

SEQUENCE LISTING

<110> Weiner, David
Guibinga, Ghiabe
Cooch, Neil
Reed, Charles

<120> OPTIMIZED NUCLEIC ACID ANTIBODY CONSTRUCTS

<130> 206194-0014-00-W0.607261

<150> US 62/504,448

<151> 2017-05-10

<150> US 62/624,320

<151> 2018-01-31

<150> US 62/504,460

<151> 2017-05-10

<150> US 62/624,367

<151> 2018-01-31

<160> 128

<170> PatentIn version 3.5

<210> 1

<211> 2193

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX9291, Ebola ZSD2 modified

<400> 1

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ccatctctga agagccggat ctccatcaca agagacacct ccaagaatca gttctttctg	300
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tattggggac agggcacact ggtgaccgtg agctccgcct ctaccaaggg accaagcgtg	420
tttccactgg caccttctag caagagcaca tccggcggca ccgccgccct gggatgtctg	480
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gtgcagtgga aggtggataa cgccctgcag agcggcaatt cccaggagtc tgtgaccgag	2040
caggacagca aggattccac atattccctg tctaacacac tgaccctgtc caaggccgac	2100
tacgagaagc acaaggtgta tgcattgcgag gtgaccacc agggcctgtc ctctcctgtg	2160

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2193

<210> 2

<211> 729

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX9291, Ebola ZSD2 modified

<400> 2

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

Pro Ser Gln Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile
35 40 45

Thr Ser Asp Tyr Ala Trp Asn Trp Ile Arg Gln Phe Pro Gly Tyr Lys
50 55 60

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

Pro Ser Leu Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn
85 90 95

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

Tyr His Cys Ala Arg Gly Leu Ala Tyr Trp Gly Gln Gly Thr Leu Val
115 120 125

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

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
145 150 155 160

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly

165

170

175

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

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

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

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

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
 245 250 255

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 260 265 270

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
 275 280 285

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 290 295 300

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 305 310 315 320

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 325 330 335

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
 340 345 350

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 355 360 365

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 370 375 380

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 385 390 395 400

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 405 410 415

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

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 435 440 445

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Arg Gly
 450 455 460

Arg Lys Arg Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys
 465 470 475 480

Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Val Leu Gln Thr
 485 490 495

Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser Gly Ala Tyr Gly Asp
 500 505 510

Val Val Leu Thr Gln Thr Pro Leu Thr Leu Ser Val Thr Ile Gly Gln
 515 520 525

Pro Ala Ser Ile Ser Cys Asn Ser Ser Gln Ser Leu Leu Asp Ser Asp
 530 535 540

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

Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Thr Asp
 565 570 575

Glu Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser
 580 585 590

Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys Trp Gln Gly Thr

595

600

605

His Ser Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys 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 Asn 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
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<210> 3

<211> 2196

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX9292, Ebola ZSD2 partial graft

<400> 3

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gtgcagctgc aggagtccgg accaggcctg gtgcgcccta gccagtcctt gtctctgacc 120

tgcacagtga ccggctacag catcacatcc gattatgcct ggaactggat cagacagttc 180

cctggcaata agctggagtg gctgggctac atcacaacaa ccggcagcac cggctttaat 240

ccatctctga agagccggat ctccatcaca agagacacct ccaagaacca gttctttctg 300

cagctgatct ctgtgaccac agaggataca gcaacctacc actgcgccag aggcctggca	360
tattggggac agggcacact ggtgaccgtg agctccgcct ctaccaaggg accaagcgtg	420
tttccactgg caccttctag caagagcaca tccggcggca ccgccgccct gggatgtctg	480
gtgaaggact acttccctga gccagtgacc gtgtcttgga acagcggcgc cctgacatcc	540
ggagtgcaca cttttccagc cgtgctgcag tcctctggcc tgtacagcct gagctccgtg	600
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tgccctccct gtccagcacc tgagctgctg ggcggccctt ccgtgttcct gtttccaccc	780
aagccaaagg acaccctgat gatctccagg acacctgagg tgacctgcgt ggtggtggac	840
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gtgacaaaga gctttaatcg gggcgagtgt tgataa 2196

<210> 4

<211> 730

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX9292, Ebola ZSD2 partial graft

<400> 4

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 Pro Gly Leu Val Arg
20 25 30

Pro Ser Gln Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile
35 40 45

Thr Ser Asp Tyr Ala Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys
50 55 60

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

Pro Ser Leu Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn
85 90 95

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

Tyr His Cys Ala Arg Gly Leu Ala Tyr Trp Gly Gln Gly Thr Leu Val
115 120 125

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala

130

135

140

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
 145 150 155 160

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
 165 170 175

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

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

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

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

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
 245 250 255

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 260 265 270

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
 275 280 285

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 290 295 300

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 305 310 315 320

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 325 330 335

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
 340 345 350

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 355 360 365

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 370 375 380

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 385 390 395 400

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 405 410 415

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

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 435 440 445

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Arg Gly
 450 455 460

Arg Lys Arg Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys
 465 470 475 480

Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Val Leu Gln Thr
 485 490 495

Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser Gly Ala Tyr Gly Glu
 500 505 510

Thr Thr Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu
 515 520 525

Arg Ala Thr Leu Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp
 530 535 540

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

Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Thr Asp

565

570

575

Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser
580 585 590

Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Trp Gln Gly Thr
595 600 605

His Ser Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg
610 615 620

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

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

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

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

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

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

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

<210> 5

<211> 2196

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX9293, Ebola ZSD2 graft on MERSYTE_1

<400> 5

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tgcaaggcct ccggctactc tatcacaagc gattatgcca tcagctgggt gcggcaggca	180
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 gattacgaga agcacaaggt gtatgcatgc gaggtgaccc accagggcct gaggagcccc 2160
 gtgacaaagt cctttaatcg cggcgagtgt tgataa 2196

<210> 6

<211> 730

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX9293, Ebola ZSD2 graft on MERSYTE_1

<400> 6

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 Lys
 20 25 30

Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Ile
 35 40 45

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

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

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

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val

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

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
325 330 335

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
340 345 350

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
355 360 365

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
370 375 380

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
385 390 395 400

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
405 410 415

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

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
435 440 445

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Arg Gly
450 455 460

Arg Lys Arg Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys
465 470 475 480

Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Val Leu Gln Thr
485 490 495

Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser Gly Ala Tyr Gly Glu
500 505 510

Thr Thr Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu
515 520 525

Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Leu Leu Asp Ser Asp

530

535

540

Gly Lys Thr Tyr Ile Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
 545 550 555 560

Arg Leu Leu Met Phe Leu Val Ser Thr Arg Ala Thr Gly Ile Pro Asp
 565 570 575

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile Ser
 580 585 590

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Trp Gln Gly Thr
 595 600 605

His Ser Pro Phe Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
 610 615 620

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

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

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

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

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

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

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

<210> 7

<211> 2196

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX9294, Ebola Z5D2 graft on MERSYTE_2

<400> 7

atggactgga cctggagaat cctgttcctg gtggcagcag caaccggaac acacgcacag	60
gtgcagctgg tgcagtctgg agccgaggtg aagaagccag gcagctccgt gaaggtgtcc	120
tgcaaggcct ccggctactc tatcacaagc gattatgcct ggagctgggt gcggcaggca	180
ccaggacagg gcctggagtg gatgggcggc atcaccaaca caggctccac caattacgcc	240
cagaagttcc agggcagagt gaccatcaca gccgacacct ccacatctac cgcctatatg	300
gagctgtcta gcctgcggag cgaggatacc gccgtgtact attgcgccag aggcttgga	360
tactggggac agggcaccac agtgaccgtg tcctctgcct ccacaaagg accaagcgtg	420
ttcccactgg cacctagctc caagagcaca tccggcggca ccgccgccct gggatgtctg	480
gtgaaggact atttccctga gccagtgacc gtgtcctgga actctggcgc cctgacaagc	540
ggagtgcaca cttttccagc cgtgctgcag tctagcggcc tgtactccct gtcctctgtg	600
gtgaccgtgc ctagctcctc tctgggcaca cagacctata tctgcaacgt gaatcacaag	660
ccttccaata caaaggtgga caagaaggtg gagccaaagt cttgtgataa gacacacacc	720
tgccctccct gtccagcacc tgagctgctg ggcggcccaa gcgtgttcct gtttccaccc	780
aagcccaagg acacactgta catcacccgg gagccagagg tgacctgcgt ggtggtggac	840
gtgtcccacg aggacccga ggtgaagttc aactggtacg tggatggcgt ggaggtgcac	900
aatgccaaga ccaagcctcg ggaggagcag tacaactcta cctatagagt ggtgagcgtg	960
ctgacagtgc tgcaccagga ctggctgaac ggcaaggagt acaagtcaa ggtgagcaat	1020
aaggccctgc cagcccccat cgagaagacc atctccaagg caaagggaca gccaaggag	1080
ccacaggtgt acacactgcc tccaagccgc gacgagctga ccaagaacca ggtgtccctg	1140
acatgtctgg tgaagggtt ctatccctcc gatatcgccg tggagtggga gtctaattggc	1200
cagcctgaga acaattacaa gaccacacc cctgtgctgg acagcgatgg ctcttcttt	1260
ctgtatagca agctgaccgt ggacaagtcc cggtggcagc agggcaacgt gttttcttgc	1320
agcgtgatgc acgaggccct gcacaatcac tacaccaga agtccctgtc tctgagccca	1380
ggcaagaggg gaaggaagcg gagatccggc tctggagcca caaacttcag cctgctgaag	1440

caggccggcg atgtggagga gaatcctggc ccaatgggtgc tgcagacca ggtgtttatc 1500
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 aaggtgcagt ggaaggtgga taacgcctg cagtctggca atagccagga gtccgtgacc 2040
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 gattacgaga agcacaaggt gtatgcatgc gaggtgaccc accagggcct gaggagcccc 2160
 gtgacaaagt cttttaatcg cggcgagtgt tgataa 2196

<210> 8

<211> 730

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX9294, Ebola ZSD2 graft on MERSYTE_2

<400> 8

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 Lys
 20 25 30

Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Ile
 35 40 45

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

Leu Glu Trp Met Gly Gly Ile Thr Asn Thr Gly Ser Thr Asn Tyr Ala

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

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 290 295 300

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 305 310 315 320

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 325 330 335

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
 340 345 350

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 355 360 365

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 370 375 380

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 385 390 395 400

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 405 410 415

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

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 435 440 445

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Arg Gly
 450 455 460

Arg Lys Arg Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys
 465 470 475 480

Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Val Leu Gln Thr
 485 490 495

Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser Gly Ala Tyr Gly Glu

500					505					510					
Thr	Thr	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Pro	Gly	Glu
		515					520					525			
Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Leu	Leu	Asp	Ser	Asp
	530					535					540				
Gly	Lys	Thr	Tyr	Ile	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro
545					550					555					560
Arg	Leu	Leu	Met	Phe	Leu	Val	Ser	Thr	Arg	Ala	Thr	Gly	Ile	Pro	Asp
				565					570					575	
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Asn	Ile	Ser
			580					585					590		
Ser	Leu	Glu	Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Trp	Gln	Gly	Thr
		595					600					605			
His	Ser	Pro	Phe	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg
	610					615					620				
Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln
625					630					635					640
Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr
				645					650					655	
Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser
			660					665					670		
Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr
	675						680					685			
Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys
	690					695					700				
His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Arg	Ser	Pro
705					710					715					720

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

<210> 9
<211> 2196
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, pGX9295, Ebola ZSD2 graft on V2L2

<400> 9
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gtgcagctgc tggagagcgg cggcggcctg gtgcagcccg gcggctctct gaggctgagc 120
tgcgccgcct ctggctacag catcacctcc gattatgcaa tgaactgggt gcgccaggca 180
cctggcaagg gcctggagtg ggtgtctgcc atcaccaata caggcagcac cggctacaca 240
gacgatgtga agggccggtt cacaatctcc agagacaact ctaagaatac cctgtatctg 300
cagatgaact ccctgagggc cgaggatacc gccgtgtact attgcgcccg cggcctggca 360
tactgggggac agggcaccac agtgacagtg agctccgcct ctaccaaggg accaagcgtg 420
tttccactgg caccttctag caagtctacc agcggcggca cagccgccct gggatgtctg 480
gtgaaggact atttccctga gccagtgacc gtgtcttgga acagcggcgc cctgaccagc 540
ggagtgcaca catttcctgc cgtgctgcag tcctctggcc tgtactccct gagctccgtg 600
gtgaccgtgc catctagctc cctgggcacc cagacatata tctgcaacgt gaatcacaag 660
ccaagcaata caaaggtgga caagaaggtg gagcccaagt cctgtgataa gaccacaca 720
tgccctccct gtccagcacc tgagctgctg ggccggccca gcgtgttcct gtttccaccc 780
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cagccagaga acaattacaa gaccacaccc cctgtgctgg actccgatgg ctctttcttt	1260
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ctggactccg atggcaagac ctacctgggc tggatatcagc agaagcctgg caaggcccca	1680
aagctgctga tctacctggt gagcacactg cagtccggag tgccatctcg cttcagcggc	1740
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acatactatt gctggcaggg caccactcc cccttcacat ttggccaggg caccaagggtg	1860
gagatcaaga ggaccgtggc agcaccaagc gtgttcatct ttccaccctc cgacgagcag	1920
ctgaagagcg gcacagcctc cgtgggtgtgc ctgctgaaca acttctaccc cagagaggcc	1980
aaggtgcagt ggaagggtgga taacgccctg cagagcggca attcccagga gtctgtgaca	2040
gagcaggaca gcaaggattc cacctatagc ctgtccaaca ccctgacact gagcaaggcc	2100
gactacgaga agcacaaggt gtatgcctgc gaggtgacac accagggcct gagctcccc	2160
gtgaccaagt cttcaatag aggcgagtgt tgataa	2196

<210> 10

<211> 730

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX9295, Ebola Z5D2 graft on V2L2

<400> 10

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	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln
			20					25					30		

Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Tyr	Ser	Ile
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35

40

45

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

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

Asp Asp 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 Arg Gly Leu Ala Tyr Trp Gly Gln Gly Thr Thr Val
115 120 125

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

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
145 150 155 160

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
165 170 175

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

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

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

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

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
245 250 255

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
260 265 270

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
275 280 285

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
290 295 300

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
305 310 315 320

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
325 330 335

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
340 345 350

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
355 360 365

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
370 375 380

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
385 390 395 400

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
405 410 415

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

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
435 440 445

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Arg Gly
450 455 460

Arg Lys Arg Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys

465		470		475		480
Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Val Leu Gln Thr						
		485		490		495
Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser Gly Ala Tyr Gly Ala						
		500		505		510
Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp						
		515		520		525
Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Leu Leu Asp Ser Asp						
		530		535		540
Gly Lys Thr Tyr Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro						
545		550		555		560
Lys Leu Leu Ile Tyr Leu Val Ser Thr Leu Gln Ser Gly Val Pro Ser						
		565		570		575
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser						
		580		585		590
Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Trp Gln Gly Thr						
		595		600		605
His Ser Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg						
		610		615		620
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln						
625		630		635		640
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr						
		645		650		655
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser						
		660		665		670
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr						
		675		680		685

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

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

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

<210> 11
<211> 2208
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, pGX9296, Ebola ZBDBV223 modified

<400> 11
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gtgcagctgc agcagtgggg cgccggcctg ctgaagccaa gcgagacact gtccctgaca 120
tgcgccgtgt acggcggcag ctttaccaca acctattgga attggatcag gcagccccct 180
ggcaagggcc tggagtggat cggcgaggtg aactactctg gcaacgcca ttataacca 240
agcctgcagg gaagggtggc aatctctgtg gacacaagca agaatcagtt ctctctgcag 300
ctgaacagcg tgaccgccgc cgatacagcc atctactatt gcaccagccg gatcagaagc 360
cacatcgctt actcctggaa gggctgggtg tggggcaagg gcacaaccgt gaccgtgagc 420
tccgcctcca caaagggacc aagcgtgttc cacttggcac cctctagcaa gagcacctcc 480
ggcggcacag ccgccctggg ctgtctggtg aaggattatt tccccgagcc tgtgaccgtg 540
agctggaatt ccggcgccct gaccagcgga gtgcacacat ttccagccgt gctgcagtcc 600
tctggcctgt actccctgag ctccgtggtg accgtgccct ctagctccct gggcacacag 660
acctatatct gcaatgtgaa ccacaagccc tctaacacaa aggtggacaa gaagggtggag 720
cctaagagct gtgataagac acacacctgc ccaccctgtc cagcaccaga gctgctgggc 780
ggccctagcg tgttcctgtt tcctccaaag ccaaaggata ccctgatgat ctcccgacc 840
cctgaggtga catgctggtt ggtggacgtg tctcacgagg accccgaggt gaagttcaat 900
tggtacgtgg acggcgtgga ggtgcacaac gccaaagacca agcctaggga ggagcagtac 960

aatagcacct atcgcgtggg gtccgtgctg acagtgtctg accaggactg gctgaatggc	1020
aaggagtata agtgcaaggt gagcaacaag gccctgcctg cccaatcga gaagaccatc	1080
tccaaggcaa agggacagcc tcgggagcca caggtgtaca cactgcccc tagcagagac	1140
gagctgacca agaatcaggt gtccctgaca tgtctgggtga agggcttcta tccatccgat	1200
atcgccgtgg agtgggagtc taacggccag cccgagaaca attacaagac aacccccacc	1260
gtgctggact ctgatggcag cttctttctg tattccaagc tgaccgtgga taagtctcgg	1320
tggcagcagg gcaacgtgtt cagctgcagc gtgatgcacg agggcctgca caaccactac	1380
accagaagt ccctgtctct gagcccaggc aagcggggca gaaagcggag atccggctct	1440
ggcgccacaa atttcagcct gctgaagcag gcaggcgacg tggaggagaa cccaggacct	1500
atggtgctgc agaccaggt gtttatctct ctgctgctgt ggatcagcgg cgcctacggc	1560
gagatcgtga tgaccagag cccaggcaca ctgagcctgt cccaggaga gcaggccacc	1620
ctgtcctgta gggcctctca gagcgtgccc cgcaactaca tcggctgggtg gcagcagaca	1680
ccaggacagg cccctcggct gctgatctat ggagcctcta gccgggccgc aggattccct	1740
gacagatfff ccggctctgg cagcggcacc gatttcacac tgaccatcac agacctggag	1800
cccgaggatt ttgccatgta ctattgccac cagtacgaca gactgcctta taccttcggc	1860
cagggcacia agctggagat caagaccgtg gccgccccta gcgtgttcat ctttcctcca	1920
tccgatgagc agctgaagag cggcacagcc tccgtgggtg gcctgctgaa caacttctac	1980
ccaagggagg ccaaggtgca gtggaaggtg gacaatgccc tgagtcagg caactctcag	2040
gagagcgtga ccgagcagga ctccaaggat tctacatatt ccctgtctaa taccctgaca	2100
ctgagcaagg ccgactacga gaagcacaag gtgtatgcat gcgaggtgac ccaccagggc	2160
ctgtcctctc ctgtgacaaa gtccttcaac agaggcgagt gttgataa	2208

<210> 12

<211> 734

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX9296, Ebola ZDBV223 modified

<400> 12

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 Trp Gly Ala Gly Leu Leu Lys	20	25	30
Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe	35	40	45
Thr Thr Thr Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu	50	55	60
Glu Trp Ile Gly Glu Val Asn Tyr Ser Gly Asn Ala Asn Tyr Asn Pro	65	70	75
Ser Leu Gln Gly Arg Val Ala Ile Ser Val Asp Thr Ser Lys Asn Gln	85	90	95
Phe Ser Leu Gln Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Ile Tyr	100	105	110
Tyr Cys Thr Ser Arg Ile Arg Ser His Ile Ala Tyr Ser Trp Lys Gly	115	120	125
Trp Val Trp Gly Lys 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
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

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

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

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

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

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

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

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

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

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

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

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

445

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
645 650 655

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

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

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

Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
705 710 715 720

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

<210> 13
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, pGX9297, Ebola ZBDBV223 partial graft

<400> 13
atggactgga cctggagaat cctgttcctg gtggcagcag caacaggaac ccacgcacag 60
gtgcagctgc agcagtgggg cgccggcctg ctgaagccaa gcgagacact gtccctgaca 120
tgcgccgtgt acggcggcag ctttaccaca acctattgga attggatcag acagccccct 180
ggcaagggcc tggagtggat cggcgaggtg aactactctg gcaacgccaa ttataacccc 240
agcctgaagg gcagggtggc catctctgtg gacacaagca agaatcagtt ctctctgcgc 300
ctgaacagcg tgaccgcagc agatacagcc atctactatt gcaccagccg gatcagaagc 360
cacatcgcct actcctggaa gggcgacgtg tggggcaagg gcacaaccgt gaccgtgagc 420
tccgcctcca caaagggacc aagcgtgttc cactggcac cctctagcaa gagcacctcc 480
ggcggcacag ccgccctggg ctgtctggtg aaggattatt tccccgagcc tgtgaccgtg 540
agctggaatt ccggcgccct gaccagcgga gtgcacacat ttccagccgt gctgcagtcc 600
tctggcctgt actccctgag ctccgtggtg accgtgccct ctagctccct gggcacacag 660
acctatatct gcaatgtgaa ccacaagccc tctaacacaa aggtggacaa gaaggtggag 720

cctaagagct gtgataagac acacacctgc ccaccctgtc cagcaccaga gctgctgggc	780
ggccctagcg tgttcctggt tcctccaaag ccaaaggaca ccctgatgat ctcccggacc	840
cctgaggtga catgctggtt ggtggacgtg tctcacgagg accccgaggt gaagttcaat	900
tggtagctgg atggcgtgga ggtgcacaac gccaaagacca agcctaggga ggagcagtac	960
aatagcacct atcgctggtt gtccgtgctg acagtgtctg accaggattg gctgaatggc	1020
aaggagtata agtgcaaggt gagcaacaag gccctgcctg ccccaatcga gaagaccatc	1080
tccaaggcaa agggacagcc tcgggagcca caggtgtaca cactgcccc tagcagagac	1140
gagctgacca agaatcaggt gtccctgaca tgtctggtga agggcttcta tccatccgat	1200
atcgccgtgg agtgggagtc taacggccag ccgagaaca attacaagac aacccccacc	1260
gtgctggact ctgatggcag cttctttctg tattccaagc tgaccgtgga caagtctaga	1320
tggcagcagg gcaacgtggt cagctgcagc gtgatgcacg aggccctgca caaccactac	1380
accagaagt ccctgtctct gagcccaggc aagcggggca gaaagcggag atccggctct	1440
ggcgccacaa atttcagcct gctgaagcag gcaggcgatg tggaggagaa cccaggacct	1500
atggtgctgc agaccaggt gtttatctct ctgctgctgt ggatcagcgg agcatcacgga	1560
gagacaacct tgaccagag cccaggcaca ctgagcctgt cccaggaga gagggccacc	1620
ctgtcctgta gggcatctca gagcgtgcca cggaactaca tcggatgggt ccagcagaag	1680
ccaggacagg cccctagact gctgatctat ggagcctcta gccgggccgc aggattccct	1740
gacagatctt ccggctctgg cagcggcacc gatttcacac tgaccatcac aaggctggag	1800
cccgaggact ttgccatgta ctattgccac cagtacgata ggctgcctta taccttcggc	1860
cagggcacia agctggagat caagaggacc gtggcagcac ctagcgtgtt catctttcct	1920
ccatccgacg agcagctgaa gagcggcaca gcctccgtgg tgtgcctgct gaacaacttc	1980
taccacgcg aggccaaaggt gcagtggaag gtggataatg ccctgcagtc cggcaactct	2040
caggagagcg tgaccgagca ggactccaag gattctacat attccctgtc taataccctg	2100
acactgagca aggccgacta cgagaagcac aaggtgtatg catgcgaggt gaccaccag	2160
ggcctgtcct ctcctgtgac aaagtccttt aacaggggag agtggtgata a	2211

<210> 14

<211> 735

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX9297, Ebola ZBDBV223 partial graft

<400> 14

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 Trp Gly Ala Gly Leu Leu Lys
20 25 30

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

Thr Thr Thr Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu
50 55 60

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

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

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

Tyr Cys Thr Ser Arg Ile Arg Ser His Ile Ala Tyr Ser Trp Lys Gly
115 120 125

Asp Val Trp Gly Lys 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

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

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

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

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

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

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

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

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

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys

405

410

415

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

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

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

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

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

Asn Pro Gly Pro Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu
 500 505 510

Leu Trp Ile Ser Gly Ala Tyr Gly Glu Thr Thr Leu Thr Gln Ser Pro
 515 520 525

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

Ala Ser Gln Ser Val Pro Arg Asn Tyr Ile Gly Trp Phe Gln Gln Lys
 545 550 555 560

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

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

Thr Leu Thr Ile Thr Arg Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr
 595 600 605

Cys His Gln Tyr Asp Arg Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys
 610 615 620

Leu Glu Ile Lys Arg 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> 15

<211> 2211

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX9298, Ebola ZBDBV223 graft on MERSYTE

<400> 15

atggactgga cctggagaat cctgttcctg gtggcagcag caacaggaac ccacgcacag	60
gtgcagctgg tgcagagcgg agccgaggtg aagaagccag gcagctccgt gaaggtgtcc	120
tgcaaggcca gcggcggctc cttcaccaca acctacatct cttgggtgcg ccaggcacca	180
ggacagggcc tggagtggat gggcggcgtg aactacagcg gcaacgcaa ttatgccag	240
aagtttcagg gccgggtgac aatcaccgcc gacacaagca cctccacagc ctacatggag	300
ctgtctagcc tgagaagcga ggataccgcc gtgtactatt gcaccagccg gatcagaagc	360
cacatcgcct attcctggaa gggcgacgtg tggggacagg gaacaaccgt gaccgtgtcc	420
tctgcctcca caaagggacc aagcgtgttc cactggcac ctagctccaa gtctaccagc	480

ggcggcacag cgcgcctggg atgtctggtg aaggattact tccctgagcc agtgaccgtg	540
tcttggaca gcggcgccct gaccagcgga gtgcacacat ttcccgccgt gctgcagtct	600
agcggcctgt actccctgtc ctctgtggtg accgtgccta gctcctctct gggcaccag	660
acatatatct gcaacgtgaa tcacaagcct tctaatacaa aggtggacaa gaaggtggag	720
ccaaagagct gtgataagac ccacacatgc cctccctgtc cagcacctga gctgctgggc	780
ggcccaagcg tgttcctgtt tccaccaag cccaaggaca ccctgtacat cacacgggag	840
ccagaggtga cctgcgtggt ggtggacgtg tcccacgagg accccgaggt gaagttcaac	900
tggtacgtgg atggcgtgga ggtgcacaat gccaaagaca agccaaggga ggagcagtac	960
aattctacct atcgcgtggt gagcgtgctg acagtgtgc accaggattg gctgaacggc	1020
aaggagtaca agtgcaaggt gtccaataag gccctgccag ccccatcga gaagaccatc	1080
tctaaggcaa agggacagcc aaggagacca caggtgtaca cactgcctcc aagccgcgac	1140
gagctgacca agaaccaggt gtccctgaca tgtctggtga agggcttcta tccctccgat	1200
atcgccgtgg agtgggagtc taatggccag cctgagaaca attacaagac aaccctccc	1260
gtgctggact ccgatggctc tttctttctg tatagcaagc tgaccgtgga caagtccaga	1320
tggcagcagg gcaacgtgtt ttctgtctct gtgatgcacg aggccctgca caatcactac	1380
accagaaga gcctgtccct gtctcctggc aagaggggaa gaaagcggag aagcggctcc	1440
ggcgccacaa acttcagcct gctgaagcag gccggcgatg tggaggagaa tcctggccca	1500
atggtgctgc agaccaggt gtttatctcc ctgctgtgtg ggatctcttg cgcctatgga	1560
gagacaacct tgaccagag ccaggcaca ctgtctctga gccctggaga gagggccacc	1620
ctgtcctgta gggcatccca gtctgtgcc aaggaactaca tcgcctggta tcagcagaag	1680
cctggccagg cccaagact gctgatgttc ggagccagct cccgggccgc aggcattcct	1740
gacagattca gcggctccgg ctctggaacc gacttcaccc tgaacatctc tagcctggag	1800
cctgaggact tcgccgtgta ctattgccac cagtacgata ggctgccata tacctttggc	1860
cagggcacia agctggagat caagaggacc gtggcagcac ctagcgtgtt catctttcca	1920
cccagcgacg agcagctgaa gtctggcaca gccagcgtgg tgtgcctgct gaacaatttc	1980
taccaaggg aggccaaggt gcagtggaag gtggataacg ccctgcagag cggcaattcc	2040
caggagtctg tgaccgagca ggacagcaag gattccacat attctctgtc ctctaccctg	2100

acactgtcca aggccgacta cgagaagcac aaggtgtatg catgcgaggt gacccaccag 2160
 ggccctgcgga gccccgtgac aaagtccttt aacagaggcg agtggtgata a 2211

<210> 16
 <211> 735
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Chemically Synthesized, pGX9298, Ebola ZBDBV223 graft on MERSYTE

<400> 16

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 Lys
 20 25 30

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

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

Glu Trp Met Gly Gly Val Asn Tyr Ser Gly Asn Ala Asn Tyr Ala Gln
 65 70 75 80

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

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

Tyr Cys Thr Ser Arg Ile Arg Ser His Ile Ala Tyr Ser Trp Lys Gly
 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

Asp Thr Leu Tyr Ile Thr Arg Glu Pro Glu Val Thr Cys Val Val Val
275 280 285

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

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

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

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

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

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys

370

375

380

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

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

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

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

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

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

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

Asn Pro Gly Pro Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu
 500 505 510

Leu Trp Ile Ser Gly Ala Tyr Gly Glu Thr Thr Leu Thr Gln Ser Pro
 515 520 525

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

Ala Ser Gln Ser Val Pro Arg Asn Tyr Ile Ala Trp Tyr Gln Gln Lys
 545 550 555 560

Pro Gly Gln Ala Pro Arg Leu Leu Met Phe Gly Ala Ser Ser Arg Ala
 565 570 575

Ala Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
 580 585 590

Thr Leu Asn Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
595 600 605

Cys His Gln Tyr Asp Arg Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys
610 615 620

Leu Glu Ile Lys Arg 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> 17
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, pGX9299, Ebola ZBDBV223 graft on V2L2

<400> 17
atggactgga cctggagaat cctgttcctg gtggcagcag caacaggaac ccacgcagag 60
gtgcagctgc tggagagcgg cggcggcctg gtgcagccag gcggtccct gaggctgtct 120
tgcgcagcat ctggcggcag cttcaccaca acctacatga actgggtgcg ccaggcacca 180
ggcaagggcc tggagtgggt gagcgccgtg aactattccg gcaatgccta ctatacagac 240

gatgtgaagg gccggtttac catcagcgtg gacacatcca agaacaccct gtacctgcag	300
atgaattccc tgagagccga ggatacagcc gtgtactatt gcaccagccg gatcagaagc	360
cacatcgcct atagctggaa gggcgacgtg tggggacagg gaacaaccgt gacagtgagc	420
tccgcctcta ccaagggccc aagcgtgttt cccctggccc cttctagcaa gtctacaagc	480
ggcggcaccg ccgccctggg atgtctggtg aaggattact tccctgagcc agtgaccgtg	540
tcctggaact ctggcgccct gacatccggc gtgcacacct ttcctgccgt gctgcagtcc	600
tctggcctgt acagcctgag ctccgtggtg accgtgccat ctagctccct gggcacacag	660
acctatatct gcaacgtgaa tcacaagcca tccaatacaa aggtggacaa gaaggtggag	720
cccaagtctt gtgataagac acacacctgc cctccctgtc cagcacctga gctgctgggc	780
ggcccaagcg tgttcctgtt tccaccaag cctaaggaca ccctgatgat cagcaggaca	840
cccgaggtga cctgcgtggt ggtggacgtg tcccacgagg accccgaggt gaagttcaac	900
tggtagctgg atggcgtgga ggtgcacaat gccaaagacca agcctcggga ggagcagtac	960
aactccacat atagagtggg gtctgtgctg accgtgctgc accaggactg gctgaacggc	1020
aaggagtata agtgcaaggt gtctaataag gccctgccag ccccatcga gaagacaatc	1080
agcaaggcaa agggacagcc aaggagacca caggtgtaca ccctgcctcc atctcgcgac	1140
gagctgacaa agaaccaggt gagcctgacc tgtctggtga agggcttcta tcctagcgat	1200
atcgccgtgg agtgggagtc caatggccag ccagagaaca attacaagac aaccctccc	1260
gtgctggaca gcgatggctc cttctttctg tattctaagc tgaccgtgga taagagccgc	1320
tggcagcagg gcaacgtgtt ttcctgctct gtgatgcacg aggccctgca caatcactac	1380
accagaaga gcctgtccct gtctccaggc aagaggggaa gaaagcggag aagcggctcc	1440
ggagcaacca acttctccct gctgaagcag gcaggcgacg tggaggagaa tcctggacca	1500
atggtgctgc agaccaggt gtttatcagc ctgctgctgt ggatctccgg agcatacggg	1560
gccatccaga tgacacagag cccctctagc ctgtctgcca gcgtgggcga tagggtgaca	1620
atcacctgtc gcgcctccca gtctgtgcct aggaattacc tgggctggta tcagcagaag	1680
cctggcaagg ccccaaagct gctgatctac ggagcatcca cactgcagtc tggagtgcct	1740
agccgcttca gcggctccgg ctctggaacc gactttacac tgaccatctc ctctctgcag	1800
ccagaggact tcgccacata ctattgccac cagtacgatc ggctgcccta tacatttggc	1860

cagggcacca aggtggagat caagagaacc gtggccgccc cttccgtgtt catctttcca 1920
 ccctctgacg agcagctgaa gtccggcaca gcctctgtgg tgtgcctgct gaacaatttc 1980
 taccacacggg aggccaaggt gcagtggaag gtggataacg ccctgcagtc tggcaatagc 2040
 caggagtccg tgacagagca ggactctaag gatagcacct atagcctgtc caacacactg 2100
 accctgtcca aggccgatta cgagaagcac aaggtgtatg cctgcgaggt gacacaccag 2160
 ggcttgagct cccccgtgac caagagcttt aatagaggcg agtgttgata a 2211

<210> 18

<211> 735

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX9299, Ebola ZDBV223 graft on V2L2

<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 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
 20 25 30

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

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

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

Asp Val Lys Gly Arg Phe Thr Ile Ser Val Asp Thr 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 Thr Ser Arg Ile Arg Ser His Ile Ala Tyr Ser Trp Lys Gly
 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

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

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

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

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

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu

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

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

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

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
595 600 605

Cys His Gln Tyr Asp Arg Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys
610 615 620

Val Glu Ile Lys Arg 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> 19

<211> 1476

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX9330, Ebola Z5D2 scFv-Fc

<400> 19

atggtgctgc agaccaggt gttcatttcc ctgctgctgt ggattagcgg agcctatgga	60
gatgtcgtgc tgaccagac cccactgacc ctgagcgtga ccatcggcca gccagcctcc	120
atctcttgca agtccagcca gtccctgctg gattctgacg gcaagaccta cctgaattgg	180
ctgctgcaga gacctggcca gagccctaag cggctgatct atctggtgtc taagctggat	240
tctggcgtga ccgatagatt caccggctcc ggctctggca ccgactttac cctgaagatc	300
tccaggggtgg aggccgagga tctgggcgtg tattactgtt ggcagggcac ccactcccc	360
tttacattcg gcagcggcac aaagctggag atcaagggcg gcggcggctc cggcggcggc	420
ggctctggcg gcggcggctc tgaggtgcag ctgcaggaga gcggcccagg cctggtgcgc	480
ccatcccaga gcctgtctct gacatgtacc gtgacaggct acagcatcac atccgattac	540
gcctggaact ggatcagaca gttcccaggc aacaagctgg agtggctggg ctatatcacc	600
aacaccggct ctacaggctt caacccttcc ctgaagtcca gaatctctat caccgcgat	660
acatccaaga accagttctt tctgcagctg atcagcgtga ccacagagga taccgccaca	720
tatcactgtg ccagaggcct ggcctactgg ggccagggca ccctggtgac cgtgtcctct	780
gagcccaagt cctgtgataa gaccacacc tgcccacctt gtcccgcccc agagctgctg	840
ggcggcccca gcgtgttctt gtttctcca aagcccaagg acaccctgat gatcagcagg	900
acaccagagg tgacatgcgt ggtggtggac gtgtctcacg aggaccaga ggtgaagttc	960
aactggtacg tggatggcgt ggaggtgcac aacgccaaga ccaagccacg ggaggagcag	1020
tacaacagca cctacagagt ggtgtccgtg ctgaccgtgc tgcaccagga ttggctgaac	1080
ggcaaggagt acaagtgtaa ggtgtctaac aaggccctgc ccgccccaat cgagaagacc	1140
atctccaagg ccaagggcca gcctagggag ccacagggtg atacactgcc accctctaga	1200
gatgagctga caaagaatca ggtgtccctg acatgcctgg tgaagggtt ctatccatcc	1260
gacatcgccg tggagtggga gagcaatggc cagccagaga ataactacaa gaccacacca	1320
cctgtgctgg attccgacgg ctctttcttc ctgtactcca agctgaccgt ggataagtcc	1380
aggtggcagc agggcaacgt gttttcttgc agcgtcatgc acgaagcact gcacaaccat	1440
tacactcaga agagcctgtc actgtcacct tgataa	1476

<210> 20

<211> 490

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX9330, Ebola Z5D2 scFv-Fc

<400> 20

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

Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

Gly Gly Ser Glu Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg
145 150 155 160

Pro Ser Gln Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile
165 170 175

Thr Ser Asp Tyr Ala Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys
180 185 190

Leu Glu Trp Leu Gly Tyr Ile Thr Asn Thr Gly Ser Thr Gly Phe Asn
195 200 205

Pro Ser Leu Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn
210 215 220

Gln Phe Phe Leu Gln Leu Ile Ser Val Thr Thr Glu Asp Thr Ala Thr
225 230 235 240

Tyr His Cys Ala Arg Gly Leu Ala Tyr Trp Gly Gln Gly Thr Leu Val
245 250 255

Thr Val Ser Ser Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
260 265 270

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
275 280 285

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
290 295 300

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
305 310 315 320

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
325 330 335

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
340 345 350

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
355 360 365

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
370 375 380

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly

405

410

415

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 420 425 430

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 435 440 445

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 450 455 460

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 465 470 475 480

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 485 490

<210> 21

<211> 1488

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX9331, Ebola Z1H3 scFv-Fc

<400> 21

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atggactgga cctggagaat cctgttcctg gtcgccgccg ctactgggac tcacgccgaa      60
gtgcagctgc agcagagtgg agccgagctg gtgaagccag gcgccagcgt gaagctgtcc      120
tgcacagcct ccggctttaa catcaaggat acctacatcc actgggtgaa gcagggccct      180
gagcagggcc tggagtggat cggcaggatc gatcccgcca acggcaatac aaagtacgat      240
ccaaagtttc agggcaaggc caccatcaca gccgacacct ctagcaatac agcctatctg      300
cagctgtctg gcctgacatc cgaggatata gccgtgtact attgtgcccc ggagtctaga      360
atcagcacia tgctgaccac aggctacttt gactactggg gccagggcac caccctgacc      420
gtgagcagcg gcggcggcgg ctctggcggc ggcggctccg gcggcggcgg cagccagatc      480
gtgctgaccc agtccccagc catcatgagc gcctccccag gcgagaaggt gaccatgacc      540
tgctccgcct ctagctccgt gtcttatatg tactggatat agcagaagcc aggctcctct      600
ccaagactgc tgatctatga taccagcaat ctggcctctg gcgtgccagt gagattctct      660

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ggacagcggct ccggcaccag ctactccctg acaatcagca ggatggaggc cgaggatgcc 720
 gccacatact attgccagca gtggtcttcc tatccctaca cctttggcgg cggcacaaaag 780
 ctggagatca aggagcctaa gtcctgcgat aagaccaca cctgtcctcc ctgcccagcc 840
 cccgagctgc tgggcggccc atccgtgttt ctgttcctc caaagcccaa ggataccctg 900
 atgatctccc ggacaccaga ggtgacatgc gtggtggtgg atgtgagcca cgaggaccca 960
 gaggtgaagt tcaactggta cgtggatggc gtggaggtgc acaatgcaa gaccaagcca 1020
 agagaggagc agtacaacag cacatacagg gtggtgtctg tgctgacagt gctgcaccag 1080
 gactggctga atggcaagga gtataagtgc aaggtgtcca ataaggccct gcctgcccct 1140
 atcgagaaga ccatctccaa ggccaagggc cagcccaggg agccacaggt gtataccctg 1200
 cctcccagcc gggatgagct gacaaagaac caggtgtccc tgacatgtct ggtgaagggc 1260
 ttctacccta gcgatatgc cgtggagtgg gagtccaacg gccagccaga gaacaattat 1320
 aagacaacc cacctgtgct ggattccgac ggcagcttct ttctgtattc caagctgaca 1380
 gtggacaaga gcaggtggca gcagggcaac gtgttttagct gtcctgcat gcacgaagcc 1440
 ctgcacaacc actacacca gaagtcactg agcctgtcac cttgataa 1488

<210> 22

<211> 494

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX9331, Ebola Z1H3 scFv-Fc

<400> 22

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 Gln Ser Gly Ala Glu Leu Val Lys
 20 25 30

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

Lys Asp Thr Tyr Ile His Trp Val Lys Gln Gly Pro Glu Gln Gly Leu
 50 55 60

Glu Trp Ile Gly Arg Ile Asp Pro Ala Asn Gly Asn Thr Lys Tyr Asp
65 70 75 80

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

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

Tyr Tyr Cys Ala Arg Glu Ser Arg Ile Ser Thr Met Leu Thr Thr Gly
115 120 125

Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ile
145 150 155 160

Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys
165 170 175

Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Tyr Trp
180 185 190

Tyr Gln Gln Lys Pro Gly Ser Ser Pro Arg Leu Leu Ile Tyr Asp Thr
195 200 205

Ser Asn Leu Ala Ser Gly Val Pro Val Arg Phe Ser Gly Ser Gly Ser
210 215 220

Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu Asp Ala
225 230 235 240

Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro Tyr Thr Phe Gly
245 250 255

Gly Gly Thr Lys Leu Glu Ile Lys Glu Pro Lys Ser Cys Asp Lys Thr
260 265 270

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser

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

<210> 23
 <211> 1488
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Chemically Synthesized, pGX9332, Ebola ZBDBV223 scFv-Fc

<400> 23
 atggattgga cttggaggat tctgtttctg gtcgccgccg ctacaggacgac tcacgctcag 60
 gtgcagctgc agcagtgggg agccgggctg ctgaagccat ctgagaccct gtctctgaca 120
 tgcgccgtgt acggcggctc cttcacaacc acctactgga actggatcag acagccaccc 180
 ggcaagggcc tggagtggat cggcgaggctg aactacagcg gcaatgccaa ctacaatccc 240
 tccctgaagg gcagggtggc catctccgtg gatacatcca agaaccagtt ttccctgcgg 300
 ctgaatagcg tgacagccgc cgacaccgcc atctattact gcacaagccg gatcagaagc 360
 cacatgcct actcttgaa gggcgacgtg tggggcaagg gcacaaccgt gacagtgtcc 420
 tctggcggcg gcggctccgg cggcggcggc agcggcggcg gcggcagcga gatcgtgatg 480
 acccagtccc caggcacact gagcctgtcc ccaggcgaga gagccaccct gagctgtagg 540
 gcctctcagt ccgtgccaa gaactatatc ggctggtttc agcagaagcc aggccaggcc 600
 cctagactgc tgatctatgg cgccagctcc agagccgccg gcttccccga taggttttct 660
 ggctccggct ctggcaccga cttcacactg accatcaca gactggagcc agaggacttt 720
 gccatgtatt actgccacca gtatgatcgg ctgccataca ccttcggcca gggcaccaag 780
 ctggagatca aggagccaaa gagctgtgac aagaccaca cctgccctcc ctgcccagcc 840
 ccagagctgc tgggcggccc atccgtgttc ctgttccac caaagccaa ggacaccctg 900
 atgatctccc gcacaccaga ggtgacctgc gtggtggtgg acgtgtctca cgaggaccca 960
 gaggtgaagt ttaactggta cgtggacggc gtggagggtgc acaacgcaa gacaaagccc 1020
 agagaggagc agtacaattc cacatacaga gtggtgtctg tgctgacagt gctgcaccag 1080
 gattggctga acggcaagga gtataagtgc aagggtgtcta acaaggccct gcccggccca 1140
 atcgagaaga caatcagcaa ggccaaggcg cagccaagag agccccaggt gtataccctg 1200
 cctccatcta gagacgagct gaccaagaat cagggtgtccc tgacatgtct ggtgaaggcg 1260
 ttctacccta gcgacatcgc cgtggagtgg gagtccaatg gccagccaga gaataactac 1320

aagaccaccc ctccagtgtt ggattctgac ggcagctttt tcctgtattc taagctgacc 1380
 gtggacaaga gcagatggca gcagggcaac gtgttttcct gcagcgcat gcacgaagcc 1440
 ctgcacaacc attacacca gaagagcctg tctactgagcc cctgataa 1488

<210> 24
 <211> 494
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Chemically Synthesized, pGX9332, Ebola ZBDBV223 scFv-Fc

<400> 24

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 Trp Gly Ala Gly Leu Leu Lys
 20 25 30

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

Thr Thr Thr Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu
 50 55 60

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

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

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

Tyr Cys Thr Ser Arg Ile Arg Ser His Ile Ala Tyr Ser Trp Lys Gly
 115 120 125

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
 130 135 140

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Met

145		150		155		160									
Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Pro	Gly	Glu	Arg	Ala	Thr
				165					170					175	
Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Pro	Arg	Asn	Tyr	Ile	Gly	Trp
			180					185					190		
Phe	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile	Tyr	Gly	Ala
		195					200					205			
Ser	Ser	Arg	Ala	Ala	Gly	Phe	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser
	210					215					220				
Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Thr	Arg	Leu	Glu	Pro	Glu	Asp	Phe
225					230					235					240
Ala	Met	Tyr	Tyr	Cys	His	Gln	Tyr	Asp	Arg	Leu	Pro	Tyr	Thr	Phe	Gly
				245					250					255	
Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr
			260					265					270		
His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser
		275					280					285			
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg
	290					295					300				
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro
305					310					315					320
Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
				325					330					335	
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val
			340					345					350		
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
		355					360					365			

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
 370 375 380

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

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
 405 410 415

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 420 425 430

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 435 440 445

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 450 455 460

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 465 470 475 480

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 485 490

<210> 25
 <211> 1482
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Chemically Synthesized, pGX9345, EBV114_scFv-Fc

<400> 25
 atggactgga cctggagaat cctgttcctg gtcgccgccg ctactgggac tcacgccgaa 60
 gtgcagctgg tcgaatctgg gggaggcctg atccagccag gcggctccct gaggtgtct 120
 tgcgccgcct ctggcttcgc cctgagaatg tacgatatgc actgggtgcg gcagacaatc 180
 gacaagagac tggagtgggt gtctgccgtg ggcccaagcg gcgacaccta ttacgccgac 240
 tctgtgaagg gccggttcgc cgtgtctaga gagaatgcca agaactccct gagcctgcag 300
 atgaacagcc tgacagccgg cgacaccgcc atctattact gcgtgagaag cgacaggggc 360

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gtggccggcc tgttcgattc ctggggccag ggcacacctg tgacagtgtc cagcggcggc      420
ggcggctctg gcggcggcgg ctccggcggc ggccggcagc atatccagat gacccagagc      480
ccctcctccc tgagcgcctc cgtgggcgac agaatcaca tcacctgtag agcctcccag      540
gcctttgata attacgtggc ctggtatcag cagcggccag gcaaggtgcc aaagctgctg      600
atcagcgccg cctctgccct gcacgccggc gtgccaagca gattctcttg ctctggctcc      660
ggcaccact tcacactgac catctctagc ctgcagcccg aggatgtggc cacctattac      720
tgccagaact acaattccgc ccactgaca tttggcggcg gcacaaaggt ggagatcaag      780
gagccaaagt cttgcgaca gaccacacc tgtccaccct gccccgcccc agagctgctg      840
ggcggccctt ccgtgttcct gtttcccca aagcctaagg ataccctgat gatctccagg      900
acaccgagg tgacatgcgt ggtggtggat gtgagccacg aggaccaga ggtgaagttc      960
aattggtacg tggacggcgt ggaggtgcac aatgccaaga caaagcctag agaggagcag     1020
tataactcca cctatagggt ggtgtccgtg ctgacagtgc tgcaccagga ttggctgaac     1080
ggcaaggagt acaagtgcaa ggtgtccaat aaggccctgc ccgcccctat cgagaagaca     1140
atctctaagg ccaagggccca gccaaagagag ccacaggtgt acaccctgcc accctccaga     1200
gacgagctga caaagaacca ggtgtccctg acatgtcttg tgaagggtt ctatccctcc     1260
gatatcgccg tggagtggga gtctaattggc cagcccgaga acaattacaa gacaaccca     1320
cctgtgctgg actccgacgg cagctttttc ctgtactcca agctgaccgt ggataagtcc     1380
cgggtggcagc agggcaacgt gttttcctgc tccgtgatgc acgaagcact gcacaaccac     1440
tacactcaga aaagcctgtc cctgtcacct ggcaaagat aa                          1482

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<210> 26

<211> 492

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX9345, EBV114_scFv-Fc

<400> 26

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

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Thr His Ala Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Ile Gln

```

20

25

30

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

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

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

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

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

Tyr Cys Val Arg Ser Asp Arg Gly Val Ala Gly Leu Phe Asp Ser Trp
 115 120 125

Gly Gln Gly Ile Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
 130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
 145 150 155 160

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Ile Thr Ile Thr Cys
 165 170 175

Arg Ala Ser Gln Ala Phe Asp Asn Tyr Val Ala Trp Tyr Gln Gln Arg
 180 185 190

Pro Gly Lys Val Pro Lys Leu Leu Ile Ser Ala Ala Ser Ala Leu His
 195 200 205

Ala Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr His Phe
 210 215 220

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr
 225 230 235 240

Cys Gln Asn Tyr Asn Ser Ala Pro Leu Thr Phe Gly Gly Gly Thr Lys
245 250 255

Val Glu Ile Lys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
260 265 270

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
275 280 285

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
290 295 300

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
305 310 315 320

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
325 330 335

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
340 345 350

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
355 360 365

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
370 375 380

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

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
405 410 415

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
420 425 430

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
435 440 445

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln

450

455

460

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 465 470 475 480

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 485 490

<210> 27

<211> 1512

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX9346, 1A2_scFv-Fc

<400> 27

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atggtgctgc agaccaggt gttcatctct ctgctgctgt ggatctcttg cgcctatggc      60
gatatcgtga tgaccagtc ccctagaagc ctgtccgtga caccggcgga gcctgccagc      120
atctcctgca gatcctctca gagcctgctg cacaggaatg gctacaacta cctggactgg      180
tatctgcaga agcctggcca gtcccctcag ctgctgatct atctgggctc taatcgcgcc      240
agcggcgtgc ctgacaggtt ctccggcagc ggctctggca ccgacttcac actgaagatc      300
agcagagtgg aggccgagga cgtgggcgtg tactattgta tgcaggccct gcagaccctt      360
tcctggacat tcggccaggg caccaaggtg gagatcaagg gcggcggcgg ctccggcggc      420
ggcggctctg gcggcggcgg ctccgaggtg cagctggttg agtctggcgg cggcctgata      480
cagccaggcg gtcctctgag actgtcttgc gccgcctctg gcttcgccgt gaggtccaac      540
tacctgtctt ggggtgcgcca ggcccctggc aagggcctgg agtgggtgtc tctgatctac      600
tccggcggcc tgacagccta cgccgattcc gtggagggcc gggtcacaat ctccagagac      660
aattccaaga acaccctgta cctgcagatg aactccctga gagtggagga tacagccctg      720
tattactgtg ccagagtggc cagctccgcc ggcacattct attacggcat ggacgtgtgg      780
ggccagggca caaccgtgac cgtgtcttcc gagcctaagt cctgtgacaa gaccacacc      840
tgtccaccct gtcctgcccc agagctgctg ggcggcccat ccgtgttcct gttccctcca      900
aagcccaagg atacactgat gatctctagg acccctgagg tgacctgcgt ggtgggtgat      960
gtgagccacg aggaccctga ggtgaagttt aactgggtac tggatggcgt ggaggtgcac     1020

```

```

aatgccaaga caaagccaag agaggagcag tacaattcta catacagagt ggtgtctgtg      1080
ctgacagtgc tgcaccagga ctggctgaat ggcaaggagt acaagtgcaa ggtgtccaac      1140
aaggccctgc cagcccctat cgagaagacc atctccaagg ccaagggcca gccccgggag      1200
ccacaggtgt ataccctgcc accaagcaga gatgagctga ccaagaatca ggtgtccctg      1260
acatgtctgg tgaagggtt ctatcccagc gatatcgccg tggagtggga gagcaacggc      1320
cagcctgaga ataactacaa gaccacacca cctgtgtctgg attccgatgg cagcttcttt      1380
ctgtattcca agctgaccgt ggacaagtcc agatggcagc agggcaacgt gttcagctgc      1440
tccgtgatgc acgaggccct gcacaatcac tacaccaga agtctctgtc cctgtctcct      1500
ggcaagtgat aa                                                              1512

```

<210> 28
 <211> 502
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Chemically Synthesized, pGX9346, 1A2_scFv-Fc

<400> 28

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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 Val Met Thr Gln Ser Pro Arg Ser Leu Ser
          20          25          30

```

```

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

```

```

Leu Leu His Arg Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys
          50          55          60

```

```

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

```

```

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

```

```

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr

```

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

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
325 330 335

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
340 345 350

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
355 360 365

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
370 375 380

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
385 390 395 400

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
405 410 415

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

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
435 440 445

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
450 455 460

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
465 470 475 480

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
485 490 495

Ser Leu Ser Pro Gly Lys
500

<210> 29

<211> 2226

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX9356, 1A2_Full length_partial graft

<400> 29

atggactgga cctggagaat cctgttcctg gtggcagcag caaccggaac acacgcagag	60
gtgcagctgg tggagagcgg cggcggcctg atccagcccg gcggctctct gaggctgagc	120
tgcgcagcat ccggatttgc cgtgaggtct aactacctga gctgggtgcg ccaggcacct	180
ggcaagggcc tggagtgggt gtccctgata tactctggcg gcctgaccgc atatgcagac	240
tccgtggagg gccggttcac catcagcaga gataactcca agaatacact gtatctgcag	300
atgaatagcc tgagggtgga ggacaccgcc ctgtactatt gcgcccgcgt ggccagctcc	360
gccggcacat tctactatgg catggacgtg tggggccagg gcaccacagt gaccgtgtct	420
agcgccagca caaagggacc atccgtgttt cacttggcac cttcctctaa gtccacctct	480
ggcggcacag ccgccctggg ctgtctggtg aaggactact tccctgagcc agtgaccgtg	540
tcttgaaca gcggcgccct gacctctgga gtgcacacat ttccagccgt gctgcagagc	600
tccggcctgt acagcctgtc tagcgtggtg accgtgccct cctctagcct gggcacccag	660
acatatatct gcaacgtgaa tcacaagcca tctaatacaa aggtggacaa gaagtgagg	720
cccaagagct gtgataagac ccacacatgc cctccctgtc cagcacctga gctgctgggc	780
ggcccaagcg tgttcctgtt tccacccaag cctaaggaca ccctgatgat ctccaggacc	840
cccagagtga catgcgtggt ggtggacgtg tctcacgagg accccgaggt gaagttaac	900
tggtagctgg atggcgtgga ggtgcacaat gccaaagaca agccccggga ggagcagtac	960
aactctacct atagagtggg gagcgtgctg acagtgtgc accaggattg gctgaacggc	1020
aaggagtata agtgcaaggt gagcaataag gccctgccag ccccatcga gaagaccatc	1080
tccaaggcaa agggacagcc acgggagcca caggtgtaca cactgcctcc aagcagagac	1140
gagctgacca agaaccaggt gtccctgaca tgtctggtga agggcttcta tccttccgat	1200
atgccgtgg agtgggagtc taatggccag ccagagaaca attacaagac cacaccccct	1260
gtgctggact ccgatggctc tttctttctg tatagcaagc tgaccgtgga caagtcccgg	1320
tggcagcagg gcaacgtgtt tagctgctcc gtgatgcacg aggccctgca caatcactac	1380
accagaagt ctctgagcct gtcccctggc aagaggggaa ggaagcggag atctggcagc	1440
ggagccacaa acttctccct gctgaagcag gccggcgatg tggaggagaa tcctggccca	1500

atggtgctgc agaccaggt gtttatctcc ctgctgctgt ggatctctgg cgcctacggc 1560
 gccatccaga tgacacagag cccatcctct ctgtccgcct ctgtgggcga cagggtgacc 1620
 atcacatgtc gcagctccca gtccctgctg cacagaaacg gctacaatta tctggattgg 1680
 tacctgcaga agcctggcca gagccacag ctgctgatct atctgggctc taacagggca 1740
 agcggagtgc cagacagatt cagcggctcc ggctctggaa ccgacttcac cctgaagatc 1800
 tcccgggtgg aggcagagga cgtgggcgtg tactattgca tgcaggccct gcagaccct 1860
 agctggacat tcggccaggg caccaaggtg gagatcaaga gaacagtggc cgccccaagc 1920
 gtgttcatct ttccaccag cgacgagcag ctgaagtccg gcaccgcctc tgtggtgtgc 1980
 ctgctgaaca acttctaccc tagggaggcc aaggtgcagt ggaaggtgga taacgccctg 2040
 cagagcggca attcccagga gtctgtgacc gagcaggaca gcaaggattc cacatatagc 2100
 ctgtccaaca ccctgacact gtccaaggcc gattacgaga agcacaaggt gtatgcctgc 2160
 gaggtgaccc accagggcct gtctagccca gtgacaaaga gcttcaatcg cggcgagtgt 2220
 tgataa 2226

<210> 30

<211> 740

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX9356, 1A2_Full length_partial graft

<400> 30

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 Ile Gln
 20 25 30

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Asn Pro Gly Pro Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu

500

505

510

Leu Trp Ile Ser Gly Ala Tyr Gly Ala Ile Gln Met Thr Gln Ser Pro
 515 520 525

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
 530 535 540

Ser Ser Gln Ser Leu Leu His Arg Asn Gly Tyr Asn Tyr Leu Asp Trp
 545 550 555 560

Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu Gly
 565 570 575

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

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
 610 615 620

Gly Gln Gly Thr Lys Val 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

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 Asn 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> 31
<211> 1512
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, pGX9357, 1A2_scFv-Fc_partial graft

<400> 31
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gctatccaga tgaccagtc cccttcaagc ctgtccgcct ctgtgggcga cagggtgaca 120
atcacctgca gatcctctca gagcctgctg cacaggaatg gctacaacta cctggactgg 180
tatctgcaga agcctggcca gtccctcag ctgctgatct atctgggctc taatcgcgcc 240
agcggcgtgc ctgacaggtt ctccggcagc ggctctggca ccgacttcac actgaagatc 300
agcagagtgg aggccgagga cgtgggcgtg tactattgta tgcaggccct gcagaccct 360
tcctggacat tcggccaggg caccaaggtg gagatcaagg gcggcggcgg ctccggcggc 420
ggcggctctg gcggcggcgg ctccgaggtg cagctggtgg agtctggcgg cggcctgac 480
cagccaggcg gctccctgag actgtcttgc gccgcctctg gcttcgccgt gaggtccaac 540
tacctgtctt ggggtgcgcca ggcccctggc aagggcctgg agtgggtgtc tctgatctac 600
tccggcggcc tgacagccta cgccgattcc gtggagggcc ggttcacaat ctccagagac 660
aattccaaga acaccctgta cctgcagatg aactccctga gagtggagga tacagccctg 720
tattactgtg ccagagtggc cagctccgcc ggcacattct attacggcat ggacgtgtgg 780
ggccagggca caaccgtgac cgtgtcttcc gagcctaagt cctgtgacaa gaccacacc 840
tgtccaccct gtcctgcccc agagctgctg ggcgggccat ccgtgttcct gttccctcca 900
aagcccaagg atacactgat gatctctagg acccctgagg tgacctgctg ggtggtggat 960
gtgagccacg aggaccctga ggtgaagttt aactggtacg tggatggcgt ggaggtgcac 1020
aatgccaaga caaagccaag agaggagcag tacaattcta catacagagt ggtgtctgtg 1080

ctgacagtgc tgcaccagga ctggctgaat ggcaaggagt acaagtgcaa ggtgtccaac 1140
aaggccctgc cagcccctat cgagaagacc atctccaagg ccaagggcca gccccgggag 1200
ccacaggtgt ataccctgcc accaagcaga gatgagctga ccaagaatca ggtgtccctg 1260
acatgtctgg tgaagggtt ctatcccagc gatatcgccg tggagtggga gagcaacggc 1320
cagcctgaga ataactacaa gaccacacca cctgtgctgg attccgatgg cagcttcttt 1380
ctgtattcca agctgaccgt ggacaagtcc agatggcagc agggcaacgt gttcagctgc 1440
tccgtgatgc acgaggccct gcacaatcac tacaccaga agtctctgtc cctgtctcct 1500
ggcaagtgat aa 1512

<210> 32

<211> 502

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX9357, 1A2_scFv-Fc_partial graft

<400> 32

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

Gly Ala Tyr Gly Ala 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 Ser Ser Gln Ser
35 40 45

Leu Leu His Arg Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys
50 55 60

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

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

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
100 105 110

Cys Met Gln Ala Leu Gln Thr Pro Ser Trp Thr Phe Gly Gln Gly Thr
115 120 125

Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130 135 140

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Ile
145 150 155 160

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala
165 170 175

Val Arg Ser Asn Tyr Leu Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
180 185 190

Leu Glu Trp Val Ser Leu Ile Tyr Ser Gly Gly Leu Thr Ala Tyr Ala
195 200 205

Asp Ser Val Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
210 215 220

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Leu
225 230 235 240

Tyr Tyr Cys Ala Arg Val Ala Ser Ser Ala Gly Thr Phe Tyr Tyr Gly
245 250 255

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Glu Pro
260 265 270

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
275 280 285

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
290 295 300

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
305 310 315 320

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly

325

330

335

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
 340 345 350

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
 355 360 365

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
 370 375 380

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
 385 390 395 400

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
 405 410 415

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

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 435 440 445

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
 450 455 460

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
 465 470 475 480

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 485 490 495

Ser Leu Ser Pro Gly Lys
 500

<210> 33

<211> 2199

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX9362, EBV114_ Full length _partial

graft

<400> 33

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gtgcagctgg tggagagcgg cggcggcctg atccagccag gcggctccct gaggctgtct	120
tgcgcagcaa gcggatttgc actgaggatg tacgacatgc actgggtgcg gcagaccatc	180
gataagagac tggagtgggt gagcgccgtg ggaccatccg gcgacacata ctatgccgat	240
agcgtgaagg gcaggttcgc cgtgtcccgc gagaacgcca agaattctct gagcctgcag	300
atgaacagcc tgaccgccgg cgacacagcc atctactatt gcgtgcggtc cgacagaggc	360
gtggcaggcc tgttcgattc ttggggccag ggcatcctgg tgaccgtgag ctccgcctct	420
acaaagggac caagcgtgtt tccactggca ctttctagca agtccacctc tggcggcaca	480
gccgccctgg gctgtctggt gaaggattac ttccctgagc cagtgaccgt gtcttggaac	540
agcggcgccc tgacctctgg agtgcacaca tttcctgccg tgctgcagtc ctctggcctg	600
tacagcctga gctccgtggt gaccgtgcc a tctagctccc tgggcaccca gacatatatc	660
tgcaacgtga atcacaagcc atctaataca aaggtggaca agaaggtgga gccaagagc	720
tgtgataaga cccacacatg ccctccctgt ccagcacctg agctgctggg cggcccatcc	780
gtgttcctgt ttccacccaa gcctaaggac accctgatga tctccaggac ccccgaggtg	840
acatgcgtgg tgggtggacgt gtctcacgag gaccccgagg tgaagttcaa ctggtacgtg	900
gatggcgtgg aggtgcacaa tgccaagacc aagccccggg aggagcagta caattccacc	960
tatagagtgg tgtctgtgct gacagtgtcg caccaggact ggctgaacgg caaggagtat	1020
aagtgcaagg tgagcaataa ggccctgcc a gccccatcg agaagaccat ctccaaggca	1080
aagggacagc cacgggagcc acaggtgtac aactgcctc caagcagaga cgagctgacc	1140
aagaaccagg tgtccctgac atgtctggtg aagggttct atccttctga tatcgccgtg	1200
gagtgggaga gcaatggcca gccagagaac aattacaaga ccacaccccc tgtgtgtggac	1260
tccgatggct ctttctttct gtattctaag ctgaccgtgg acaagagccg ctggcagcag	1320
ggcaacgtgt ttagctgctc cgtgatgcac gaggccctgc acaatcacta caccagaag	1380
tctctgagcc tgtcccctgg caagagggga aggaagcgga gatctggcag cggagccaca	1440
aacttcagcc tgctgaagca ggccggcgat gtggaggaga atcctggccc aatggtgctg	1500
cagaccaggg tgtttatcag cctgctgctg tggatctccg gcgcctatgg cgccatccag	1560

atgacacagt ccccttctag cctgtccgcc tctgtgggcg acagggtgac catcacatgt 1620
 cgcgccagcc aggccttcga taactacgtg gcctgggtatc agcagaggcc tggcaaggtg 1680
 ccaaagctgc tgatcagcgc cgcatccgcc ctgcacgcag gagtgccatc ccgcttcagc 1740
 ggctccggct ctggaacca ctttaccctg acaatctcct ctctgcagcc agaggacgtg 1800
 gccacatact attgccagaa ctacaatagc gcacccctga ccttcggggg cgggacaaaag 1860
 gtggagatca agaggaccgt ggcagcacca tccgtgttca tctttccacc ctctgacgag 1920
 cagctgaagt ccggcacagc ctctgtggtg tgcctgctga acaacttcta ccctagagag 1980
 gccaaaggtgc agtgaaggt ggataacgcc ctgcagtctg gcaatagcca ggagtccgtg 2040
 accgagcagg actctaagga tagcacatat agcctgtcca acaccctgac actgtccaag 2100
 gccgattacg agaagcaciaa ggtgtatgca tgcgaggtga cccaccaggg cctgagctcc 2160
 ccagtgacaa agagctttaa tagaggcgag tgttgataa 2199

<210> 34

<211> 731

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX9362, EBV114_ Full length _partial graft

<400> 34

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 Ile Gln
 20 25 30

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

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

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

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

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

Tyr Cys Val Arg Ser Asp Arg Gly Val Ala Gly Leu Phe Asp Ser Trp
115 120 125

Gly Gln Gly Ile 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
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

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 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 Met 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

Ala Phe Asp Asn Tyr Val Ala Trp Tyr Gln Gln Arg Pro Gly Lys Val
545 550 555 560

Pro Lys Leu Leu Ile Ser Ala Ala Ser Ala Leu His Ala Gly Val Pro
565 570 575

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr His Phe Thr Leu Thr Ile
580 585 590

Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Asn Tyr
595 600 605

Asn Ser Ala 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 Asn 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

<210> 35
 <211> 1485
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Chemically Synthesized, pGX9363, EBV114_scFv-Fc_partial graft

<400> 35
 atggtgctgc agactcaggt gtttatttca ctgctgctgt ggatttcagg agcctatgga 60
 gctattcaga tgactcagag cccaagcagc ctgtctgcct ccgtgggcga tagagtgaca 120
 atcacctgta gagccagcca ggccttcgac aattacgtgg cctggtagca gcagagaccc 180
 ggcaaggtgc caaagctgct gatcagcgcc gcctccgccc tgcacgccgg cgtgccttct 240
 cgcttttccg gcagcggcag cggcacccac tttaccctga caatctccag cctgcagcct 300
 gaggatgtgg ccacctaata ttgtcagaat tacaactctg cccactgac cttcggcggc 360
 ggaccaagg tggagatcaa gggcggcggc ggcagcggcg gcggcggctc cggcggcggc 420
 ggctctgagg tgcagctggt ggagtctggc ggcggcctga tccagcccgg cggctctctg 480
 aggctgtcct gcgccgcctc cggctttgcc ctgcggatgt atgacatgca ctgggtgctc 540
 cagacaatcg acaagagact ggagtgggtg tctgccgtgg gcccttccgg cgatacctac 600
 tatgccgata gcgtgaaggg cagatttgcc gtgagcagag agaacgcaa gaactctctg 660
 agcctgcaga tgaacagcct gaccgccggc gatacagcca tctactattg cgtgagaagc 720
 gacagaggcg tggccggcct gttcgactct tggggccagg gcatcctggt gacagtgtcc 780
 agcgagccta agtcttgca taagaccac acctgtcccc cttgccagc ccctgagctg 840
 ctgggcggcc ccagcgtgtt cctgttccca cctaagccta aggatacact gatgatctcc 900
 aggacaccag aggtgacatg cgtggtggtg gacgtgtccc acgaggaccc tgaggatgaag 960
 ttcaactggt acgtggatgg cgtggaggtg cacaacgcca agacaaagcc caggaggagg 1020
 cagtacaaca gcacctatag agtggtgtcc gtgctgacag tgctgcacca ggattggctg 1080
 aatggcaagg agtacaagt caaggtgtcc aacaaggccc tgcccgcccc tatcgagaag 1140
 accatctcca aggccaaggg ccagcctaga gagccccagg tgtataccct gcctccctct 1200
 agggatgagc tgacaaagaa ccaggtgtcc ctgacctgtc tggatgaagg cttctatcca 1260

agcgatatcg ccgtggagtg ggagtctaac ggccagcccg agaataacta caagacaacc 1320
cctccagtgc tggacagcga tggctccttc tttctgtaca gcaagctgac cgtggacaag 1380
tccaggtggc agcagggcaa cgtgttttagc tgttccgtga tgcacgaagc cctgcacaac 1440
cactacactc agaagtcact gtcactgtct cctgggaagt gataa 1485

<210> 36
<211> 493
<212> PRT
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, pGX9363, EBV114_scFv-Fc_partial graft

<400> 36

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

Gly Ala Tyr Gly Ala 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 Ala Ser Gln Ala
35 40 45

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

Lys Leu Leu Ile Ser Ala Ala Ser Ala Leu His Ala Gly Val Pro Ser
65 70 75 80

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

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

Ser Ala Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val
130 135 140

Gln Leu Val Glu Ser Gly Gly Gly Leu Ile Gln Pro Gly Gly Ser Leu
 145 150 155 160

Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Leu Arg Met Tyr Asp Met
 165 170 175

His Trp Val Arg Gln Thr Ile Asp Lys Arg Leu Glu Trp Val Ser Ala
 180 185 190

Val Gly Pro Ser Gly Asp Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg
 195 200 205

Phe Ala Val Ser Arg Glu Asn Ala Lys Asn Ser Leu Ser Leu Gln Met
 210 215 220

Asn Ser Leu Thr Ala Gly Asp Thr Ala Ile Tyr Tyr Cys Val Arg Ser
 225 230 235 240

Asp Arg Gly Val Ala Gly Leu Phe Asp Ser Trp Gly Gln Gly Ile Leu
 245 250 255

Val Thr Val Ser Ser Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
 260 265 270

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
 275 280 285

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 290 295 300

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
 305 310 315 320

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
 325 330 335

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

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

355

360

365

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
 370 375 380

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

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 405 410 415

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
 420 425 430

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
 435 440 445

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
 450 455 460

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
 465 470 475 480

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 485 490

<210> 37

<211> 2193

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX9224, Ebola Z5D2

<400> 37

atggattgga cttggaggat tctgtttctg gtcgccgccg ctactgggac acacgccgag 60

gtgcagctgc aggagagtgg gcctggactg gtgcgaccca gccagtccct gtctctgaca 120

tgcactgtga ccggctacag tatcacatca gactatgcct ggaactggat tcgccagttc 180

ccaggcaata agctggaatg gctgggatac atcacaacaa ctggcagcac cgggtttaat 240

cccagcctga agtcccgaat ctctattaca agggacactt ctaaaaacca gttctttctg 300

cagctgatta gtgtgaccac agaggatacc gcaacatacc actgcgcccg gggactggct	360
tattggggac aggggaccct ggtcacagtg agctccgcta gtacaaaggg gccttcagtg	420
ttccccctgg caccttctag taaaagtaca tcaggcggaa ctgccgctct gggctgtctg	480
gtgaaggatt acttcctga gccagtcacc gtgagttgga actcaggagc actgacctcc	540
ggggtccata catttccgc cgtgctgcag tcaagcggcc tgtactctct gtcctctgtg	600
gtcactgtgc ctagttcaag cctgggaact cagacctata tctgcaacgt gaatcacaag	660
cctagcaata ccaaagtcga caagaaagtg gaaccaaaga gctgtgataa aacacatact	720
tgcccacctt gtccagcacc tgagctgctg ggaggaccaa gcgtgttcct gtttccaccc	780
aagcctaaag acacactgat gatctccgc accccagaag tcacatgtgt ggtcgtggac	840
gtgtctcacg aggacccga agtcaagttc aactggtagc tggatggcgt cgaggtgcat	900
aatgctaaga ccaaaccacg cgaggaacag tacaacagca catatcgagt cgtgtccgtc	960
ctgactgtgc tgcaccagga ctggctgaac ggcaaggagt ataagtcaa agtgagcaat	1020
aaggctctgc cagcacccat cgagaaaaca attagcaagg caaaaggaca gccaagggaa	1080
ccccaggtgt acactctgcc tccatccaga gacgagctga ctaagaacca ggtctctctg	1140
acctgtctgg tgaaaggatt ctatcccagc gatatcgccg tggagtggga atccaatggg	1200
cagcctgaaa acaattacaa gactaccccc cctgtgctgg acagcgatgg gtccttcttt	1260
ctgtattcca agctgaccgt ggataaatct cggtggcagc agggcaacgt ctttagctgc	1320
tccgtgatgc atgaggccct gcacaatcat tacacacaga agtctctgag tctgtcacct	1380
ggcaagcggg gacgcaaaag gagaagcggc tccggagcaa ctaacttcag cctgctgaaa	1440
caggccgggg acgtggagga aaatcctggc ccaatgggcc tgcagacca ggtgtttatc	1500
tctctgctgc tgtggattag tggggcctat ggcgatgtcg tgctgacca gacaccactg	1560
actctgagcg tgaccatcgg acagcccgct tctattagtt gtaagtcctc tcagtctctg	1620
ctggacagtg atggcaaaac ctacctgaac tggctgctgc agagacctgg acagtcccca	1680
aagcggctga tctatctggt ctcaaaactg gacagcggcg tgacagatcg gttcactggg	1740
tcaggcagcg gaactgactt taccctgaag atttctcgcg tcgaggctga agatctggga	1800
gtgtactatt gctggcaggg gactcactca cttttcacct ttgggagcgg cacaaagctg	1860
gaaatcaaaa ccgtcgcagc cccaagtgtg ttcatTTTTT caccctcaga cgagcagctg	1920

aagtccggga cagcatctgt cgtgtgtctg ctgaacaatt tctaccctag ggaggctaag 1980
gtccagtgga aagtggataa cgcactgcag tctggcaata gtcaggagtc agtgaccgaa 2040
caggacagca aggattccac atattccctg tctaacactc tgaccctgag caaagccgac 2100
tacgagaagc acaaagtcta tgcttgcgaa gtgactcatc aggggctgag ttcaccagtg 2160
accaagagct ttaatagagg cgagtgttga taa 2193

<210> 38
<211> 729
<212> PRT
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, pGX9224, Ebola Z5D2

<400> 38

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 Pro Gly Leu Val Arg
20 25 30

Pro Ser Gln Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile
35 40 45

Thr Ser Asp Tyr Ala Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys
50 55 60

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

Pro Ser Leu Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn
85 90 95

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

Tyr His Cys Ala Arg Gly Leu Ala Tyr Trp Gly Gln Gly Thr Leu Val
115 120 125

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala

130

135

140

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
 145 150 155 160

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
 165 170 175

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

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

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

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

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
 245 250 255

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 260 265 270

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
 275 280 285

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 290 295 300

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 305 310 315 320

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 325 330 335

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
 340 345 350

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
355 360 365

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
370 375 380

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
385 390 395 400

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
405 410 415

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

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
435 440 445

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Arg Gly
450 455 460

Arg Lys Arg Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys
465 470 475 480

Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Val Leu Gln Thr
485 490 495

Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser Gly Ala Tyr Gly Asp
500 505 510

Val Val Leu Thr Gln Thr Pro Leu Thr Leu Ser Val Thr Ile Gly Gln
515 520 525

Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp
530 535 540

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

Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Thr Asp

565

570

575

Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser
 580 585 590

Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Trp Gln Gly Thr
 595 600 605

His Ser Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys 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 Asn 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> 39

<211> 2208

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX9225, Ebola Z1H3

<400> 39

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60

gtgcagctgc agcagagtgg agccgagctg gtcaaacctg gggcatccgt gaagctgtct	120
tgcactgcca gtggcttcaa catcaaagac acctacattc actgggtgaa gcagggccca	180
gagcagggaac tggaatggat cggacggatt gacccagcaa acgggaatac caagtatgat	240
cccaaatttc aggggaaggc aaccatcaca gccgacacaa gctccaatac tgcctacctg	300
cagctgtcag gcctgaccag cgaggataca gccgtgtact attgcccag ggagagcagg	360
atttccacca tgctgaccac aggatatttc gactactggg gacaggggac taccctgacc	420
gtctctagtgc ccagcacaaa agggccttcc gtgtttcccc tggctccttc aagcaagtct	480
actagtggag gaaccgcagc tctgggatgt ctggtgaagg attacttccc tgagccagtc	540
accgtgtctt ggaacagtgg ggctctgacc tccggcgtcc acacatttcc agcagtgtctg	600
cagtcctctg ggctgtattc tctgagttca gtggtcaccg tgcccagctc ctctctgggc	660
actcagacct acatctgcaa cgtgaatcac aaaccctcca atacaaaggt cgacaagaaa	720
gtggaaccta aatcttgtga taagacacat acttgcccac cttgtccagc acctgagctg	780
ctgggaggac ctagcgtgtt cctgtttcca cccaagccaa aagacaccct gatgatcagc	840
cgcacacctg aagtcacttg tgtggctgtg gacgtgtccc acgaggaccc cgaagtcaag	900
ttcaactggg acgtggatgg cgtcgaggtg cataatgcca agacaaaacc cagagaggaa	960
cagtataact ctacataccg ggtcgtgagt gtcctgactg tgctgcacca ggattggctg	1020
aacggcaagg agtacaagtg caaagtgtct aacaaggccc tgccagctcc catcgagaag	1080
accattagca aggccaaagg acagccacgc gaaccccagg tgtatacact gcctcccagc	1140
agggacgagc tgactaaaaa ccaggtcagc ctgacctgtc tgggtgaaggg cttctacca	1200
agcgatatcg ctgtggagtg ggaatccaat ggacagcccg aaaacaatta taagacaact	1260
ccccctgtgc tggactcaga tggcagcttc tttctgtaca gtaaaactgac cgtggacaag	1320
tcaagatggc agcagggaaa cgtcttttca tgcagcgtga tgcatgaggc cctgcacaat	1380
cattatactc agaagtcctt gtctctgagt ccagggaac ggggccgcaa gaggagatca	1440
ggcagcggag ctacaaactt cagcctgctg aagcaggcag gcgatgtgga ggaaaatcct	1500
ggaccaatgg tcctgcagac tcaggtgttt atctcactgc tgctgtggat tagcggagcc	1560
tacggacaga tcgtgctgac ccagtcccca gctattatgt ccgcatctcc tggcgagaaa	1620
gtgacctga catgttccgc tagttcaagc gtgtcttaca tgtattggta ccagcagaag	1680

cctggcagca gcccaaggct gctgatctat gacacctcca acctggcttc tgggggtcccc 1740
 gtgagattca gtgggtcagg cagcggaact tcctactctc tgaccatttc ccggatggag 1800
 gcagaagatg cagccacata ctattgccag cagtggagtt catatcccta cacatttgga 1860
 gggggcacta aactggaaat caagacagtc gctgcacctt ctgtgttcat ttttccaccc 1920
 agtgacgagc agctgaagag tggcactgcc tcagtcgtgt gtctgctgaa caatttctat 1980
 ccccgcgagg ccaaagtcca gtggaaggtg gataacgctc tgcagtccgg caatttctag 2040
 gagagtgtga ccgaacagga ctcaaaagat agcacatata gtctgtcaaa cactctgacc 2100
 ctgagcaagg cagactatga gaagcacaaa gtctacgcct gcgaagtga acatcaggga 2160
 ctgagctccc ctgtgactaa gtcctttaat cgagggggagt gttgataa 2208

<210> 40
 <211> 734
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Chemically Synthesized, pGX9225, Ebola Z1H3

<400> 40

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 Gln Ser Gly Ala Glu Leu Val Lys
 20 25 30

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

Lys Asp Thr Tyr Ile His Trp Val Lys Gln Gly Pro Glu Gln Gly Leu
 50 55 60

Glu Trp Ile Gly Arg Ile Asp Pro Ala Asn Gly Asn Thr Lys Tyr Asp
 65 70 75 80

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

Thr Ala Tyr Leu Gln Leu Ser Gly Leu Thr Ser Glu Asp Thr Ala Val

100	105	110
Tyr Tyr Cys Ala Arg Glu Ser Arg Ile Ser Thr Met Leu Thr Thr Gly 115 120 125		
Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu 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 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
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 Gln Ile Val Leu Thr Gln
515 520 525

Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr

530

535

540

Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Tyr Trp Tyr Gln Gln Lys
 545 550 555 560

Pro Gly Ser Ser Pro Arg Leu Leu Ile Tyr Asp Thr Ser Asn Leu Ala
 565 570 575

Ser Gly Val Pro Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr
 580 585 590

Ser Leu Thr Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr
 595 600 605

Cys Gln Gln Trp Ser Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys
 610 615 620

Leu Glu Ile Lys Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
 625 630 635 640

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
 645 650 655

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

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

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

Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
 705 710 715 720

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

<210> 41

<211> 2208

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX9228, Ebola ZBDBV223

<400> 41

atggattgga cttggagaat tctgtttctg gtggccgccg ctacaggaac tcacgctcag	60
gtgcagctgc agcagtgggg agccgggctg ctgaagccaa gcgagacact gtccctgact	120
tgcgccgtgt acggcggaag cttcaccaca acttattgga attggatcag gcagccccct	180
ggcaagggaac tggagtggat tggggaagtg aactacagcg gcaacgctaa ttataacccc	240
tccctgaagg gccgagtcgc aatctctgtg gacactagta aaaatcagtt tagtctgagg	300
ctgaactcag tgaccgccgc tgatacagca atctactatt gcaccagcag gatcaggagc	360
cacattgcct actcctggaa gggagacgtg tgggggaaag gcaccacagt caccgtgagc	420
tccgccagca caaagggacc atccgtgttc ccactggctc cctctagtaa aagtacttca	480
gggggcaccg cagccctggg atgtctggtg aaggattact tccccgagcc tgtcaccgtg	540
tcctggaatt ctggcgcact gacctctgga gtccatacat ttccagccgt gctgcagtca	600
agcgggctgt acagcctgtc ctctgtggtc accgtcccca gttcaagcct gggcacacag	660
acttatatct gcaatgtgaa ccacaagccc tctaacacaa aagtcgacaa gaaagtggaa	720
cctaagagct gtgataaaac ccatacatgc ccaccctgtc cagcaccaga gctgctggga	780
gggcctagcg tgttcctgtt tcctccaaag ccaaaagaca cactgatgat tagcaggaca	840
cctgaagtca cttgcgtggt cgtggacgtg tcccacgagg accccgaagt caagtttaat	900
tggtagctgg atggcgctga ggtgcataac gctaagacca aacctaggga ggaacagtac	960
aactctacat atagagtcgt gagtgtcctg actgtgctgc accaggactg gctgaatggg	1020
aaggagtata agtgcaaagt gtctaacaag gcactgcctg ccccaatcga gaaaactatt	1080
agcaaggcta aaggccagcc tcgggaacca cagggtgtaca ccctgcccc tagccgcgac	1140
gagctgacta agaatcaggt ctccctgacc tgtctggtga aaggcttcta tccatctgat	1200
atcgcagtgg agtgggaaag taacggacag cccgaaaaca attacaagac taccacccc	1260
gtcctggaca gtgatggctc attctttctg tattccaagc tgaccgtgga caaatctaga	1320
tggcagcagg gaaatgtctt tagctgctcc gtgatgcacg aggcctgca caaccattac	1380
actcagaagt ctctgagtct gtcaccaggg aagcgaggca ggaaaaggag aagcggcagc	1440

ggggcaacca atttctctct gctgaaacag gccggagatg tggaggaaaa ccccgggcct 1500
 atggtcctgc agacacaggt gtttatctca ctgctgctgt ggattagcgg agcctacggg 1560
 gaaatcgtga tgactcagag cccaggcacc ctgtctctga gtcccggaga gagagctaca 1620
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 ccaggacagg cccctcggct gctgatctac ggagcttcct ctcgctgctgc agggttccct 1740
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 caggaacta agctggaaat caaaacagtc gccgctccta gcgtgttcat ctttcctcca 1920
 tcagacgagc agctgaagtc cggaactgct tctgtggtgt gcctgctgaa caacttctac 1980
 ccacgcgaag ctaaggtcca gtggaaagt gataatgcac tgacagcgg caactcccag 2040
 gagtctgtga ccgaacagga cagtaaggat tcaacatatt cactgagcaa cactctgacc 2100
 ctgtccaaag ccgactacga gaagcataaa gtgtatgctt gcgaggtcac ccaccagggg 2160
 ctgtcatctc cagtcactaa gtccttcaat agaggcgaat gttgataa 2208

<210> 42

<211> 734

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX9228, Ebola ZBDBV223

<400> 42

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 Trp Gly Ala Gly Leu Leu Lys
 20 25 30

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

Thr Thr Thr Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu
 50 55 60

Glu Trp Ile Gly Glu Val Asn Tyr Ser Gly Asn Ala Asn Tyr Asn Pro

65		70		75		80									
Ser	Leu	Lys	Gly	Arg	Val	Ala	Ile	Ser	Val	Asp	Thr	Ser	Lys	Asn	Gln
			85						90					95	
Phe	Ser	Leu	Arg	Leu	Asn	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Ile	Tyr
			100					105					110		
Tyr	Cys	Thr	Ser	Arg	Ile	Arg	Ser	His	Ile	Ala	Tyr	Ser	Trp	Lys	Gly
		115					120					125			
Asp	Val	Trp	Gly	Lys	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		
Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val
		275					280					285			

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

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

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

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

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

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

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

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

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

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

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

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

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

Asn Pro Gly Pro Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu

500	505	510
Leu Trp Ile Ser Gly Ala Tyr Gly Glu Ile Val Met Thr Gln Ser Pro		
515	520	525
Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg		
530	535	540
Ala Ser Gln Ser Val Pro Arg Asn Tyr Ile Gly Trp Phe Gln Gln Lys		
545	550	555
Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala		
565	570	575
Ala Gly Phe Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe		
580	585	590
Thr Leu Thr Ile Thr Arg Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr		
595	600	605
Cys His Gln Tyr Asp Arg Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys		
610	615	620
Leu Glu Ile Lys Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro		
625	630	635
Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu		
645	650	655
Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn		
660	665	670
Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser		
675	680	685
Lys Asp Ser Thr Tyr Ser Leu Ser Asn Thr Leu Thr Leu Ser Lys Ala		
690	695	700
Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly		
705	710	715
		720

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

<210> 43
<211> 2223
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, pGX9256, 1A2

<400> 43
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gtgcagctgg tggagagcgg cggcggcctg atccagccag gcggcagcct gaggctgtcc 120
tgcgcagcat ctggatttgc cgtgaggagc aactacctgt cctgggtgag acaggcacca 180
ggcaagggac tggagtgggt gtctctgata tacagcggcg gcctgaccgc atatgcagac 240
agcgtggagg gcaggttcac catctccaga gataactcta agaatacact gtatctgcag 300
atgaattccc tgcgggtgga ggacaccgcc ctgtactatt gcgcccgcgt ggccagctcc 360
gccggcacat tctactatgg catggacgtg tggggccagg gcaccacagt gaccgtgtct 420
agcgcctcca caaagggacc aagcgtgttc ccactggcac cttcctctaa gtccacctct 480
ggcggcacag ccgccctggg ctgtctggtg aaggattact tccctgagcc agtgaccgtg 540
tcttggaaca gcggcgccct gaccagcggg gtgcacacat ttcctgccgt gctgcagagc 600
tccggcctgt actccctgtc tagcgtggtg accgtgccat cctctagcct gggcacccag 660
acatatatct gcaacgtgaa tcacaagcct agcaatacaa aggtggacaa gaaggtggag 720
ccaaagtcct gtgataagac ccacacatgc cctccctgtc cagcacctga gctgctgggc 780
ggcccaagcg tgttcctgtt tccacccaag cccaaggaca cactgatgat ctctaggacc 840
ccagaggtga catgcgtggt ggtggacgtg agccacgagg accccgaggt gaagtttaac 900
tggtacgtgg atggcgtgga ggtgcacaat gccaaagaca agccaaggga ggagcagtac 960
aacagcacct atagagtgggt gtccgtgctg acagtgtgtc accaggactg gctgaacggc 1020
aaggagtata agtgcaaggt gtccaataag gccctgccag ccccatcga gaagaccatc 1080
tctaaggcaa agggacagcc aaggagacca caggtgtaca cactgcctcc atccagagac 1140
gagctgacca agaaccaggt gtctctgaca tgtctggtga agggcttcta tccctctgat 1200

atcgccgtgg agtgggagag caatggccag cctgagaaca attacaagac cacaccccct	1260
gtgctggact ccgatggctc tttctttctg tattccaagc tgaccgtgga taagtctcgg	1320
tggcagcagg gcaacgtggt tagctgctcc gtgatgcacg aggccctgca caatcactac	1380
accagaagt ctctgagcct gtcccctggc aagaggggaa ggaagaggag atctggcagc	1440
ggcgccacaa acttcagcct gctgaagcag gcaggcgacg tggaggagaa tcctggacca	1500
atggtgctgc agaccaggt gtttatctct ctgctgctgt ggatcagcgg cgcctacggc	1560
gatatcgtga tgaccagtc ccctcgctcc ctgtctgtga cacctggcga gccagccagc	1620
atctcctgtc ggtcctctca gtctctgtg caccgcaacg gctacaatta tctggactgg	1680
tacctgcaga agcccggcca gtcccctcag ctgctgatct atctgggcag caacagggca	1740
tccggagtgc cagaccgctt ctctggcagc ggctccggaa ccgacttcac cctgaagatc	1800
agcagggtgg aggccgagga tgtgggcgtg tactattgca tgcaggccct gcagaccccc	1860
tcctggacat tcggccaggg caccaaggtg gagatcaaga cagtggccgc ccctagcgtg	1920
ttcatctttc caccctccga cgagcagctg aagtctggca ccgccagcgt ggtgtgcctg	1980
ctgaacaact tctaccccag agaggccaag gtgcagtgga aggtggataa cgccctgcag	2040
agcggcaatt cccaggagtc tgtgaccgag caggacagca aggattccac atattctctg	2100
agctccaccc tgacactgag caaggccgac tacgagaagc acaagggtga tgcctgcgag	2160
gtgaccacc agggcctgtc tagccctgtg acaaagtcct tcaacagagg cgagtgttga	2220
taa	2223

<210> 44
 <211> 739
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Chemically Synthesized, pGX9256, 1A2

<400> 44

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	Ile	Gln
			20					25					30		

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

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

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

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

Asn Pro Gly Pro Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu
 500 505 510

Leu Trp Ile Ser Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro
 515 520 525

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

Ser Ser Gln Ser Leu Leu His Arg Asn Gly Tyr Asn Tyr Leu Asp Trp
 545 550 555 560

Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu Gly
 565 570 575

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

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
 610 615 620

Gly Gln Gly Thr Lys Val Glu Ile Lys 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
705 710 715 720

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
725 730 735

Gly Glu Cys

<210> 45

<211> 2196

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX9290, EBV114

<400> 45

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gtgcagctgg tcgaaagtgg aggggggactg atccagccag gcggaagcct gcgactgtcc      120
tgcgcagctt ctggattcgc actgcgcatg tacgacatgc actgggtgcg ccagacaatt      180
gataagcgac tggaatgggt cagcgccgtg ggaccatccg gggacactta ctatgctgat      240
tctgtgaagg ggagatttgc tgtcagtcgg gagaacgcaa aaaattctct gagtctgcag      300
atgaactctc tgaccgcagg cgacacagcc atctactatt gcgtgcatc cgacaggggc      360
gtcgcaggac tgttcgattc ttggggccag ggaattctgg tcacagttag ctccgcctct      420
actaagggac caagcgtggt cccactggct ctttctagta aatcaactag cgggggcacc      480
gcagccctgg gatgtctggt gaaggattac ttccctgagc cagtcaccgt gagttggaac      540
tcaggcgcac tgaccagcgg agtgcataca tttcctgccg tcctgcagtc aagcggcctg      600
tactccctgt cctctgtggt cacagtgcca agttcaagcc tgggaactca gacctatata      660
tgcaacgtga atcacaagcc atctaatact aaagtcgaca agaaagtgga acccaagagc      720
tgtgataaaa cacatacttg ccctccctgt ccagcacctg agctgctggg agggccaagc      780

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gatggcgtcg aggtgcataa tgctaagaca aaaccccggg aggaacagta caattcaact	960
tatcgcgtcg tgagcgtcct gaccgtgctg caccaggact ggctgaacgg aaaggagtat	1020
aagtgcaaag tgtctaataa ggcaactgcc gccccatcg agaaaaccat tagcaaggcc	1080
aaagggcagc caaggggaacc ccaggtgtac aactgcctc caagtagaga cgagctgacc	1140
aagaaccagg tgtccctgac atgtctggtc aaaggattct atccttcaga tatcgtctgtg	1200
gagtgggaaa gcaatgggca gccagaaaac aattacaaga ccacaccccc tgtgctggac	1260
agcgatggca gcttcttcct gtatagtaag ctgaccgtgg ataaatcaag gtggcagcag	1320
gggaacgtct tttcctgctc tgtgatgcat gaggccctgc acaatcatta caccagaag	1380
agtctgtcac tgagccctgg gaagcgagga cgaaaaagga gatccgggtc tggcgccaca	1440
aacttcagcc tgctgaagca ggctggggac gtggaggaaa atcctggccc aatggtcctg	1500
cagaccaggg tgtttatctc cctgctgctg tggatttctg gagcatatgg ggatatccag	1560
atgacacagt ctccttcctc tctgagtgtc tcagtgggcg acaggatcac cattacatgt	1620
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ccaaaactgc tgatctctgc tgcaagtgcc ctgcacgctg gagtgccaaag ccgcttcagc	1740
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gtacctact attgccagaa ctacaattcc gcaccctga ctttcggcgg agggaccaag	1860
gtcgaaatca aaactgtggc cgctcccagc gtcttcattt ttccaccctc cgacgagcag	1920
ctgaagagtg gcaccgcctc agtgggtgtc ctgctgaaca acttctaccc tagagaagca	1980
aaggtccagt ggaaagtgga taacgccctg cagtcaggaa atagccagga gtccgtgaca	2040
gaacaggact ctaaggatag tacttattca ctgagctcca cactgactct gtccaaagct	2100
gactacgaga agcacaaagt gtatgcatgc gaagtgacct accagggact gagcagcccc	2160
gtgaccaaga gctttaatag aggagaatgt tgataa	2196

<210> 46

<211> 730

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX9290, EBV114

<400> 46

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 Ile Gln
20 25 30

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

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

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

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

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

Tyr Cys Val Arg Ser Asp Arg Gly Val Ala Gly Leu Phe Asp Ser Trp
115 120 125

Gly Gln Gly Ile 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 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

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 Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile
500 505 510

Ser Gly Ala Tyr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
515 520 525

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

Ala Phe Asp Asn Tyr Val Ala Trp Tyr Gln Gln Arg Pro Gly Lys Val
545 550 555 560

Pro Lys Leu Leu Ile Ser Ala Ala Ser Ala Leu His Ala Gly Val Pro
565 570 575

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr His Phe Thr Leu Thr Ile
580 585 590

Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Asn Tyr
595 600 605

Asn Ser Ala Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
610 615 620

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln

<220>

<223> Chemically Synthesized

<400> 49

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

Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Tyr Ser Tyr
20 25 30

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

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

Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Asn Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Gly Ser Tyr Phe Cys Gln His His Phe Gly Thr Pro Phe
85 90 95

Thr Phe Gly Ser Gly Thr Glu Leu Glu Ile Lys
100 105

<210> 50

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized

<400> 50

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

Glu Thr Val Thr Ile Thr Cys Asn Ala Ser Glu Asn Ile Tyr Ser Tyr
20 25 30

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

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

Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Asn Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Gly Ser Tyr Trp Cys Gln His His Phe Gly Thr Pro Phe
85 90 95

Thr Phe Gly Ser Gly Thr Glu Leu Glu Ile Lys
100 105

<210> 51

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized

<400> 51

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

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

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
115

<210> 52
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Chemically Synthesized

<400> 52

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

Ser Val Lys Ile Ser Cys Gln Ala Ser Gly Ser Ser Phe Thr Gly Phe
20 25 30

Ser Met Asn Trp Val Lys Tyr 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

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

Met Gln Leu Gln 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
115

<210> 53
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Chemically Synthesized

<400> 53

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 54

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized

<400> 54

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

Glu Pro Ala Ser Ile Ser Cys Arg Ala Ser Gln Ser Leu Leu His Arg
20 25 30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

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

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
85 90 95

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

Lys

<210> 55

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized

<400> 55

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

Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser Gln Ala Phe Asp Asn Tyr
20 25 30

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

Ser Ala Ala Ser Ala Leu His Ala Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr His Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

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

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 56

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized

<400> 56

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 57

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized

<400> 57

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
20 25 30

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

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Tyr Asn Tyr Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 58
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> Chemically Synthesized

<400> 58

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

Glu Arg Ala Thr Leu Ser Cys Arg Ser Ser Gln Ser Leu Leu His Arg
20 25 30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

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

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
85 90 95

Leu Gln Thr Pro Ser Trp Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
100 105 110

Lys Arg

<210> 59
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Chemically Synthesized

<400> 59

Glu Thr Thr Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly

1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ala Phe Asp Asn Tyr
 20 25 30
 Val Ala Trp Tyr Gln Gln Arg Pro Gly Lys Val Pro Lys Leu Leu Ile
 35 40 45
 Ser Ala Ala Ser Ala Leu His Ala Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr His Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Val Ala Thr Tyr Tyr Cys Gln Asn Tyr Asn Ser Ala Pro Leu
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
 100 105

<210> 60
 <211> 114
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Chemically Synthesized

<400> 60

Ala Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Ser Leu Leu His Arg
 20 25 30
 Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45
 Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile

65		70		75		80									
Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	Cys	Met	Gln	Ala
			85					90						95	

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

Lys Arg

<210> 61
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Chemically Synthesized

<400> 61

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

Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Ala	Phe	Asp	Asn	Tyr
			20					25					30		

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

Ser	Ala	Ala	Ser	Ala	Leu	His	Ala	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				

Ser	Gly	Ser	Gly	Thr	His	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65					70					75				80	

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

Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg
			100					105			

<210> 62

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

<220>
 <223> Chemically Synthesized

<400> 62

Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys
 1 5 10 15

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

Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile
 35 40 45

<210> 63
 <211> 2235
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Chemically Synthesized, pRD211, 190-FP2A-mouse-GeneArt

<400> 63

atggattgga cttggagaat cctgttcctg gtggccgctg ctacaggcac acatgctcag	60
gtgcagctgg ttgaaagcgg aggcggagtt gtgcagcctg gcagatctct gagactgtct	120
tgtgccgcca gcggcttcac cttctctaag tacggaatgc actgggtccg acaggcccct	180
ggaaaaggac tggaatgggt cgccgtgatc agctacgagg gcagcaacaa gtactacgcc	240
gacagcgtga agggcagatt caccatcagc agagacaaca gcaagaacac cctgtacctg	300
cagatgaaca gcctgagagc cgaggacacc gccgtgtact actgtgctaa gagcggcacc	360
cagtactacg acaccaccgg ctacgagtac agaggcctgg aatacttttg ctactggggc	420
cagggaaccc tggtcacagt tagctctgct agcacaaagg gccccagcgt tttcccactg	480
gctcctagct ctaagagcac atctggcgga acagctgctc tgggctgtct ggtcaaggac	540
tactttcctg agcctgtgac cgtgtcctgg aactctgggtg ctctgacaag cggcgtgcac	600
acatttccag ctgtgctgca gtctagcggc ctgtactctc tgtctagcgt cgtgacagtg	660
cctagcagct ctctgggaac ccagacctac atctgcaacg tgaaccacaa gcctagcaac	720

accaaggtgg acaagagagt ggaacccaag agctgcgaca agaccacac ctgtcctcca	780
tgtcctgctc cagaagctgc aggcggaccc tctgtgttcc tgtttcctcc aaagcctaag	840
gacaccctga tgatcagcag aaccctgaa gtgacctgcg tgggtggtgga tgtgtctcac	900
gaggaccccg aagtgaagtt caattggtac gtggacggcg tggaagtgca caacgccaag	960
accaagccta gagaggaaca gtacaacagc acctacagag tgggtgtccgt gctgacagtg	1020
ctgcaccagg attggctgaa cggcaaagag tacaagtgca aggtgtccaa caaggccctg	1080
cctgctccta tcgaaaagac catctccaag gctaagggcc agcctaggga accccaggtt	1140
tacacactgc ctccaagcag agaagagatg accaagaacc aggtgtccct gacctgcctc	1200
gtgaagggat tctacccttc cgatatcgcc gtggaatggg agtctaacgg ccagccagag	1260
aacaactaca agacaacccc tcctgtgctg gacagcgacg gctcattctt cctgtacagc	1320
aagctgaccg tggacaagtc cagatggcag cagggaacg tgttcagctg ttctgtgatg	1380
cacgaggccc tgcacaacca ctacaccag aagtctctgt ctctgagccc cggcaagcgc	1440
ggcagaaaga gaagatctgg aagcggcgcc accaacttca gtctgctgaa acaggctggc	1500
gacgtggaag agaaccctgg acctatggtg ctgcagaccc aggtgttcat tagcctgctg	1560
ctgtggatct ctggcgcccta tggcgagatc gtgctgaccc agtctcctgg cacattgagc	1620
ctgtctccag gcgagagagc cacactgagc tgtagagcct ctgagagcgt gtcctctagc	1680
tacctggcct ggtatcagca aaagagaggc caggctccta gactgctgat ctacgacgcc	1740
tcttccagag ccacaggcat ccctgataga ttacgcggct ctggcagcgg caccgacttc	1800
acactgacca tctctagact ggaacccgag gatttcgctg tgtactattg ccagcagtac	1860
ggcagatcca gatggacctt tggacagggc acaaaggtgg aaatcaagag aaccgtggcc	1920
gtccttagcg tgttcatctt tccaccaagc gacgagcagc tgaagtctgg cacagcttct	1980
gtcgtgtgcc tgctgaacaa cttctacccc agagaagcca aggtgcagtg gaaggctgac	2040
aacgctctgc agtccggcaa cagccaagag agcgtgacag agcaggactc caaggacagc	2100
acatactccc tgagcagcac cctgacactg agcaaggccg actacgaaaa gcacaaggctg	2160
tacgcctgcg aagtgacaca ccagggactg agcagccctg tgaccaagtc tttcaacaga	2220
ggcgagtgcg gatga	2235

<211> 743
<212> PRT
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, pRD211, 190-FP2A-mouse-GeneArt

<400> 64

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

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

Tyr Tyr Cys Ala Lys Ser Gly Thr Gln Tyr Tyr Asp Thr Thr Gly Tyr
115 120 125

Glu Tyr Arg Gly Leu Glu Tyr Phe Gly Tyr Trp Gly Gln Gly Thr Leu
130 135 140

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

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

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser

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

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

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

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

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

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

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

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

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

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
530 535 540

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
545 550 555 560

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

Ile Tyr Asp Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
580 585 590

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

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Arg Ser Arg

610

615

620

Trp Thr Phe Gly Gln Gly Thr Lys Val 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> 65

<211> 2235

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pRD212, 190-FP2A-mouse-Synbio

<400> 65

atggactgga cttggagaat cctgttcctg gtggcagcag ctacaggaac acacgctcag 60

gtgcagctgg tggaatcagg aggaggagtg gtgcagccag gcagaagcct gagactgtct 120

tgcgccgcta gcggcttcac attcagcaag tacggcatgc attgggtccg acaggctcca 180

ggaaagggac tggagtgggt ggccgtgatt agctacgagg gcagcaacaa gtactacgcc 240

gacagcgtga agggcaggtt caccatcagc cgggacaaca gcaagaacac cctgtacctg 300

cagatgaaca gcctgagggc cgaggataacc gccgtgtact attgcgcaa gagcggaacc	360
cagtactacg acaccaccgg ctacgagtac aggggactgg agtacttcgg ctattggggc	420
cagggaaacac tggtgaccgt gtctagcgct agcaccaagg gacctagcgt gttccctctg	480
gccccttcta gcaagtctac cagcggagga acagccgctc tgggttgtct ggtgaaggac	540
tacttcccag agcccgtgac cgtgtcttgg aatagcggag ctctgaccag cggagtgcac	600
acattcccag cagtgtctga gagcagcggg ctgtactctc tgagcagcgt ggtgaccgtg	660
ccttcttcta gcctgggcac ccagacctac atctgcaacg tgaaccacaa gccagcaac	720
accaaggtgg acaagagggt ggagcccaag tcttgcgaca agaccacac ctgtccccct	780
tgtccagctc cagaagcagc aggaggacct agcgtgttcc tgttccctcc caagcccaag	840
gacaccctga tgatcagccg gaccccagaa gtgacttgcg tggtggtgga cgtgtctcac	900
gaggacccc aggtcaagtt caattggtac gtggacggag tggagggtgca caacgctaag	960
accaagccca gggaggagca gtacaacagc acctacaggg tgggtgtccgt gctgacagtg	1020
ctgcaccagg attggctgaa cggcaaggag tacaagtga aggtgtccaa caaggctctg	1080
ccagccccca tcgagaagac catcagcaag gctaaggagc agcctaggga acctcaggtg	1140
tacaccctgc ctctagcag ggaggagatg accaagaacc aggtgtccct gacttgcttc	1200
gtgaagggt tctaccctag cgacatcgcc gtggagtggg aatctaacgg ccagccagag	1260
aacaactaca agaccacccc ccagtgctg gacagcgacg gcagcttctt cctgtacagc	1320
aagctgaccg tggacaagag ccgttggcag cagggaacg tgttctcttg cagcgtgatg	1380
cacgaggccc tgcacaacca ctacaccag aagagcctga gcctgagccc aggaaagg	1440
ggcagaaaga gaagaagcgg aagcggcgct accaacttca gcctgctgaa gcaggccgga	1500
gacgtggagg agaatccagg acccatggtg ctgcagaccc aggtgttcat cagcctcctc	1560
ctgtggatca gcggagctta cggcgagatc gtgctgacac agagcccagg aaccctgtct	1620
ctgtctccag gagagagagc caccctgtct tgcagagcta gccagagcgt gtctagcagc	1680
tacctggctt ggtaccagca gaagaggggc caggctccta gactgctgat ctacgacgcc	1740
agctctagag ccaccggaat ccccgacaga ttacgcggaa gcggaagcgg aaccgacttc	1800
accctgacca tcagcagact ggagccagag gacttcgccg tctactactg ccagcagtac	1860
ggcagatctc gttggacctt cggacaggga accaaggtgg agatcaagcg gaccgtggca	1920

gccctagcg tgttcattt ccttcctagc gacgagcagc tgaagagcgg aacagctagc 1980
 gtcgtctgcc tgctgaacaa cttctacccc agggaggcca aggtccagtg gaaggtcgat 2040
 aacgccctgc agagcggaaa ctctcaggag agcgtgaccg agcaggactc taaggacagc 2100
 acctacagcc tgagcagcac actgaccctg agcaaggccg actacgagaa gcacaagggtg 2160
 tacgcttgcg aagtgaccca ccagggactg tctagccccg tgaccaagag cttcaaccgg 2220
 ggcgagtgtt gataa 2235

<210> 66
 <211> 743
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Chemically Synthesized, pRD212, 190-FP2A-mouse-Synbio

<400> 66

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

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

Tyr Tyr Cys Ala Lys Ser Gly Thr Gln Tyr Tyr Asp Thr Thr Gly Tyr
 115 120 125

Glu Tyr Arg Gly Leu Glu Tyr Phe Gly Tyr Trp Gly Gln Gly Thr Leu
130 135 140

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

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

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

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

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

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

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

Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
260 265 270

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

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

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

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

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys

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

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

Ile Tyr Asp Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
580 585 590

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

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Arg Ser Arg
610 615 620

Trp Thr Phe Gly Gln Gly Thr Lys Val 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> 67

<211> 2235

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pRD213, 190-FP2A-mouse-Genewiz

<400> 67

atggactgga cctggagaat cctgttcctc gtcgctgccg ctacaggcac ccatgcccag	60
gtgcagctgg tggaaagcgg cggaggcgctc gtgcagcctg gaaggagcct gagactgagc	120
tgcgccgcct ccggcttcac cttctccaaa tacggcatgc actgggtgag gcaggcccc	180
ggcaagggcc tggagtgggt cgctgtgatc agctacgaag gcagcaaca gtactacgcc	240
gacagcgtca agggcaggtt caccatctcc agagacaact ccaagaatac actgtacctg	300
cagatgaaca gcctgagggc tgaggacacc gctgtgtact actgcgcaa gagcggcacc	360
cagtactatg ataccaccgg ctatgagtac aggggcctgg aatacttcgg atattggggc	420
cagggcaccc tggtgacagt gagctccgct agcacaaagg gaccagcgt gttccctctc	480
gctcccagct ccaagtccac aagcggcgga acagccgctc tgggctgcct cgtgaaagac	540
tatttcctg agcccgtgac agtcagctgg aattccggcg ccctgacaag cggcgtccat	600
accttcctg ccgtcctcca aagctccggc ctgtactccc tgtcctccgt ggtcacagt	660
cccagctcct ccctgggaac ccagacctac atttgcaacg tcaatcaca gcccagcaac	720
accaaggtcg acaaaagggc cgaacccaag agctgcgaca aaaccacac ctgtcctccc	780
tgccctgctc ctgaagccgc tggaggacct agcgtgttcc tctttcctcc taagcccaag	840
gacaccctga tgatctccag gaccctgag gtgacctgtg tggctgtgga cgtgagccac	900
gaagatcccg aggtcaagtt caactggtac gtggacggcg tcgaagtga caatgcaaaa	960
accaagccca gagaggagca atacaactcc acctacagag tgggtgtccgt gtcacagt	1020
ctgcaccagg actggctgaa tggcaaagag tacaagtgtg aagtcagcaa taaggctctg	1080
cccgctccta ttgagaaaac catcagcaag gctaaaggac agcccaggga gcccaggtg	1140
tacacactgc ctcccagcag ggaggagatg acaaagaatc aggtgtccct gacatgcctg	1200
gtgaagggat tctaccctc cgatatcgct gtcgagtggg agtccaacgg ccaacccgaa	1260
aacaactata agaccacacc cccgctcctc gattccgacg gctccttctt tctgtattcc	1320
aagctgaccg tggacaagtc caggtggcag cagggaacg tcttctcctg tagcgtgatg	1380
cacgaggctc tgcacaatca ctacaccag aaaagcctgt ccctgagccc tggcaagaga	1440
ggcaggaaga gaagatccgg aagcggagcc acaaacttct ccctgctgaa gcaggccgga	1500

gacgtcgaag agaaccctgg ccccatggtc ctgcagacac aggtgttcat ttccctgctg 1560
 ctgtggatct ccggagccta cggcgagatc gtcctcacc agagccctgg cacactgtcc 1620
 ctgagccctg gcgagagagc caccctgtcc tgtagagcca gccaaagcgt ctccagcagc 1680
 tatctggcct ggtaccagca gaagaggggc caagctccca gactcctgat ctatgacgct 1740
 tcctccaggg ctaccggcat ccccgatagg tttagcggca gcggcagcgg caccgatttc 1800
 accctcacia tctccaggct ggagcctgag gactttgctg tgtattactg ccagcagtac 1860
 ggagggagca ggtggacctt cggacaggga accaaggtgg agatcaaaag gaccgtcgct 1920
 gctcccagcg tcttcatctt cccccccagc gatgagcagc tgaagtccgg cacagctagc 1980
 gtcgtgtgcc tcctgaacia tttctatccc agagaggcca aagtccagtg gaaggtggat 2040
 aacgccctgc agagcggaaa cagccaagaa tccgtcaccg aacaggacag caaggacagc 2100
 acctacagcc tctcctccac actcaccctc agcaaagccg actacgagaa gcacaaggctg 2160
 tacgcttgcg aggtgaccca ccagggcctg agctcccctg tgaccaagag cttcaatagg 2220
 ggcgagtgcct gataa 2235

<210> 68

<211> 743

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pRD213, 190-FP2A-mouse-Genewiz

<400> 68

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Val Leu Gln

500					505					510					
Thr	Gln	Val	Phe	Ile	Ser	Leu	Leu	Leu	Trp	Ile	Ser	Gly	Ala	Tyr	Gly
		515					520					525			
Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Pro	Gly
	530					535					540				
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Ser
545					550					555					560
Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Arg	Gly	Gln	Ala	Pro	Arg	Leu	Leu
				565					570					575	
Ile	Tyr	Asp	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro	Asp	Arg	Phe	Ser
			580						585					590	
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu
		595					600						605		
Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Gly	Arg	Ser	Arg
	610					615						620			
Trp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	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> 69
<211> 2235
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, pRD214, 190-FP2A-mouse-Blue heron

<400> 69
atggactgga cctggcgaat tctgttcttg gttgcagcag cgactggtac acacgctcag 60
gtccagctgg tcgaatctgg gggcggcgtg gtacagccag ggagatcact gaggctgagt 120
tgcgctgcat ccggcttcac cttctccaaa tacggcatgc attgggtgcg gcaagctccc 180
gggaaaggct tggaatgggt ggccgtaatt tcatacgaag ggtctaacaa gtattacgcc 240
gattctgtca agggccgctt tacaataagc cgcgataata gcaaaaacac gctttacctg 300
cagatgaact ctctgagagc agaggacact gctgtgtatt actgtgctaa atctgggacg 360
cagtactatg atacaactgg atacgagtac agaggcctcg aatacttcgg atactgggggt 420
caggggaacac tggtcacggt tagtagcgcc tccactaagg gtccttcagt cttccccctg 480
gcaccagta gtaaatccac ctccggcgggt actgcagctc ttggttgcct cgtgaaagac 540
tacttccctg aaccagtgac cgtctcctgg aactccggtg cactcaccag cggcgtagat 600
acattcccag ctgtgttgca aagttctggt ctgtatagct tgtcttccgt ggtgactgtc 660
cccagctcca gcctggggac ccaaacttac atttgtaatg tcaaccacaa gccgtctaata 720
acaaaggtgg acaagcgggt tgagccaaag agctgcgaca aaacgcacac ctgcccacct 780
tgccccgccc cagaagccgc ggggggaccc tcagtattcc tgttcccccc caagcccaag 840
gacactttga tgattagtcg cactcctgag gtcacctgag tagtagtcga cgtgagccat 900
gaagatcctg aagtgaagtt taactggtac gtcgacggag tggaggtcca taacgcaaaa 960
accaagccgc gcgaagaaca atacaactca acctacaggg tgggtctctgt gcttacagtc 1020
ctccatcagg actggctcaa cggcaaagaa tacaagtgtg aggtctccaa caaggcgctg 1080

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cccgcgccca tcgagaagac aatcagcaag gccaaaggcc agcccaggga gccccagggtg 1140
tatactctgc caccagtcg agaggagatg acaaaaaatc aagtgtccct cacatgcttg 1200
gtaaagggtt tctatccgtc tgacatagcc gtggagtggg agtctaattgg ccaaccagaa 1260
aacaactata agactacacc tcccgtcctt gactctgacg gcagcttttt tctttactcc 1320
aaacttacag tcgataagag tcggtggcag caaggtaatg tgttcagctg cagcgttatg 1380
cacgaagcgc tgcacaatca ctacacgcag aagtccttga gtctgtctcc cggaaaacgg 1440
ggccgcaagc ggcgagtggt ctcagggggc acaaatttct cactcctcaa acaggctggc 1500
gacgtggagg aaaaccccg gccaatggtg ctgcagaccc aagtcttcat aagcttggtg 1560
ctttggattt ccggggccta cggagaaatc gttctcactc agtctccagg cacacttca 1620
ctgtcacctg gagagcgcgc taccctcagt tgcagagcaa gtcaaagcgt gagctcttcc 1680
taccttgctt ggtaccaaca gaagagaggt caggccccgc gcttgctgat ctatgatgct 1740
tcatccccgg cgactggtat ccccgaccga ttctccggct ccggcagcgg taccgatttt 1800
actttgacta ttagccgcct tgaacctgag gacttcgccg tctactactg tcagcagtac 1860
ggaagaagcc gatggacatt cgggcagggt accaaggtag agatcaagcg gactgtggca 1920
gccccatctg tgtttatctt ccctcctagc gatgaacaac ttaagtccgg aactgcctcc 1980
gtagtatgcc ttctgaacaa tttttatcca cgcgaggcaa aggtgcagtg gaaagtggac 2040
aacgcccttc agtctggcaa ttcccaggaa agcgtcacag aacaggatag caaggactca 2100
acctactccc tctccagtac tctgacattg tccaaagccg attatgaaaa gcacaaagtg 2160
tatgcctgcg aagtaacaca ccaagggtg tcatctccag taaccaagag cttcaaccgc 2220
ggtgagtgtt gatga 2235

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<210> 70

<211> 743

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pRD214, 190-FP2A-mouse-Blue heron

<400> 70

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

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

Tyr Tyr Cys Ala Lys Ser Gly Thr Gln Tyr Tyr Asp Thr Thr Gly Tyr
115 120 125

Glu Tyr Arg Gly Leu Glu Tyr Phe Gly Tyr Trp Gly Gln Gly Thr Leu
130 135 140

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

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

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

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

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

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

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

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

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

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

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

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

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
530 535 540

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
545 550 555 560

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

Ile Tyr Asp Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
580 585 590

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

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Arg Ser Arg
610 615 620

Trp Thr Phe Gly Gln Gly Thr Lys Val 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> 71

<211> 2235

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pRD215, 190-FP2A-mammal-DNA2.0

<400> 71

atggactgga cctggcgcac cctgtttctc gtcgctgccg ccactgggtac ccatgcccag	60
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tgcgccgcct caggcttcac cttctcgaag tacgggatgc actgggtcag acaggctccc	180
gggaaaggcc tggaatgggt ggccgtcatc tcgtacgagg gctcaaaca gtactatgcc	240
gattccgtga agggacggtt caccatctcc cgggacaaca gcaagaacac cctgtacctc	300
caaatgaaca gcctgagggc cgaggacact gcagtgtact actgcgcca gtcgggcact	360
cagtactacg acaccacggg atacgagtac aggggactcg aatacttcgg atactggggc	420
cagggcacac tcgtgaccgt cagctccgcc tccactaagg gaccttcagt gttccctctg	480
gcgccatcct ccaagtgcac cagcggtgga actgcagccc tgggatgtct cgtgaaggac	540
tacttcctg aacctgtcac cgtgtcctgg aacagcggag cactgacctc cgggggtccac	600
actttcccg cggtgttgca gagctccggc ctgtactccc tgtcgtccgt cgtgacagtg	660

ccgtccagct cgttggggac ccagacttac atctgcaacg tgaaccacaa gccgtccaac	720
actaaagtgg acaaacgggt ggaaccaag tcgtgtgaca agactcatac ttgtccgcca	780
tgtcccgcctc ctgaagcggc gggaggacct tccgtgttcc tcttcccccc gaagcctaag	840
gacaccctca tgattagcag gaccccggaa gtgacctgtg tcgtggtcga cgtgtcacac	900
gaggaccccg aagtgaagtt taattggtac gtggacggcg tcgaagtga caacgccaag	960
accaagccac gcgaagaaca gtacaactcc acctaccggg tgggtgtccgt gcttactgtg	1020
ctccatcagg actggctcaa cggaaaggag tacaagtga aagtgtccaa caaagcgctc	1080
ccggctccta ttgaaaagac gatttccaag gccaaaggac agcctcggga acctcaggtc	1140
tacaccctgc ctcttcgcg cgaggagatg accaagaatc aggtgtccct gacttgcctg	1200
gtcaagggat tctatccatc cgacatcgcc gtggagtggg agtccaacgg ccagccggaa	1260
aacaactaca agaccacccc acccgtcctg gacagcgacg ggtccttctt cctgtactca	1320
aagctgactg tggataagtc ccgctggcaa cagggcaacg tgttctcctg ctccgtgatg	1380
cacgaggccc tgcacaacca ctacaccag aagtcgctta gcctctcgcc gggcaaacga	1440
ggaagaaagc gccggtccgg atcaggagcg actaacttct ccctcctgaa gcaggccggg	1500
gatgtggagg aaaatccagg acctatggtg ctgcaaacc aggtgttcat cagcctctc	1560
ctgtggatct ccggagccta cggcgaaatt gtgctgacct agtcccctgg gaccctgtcc	1620
ctgtcccccg gagagagagc caccctttcc tgccgggcat cgagagcgt cagctccagc	1680
tatctggcct ggtaccagca aaagcgcgga caagctccga gactgctgat ctacgatgcc	1740
tcatcacgcg ccaccggaat cccggatagg ttctcaggat cgggctccgg tactgatttc	1800
accctgacca tcagccggct ggaacctgag gacttcgctg tgtattactg ccagcagtac	1860
ggccggtcca gatggacttt cggacagggc actaaggctc aaatcaagcg gactgtcgct	1920
gcaccgagcg tgttcatttt cccaccctcc gacgagcagc ttaagagcgg aactgcttcc	1980
gtggtgtgcc ttctgaacaa tttctacccc cgggaagcca aggtccagtg gaaggctgac	2040
aacgccctgc aatccgggaa ctccaagaa tccgtcaccg aacaggactc caaggacagc	2100
acctactccc tctcatctac cctgaccctg tctaaggccg actacgagaa gcataaggctc	2160
tacgcctgcg aagtgcaca ccaaggcctt tcttcccccg tgaccaaatac cttcaaccgc	2220
ggagagtgcg gataa	2235

<210> 72
<211> 743
<212> PRT
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, pRD215, 190-FP2A-mammal-DNA2.0

<400> 72

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

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

Tyr Tyr Cys Ala Lys Ser Gly Thr Gln Tyr Tyr Asp Thr Thr Gly Tyr
115 120 125

Glu Tyr Arg Gly Leu Glu Tyr Phe Gly Tyr Trp Gly Gln Gly Thr Leu
130 135 140

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

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

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

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

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

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

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

Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
260 265 270

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

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

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

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

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

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

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

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu

385		390		395		400									
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn
				405					410					415	
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser
			420					425					430		
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg
		435					440					445			
Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu
	450					455					460				
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys	Arg
465					470					475					480
Gly	Arg	Lys	Arg	Arg	Ser	Gly	Ser	Gly	Ala	Thr	Asn	Phe	Ser	Leu	Leu
				485					490					495	
Lys	Gln	Ala	Gly	Asp	Val	Glu	Glu	Asn	Pro	Gly	Pro	Met	Val	Leu	Gln
			500					505					510		
Thr	Gln	Val	Phe	Ile	Ser	Leu	Leu	Leu	Trp	Ile	Ser	Gly	Ala	Tyr	Gly
		515					520					525			
Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Pro	Gly
	530					535					540				
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Ser
545					550					555					560
Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Arg	Gly	Gln	Ala	Pro	Arg	Leu	Leu
				565					570					575	
Ile	Tyr	Asp	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro	Asp	Arg	Phe	Ser
			580					585					590		
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu
		595					600					605			

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Arg Ser Arg
610 615 620

Trp Thr Phe Gly Gln Gly Thr Lys Val 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> 73

<211> 2235

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pRD216, 190-FP2A-mouse-Genscript

<400> 73

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gtgcagctcg tcgaatcagg gggaggggtg gtgcagccag gcaggagcct gaggctgagc 120

tgcgctgctt ccggcttcac cttttccaag tacggaatgc actgggtgag gcaggctcct 180

ggcaagggac tggagtgggt ggctgtgatc tcttacgagg gcagcaacaa gtactacgcc 240

gatagcgtga aggggaaggtt caccatctcc agagacaact ctaagaacac actgtacctg	300
cagatgaact ccctgagggc cgaggatacc gccgtgtact actgcgctaa gtctggcaca	360
cagtactacg acaccacagg atacgagtac agaggcctgg agtacttcgg atactggggc	420
cagggaaacc tggtgacagt gagctccgcc tctacaaagg gccccagcgt gtttcccctg	480
gctccttcta gcaagagcac ctccggcgga acagccgctc tgggatgtct ggtgaaggac	540
tacttccctg agccagtgac cgtgtcctgg aactctggcg ccctgacctc tggagtgcac	600
acatttcctg ctgtgctgca gtcctctggc ctgtacagcc tgagctccgt ggtgaccgtg	660
ccatctagct ccctgggaac ccagacatac atctgcaacg tgaaccacaa gccatccaac	720
acaaaggtgg acaagagggt ggagcccaag tcttgtgata agaccacac atgccctccc	780
tgtccagctc ctgaggctgc tggcggacca tccgtgttcc tgtttccacc caagcctaag	840
gatacactga tgatcagcag aacccccgag gtgacatgcg tgggtggtgga cgtgtccac	900
gaggaccccg aggtgaagtt caactggtac gtggacggcg tggaggtgca caacgccaag	960
accaagccta gggaggagca gtacaactcc acctacagag tgggtgtctgt gctgacagtg	1020
ctgcaccagg attggctgaa cggcaaggag tacaagtgcag aggtgtctaa caaggccctg	1080
ccagctcca tcgagaagac catcagcaag gctaaggagc agccacggga gccacagggtg	1140
tacacactgc ctccatctcg cgaggagatg accaagaacc aggtgagcct gacatgtctg	1200
gtgaagggtt tctaccctag cgatatcgct gtggagtggg agtccaacgg acagccagag	1260
aacaactaca agaccacacc ccctgtgtcg gacagcgatg gctccttctt tctgtactct	1320
aagctgaccg tggacaagag ccggtggcag cagggaaacg tgttttcttg cagcgtgatg	1380
cacgaggccc tgcacaacca ctacaccag aagtccctgt ctctgagccc tggaaagagg	1440
ggaaggaaga ggagatccgg ctctggagcc acaaacttct ccctgctgaa gcaggctggc	1500
gacgtggagg agaaccctgg accaatggtg ctgcagaccc aggtgtttat cagcctgctg	1560
ctgtggatct ccggagccta cggcgagatc gtgctgaccc agagccctgg cacactgagc	1620
ctgtccccag gagagagggc caccctgtcc tgtagagctt ctgagagcgt gtctagctcc	1680
tacctggctt ggtaccagca gaagagggga caggctccac gcctgctgat ctacgacgcc	1740
tctagccggg ctaccggaat ccccgatcgc ttctccggct ctggaagcgg cacagacttt	1800
accctgacaa tctcccggct ggagccagag gatttcgccg tgtactactg ccagcagtac	1860

ggcaggagca gatggacctt tggacagggc acaaaggtgg agatcaagcg caccgtggcc 1920
gctccatccg tgttcacctt tccaccctct gatgagcagc tgaagagcgg cacagcttcc 1980
gtggtgtgcc tgctgaacaa cttctacccc agggaggcca aggtgcagtg gaaggtggac 2040
aacgctctgc agtctggcaa cagccaggag tccgtgaccg agcaggactc taaggatagc 2100
acatactccc tgtcctctac cctgacactg agcaaggccg actacgagaa gcacaaggtg 2160
tacgcttgcg aagtgaccca ccaggggctg agcagtcagc tgacaaagtc cttcaataga 2220
ggggaatgct gataa 2235

<210> 74

<211> 743

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pRD216, 190-FP2A-mouse-Genscript

<400> 74

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

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

Tyr Tyr Cys Ala Lys Ser Gly Thr Gln Tyr Tyr Asp Thr Thr Gly Tyr

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

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

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

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

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

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

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

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

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

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

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

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

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

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
530 535 540

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser

545		550		555		560									
Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Arg	Gly	Gln	Ala	Pro	Arg	Leu	Leu
				565					570					575	
Ile	Tyr	Asp	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro	Asp	Arg	Phe	Ser
			580					585					590		
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu
		595					600					605			
Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Gly	Arg	Ser	Arg
	610					615					620				
Trp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	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> 75
 <211> 2211
 <212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pRD225, 185-mouse-GeneArt

<400> 75

atggactgga cttggagaat cctgttcctg gtggccgctg ctacaggcac acatgctgaa	60
gtgcagctgg tgcagtctgg cgccgaagtg aagaaacctg gcgagagcct gagaatcagc	120
tgcaaaggca gcggtctacag cttcaccagc tactggatca cctgggtccg acagatgcct	180
ggcaaaggcc tggaatggat ggccaagttc gaccctagcg acagccagac caactacagc	240
cctagctttc agggccacgt gaccatcagc gtggacaaga gcatcagcac agcctacctg	300
cagtggctcta gcctgaaggc cagcgacacc gccatgtact actgcgccag aagatactgc	360
agcagcagct cctgctacgt ggacaactgg ggacagggca ccctggtcac aatcttctct	420
gcctctacaa agggccccag cgtgttcctt ctggctccta gctctaagag cacatctggc	480
ggaacagctg ctctgggctg tctgggtcaag gactactttc ctgagcctgt gaccgtgtcc	540
tggaactctg gtgctctgac aagcggcgctg cacacatttc cagcagtgtg gcagtctagc	600
ggcctgtact ctctgtctag cgtgggtcaca gtgcctagca gcagcctggg aaccagacc	660
tacatctgca acgtgaacca caagcctagc aacaccaagg tcgacaagaa ggtggaaccc	720
aagagctgcg acaagaccca cacctgtcct ccatgtcctg ctccagaagc tgctggcgga	780
ccctctgtgt tcctgtttcc tccaaagcct aaggacaccc tgatgatcag cagaacccct	840
gaagtgacct gcgtgggtggg ggatgtgtct cacgaggacc cagaagtga gttcaattgg	900
tacgtggacg gcgtggaagt gcacaacgcc aagaccaagc ctagagagga acagtacaac	960
agcacctaca gagtgggtgtc cgtgctgacc gtgctgcacc aggattggct gaacggcaaa	1020
gagtacaagt gcaaggtgtc caacaaggcc ctgcctgctc ctatcgaaaa gaccatctcc	1080
aaggctaagg gccagccaag agaaccacag gtgtacacac tgcctccaag cagggacgag	1140
ctgaccaaga atcaggtgtc cctgacctgc ctctgtgaagg gcttctaccc ttccgatatc	1200
gccgtggaat gggagtctaa cggacagccc gagaacaact acaagacaac ccctcctgtg	1260
ctggacagcg acggctcatt cttcctgtac agcaagctga cagtggacaa gtccagatgg	1320
cagcagggca acgtgttcag ctgttctgtg atgcacgagg ccctgcacaa ccactacaca	1380
cagaagtccc tgtctctgag ccccggaag aggggcagaa agagaagatc tggcagcggc	1440

gccacaaact tcagtctgct gaaacaggct ggcgacgtgg aagagaatcc cggacctatg 1500
gtgctgcaga cacaggtggt catcagcctg ctgctgtgga tctctggcgc ctacggaagc 1560
agctatgagc tgacacagcc tcctagcgtg tccgtgtctc ctggccagac cgccagaatc 1620
acatgtagcg gagatgccct gcctaacaag ttcgcctact ggtacaggca gaagtccgga 1680
caggctcccc tgctgggtcat ctacgaggac aacaagaggc ctagcggcat ccctgagaga 1740
ttcagcggct ctagctctgg caccatggcc aactgacaa tcagtggcgc tcaggtggaa 1800
gatgaggccg actaccactg ttacagcacc gacagcagct ctaaccctct gggagtgttt 1860
ggcggcggaa caaagcttac agtgctgggc caacctaagg ctgccccttc tgtgacactg 1920
ttcccaccta gctctgagga actgcaggct aacaaggcca cactcgtgtg cctgatcagc 1980
gatttctacc ctggcgctgt gacagtggct tggaaggctg atagctctcc tgtgaaggcc 2040
ggcgtcgaga caacaacacc tagcaagcag agcaacaaca aatacgccgc cagctcctat 2100
ctgagcctga cacctgagca gtggaagtcc cacagatcct acagctgcca agtgaccac 2160
gagggcagca ccgtggaaaa gactgtggct cctaccgagt gctcctgatg a 2211

<210> 76

<211> 735

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pRD225, 185-mouse-GeneArt

<400> 76

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 Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe
35 40 45

Thr Ser Tyr Trp Ile Thr Trp Val Arg Gln Met Pro Gly Lys Gly Leu
50 55 60

Glu Trp Met Ala Lys Phe Asp Pro Ser Asp Ser Gln Thr Asn Tyr Ser

65		70		75		80									
Pro	Ser	Phe	Gln	Gly	His	Val	Thr	Ile	Ser	Val	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	Arg	Tyr	Cys	Ser	Ser	Ser	Ser	Cys	Tyr	Val	Asp
		115					120					125			
Asn	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Ile	Phe	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	
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	
Ala	Ala	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
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 Ser Ser Tyr Glu Leu Thr Gln Pro Pro		
515	520	525
Ser Val Ser Val Ser Pro Gly Gln Thr Ala Arg Ile Thr Cys Ser Gly		
530	535	540
Asp Ala Leu Pro Asn Lys Phe Ala Tyr Trp Tyr Arg Gln Lys Ser Gly		
545	550	555
Gln Ala Pro Val Leu Val Ile Tyr Glu Asp Asn Lys Arg Pro Ser Gly		
565	570	575
Ile Pro Glu Arg Phe Ser Gly Ser Ser Ser Gly Thr Met Ala Thr Leu		
580	585	590
Thr Ile Ser Gly Ala Gln Val Glu Asp Glu Ala Asp Tyr His Cys Tyr		
595	600	605
Ser Thr Asp Ser Ser Ser Asn Pro Leu Gly Val Phe Gly Gly Gly Thr		
610	615	620
Lys Leu Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu		
625	630	635
Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val		
645	650	655
Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys		
660	665	670
Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser		
675	680	685
Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr		
690	695	700
Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His		
705	710	715
		720

Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
725 730 735

<210> 77
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, pRD227, 185-mouse-Synbio

<400> 77
atggactgga cttggagaat cctgttcctg gtggcagccg ctacaggaac acacgcagaa 60
gtgcagctgg tgcagagcgg agcagaagtg aagaagccag gcgagagcct gcggatctct 120
tgcaagggaa gcggctacag cttcaccagc tactggatca cttgggtgcg ccagatgcca 180
ggcaagggac tggagtggat ggccaagttc gaccctagcg acagccagac caactacagc 240
cctagcttcc agggccacgt gacaatcagc gtggacaaga gcatcagcac cgcctacctc 300
cagtggctta gcctgaaggc cagcgatacc gccatgtact attgcgcccc gcggtattgc 360
agcagcagct cttgctacgt ggacaattgg ggccagggaa cactggtgac catcttcagc 420
gccagcacca agggacctag cgtgtttcct ctggcccctt ctagcaagag cacaagcgga 480
ggaacagccg ctctgggctg tctggtgaaa gactacttcc ccgagccagt gaccgtgtct 540
tggaactcag gagccctgac aagcggagtg cacacatttc cagccgtgct gcagagcagc 600
ggactgtact ctctgagcag cgtggtgacc gtgccttctt cttctctggg caccagacc 660
tacatctgca acgtgaacca caagcccagc aacaccaagg tggacaagaa ggtggagccc 720
aagtcttgcg acaagaccca cacttgcccc ctttgtccag ctccagaagc agcaggagga 780
cctagcgtgt tcctgttccc tcctaagccc aaggacaccc tgatgatcag ccggacccca 840
gaagtgactt gcgtggtggt ggacgtgtcc cacgaagacc ccgaggtcaa gttcaattgg 900
tacgtggacg gagtggaggt gcacaacgct aagaccaagc ccagggagga gcagtacaac 960
agcacctaca ggggtggtgtc cgtgctgaca gtgctgcacc aggattggct gaacggcaag 1020
gagtacaagt gcaaggtgtc caacaaggcc ctgccagctc ccatcgagaa gaccatcagc 1080
aaggccaagg gacagcctag agagcctcag gtgtacaccc tgccctcctt tagggacgag 1140
ctgaccaaga accaggtgtc cctgacttgc ctcgtgaagg gcttctaccc cagcgacatc 1200

gcagtggagt gggaaagcaa cggtcagcca gagaacaact acaagaccac cccccagtg 1260
ctggacagcg acggcagctt cttcctgtac agcaagctga ccgtggacaa aagccgctgg 1320
cagcagggca acgtgttctc ttgcagcgtg atgcacgagg ccctgcacaa ccactacacc 1380
cagaagagcc tgtctctgag cccaggcaag aggggcagaa agagaagaag cggcagcggg 1440
gccaccaact tcagcctgct gaagcaggca ggagacgtgg aggagaaccc aggacctatg 1500
gtgctgcaga cccaggtgtt catcagcctc ctgctgtgga tcagcggagc ttacggaagc 1560
agctacgagc tgacacagcc tcctagcgtg tccgtgtctc caggacagac cgccagaatc 1620
acttgtagcg gcgacgccct gcctaacaag ttcgcctatt ggtaccggca gaagagcggg 1680
caggctccag tgctgggtcat ctacaggagc aacaagaggc ctagcggcat cccagagagg 1740
ttcagcggat ctagcagcgg cacaatggcc aactgacca tcagcggagc tcaggtggag 1800
gacgaggccg actaccattg ctacagcacc gacagcagct ctaaccact gggcgtgttc 1860
ggaggaggaa caaagctgac cgtgctggga cagcctaagg cagctcctag cgtgacactg 1920
ttccctcctt ctagcgagga gctgcaggct aacaaggcca cactcgtctg cctgatcagc 1980
gacttctatc caggcgccgt gacagtggct tggaaggccg atagcagccc agtgaaagcc 2040
ggagtggaga caaccacccc tagcaagcag agcaacaaca agtacgccgc cagcagctac 2100
ctgagcctga caccagagca gtggaagagc cacaggagct actcttgcca ggtcaccac 2160
gaggggaagca cagtggagaa gacagtggcc cctacagagt gctcctgata a 2211

<210> 78

<211> 735

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pRD227, 185-mouse-Synbio

<400> 78

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 Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe

35

40

45

Thr Ser Tyr Trp Ile Thr Trp Val Arg Gln Met Pro Gly Lys Gly Leu
 50 55 60

Glu Trp Met Ala Lys Phe Asp Pro Ser Asp Ser Gln Thr Asn Tyr Ser
 65 70 75 80

Pro Ser Phe Gln Gly His Val Thr Ile Ser Val 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 Arg Tyr Cys Ser Ser Ser Ser Cys Tyr Val Asp
 115 120 125

Asn Trp Gly Gln Gly Thr Leu Val Thr Ile Phe 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

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

Ala Ala 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
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 Ser Ser Tyr Glu Leu Thr Gln Pro Pro						
	515			520		525
Ser Val Ser Val Ser Pro Gly Gln Thr Ala Arg Ile Thr Cys Ser Gly						
	530			535		540
Asp Ala Leu Pro Asn Lys Phe Ala Tyr Trp Tyr Arg Gln Lys Ser Gly						
545		550		555		560
Gln Ala Pro Val Leu Val Ile Tyr Glu Asp Asn Lys Arg Pro Ser Gly						
	565			570		575
Ile Pro Glu Arg Phe Ser Gly Ser Ser Ser Gly Thr Met Ala Thr Leu						
	580			585		590
Thr Ile Ser Gly Ala Gln Val Glu Asp Glu Ala Asp Tyr His Cys Tyr						
	595			600		605
Ser Thr Asp Ser Ser Ser Asn Pro Leu Gly Val Phe Gly Gly Gly Thr						
	610			615		620
Lys Leu Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu						
625		630		635		640
Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val						
	645			650		655
Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys						
	660			665		670
Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser						
	675			680		685

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

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

Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
725 730 735

<210> 79

<211> 2211

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pRD229, 185-mouse-Genewiz

<400> 79

atggactgga catggagaat cctcttcctg gtggccgccg ctaccggcac acatgctgag	60
gtgcagctgg tgcagtccgg cgctgaagtg aagaaacccg gagagagcct gagaatctcc	120
tgtaaaggct ccggctacag cttcacctcc tactggatta cctgggtgag acagatgccc	180
ggcaaaggac tggagtggat ggccaagttc gatccctccg acagccagac caactacagc	240
cccagctttc agggacatgt gaccatcagc gtggataaga gcatctccac cgcttatctg	300
cagtggagca gcctcaaggc cagcgatacc gccatgtact actgcgccag gaggtattgc	360
tccagctcca gctgctacgt cgacaactgg ggccagggaa cactggtcac aatcttctcc	420
gcctccacca agggcccctc cgtgtttcct ctggctccta gcagcaagtc cacctccgga	480
ggaacagctg ccctcggctg cctcgtgaaa gactacttcc ccgagcccgt gaccgtgtcc	540
tggaactccg gagccctgac ctccggagtc cataccttcc ctgccgtgct ccagagcagc	600
ggcctctaca gcctgagctc cgtgggtgacc gtcccttcca gcagcctggg caccagaca	660
tatatctgca acgtgaacca taagcctagc aacacaaagg tggacaagaa ggtcgaaccc	720
aagagctgtg acaagaccca cacctgtcct cttgttccg cccctgaagc tgctggcgga	780
cctagcgtgt tcctgttccc tcctaagccc aaggacaccc tcatgatctc cagaaccctt	840
gaagtgacct gcgtggtcgt ggacgtgagc cacgaggacc ccgaggtcaa gttcaattgg	900
tatgtggacg gcgtcgaggt gcacaatgcc aagaccaaac ccagagagga gcaatacaac	960

agcacctaca	gagtgggtgtc	cgtgctgaca	gtgctgcacc	aggattggct	caatggcaag	1020
gagtacaaat	gcaaagtgtc	caacaaggcc	ctgcccgtc	ccatcgaaaa	gacaatcagc	1080
aaggccaagg	gccagcccag	ggaacctcag	gtctataccc	tccctcccag	cagggatgag	1140
ctcaccaaga	accaagtgtc	cctgacctgt	ctgggtcaaag	gattctaccc	ctccgatatt	1200
gctgtcgagt	gggagagcaa	cggccagccc	gaaaacaact	acaagacaac	ccctcctgtg	1260
ctggatagcg	acggttcttt	cttcctgtac	tccaagctca	cagtggacaa	atccaggtgg	1320
cagcagggca	acgtgttctc	ctgctccgtc	atgcatgagg	ccctgcacaa	ccactatacc	1380
cagaagtccc	tgtccctgag	ccccggaaaa	agaggcagaa	aaagaaggtc	cggctccggc	1440
gccacaaact	tctccctgtc	gaagcaggct	ggcgacgtgg	aggagaaccc	cggccctatg	1500
gtcctccaga	cccaggtgtt	tattagcctg	ctgctgtgga	tcagcggcgc	ctatggcagc	1560
tcctacgaac	tgacacagcc	ccctagcgtg	agcgtgagcc	ctggacagac	cgccagaatt	1620
acctgcagcg	gcgatgccct	gcccacaag	tttgcttact	ggtacaggca	gaaatccggc	1680
caagcccctg	tgctgggtcat	ttacgaggac	aacaagaggc	ccagcggcat	tcctgagagg	1740
ttcagcggca	gcagcagcgg	aacctatggc	accctgacaa	tcagcggcgc	ccaagtggaa	1800
gacgaggctg	actaccactg	ttacagcaca	gactcctcct	ccaatcctct	cggcgtgttc	1860
ggcggcggca	caaaactgac	agtgtctgga	cagcctaagg	ccgcccctag	cgtgacactg	1920
tttcctcctt	cctccgagga	actgcaggcc	aacaaggcca	cactgggtgtg	tctgatctcc	1980
gacttctacc	ccggcgtgtg	gaccgtggct	tggaaggccg	attccagccc	cgtgaaggct	2040
ggcgtcgaga	ccacaacccc	cagcaagcag	agcaacaaca	agtatgctgc	ctcctcctac	2100
ctgtccctca	caccgaaca	gtggaagagc	cataggtcct	acagctgcca	ggtgacacac	2160
gaaggcagca	cagtggaaaa	gaccgtggcc	cctaccgaat	gctcctgata	a	2211

<210> 80

<211> 735

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pRD229, 185-mouse-Genewiz

<400> 80

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	Gln Ser Gly Ala Glu Val Lys Lys	
	20	25	30
Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe			
	35	40	45
Thr Ser Tyr Trp Ile Thr Trp Val Arg Gln Met Pro Gly Lys Gly Leu			
	50	55	60
Glu Trp Met Ala Lys Phe Asp Pro Ser Asp Ser Gln Thr Asn Tyr Ser			
65	70	75	80
Pro Ser Phe Gln Gly His Val Thr Ile Ser Val 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 Arg Tyr Cys Ser Ser Ser Ser Cys Tyr Val Asp			
	115	120	125
Asn Trp Gly Gln Gly Thr Leu Val Thr Ile Phe 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
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

Ala Ala 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
 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	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 Ser Ser Tyr Glu Leu Thr Gln Pro Pro		
515	520	525
Ser Val Ser Val Ser Pro Gly Gln Thr Ala Arg Ile Thr Cys Ser Gly		
530	535	540
Asp Ala Leu Pro Asn Lys Phe Ala Tyr Trp Tyr Arg Gln Lys Ser Gly		
545	550	560
Gln Ala Pro Val Leu Val Ile Tyr Glu Asp Asn Lys Arg Pro Ser Gly		
565	570	575
Ile Pro Glu Arg Phe Ser Gly Ser Ser Ser Gly Thr Met Ala Thr Leu		
580	585	590
Thr Ile Ser Gly Ala Gln Val Glu Asp Glu Ala Asp Tyr His Cys Tyr		
595	600	605
Ser Thr Asp Ser Ser Ser Asn Pro Leu Gly Val Phe Gly Gly Gly Thr		
610	615	620
Lys Leu Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu		
625	630	640
Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val		
645	650	655

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

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

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

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

Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
725 730 735

<210> 81
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, pRD231, 185-mouse-GenScript

<400> 81
atggattgga catggaggat tctgtttctg gtcgccgccg ctactggaac tcacgccgaa 60
gtgcagctgg tgcagtcagg agccgaagtg aagaagccag gcgagagcct gcggatctcc 120
tgtaagggaa gcggctactc ctttacatct tactggatca cctgggtgcg ccagatgcca 180
ggaaagggcc tggagtggat ggccaagttc gacccttctg atagccagac aaactactcc 240
ccatcttttc agggccacgt gacaatcagc gtggacaaga gcatctccac cgcctacctg 300
cagtggagct ccctgaaggc ctccgatacc gctatgtact actgcgctag gagatactgt 360
tctagctcct cttgctacgt ggacaactgg ggacagggca cactggtgac catcttctct 420
gccagcacia agggacccag cgtgtttcca ctggctccca gctccaagtc cacatctggc 480
ggaaccgccg ctctgggatg tctggtgaag gattacttcc ccgagcctgt gaccgtgagc 540
tggaactccg gagccctgac aagcggcgtg cacacctttc ccgctgtgct gcagtctagc 600
ggactgtact ccctgtcctc tgtggtgaca gtgcctagct cctctctggg cacacagacc 660
tacatctgta acgtgaacca caagccttcc aacaccaagg tggacaagaa ggtggagcca 720

aagtcttgcg ataagacaca cacctgccct ccctgtccag ctccagaggc tgctggcgga	780
ccatccgtgt tcctgtttcc acccaagcct aaggacaccc tgatgatcag caggacacca	840
gaggtgacct gcgtgggtgt ggacgtgtcc cacgaggacc ccgaggtgaa gttcaactgg	900
tacgtggatg gcgtggaggt gcacaacgcc aagacaaagc caagggagga gcagtacaac	960
tctacataca gagtgggtgag cgtgctgacc gtgctgcacc aggactggct gaacggaaag	1020
gagtacaagt gtaaggtgtc taacaaggcc ctgcctgctc caatcgagaa gacaatcagc	1080
aaggctaagg gacagcctcg ggagccacag gtgtacaccc tgcctccatc tcgcgacgag	1140
ctgacaaaga accaggtgag cctgacctgc ctggtgaagg gcttctaccc ctccgatatc	1200
gctgtggagt gggagtctaa cggccagcct gagaacaact acaagaccac accccctgtg	1260
ctggactctg atggaagctt ctttctgtac agcaagctga ccgtggacaa gtccagatgg	1320
cagcagggca acgtgttcag ctgttccgtg atgcacgagg ccctgcacaa ccactacaca	1380
cagaagtctc tgagcctgtc ccctggaaag aggggaagaa agcggcgctc tggaagcgga	1440
gccaccaact ttagcctgct gaagcaggct ggagatgtgg aggagaaccc cggccctatg	1500
gtgctgcaga cacaggtgtt catctccctg ctgctgtgga tctctggagc ctacggcagc	1560
tcctacgagc tgaccagcc accctccgtg tctgtgagcc ctggacagac agctaggatc	1620
acctgctctg gcgacgccct gccaaacaag tttgcttact ggtacagaca gaagtccgga	1680
caggcccccg tgctgggtcat ctacaggat aacaagcggc cctctggcat ccctgagagg	1740
ttcagcggat ctagctccgg cacaatggct aactgacca tctccggagc tcaggtggag	1800
gacgaggctg attaccactg ttactctacc gactctagct ccaaccctct gggagtgttc	1860
ggcggaggca caaagctgac cgtgctggga cagccaaagg ctgctccaag cgtgaccctg	1920
tttcctccat ctagcgagga gctgcaggcc aacaaggcta cactgggtgtg cctgatctcc	1980
gacttctacc ctggagctgt gaccgtggct tggaaggctg attcctctcc agtgaaggct	2040
ggcgtggaga caacaacccc ctccaagcag tctaacaaca agtacgccgc tagctcctac	2100
ctgagcctga cccagagca gtggaagtcc caccggctcct actcttgcca ggtcactcac	2160
gaaggaagca ctgtggaaaa aactgtcgcc cctaccgaat gttcttgata a	2211

<210> 82

<211> 735

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pRD231, 185-mouse-GenScript

<400> 82

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 Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe
35 40 45

Thr Ser Tyr Trp Ile Thr Trp Val Arg Gln Met Pro Gly Lys Gly Leu
50 55 60

Glu Trp Met Ala Lys Phe Asp Pro Ser Asp Ser Gln Thr Asn Tyr Ser
65 70 75 80

Pro Ser Phe Gln Gly His Val Thr Ile Ser Val 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 Arg Tyr Cys Ser Ser Ser Ser Cys Tyr Val Asp
115 120 125

Asn Trp Gly Gln Gly Thr Leu Val Thr Ile Phe 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

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

Ala Ala 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		
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
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 Ser Ser Tyr Glu Leu Thr Gln Pro Pro		
515	520	525
Ser Val Ser Val Ser Pro Gly Gln Thr Ala Arg Ile Thr Cys Ser Gly		
530	535	540
Asp Ala Leu Pro Asn Lys Phe Ala Tyr Trp Tyr Arg Gln Lys Ser Gly		
545	550	555
Gln Ala Pro Val Leu Val Ile Tyr Glu Asp Asn Lys Arg Pro Ser Gly		
565	570	575
Ile Pro Glu Arg Phe Ser Gly Ser Ser Ser Gly Thr Met Ala Thr Leu		
580	585	590
Thr Ile Ser Gly Ala Gln Val Glu Asp Glu Ala Asp Tyr His Cys Tyr		
595	600	605
Ser Thr Asp Ser Ser Ser Asn Pro Leu Gly Val Phe Gly Gly Gly Thr		
610	615	620

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

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

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

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

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

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

Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
725 730 735

<210> 83

<211> 2211

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pRD233, 185-mouse-Blue Heron

<400> 83

atggactgga cctggaggat actgtttctg gtggctgccg caaccggaac acatgccgaa	60
gtacagctgg ttcagtctgg agcggaggtc aagaagcccg gggaaagtct gaggatctct	120
tgcaaggggt caggttatag tttcacaagt tattggatca cttgggtcag acaaatgccg	180
gggaagggac tggagtggat ggctaagttt gatccctccg attctcagac taattactcc	240
ccgtcatttc agggatcatgt gactatcagc gtcgataaat ctatttcaac tgcctacctg	300
caatggagca gcttgaaggc ttccgatacc gccatgtatt actgtgcacg gaggtattgt	360
tccagctcct cttgttacgt ggataactgg gggcagggga cattggtaac gattttttca	420
gcttctacaa agggcccctc tgtctttcct ctcgctcctt ctagcaaadc cacttctggg	480

ggaaccgctg cactgggatg cctcgtgaaa gactacttcc ccgaacccgt gaccgtgtca	540
tggaactcag gtgcccttac cagcggagtc cacacgttcc cggctgtgct tcagagttcc	600
ggtctgtatt ccctctcctc tgtggtgacg gtgccctcca gctcactggg aacgcagaca	660
tatatctgta acgtgaacca caaaccttcc aataccaagg tcgacaagaa ggtggagccg	720
aaatcctgtg ataagacca tacctgtcct ccatgccccg cccagaagc agctggagga	780
ccctctgtgt tcttgtttcc ccccaaaccg aaagatactt tgatgatctc ccggacccca	840
gaagtcacgt gtgtagtggg cgatgttagt catgaagacc ccgaagtga attcaactgg	900
tacgtagacg gcgtggaggt ccataatgct aagacgaagc cacgagaaga acagtataat	960
tccacctacc gggttgtcag cgtgcttacc gttttgcatc aggattgggt gaatggaaaag	1020
gaatacaaat gcaaggtgtc caataaggcc ctgcccgtc ctatcgagaa gacaattagt	1080
aaggcaaaag gccaacctcg cgagccccag gtgtataccc tccctccctc cagggacgaa	1140
ctgacaaaga accaagtgag cctgacatgt ctggtcaagg gattttatcc ttcagatatc	1200
gctgtggagt gggaaagcaa tggccagcca gaaaacaact acaaaacaac tccgcccgtc	1260
ctggactctg acggttcctt tttcctgtac tctaagctga ctgtggataa gtcaagatgg	1320
cagcagggga atgtgttttc ttgtagcgtt atgcacgagg ctctgcacaa ccattatacg	1380
cagaagagtt tgagcctgag tcctggtaaa aggggccgga aacgcaggtc tggatctggg	1440
gctactaact tcagcctttt gaaacaagcc ggggatgtgg aggaaaaccc agggcccatg	1500
gtcctgcaga ctcaggtttt tatcagtctg ctgctctgga tttcaggcgc ttacggtagc	1560
agctacgagc tgaccagcc cccttcagt tccgtctcac caggacagac cgcgaggatc	1620
acttgacgtg gggatgccct gccgaataag tttgcgtatt ggtacagaca aaagtccggt	1680
caggcaccag tcctggtgat ttatgaagac aacaagcgac caagcggcat ccctgagcgc	1740
ttctccggtt ccagcagcgg gaccatggcc aactgacaa tcagtggggc ccaggtcgag	1800
gacgaggccg actaccactg ctattctacc gatagctctt caaatccatt gggagtgttt	1860
ggcgggtggaa caaaactcac cgtgctgggg cagccaaagg cagctccaag tgtcactctt	1920
tttccaccta gcagtgaaga gtcacaggcc aacaaagcaa ccctggtgtg tcttatcagc	1980
gatttttacc ctggggcggt gacagtggcc tggaaagccg attccagccc cgtgaaagcc	2040
ggtgtcga aa ccactactcc tagcaagcag agcaacaata aatatgccgc gagttcctac	2100

ctgagcctta ctccagagca gtggaagtca caccggctct atagttgtca ggttacacac 2160
 gaaggaagta ctgttgaaaa gactgttgct ccgacagaat gcagctgata a 2211

<210> 84
 <211> 735
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Chemically Synthesized, pRD233, 185-mouse-Blue Heron

<400> 84

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 Gln Ser Gly Ala Glu Val Lys Lys
 20 25 30

Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe
 35 40 45

Thr Ser Tyr Trp Ile Thr Trp Val Arg Gln Met Pro Gly Lys Gly Leu
 50 55 60

Glu Trp Met Ala Lys Phe Asp Pro Ser Asp Ser Gln Thr Asn Tyr Ser
 65 70 75 80

Pro Ser Phe Gln Gly His Val Thr Ile Ser Val 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 Arg Tyr Cys Ser Ser Ser Ser Cys Tyr Val Asp
 115 120 125

Asn Trp Gly Gln Gly Thr Leu Val Thr Ile Phe 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

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

Ala Ala 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
 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 Ser Ser Tyr Glu Leu Thr Gln Pro Pro
 515 520 525

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

Asp Ala Leu Pro Asn Lys Phe Ala Tyr Trp Tyr Arg Gln Lys Ser Gly
 545 550 555 560

Gln Ala Pro Val Leu Val Ile Tyr Glu Asp Asn Lys Arg Pro Ser Gly
 565 570 575

Ile Pro Glu Arg Phe Ser Gly Ser Ser Ser Gly Thr Met Ala Thr Leu
 580 585 590

Thr Ile Ser Gly Ala Gln Val Glu Asp Glu Ala Asp Tyr His Cys Tyr
595 600 605

Ser Thr Asp Ser Ser Ser Asn Pro Leu Gly Val Phe Gly Gly Gly Thr
610 615 620

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

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

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

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

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

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

Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
725 730 735

<210> 85

<211> 2211

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pRD234, 185-mammal-DNA2.0

<400> 85

atggactgga cttggcggat tttgttcctg gtggcggcgg ctactggaac tcatgcagaa	60
gtgcagcttg tgcagtccgg cgctgaagtc aagaagcctg gagagtccct gagaatcagc	120
tgcaagggca gcggctactc cttcacctcg tactggatca cttgggtcag acaaatgccg	180
ggaaagggac tggaatggat ggctaaattc gacccgtcgg acagccagac taactacagc	240

ccgtcgttcc aaggacatgt caccatctcc gtggacaaat cgatcagcac cgcgtacctc	300
cagtggagct cactcaaagc atccgacacc gcgatgtact actgcgcccg ccgctactgc	360
tcgtcctcgt cctgctacgt ggacaattgg ggacagggtta ctcttgtgac aatcttctcc	420
gcctccacca agggcccctc agtggttccc ctggcaccat cctctaagtc cacctccgga	480
ggcaccgccg ccttgggttg cctgggtcaag gactacttcc cggaacctgt gaccgtgtcc	540
tggaacagcg gggcactgac ctccggcgtg catacttttc ccgccgtcct gcaatcttcc	600
ggcctgtact cactgtcatc agtggtcacc gtgccctcgt cctccctggg caccagact	660
tacatctgta acgtgaacca taagccctcc aacaccaaag tggacaagaa agtggagcca	720
aagtcgtgtg acaagactca cacttgcccg ccgtgcccgg ccccggaagc cgccgggtgga	780
ccgagcgtgt ttctcttccc acccaagccg aaggataccc tgatgatttc gcggacccct	840
gaagtgacct gtgtggtggt cgacgtgtcc cacgaggacc ccgaagtcaa gttcaattgg	900
tacgtggacg gtgtcgaagt gcacaacgcc aagacgaagc ctcgcgagga acagtacaac	960
agcacttacc gggtcgtgtc cgtcctcacc gtgctgcacc aagattggct caacgggaag	1020
gagtacaagt gcaaagtgtc aaataaggcc ctgccggccc cgattgaaaa gaccattagc	1080
aaggccaagg gacagcctag ggaacctcaa gtgtacacgc tgccccgctc gcgggacgag	1140
ctgaccaaga accaagtgtc gctgacttgc cttgtgaagg gattctaccc gtccgacatt	1200
gccgtggagt gggagtccaa cggacagccc gaaaacaact acaagaccac ccctcctgtg	1260
ctggactctg atggatcatt cttcctttac tcgaaactca ccgtggacaa gtcccgtggtg	1320
caacagggaa acgtgttcag ctgctccgtg atgcacgagg ccctgcacaa ccactatacc	1380
cagaagtccc tgtcactgag ccccggggaag cgcggcagga agcggagaag cggaagcgga	1440
gctacaaact tttcgctgct gaagcaggcc ggcgatgtgg aagaaaacc agggcctatg	1500
gtgctgcaga ctcaagtgtt tatctccctg ctctgttgga tctccggagc gtatgggtcc	1560
agctacgagc tcaccagcc tccttccgtg tcggtgtcac caggacagac cgcccggatt	1620
acctgttccg gggatgccct cccaacaag ttgcctact ggtaccgcca gaagtccggc	1680
caggctccag tgcttgtgat ctacaggac aacaagcggc cttctggcat ccccgagcgg	1740
ttctccgggt cctcctccgg caccatggca accctgacca tctcgggagc tcaggtcgaa	1800
gatgaagccg actatcactg ctactcgacc gatagctcct caaaccggtt gggggtcttt	1860

ggcgaggagaa ccaagctgac tgtgctggga cagccgaagg ccgcgccgtc cgtcacccctg 1920
 ttcccgccga gcagcgagga actccaggcc aacaaggcca ctctcgtgtg cctgatttcc 1980
 gacttctacc ctgggtgccgt gactgtggcg tggaaggccg actcgtcgcc ggtcaaggcc 2040
 ggcggtggaga ctaccacccc gtcaaaacag agcaacaata agtacgccgc ctcttcctat 2100
 ttgtcactga ctcccagca gtggaagtcc caccggtcct actcatgcca agtcacccat 2160
 gaagggtcca ccgtggaaaa gactgtggcc cccactgagt gttcgtaatg a 2211

<210> 86

<211> 735

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pRD234, 185-mammal-DNA2.0

<400> 86

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 Gln Ser Gly Ala Glu Val Lys Lys
 20 25 30

Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe
 35 40 45

Thr Ser Tyr Trp Ile Thr Trp Val Arg Gln Met Pro Gly Lys Gly Leu
 50 55 60

Glu Trp Met Ala Lys Phe Asp Pro Ser Asp Ser Gln Thr Asn Tyr Ser
 65 70 75 80

Pro Ser Phe Gln Gly His Val Thr Ile Ser Val 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 Arg Tyr Cys Ser Ser Ser Ser Cys Tyr Val Asp
 115 120 125

Asn Trp Gly Gln Gly Thr Leu Val Thr Ile Phe 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

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

Ala Ala 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	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		
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	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 Ser Ser Tyr Glu Leu Thr Gln Pro Pro		
515	520	525
Ser Val Ser Val Ser Pro Gly Gln Thr Ala Arg Ile Thr Cys Ser Gly		
530	535	540
Asp Ala Leu Pro Asn Lys Phe Ala Tyr Trp Tyr Arg Gln Lys Ser Gly		
545	550	560

Gln Ala Pro Val Leu Val Ile Tyr Glu Asp Asn Lys Arg Pro Ser Gly
565 570 575

Ile Pro Glu Arg Phe Ser Gly Ser Ser Ser Gly Thr Met Ala Thr Leu
580 585 590

Thr Ile Ser Gly Ala Gln Val Glu Asp Glu Ala Asp Tyr His Cys Tyr
595 600 605

Ser Thr Asp Ser Ser Ser Asn Pro Leu Gly Val Phe Gly Gly Gly Thr
610 615 620

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

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

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

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

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

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

Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
725 730 735

<210> 87

<211> 2235

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX9382, 190

<400> 87

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gtgcagctgg tggagagcgg cggcggcgtg gtgcagccag gccgggtccct gaggctgtct	120
tgcgcagcaa gcggcttcac ctttagcaag tacggaatgc actgggtgag acaggcacct	180
ggcaagggcc tggagtgggt ggccgtgatc tcctatgagg gctctaaca gtactatgcc	240
gattccgtga agggcaggtt taccatcagc agagacaact ccaagaatac actgtacctg	300
cagatgaata gcctgagggc cgaggatacc gccgtgtact attgcgcaa gtccggcaca	360
cagtactatg acaccacagg ctacgagtat agaggcctgg agtacttcgg ctattggggc	420
cagggcaccc tggtgacagt gagctccgcc tccacaaagg gaccaagcgt gttcccactg	480
gcaccttcta gcaagtctac cagcggcggc acagccggcc tgggatgtct ggtgaaggat	540
tacttcctg agccagtgc cgtgagctgg aactccggcg ccctgacctc cggagtgcac	600
acatttcctg ccgtgctgca gtcctctggc ctgtactctc tgagctccgt ggtgaccgtg	660
ccatctagct ccctgggcac ccagacatat atctgcaacg tgaatcaca gccaaagcaat	720
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tgtccagcac ctgaggcagc cggcggccca agcgtgttcc tgtttccacc caagcctaag	840
gatacactga tgatctctag aacccccgag gtgacatgcg tgggtggtgga cgtgagccac	900
gaggaccccg aggtgaagtt caactggtac gtggacggcg tggaggtgca caatgccaag	960
accaagccca gggaggagca gtacaacagc acctatagag tgggtgtccgt gctgacagtg	1020
ctgcaccagg actggctgaa cggcaaggag tataagtgc aggtgtccaa taaggccctg	1080
ccagcccca tcgagaagac catctctaag gcaaaggac agccacggga gccacaggtg	1140
tacacactgc ctccatccc cgaggagatg accaagaacc aggtgtctct gacatgtctg	1200
gtgaagggt tctatccttc tgatatcgcc gtggagtggg agagcaatgg ccagccagag	1260
aacaattaca agaccacacc ccctgtgctg gactctgatg gcagcttctt tctgtattcc	1320
aagctgaccg tggacaagtc taggtggcag cagggaacg tgttttcctg ctctgtgatg	1380
cacgaggccc tgcacaatca ctacaccag aagagcctgt ccctgtctcc tggcaagagg	1440
ggaaggaaga ggagaagcgg ctccggcgcc acaaacttca gcctgctgaa gcaggcaggc	1500
gacgtggagg agaatcctgg accaatggtg ctgcagaccc aggtgtttat ctctctgctg	1560
ctgtggatca gcggagcata cggagagatc gtgctgaccc agtctcctgg cacactgtct	1620

ctgagcccag gagagagggc caccctgagc tgtagagcct cccagagcgt gagcagcagc 1680
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 tctagccggg ccaccggcat ccccgatcgc ttcagcggct ccggctctgg cacagacttt 1800
 accctgacaa tctcccggct ggagcctgag gatttcgccg tgtactattg ccagcagtat 1860
 ggcaggagca gatggacctt tggccagggc acaaaggtgg agatcaagag gaccgtggca 1920
 gcaccaagcg tgttcatctt tccaccctcc gatgagcagc tgaagtctgg cacagccagc 1980
 gtggtgtgcc tgctgaacaa tttctacccc agggaggcca aggtgcagtg gaaggtggac 2040
 aacgccctgc agtccggcaa ttctcaggag agcgtgaccg agcaggactc caaggattct 2100
 acatatagcc tgtcctctac cctgacactg tccaaggccg actacgagaa gcacaagggtg 2160
 tatgcatgcg aggtgaccca ccagggcctg agctccccag tgacaaagag ctttaaccgc 2220
 ggcgagtgtt gataa 2235

<210> 88
 <211> 743
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Chemically Synthesized, pGX9382, 190

<400> 88

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

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

Tyr Tyr Cys Ala Lys Ser Gly Thr Gln Tyr Tyr Asp Thr Thr Gly Tyr
 115 120 125

Glu Tyr Arg Gly Leu Glu Tyr Phe Gly Tyr Trp Gly Gln Gly Thr Leu
 130 135 140

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

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

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

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

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

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

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

Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
 260 265 270

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser Gly Ala Tyr Gly

515

520

525

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 530 535 540

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 545 550 555 560

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

Ile Tyr Asp Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 580 585 590

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

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Arg Ser Arg
 610 615 620

Trp Thr Phe Gly Gln Gly Thr Lys Val 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> 89

<211> 1518

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX93100, 190.scFv_Fc.VH.G4S3.VL

<400> 89

atggattgga cctggagaat cctgttcctg gtggcagcag caaccggaac acacgcacag	60
gtgcagctgg tggagagcgg cggcggcgtg gtgcagccag gccgggtccct gaggctgtct	120
tgcgcagcaa gcggcttcac ctttagcaag tacggaatgc actgggtgag acaggcacct	180
ggcaagggcc tggagtgggt ggccgtgatc tcctatgagg gctctaaca gtactatgcc	240
gattccgtga agggcaggtt taccatcagc agagacaact ccaagaatac actgtacctg	300
cagatgaata gcctgagggc cgaggatacc gccgtgtact attgcgcaa gtccggcaca	360
cagtactatg acaccacagg ctacgagtat agaggcctgg agtacttcgg ctattggggc	420
cagggcaccc tggtgacagt gagctccggc ggccggcggct ccggcggcgg cggcagcggc	480
ggcggcggca gcgagatcgt gctgaccag tctcctggca cactgtctct gagcccagga	540
gagagggcca ccctgagctg tagagcctcc cagagcgtga gcagcagcta cctggcctgg	600
tatcagcaga agaggggaca ggccccacgc ctgctgatct acgacgcctc tagccggggc	660
accggcatcc ccgatcgctt cagcggctcc ggctctggca cagactttac cctgacaatc	720
tcccggctgg agcctgagga tttcgccgtg tactattgcc agcagtatgg caggagcaga	780
tggacctttg gccagggcac aaaggtggag atcaaggagc ccaagtcctg tgataagacc	840
cacacatgcc ctccctgtcc agcacctgag gcagccggcg gcccaagcgt gttcctgttt	900
ccaccaagc ctaaggatac actgatgatc tctagaacct ccgaggtgac atgcgtgggtg	960
gtggacgtga gccacgagga ccccaggtg aagttcaact ggtacgtgga cggcgtggag	1020
gtgcacaatg ccaagaccaa gccagggag gagcagtaca acagcaccta tagagtgggtg	1080
tccgtgctga cagtgtgca ccaggactgg ctgaacggca aggagtataa gtgcaaggtg	1140
tccaataagg ccctgccagc ccccatcgag aagaccatct ctaaggcaaa gggacagcca	1200

cgggagccac aggtgtacac actgcctcca tcccgcgagg agatgaccaa gaaccaggtg 1260
 tctctgacat gtctggtgaa gggcttctat ctttctgata tcgccgtgga gtgggagagc 1320
 aatggccagc cagagaacaa ttacaagacc acaccccctg tgctggactc tgatggcagc 1380
 ttctttctgt attccaagct gaccgtggac aagtctaggt ggcagcaggg caacgtgttt 1440
 tcctgctctg tgatgcacga ggccctgcac aatcactaca cccagaagag cctgtccctg 1500
 tctcctggca agtgataa 1518

<210> 90

<211> 504

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX93100, 190.scFv_Fc.VH.G4S3.VL

<400> 90

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

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

Tyr Tyr Cys Ala Lys Ser Gly Thr Gln Tyr Tyr Asp Thr Thr Gly Tyr
 115 120 125

Glu Tyr Arg Gly Leu Glu Tyr Phe Gly Tyr Trp Gly Gln Gly Thr Leu
130 135 140

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
145 150 155 160

Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
165 170 175

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
180 185 190

Val Ser Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Arg Gly Gln Ala
195 200 205

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

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
225 230 235 240

Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
245 250 255

Gly Arg Ser Arg Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
260 265 270

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
275 280 285

Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
290 295 300

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
305 310 315 320

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
325 330 335

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln

340

345

350

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 355 360 365

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 370 375 380

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 385 390 395 400

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
 405 410 415

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

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 435 440 445

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 450 455 460

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 465 470 475 480

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 485 490 495

Ser Leu Ser Leu Ser Pro Gly Lys
 500

<210> 91

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX93101, 190.scFv_Fc.VL.G4S3.VH

<400> 91

atggtgctgc agaccaggt gtttatctct ctgctgctgt ggatcagcgg agcatacgga

60

gagatcgtgc tgacccagtc tcctggcaca ctgtctctga gcccaggaga gagggccacc	120
ctgagctgta gaggctccca gagcgtgagc agcagctacc tggcctggta tcagcagaag	180
aggggacagg cccacgcct gctgatctac gacgcctcta gccgggccac cggcatcccc	240
gatcgcttca gcggctccgg ctctggcaca gactttaccc tgacaatctc ccggctggag	300
cctgaggatt tcgccgtgta ctattgccag cagtatggca ggagcagatg gacctttggc	360
cagggcacaa aggtggagat caagggcggc ggcggtccg gcggcggcgg cagcggcggc	420
ggcggcagcc aggtgcagct ggtggagagc ggcggcggcg tggcgcagcc aggccggtcc	480
ctgaggctgt cttgcgcagc aagcggcttc acctttagca agtacggaat gcaactgggtg	540
agacaggcac ctggcaaggg cctggagtgg gtggccgtga tctcctatga gggctctaac	600
aagtactatg ccgattccgt gaagggcagg tttaccatca gcagagacaa ctccaagaat	660
acactgtacc tgcagatgaa tagcctgagg gccgaggata ccgccgtgta ctattgcgcc	720
aagtccggca cacagtacta tgacaccaca ggctacgagt atagaggcct ggagtacttc	780
ggctattggg gccagggcac cctggtgaca gtgagctccg agcccaagtc ctgtgataag	840
accacacat gccctccctg tccagcacct gaggcagccg gcggcccaag cgtgttcctg	900
tttccacca agcctaagga tacactgatg atctctagaa ccccgagggt gacatgcgtg	960
gtggtggacg tgagccacga ggaccccgag gtgaagttca actggtacgt ggacggcgtg	1020
gaggtgcaca atgccaagac caagcccagg gaggagcagt acaacagcac ctatagagtg	1080
gtgtccgtgc tgacagtgtc gcaccaggac tggctgaacg gcaaggagta taagtgaag	1140
gtgtccaata aggccctgcc agccccatc gagaagacca tctctaaggc aaaggacag	1200
ccacgggagc cacaggtgta cacactgcct ccatcccgcg aggagatgac caagaaccag	1260
gtgtctctga catgtctggt gaagggcttc tatccttctg atatcgccgt ggagtgggag	1320
agcaatggcc agccagagaa caattacaag accacacccc ctgtgctgga ctctgatggc	1380
agcttctttc tgtattccaa gctgaccgtg gacaagtcta ggtggcagca gggcaacgtg	1440
ttttcctgct ctgtgatgca cgaggccctg cacaatcact acaccagaa gagcctgtcc	1500
ctgtctcctg gcaagtgata a	1521

<210> 92
 <211> 505
 <212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX93101, 190.scFv_Fc.VL.G4S3.VH

<400> 92

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

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

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

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

Pro Arg Leu Leu Ile Tyr Asp Ala Ser Ser Arg Ala Thr Gly Ile Pro
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 Arg Ser Arg Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
130 135 140

Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser
145 150 155 160

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

Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
180 185 190

Val Ile Ser Tyr Glu Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
195 200 205

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
210 215 220

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
225 230 235 240

Lys Ser Gly Thr Gln Tyr Tyr Asp Thr Thr Gly Tyr Glu Tyr Arg Gly
245 250 255

Leu Glu Tyr Phe Gly Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
260 265 270

Ser Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
275 280 285

Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
290 295 300

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
305 310 315 320

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
325 330 335

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
340 345 350

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
355 360 365

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
370 375 380

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
385 390 395 400

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met

405

410

415

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 435 440 445

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 450 455 460

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 465 470 475 480

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 485 490 495

Lys Ser Leu Ser Leu Ser Pro Gly Lys
 500 505

<210> 93

<211> 1527

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX93102, 190.scFv_Fc VH.Whitlow.VL

<400> 93

atggattgga cctggagaat cctgttcctg gtggcagcag caaccggaac acacgcacag 60

gtgcagctgg tggagagcgg cggcggcgtg gtgcagccag gccggtcctt gaggctgtct 120

tgcgcagcaa gcggcttcac ctttagcaag tacggaatgc actgggtgag acaggcacct 180

ggcaagggcc tggagtgggt ggccgtgata tcctatgagg gctctaaca gtactatgcc 240

gattccgtga agggcagggt taccatcagc agagacaact ccaagaatac actgtacctg 300

cagatgaata gcctgagggc cgaggatacc gccgtgtact attgcgcaa gtccggcaca 360

cagtactatg acaccacagg ctacgagtat agaggcctgg agtacttcgg ctattggggc 420

cagggcaccc tggtgacagt gagctccggc agcacctctg gctccggcaa gcccggtctt 480

ggcgagggca gcaccaaggg cgagatcgtg ctgacccagt ctcctggcac actgtctctg 540

agcccaggag agagggccac cctgagctgt agagcctccc agagcgtgag cagcagctac 600
 ctggcctggt atcagcagaa gaggggacag gccccacgcc tgctgatcta cgacgcctct 660
 agccggggcca ccggcatccc cgatcgcttc agcggctccg gctctggcac agactttacc 720
 ctgacaatct cccggctgga gcctgaggat ttcgccgtgt actattgcca gcagtatggc 780
 aggagcagat ggacctttgg ccagggcaca aaggtggaga tcaaggagcc caagtcctgt 840
 gataagaccc acacatgccc tccctgtcca gcacctgagg cagccggcgg cccaagcgtg 900
 ttcctgtttc cacccaagcc taaggataca ctgatgatct ctagaacccc cgaggtgaca 960
 tgcgtggtgg tggacgtgag ccacgaggac cccgagggtga agttcaactg gtacgtggac 1020
 ggcgtggagg tgcacaatgc caagaccaag cccagggagg agcagtacaa cagcacctat 1080
 agagtgggtgt ccgtgctgac agtgctgcac caggactggc tgaacggcaa ggagtataag 1140
 tgcaaggtgt ccaataaggc cctgccagcc cccatcgaga agaccatctc taaggcaaag 1200
 ggacagccac gggagccaca ggtgtacaca ctgcctccat cccgcgagga gatgaccaag 1260
 aaccaggtgt ctctgacatg tctggtgaag ggcttctatc cttctgatat cgccgtggag 1320
 tgggagagca atggccagcc agagaacaat tacaagacca caccctgtgt gctggactct 1380
 gatggcagct tctttctgta ttccaagctg accgtggaca agtctaggtg gcagcagggc 1440
 aacgtgtttt cctgctctgt gatgcacgag gccctgcaca atcactacac ccagaagagc 1500
 ctgtccctgt ctctggcaa gtgataa 1527

<210> 94

<211> 507

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX93102, 190.scFv_Fc VH.Whitlow.VL

<400> 94

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

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

Tyr Tyr Cys Ala Lys Ser Gly Thr Gln Tyr Tyr Asp Thr Thr Gly Tyr
 115 120 125

Glu Tyr Arg Gly Leu Glu Tyr Phe Gly Tyr Trp Gly Gln Gly Thr Leu
 130 135 140

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

Gly Glu Gly Ser Thr Lys Gly Glu Ile Val Leu Thr Gln Ser Pro Gly
 165 170 175

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
 180 185 190

Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Arg
 195 200 205

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

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 225 230 235 240

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
 245 250 255

Gln Gln Tyr Gly Arg Ser Arg Trp Thr Phe Gly Gln Gly Thr Lys Val
 260 265 270

Glu Ile Lys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
 275 280 285

Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro
 290 295 300

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 305 310 315 320

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
 325 330 335

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 340 345 350

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 355 360 365

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 370 375 380

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
 385 390 395 400

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
 405 410 415

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 420 425 430

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 435 440 445

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 450 455 460

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

465		470		475		480									
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr
				485					490				495		
Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys					
			500					505							

<210> 95
 <211> 1530
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Chemically Synthesized, pGX93103, 190.scFv_Fc.VL.Whitlow.VH

<400> 95
 atggtgctgc agaccaggt gtttatctct ctgctgctgt ggatcagcgg agcatcacgga 60
 gagatcgtgc tgaccagtc tcctggcaca ctgtctctga gcccaggaga gagggccacc 120
 ctgagctgta gagcctccca gagcgtgagc agcagctacc tggcctggta tcagcagaag 180
 aggggacagg cccacgcct gctgatctac gacgcctcta gccgggccac cggcatcccc 240
 gatcgcttca gcggctccgg ctctggcaca gactttaccc tgacaatctc ccggctggag 300
 cctgaggatt tcgccgtgta ctattgccag cagtatggca ggagcagatg gacctttggc 360
 cagggcacaa aggtggagat caagggcagc acctctggct ccggcaagcc cggctctggc 420
 gagggcagca ccaagggcca ggtgcagctg gtggagagcg gcggcggcgt ggtgcagcca 480
 ggccgggtccc tgaggctgtc ttgcgcagca agcggcttca cctttagcaa gtacggaatg 540
 cactgggtga gacaggcacc tggcaagggc ctggagtggg tggccgtgat ctctatgag 600
 ggctctaaca agtactatgc cgattccgtg aagggcaggt ttaccatcag cagagacaac 660
 tccaagaata cactgtacct gcagatgaat agcctgaggg ccgaggatac cgccgtgtac 720
 tattgcgcca agtccggcac acagtactat gacaccacag gctacgagta tagaggcctg 780
 gagtacttcg gctattgggg ccagggcacc ctggtgacag tgagctccga gcccgaagtcc 840
 tgtgataaga cccacacatg ccctccctgt ccagcacctg aggcagccgg cggcccaagc 900
 gtgttcctgt ttccaccaa gcctaaggat aactgatga tctctagaac ccccgaggtg 960
 acatgcgtgg tggtggacgt gagccacgag gaccccgagg tgaagttcaa ctggtacgtg 1020

gacggcgtgg aggtgcacaa tgccaagacc aagcccaggg aggagcagta caacagcacc 1080
 tatagagtgg tgtccgtgct gacagtgtg caccaggact ggctgaacgg caaggagtat 1140
 aagtgaagg tgtccaataa ggccctgcca gccccatcg agaagaccat ctctaaggca 1200
 aaggacagc cacgggagcc acaggtgtac acactgcctc catcccgcga ggagatgacc 1260
 aagaaccagg tgtctctgac atgtctggtg aagggttct atccttctga tatcgccgtg 1320
 gagtgggaga gcaatggcca gccagagaac aattacaaga ccacaccccc tgtgctggac 1380
 tctgatggca gcttcttct gtattccaag ctgaccgtgg acaagtctag gtggcagcag 1440
 ggcaacgtgt tttcctgctc tgtgatgcac gaggccctgc acaatcacta caccagaag 1500
 agcctgtccc tgtctcctgg caagtgataa 1530

<210> 96

<211> 508

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX93103, 190.scFv_Fc.VL.Whitlow.VH

<400> 96

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

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

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

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

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

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
325 330 335

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
340 345 350

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
355 360 365

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
370 375 380

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
385 390 395 400

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
405 410 415

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
420 425 430

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
435 440 445

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
450 455 460

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
465 470 475 480

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
485 490 495

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
500 505

<210> 97

<211> 2211

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX93134, 185

<400> 97

atggactgga cttggagaat cctgttcctg gtcgccgcag caaccgggac ccacgccgag	60
gtgcagctgg tgcagagcgg ggcagaagtg aagaagccag gcgagagcct gcggatctcc	120
tgtaagggca gcggctactc ctttacatct tattggatca cctgggtgcg ccagatgcca	180
ggcaagggcc tggagtggat ggccaagttc gacccttctg atagccagac aaactactcc	240
ccatcttttc agggccacgt gacaatcagc gtggacaaga gcatctccac cgcctatctg	300
cagtggagct ccctgaaggc ctccgatacc gccatgtact attgcgccag gagatactgt	360
tctagctcct cttgctatgt ggacaattgg ggccagggca cactggtgac catcttctct	420
gccagcacia agggaccaag cgtgtttcca ctggcaccca gctccaagtc cacatctggc	480
ggcaccgccg ccctgggatg tctggtgaag gattacttcc ccgagcctgt gaccgtgagc	540
tggaactccg gcgccctgac aagcggagtg cacacctttc cagccgtgct gcagtctagc	600
ggcctgtact ccctgtcctc tgtggtgaca gtgcctagct cctctctggg cacacagacc	660
tatatctgta acgtgaatca caagccttcc aataccaagg tggacaagaa ggtggagcca	720
aagtcttgcg ataagacaca cacctgccct ccctgtccag caccagaggc agccggcgga	780
ccatccgtgt tcctgtttcc acccaagcct aaggacaccc tgatgatcag caggacacca	840
gaggtgacct gcgtgggtgt ggacgtgtcc cacgaggacc ccgaggtgaa gttcaactgg	900
tacgtggatg gcgtggaggt gcacaatgcc aagacaaagc caagggagga gcagtacaac	960
tctacatata gagtggtag cgtgctgacc gtgctgcacc aggactggct gaacggcaag	1020
gagtataagt gtaaggtgtc taataaggcc ctgcctgccc caatcgagaa gacaatcagc	1080
aaggcaaagg gacagcctcg ggagccacag gtgtacaccc tgcctccatc tcgcgacgag	1140
ctgacaaaga accaggtgag cctgacctgc ctggtgaagg gcttttatcc ctccgatatc	1200
gccgtggagt gggagtctaa tggccagcct gagaacaatt acaagaccac acccctgtg	1260
ctggactctg atggcagctt ctttctgtat agcaagctga ccgtggacaa gtcccgggtg	1320
cagcagggca acgtgttcag ctgttcctg atgcacgagg ccctgcacaa tcactacaca	1380
cagaagtctc tgagcctgtc ccctggcaag aggggaagaa agcggcgctc tggcagcgga	1440
gcaaccaact ttagcctgct gaagcaggca ggcgatgtgg aggagaatcc aggacctatg	1500

gtgctgcaga cacaggtggt catctccctg ctgctgtgga tctctggcgc ctacggcagc 1560
 tcctatgagc tgaccagacc accctccgtg tctgtgagcc ctggccagac agcaaggatc 1620
 acctgcagcg gcgacgcact gccaaacaag tttgcctact ggtatagaca gaagtccgga 1680
 caggcacccg tgctgggtcat ctacgaggat aataagcggc cctctggcat ccctgagagg 1740
 ttcagcggct ctagctccgg cacaatggcc aactgacca tctccggagc acaggtggag 1800
 gacgaggcag attaccactg ttattctacc gactctagct ccaaccctct gggcgtgttc 1860
 ggcggcggaa caaagctgac cgtgctggga cagccaaagg cagcaccaag cgtgaccctg 1920
 tttcctccat ctagcgagga gctgcaggcc aataaggcca cactggtgtg cctgatctcc 1980
 gacttctacc ctggagcagt gaccgtggca tggaaggccg attcctctcc agtgaaggcc 2040
 ggcgtggaga caacaacccc ctccaagcag tctaacaata agtacgccgc cagctcctat 2100
 ctgagcctga cccagagca gtggaagtcc cacaggctct attcttgtca ggtcacccat 2160
 gaaggctcaa cagtggagaa aacagtcgcc cctacagaat gctcatgata a 2211

<210> 98

<211> 735

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX93134, 185

<400> 98

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 Gln Ser Gly Ala Glu Val Lys Lys
 20 25 30

Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe
 35 40 45

Thr Ser Tyr Trp Ile Thr Trp Val Arg Gln Met Pro Gly Lys Gly Leu
 50 55 60

Glu Trp Met Ala Lys Phe Asp Pro Ser Asp Ser Gln Thr Asn Tyr Ser
 65 70 75 80

Pro Ser Phe Gln Gly His Val Thr Ile Ser Val 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 Arg Tyr Cys Ser Ser Ser Ser Cys Tyr Val Asp
115 120 125

Asn Trp Gly Gln Gly Thr Leu Val Thr Ile Phe 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

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

Ala Ala 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
 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 Ser Ser Tyr Glu Leu Thr Gln Pro Pro
515 520 525

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

Asp Ala Leu Pro Asn Lys Phe Ala Tyr Trp Tyr Arg Gln Lys Ser Gly
545 550 555 560

Gln Ala Pro Val Leu Val Ile Tyr Glu Asp Asn Lys Arg Pro Ser Gly
565 570 575

Ile Pro Glu Arg Phe Ser Gly Ser Ser Ser Gly Thr Met Ala Thr Leu
580 585 590

Thr Ile Ser Gly Ala Gln Val Glu Asp Glu Ala Asp Tyr His Cys Tyr
595 600 605

Ser Thr Asp Ser Ser Ser Asn Pro Leu Gly Val Phe Gly Gly Gly Thr
610 615 620

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

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

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

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

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

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

Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser

<210> 99

<211> 1497

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX93129, 185.scFv_Fc.VH.G4S3.VL

<400> 99

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gtgcagctgg tgcagtctgg agccgaagtg aagaagccag gcgagtctct gagaatcagc	120
tgcaagggca gcggtacttc tttcacatcc tactggatca cctgggtgcg ccagatgcca	180
ggcaagggcc tggagtggat ggccaagtgc gacccatctg atagccagac aaactacagc	240
ccctccttcc agggccacgt gacaatctcc gtggacaagt ccatcagcac agcctatctg	300
cagtggctct ccctgaaggc ctctgacacc gccatgtact attgcgcccc gagatattgc	360
agctcttcca gctgttacgt ggacaactgg ggccagggca ccctgggtgac aatcttctct	420
ggcggcgggcg gctctggcgg cggcggcagc ggcggcgggcg gctccagctc ctatgagctg	480
accagcccc catccgtgag cgtgtctcca ggccagacag cccggatcac atgtagcggc	540
gacgccctgc ctaataagtt tgcctactgg tacaggcaga agagcggcca ggccccagtg	600
ctggtaatct acgaggacaa caagcgccca tctggcatcc ccgagagatt ttctggctct	660
tccagcggca ccatggccac cctgacaatc tccggcgccc aggtggagga tgaggccgat	720
tatcactgct acagcacaga ttccagctcc aatcccctgg gcgtgtttgg cggcggcacc	780
aagctgaccg tgctggagcc aaagagctcc gataagacc acacctgtcc accttgcccc	840
gccccagagg ccgccggcgg cccaagcgtg ttctgtttcc cacctaagcc caaggacacc	900
ctgatgatct ccagaacccc tgaggtgaca tgcgtggtgg tggacgtgtc tcacgaggac	960
ccagaggtga agttcaactg gtatgtggac ggcgtggagg tgcacaacgc caagacaaag	1020
cctagagagg agcagtacaa cagcacctac agagtgggtg ctgtgctgac agtgctgcac	1080
caggactggc tgaacggcaa ggagtacaag tgtaaggtgt ccaataaggc cctgccagcc	1140
cctatcgaga agaccatctc taaggccaag ggccagccaa gagagccaca ggtgtatacc	1200
ctgccaccct ctagagacga gctgacaaag aaccaggtgt ctctgacatg tctggtgaag	1260

ggcttctacc cctctgatat cgccgtggag tgggagtcta atggccagcc agagaataac 1320
tacaagacca caccacctgt gctggactcc gatggcagct ttttcctgta cagcaagctg 1380
acagtggata agtccagatg gcagcagggc aacgtgttta gctgctccgt gatgcacgaa 1440
gcactgcaca accactacac ccagaagtcc ctgagcctgt caccggcaa gtgataa 1497

<210> 100

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX93129, 185.scFv_Fc.VH.G4S3.VL

<400> 100

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 Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe
35 40 45

Thr Ser Tyr Trp Ile Thr Trp Val Arg Gln Met Pro Gly Lys Gly Leu
50 55 60

Glu Trp Met Ala Lys Phe Asp Pro Ser Asp Ser Gln Thr Asn Tyr Ser
65 70 75 80

Pro Ser Phe Gln Gly His Val Thr Ile Ser Val 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 Arg Tyr Cys Ser Ser Ser Ser Cys Tyr Val Asp
115 120 125

Asn Trp Gly Gln Gly Thr Leu Val Thr Ile Phe Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Ser Tyr Glu Leu
 145 150 155 160

Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln Thr Ala Arg Ile
 165 170 175

Thr Cys Ser Gly Asp Ala Leu Pro Asn Lys Phe Ala Tyr Trp Tyr Arg
 180 185 190

Gln Lys Ser Gly Gln Ala Pro Val Leu Val Ile Tyr Glu Asp Asn Lys
 195 200 205

Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Ser Ser Gly Thr
 210 215 220

Met Ala Thr Leu Thr Ile Ser Gly Ala Gln Val Glu Asp Glu Ala Asp
 225 230 235 240

Tyr His Cys Tyr Ser Thr Asp Ser Ser Ser Asn Pro Leu Gly Val Phe
 245 250 255

Gly Gly Gly Thr Lys Leu Thr Val Leu Glu Pro Lys Ser Ser Asp Lys
 260 265 270

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro
 275 280 285

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 290 295 300

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 305 310 315 320

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 325 330 335

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 340 345 350

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu

355

360

365

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 370 375 380

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 385 390 395 400

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
 405 410 415

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

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
 435 440 445

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 450 455 460

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 465 470 475 480

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 485 490 495

Lys

<210> 101

<211> 1500

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX93130, 185.scFv_Fc.VL.G4S3.VH

<400> 101

atggtcctgc agactcaggt gtttatttca ctgctgctgt ggatttccgg cgcttatggg 60

tcatcttacg aactgactca gcctccttcc gtgagcgtgt ctccaggcca gacagccaga 120

atcacatgct ccggcgacgc cctgccaaac aagtttgcct actggtatag gcagaagtcc 180

ggccaggccc cagtgtggt aatctatgag gacaacaagc ggccaagcgg catcccagag	240
cggtttagcg gctccagctc tggcaccatg gccaccctga caatctccgg cgcccagggtg	300
gaggatgagg ccgattatca ctgttactcc acagatagct cctccaatcc actgggcgtg	360
ttcggcggcg gcaccaagct gaccgtgctg ggcggcggcg gctccggcgg cggcggctct	420
ggcggcggcg gctccgaggt gcagctggtg cagtctggcg ccgaggtgaa gaagccaggc	480
gagtcctgc gcatcagctg caagggctct ggctatagct tcacaagcta ctggatcacc	540
tgggtgcggc agatgccagg caagggcctg gagtggatgg ccaagtttga cccctctgat	600
agccagacca attactctcc cagcttccag ggccacgtga caatcagcgt ggacaagtcc	660
atcagcacag cctacctgca gtggtctagc ctgaaggcca gcgatacagc catgtattat	720
tgcgcccggg gatactgttc cagctctagc tgttacgtgg acaattgggg ccagggcaca	780
ctggtgacaa tcttttccga gccaaagtct tccgataaga cccacacctg tccaccctgt	840
cctgccccag aggccgccgg cggccccagc gtgttcctgt ttcctccaaa gccaaggac	900
accctgatga tctccagaac accagagggtg acctgcgtgg tggaggacgt gtctcacgag	960
gaccagagg tgaagtttaa ctggtacgtg gacggcgtgg aggtgcacaa cgccaagaca	1020
aagcctagag aggagcagta caatagcacc tacagagtgg tgtctgtgct gacagtgtg	1080
caccaggatt ggctgaacgg caaggagtac aagtgtgaagg tgtccaataa ggccctgccc	1140
gcccctatcg agaagaccat ctctaaggcc aagggccagc ctagagagcc acagggtgtat	1200
acactgcccc catccaggga cgagctgacc aagaaccagg tgtccctgac atgtctggtg	1260
aagggttttt accctagcga tatcgccgtg gagtgggagt ctaacggcca gcctgagaat	1320
aactacaaga ccacaccacc tgtgctggac tctgacggca gctttttcct gtacagcaag	1380
ctgacagtgg acaagagcag gtggcagcag ggcaacgtgt tcagctgctc cgtgatgcac	1440
gaagcactgc acaaccacta cactcagaaa tccctgtcac tgtcccctgg aaaatgataa	1500

<210> 102

<211> 498

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX93130, 185.scFv_Fc.VL.G4S3.VH

<400> 102

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

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

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

Pro Asn Lys Phe Ala Tyr Trp Tyr Arg Gln Lys Ser Gly Gln Ala Pro
 50 55 60

Val Leu Val Ile Tyr Glu Asp Asn Lys Arg Pro Ser Gly Ile Pro Glu
 65 70 75 80

Arg Phe Ser Gly Ser Ser Ser Gly Thr Met Ala Thr Leu Thr Ile Ser
 85 90 95

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

Ser Ser Ser Asn Pro Leu Gly Val Phe Gly Gly Gly Thr Lys Leu Thr
 115 120 125

Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 130 135 140

Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
 145 150 155 160

Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser
 165 170 175

Tyr Trp Ile Thr Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp
 180 185 190

Met Ala Lys Phe Asp Pro Ser Asp Ser Gln Thr Asn Tyr Ser Pro Ser
 195 200 205

Phe Gln Gly His Val Thr Ile Ser Val Asp Lys Ser Ile Ser Thr Ala

210

215

220

Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr
 225 230 235 240

Cys Ala Arg Arg Tyr Cys Ser Ser Ser Ser Cys Tyr Val Asp Asn Trp
 245 250 255

Gly Gln Gly Thr Leu Val Thr Ile Phe Ser Glu Pro Lys Ser Ser Asp
 260 265 270

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
 275 280 285

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 290 295 300

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 305 310 315 320

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 325 330 335

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 340 345 350

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

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 370 375 380

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 385 390 395 400

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 405 410 415

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

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
435 440 445

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
450 455 460

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
465 470 475 480

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
485 490 495

Gly Lys

<210> 103

<211> 1506

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX93131, 185.scFv_Fc VH.Whitlow.VL

<400> 103

atggactgga catggagaat cctgttcctg gtcgccgccg ctaccgggac ccacgcagaa	60
gtgcagctgg tgcagagtgg agccgaagtg aagaagccag gcgagtctct gagaatcagc	120
tgcaagggca gcggctattc ctttacaagc tactggatca cctgggtgcg gcagatgccc	180
ggcaagggcc tggagtggat ggccaagttc gatccatccg atagccagac caattacagc	240
ccttctttcc agggccacgt gacaatctcc gtggacaagt ccatcagcac agcctacctg	300
cagtggtcct ctctgaaggc cagcgacacc gccatgtact actgtgcccc gagatattgc	360
tcctcttcca gctgctatgt ggacaattgg ggccagggca ccctggtgac catcttcagc	420
ggctctacaa gcggctctgg caagccaggc tctggcgagg gctctaccaa gggctccagc	480
tatgagctga cccagcctcc atccgtgagc gtgtccccag gccagacagc cagaatcacc	540
tgtagcggcg acgccctgcc taacaagttt gcctactggt ataggcagaa gtctggccag	600
gccctgtgc tggtaatcta cgaggataac aagaggccat ccggcatccc tgagagattt	660
tctggctcct ctagcggcac catggccacc ctgacaatct ctggcgccca ggtggaggat	720

gaggccgact accactgcta ctccacagac tcttccagca accctctggg cgtgttcggc 780
 ggccggcacca agctgacagt gctggagccc aagagctctg acaagacca cacctgccct 840
 ccatgtccag cccagaggc cgccggcggc ccaagcgtgt tcctgtttcc acctaagcca 900
 aaggacaccc tgatgatctc tcggacccca gaggtgacat gcgtgggtggg ggacgtgtcc 960
 cacgaggacc ctgaggtgaa gtttaattgg tatgtggatg gcgtggaggt gcacaatgcc 1020
 aagaccaagc cacgggagga gcagtataac agcacctaca gagtggtgtc tgtgctgacc 1080
 gtgctgcacc aggactggct gaacggcaag gagtacaagt gtaaggtgtc caacaaggcc 1140
 ctgcccggcc ctatcgagaa gaccatctct aaggccaagg gccagccaag agagccacag 1200
 gtgtataccc tgccaccctc cagagatgag ctgacaaaga atcaggtgtc tctgacctgt 1260
 ctggtgaagg gcttctaccc aagcgatata gccgtggagt gggagtctaa cggccagcct 1320
 gagaacaact ataagaccac acctcccgtg ctggattccg acggctcttt cttcctgtac 1380
 agcaagctga ccgtggataa gagcagatgg cagcagggca acgtgttctc ctgtagcgtg 1440
 atgcacgaag cactgcacaa ccattacacc cagaagtccc tgagcctgag ccctggcaaa 1500
 tgataa 1506

<210> 104

<211> 500

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX93131, 185.scFv_Fc VH.Whitlow.VL

<400> 104

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 Gln Ser Gly Ala Glu Val Lys Lys
 20 25 30

Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe
 35 40 45

Thr Ser Tyr Trp Ile Thr Trp Val Arg Gln Met Pro Gly Lys Gly Leu
 50 55 60

Glu Trp Met Ala Lys Phe Asp Pro Ser Asp Ser Gln Thr Asn Tyr Ser
65 70 75 80

Pro Ser Phe Gln Gly His Val Thr Ile Ser Val 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 Arg Tyr Cys Ser Ser Ser Ser Cys Tyr Val Asp
115 120 125

Asn Trp Gly Gln Gly Thr Leu Val Thr Ile Phe Ser Gly Ser Thr Ser
130 135 140

Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Ser Ser
145 150 155 160

Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln Thr
165 170 175

Ala Arg Ile Thr Cys Ser Gly Asp Ala Leu Pro Asn Lys Phe Ala Tyr
180 185 190

Trp Tyr Arg Gln Lys Ser Gly Gln Ala Pro Val Leu Val Ile Tyr Glu
195 200 205

Asp Asn Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Ser
210 215 220

Ser Gly Thr Met Ala Thr Leu Thr Ile Ser Gly Ala Gln Val Glu Asp
225 230 235 240

Glu Ala Asp Tyr His Cys Tyr Ser Thr Asp Ser Ser Ser Asn Pro Leu
245 250 255

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

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala

275

280

285

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 290 295 300

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 305 310 315 320

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 325 330 335

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 340 345 350

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

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 370 375 380

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 385 390 395 400

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 405 410 415

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

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 435 440 445

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 450 455 460

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 465 470 475 480

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 485 490 495

Ser Pro Gly Lys
500

<210> 105
<211> 1509
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, pGX93132, 185.scFv_Fc.VL.Whitlow.VH

<400> 105
atggtcctgc agactcaggt gtttatttca ctgctgctgt ggatttccgg ggcatacggg 60
tcctcatagc aactgactca gcctcccagc gtgtccgtgt ctctggcca gaccgccagg 120
atcacctgca gcggcgatgc cctgccaaac aagttcgcct attggtacag gcagaagtcc 180
ggccaggccc cagtgtggt aatctacgag gacaataagc ggcttcttg catccctgag 240
aggttcagcg gctcttcctc tggcacaatg gccacactga ccatctctgg cgcccagggtg 300
gaggatgagg ccgactacca ctgctacagc accgattcct ctagcaatcc tctgggcgtg 360
tttggcggcg gcaccaagct gacagtgtg ggctccacct ctggctccgg caagccaggc 420
tctggcgagg gctctacaaa gggcgagggtg cagctgggtgc agtccggcgc cgagggtgaag 480
aagcctggcg agtctctgcg gatcagctgc aagggcagcg gctactcctt cacctcttac 540
tggatcacct ggggtgcggca gatgccaggc aagggcctgg agtggatggc caagttcgac 600
cctagcgaca gccagaccaa ctacagccct tcttttcagg gccacgtgac aatcagcgtg 660
gataagtcta tctccaccgc ctatctgcag tggagctccc tgaaggcctc tgataccgcc 720
atgtattact gcgccagacg ctactgttct agcagctcct gctatgtgga caactggggc 780
cagggcacac tggtgaccat cttcagcgag cctaagagct ccgataagac ccacacctgc 840
cctccctgcc cagccccga ggccgccggc ggcccatccg tgtttctgtt ccctccaaag 900
cccaaggata ccctgatgat cagccgcacc cctgagggtga catgcgtggt ggtggacgtg 960
tctcacgagg acccagaggt gaagttcaac tggtagtggt atggcgtgga ggtgcacaat 1020
gccaagacca agcccagaga ggagcagtac aattccacct acagagtgggt gtctgtgctg 1080
accgtgctgc accaggattg gctgaacggc aaggagtaca agtgtaaggt gtccaataag 1140
gccctgccag ccccatcga gaagaccatc agcaaggcca agggccagcc aagagagcct 1200

Val Leu Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly
130 135 140

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

Lys Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser
165 170 175

Phe Thr Ser Tyr Trp Ile Thr Trp Val Arg Gln Met Pro Gly Lys Gly
180 185 190

Leu Glu Trp Met Ala Lys Phe Asp Pro Ser Asp Ser Gln Thr Asn Tyr
195 200 205

Ser Pro Ser Phe Gln Gly His Val Thr Ile Ser Val Asp Lys Ser Ile
210 215 220

Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala
225 230 235 240

Met Tyr Tyr Cys Ala Arg Arg Tyr Cys Ser Ser Ser Ser Cys Tyr Val
245 250 255

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

Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
275 280 285

Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
290 295 300

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
305 310 315 320

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
325 330 335

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser

340

345

350

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 355 360 365

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
 370 375 380

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 385 390 395 400

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
 405 410 415

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

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 435 440 445

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
 450 455 460

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
 465 470 475 480

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 485 490 495

Leu Ser Pro Gly Lys
 500

<210> 107

<211> 1497

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX93141, DVSF3 LALA scFv-Fc VH.G4S3.VL

<400> 107

atggactgga cttggagaat cctgtttctg gtcgcagcag ccactggaac ccacgccgag

60

gtgcagctgg	tcgagagcgg	gggaggcctg	gtgcagccag	gcagatccct	gaggctgtct	120
tgtgccgcct	ctggcttcac	atttgatgac	tacgccatgt	tctgggtgcg	gcaggcccca	180
ggcaagggcc	tggagtggat	ctccggcatc	agctggaact	ctgccaccat	cggctatgcc	240
gactccgtga	agggcaggtt	caccatctcc	cgggacaatg	ccaagaagtc	tctggacctg	300
cagatgaaca	gcctgagacc	cgacgatacc	gccctgtact	attgtgcca	gggcggccca	360
agaggcctgc	agctgctgtc	ctcttgggtg	gattactggg	gccagggcac	cctggtgaca	420
gtgtcttccg	gcggcggcgg	ctctggcggc	ggcggcagcg	gcggcggcgg	ctccgatatc	480
cagatgaccc	agtctccctc	ttccctgagc	gcctccgtgg	gcgatcgggt	gacaatcacc	540
tgcagagcca	gccaggatat	ccggagatac	ctgaactggt	accagcagag	gcctggcaga	600
tgccacagc	tgctgatcta	caccacatcc	accctgcagt	ctggcgtgcc	aagcagattt	660
tccggcagcg	gctccgtgac	agacttcacc	ctgacaatct	ccagcctgca	gccagaggat	720
ttcggcacat	attactgcca	gcagagctac	tccccacctc	acacctttgg	ccagggcaca	780
aagctggaga	tcaaggagcc	caagtcttcc	gacaagaccc	acacctgtcc	accttgtccc	840
gccccagagg	ccgccggcgg	ccctagcgtg	tttctgttcc	ctccaaagcc	taaggatacc	900
ctgatgatct	ccagaacccc	agaggtgaca	tgcgtgggtg	tggacgtgtc	tcacaggagc	960
cccgaggtga	agtttaactg	gtacgtggat	ggcgtggagg	tgcacaatgc	caagaccaag	1020
ccaagggagg	agcagtacaa	cagcacctac	agagtgggtg	ccgtgctgac	agtgtgtcac	1080
caggactggc	tgaatggcaa	ggagtataag	tgcaaggtgt	ccaacaaggc	cctgccagcc	1140
cccatcgaga	agaccatcag	caaggccaag	ggccagccta	gggagccaca	ggtgtacacc	1200
ctgccaccct	ccagagacga	gctgacaaa	aatcaggtgt	ctctgacatg	cctggtgaag	1260
ggcttctacc	cttccgacat	cgccgtggag	tgggagtcta	acggccagcc	cgagaacaat	1320
tacaagacca	caccacctgt	gctggactcc	gatggcagct	tcttcctgta	tagcaagctg	1380
accgtggata	agtctagatg	gcagcagggc	aacgtgttct	cctgttccgt	gatgcacgaa	1440
gcactgcaca	accactacac	tcagaagagc	ctgtccctgt	cccctggaaa	atgataa	1497

<210> 108

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX93141, DVSF3 LALA scFv-Fc VH.G4S3.VL

<400> 108

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

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 Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
145 150 155 160

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
165 170 175

Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg Arg Tyr Leu Asn
180 185 190

Trp Tyr Gln Gln Arg Pro Gly Arg Val Pro Gln Leu Leu Ile Tyr Thr

195

200

205

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

Ser Val Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
 225 230 235 240

Phe Gly Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Pro Pro His Thr Phe
 245 250 255

Gly Gln Gly Thr Lys Leu Glu Ile Lys Glu Pro Lys Ser Ser Asp Lys
 260 265 270

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro
 275 280 285

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 290 295 300

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 305 310 315 320

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 325 330 335

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 340 345 350

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 355 360 365

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 370 375 380

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 385 390 395 400

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
 405 410 415

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

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
435 440 445

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
450 455 460

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
465 470 475 480

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
485 490 495

Lys

<210> 109
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Chemically Synthesized

<400> 109

Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
1 5 10 15

Lys Gly

<210> 110
<211> 2199
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, gene optimized anti-RSV, pGX9368

<400> 110
atggactgga catggagaat cctgttcctg gtggcagcag caaccggaac acacgcacag 60

gtgaccctga gagagtccgg accagccctg gtgaagccaa cccagacact gaccctgaca	120
tgcaccttct ccggcttttc tctgagcacc tccggcatgt ctgtgggatg gatcaggcag	180
ccccctggca aggccctgga gtggctggcc gacatctggt gggacgataa gaaggattac	240
aaccctagcc tgaagtcccg cctgacaatc agcaaggaca cctccaagaa ccagggtggtg	300
ctgaaggtga caaatatgga cccagccgat acagccacct actattgcg cggagcatg	360
atcaccaatt ggtatttcga cgtgtggggc gccggaacca cagtgcaggt gagctccgcc	420
tccaccaagg gaccaagcgt gttcccactg gcaccctcta gcaagtctac aagcggcggc	480
accgccgccc tgggatgtct ggtgaaggac tacttccccg agcctgtgac cgtgtcttgg	540
aacagcggcg ccctgacatc cggagtgcac acctttccag ccgtgctgca gtcctctggc	600
ctgtacagcc tgagctccgt ggtgacagtg ccctctagct ccctgggcac acagacctat	660
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agctgtgata agacacacac ctgcccaccc tgtccagcac cagagctgct gggcggccct	780
agcgtgttcc tgtttctctc aaagccaaag gacaccctga tgatctccag aacacctgag	840
gtgacctgcg tgggtggtgga cgtgtctcac gaggaccccc aggtgaagtt caactggtac	900
gtggatggcg tggaggtgca caatgccaa accaagcctc gggaggagca gtacaacagc	960
acatatagag tgggtgtccgt gctgaccgtg ctgcaccagg attggctgaa cggcaaggag	1020
tataagtgca aggtgtccaa taaggccctg cctgccccaa tcgagaagac aatcagcaag	1080
gccaagggcc agcctaggga gccacaggtg tacaccctgc cccctagccg cgacgagctg	1140
acaaagaacc aggtgtccct gacctgtctg gtgaagggct tctatccatc tgatatcgcc	1200
gtggagtggg agagcaatgg ccagcccgag aacaattaca agaccacacc acccgtgctg	1260
gactccgatg gctctttctt tctgtattcc aagctgaccg tggacaagtc taggtggcag	1320
cagggaacg tgttttcctg ttctgtgatg cacgaggccc tgcacaatca ctacacacag	1380
aagagcctgt ccctgtctcc aggcaagagg ggaaggaagc ggagaagcgg ctccggagca	1440
accaacttct ccctgctgaa gcaggcaggc gatgtggagg agaattccagg acctatggtg	1500
ctgcagaccc aggtgtttat ctctctgctg ctgtggatca gcggcgcccta cggcgacatc	1560
cagatgacac agtctccaag caccctgtcc gcctctgtgg gcgatagggt gacaatcacc	1620
tgcaagtgtc agctgagcgt gggctacatg cactggatatc agcagaagcc cggcaaggcc	1680

cctaagctgc tgatctacga cacctctaag ctggcaagcg gagtgcctc ccgcttcagc 1740
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gccacctact attgctttca gggcagcggc tatcccttca ccttcggcgg cggcaccaag 1860
ctggagatca agcggacagt ggccgcccc agcgtgttca tctttcctcc atccgacgag 1920
cagctgaagt ctggcaccgc cagcgtggtg tgcctgctga acaatttcta ccctagagag 1980
gccaaggtgc agtgaaggt ggataacgcc ctgcagagcg gcaattccca ggagtctgtg 2040
acagagcagg acagcaagga ttccacctat tctctgtcct ctacactgac cctgtccaag 2100
gccgattacg agaagcaca ggtgtatgcc tgcgaggtga cacaccaggg cctgagctcc 2160
cctgtgacca agagctttaa cagaggcgag tgttgataa 2199

<210> 111
<211> 731
<212> PRT
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, gene optimized anti-RSV, pGX9368

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

Pro Thr Gln Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu
35 40 45

Ser Thr Ser Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys
50 55 60

Ala Leu Glu Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr
65 70 75 80

Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys
85 90 95

Asn Gln Val Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala

100	105	110
Thr Tyr Tyr Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val		
115	120	125
Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala 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 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 Val Glu Pro Lys		
225	230	235
240		
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu		
245	250	255
Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr		
260	265	270
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val		
275	280	285
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val		
290	295	300
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser		
305	310	315
320		

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
325 330 335

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
340 345 350

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

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

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
385 390 395 400

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
405 410 415

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

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
435 440 445

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

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

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

Gly Pro Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp
500 505 510

Ile Ser Gly Ala Tyr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Thr
515 520 525

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Cys Gln

530

535

540

Leu Ser Val Gly Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala
 545 550 555 560

Pro Lys Leu Leu Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro
 565 570 575

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile
 580 585 590

Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly
 595 600 605

Ser Gly Tyr Pro Phe 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> 112

<211> 1485

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, scFv-Fc anti-RSV, pGX9369

<400> 112

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gacattcaga tgaccagag cccttcaaca ctgtccgcca gcgtgggcga cagagtgaca	120
atcacctgta agtgccagct gagcgtgggc tatatgcact ggtatcagca gaagcctggc	180
aaggcccaa agctgctgat ctatgacacc agcaagctgg cctctggcgt gccatccaga	240
ttctccggct ctggcagcgg caccgagttt aactgacca tctccagcct gcagccagat	300
gacttcgcca cctactattg cttccagggc agcggctatc cttcacctt tggcggcggc	360
acaaagctgg agatcaaggg cggcggcggc tccggcggcg gcggctctgg cggcggcggc	420
tctcaggtga ccctgagaga gtccggccca gccctggtga agccaacca gaccctgaca	480
ctgacatgca ctttctccgg cttcagcctg tccaccagcg gcatgtccgt gggctggatc	540
aggcagcccc caggcaaggc cctggagtgg ctggccgata tctggtggga cgataagaag	600
gactacaacc cctccctgaa gagcagactg accatcagca aggataccag caagaaccag	660
gtggtgctga aggtgacaaa tatggacca gccgataccg ccacatacta ctgtgccaga	720
tccatgatca caaattggta cttcgacgtg tggggcgccg gcacaaccgt gacagtgagc	780
tctgagccaa agtcctgcga caagaccac acctgtcctc cttgtccagc ccccgagctg	840
ctgggcggcc caagcgtgtt cctgtttccc cctaagccaa aggataccct gatgatctcc	900
agaaccccag aggtgacatg cgtggtggtg gacgtgagcc acgaggacc cggagtgaag	960
ttcaattggg acgtggatgg cgtggaggtg cacaatgcca agaccaagcc aagagaggag	1020
cagtataact ctacatatcg cgtggtgtcc gtgctgacag tgctgcacca ggactggctg	1080
aatggcaagg agtacaagtg caaggtgtcc aataaggccc tgccagcccc tatcgagaag	1140
acaatctcca aggccaaggg ccagcccaga gagccacagg tgtatacact gccaccctcc	1200
agagatgagc tgacaaagaa tcaggtgtcc ctgacatgtc tggagaaggg cttttatccc	1260
tccgatatcg ccgtggagtg ggagtctaata ggccagcccg agaataacta taagacaacc	1320
cctccagtgc tggactccga tggctccttt ttcctgtatt ccaagctgac cgtggataag	1380
agcaggtggc agcagggcaa cgtgttctct tgttccgtga tgcacgaagc actgcacaac	1440

cactacaccc agaagtcact gtcactgtca ccaggaaaat gataa

1485

<210> 113

<211> 493

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, scFv-Fc anti-RSV, pGX9369

<400> 113

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 Thr Leu Ser
20 25 30

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

Val Gly Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
50 55 60

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

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

Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly
100 105 110

Tyr Pro Phe Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Thr
130 135 140

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

Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser Gly Met Ser

165

170

175

Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu Trp Leu Ala
 180 185 190

Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser Leu Lys Ser
 195 200 205

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

Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr Cys Ala Arg
 225 230 235 240

Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr
 245 250 255

Val Thr Val Ser Ser Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
 260 265 270

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
 275 280 285

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 290 295 300

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
 305 310 315 320

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
 325 330 335

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

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 355 360 365

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
 370 375 380

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

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
405 410 415

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
420 425 430

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
435 440 445

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
450 455 460

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
465 470 475 480

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
485 490

<210> 114

<211> 2199

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, gene optimized anti-RSV, pGX9370

<400> 114

atggactgga cctggagaat cctgttcctg gtggcagcag caaccggaac acacgcacag	60
gtgacactga gggagagcgg acctgccctg gtgaagccaa cccagacact gaccctgaca	120
tgcaccttct ctggcttttc cctgtctacc agcggcatga gcgtgggatg gatcaggcag	180
ccccctggca aggccctgga gtggctggcc gacatctggg gggacgataa gaaggattac	240
aaccctctc tgaagagccg cctgaccatc agcaaggata catccaagaa ccaggtgggtg	300
ctgaagggtga ccaatatgga ccctgccgat acagccacct actattgtgc ccggagcatg	360
atcaccaatt ggtactttga cgtgtggggc gccggcacca cagtgacagt gagctccgcc	420
aagaccacag ccccttcctg gtatcctctg gccccagtgt gcggcgatac cacaggctct	480

agcgtgaccc tgggctgtct ggtgaagggc tacttcccag agcccgtgac actgacctgg	540
aactccggct ctctgtcctc tggcgtgcac acctttccag ccgtgctgca gagcgacctg	600
tacacactga gctcctctgt gacagtgacc agctccacct ggccaagcca gtccatcaca	660
tgcaacgtgg cccaccccg cctctagcacc aagggtggata agaagatcga gcccagaggc	720
cctacaatca agccctgtcc accctgcaag tgtcctgccc caaatctgct gggcggccct	780
tccgtgttca tctttcctcc aaagatcaag gacgtgctga tgatctctct gagccctatc	840
gtgacctgcg tggtggtgga cgtgtccgag gacgatccag atgtgcagat ctcttggttc	900
gtgaacaatg tggaggtgca caccgcccag acacagaccc accgggagga ttataacagc	960
acactgagag tgggtgtccgc cctgccaatc cagcaccagg actggatgag cggcaaggag	1020
tttaagtgca aggtgaacaa taaggatctg cccgccccta tcgagcggac catctccaag	1080
cccaagggct ctgtgagagc ccctcaggtg tacgtgctgc cccctccaga ggaggagatg	1140
accaagaagc aggtgacact gacctgtatg gtgacagact tcatgcctga ggatatctac	1200
gtggagtgga ccaacaatgg caagacagag ctgaactata agaataccga gccagtgtg	1260
gactccgatg gctcttactt tatgtatagc aagctgaggg tggagaagaa gaactgggtg	1320
gagcgcaatt cctattcttg tagcgtggtg cacgagggcc tgcacaatca ccacaccaca	1380
aagtccttct ctagaacccc aggcaagagg ggaaggaagc ggagaagcgg ctccggagcc	1440
acaaactttt ccctgctgaa gcaggcaggc gacgtggagg agaatccagg acccatggtg	1500
ctgcagaccc aggtgttcat ctctctgtg ctgtggatca gcggcgccta cggcgacatc	1560
cagatgaccc agtctcccag cacactgtcc gcctctgtgg gcgatcgggt gacaatcacc	1620
tgcaagtgtc agctgtccgt gggctacatg cactggatatc agcagaagcc aggcaaggcc	1680
cccaagctgc tgatctatga cacctctaag ctggccagcg gcgtgccttc cagattcagc	1740
ggctccggct ctggcaccga gtttacactg accatctcct ctctgcagcc agacgatttc	1800
gccacatact attgctttca gggcagcggg tacccttca ccttcggcgg cggcacaaaag	1860
ctggagatca agagggccga tgccgcccc aaccgtgtcca tcttccctcc cagcagcgag	1920
cagctgacat ctggcggcgc cagcgtggtg tgcttctga acaacttcta cccaaggac	1980
atcaacgtga agtggaagat cgatggcagc gagcgccaga acggcgtgct gaattcctgg	2040
accgaccagg atagcaagga ctccacatac tctatgtcta gcacactgac cctgacaaaag	2100

gatgagtacg agcggcacaa ttcctatacc tgcgaggcca cacacaagac cagcacatcc 2160
cctatcgtga agtcttttaa cagaaatgag tgttgataa 2199

<210> 115
<211> 731
<212> PRT
<213> Artificial Sequence

<220>
<223> Chemically Synthesized, gene optimized anti-RSV, pGX9370

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

Pro Thr Gln Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu
35 40 45

Ser Thr Ser Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys
50 55 60

Ala Leu Glu Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr
65 70 75 80

Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys
85 90 95

Asn Gln Val Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala
100 105 110

Thr Tyr Tyr Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val
115 120 125

Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Lys Thr Thr Ala
130 135 140

Pro Ser Val Tyr Pro Leu Ala Pro Val Cys Gly Asp Thr Thr Gly Ser
145 150 155 160

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

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

Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr
195 200 205

Val Thr Ser Ser Thr Trp Pro Ser Gln Ser Ile Thr Cys Asn Val Ala
210 215 220

His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Glu Pro Arg Gly
225 230 235 240

Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu
245 250 255

Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val
260 265 270

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

Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val
290 295 300

Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser
305 310 315 320

Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met
325 330 335

Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala
340 345 350

Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro
355 360 365

Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln

370

375

380

Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr
 385 390 395 400

Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr
 405 410 415

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

Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser
 435 440 445

Val Val His Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser
 450 455 460

Arg Thr Pro Gly Lys Arg Gly Arg Lys Arg Arg Ser Gly Ser Gly Ala
 465 470 475 480

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

Gly Pro Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp
 500 505 510

Ile Ser Gly Ala Tyr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Thr
 515 520 525

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Cys Gln
 530 535 540

Leu Ser Val Gly Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala
 545 550 555 560

Pro Lys Leu Leu Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro
 565 570 575

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile
 580 585 590

Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly
 595 600 605

Ser Gly Tyr Pro Phe Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 610 615 620

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

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

Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg
 660 665 670

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

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

Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser
 705 710 715 720

Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
 725 730

<210> 116
 <211> 1488
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Chemically Synthesized, scFv-Fc anti-RSV, pGX9371

<400> 116
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 gacattcaga tgaccagag cccctccaca ctgagcgcct ccgtgggcga cagagtgaca 120
 atcacatgca agtgtcagct gtctgtgggc tatatgcact ggtatcagca gaagcccggc 180
 aaggcccaa agctgctgat ctatgacacc tctaagctgg cctctggcgt gccaagcaga 240

ttctccggca gcggtccgg caccgagttc accctgacaa tctcctctct gcagccagac	300
gatttcgcca catactactg ctttcagggc tccggctacc cattcacatt tggcggcggc	360
acaaagctgg agatcaaggg cggcggcggc tccggcggcg gcggctctgg cggcggcggc	420
tctcaggtga cactgcggga gtccggccca gccctggtga agccaacca gacactgaca	480
ctgacctgta cattttccgg cttctctctg tccaccagcg gcatgagcgt gggctggatc	540
agacagcccc ctggcaaggc cctggagtgg ctggccgata tctggtggga cgataagaag	600
gactacaatc cttccctgaa gtctagactg accatctcca aggatacctc caagaatcag	660
gtggtgctga aggtgaccaa catggaccct gccgatacag ccacctatta ctgcgccaga	720
agcatgatca ccaactggta ctttgacgtg tggggcgccg gcacaaccgt gacagtgtct	780
tccgagccta gaggcccaac catcaagcca tgcccaccct gtaagtgtcc cgccccaaac	840
ctgctgggcg gcccatccgt gttcatcttt cccctaaga tcaaggacgt gctgatgatc	900
agcctgagcc caatcgtgac atgcgtggtg gtggacgtgt ccgaggatga cccagatgtg	960
cagatctctt ggttcgtgaa taacgtggag gtgcacaccg cccagaccca gaccacaga	1020
gaggattaca attccacact gagagtgggtg tccgccctgc ctatccagca ccaggattgg	1080
atgagcggca aggagtttaa gtgcaagggtg aacaataagg acctgcccgc cccaatcgag	1140
agaaccatct ccaagccaaa gggctctgtg agggccccac aggtgtacgt gctgcctcct	1200
ccagaggagg agatgacaaa gaagcaggtg acactgacct gcatggtgac cgacttcatg	1260
cccgaggaca tctacgtgga gtggacaaac aatggcaaga cagagctgaa ctataagaac	1320
accgagccag tgctggattc cgacggctct tacttcatgt actccaagct gagagtggag	1380
aagaagaact ggggtggagcg gaatagctac tcctgttccg tgggtccacga agggctgcat	1440
aaccaccaca ccactaagtc attttcaaga accccaggca aatgataa	1488

<210> 117

<211> 494

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, scFv-Fc anti-RSV, pGX9371

<400> 117

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

Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr Cys Ala Arg
225 230 235 240

Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr
245 250 255

Val Thr Val Ser Ser Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro
260 265 270

Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe
275 280 285

Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro
290 295 300

Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val
305 310 315 320

Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr
325 330 335

Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala
340 345 350

Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys
355 360 365

Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser
370 375 380

Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro
385 390 395 400

Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val
405 410 415

Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly
420 425 430

Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp

435

440

445

Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp
 450 455 460

Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His
 465 470 475 480

Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
 485 490

<210> 118

<211> 2220

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, gene optimized anti-RSV, pGX9283

<400> 118

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gtgcagctgg tgcagagcgg ggcagaggtg aagaagccag gcagctccgt gaaggtgtct	120
tgcaaggcaa gcggcggctc tctgagcacc tacggcatcc actgggtgag gcaggcacca	180
ggacagggcc tggagtgggt gggcggcgtg atgaccgtgt acggcaagac cacatatggc	240
cagaacttcc agggcagggt gacaatcgcc gtggaccgct ctaccaatac agcctacatg	300
gagctgtcta gcctgaccag cgacgatacc ggcacatact attgcgccac cgactcttac	360
tacgtgtgga caggcagcta tccccctcca ttgatctgt ggggccaggg caccctggtg	420
acagtgtcct ctgcctctac aaagggacca agcgtgtttc cactggcacc tagctccaag	480
tccacctctg gcggcacagc cgccctgggc tgtctggtga aggattactt ccctgagcca	540
gtgaccgtgt cctggaactc tggcgcctg accagcggag tgcacacatt tccgccgtg	600
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aaggtggagc caaagtcctg tgataagacc cacacatgcc ctccctgtcc agcacctgag	780
ctgctgggcg gcccaagcgt gttcctgttt ccaccaagc ccaaggacac cctgatgatc	840
tccagaacct cagaggtgac atgcgtggtg gtggacgtgt ctacagagga ccccgaggtg	900

aagttaaact ggtacgtgga tggcgtggag gtgcacaatg ccaagaccaa gccccgggag	960
gagcagtaca actccaccta tagagtgggtg tctgtgctga cagtgtgca ccaggactgg	1020
ctgaacggca aggagtataa gtgcaagggtg agcaataagg ccctgccagc ccccatcgag	1080
aagaccatct ccaaggcaaa gggacagcca agggagccac aggtgtacac actgcctcca	1140
tcccgcgacg agctgaccaa gaaccagggtg tctctgacat gtctggtgaa gggcttctat	1200
ccctctgata tcgccgtgga gtgggagagc aatggccagc ctgagaacaa ttacaagacc	1260
acaccccctg tgctggacag cgatggctcc ttctttctgt attccaagct gaccgtggac	1320
aagtctcggt ggcagcaggg caacgtgttt agctgctccg tgatgcacga ggccctgcac	1380
aatcactaca cccagaagtc tctgagcctg tccccaggca agaggggaag aaagcggaga	1440
tctggcagcg gcgccacaaa cttcagcctg ctgaagcagg ccggcgatgt ggaggagaat	1500
cctggcccaa tgggtgctga gaccaggtg tttatcagcc tgctgctgtg gatctccgga	1560
gcatacggag agatcgtgct gaccagaca ccaggaacct agtccctgtc tcctggacag	1620
tccgccacac tgtctttag agccagccac tccgtgggca atgactacct ggcctggtat	1680
cagcagaagc ctggacagag cccacggctg ctgatccacg gagcatacag gagggactcc	1740
ggcatccctg atagattcat cggtcttggc agcggcaccc actttaccct gacaatcgat	1800
agcctggagc ctgacgattg cgccgtgtac tattgtcagc agtatggctc ctggccactg	1860
accttcggcg gcggcacaaa ggtggacatc aagaggaccg tggccgcccc tagcgtgttc	1920
atctttccac cctccgatga gcagctgaag agcggcacag cctccgtgggt gtgcctgctg	1980
aacaacttct acccacgcga ggccaagggtg cagtgggaagg tggacaacgc cctgcagtct	2040
ggcaatagcc aggagtccgt gaccgagcag gactctaagg atagcacata ttccctgagc	2100
tccaccctga cactgtccaa ggccgattac gagaagcaca aggtgtatgc ctgtgaggtc	2160
accaccagg gactgtcttc acccgtcaca aaatccttca ataggggaga atgctgataa	2220

<210> 119

<211> 738

<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, gene optimized anti-RSV, pGX9283

<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 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

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

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

Glu Trp Val Gly Gly Val Met Thr Val Tyr Gly Lys Thr Thr Tyr Gly
65 70 75 80

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

Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Asp Asp Thr Gly Thr
100 105 110

Tyr Tyr Cys Ala Thr Asp Ser Tyr Tyr Val Trp Thr Gly Ser Tyr Pro
115 120 125

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

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

Thr Asp Phe Thr Leu Thr Ile Asp Ser Leu Glu Pro Asp Asp Cys Ala
595 600 605

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

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

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

645

650

655

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

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

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

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

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<212> PRT

<213> Artificial Sequence

<220>

<223> Chemically Synthesized

<400> 120

Ala Met Glu Lys Ile Val Ile Leu
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<210> 121

<211> 5153

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX9368 full plasmid sequence

<400> 121

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 <211> 4439
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Chemically Synthesized, pGX9369 full plasmid sequence

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<212> DNA

<213> Artificial Sequence

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<223> Chemically Synthesized, pGX9370 full plasmid sequence

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<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX371 full plasmid sequence

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<212> DNA

<213> Artificial Sequence

<220>

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<211> 6990

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pRD245 full plasmid sequence

<400> 126

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<210> 127

<211> 4472

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX 93100 full plasmid sequence

<400> 127

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<210> 128

<211> 4451

<212> DNA

<213> Artificial Sequence

<220>

<223> Chemically Synthesized, pGX 93141 full plasmid sequence

<400> 128

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