacgtctta gctgctccgt gatgcacgag
1440 gccctgcaca atcatatcac tcagaaatc ctgagctgt caccgggaaa acgagagga
1500 aagagagaa gccgctccgg agtaccac ttctccctgc tgaagcaggc aggggatgtg
1560 gaggaaaatc ctgcccacat ggtccctgag acaaggtgt ttatcttct gctgctgtg
1620 atagtgtcg cttaaggaga catccagatg actcagcttc ctggttcaat gtcgcaagt
1680 gtcggcgatc gcgtgactat tactgtcga acctcacaga gcttgagctc ctaccgtcat
1740 tgttatcag agaagccgtg gaaagcaca aagctgtcga tctatgcagc ctctagtctg
1800 cagtccggcg tgcctctag gtctccgg tctggcagtg gaactgact tacactgact
1860 attcaagcc tgcagccctga ggtttcgt acctactt gccagcagag cagaacttt
1920 gggcagggca ccaaaagtcga aatcaagaca gtgctgcac catccgtctt catttttcca
1980 cctctgacg agcagctgaa ggttggaact gcctcagtg tgtgctctgt gaaacaattc
2040 taccctggg aagcacaagt ccagtggaa gtgataacg ctctgcagtc aggcataagc
2100 caggtgtccg tgacagaaac ggaactaaa gatagtact attcactgag caaacacctg
2160 acactgagca aggcagacta cgagaagcac aaagtgtatg cctgcgaagt gaccaccag
2211 gggctgagca gtccagtgaac caaatcttc aacaggggag aatgttgata a

<210> 164
<211> 2241
<212> DNA
<213> Artificial Sequence

<220>
<223> Influenza B DMab

<400> 164
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gtgcagcttg tggaatcagg gggaggactg gtgaagcctg gcgatcact gcgacttgagc
120 tgcgcagctt ccggaactgac ctctcctgaac gcttgatga gcttggtgtcg acaaggcaca
180 gggaaaggcc tggaaatgggt cgggcgcac aagagcaata cagacggcgg aaccacagat
240 tagcagcccc ccgtgaaagg caggttcacc atttctcgg acgatagtaa gaacacacactg
300 tatctcagaa tgaagctcccc gaataccggg gacacagccg tgaactatgt cactaacggat
360 ggcctccaca gcgtaagattt ccgtccgga tatgctgcac ggtaccgcta ttttgggatg
420 gacgtgtggg gacaggggac aactgtcaca gtgtctagtg catctaataa gggaccctagc
480 gtgttccccac tggccccctc aagcaataca actagcggag ggaaccgccg tctgggatgt
540 ctgtgtgaagg attaactccc cgaagcctgt accgttagct ggaactccgg ggccttgacc
600 tccggagtgc acacatttcc tgcgttcttg cagtctcttg ggcgtgtact tctgagtca
660 gtgtgtcagag tgcctaagctc ctctcttggc actcagacct atatctgcaa cgtgaatacac
720 aaacctagca atactaaagt cgacaagaaa gtggaacca aagctgtga taagacacacat
780 actgtccccc cctgtccagc tccagagctg ctgggcggac catccgtgtt cctgtttcca
840 cccaagcccc aagacacacct gatgatccc cggacaaccag aagtgaactg cgtgtgtcgtg
900 gacgtgtagcc acgagggcccc cgaagtgaag ttcaactgtt acgtgtgatg cgtcgaagtgtg
960 cataatgcca agacaataacc caggaggaac cagtacaact caactatag agtcgtgagc
1020 gtctctgaccc tgcctgcacca ggaactggctg aacggcaagg agtataagt caaagttagc
1080 aacaaggccc tgcctgtccc aatcgaagaa actatagca aggttaagg acagcctcgg
1140 gaaaccaagg tgtacacctt gcttccatcc cgcgacgagc tgaaccaaaa ccaggtgtct
1200 ctgaactgtc tgttcaaaagg ctctatccc tctgatatcg ccgttgatgtg ggaagttaat
1260 ctgaacgctt aaaaataa caagaccaca cccctgtgc tggactctga tggcagtttc
1320 tttctgtata gtaaacctgac cgtggacaag tcaagatggc agcaggggaaa cgtgttttcc
1380 tgcctgtca tgcatagggc cctgcacaat catcacacc agaagagtct gtcaactgagc
1440 ccaggaaaaa cgaaggagaaa gaggagatcc ggtcttgag ccacaacctt ctccctcgtg
1500 aagcaggtctg gagaagtgga ggaataccc gggcctatgg tgcctgcagac ccaggtctt
1560 atctccctgc tgcgtgtggat ttctggcgtt tacggagata tccagatgac acagctctcc
1620 agttcagtca gtgcatacagt gggcgaccgc gtacacatca catgtcggagc atcacaggat
1680 attagcacct ggcctggcctg gtaccagag aagcccgga aagcttccaa gctgtgtgatc
1740 tatgcagcca gctcctcgtca gtccggagt cctctaggt tcaagcgggtc cggctctgga
1800 acagactta ctctgaacct ttctagtctg cagccttagg atttcgcaac ttactatgtc
1860 cagcagggcca acagcttccc acccaattt gggcaggga ccaactgga aatcaagact
1920 gtgtgtgacac ctagcgtctt catttttctt ccattccgag agcagctgaa gagtgtgaccc
1980

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gcctcagtgg	tgtgcctgct	gaacaacttc	tacccaagag	aagcaaaagt	gcagtggaag	2040
gtcgataacg	ccctgcagtc	aggcaatagc	caggagtccg	tgacagaaca	ggactctaag	2100
gatagtactt	atagtctgtc	aaatacactg	actctgagca	aagctgacta	cgagaagcat	2160
aaagtgtatg	catgcgaggt	cactcaccag	ggactgtctt	cacccgtcac	caaatctttc	2220
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<220>
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<400> 171

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