

eolf-seq1
SEQUENCE LISTING

<110> Roche Glycart AG
<120> Novel Immunoconjugates
<130> 27444
<150> EP 11164237.7
<151> 2011-04-29
<160> 300
<170> PatentIn version 3.5
<210> 1
<211> 227
<212> PRT
<213> Homo sapiens
<400> 1

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65 70 75 80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
85 90 95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110

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

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
130 135 140

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145 150 155 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175

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

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Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220

Pro Gly Lys
225

<210> 2
<211> 133
<212> PRT
<213> Artificial sequence

<220>
<223> Human IL-2 (C125A)

<400> 2

Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
1 5 10 15

Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
20 25 30

Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys
35 40 45

Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
50 55 60

Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65 70 75 80

Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
85 90 95

Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
100 105 110

Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
115 120 125

Ile Ser Thr Leu Thr
130

<210> 3
<211> 133
<212> PRT
<213> Artificial sequence

<220>
<223> Quadruple mutant human IL-2 (IL-2 qm)

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<400> 3

Ala Pro Ala Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
1 5 10 15
Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
20 25 30
Asn Pro Lys Leu Thr Arg Met Leu Thr Ala Lys Phe Ala Met Pro Lys
35 40 45
Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
50 55 60
Pro Leu Glu Glu Val Leu Asn Gly Ala Gln Ser Lys Asn Phe His Leu
65 70 75 80
Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
85 90 95
Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
100 105 110
Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
115 120 125
Ile Ser Thr Leu Thr
130

<210> 4

<211> 518

<212> PRT

<213> Artificial Sequence

<220>

<223> single chain IL-12 (p40-linker-p35)

<400> 4

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

Leu Leu His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys
 85 90 95

Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe Leu Arg Cys Glu Ala Lys
 100 105 110

Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Thr Ile Ser Thr
 115 120 125

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

Gly Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Arg Val Arg Gly
 145 150 155 160

Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu Cys Gln Glu Asp Ser Ala
 165 170 175

Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Met Val Asp Ala
 180 185 190

Val His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile Arg
 195 200 205

Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro Leu
 210 215 220

Lys Asn Ser Arg Gln Val Glu Val Ser Trp Glu Tyr Pro Asp Thr Trp
 225 230 235 240

Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Val Gln Val Gln
 245 250 255

Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg Val Phe Thr Asp Lys Thr
 260 265 270

Ser Ala Thr Val Ile Cys Arg Lys Asn Ala Ser Ile Ser Val Arg Ala
 275 280 285

Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Glu Trp Ala Ser Val Pro
 290 295 300

Cys Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 305 310 315 320

Ser Arg Asn Leu Pro Val Ala Thr Pro Asp Pro Gly Met Phe Pro Cys
 325 330 335

Leu His His Ser Gln Asn Leu Leu Arg Ala Val Ser Asn Met Leu Gln
 340 345 350

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Lys Ala Arg Gln Thr Leu Glu Phe Tyr Pro Cys Thr Ser Glu Glu Ile
355 360 365

Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys
370 375 380

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

Thr Ser Phe Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser
405 410 415

Phe Met Met Ala Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met
420 425 430

Tyr Gln Val Glu Phe Lys Thr Met Asn Ala Lys Leu Leu Met Asp Pro
435 440 445

Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Ala Val Ile Asp Glu
450 455 460

Leu Met Gln Ala Leu Asn Phe Asn Ser Glu Thr Val Pro Gln Lys Ser
465 470 475 480

Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile
485 490 495

Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asp Arg Val Met
500 505 510

Ser Tyr Leu Asn Ala Ser
515

<210> 5
<211> 340
<212> PRT
<213> Artificial sequence

<220>
<223> single chain human IL-10
<400> 5

Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro
1 5 10 15

Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg
20 25 30

Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu
35 40 45

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

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Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala
 65 70 75 80
 Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly Glu
 85 90 95
 Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu
 100 105 110
 Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe
 115 120 125
 Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp
 130 135 140
 Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn
 145 150 155 160
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 165 170 175
 Gly Gly Gly Ser Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys
 180 185 190
 Thr His Phe Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp
 195 200 205
 Ala Phe Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp
 210 215 220
 Asn Leu Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu
 225 230 235 240
 Gly Cys Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val
 245 250 255
 Met Pro Gln Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn
 260 265 270
 Ser Leu Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys
 275 280 285
 His Arg Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val
 290 295 300
 Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met
 305 310 315 320
 Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met
 325 330 335

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Lys Ile Arg Asn
340

<210> 6
<211> 166
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IL-10 monomer (IL-10M1)

<400> 6

Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro
1 5 10 15

Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg
20 25 30

Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu
35 40 45

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

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

Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly Glu
85 90 95

Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu
100 105 110

Pro Cys Glu Asn Gly Gly Gly Ser Gly Gly Lys Ser Lys Ala Val Glu
115 120 125

Gln Val Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys
130 135 140

Ala Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met
145 150 155 160

Thr Met Lys Ile Arg Asn
165

<210> 7
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> Mutant human IL-15 (E53A, N79A)

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<400> 7

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Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile
1      5      10      15
Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His
20      25      30
Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln
35      40      45
Val Ile Ser Leu Ala Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu
50      55      60
Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Ala Val
65      70      75      80
Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile
85      90      95
Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn
100     105     110

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Thr Ser

<210> 8
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> leader sequence

<400> 8

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

```

Ala His Ser

<210> 9
 <211> 57
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> leader sequence

<400> 9
 atggactgga cctggagaat cctcttcttg gtggcagcag ccacaggagc ccactcc

57

<210> 10
 <211> 57
 <212> DNA
 <213> Artificial Sequence

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<220>
<223> leader sequence

<400> 10
atggactgga cctggaggat cctcttcttg gtggcagcag ccacaggagc ccactcc 57

<210> 11
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> leader sequence

<400> 11

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Phe Pro Gly Ala Arg Cys
20

<210> 12
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> leader sequence

<400> 12
atggacatga ggggtccccgc tcagctcctg ggcctcctgc tgctctgggt cccaggtgcc 60
aggtgt 66

<210> 13
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> leader sequence

<400> 13

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser

<210> 14
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> leader sequence

<400> 14
atgggatgga gctgtatcat cctcttcttg gtagcaacag ctaccgggtg gcattcc 57

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<210> 15
 <211> 57
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> leader sequence

<400> 15
 atgggctggt cctgcatcat cctgtttctg gtggctaccg ccactggagt gcattcc 57

<210> 16
 <211> 57
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> leader sequence

<400> 16
 atgggctggt cctgcatcat cctgtttctg gtcgccacag ccaccggcgt gcactct 57

<210> 17
 <211> 466
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human IL-2R-beta-Fc(hole) fusion protein

<400> 17

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
 1 5 10 15

Phe Pro Gly Ala Arg Cys Ala Val Asn Gly Thr Ser Gln Phe Thr Cys
 20 25 30

Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val Trp Ser Gln Asp Gly
 35 40 45

Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala Trp Pro Asp Arg Arg
 50 55 60

Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val Ser Gln Ala Ser Trp
 65 70 75 80

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

Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg Glu Gly Val Arg Trp
 100 105 110

Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe Glu Asn Leu Arg Leu
 115 120 125

Met Ala Pro Ile Ser Leu Gln Val Val His Val Glu Thr His Arg Cys
 130 135 140

Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His Tyr Phe Glu Arg His
 145 150 155 160

Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly His Thr Trp Glu Glu
 165 170 175

Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu Trp Ile Cys Leu Glu
 180 185 190

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

Leu Gln Gly Glu Phe Thr Thr Trp Ser Pro Trp Ser Gln Pro Leu Ala
 210 215 220

Phe Arg Thr Lys Pro Ala Ala Leu Gly Lys Asp Thr Gly Ala Gln Asp
 225 230 235 240

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
 245 250 255

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

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

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

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

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 325 330 335

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

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

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

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

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

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

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 435 440 445

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 450 455 460

Gly Lys
 465

<210> 18
 <211> 1401
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human IL-2R-beta-Fc(hole) fusion protein

<400> 18
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 tcctgtgtct ggagccaaga tggggctctg caggacactt cctgccaagt ccatgcctgg 180
 ccggacagac ggcggtggaa ccaaacctgt gagctgctcc ccgtgagtca agcatcctgg 240
 gcctgcaacc tgatcctcgg agccccagat tctcagaaac tgaccacagt tgacatcgtc 300
 accctgaggg tgctgtgccg tgaggggggtg cgatggaggg tgatggccat ccaggacttc 360
 aagccctttg agaaccttcg cctgatggcc cccatctccc tccaagttgt ccacgtggag 420
 acccacagat gcaacataag ctgggaaatc tcccaagcct ccactactt tgaaagacac 480
 ctggagttcg agggccggac gctgtcccca ggccacacct gggaggaggc ccccctgctg 540
 actctcaagc agaagcagga atggatctgc ctggagacgc tcaccccaga caccagtat 600
 gagtttcagg tgcggtgcaa gcctctgcaa ggcgagttca cgacctggag cccctggagc 660
 cagccccctg ccttcagaac aaagcctgca gcccttgagg aggacaccgg agctcaggac 720
 aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc 780
 ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 840
 gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 900
 gtggaggtgc ataatgcaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 960
 gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1020
 aaggtctcca acaaagccct cccagcccc atcgagaaaa ccatctcaa agccaaaggg 1080
 cagccccgag aaccacaggt gtgcaccctg ccccatccc gggatgagct gaccaagaac 1140
 caggtcagcc tctcgtgcgc agtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1200

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gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1260
 ggctccttct tcctcgtgag caagctcacc gtggacaaga gcagggtggca gcaggggaac 1320
 gtctttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1380
 tccctgtctc cgggtaaata a 1401

<210> 19
 <211> 492
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human IL-2R-gamma-Fc(knob) fusion protein
 <400> 19

Met Leu Lys Pro Ser Leu Pro Phe Thr Ser Leu Leu Phe Leu Gln Leu
 1 5 10 15

Pro Leu Leu Gly Val Gly Leu Asn Thr Thr Ile Leu Thr Pro Asn Gly
 20 25 30

Asn Glu Asp Thr Thr Ala Asp Phe Phe Leu Thr Thr Met Pro Thr Asp
 35 40 45

Ser Leu Ser Val Ser Thr Leu Pro Leu Pro Glu Val Gln Cys Phe Val
 50 55 60

Phe Asn Val Glu Tyr Met Asn Cys Thr Trp Asn Ser Ser Ser Glu Pro
 65 70 75 80

Gln Pro Thr Asn Leu Thr Leu His Tyr Trp Tyr Lys Asn Ser Asp Asn
 85 90 95

Asp Lys Val Gln Lys Cys Ser His Tyr Leu Phe Ser Glu Glu Ile Thr
 100 105 110

Ser Gly Cys Gln Leu Gln Lys Lys Glu Ile His Leu Tyr Gln Thr Phe
 115 120 125

Val Val Gln Leu Gln Asp Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln
 130 135 140

Met Leu Lys Leu Gln Asn Leu Val Ile Pro Trp Ala Pro Glu Asn Leu
 145 150 155 160

Thr Leu His Lys Leu Ser Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn
 165 170 175

Arg Phe Leu Asn His Cys Leu Glu His Leu Val Gln Tyr Arg Thr Asp
 180 185 190

Trp Asp His Ser Trp Thr Glu Gln Ser Val Asp Tyr Arg His Lys Phe
 195 200 205
 Ser Leu Pro Ser Val Asp Gly Gln Lys Arg Tyr Thr Phe Arg Val Arg
 210 215 220
 Ser Arg Phe Asn Pro Leu Cys Gly Ser Ala Gln His Trp Ser Glu Trp
 225 230 235 240
 Ser His Pro Ile His Trp Gly Ser Asn Thr Ser Lys Glu Asn Pro Phe
 245 250 255
 Leu Phe Ala Leu Glu Ala Gly Ala Gln 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 Cys Arg
 385 390 395 400
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp 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

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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> 20
 <211> 1479
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Human IL-2R-gamma-Fc(knob) fusion protein

<400> 20
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 ttcttgacca ctatgccac tgactccctc agtgtttcca ctctgcccct cccagaggtt 180
 cagtgttttg tgttcaatgt cgagtacatg aattgcactt ggaacagcag ctctgagccc 240
 cagcctacca acctcactct gcattattgg tacaagaact cggataatga taaagtccag 300
 aagtgcagcc actatctatt ctctgaagaa atcacttctg gctgtcagtt gcaaaaaaag 360
 gagatccacc tctaccaaac atttgttggt cagctccagg acccacggga acccaggaga 420
 caggccacac agatgctaaa actgcagaat ctggtgatcc cctgggctcc agagaaccta 480
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 cactgttttg agcacttggt gcagtaccgg actgactggg accacagctg gactgaacaa 600
 tcagtggatt atagacataa gttctccttg cctagtgtgg atgggcagaa acgctacacg 660
 tttcgtgttc ggagccgctt taaccactc tgtggaagtg ctacagcattg gagtgaatgg 720
 agccacccaa tccactgggg gagcaatact tcaaaagaga atcctttcct gtttgcattg 780
 gaagccggag ctacaggaaa aactcacaca tgcccaccgt gccacgacc tgaactcctg 840
 gggggaccgt cagtcttcct cttccccca aaacccaagg acaccctcat gatctcccgg 900
 acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagtgc 960
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 ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc 1140
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 gatgagctga ccaagaacca ggtcagcctg tgggtgcctg tcaaaggctt ctatcccagc 1260
 gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1320
 cccgtgctgg actccgacgg ctcttcttct ctctacagca agctcaccgt ggacaagagc 1380
 aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1440
 tacacgcaga agagcctctc cctgtctccg ggtaaataga 1479

eo1f-seq1

<210> 21
 <211> 219
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human IL-2R alpha subunit + Avi-tag + His-tag

<400> 21

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Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1          5          10          15

Val His Ser Glu Leu Cys Asp Asp Asp Pro Pro Glu Ile Pro His Ala
          20          25          30

Thr Phe Lys Ala Met Ala Tyr Lys Glu Gly Thr Met Leu Asn Cys Glu
          35          40          45

Cys Lys Arg Gly Phe Arg Arg Ile Lys Ser Gly Ser Leu Tyr Met Leu
          50          55          60

Cys Thr Gly Asn Ser Ser His Ser Ser Trp Asp Asn Gln Cys Gln Cys
65          70          75          80

Thr Ser Ser Ala Thr Arg Asn Thr Thr Lys Gln Val Thr Pro Gln Pro
          85          90          95

Glu Glu Gln Lys Glu Arg Lys Thr Thr Glu Met Gln Ser Pro Met Gln
          100          105          110

Pro Val Asp Gln Ala Ser Leu Pro Gly His Cys Arg Glu Pro Pro Pro
          115          120          125

Trp Glu Asn Glu Ala Thr Glu Arg Ile Tyr His Phe Val Val Gly Gln
          130          135          140

Met Val Tyr Tyr Gln Cys Val Gln Gly Tyr Arg Ala Leu His Arg Gly
145          150          155          160

Pro Ala Glu Ser Val Cys Lys Met Thr His Gly Lys Thr Arg Trp Thr
          165          170          175

Gln Pro Gln Leu Ile Cys Thr Gly Val Asp Glu Gln Leu Tyr Phe Gln
          180          185          190

Gly Gly Ser Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp
          195          200          205

His Glu Ala Arg Ala His His His His His His
          210          215

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<210> 22
 <211> 660

eolf-seq1

<212> DNA
<213> Artificial Sequence

<220>
<223> Human IL-2R alpha subunit + Avi-tag + His-tag

<400> 22
atgggatgga gctgtatcat cctcttcttg gtagcaacag ctaccggtgt gcattccgag 60
ctctgtgacg atgacccgcc agagatccca cacgccacat tcaaagccat ggcctacaag 120
gaaggaacca tgttgaactg tgaatgcaag agagggtttcc gcagaataaa aagcgggtca 180
ctctatatgc tctgtacagg aaactctagc cactcgtcct gggacaacca atgtcaatgc 240
acaagctctg ccactcggaa cacaacgaaa caagtgcacac ctcaacctga agaacagaaa 300
gaaaggaaaa ccacagaaat gcaaagtcca atgcagccag tggaccaagc gagccttcca 360
ggtcactgca gggaaacctcc accatgggaa aatgaagcca cagagagaat ttatcatttc 420
gtggtggggc agatggttta ttatcagtgc gtccagggat acaggggtct acacagaggt 480
cctgctgaga gcgtctgcaa aatgaccac ggggaagaaa ggtggaccca gcccagctc 540
atatgcacag gtgtcgacga acagttatat tttcagggcg gctcaggcct gaacgacatc 600
ttcgaggccc agaagatcga gtggcacgag gctcgagctc accaccatca ccatcactga 660

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

<220>
<223> 2B10; VL

<400> 23

Asp 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 Arg Leu Ile
35 40 45

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

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

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

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

eolf-seq1

<210> 24
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 2B10; VL

<400> 24
 gatatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtcggaga ccgggtcacc 60
 atcacctgcc gggcaagtca gggcattaga aatgatttag gctggtacca gcagaagcca 120
 gggaaagccc ctaagcgcct gatctatgct gcatccagtt tgcagagtgg cgtcccatca 180
 aggttcagcg gcggtggatc cgggacagag ttactctca ccatcagcag cttgcagcct 240
 gaagattttg ccacctatta ctgcttgcat aatgggtctgc agcccgcgac gtttggccag 300
 ggcaccaaag tcgagatcaa g 321

<210> 25
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 2B10(GS); VL

<400> 25

Asp 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 Arg Leu Ile
 35 40 45

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

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

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

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

<210> 26
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 2B10(GS); VL

eolf-seq1

<400> 26
 gatatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtcggaga ccgggtcacc 60
 atcacctgcc gggcaagtca gggcattaga aatgatttag gctggtacca gcagaagcca 120
 gggaaagccc ctaagcgcct gatctatgct gcatccagtt tgcagagtgg cgtcccatca 180
 aggttcagcg gcagtggatc cgggacagag ttcactctca ccatcagcag cttgcagcct 240
 gaagattttg ccacctatta ctgcttgag aatgggtctgc agcccgcgac gtttggccag 300
 ggcaccaaag tcgagatcaa g 321

<210> 27
 <211> 121
 <212> PRT
 <213> Artificial sequence

<220>
 <223> 2B10; VH

<400> 27

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

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

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

Ala Arg Leu Tyr Gly Tyr Ala Tyr Tyr Gly Ala Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 28
 <211> 363
 <212> DNA
 <213> Artificial sequence

<220>
 <223> 2B10; VH

<400> 28
 caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
 tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
 Page 19

eolf-seq1

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cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac      180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac      240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagactgtac      300
ggttacgctt actacggtgc ttttgactac tggggccaag ggaccaccgt gaccgtctcc      360
tca                                                                    363

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<210> 29
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> 2F11; VL

<400> 29

Glu Ile Val 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

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

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

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

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

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

<210> 30
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 2F11; VL

<400> 30

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gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc      60
ctctcttgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa      120
cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcgtccca      180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag      240
cctgaagatt ttgcagtgta ttactgtcag cagggtcagt atactccccc cacgttcggc      300

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eof-seq1

caggggacca aagtggaaat caaa

324

<210> 31
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> 2F11(VI); VL

<400> 31

Glu Ile Val 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

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

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

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

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

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

<210> 32
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 2F11(VI); VL

<400> 32

gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
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cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgt ttactgtcag cagggtcagt atactcccc cagtttcggc 300
caggggacca aagtggaaat caaa 324

<210> 33
<211> 117
<212> PRT
<213> Artificial Sequence

eo1f-seq1

<220>

<223> 2F11; VH

<400> 33

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Trp Arg Trp Met Met Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 34

<211> 351

<212> DNA

<213> Artificial Sequence

<220>

<223> 2F11; VH

<400> 34

gaggtgcaat tggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctccggatt caccttttagc agttatgcc a tgagctgggt ccgccaggct 120

ccaggggaagg ggctggagtg ggtctcagct attagtggta gtgggtgtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcagatga acagcctgag agccgaggac atggccgtat attactgtgc gaaatggaga 300

tggatgatgt ttgactactg gggccaagga accctgggtca ccgtctcgag t 351

<210> 35

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> 2F11(MT); VH

eo1f-seq1

<400> 35

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Trp Arg Trp Met Met Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 36

<211> 351

<212> DNA

<213> Artificial Sequence

<220>

<223> 2F11(MT); VH

<400> 36

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tcctgtgcag cctccggatt caccttttagc agttatgcc a tgagctgggt ccgccaggct 120

ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcagatga acagcctgag agccgaggac accgccgtat attactgtgc gaaatggaga 300

tggatgatgt ttgactactg gggccaagga accctgggtca ccgtctcgag t 351

<210> 37

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> 3F2; VL

<400> 37

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

eof-seq1

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

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

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

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

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

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

<210> 38
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 3F2; VL

<400> 38
gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt atccagggga aagagccacc 60
ctctcttgca gggccagtca gagtgttacc agtagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatcaat gtgggctccc gtagggccac tggcatccca 180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta ttactgtcag caggggtatta tgcttcccc gacgttcggc 300
caggggacca aagtggaaat caaa 324

<210> 39
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> 3F2(YS); VL

<400> 39

Glu Ile Val 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 Thr Ser Ser
20 25 30

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

eo1f-seq1

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

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

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

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

<210> 40
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 3F2(YS); VL

<400> 40
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ctctcttgca gggccagtca gagtggtacc agtagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatcaat gtgggctccc gtagggccac tggcatccca 180
gacaggttca gtggcagtggt atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtta ttactgtcag caggggtatta tgcttcccc gacgttcggc 300
caggggacca aagtggaaat caaa 324

<210> 41
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> 3F2; VH

<400> 41

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

eolf-seq1

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

Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 42
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> 3F2; VH

<400> 42
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tcctgtgcag cctccggatt caccttttagc agttatgccca tgagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggttag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300
tttggtgggt ttaactactg gggccaagga accctgggtca ccgtctcgag t 351

<210> 43
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> 3D9, VL

<400> 43

Glu Ile Val 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

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

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

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

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

eolf-seq1

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

<210> 44
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 3D9, VL

<400> 44
gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcttgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta ttactgtcag caggggtcagc ttattcccc tacgttcggc 300
caggggacca aagtggaaat caaa 324

<210> 45
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> 3D9, VH

<400> 45

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ala Ile Gly Val Ser Thr Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

eolf-seq1

<210> 46
 <211> 351
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 3D9, VH

<400> 46
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 tcctgtgcag cctccggatt caccttttagc agttatgcta tgagctgggt ccgccagact 120
 ccaggggaagg ggctggagtg ggtctcagct attgggtgta gtactggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggttgg 300
 ctgggtcctt ttgactactg gggccaagga accctgggtca ccgtctcgag t 351

<210> 47
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 3D9(TA); VH

<400> 47

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

Ser Ala Ile Gly Val Ser Thr Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Lys Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 48
 <211> 351

eolf-seq1

<212> DNA
<213> Artificial Sequence

<220>
<223> 3D9(TA); VH

<400> 48
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tcctgtgcag cctccggatt cacctttagc agttatgcta tgagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcagct attggtgtta gtactggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggttgg 300
ctgggtcctt ttgactactg gggccaagga accctgggtca ccgtctcgag t 351

<210> 49
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> 4G8; VL

<400> 49

Glu Ile Val 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 Arg Ser
20 25 30

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

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

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

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

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

<210> 50
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 4G8; VL

<400> 50
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eolf-seq1

ctctcttgca gggccagtca gagtgttagc cgcagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatcatt ggggcctcca ccaggggccac tggcatccca 180
 gacaggttca gtggcagtgg atccgggacg gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgtg ttactgtcag cagggtcagg ttattccccc tacgttcggc 300
 caggggacca aagtggaaat caaa 324

<210> 51
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 4G8; VH

<400> 51

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 52
 <211> 351
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 4G8; VH

<400> 52

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tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120

ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

eolf-seq1

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtgg 300
ctgggtaatt ttgactactg gggccaagga accctgggtca ccgtctcgag t 351

<210> 53
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> 4B3; VL

<400> 53

Glu Ile Val 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 Asn
20 25 30

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

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

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

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

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

<210> 54
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 4B3; VL

<400> 54

gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcttgca gggccagtca gagggttagc agcaattact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggcgccata tcagggccac tggcatccca 180
gacaggttca gtggcagtg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgt ttactgtcag cagggtcagg ttattcccc tacgttcggc 300
caggggacca aagtggaaat caaa 324

eolf-seq1

<210> 55
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 4B3; VH

<400> 55

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 56
 <211> 351
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 4B3; VH

<400> 56

gaggtgcaat tgttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc	60
tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct	120
ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg	300
ctgggtaatt ttgactactg gggccaagga accctgggtca ccgtctcgag t	351

<210> 57
 <211> 108
 <212> PRT
 <213> Artificial Sequence

eolf-seq1

<220>

<223> 4D6; VL

<400> 57

Glu Ile Val 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 Asn
20 25 30

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

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

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

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

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

<210> 58

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> 4D6; VL

<400> 58

gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcttgca gggccagtca gagtgttagc agcaactact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatccag ggcgcctcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgtg ttactgtcag cagggtcagg ttattcccc tacgttcggc 300

caggggacca aagtggaaat caaa 324

<210> 59

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> 4D6; VH

<400> 59

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

eo1f-seq1

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 60
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> 4D6; VH

<400> 60
gaggtgcaat tgttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt cacctttagc agttatgcc a tgagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300
ctgggtaatt ttgactactg gggccaagga accctgggtca ccgtctcgag t 351

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

<220>
<223> 2C6; VL

<400> 61

Glu Ile Val 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

eolf-seq1

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

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

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

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

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

<210> 62
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 2C6; VL

<400> 62
gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcttgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag caggctggag 240
cctgaagatt ttgcagtgtg ttactgtcag cagggtcagc agattccccc tacgttcggc 300
caggggacca aagtggaaat caaa 324

<210> 63
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> 2C6; VH

<400> 63

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ala Ile Ser Gly Ser Ala Gly Tyr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

eolf-seq1

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

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

Ala Lys Gly Trp Phe Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 64
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> 2C6; VH

<400> 64
gaggtgcaat tggttgagtc tgggggaggc ttgttacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatc cacctttagc agttatgccca tgagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcagct attagtggga gtgctgggta tacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggttg 300
tttggaatt ttgactactg gggccaagga accctgggtca ccgtctcgag t 351

<210> 65
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> 5H5; VL

<400> 65

Glu Ile Val 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

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

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

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

eolf-seq1

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Gly Asn Gln Ile Pro
85 90 95

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

<210> 66
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 5H5; VL

<400> 66
gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcttgca gggccagtca gagggttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg ttactgtcag cagggtaatc agattccccc tacgttcggt 300
caggggacca aagtggaaat caaa 324

<210> 67
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> 5H5; VH

<400> 67

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Thr Met Ser Trp Val Arg Arg Ser Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

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

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

Lys Gly Trp Phe Thr Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

eolf-seq1

Thr Val Ser Ser
115

<210> 68
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<223> 5H5; VH

<400> 68
gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt caccttttagc agttatacca tgagctgggt ccgccggtct 120
ccaggaagg ggctggagtg ggtctcagct attagtgggt gtggtaggac atactacgca 180
gactccgtga agggccggtt caccatctcc agagacaatt ccaagaacac gctgtatctg 240
cagatgaaca gcctgagagc cgaggacacg gccgtatatatt actgtgcaaa aggttggttt 300
acgccttttg actactgggg ccaaggaacc ctggtcaccg tctcgagt 348

<210> 69
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> 2C4; VL

<400> 69

Glu Ile Val 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 Asn
20 25 30

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

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

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

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Gly Asn Gln Ile Pro
85 90 95

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

<210> 70
<211> 324

eolf-seq1

<212> DNA
<213> Artificial Sequence

<220>
<223> 2C4; VL

<400> 70
gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcttgca gggccagtca gagtgtagc agtaactact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggtgcctcca ttagggccac tggcatccca 180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta ttactgtcag cagggtaatc agattccccc tacgttcggg 300
caggggacca aagtggaaat caaa 324

<210> 71
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> 2C4; VH

<400> 71

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Gly Trp Phe Thr Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 72
<211> 351
<212> DNA
<213> Artificial Sequence

<220>

eolf-seq1

<223> 2C4; VH

<400> 72
gaggtgcaat tgttgagtc tgggggaggc ttgttacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt caccttttagc agttatgccca tgagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcagct attagcggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggttg 300
tttacgcctt ttgactactg gggccaagga accctgggtca ccgtctcgag t 351

<210> 73
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> 2D9; VL

<400> 73
Glu Ile Val 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
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Gly Asn Gln Ile Pro
85 90 95
Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 74
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 2D9; VL

<400> 74
gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcttgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180

eolf-seq1

gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg ttactgtcag cagggtaatc agattccccc tacgttcggt 300
caggggacca aagtggaaat caaa 324

<210> 75
<211> 117
<212> PRT
<213> Artificial sequence

<220>
<223> 2D9; VH

<400> 75

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Gly Trp Phe Thr Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 76
<211> 351
<212> DNA
<213> Artificial sequence

<220>
<223> 2D9; VH

<400> 76

gaggtgcaat tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt caccttttagc agttatgccg tgagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcagct attagcggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggttg 300

eolf-seq1

tttacgcctt ttgactactg gggccaagga accctggtca ccgtctcgag t 351

<210> 77
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> 4B8; VL

<400> 77

Glu Ile Val 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

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

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

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

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

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

<210> 78
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 4B8; VL

<400> 78

gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcttgca gggccagtca gagtgtagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgt ttactgtcag cagggtcagg ttattccccc tacgttcggc 300
caggggacca aagtggaaat caaa 324

<210> 79
<211> 117
<212> PRT
<213> Artificial Sequence

eolf-seq1

<220>

<223> 4B8; VH

<400> 79

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 80

<211> 351

<212> DNA

<213> Artificial Sequence

<220>

<223> 4B8; VH

<400> 80

gaggtgcaat tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctccggatt caccttttagc agttatgcc a tgagctgggt ccgccaggct 120

ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtgg 300

ctgggtaatt ttgactactg gggccaagga accctgggtca ccgtctcgag t 351

<210> 81

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> 7A1; VL

eof-seq1

<400> 81

Glu Ile Val 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

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

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

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

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

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

<210> 82

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> 7A1; VL

<400> 82

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ctctcttgca gggccagtca gagggttagc agcagctact tagcctggta ccagcagaaa	120
cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatcca	180
gacaggttca gtggcagtg atccgggaca gacttcactc tcaccatcag cagactggag	240
cctgaagatt ttgcagtgt ttactgtcag cagggtcagc agattccccc tacgttcggc	300
caggggacca aagtggaaat caaa	324

<210> 83

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> 7A1; VH

<400> 83

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

eolf-seq1

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Gly Trp Phe Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 84
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> 7A1; VH

<400> 84
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tcctgtgcag cctccggatt caccttttagc agttatgcc a tgagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggttg 300
tttggaatt ttgactactg gggccaagga accctgggtca ccgtctcgag t 351

<210> 85
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> 13C2; VL

<400> 85

Glu Ile Val 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

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

eo1f-seq1

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

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

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

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

<210> 86
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 13C2; VL

<400> 86
gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcttgca gggccagtca gagtgtagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatcca 180
gacaggttca gtggcagtg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgt ttactgtcag cagggtcagc ttattccccc tacgttcggc 300
caggggacca aagtggaaat caaa 324

<210> 87
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> 13C2; VH

<400> 87

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

eolf-seq1

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

Ala Lys Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 88
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> 13C2; VH

<400> 88
gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt caccttttagc agttatgcca tgagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggttg 300
ctgggtcctt ttgactactg gggccaagga accctgggtca ccgtctcgag t 351

<210> 89
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> 13E8; VL

<400> 89

Glu Ile Val 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

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

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

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

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

eolf-seq1

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

<210> 90
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 13E8; VL

<400> 90
gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcttgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta ttactgtcag caggggtctga atattccctc gacgttcggc 300
caggggacca aagtggaaat caaa 324

<210> 91
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> 13E8; VH

<400> 91

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

eolf-seq1

<210> 92
 <211> 351
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 13E8; VH

<400> 92
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 tcctgtgcag cctccggatt cacctttagc agttatgcc a tgagctgggt ccgccaggct 120
 ccaggggaagg ggctggagtg ggtctcagct attagtggta gtgggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggttgg 300
 ttgggtccgt ttgactactg gggccaagga accctgggtca ccgtctcgag t 351

<210> 93
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 14C10; VL

<400> 93

Glu Ile Val 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

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

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

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

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Gly His Ile Ile Pro
 85 90 95

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

<210> 94
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>

eolf-seq1

<223> 14C10; VL

<400> 94
gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctctttgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta ttactgtcag caggggtcata ttattcccc gaggttcggc 300
caggggacca aagtggaaat caaa 324

<210> 95

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> 14C10; VH

<400> 95

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Lys Ala Trp Met Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110
Val Thr Val Ser Ser
115

<210> 96

<211> 351

<212> DNA

<213> Artificial Sequence

<220>

<223> 14C10; VH

<400> 96

gaggtgcaat tgttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

eolf-seq1

tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct	120
ccaggggaagg ggctggagtg ggtctcagct attagtggta gtgggtggtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagcttgg	300
atggggcctt ttgactactg gggccaagga accctgggtca ccgtctcgag t	351

<210> 97
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 17A11; VL

<400> 97

Glu Ile Val 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

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

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

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

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

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

<210> 98
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 17A11; VL

<400> 98

gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc	60
ctctcttgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa	120
cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca	180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag	240
cctgaagatt ttgcagtgta ttactgtcag caggggtctga atattccctc gacgttcggc	300

eolf-seq1

caggggacca aagtggaaat caaa

324

<210> 99
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> 17A11; VH

<400> 99

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 100
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> 17A11; VH

<400> 100

gaggtgcaat tgttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt cacctttagc agttatgccca tgagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggttgg 300
ttgggtccgt ttgactactg gggccaagga accctgggtca ccgtctcgag t 351

eof-seq1

<210> 101
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 19G1; VL

<400> 101

Glu Ile Val 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 Thr Ser Ser
 20 25 30

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

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

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

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

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

<210> 102
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 19G1; VL

<400> 102

gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc	60
ctctcttgca gggccagtca gagggttacc agtagctact tagcctggta ccagcagaaa	120
cctggccagg ctcccaggct cctcatcaat gtgggctccc gtagggccac tggcatccca	180
gacaggttca gtggcagtg atccgggaca gacttcactc tcaccatcag cagactggag	240
cctgaagatt ttgcagtgt ttactgtcag cagggtatta tgcttcccc gacgttcggc	300
caggggacca aagtggaaat caaa	324

<210> 103
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 19G1; VH

eo1f-seq1

<400> 103

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ala Ile Ile Ser Ser Gly Gly Leu Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 104

<211> 351

<212> DNA

<213> Artificial Sequence

<220>

<223> 19G1; VH

<400> 104

gaggtgcaat tgttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc	60
tcctgtgcag cctccggatt caccttttagc agttatgcga tgagctgggt ccgccaggct	120
ccaggggaagg ggctggagtg ggtctcagcg attattagta gtggtggtct cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg	300
tttgggtggtt ttaactactg gggccaagga accctgggtca ccgtctcgtc c	351

<210> 105

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> 20G8; VL

<400> 105

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

eof-seq1

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

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

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

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

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

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

<210> 106
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 20G8; VL

<400> 106
gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcttgca gggccagtca gagtgttacc agtagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatcaat gtgggctccc gtagggccac tggcatccca 180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta ttactgtcag caggggtatta tgcttcccc gacgttcggc 300
caggggacca aagtggaaat caaa 324

<210> 107
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> 20G8; VH

<400> 107

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

eolf-seq1

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

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

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

Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 108
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> 20G8; VH

<400> 108
gaggtgcaat tgttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt cacctttagc agttatgcaa tgagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcagct attattggga gtggtagtcg tacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300
tttgggtggtt ttaactactg gggccaagga accctgggtca ccgtctcgtc c 351

<210> 109
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> 4B9; VL

<400> 109

Glu Ile Val 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 Thr Ser Ser
20 25 30

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

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

eof-seq1

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

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

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

<210> 110
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 4B9; VL

<400> 110
gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcttgca gggccagtca gagggttacc agtagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatcaat gtgggctccc gtagggccac tggcatccca 180
gacaggttca gtggcagtggt atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta ttactgtcag caggggtatta tgcttcccc gacgttcggc 300
caggggacca aagtggaaat caaa 324

<210> 111
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> 4B9; VH

<400> 111

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ala Ile Ile Gly Ser Gly Ala Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

eof-seq1

Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 112
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> 4B9; VH

<400> 112
gaggtgcaat tgttgagatc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt caccttttagc agttatgcta tgagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcagct attattggta gtggtgctag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtgg 300
tttggtgggtt ttaactactg gggccaagga accctgggtca ccgtctcgtc c 351

<210> 113
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> 5B8; VL

<400> 113

Glu Ile Val 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 Thr Ser Ser
20 25 30

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

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

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

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

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

eolf-seq1

<210> 114
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 5B8; VL

<400> 114
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ctctcttgca gggccagtca gagtgttacc agtagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatcaat gtgggctccc gtagggccac tggcatccca 180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg ttactgtcag caggggtatta tgcttcccc gacgttcggc 300
caggggacca aagtggaaat caaa 324

<210> 115
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> 5B8; VH

<400> 115

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Ala Ile Trp Gly Gly Gly Arg Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu
100 105 110
Val Thr Val Ser Ser
115

<210> 116
<211> 351

eolf-seq1

<212> DNA
<213> Artificial Sequence

<220>
<223> 5B8; VH

<400> 116
gaggtgcaat tgttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt caccttttagc agttatgcta tgagctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcagct atttgggggtg gtggtcgtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300
tttggtggtt ttaactactg gggccaagga accctgggtca ccgtctcgtc c 351

<210> 117
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> 5F1; VL

<400> 117

Glu Ile Val 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 Thr Ser Ser
20 25 30

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

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

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

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

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

<210> 118
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 5F1; VL

<400> 118
gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

eolf-seq1

ctctcttgca gggccagtca gagtgttacc agtagctact tagcctggta ccagcagaaa	120
cctggccagg ctcccaggct cctcatcaat gtgggctccc gtagggccac tggcatccca	180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag	240
cctgaagatt ttgcagtgtg ttactgtcag caggggtatta tgcttcccc gacgttcggc	300
caggggacca aagtggaaat caaa	324

<210> 119
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 5F1; VH

<400> 119

Glu Val Gln Leu	Leu Glu Ser Gly Gly Gly	Leu Val Gln Pro Gly Gly
1	5	10

Ser Leu Arg	Leu Ser Cys Ala Ala	Ser Gly Phe Thr Phe	Ser Ser Tyr
20	25	30	

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

Ser Ala Ile Ile Ser Ser Gly Ala Ser Thr Tyr Tyr	Ala Asp Ser Val
50	55

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn	Ser Lys Asn Thr Leu Tyr
65	70

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85

Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu
100

Val Thr Val Ser Ser
115

<210> 120
 <211> 351
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 5F1; VH

<400> 120

gaggtgcaat tgttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc	60
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tcctgtgcag cctccggatt cacctttagc agttatgcta tgagctgggt ccgccaggct	120
---	-----

ccaggggaagg ggctggagtg ggtctcagct attattagta gtgggggctag cacatactac	180
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eolf-seq1

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtgg 300
 tttggtggtt ttaactactg gggccaagga accctgggtca ccgtctcgtc c 351

<210> 121
 <211> 108
 <212> PRT
 <213> Artificial sequence

<220>
 <223> 14B3; VL

<400> 121

Glu Ile Val 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 Thr Ser Ser
 20 25 30

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

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

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

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

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

<210> 122
 <211> 324
 <212> DNA
 <213> Artificial sequence

<220>
 <223> 14B3; VL

<400> 122

gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcttgca gggccagtca gagggttacc agtagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatcaat gtgggctccc gtagggccac tggcatccca 180
 gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgtg ttactgtcag caggggtatta tgcttcccc gacgttcggc 300
 caggggacca aagtggaaat caaa 324

eolf-seq1

<210> 123
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 14B3; VH

<400> 123

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

Ser Ala Ile Leu Ala Ser Gly Ala Ile Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 124
 <211> 351
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 14B3; VH

<400> 124

gaggtgcaat tgttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc	60
tcctgtgcag cctccggatt cacctttagc agttatgcta tgagctgggt ccgccaggct	120
ccaggggaagg ggctggagtg ggtctcagct attttggcta gtggtgcat cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg	300
tttggtggtt ttaactactg gggccaagga accctgggtca ccgtctcgtc c	351

<210> 125
 <211> 108
 <212> PRT
 <213> Artificial Sequence

eof-seq1

<220>

<223> 16F1; VL

<400> 125

Glu Ile Val 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 Thr Ser Ser
20 25 30

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

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

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

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

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

<210> 126

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> 16F1; VL

<400> 126

gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcttgca gggccagtca gagtgttacc agtagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatcaat gtgggctccc gtagggccac tggcatccca 180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg ttactgtcag caggggtatta tgcttcccc gacgttcggc 300
caggggacca aagtggaaat caaa 324

<210> 127

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> 16F1; VH

<400> 127

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

eolf-seq1

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Gly Ile Ile Gly Ser Gly Gly Ile Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 128
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> 16F1; VH

<400> 128
gaggtgcaat tgttgagtc tgggggaggc ttgtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt cacctttagc agttatgcta tgagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcaggt attattggta gtggtggat cacatactac 180
gcagactccg tgaagggccg gtccaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300
tttggtggtt ttaactactg gggccaagga accctgggtca ccgtctcgtc c 351

<210> 129
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> 16F8; VL

<400> 129

Glu Ile Val 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 Thr Ser Ser
20 25 30

eolf-seq1

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

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

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

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

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

<210> 130
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 16F8; VL

<400> 130
gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcttgca gggccagtca gagtgttacc agtagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatcaat gtgggctccc gtagggccac tggcatccca 180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg ttactgtcag caggggtatta tgcttcccc gacgttcggc 300
caggggacca aagtggaaat caaa 324

<210> 131
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> 16F8; VH

<400> 131

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ala Ile Leu Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

eo1f-seq1

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

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

Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 132
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> 16F8; VH

<400> 132
gagggtgcaat tggttgagtc tgggggaggc ttgttacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt cacctttagc agttatgccca tgagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcagct attcttggtg gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300
tttggtggtt ttaactactg gggccaagga accctgggtca ccgtctcgtc c 351

<210> 133
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> O3C9; VL

<400> 133

Glu Ile Val 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 Thr Ser Ser
20 25 30

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

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

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

eolf-seq1

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

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

<210> 134
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> O3C9; VL

<400> 134
gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcttgca gggccagtca gagggttacc agtagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatcaat gtgggctccc gtagggccac tggcatccca 180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg ttactgtcag cagggtatta tgcttcccc gacgttcggc 300
caggggacca aagtggaaat caaa 324

<210> 135
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> O3C9; VH

<400> 135

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe
20 25 30

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

Ser Ala Ile Ile Gly Ser Gly Ser Asn Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu
100 105 110

eolf-seq1

Val Thr Val Ser Ser
115

<210> 136
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> O3C9; VH

<400> 136
gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt caccttttagc agttttgcca tgagctgggt ccgtcagtct 120
ccaggaagg ggctggagtg ggtctcagct attattggta gtggtagtaa cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300
tttggtggtt ttaactactg gggccaagga accctgggtca ccgtctcgtc c 351

<210> 137
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> O2D7; VL

<400> 137

Glu Ile Val 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 Thr Ser Ser
20 25 30

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

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

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

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ala Ile Met Leu Pro
85 90 95

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

<210> 138
<211> 324

eolf-seq1

<212> DNA
<213> Artificial Sequence

<220>
<223> O2D7; VL

<400> 138
gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctctttgca gggccagtca gagtggtacc agtagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatcaat gtgggctccc gtagggccac tggcacccca 180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg ttactgtcag caggctatta tgcttcctcc gacgttcggc 300
caggggacca aagtggaaat caaa 324

<210> 139
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> O2D7; VH

<400> 139

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 140
<211> 351
<212> DNA
<213> Artificial Sequence

<220>

eolf-seq1

<223> O2D7; VH

<400> 140
gaggtgcaat tgttgagtc tgggggaggc ttgttacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt caccttttagc agttatgccca tgagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggtag 300
tttggtggtt ttaactactg gggccaagga accctgggtca ccgtctcgtc c 351

<210> 141
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> 28H1; VL

<400> 141
Glu Ile Val 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 Arg Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Ile Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Gly Gln Val Ile Pro
85 90 95
Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 142
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 28H1; VL

<400> 142
gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcttgca gggccagtca gagtgttagc cgcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatcatt ggggcctcca ccagggccac tggcatccca 180

eolf-seq1

gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg ttactgtcag cagggtcagg ttattccccc tacgttcggc 300
caggggacca aagtggaaat caaa 324

<210> 143
<211> 116
<212> PRT
<213> Artificial sequence

<220>
<223> 28H1; VH

<400> 143

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser His
20 25 30

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

Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp Ser Val Lys
50 55 60

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

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

Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 144
<211> 348
<212> DNA
<213> Artificial sequence

<220>
<223> 28H1; VH

<400> 144

gaggtgcaat tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt caccttttagc agtcatgcta tgagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcagct atttgggcta gtggggagca atactacgca 180
gactccgtga agggccggtt caccatctcc agagacaatt ccaagaacac gctgtatctg 240
cagatgaaca gcctgagagc cgaggacacg gccgtatatt actgtgcgaa aggggtggctg 300

eolf-seq1

ggtaattttg actactgggg ccaaggaacc ctggtcaccg tctcgagt

348

<210> 145
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> 22A3; VL

<400> 145

Glu Ile Val 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 Thr Ser Ser
20 25 30

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

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

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

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

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

<210> 146
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 22A3; VL

<400> 146

gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcttgca gggccagtca gagggttacc agtagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatcaat gtgggctccc gtagggccac tggcatccca 180
gacaggttca gtggcagtg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgt ttactgtcag cagggtatta tgcttcccc gacgttcggc 300
caggggacca aagtggaaat caaa 324

<210> 147
<211> 117
<212> PRT
<213> Artificial Sequence

eo1f-seq1

<220>

<223> 22A3; VH

<400> 147

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ala Ile Ile Gly Ser Gly Ser Ile Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 148

<211> 351

<212> DNA

<213> Artificial Sequence

<220>

<223> 22A3; VH

<400> 148

gaggtgcaat tggttgagtc tgggggaggc ttgttacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctccggatt caccttttagc agttatgcc a tgagctgggt ccgccaggct 120

ccaggggaagg ggctggagtg ggtctcagct attattggta gtggtagtat cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300

tttggtgggt ttaactactg gggccaagga accctgggtca ccgtctcgag t 351

<210> 149

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> 29B11; VL

eof-seq1

<400> 149

Glu Ile Val 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 Thr Ser Ser
20 25 30

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

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

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

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

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

<210> 150

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> 29B11; VL

<400> 150

gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc	60
ctctcttgca gggccagtca gagtgttacc agtagctact tagcctggta ccagcagaaa	120
cctggccagg ctcccaggct cctcatcaat gtgggctccc gtagggccac tggcatccca	180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag	240
cctgaagatt ttgcagtgtg ttactgtcag caggggtatta tgcttcccc gacgttcggc	300
caggggacca aagtggaaat caaa	324

<210> 151

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> 29B11; VH

<400> 151

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

eolf-seq1

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

Ser Ala Ile Ile Gly Ser Gly Gly Ile Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 152
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> 29B11; VH

<400> 152
gaggtgcaat tggttgagtc tgggggaggc ttgttacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt caccttttagc agttatgcta tgagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcagct attattggta gtggtgggtat cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300
tttggtgggtt ttaactactg gggccaagga accctgggtca ccgtctcgag t 351

<210> 153
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> 23C10; VL

<400> 153

Glu Ile Val 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 Arg Ser
20 25 30

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

eo1f-seq1

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

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

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

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

<210> 154
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 23C10; VL

<400> 154
gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcttgca gggccagtca gagtggttagc cgcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatcatt ggggcctcca ccagggccac tggcatccca 180
gacaggttca gtggcagtggt atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta ttactgtcag cagggtcagg ttattccccc tacgttcggc 300
caggggacca aagtggaaat caaa 324

<210> 155
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> 23C10; VH

<400> 155

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Ser
20 25 30

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

Ser Ala Ile Ser Thr Asn Gly Asn Tyr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

eof-seq1

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

Ala Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 156
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> 23C10; VH

<400> 156
gaggtgcaat tgttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt caccttttagc agttctgccg tgagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcagct attagtacta atggtaatta tacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300
ctgggtaatt ttgactactg gggccaagga accctgggtca ccgtctcgag t 351

<210> 157
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> 2B10_C3B6; VL

<400> 157

Asp 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 Arg Leu Ile
35 40 45

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

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

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

eolf-seq1

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

<210> 158
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> 2B10_C3B6; VL

<400> 158
gatatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtcggaga ccgggtcacc 60
atcacctgcc gggcaagtca gggcattaga aatgatttag gctggtacca gcagaagcca 120
gggaaagccc ctaagcgctt gatctatgct gcatccagtt tgcagagtgg cgtcccatca 180
aggttcagcg gcagtggatc cgggacagag ttactctca ccatcagcag cttgcagcct 240
gaagattttg ccacctatta ctgcttgcat aatgggtctgc agcccgcgac gtttggccag 300
ggcaccaaag tcgagatcaa g 321

<210> 159
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> 2B10_C3B6; VH

<400> 159
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Ala Ile Ile Pro Ile Leu Gly Ile Ala Asn Tyr Ala Gln Lys Phe
50 55 60
Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Leu Tyr Gly Tyr Ala Tyr Tyr Gly Ala Phe Asp Tyr Trp Gly
100 105 110
Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

eolf-seq1

<210> 160
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> 2B10_C3B6; VH

<400> 160
caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
cctggacaag ggctcgagtg gatgggagct atcatcccga tccttgggtat cgcaaactac 180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagactgtac 300
ggttacgctt actacggtgc ttttgactac tggggccaag ggaccaccgt gaccgtctcc 360
tca 363

<210> 161
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> 2B10_6A12; VL

<400> 161

Asp 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 Arg Leu Ile
35 40 45

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

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

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

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

<210> 162
<211> 321
<212> DNA
<213> Artificial Sequence

eof-seq1

<220>
 <223> 2B10_6A12; VL
 <400> 162
 gatatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtcggaga ccgggtcacc 60
 atcacctgcc gggcaagtca gggcattaga aatgatttag gctggtacca gcagaagcca 120
 gggaaagccc ctaagcgcct gatctatgct gcatccagtt tgcagagtgg cgtcccatca 180
 aggttcagcg gcagtggatc cgggacagag ttcactctca ccatcagcag cttgcagcct 240
 gaagattttg ccacctatta ctgcttgtag aatgggtctgc agcccgcgac gtttggccag 300
 ggcaccaaag tcgagatcaa g 321

<210> 163
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 2B10_6A12; VH
 <400> 163
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
 20 25 30
 Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Val Ile Ile Pro Ile Leu Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60
 Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Leu Tyr Gly Tyr Ala Tyr Tyr Gly Ala Phe Asp Tyr Trp Gly
 100 105 110
 Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 164
 <211> 363
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 2B10_6A12; VH

eolf-seq1

<400> 164
caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
tcctgcaagg cctccggagg cacattcagc agctatgcta taagctgggt gcgacaggcc 120
cctggacaag ggctcgagtg gatgggagtg atcatcccta tccttgggtac cgcaaactac 180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagactgtac 300
ggttacgctt actacggtgc ttttgactac tggggccaag ggaccaccgt gaccgtctcc 360
tca 363

<210> 165
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> 2B10_C3A6; VL

<400> 165
Asp 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 Val
20 25 30
Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
35 40 45
Tyr Asp Ser Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Gly Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asn Gly Leu Gln Pro Ala
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 166
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> 2B10_C3A6; VL

<400> 166
gacatccaga tgaccagtc tccttcctcc ctgtctgcat ctgtcggaga ccgggtcacc 60
atcacctgcc gggcaagtca gggcattcgt aatgttttag gctggtacca gcagaagcca 120
gggaaagccc ctaagcgctt gatctatgat tcgtccagtt tgcagagtgg cgtcccatca 180

eolf-seq1

aggttcagcg gcggtggatc cgggacagag ttactctca ccatcagcag cttgcagcct 240
 gaagattttg ccacctatta ctgcttgag aatgggtctgc agcccgcgac gtttggccag 300
 ggcaccaaag tcgagatcaa g 321

<210> 167
 <211> 121
 <212> PRT
 <213> Artificial sequence

<220>
 <223> 2B10_C3A6; VH

<400> 167

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

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

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

Ala Arg Leu Tyr Gly Tyr Ala Tyr Tyr Gly Ala Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 168
 <211> 363
 <212> DNA
 <213> Artificial sequence

<220>
 <223> 2B10_C3A6; VH

<400> 168

caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
 tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
 cctggacaag ggctcgagt gatgggagg atcatcccta tctttgttac agcaaactac 180
 gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
 atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagactgtac 300

eolf-seq1

ggttacgctt actacggtgc ttttgactac tggggccaag ggaccaccgt gaccgtctcc 360
tca 363

<210> 169
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> 2B10_D1A2_wt; VL

<400> 169

Asp 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 Val
20 25 30

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

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

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

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

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

<210> 170
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> 2B10_D1A2_wt; VL

<400> 170

gatatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtcggaga ccgggtcacc 60
atcacctgcc gggcaagtca ggggattcgt aatgttttag gctggtacca gcagaagcca 120
gggaaagccc ctaagcgct gatctatgat gcttacagct tgcagagtgg cgtcccatca 180
aggttcagcg gcggtggatc cgggacagag ttactctca ccatcagcag cttgcagcct 240
gaagattttg ccacctatta ctgcttgag aatgggtctgc agcccgcgac gtttgccag 300
ggcaccaaag tcgagatcaa g 321

<210> 171
<211> 121

eof-seq1

<212> PRT
<213> Artificial Sequence

<220>
<223> 2B10_D1A2_wt; VH

<400> 171

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

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

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

Ala Arg Leu Tyr Gly Tyr Ala Tyr Tyr Gly Ala Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 172
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> 2B10_D1A2_wt; VH

<400> 172

caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc	60
tcttgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc	120
cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac	180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac	240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagactgtac	300
ggttacgctt actacggtgc ttttgactac tggggccaag ggaccaccgt gaccgtctcc	360
tca	363

<210> 173
<211> 107
<212> PRT
<213> Artificial Sequence

eo1f-seq1

<220>

<223> 2B10_D1A2_VD; VL

<400> 173

Asp 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 Arg Leu Ile
35 40 45

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

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

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

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

<210> 174

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> 2B10_D1A2_VD; VL

<400> 174

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtcggaga ccgggtcacc 60

atcacctgcc gggcaagtca ggggattcgt aatgatttag gctggtacca gcagaagcca 120

gggaaagccc ctaagcgcct gatctatgat gcttacagct tgcagagtgg cgtcccatca 180

aggttcagcg gcggtggatc cgggacagag ttactctca ccatcagcag cttgcagcct 240

gaagattttg ccacctatta ctgcttcgag aatgggtctgc agcccgcgac gtttgccag 300

ggcaccaaag tcgagatcaa g 321

<210> 175

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> 2B10_D1A2_VD; VH

<400> 175

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

eolf-seq1

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

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

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

Ala Arg Leu Tyr Gly Tyr Ala Tyr Tyr Gly Ala Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 176
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> 2B10_D1A2_VD; VH

<400> 176
caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagactgtac 300
ggttacgctt actacggtgc ttttgactac tggggccaag ggaccaccgt gaccgtctcc 360
tca 363

<210> 177
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> 2B10_07D8; VL

<400> 177

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

eolf-seq1

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

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

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

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

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

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

<210> 178
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 2B10_O7D8; VL

<400> 178
 gatatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtcggaga ccgggtcacc 60
 atcacctgcc gggcaagtca gagcattcgt aatgttttag gctggtacca gcagaagcca 120
 gggaaagccc ctaagcgcct gatctatgat gtgtccagtt tgcagagtgg cgtcccatca 180
 aggttcagcg gcggtggatc cgggacagag ttcaactctca ccatcagcag cttgcagcct 240
 gaagattttg ccacctatta ctgcttgtag aatgggtctgc agcccgcgac gtttggccag 300
 ggcaccaaag tcgagatcaa g 321

<210> 179
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 2B10_O7D8; VH

<400> 179
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

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

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

eolf-seq1

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

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

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

Ala Arg Leu Tyr Gly Tyr Ala Tyr Tyr Gly Ala Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 180
 <211> 363
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 2B10_07D8; VH

<400> 180
 caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
 tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
 cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180
 gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
 atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagactgtac 300
 ggttacgctt actacggtgc ttttgactac tggggccaag ggaccaccgt gaccgtctcc 360
 tca 363

<210> 181
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 2B10_01F7; VL

<400> 181

Asp 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 Val
 20 25 30

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

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

eof-seq1

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

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

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

<210> 182
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> 2B10_01F7; VL

<400> 182
gatatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtcggaga ccgggtcacc 60
atcacctgcc gggcaagtca gggcattcgt aatgttttag gctggtacca gcagaagcca 120
gggaaagccc ctaagcgcct gatctatgat gcgtccagtt tgcagagtgg cgtcccatca 180
aggttcagcg gcggtggatc cgggacagag ttactctca ccatcagcag cttgcagcct 240
gaagattttg ccacctatta ctgcctgcag aatgggtctgc agcccgcgac gtttggccag 300
ggcaccaaag tcgagatcaa g 321

<210> 183
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> 2B10_01F7; VH

<400> 183

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

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

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

eolf-seq1

Ala Arg Leu Tyr Gly Tyr Ala Tyr Tyr Gly Ala Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 184
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> 2B10_O1F7; VH

<400> 184
caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggctc 60
tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagactgtac 300
ggttacgctt actacggtgc ttttgactac tggggccaag ggaccaccgt gaccgtctcc 360
tca 363

<210> 185
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> 2B10_6H10; VL

<400> 185
Asp 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 Val
20 25 30
Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
35 40 45
Gln Ala Ala Thr Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Gly Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asn Gly Leu Gln Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105 eolf-seq1

<210> 186
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 2B10_6H10; VL

<400> 186
 gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtcggaga ccgggtcacc 60
 atcacctgcc gggcaagtca gggcattcgt aatgttttag gctggtacca gcagaagcca 120
 gggaaagccc ctaagcgcct gatccaggct gctaccagtt tgcagagtgg cgtcccatca 180
 aggttcagcg gcggtggatc cgggacagag ttactctca ccatcagcag cttgcagcct 240
 gaagattttg ccacctatta ctgcttgag aatgggtctgc agcccgcgac gtttggccag 300
 ggcaccaaag tcgagatcaa g 321

<210> 187
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 2B10_6H10; VH

<400> 187

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
 20 25 30
 Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60
 Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Leu Tyr Gly Tyr Ala Tyr Tyr Gly Ala Phe Asp Tyr Trp Gly
 100 105 110
 Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

eolf-seq1

<210> 188
 <211> 363
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 2B10_6H10; VH

<400> 188
 caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
 tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
 cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180
 gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
 atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagactgtac 300
 ggttacgctt actacggtgc ttttgactac tggggccaag ggaccaccgt gaccgtctcc 360
 tca 363

<210> 189
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CH1A1A; VL

<400> 189

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

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

Tyr Ser Ala Ser Tyr Arg Lys Arg 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 His Gln Tyr Tyr Thr Tyr Pro Leu
 85 90 95

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

<210> 190
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>

eolf-seq1

<223> CH1A1A; VL

<400> 190
 gatatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtgggaga cagagtcacc 60
 atcacttgca aggccagtc ggctgtgggt acgtatgttg cgtggatatca gcagaaacca 120
 gggaaagcac ctaagctcct gatctattcg gcatcctacc gcaaaagggg agtcccatca 180
 aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
 gaagatttcg caacttacta ctgtcaccaa tattacacct atcctctatt cacgtttggc 300
 cagggcacca agctcgagat caag 324

<210> 191
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CH1A1A; VH

<400> 191
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Glu Phe
 20 25 30
 Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Trp Ile Asn Thr Lys Thr Gly Glu Ala Thr Tyr Val Glu Glu Phe
 50 55 60
 Lys Gly Arg Val Thr Phe Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Trp Asp Phe Ala Tyr Tyr Val Glu Ala Met Asp Tyr Trp Gly
 100 105 110
 Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 192
 <211> 363
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CH1A1A; VH

<400> 192
 caggtgcagc tgggtgcagtc tggcgccgaa gtgaagaaac ctggagctag tgtgaagggtg 60

eolf-seq1

tcctgcaagg ccagcggcta caccttcacc gagttcggca tgaactgggt ccgacaggct	120
ccaggccagg gcctcgaatg gatgggctgg atcaacacca agaccggcga ggccacctac	180
gtggaagagt tcaagggcag agtgaccttc accacggaca ccagcaccag caccgcctac	240
atggaactgc ggagcctgag aagcgacgac accgccgtgt actactgcg cagatgggac	300
ttcgcttatt acgtggaagc catggactac tggggccagg gcaccaccgt gaccgtgtct	360
agc	363

<210> 193
 <211> 446
 <212> PRT
 <213> Artificial sequence

<220>
 <223> 28H1 Fab HC-Fc hole (LALA P329G)

<400> 193

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser His
 20 25 30

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

Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp Ser Val Lys
 50 55 60

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

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

Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

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

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
 130 135 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
 145 150 155 160

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
 165 170 175

eolf-seq1
 Gly Leu Tyr Ser₁₈₀ Leu Ser Ser Val₁₈₅ Val Thr Val Pro Ser Ser₁₉₀ Ser Leu
 Gly Thr Gln₁₉₅ Thr Tyr Ile Cys Asn₂₀₀ Val Asn His Lys Pro₂₀₅ Ser Asn Thr
 Lys Val₂₁₀ Asp Lys Lys Val₂₁₅ Glu Pro Lys Ser Cys Asp₂₂₀ Lys Thr His Thr
 Cys₂₂₅ Pro Pro Cys Pro Ala₂₃₀ Pro Glu Ala Ala Gly₂₃₅ Gly Pro Ser Val Phe₂₄₀
 Leu Phe Pro Pro Lys₂₄₅ Pro Lys Asp Thr Leu₂₅₀ Met Ile Ser Arg Thr₂₅₅ Pro
 Glu Val Thr Cys₂₆₀ Val Val Val Asp Val₂₆₅ Ser His Glu Asp Pro₂₇₀ Glu Val
 Lys Phe Asn₂₇₅ Trp Tyr Val Asp Gly₂₈₀ Val Glu Val His Asn₂₈₅ Ala Lys Thr
 Lys Pro₂₉₀ Arg Glu Glu Gln Tyr₂₉₅ Asn Ser Thr Tyr Arg₃₀₀ Val Val Ser Val
 Leu₃₀₅ Thr Val Leu His Gln₃₁₀ Asp Trp Leu Asn Gly₃₁₅ Lys Glu Tyr Lys Cys₃₂₀
 Lys Val Ser Asn₃₂₅ Lys Ala Leu Gly Ala Pro₃₃₀ Ile Glu Lys Thr Ile₃₃₅ Ser
 Lys Ala Lys Gly₃₄₀ Gln Pro Arg Glu Pro₃₄₅ Gln Val Cys Thr Leu₃₅₀ Pro Pro
 Ser Arg Asp₃₅₅ Glu Leu Thr Lys Asn₃₆₀ Gln Val Ser Leu Ser₃₆₅ Cys Ala Val
 Lys Gly₃₇₀ Phe Tyr Pro Ser Asp₃₇₅ Ile Ala Val Glu Trp₃₈₀ Glu Ser Asn Gly
 Gln₃₈₅ Pro Glu Asn Asn Tyr₃₉₀ Lys Thr Thr Pro Pro₃₉₅ Val Leu Asp Ser Asp₄₀₀
 Gly Ser Phe Phe₄₀₅ Leu Val Ser Lys Leu Thr₄₁₀ Val Asp Lys Ser Arg₄₁₅ Trp
 Gln Gln Gly Asn₄₂₀ Val Phe Ser Cys Ser₄₂₅ Val Met His Glu Ala₄₃₀ Leu His
 Asn His Tyr₄₃₅ Thr Gln Lys Ser Leu₄₄₀ Ser Leu Ser Pro Gly₄₄₅ Lys

eolf-seq1

<210> 194
 <211> 1338
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 28H1 Fab HC-Fc hole (LALA P329G)

<400> 194
 gaagtgcagc tgctggaatc cggcggaggc ctggtgcagc ctggcggatc tctgagactg 60
 tcctgcgccg cctccggctt caccttctcc tcccacgcca tgtcctgggt ccgacaggct 120
 cctggcaaag gcctggaatg ggtgtccgcc atctgggcct ccggcgagca gtactacgcc 180
 gactctgtga agggccggtt caccatctcc cgggacaact ccaagaacac cctgtacctg 240
 cagatgaact ccctgcgggc cgaggacacc gccgtgtact actgtgcca gggctggctg 300
 ggcaacttcg actactgggg acagggcacc ctggtcaccg tgtccagcg tagcaccaag 360
 ggccccctcg tgttccccct ggcccccagc agcaagagca ccagcggcgg cacagccgct 420
 ctgggctgcc tgggtcaagga ctacttcccc gagcccgtga ccgtgtcctg gaacagcgga 480
 gccctgacct ccggcgtgca caccttcccc gccgtgctgc agagttctgg cctgtatagc 540
 ctgagcagcg tggtcaccgt gccttctagc agcctgggca cccagacct catctgcaac 600
 gtgaaccaca agcccagcaa caccaagggt gacaagaagg tggagcccaa gagctgcgac 660
 aaaactcaca catgcccacc gtgcccagca cctgaagctg cagggggacc gtcagtcttc 720
 ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 780
 gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840
 gtggaggtgc ataatgcca gacaaagccg cgggaggagc agtacaacag cacgtaccgt 900
 gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960
 aaggtctcca acaaagccct cggcgccccc atcgagaaaa ccatctccaa agccaaaggg 1020
 cagccccgag aaccacaggt gtgcaccctg ccccatccc gggatgagct gaccaagaac 1080
 caggtcagcc tctcgtgcgc agtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1140
 gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200
 ggctccttct tcctcgtgag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1260
 gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1320
 tccctgtctc cgggtaaa 1338

<210> 195
 <211> 592
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 28H1 Fab HC-Fc knob (LALA P329G)-IL-2 qm

<400> 195

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

eo1f-seq1

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser His
20 25 30

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

Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp Ser Val Lys
50 55 60

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

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

Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

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

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
130 135 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145 150 155 160

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
165 170 175

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
180 185 190

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
195 200 205

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

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

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

eo1f-seq1

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

eof-seq1

Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe
565 570 575

Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
580 585 590

<210> 196
<211> 1776
<212> DNA
<213> Artificial Sequence

<220>
<223> 28H1 Fab HC-Fc knob (LALA P329G)-IL-2 qm

<400> 196
gaagtgcagc tgctggaatc cggcggaggc ctggtgcagc ctggcggatc tctgagactg 60
tcctgcgccg cctccggctt cacccttctcc tcccacgccca tgtcctgggt cgcacaggct 120
cctggcaaaag gcctggaatg ggtgtccgcc atctgggcct ccggcgagca gtactacgcc 180
gactctgtga agggccggtt caccatctcc cgggacaact ccaagaacac cctgtacctg 240
cagatgaact ccctgcgggc cgaggacacc gccgtgtact actgtgccaa gggctggctg 300
ggcaacttcg actactgggg acagggcacc ctggtcaccg tgtccagcgc tagcaccaag 360
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420
ctgggctgcc tgggtcaagga ctacttcccc gaaccgggtga cgggtgcgtg gaactcaggc 480
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc 540
ctcagcagcg tgggtaccgt gccctccagc agcttgggca ccagaccta catctgcaac 600
gtgaatcaca agcccagcaa caccaagggtg gacaagaaag ttgagcccaa atcttgtgac 660
aaaactcaca catgcccacc gtgcccagca cctgaagctg cagggggacc gtcagtcttc 720
ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 780
gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840
gtggagggtgc ataatgcaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 900
gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960
aaggctctca acaaagccct cggcgcccc atcgagaaaa ccatctccaa agccaaaggg 1020
cagccccgag aaccacaggt gtacaccctg ccccatgcc gggatgagct gaccaagaac 1080
caggtcagcc tgtggtgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1140
gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200
ggctccttct tcctctacag caagctcacc gtggacaaga gcagggtggca gcaggggaac 1260
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1320
tcctgtctc cgggtggcgg cggaggctcc ggaggcggag gttctggcgg aggtggcgct 1380
cctgcctcct ccagcaccaa gaaaaccag ctccagctgg aacatctcct gctggatctg 1440
cagatgatcc tgaacggcat caacaactac aagaacccca agctgaccgc gatgctgacc 1500

eolf-seq1

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gccaagttcg ccatgccccaa gaaggccacc gagctgaaac atctgcagtg cctggaagag 1560
gaactgaagc ctctggaaga ggtgctgaac ggcgcccagt ccaagaactt ccacctgagg 1620
cctcgggacc tgatctccaa catcaacgtg atcgtgctgg aactgaaggg ctccgagaca 1680
accttcatgt gcgagtacgc cgacgagaca gctaccatcg tggaatttct gaaccggtgg 1740
atcaccttcg cccagtccat catctccacc ctgacc 1776

```

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<210> 197
<211> 592
<212> PRT
<213> Artificial Sequence

```

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<220>
<223> 28H1 Fab HC-Fc knob (LALA P329G)-IL-2 wt
<400> 197

```

```

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

```

```

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser His
20 25 30

```

```

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

```

```

Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp Ser Val Lys
50 55 60

```

```

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

```

```

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

```

```

Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

```

```

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

```

```

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
130 135 140

```

```

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145 150 155 160

```

```

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
165 170 175

```

```

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
180 185 190

```

eo1f-seq1

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
195 200 205

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

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

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
435 440 445

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Thr Ser Ser
450 455 460

eolf-seq1

Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu
465 470 475 480

Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr
485 490 495

Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu
500 505 510

Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
515 520 525

Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu
530 535 540

Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr
545 550 555 560

Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe
565 570 575

Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
580 585 590

<210> 198
<211> 1776
<212> DNA
<213> Artificial sequence

<220>
<223> 28H1 Fab HC-Fc knob (LALA P329G)-IL-2 wt

<400> 198
gaagtgcagc tgctggaatc cggcggaggc ctggtgcagc ctggcggatc tctgagactg 60
tcttgcgccg cctccggctt cactttctcc tcccacgcca tgtcctgggt ccgacaggct 120
cctggcaaag gcctggaatg ggtgtccgcc atctgggcct ccggcggagca gtactacgcc 180
gactctgtga agggccggtt caccatctcc cgggacaact ccaagaacac cctgtacctg 240
cagatgaact ccctgcgggc cgaggacacc gccgtgtact actgtgcca gggctggctg 300
ggcaacttcg actactgggg acagggcacc ctggtcaccg tgtccagcgc tagcaccaag 360
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420
ctgggctgcc tgggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 480
gccctgacca gcggcgtgca cacttcccc gctgtcctac agtcctcagg actctactcc 540
ctcagcagcg tgggtgaccgt gccctccagc agcttgggca ccagaccta catctgcaac 600
gtgaatcaca agcccagcaa caccaagggtg gacaagaaag ttgagccaa atcttgtgac 660
aaaactcaca catgcccacc gtgcccagca cctgaagctg caggggggacc gtcagtcttc 720
ctcttcccc caaaaccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 780

eof-seq1

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840
gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 900
gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960
aaggtctcca acaaagccct cggcgccccc atcgagaaaa ccatctccaa agccaaaggg 1020
cagccccgag aaccacaggt gtacaccctg ccccatgcc gggatgagct gaccaagaac 1080
caggtcagcc tgtggtgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1140
gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200
ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1260
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1320
tcctgtctc cgggtggcgg cggaggctcc ggaggcggag gttctggcgg aggtggcgct 1380
cctacatcct ccagcaccaa gaaaaccag ctccagctgg aacatctcct gctggatctg 1440
cagatgatcc tgaacggcat caacaactac aagaacccca agctgacccg gatgctgacc 1500
ttcaagttct acatgccccaa gaaggccacc gagctgaaac atctgcagtg cctggaagag 1560
gaactgaagc ctctggaaga ggtgctgaac ctggcccagt ccaagaactt ccacctgagg 1620
cctcgggacc tgatctccaa catcaacgtg atcgtgctgg aactgaaggg ctccgagaca 1680
accttcatgt gcgagtacgc cgacgagaca gctaccatcg tggaatttct gaaccggtgg 1740
atcaccttcg cccagtccat catctccacc ctgacc 1776

<210> 199
<211> 574
<212> PRT
<213> Artificial Sequence

<220>
<223> 28H1 Fab HC-Fc knob (LALA P329G)-IL-15 (E53A N79A)
<400> 199

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser His
20 25 30

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

Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp Ser Val Lys
50 55 60

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

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

eo1f-seq1

Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
 115 120 125
 Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
 130 135 140
 Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
 145 150 155 160
 Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
 165 170 175
 Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
 180 185 190
 Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
 195 200 205
 Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
 210 215 220
 Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
 225 230 235 240
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255
 Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
 260 265 270
 Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 275 280 285
 Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 290 295 300
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 305 310 315 320
 Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
 325 330 335
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 340 345 350
 Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
 355 360 365

eolf-seq1

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Ser Gly Gly
435 440 445

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Asn Trp Val Asn
450 455 460

Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His
465 470 475 480

Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys
485 490 495

Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu
500 505 510

Ala Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile
515 520 525

Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Ala Val Thr Glu Ser Gly
530 535 540

Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu
545 550 555 560

Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser
565 570

<210> 200
<211> 1722
<212> DNA
<213> Artificial Sequence

<220>
<223> 28H1 Fab HC-Fc knob (LALA P329G)-IL-15 (E53A N79A)

<400> 200
gaagtgcagc tgctggaatc cggcggaggc ctggtgcagc ctggcggatc tctgagactg 60
tcctgcgccg cctccggctt caccttctcc tcccacgcca tgtcctgggt ccgacaggct 120
cctggcaaag gcctggaatg ggtgtccgcc atctgggcct ccggcgagca gtactacgcc 180

eolf-seq1

gactctgtga agggccggtt caccatctcc cgggacaact ccaagaacac cctgtacctg 240
cagatgaact ccctgcgggc cgaggacacc gccgtgtact actgtgccaa gggctggctg 300
ggcaacttcg actactgggg acagggcacc ctggtcaccg tgtccagcgc tagcaccaag 360
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420
ctgggctgcc tgggtcaagga ctacttcccc gaaccgggtga cgggtgcgtg gaactcaggc 480
gccctgacca gcggcggtgca caccttcccc gctgtcctac agtcctcagg actctactcc 540
ctcagcagcg tgggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 600
gtgaatcaca agcccagcaa caccaagggtg gacaagaaaag ttgagcccaa atcttgtgac 660
aaaactcaca catgcccacc gtgcccagca cctgaagctg caggggggacc gtcagtcttc 720
ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 780
gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840
gtggaggtgc ataattgcaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 900
gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960
aaggtctcca acaaagccct cggcgccccc atcgagaaaa ccatctccaa agccaaaggg 1020
cagccccgag aaccacaggt gtacaccctg ccccatgcc gggatgagct gaccaagaac 1080
caggtcagcc tgtggtgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1140
gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200
ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1260
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1320
tcctgtctc cgggttccgg cggcgagggc tccggaggcg gaggttctgg cggaggtggc 1380
aactgggtga atgtaataag tgatttgaaa aaaattgaag atcttattca atctatgcat 1440
attgatgcta ctttatatac ggaaagtgat gttcacccca gttgcaaagt aacagcaatg 1500
aagtgccttc tcttgagatt acaagttatt tcaattgcgt ccggagatgc aagtattcat 1560
gatacagtag aaaatctgat catcctagca aacaacagtt tgtcttctaa tggggctgta 1620
acagaatctg gatgcaaaga atgtgaggaa ctggaggaaa aaaatattaa agaatttttg 1680
cagagttttg tacatattgt ccaaattgtc atcaacactt ct 1722

<210> 201
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> 4G8 Fab HC-Fc hole (LALA P329G)

<400> 201

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

eolf-seq1

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

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

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
195 200 205

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
210 215 220

Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

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

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

eolf-seq1

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
 290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 305 310 315 320

Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile
 325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro
 340 345 350

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala
 355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 370 375 380

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

Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg
 405 410 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
 420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 202
 <211> 1341
 <212> DNA
 <213> Artificial sequence

<220>
 <223> 4G8 Fab HC-Fc hole (LALA P329G)

<400> 202
 gaggtgcaat tgttgagatc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctccggatt caccttttagc agttatgccca tgagctgggt ccgccaggct 120
 ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300
 ctgggtaatt ttgactactg gggccaagga accctgggtca ccgtctcgag tgctagcacc 360
 aagggcccct ccgtgttccc cctggccccc agcagcaaga gcaccagcgg cggcacagcc 420
 gctctgggct gcctgggtcaa ggactacttc cccgagcccg tgaccgtgtc ctggaacagc 480
 ggagccctga cctccggcgt gcacaccttc cccgccgtgc tgcagagttc tggcctgtat 540
 agcctgagca gcgtgggtcac cgtgccttct agcagcctgg gcacccagac ctacatctgc 600

eolf-seq1

aacgtgaacc acaagcccag caacaccaag gtggacaaga aggtggagcc caagagctgc 660
gacaaaactc acacatgccc accgtgcccga gcacctgaag ctgcaggggg accgtcagtc 720
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 780
tgcgtggtgg tggacgtgag ccacgaagac cctgagggtca agttcaactg gtacgtggac 840
ggcgtggagg tgcataatgc caagacaaaag ccgcggggagg agcagtacaa cagcacgtac 900
cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 960
tgcaaggtct ccaacaaagc cctcggcgcc cccatcgaga aaaccatctc caaagccaaa 1020
gggcagcccc gagaaccaca ggtgtgcacc ctgcccccat cccgggatga gctgaccaag 1080
aaccagggtca gcctctcgtg cgcagtcaaa ggcttctatc ccagcgacat cgccgtggag 1140
tgggagagca atgggcagcc ggagaacaac tacaagacca cgctcccgt gctggactcc 1200
gacggctcct tcttctcgt gagcaagctc accgtggaca agagcaggtg gcagcagggg 1260
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 1320
ctctccctgt ctccgggtaa a 1341

<210> 203
<211> 593
<212> PRT
<213> Artificial sequence

<220>
<223> 4G8 Fab HC-Fc knob (LALA P329G)-IL-2 qm
<400> 203

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

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

eo1f-seq1

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
195 200 205

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
210 215 220

Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

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

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

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

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Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
405 410 415
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly
435 440 445
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Ala Ser
450 455 460
Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp
465 470 475 480
Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu
485 490 495
Thr Arg Met Leu Thr Ala Lys Phe Ala Met Pro Lys Lys Ala Thr Glu
500 505 510
Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu
515 520 525
Val Leu Asn Gly Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp
530 535 540
Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu
545 550 555 560
Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu
565 570 575
Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu
580 585 590

Thr

<210> 204
<211> 1779
<212> DNA
<213> Artificial Sequence

<220>
<223> 4G8 Fab HC-Fc knob (LALA P329G)-IL-2 qm

<400> 204
gaggtgcaat tgttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
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gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtgg	300
ctgggtaatt ttgactactg gggccaagga accctgggtca ccgtctcgag tgctagcacc	360
aagggcccat cgggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	420
gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca	480
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac	540
tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcaccagac ctacatctgc	600
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	660
gacaaaactc acacatgccc accgtgcccc gcacctgaag ctgcaggggg accgtcagtc	720
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca	780
tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac	840
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac	900
cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag	960
tgcaaggctc ccaacaaagc cctcggcgcc cccatcgaga aaaccatctc caaagccaaa	1020
gggcagcccc gagaaccaca ggtgtacacc ctgcccccat gccgggatga gctgaccaag	1080
aaccagggtca gcctgtggtg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag	1140
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc	1200
gacggctcct tcttctctta cagcaagctc accgtggaca agagcaggtg gcagcagggg	1260
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc	1320
ctctccctgt ctccgggtgg cggcggaggc tccggaggcg gaggttctgg cggagggtggc	1380
gctcctgcct cctccagcac caagaaaacc cagctccagc tggaacatct cctgctggat	1440
ctgcagatga tcctgaacgg catcaacaac tacaagaacc ccaagctgac ccggatgctg	1500
accgccaagt tcgcatgcc caagaaggcc accgagctga aacatctgca gtgcctggaa	1560
gaggaactga agcctctgga agagggtgctg aacggcgccc agtccaagaa cttccacctg	1620
aggcctcggg acctgatctc caacatcaac gtgatcgtgc tggaactgaa gggctccgag	1680
acaaccttca tgtgcgagta cgccgacgag acagctacca tcgtggaatt tctgaaccgg	1740
tggatcacct tcgcccagtc catcatctcc accctgacc	1779

<210> 205
 <211> 215
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 4G8 Fab LC

<400> 205

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

eolf-seq1

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

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

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

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

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

Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

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

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

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 206
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> 4G8 Fab LC

<400> 206
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ctgtcctgca gagcctccca gtccgtgtcc cggtcctacc tcgcctggta tcagcagaag 120
cccggccagg cccctcggct gctgatcatc ggcgccctcta ccagagccac cggcatccct 180
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gaccggttct ccggctctgg ctccggcacc gacttcaccc tgaccatctc ccggctggaa	240
cccgaggact tcgccgtgta ctactgccag cagggccagg tcatccctcc cacctttggc	300
cagggcacca aggtggaaat caagcgtacg gtggctgcac catctgtctt catcttccc	360
ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc	420
tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc	480
caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcacctg	540
acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag	600
ggcctgagct cgcccgtcac aaagagcttc aacagggggag agtgt	645

<210> 207
 <211> 447
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 4B9 Fab HC-Fc hole (LALA P329G)

<400> 207

Glu Val Gln Leu	Leu Glu Ser Gly Gly Gly	Leu Val Gln Pro Gly Gly
1	5	10
Ser Leu Arg	Leu Ser Cys Ala Ala	Ser Gly Phe Thr Phe Ser Ser Tyr
20	25	30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly	Leu Glu Trp Val	
35	40	45
Ser Ala Ile Ile Gly Ser Gly Ala Ser Thr Tyr Tyr Ala Asp Ser Val		
50	55	60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr		
65	70	75
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys		
85	90	95
Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu		
100	105	110
Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu		
115	120	125
Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys		
130	135	140
Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser		
145	150	155
		160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 165 170 175 eolf-seq1
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 180 185 190
 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 195 200 205
 Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
 210 215 220
 Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
 225 230 235 240
 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 245 250 255
 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
 260 265 270
 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 275 280 285
 Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
 290 295 300
 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 305 310 315 320
 Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile
 325 330 335
 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro
 340 345 350
 Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala
 355 360 365
 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 370 375 380
 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
 385 390 395 400
 Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg
 405 410 415
 Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
 420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445
 eolf-seq1

<210> 208
 <211> 1341
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 4B9 Fab HC-Fc hole (LALA P329G)

<400> 208
 gaggtgcagc tgctcgaaag cggcggagga ctggtgcagc ctggcggcag cctgagactg 60
 tcttgcgccg ccagcggctt caccttcagc agctacgccca tgagctgggt ccgccaggcc 120
 cctggcaagg gactggaatg ggtgtccgcc atcatcggct ctggcgccag cacctactac 180
 gccgacagcg tgaagggccg gttcaccatc agccgggaca acagcaagaa caccctgtac 240
 ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcgc caagggatgg 300
 ttcggcggct tcaactactg gggacagggc accctgggtca cagtgtccag cgctagcacc 360
 aagggcccct ccgtgttccc cctggcccc agcagcaaga gcaccagcgg cggcacagcc 420
 gctctgggct gcctgggtcaa ggactacttc cccgagcccg tgaccgtgtc ctggaacagc 480
 ggagccctga cctccggcgt gcacaccttc cccgccgtgc tgcagagttc tggcctgtat 540
 agcctgagca gcgtgggtcac cgtgccttct agcagcctgg gcaccagac ctacatctgc 600
 aacgtgaacc acaagcccag caacaccaag gtggacaaga aggtggagcc caagagctgc 660
 gacaaaactc acacatgccc accgtgcccc gcacctgaag ctgcaggggg accgtcagtc 720
 ttctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 780
 tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 840
 ggcgtggagg tgcataatgc caagacaaa cgcggggagg agcagtacaa cagcacgtac 900
 cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 960
 tgcaaggtct ccaacaaagc cctcggcgcc cccatcgaga aaaccatctc caaagccaaa 1020
 gggcagcccc gagaaccaca ggtgtgcacc ctgcccccat cccgggatga gctgaccaag 1080
 aaccagggtca gcctctcgtg cgcagtcaaa ggcttctatc ccagcgacat cgccgtggag 1140
 tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1200
 gacggctcct tcttcctcgt gagcaagctc accgtggaca agagcaggtg gcagcagggg 1260
 aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 1320
 ctctccctgt ctccgggtaa a 1341

<210> 209
 <211> 593
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 4B9 Fab HC-Fc knob (LALA P329G)-IL-2 qm

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<400> 209

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ala Ile Ile Gly Ser Gly Ala Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu
100 105 110

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

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
195 200 205

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
210 215 220

Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

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

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

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Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu
545 550 555 560

Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu
565 570 575

Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu
580 585 590

Thr

<210> 210
<211> 1779
<212> DNA
<213> Artificial Sequence

<220>
<223> 4B9 Fab HC-Fc knob (LALA P329G)-IL-2 qm

<400> 210
gaggtgcagc tgctcgaaag cggcggagga ctggtgcagc ctggcggcag cctgagactg 60
tcttgcgccg ccagcggcctt caccttcagc agctacgccca tgagctgggt ccgccaggcc 120
cctggcaagg gactggaatg ggtgtccgcc atcatcggct ctggcgccag cacctactac 180
gccgacagcg tgaaggggcg gttcaccatc agccgggaca acagcaagaa caccctgtac 240
ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcgc caagggatgg 300
ttcggcggct tcaactactg gggacagggc accctgggtca cagtgtccag cgctagcacc 360
aagggcccat cgggtcttccc cctggcacc cctccaaga gcacctctgg gggcacagcg 420
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca 480
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540
tccttcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 660
gacaaaactc acacatgccc accgtgccc gcacctgaag ctgcaggggg accgtcagtc 720
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 780
tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 840
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 900
cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 960
tgcaaggtct ccaacaaagc cctcggcgcc cccatcgaga aaaccatctc caaagccaaa 1020
gggcagcccc gagaaccaca ggtgtacacc ctgcccccat gccgggatga gctgaccaag 1080
aaccagggtca gcctgtggtg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 1140
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1200
gacggctcct tcttctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 1260

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aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 1320
 ctctccctgt ctccgggtgg cggcggaggc tccggaggcg gaggttctgg cggagggtggc 1380
 gctcctgcct cctccagcac caagaaaacc cagctccagc tggaacatct cctgctggat 1440
 ctgcagatga tcctgaacgg catcaacaac tacaagaacc ccaagctgac ccggatgctg 1500
 accgccaagt tcgcatgcc caagaaggcc accgagctga aacatctgca gtgcctggaa 1560
 gaggaactga agcctctgga agagggtgctg aacggcgccc agtccaagaa cttccacctg 1620
 aggctcggg acctgatctc caacatcaac gtgatcgtgc tggaactgaa gggctccgag 1680
 acaaccttca tgtgcgagta cgccgacgag acagctacca tcgtggaatt tctgaaccgg 1740
 tggatcacct tcgcccagtc catcatctcc accctgacc 1779

<210> 211
 <211> 215
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 3F2 Fab LC

<400> 211

Glu Ile Val 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 Thr Ser Ser
 20 25 30

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

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

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

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

Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
 100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
 115 120 125

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

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

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Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 212
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> 3F2 Fab LC

<400> 212
gagatcgtgc tgaccagtc ccccggcacc ctgtctctga gccctggcga gagagccacc 60
ctgtcctgca gagcctccca gtccgtgacc tcctcctacc tcgcctggta tcagcagaag 120
cccgccagc cccctcggct gctgatcaac gtgggcagtc ggagagccac cggcatcctt 180
gaccggttct ccggtctctg ctccggcacc gacttcaccc tgaccatctc ccggtctggaa 240
cccaggagct tcgccgtgta ctactgccag cagggcatca tgctgcccc cacttttggc 300
cagggcacca aggtggaat caagcgtacg gtggccgctc cctccgtgtt catcttccca 360
ccctccgacg agcagctgaa gtccggcacc gcctccgctg tgtgcctgct gaacaacttc 420
tacccccgcg aggccaaggt gcagtggaag gtggacaacg ccctgcagtc cggcaactcc 480
caggaatccg tcaccgagca ggactccaag gacagcacct actccctgtc ctccaccctg 540
accctgtcca aggccgacta cgagaagcac aaggtgtacg cctgcgaagt gaccaccag 600
ggcctgtcca gccccgtgac caagtccttc aaccggggcg agtgc 645

<210> 213
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> L19 Fab HC-Fc hole (LALA P329G)

<400> 213

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe
20 25 30

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

Ser Ser Ile Ser Gly Ser Ser Gly Thr Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Lys Pro Phe Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

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

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
 130 135 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
 145 150 155 160

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
 165 170 175

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
 180 185 190

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
 195 200 205

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
 210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
 225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255

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

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 275 280 285

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 290 295 300

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Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 305 310 315 320

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
 325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro
 340 345 350

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val
 355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 385 390 395 400

Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 214
 <211> 1338
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> L19 Fab HC-Fc hole (LALA P329G)

<400> 214
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctctggatt cacctttagc agtttttcga tgagctgggt ccgccaggct 120
 ccaggggaagg ggctggagtg ggtctcatct atttccggtg gttcgggtac cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcaaatac acagcctgag agccgaggac acggccgtat attactgtgc gaaaccgttt 300
 ccgtattttg actactgggg ccaggggaacc ctggtcaccg tctcgagtgc tagcaccaag 360
 ggccccctccg tgttccccct ggccccccagc agcaagagca ccagcggcgg cacagccgct 420
 ctgggctgcc tgggtcaagga ctacttcccc gagcccgtga ccgtgtcctg gaacagcgga 480
 gccctgacct ccggcgtgca caccttcccc gccgtgctgc agagttctgg cctgtatagc 540
 ctgagcagcg tggtcaccgt gccttctagc agcctgggca ccagaccta catctgcaac 600
 gtgaaccaca agcccagcaa caccaagggtg gacaagaagg tggagcccaa gagctgcgac 660
 aaaactcaca catgcccacc gtgcccagca cctgaagctg caggggggacc gtcagtcttc 720

eolf-seq1

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ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc      780
gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc      840
gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt      900
gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc      960
aaggtctcca acaaagccct cggcgccccc atcgagaaaa ccatctccaa agccaaaggg    1020
cagccccgag aaccacaggt gtgcaccctg ccccatccc gggatgagct gaccaagaac    1080
caggtcagcc tctcgtgcmc agtcaaaggc ttctatccca gcgacatcmc cgtggagtgg    1140
gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac    1200
ggctccttct tcctcgtgag caagctcacc gtggacaaga gcaggtggca gcaggggaac    1260
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc    1320
tccctgtctc cgggtaaa                                     1338

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<210> 215
<211> 592
<212> PRT
<213> Artificial Sequence

<220>
<223> L19 Fab HC-Fc knob (LALA P329G)-IL-2 qm

<400> 215

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe
20 25 30

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

Ser Ser Ile Ser Gly Ser Ser Gly Thr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Pro Phe Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

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

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
130 135 140

eo1f-seq1

Val₁₄₅ Lys Asp Tyr Phe Pro₁₅₀ Glu Pro Val Thr Val₁₅₅ Ser Trp Asn Ser Gly₁₆₀
 Ala Leu Thr Ser Gly₁₆₅ Val His Thr Phe Pro₁₇₀ Ala Val Leu Gln Ser₁₇₅ Ser
 Gly Leu Tyr Ser₁₈₀ Leu Ser Ser Val Val₁₈₅ Thr Val Pro Ser Ser₁₉₀ Ser Leu
 Gly Thr Gln₁₉₅ Thr Tyr Ile Cys Asn₂₀₀ Val Asn His Lys Pro₂₀₅ Ser Asn Thr
 Lys Val₂₁₀ Asp Lys Lys Val Glu₂₁₅ Pro Lys Ser Cys Asp₂₂₀ Lys Thr His Thr
 Cys₂₂₅ Pro Pro Cys Pro Ala₂₃₀ Pro Glu Ala Ala Gly₂₃₅ Gly Pro Ser Val Phe₂₄₀
 Leu Phe Pro Pro Lys₂₄₅ Pro Lys Asp Thr Leu₂₅₀ Met Ile Ser Arg Thr₂₅₅ Pro
 Glu Val Thr Cys₂₆₀ Val Val Val Asp Val₂₆₅ Ser His Glu Asp Pro₂₇₀ Glu Val
 Lys Phe Asn₂₇₅ Trp Tyr Val Asp Gly₂₈₀ Val Glu Val His Asn₂₈₅ Ala Lys Thr
 Lys Pro₂₉₀ Arg Glu Glu Gln Tyr₂₉₅ Asn Ser Thr Tyr Arg₃₀₀ Val Val Ser Val
 Leu Thr Val Leu His Gln₃₁₀ Asp Trp Leu Asn Gly₃₁₅ Lys Glu Tyr Lys Cys₃₂₀
 Lys Val Ser Asn Lys₃₂₅ Ala Leu Gly Ala Pro₃₃₀ Ile Glu Lys Thr Ile₃₃₅ Ser
 Lys Ala Lys Gly₃₄₀ Gln Pro Arg Glu Pro₃₄₅ Gln Val Tyr Thr Leu₃₅₀ Pro Pro
 Cys Arg Asp₃₅₅ Glu Leu Thr Lys Asn₃₆₀ Gln Val Ser Leu Trp₃₆₅ Cys Leu Val
 Lys Gly₃₇₀ Phe Tyr Pro Ser Asp₃₇₅ Ile Ala Val Glu Trp₃₈₀ Glu Ser Asn Gly
 Gln₃₈₅ Pro Glu Asn Asn Tyr₃₉₀ Lys Thr Thr Pro Pro₃₉₅ Val Leu Asp Ser Asp₄₀₀
 Gly Ser Phe Phe Leu₄₀₅ Tyr Ser Lys Leu Thr₄₁₀ Val Asp Lys Ser Arg Trp₄₁₅

eo1f-seq1

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
435 440 445

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Ala Ser Ser
450 455 460

Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu
465 470 475 480

Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr
485 490 495

Arg Met Leu Thr Ala Lys Phe Ala Met Pro Lys Lys Ala Thr Glu Leu
500 505 510

Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
515 520 525

Leu Asn Gly Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu
530 535 540

Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr
545 550 555 560

Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe
565 570 575

Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
580 585 590

<210> 216
<211> 1776
<212> DNA
<213> Artificial Sequence

<220>
<223> L19 Fab HC-Fc knob (LALA P329G)-IL-2 qm

<400> 216
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt caccttttagc agtttttcga tgagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcatct atttccggtg gttcgggtac cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaccgttt 300
ccgtatatttg actactgggg ccaggggaacc ctggtcaccg tctcgagtgc tagcaccaag 360
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420

eolf-seq1

ctgggctgcc tgggtcaagga ctacttcccc gaaccggtga cgggtgtcgtg gaactcaggc 480
gccctgacca gcggcggtgca caccttcccc gctgtcctac agtcctcagg actctactcc 540
ctcagcagcg tgggtgaccgt gccctccagc agcttgaggca cccagaccta catctgcaac 600
gtgaatcaca agcccagcaa caccaagggtg gacaagaaag ttgagcccaa atcttgtgac 660
aaaactcaca catgcccacc gtgcccagca cctgaagctg caggggggacc gtcagtcttc 720
ctcttcccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 780
gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840
gtggagggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 900
gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960
aaggtctcca acaaagccct cggcgcccc atcgagaaaa ccatctcaa agccaaaggg 1020
cagccccgag aaccacaggt gtacaccctg ccccatgcc gggatgagct gaccaagaac 1080
caggtcagcc tgtggtgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1140
gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200
ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1260
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1320
tcctgtctc cgggtggcgg cggaggctcc ggaggcggag gttctggcgg aggtggcgct 1380
cctgcctcct ccagcaccaa gaaaaccag ctccagctgg aacatctcct gctggatctg 1440
cagatgatcc tgaacggcat caacaactac aagaacccca agctgaccgc gatgctgacc 1500
gccaagttcg ccatgccccaa gaaggccacc gagctgaaac atctgcagtg cctggaagag 1560
gaactgaagc ctctggaaga ggtgctgaac ggcgcccagt ccaagaactt ccacctgagg 1620
cctcgggacc tgatctccaa catcaacgtg atcgtgctgg aactgaaggg ctccgagaca 1680
accttcatgt gcgagtacgc cgacgagaca gctaccatcg tggaatttct gaaccggtgg 1740
atcaccttcg ccagttccat catctccacc ctgacc 1776

<210> 217
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> L19 Fab LC

<400> 217

Glu Ile Val 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

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

eolf-seq1

Ile Tyr Tyr Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Thr Gly Arg Ile Pro
85 90 95
Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
100 105 110
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125
Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140
Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160
Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175
Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190
Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205
Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 218
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> L19 Fab LC

<400> 218
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
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cctggccagg ctcccaggct cctcatctat tatgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta ttactgtcag cagacggggtc gtattcctcc gacgttcggc 300
caagggacca aggtggaaat caaacgtacg gtggctgcac catctgtctt catcttcccg 360
ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420

eolf-seq1

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc	480
caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg	540
acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag	600
ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt	645

<210> 219
 <211> 445
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DP47 GS Fab HC-Fc hole (LALA P329G)

<400> 219

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Lys Gly Ser Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

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

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
 130 135 140

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
 145 150 155 160

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
 165 170 175

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
 180 185 190

eolf-seql

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
195 200 205

Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

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

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
275 280 285

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys
325 330 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser
340 345 350

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys
355 360 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
370 375 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385 390 395 400

Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
405 410 415

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 220
<211> 1335
<212> DNA
<213> Artificial Sequence

eolf-seq1

<220>

<223> DP47 GS Fab HC-Fc hole (LALA P329G)

<400> 220

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gaggtgcaat tgttgagagtc tgggggagggc ttggtacagc ctgggggggtc cctgagactc      60
tcctgtgcag cctccggatt caccttttagc agttatgccca tgagctgggt ccgccaggct      120
ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat      240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggcagc      300
ggatttgact actggggcca aggaaccctg gtcaccgtct cgagtgcctag caccaagggc      360
ccctccgtgt tccccctggc ccccagcagc aagagcacca gcggcggcac agccgctctg      420
ggctgcctgg tcaaggacta cttccccgag cccgtgaccg tgtcctggaa cagcggagcc      480
ctgacctccg gcgtgcacac cttccccgcc gtgctgcaga gttctggcct gtatagcctg      540
agcagcgtgg tcaccgtgcc ttctagcagc ctgggcaccc agacctacat ctgcaacgtg      600
aaccacaagc ccagcaacac caaggtggac aagaagggtg agcccaagag ctgcgacaaa      660
actcacacat gcccaccgtg cccagcacct gaagctgcag ggggaccgtc agtcttcctc      720
ttccccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg      780
gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg      840
gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg      900
gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgaag      960
gtctccaaca aagccctcgg cgcccccatc gagaaaacca tctccaaagc caaagggcag     1020
ccccgagaac cacagggtgtg caccctgccc ccatcccggg atgagctgac caagaaccag     1080
gtcagcctct cgtgcgcagt caaaggcttc tatcccagcg acatcgccgt ggagtgggag     1140
agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc     1200
tcctttcttc tcgtgagcaa gtcaccgtg gacaagagca ggtggcagca ggggaacgtc     1260
ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc     1320
ctgtctccgg gtaaa                                           1335

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<210> 221

<211> 591

<212> PRT

<213> Artificial Sequence

<220>

<223> DP47 GS Fab HC-Fc knob (LALA P329G)-IL-2 qm

<400> 221

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

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20           25           30

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eo1f-seq1

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Gly Ser Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

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

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
130 135 140

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
145 150 155 160

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
165 170 175

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
180 185 190

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
195 200 205

Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

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

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
275 280 285

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

eo1f-seq1

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 305 310 315 320
 Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys
 325 330 335
 Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys
 340 345 350
 Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys
 355 360 365
 Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
 370 375 380
 Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
 385 390 395 400
 Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
 405 410 415
 Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
 420 425 430
 His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
 435 440 445
 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Ala Ser Ser Ser
 450 455 460
 Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln
 465 470 475 480
 Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg
 485 490 495
 Met Leu Thr Ala Lys Phe Ala Met Pro Lys Lys Ala Thr Glu Leu Lys
 500 505 510
 His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu
 515 520 525
 Asn Gly Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile
 530 535 540
 Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr
 545 550 555 560
 Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu
 565 570 575

eolf-seq1

Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
580 585 590

<210> 222
<211> 1773
<212> DNA
<213> Artificial Sequence

<220>
<223> DP47 GS Fab HC-Fc knob (LALA P329G)-IL-2 qm

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<400> 222
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tcctgtgcag cctccggatt cacctttagc agttatgccca tgagctgggt ccgccaggct      120
ccaggaaggg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat      240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggcagc      300
ggatttgact actggggcca aggaaccctg gtcaccgtct cgagtgctag caccaagggc      360
ccatcgggtct tccccctggc accctcctcc aagagcacct ctggggggcac agcggccctg      420
ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc      480
ctgaccagcg gcgtgcacac cttcccggtc gtcctacagt cctcaggact ctactccctc      540
agcagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg      600
aatcacaagc ccagcaacac caaggtggac aagaaaagttg agcccaaadc ttgtgacaaa      660
actcacacat gcccaccgtg cccagcacct gaagctgcag ggggaccgtc agtcttcctc      720
ttccccccaa aaccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg      780
gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg      840
gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg      900
gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgaag      960
gtctccaaca aagccctcgg cgtcccccac gagaaaacca tctccaaagc caaagggcag     1020
ccccgagaac cacaggtgta caccctgccc ccatgccggg atgagctgac caagaaccag     1080
gtcagcctgt ggtgcctggt caaaggcttc tatccagcg acatcgccgt ggagtgggag     1140
agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc     1200
tccttcttcc tctacagcaa gtcaccgtg gacaagagca ggtggcagca ggggaacgtc     1260
ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc     1320
ctgtctccgg gtggcggcgg aggctccgga ggcggagggt ctggcggagg tggcgctcct     1380
gcctcctcca gcaccaagaa aaccagctc cagctggaac atctcctgct ggatctgcag     1440
atgatcctga acggcatcaa caactacaag aacccaagc tgaccgggat gctgaccgcc     1500
aagttcgcca tgccaagaa ggccaccgag ctgaaacatc tgcagtgcct ggaagaggaa     1560
ctgaagcctc tggaagaggt gctgaacggc gcccagtcga agaacttcca cctgaggcct     1620

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eolf-seq1

cgggacctga tctccaacat caacgtgatc gtgctggaac tgaagggctc cgagacaacc 1680
 ttcatgtgcg agtacgccga cgagacagct accatcgtgg aatttctgaa ccggtggatc 1740
 accttcgccc agtccatcat ctccaccctg acc 1773

<210> 223
 <211> 591
 <212> PRT
 <213> Artificial sequence

<220>
 <223> DP47GL Fab HC-Fc knob (LALA P329G)- IL-2 wt

<400> 223

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Lys Gly Ser Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

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

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
 130 135 140

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
 145 150 155 160

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
 165 170 175

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
 180 185 190

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
 195 200 205

eo1f-seq1

Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
 210 215 220
 Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu
 225 230 235 240
 Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 245 250 255
 Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
 260 265 270
 Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
 275 280 285
 Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
 290 295 300
 Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 305 310 315 320
 Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys
 325 330 335
 Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys
 340 345 350
 Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys
 355 360 365
 Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
 370 375 380
 Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
 385 390 395 400
 Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
 405 410 415
 Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
 420 425 430
 His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
 435 440 445
 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Thr Ser Ser Ser
 450 455 460
 Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln
 465 470 475 480

eolf-seq1

Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg
485 490 495

Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys
500 505 510

His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu
515 520 525

Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile
530 535 540

Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr
545 550 555 560

Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu
565 570 575

Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
580 585 590

<210> 224
<211> 1773
<212> DNA
<213> Artificial Sequence

<220>
<223> DP47GS Fab HC-Fc knob (LALA P329G)- IL-2 wt

<400> 224
gagggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggcagc 300
ggatttgact actggggcca aggaaccctg gtcaccgtct cgagtgctag caccaagggc 360
ccatcgggtct tccccctggc accctcctcc aagagcacct ctggggggcac agcggccctg 420
ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc 480
ctgaccagcg gcgtgcacac cttcccggct gtcctacagt cctcaggact ctactccctc 540
agcagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg 600
aatcacaagc ccagcaacac caaggtggac aagaaagttg agcccaaadc ttgtgacaaa 660
actcacacat gcccaccgtg cccagcacct gaagctgcag ggggaccgtc agtcttcctc 720
ttccccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg 780
gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 840
gagggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg 900

eof-seq1

gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgaag 960
gttccaaca aagccctcgg cgcccccatc gagaaaacca tctccaaagc caaagggcag 1020
ccccgagaac cacaggtgta caccctgccc ccatgccggg atgagctgac caagaaccag 1080
gtcagcctgt ggtgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 1140
agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1200
tcctttcttc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1260
ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc 1320
ctgtctccgg gtggcggcgg aggctccgga ggcggagggt ctggcggagg tggcgctcct 1380
acatcctcca gcaccaagaa aaccagctc cagctggaac atctcctgct ggatctgcag 1440
atgatcctga acggcatcaa caactacaag aacccaagc tgaccggat gctgacctc 1500
aagttctaca tgccaagaa ggccaccgag ctgaaacatc tgcagtgcct ggaagaggaa 1560
ctgaagcctc tggaagaggt gctgaacctg gcccagtcca agaacttcca cctgaggcct 1620
cgggacctga tctcaacat caacgtgatc gtgctggaac tgaagggtc cgagacaacc 1680
ttcatgtgcg agtacgccga cgagacagct accatcgctg aatttctgaa ccggtggatc 1740
accttcgccc agtccatcat ctccaccctg acc 1773

<210> 225
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> DP47GS Fab LC
<400> 225

Glu Ile Val 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

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

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

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

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

Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
100 105 110

eolf-seq1

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

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

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

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 226
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> DP47GS Fab LC

<400> 226
gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
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cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtggt atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccgct gacgttcggc 300
caggggacca aagtggaaat caaacgtacg gtggctgcac catctgtctt catcttcccg 360
ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420
tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480
caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540
acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt caccatcag 600
ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 645

<210> 227
<211> 451
<212> PRT
<213> Artificial Sequence

<220>

eof-seq1

<223> CH1A1A Fab HC-Fc hole (wt)

<400> 227

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

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

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

Gly Trp Ile Asn Thr Lys Thr Gly Glu Ala Thr Tyr Val Glu Glu Phe
50 55 60

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

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

Ala Arg Trp Asp Phe Ala Tyr Tyr Val Glu Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

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

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 260 265 270
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 275 280 285
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 290 295 300
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 305 310 315 320
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 325 330 335
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 340 345 350
 Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 355 360 365
 Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 385 390 395 400
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
 405 410 415
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 435 440 445
 Pro Gly Lys
 450

<210> 228
 <211> 1353
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CH1A1A Fab HC-Fc hole (wt)

<400> 228
 caggtgcagc tgggtgcagtc tggcgccgaa gtgaagaaac ctggagctag tgtgaagggtg 60
 tcctgcaagg ccagcggcta caccttcacc gagttcggca tgaactgggt ccgacaggct 120
 ccaggccagg gcctcgaatg gatgggctgg atcaacacca agaccggcga ggccacctac 180
 gtggaagagt tcaagggcag agtgaccttc accacggaca ccagcaccag caccgcctac 240
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atggaactgc ggagcctgag aagcgacgac accgccgtgt actactgcg cagatgggac 300
 ttgcctatt acgtggaagc catggactac tggggccagg gcaccaccgt gaccgtgtct 360
 agcgctagca ccaagggccc aagcgtgttc cctctggccc ccagcagcaa gagcacaagc 420
 ggcggaacag ccgccctggg ctgcctgggtc aaggactact tccccgagcc cgtgacagtg 480
 tcctggaaca gcggagccct gaccagcggc gtgcacacct ttccagccgt gctgcagagc 540
 agcggcctgt acagcctgag cagcgtgggtc acagtgccta gcagcagcct gggcacccag 600
 acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggag 660
 cccaagagct gcgacaagac ccacacctgt cccccttggtc ctgcccctga gctgctgggc 720
 ggacccagcg tgttcctgtt ccccccaaag cccaaggaca ccctgatgat cagccggacc 780
 cccgaagtga cctgcgtggt ggtggacgtg tcccacgagg accctgaagt gaagttcaat 840
 tggtagctgg acggcgtgga ggtgcacaat gccaagacca agccccggga ggaacagtac 900
 aacagcacct accgggtggt gtccgtgctg accgtgctgc accaggactg gctgaacggc 960
 aaagagtaca agtgcaaggt ctccaacaag gccctgcctg ccccatcga gaaaaccatc 1020
 agcaaggcca agggccagcc cagagaaccc cagggtgtgca ccctgcccc cagcagagat 1080
 gagctgacca agaaccaggt gtccctgagc tgtgccgtca agggcttcta cccagcgat 1140
 atcgccgtgg agtgggagag caacggccag cctgagaaca actacaagac cccccccct 1200
 gtgctggaca gcgacggcag cttcttcctg gtgtccaaac tgaccgtgga caagagccgg 1260
 tggcagcagg gcaacgtgtt cagctgcagc gtgatgcacg aggccctgca caaccactac 1320
 acccagaagt ccctgagcct gagccccggc aag 1353

<210> 229
 <211> 599
 <212> PRT
 <213> Artificial sequence

<220>
 <223> CH1A1A Fab HC-Fc knob (wt)-IL-2 qm
 <400> 229

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

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

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

Gly Trp Ile Asn Thr Lys Thr Gly Glu Ala Thr Tyr Val Glu Glu Phe
 50 55 60

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

eo1f-seq1

Met Glu Leu Arg Ser₈₅ Leu Arg Ser Asp₉₀ Thr Ala Val Tyr₉₅ Tyr Cys
Ala Arg Trp Asp₁₀₀ Phe Ala Tyr Tyr Val₁₀₅ Glu Ala Met Asp Tyr₁₁₀ Trp Gly
Gln Gly Thr₁₁₅ Thr Val Thr Val Ser₁₂₀ Ser Ala Ser Thr Lys₁₂₅ Gly Pro Ser
Val Phe₁₃₀ Pro Leu Ala Pro Ser₁₃₅ Ser Lys Ser Thr Ser₁₄₀ Gly Gly Thr Ala
Ala₁₄₅ Leu Gly Cys Leu Val₁₅₀ Lys Asp Tyr Phe Pro₁₅₅ Glu Pro Val Thr Val₁₆₀
Ser Trp Asn Ser Gly₁₆₅ Ala Leu Thr Ser Gly₁₇₀ Val His Thr Phe Pro₁₇₅ Ala
Val Leu Gln Ser₁₈₀ Ser Gly Leu Tyr Ser₁₈₅ Leu Ser Ser Val Val₁₉₀ Thr Val
Pro Ser Ser₁₉₅ Ser Leu Gly Thr Gln₂₀₀ Thr Tyr Ile Cys Asn₂₀₅ Val Asn His
Lys Pro₂₁₀ Ser Asn Thr Lys Val₂₁₅ Asp Lys Lys Val Glu₂₂₀ Pro Lys Ser Cys
Asp₂₂₅ Lys Thr His Thr Cys₂₃₀ Pro Pro Cys Pro Ala₂₃₅ Pro Glu Leu Leu Gly₂₄₀
Gly Pro Ser Val Phe₂₄₅ Leu Phe Pro Pro Lys₂₅₀ Pro Lys Asp Thr Leu₂₅₅ Met
Ile Ser Arg Thr₂₆₀ Pro Glu Val Thr Cys₂₆₅ Val Val Val Asp Val₂₇₀ Ser His
Glu Asp Pro₂₇₅ Glu Val Lys Phe Asn₂₈₀ Trp Tyr Val Asp Gly₂₈₅ Val Glu Val
His Asn Ala Lys Thr Lys Pro₂₉₅ Arg Glu Glu Gln Tyr₃₀₀ Asn Ser Thr Tyr
Arg Val Val Ser Val Leu₃₁₀ Thr Val Leu His Gln₃₁₅ Asp Trp Leu Asn Gly₃₂₀
Lys Glu Tyr Lys Cys₃₂₅ Lys Val Ser Asn Lys₃₃₀ Ala Leu Pro Ala Pro₃₃₅ Ile
Glu Lys Thr Ile₃₄₀ Ser Lys Ala Lys Gly₃₄₅ Gln Pro Arg Glu Pro₃₅₀ Gln Val

eo1f-seq1

Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 355 360 365
 Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 385 390 395 400
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 405 410 415
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 435 440 445
 Pro Gly Lys Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 450 455 460
 Gly Gly Ala Pro Ala Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
 465 470 475 480
 Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
 485 490 495
 Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Ala Lys Phe Ala Met
 500 505 510
 Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
 515 520 525
 Leu Lys Pro Leu Glu Glu Val Leu Asn Gly Ala Gln Ser Lys Asn Phe
 530 535 540
 His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
 545 550 555 560
 Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
 565 570 575
 Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
 580 585 590
 Ser Ile Ile Ser Thr Leu Thr
 595

<210> 230
 <211> 1797

eolf-seq1

<212> DNA

<213> Artificial Sequence

<220>

<223> CH1A1A Fab HC-Fc knob (wt)-IL-2 qm

<400> 230

caggtgcagc	tggtgcagtc	tggcgccgaa	gtgaagaaac	ctggagctag	tgtgaagggtg	60
tcctgcaagg	ccagcggcta	caccttcacc	gagttcggca	tgaactgggt	ccgacaggct	120
ccaggccagg	gcctcgaatg	gatgggctgg	atcaacacca	agaccggcga	ggccacctac	180
gtggaagagt	tcaagggcag	agtgaccttc	accacggaca	ccagcaccag	caccgcctac	240
atggaactgc	ggagcctgag	aagcgacgac	accgccgtgt	actactgctc	cagatgggac	300
ttcgctatt	acgtggaagc	catggactac	tggggccagg	gcaccaccgt	gaccgtgtct	360
agcgctagca	ccaagggccc	aagcgtgttc	cctctggccc	ccagcagcaa	gagcacaagc	420
ggcggaacag	ccgccctggg	ctgcctggtc	aaggactact	tccccgagcc	cgtgacagtg	480
tcctggaaca	gcggagccct	gaccagcggc	gtgcacacct	ttccagccgt	gctgcagagc	540
agcggcctgt	acagcctgag	cagcgtggtc	acagtgccta	gcagcagcct	gggcacccag	600
acctacatct	gcaacgtgaa	ccacaagccc	agcaacacca	aggtggacaa	gaagggtggag	660
cccaagagct	gcgacaagac	ccacacctgt	cccccttgct	ctgccccctga	gctgctgggc	720
ggacccagcg	tgttcctgtt	ccccccaaag	cccaaggaca	ccctgatgat	cagccggacc	780
cccgaagtga	cctgcgtggg	ggtggacgtg	tcccacgagg	accctgaagt	gaagttcaat	840
tggtacgtgg	acggcgtgga	ggtgcacaat	gccaagacca	agccccggga	ggaacagtac	900
aacagcacct	accgggtggg	gtccgtgctg	accgtgctgc	accaggactg	gctgaacggc	960
aaagagtaca	agtgcaagggt	ctccaacaag	gccctgcctg	cccccatcga	gaaaaccatc	1020
agcaaggcca	agggccagcc	cagagaaccc	caggtgtaca	ccctgcccc	ctgcagagat	1080
gagctgacca	agaaccagggt	gtccctgtgg	tgtctgggtca	agggcttcta	ccccagcgat	1140
atcgccgtgg	agtgggagag	caacggccag	cctgagaaca	actacaagac	cacccccctt	1200
gtgctggaca	gcgacggcag	cttcttcctg	tactccaaac	tgaccgtgga	caagagccgg	1260
tggcagcagg	gcaacgtgtt	cagctgcagc	gtgatgcacg	aggccctgca	caaccactac	1320
accagaagt	ccctgagcct	gagccccggc	aagtccggag	gcggagggtc	cggcggcgga	1380
ggttctggcg	gaggtggcgc	tcctgcctcc	tccagcacca	agaaaaccca	gctccagctg	1440
gaacatctcc	tgctggatct	gcagatgatc	ctgaacggca	tcaacaacta	caagaacccc	1500
aagctgaccc	ggatgctgac	cgccaagtgc	gccatgccca	agaaggccac	cgagctgaaa	1560
catctgcagt	gcctggaaga	ggaactgaag	cctctggaag	aggtgctgaa	cggcgcccag	1620
tccaagaact	tccacctgag	gcctcgggac	ctgatctcca	acatcaacgt	gatcgtgctg	1680
gaactgaagg	gctccgagac	aaccttcatt	tgcgagtacg	ccgacgagac	agctaccatc	1740
gtggaatttc	tgaaccgggtg	gatcaccttc	gcccagtcca	tcattctccac	cctgacc	1797

eof-seq1

<210> 231
 <211> 215
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 2F1 Fab LC

<400> 231

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

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

Tyr Ser Ala Ser Tyr Arg Lys Arg 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 His Gln Tyr Tyr Thr Tyr Pro Leu
 85 90 95

Phe Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala
 100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
 115 120 125

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

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

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
 165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
 180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
 195 200 205

Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 232
 <211> 645

eolf-seq1

<212> DNA
<213> Artificial Sequence

<220>
<223> 2F1 Fab LC

<400> 232
gatatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtgggaga cagagtcacc 60
atcacttgca aggccagtcg ggctgtgggt acgtatgttg cgtgggtatca gcagaaacca 120
gggaaagcac ctaagctcct gatctattcg gcatcctacc gcaaaagggg agtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagatttcg caacttacta ctgtcaccaa tattacacct atcctctatt cacgtttggc 300
cagggcacca agctcgagat caagcgtacg gtggctgcac catctgtctt catcttcccg 360
ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420
tatccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480
caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540
acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt caccatcag 600
ggcctgagct cgcccgtcac aaagagcttc aacagggggag agtgt 645

<210> 233
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> 2B10 Fab HC-Fc knob (LALA P329G)

<400> 233
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60
Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Leu Tyr Gly Tyr Ala Tyr Tyr Gly Ala Phe Asp Tyr Trp Gly
100 105 110

eolf-seq1
 Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125
 Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
 130 135 140
 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 145 150 155 160
 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 165 170 175
 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 180 185 190
 Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 195 200 205
 Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
 210 215 220
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
 225 230 235 240
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 245 250 255
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 260 265 270
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 275 280 285
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 290 295 300
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 305 310 315 320
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
 325 330 335
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 340 345 350
 Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 355 360 365
 Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 435 440 445

Pro Gly Lys
 450

<210> 234
 <211> 1353
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 2B10 Fab HC-Fc knob (LALA P329G)

<400> 234
 caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
 tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
 cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180
 gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
 atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagactgtac 300
 ggttacgctt actacgggtgc ttttgactac tggggccaag ggaccaccgt gaccgtctcc 360
 tcagctagca ccaagggccc atcgggtcttc cccctggcac cctcctccaa gagcacctct 420
 gggggcacag cggccctggg ctgcctgggtc aaggactact tccccgaacc ggtgacgggtg 480
 tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggtgt cctacagtcc 540
 tcaggactct actccctcag cagcgtgggt accgtgccct ccagcagctt gggcacccag 600
 acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660
 cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720
 ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 780
 cctgagggtca catgcgtgggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840
 tggtagctgg acggcggtga ggtgcataat gccaagacaa agccgcggga ggagcagtag 900
 aacagcacgt accgtgtgggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960
 aaggagtaca agtgcaagggt ctccaacaaa gccctcggcg ccccatcga gaaaaccatc 1020
 tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atgccgggat 1080
 gagctgacca agaaccagggt cagcctgtgg tgcctgggtca aaggcttcta tcccagcgac 1140
 atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc 1200

eolf-seq1

```

gtgctggact cgcacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg      1260
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac      1320
acgcagaaga gcctctccct gtctccgggt aaa                                  1353

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<210> 235
<211> 805
<212> PRT
<213> Artificial sequence

```

```

<220>
<223> 2B10 Fab HC-Fc hole (LALA P329G)-scIL-10

```

```

<400> 235

```

```

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

```

```

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

```

```

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

```

```

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50          55          60

```

```

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

```

```

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

```

```

Ala Arg Leu Tyr Gly Tyr Ala Tyr Tyr Gly Ala Phe Asp Tyr Trp Gly
100          105          110

```

```

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115          120          125

```

```

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

```

```

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145          150          155          160

```

```

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165          170          175

```

```

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180          185          190

```

```

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195          200          205

```

eo1f-seq1

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
 210 215 220
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
 225 230 235 240
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 245 250 255
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 260 265 270
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 275 280 285
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 290 295 300
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 305 310 315 320
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
 325 330 335
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 340 345 350
 Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 355 360 365
 Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 385 390 395 400
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
 405 410 415
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 435 440 445
 Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 450 455 460
 Ser Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe
 465 470 475 480

eo1f-seq1

Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser
485 490 495

Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu
500 505 510

Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln
515 520 525

Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln
530 535 540

Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly
545 550 555 560

Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe
565 570 575

Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala
580 585 590

Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe
595 600 605

Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg
610 615 620

Asn Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
625 630 635 640

Gly Gly Gly Gly Ser Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser
645 650 655

Cys Thr His Phe Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg
660 665 670

Asp Ala Phe Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu
675 680 685

Asp Asn Leu Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr
690 695 700

Leu Gly Cys Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu
705 710 715 720

Val Met Pro Gln Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val
725 730 735

Asn Ser Leu Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg
740 745 750

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Cys His Arg Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln
755 760 765

Val Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala
770 775 780

Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr
785 790 795 800

Met Lys Ile Arg Asn
805

<210> 236
<211> 2415
<212> DNA
<213> Artificial Sequence

<220>
<223> 2B10 Fab HC-Fc hole (LALA P329G)-scIL-10

<400> 236
caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagactgtac 300
ggttacgctt actacggtgc ttttgactac tggggccaag ggaccaccgt gaccgtctcc 360
tcagctagca ccaagggccc atcgggtcttc cccctggcac cctcctccaa gagcacctct 420
gggggacacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacgggtg 480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540
tcaggactct actccctcag cagcgtgggt accgtgccct ccagcagctt gggcacccag 600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660
cccaaattctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccgacc 780
cctgagggtca catgcgtggg ggtggacgtg agccacgaag accctgaggt caagttcaac 840
tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 900
aacagcacgt accgtgtggg cagcgtcctc accgtcctgc accaggactg gctgaatggc 960
aaggagtaca agtgcaaggc ctccaacaaa gccctcggcg ccccatcga gaaaaccatc 1020
tccaaagcca aagggcagcc ccgagaacca cagggtgtgca ccctgcccc atcccgggat 1080
gagctgacca agaaccaggc cagcctctcg tgcgcagtca aaggcttcta tcccagcgac 1140
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc 1200
gtgctggact ccgacggctc cttcttcctc gtgagcaagc tcaccgtgga caagagcagg 1260

eolf-seq1

tggcagcagg ggaacgtctt ctcagtctcc gtgatgcatg aggctctgca caaccactac	1320
acgcagaaga gcctctccct gtctccgggt ggcggcggag gctccggagg cggaggatct	1380
gggggaggcg gaagtagccc gggccagggc acccagagcg agaacagctg caccacttc	1440
cccggcaacc tgcccaacat gctgcgggac ctgagggacg ccttcagcag agtgaaaacc	1500
ttctttccaga tgaaggacca gctggacaac ctgctgctga aagagagcct gctggaagat	1560
ttcaagggct acctgggctg tcaggccctg agcgagatga tccagttcta cctggaagaa	1620
gtgatgcccc aggccgagaa ccaggacccc gacatcaagg cccacgtgaa cagcctgggc	1680
gagaacctga aaacctgcg gctgagactg cggcggtgcc acagatttct gccctgagag	1740
aacaagagca aggccgtgga acaggatgaag aacgccttca acaagctgca ggaaaagggc	1800
atctacaagg ccatgtccga gttcgacatc ttcataact acatcgaagc ttacatgacc	1860
atgaagatca gaaacggcgg aggcggatct ggcggcggtg gaagtggagg cggaggatct	1920
gggggaggcg gaagtagccc gggccagggc acccagagcg agaacagctg caccacttc	1980
cccggcaacc tgcccaacat gctgcgggac ctgagggacg ccttcagcag agtgaaaacc	2040
ttctttccaga tgaaggacca gctggacaac ctgctgctga aagagagcct gctggaagat	2100
ttcaagggct acctgggctg tcaggccctg agcgagatga tccagttcta cctggaagaa	2160
gtgatgcccc aggccgagaa ccaggacccc gacatcaagg cccacgtgaa cagcctgggc	2220
gagaacctga aaacctgcg gctgagactg cggcggtgcc acagatttct gccctgagag	2280
aacaagagca aggccgtgga acaggatgaag aacgccttca acaagctgca ggaaaagggc	2340
atctacaagg ccatgtccga gttcgacatc ttcataact acatcgaggc ctacatgaca	2400
atgaaaatcc gcaat	2415

<210> 237
 <211> 631
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 2B10 Fab HC-Fc hole (LALA P329G)-IL-10M1

<400> 237

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe	
50 55 60	

eolf-seq1
 Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Leu Tyr Gly Tyr Ala Tyr Tyr Gly Ala Phe Asp Tyr Trp Gly
 100 105 110
 Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125
 Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
 130 135 140
 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 145 150 155 160
 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 165 170 175
 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 180 185 190
 Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 195 200 205
 Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
 210 215 220
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
 225 230 235 240
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 245 250 255
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 260 265 270
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 275 280 285
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 290 295 300
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 305 310 315 320
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
 325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 340 345 350
 Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 355 360 365
 Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 385 390 395 400
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
 405 410 415
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 435 440 445
 Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 450 455 460
 Ser Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe
 465 470 475 480
 Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser
 485 490 495
 Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu
 500 505 510
 Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln
 515 520 525
 Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln
 530 535 540
 Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly
 545 550 555 560
 Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe
 565 570 575
 Leu Pro Cys Glu Asn Gly Gly Gly Ser Gly Gly Lys Ser Lys Ala Val
 580 585 590
 Glu Gln Val Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr
 595 600 605

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Lys Ala Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr
 610 615 620

Met Thr Met Lys Ile Arg Asn
 625 630

<210> 238
 <211> 1893
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 2B10 Fab HC-Fc hole (LALA P329G)-IL-10M1

<400> 238
 caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
 tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
 cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180
 gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
 atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagactgtac 300
 ggttacgctt actacgggtgc ttttgactac tggggccaag ggaccaccgt gaccgtctcc 360
 tcagctagca ccaagggccc atcgggtcttc cccctggcac cctcctcaa gagcacctct 420
 gggggcacag cgcccttggg ctgcctgggtc aaggactact tccccgaacc ggtgacgggtg 480
 tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540
 tcaggactct actccctcag cagcgtgggtg accgtgccct ccagcagctt gggcacccag 600
 acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttag 660
 cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720
 ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 780
 cctgagggtca catgcgtgggt ggtggacgtg agccacgaag accctgagggt caagttcaac 840
 tggtagctgg acggcggtga ggtgcataat gccaagacaa agccgcggga ggagcagtac 900
 aacagcacgt accgtgtgggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960
 aaggagtaca agtgcaagggt ctccaacaaa gccctcggcg ccccatcga gaaaaccatc 1020
 tccaaagcca aagggcagcc ccgagaacca cagggtgtgca ccctgcccc atcccgggat 1080
 gagctgacca agaaccagggt cagcctctcg tgcgcagtca aaggcttcta tcccagcgac 1140
 atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc 1200
 gtgctggact ccgacggctc cttcttcctc gtgagcaagc tcaccgtgga caagagcagg 1260
 tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1320
 acgcagaaga gcctctccct gtctccgggt ggcggcggag gctccggagg cggaggaagt 1380
 ggcggcggtg gcagctctcc aggccagggc acccagagcg agaacagctg caccacttc 1440
 cccggcaacc tgcccaacat gctgcgggac ctgagggacg ccttcagcag agtgaaaacc 1500
 ttcttccaga tgaaggacca gctggacaac ctgctgctga aagagagcct gctggaagat 1560

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ttcaagggct acctgggctg tcaggccctg agcgagatga tccagttcta cctggaagaa 1620
 gtgatgcccc aggccgagaa ccaggacccc gacatcaagg cccacgtgaa cagcctgggc 1680
 gagaacctga aaacctgcg gctgagactg cggcggtgcc acagatttct gccctgcgag 1740
 aacggcggag gctctggcgg aaagtccaag gccgtggaac aggtgaagaa cgccttcaac 1800
 aagctgcagg aaaagggcat ctacaaggcc atgagcgagt tcgacatctt catcaactac 1860
 atcgaagctt acatgacaat gaagatacga aac 1893

<210> 239
 <211> 214
 <212> PRT
 <213> Artificial sequence

<220>
 <223> 2B10 Fab LC

<400> 239

Asp 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 Arg Leu Ile
 35 40 45

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

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

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

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Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
 210

<210> 240
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 2B10 Fab LC

<400> 240
 gatatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtcggaga ccgggtcacc 60
 atcacctgcc gggcaagtca gggcattaga aatgatttag gctggtacca gcagaagcca 120
 gggaaagccc ctaagcgcct gatctatgct gcatccagtt tgcagagtgg cgtcccatca 180
 aggttcagcg gcggtggatc cgggacagag ttcaactctca ccatcagcag cttgcagcct 240
 gaagattttg ccacctatta ctgcttgtag aatgggtctgc agcccgcgac gtttggccag 300
 ggcaccaaag tcgagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagaggt gt 642

<210> 241
 <211> 447
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 4G8 Fab HC-Fc knob (LALA P329G)

<400> 241

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

eolf-seq1

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

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

Ala Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

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

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
195 200 205

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
210 215 220

Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

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

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile
325 330 335

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Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

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

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 242
<211> 1341
<212> DNA
<213> Artificial Sequence

<220>
<223> 4G8 Fab HC-Fc knob (LALA P329G)

<400> 242
gagggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300
ctgggtaatt ttgactactg gggccaagga accctgggtca ccgtctcgag tgctagcacc 360
aagggcccat cggctcttccc cctggcacc tcctccaaga gcacctctgg gggcacagcg 420
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540
tccttcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 660
gacaaaactc acacatgccc accgtgccc gcacctgaag ctgcaggggg accgtcagtc 720
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 780
tgcgtggtgg tggacgtgag ccacgaagac cctgagggtca agttcaactg gtacgtggac 840
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 900

eof-seq1

cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 960
 tgcaagggtct ccaacaaagc cctcggcgcc cccatcgaga aaaccatctc caaagccaaa 1020
 gggcagcccc gagaaccaca ggtgtacacc ctgcccccat gccgggatga gctgaccaag 1080
 aaccagggtca gcctgtggtg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 1140
 tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1200
 gacggctcct tcttcctcta cagcaagctc accgtggaca agagcagggtg gcagcagggg 1260
 aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 1320
 ctctccctgt ctccgggtaa a 1341

<210> 243
 <211> 801
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 4G8 Fab HC-Fc hole (LALA P329G)-scIL-10

<400> 243

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

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

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 165 170 175 eolf-seq1
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 180 185 190
 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 195 200 205
 Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
 210 215 220
 Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
 225 230 235 240
 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 245 250 255
 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
 260 265 270
 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 275 280 285
 Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
 290 295 300
 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 305 310 315 320
 Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile
 325 330 335
 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro
 340 345 350
 Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala
 355 360 365
 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 370 375 380
 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
 385 390 395 400
 Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg
 405 410 415
 Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
 420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly
 435 440 445
 Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Pro Gly
 450 455 460
 Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro Gly Asn Leu
 465 470 475 480
 Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg Val Lys Thr
 485 490 495
 Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu Lys Glu Ser
 500 505 510
 Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala Leu Ser Glu
 515 520 525
 Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala Glu Asn Gln
 530 535 540
 Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly Glu Asn Leu Lys
 545 550 555 560
 Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu Pro Cys Glu
 565 570 575
 Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe Asn Lys Leu
 580 585 590
 Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp Ile Phe Ile
 595 600 605
 Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn Gly Gly Gly
 610 615 620
 Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 625 630 635 640
 Ser Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe
 645 650 655
 Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser
 660 665 670
 Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu
 675 680 685
 Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln
 690 695 700

Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln
 705 710 715 720

Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly
 725 730 735

Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe
 740 745 750

Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala
 755 760 765

Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe
 770 775 780

Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg
 785 790 795 800

Asn

<210> 244
 <211> 2403
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 4G8 Fab HC-Fc hole (LALA P329G)-scIL-10

<400> 244
 gaggtgcaat tgttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctccggatt caccttttagc agttatgcc a tgagctgggt ccgccaggct 120
 ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggtgg 300
 ctgggtaatt ttgactactg gggccaagga accctgggtca ccgtctcgag tgctagcacc 360
 aagggcccat cggctcttccc cctggcacc cctccaaga gcacctctgg gggcacagcg 420
 gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480
 ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540
 tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcaccagac ctacatctgc 600
 aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 660
 gacaaaactc acacatgccc accgtgccc gcacctgaag ctgcaggggg accgtcagtc 720
 ttctcttccc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 780
 tgcgtggtgg tggacgtgag ccacgaagac cctgagggtca agttcaactg gtacgtggac 840
 ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 900
 cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 960

eolf-seq1

tgcaaggtct	ccaacaaagc	cctcggcgcc	cccacgcaga	aaaccatctc	caaagccaaa	1020
gggcagcccc	gagaaccaca	ggtgtgcacc	ctgcccccat	cccgggatga	gctgaccaag	1080
aaccaggtca	gcctctcgtg	cgcagtcaaa	ggcttctatc	ccagcgacat	cgccgtggag	1140
tgggagagca	atgggcagcc	ggagaacaac	tacaagacca	cgcctcccgt	gctggactcc	1200
gacggctcct	tcttcctcgt	gagcaagctc	accgtggaca	agagcaggtg	gcagcagggg	1260
aacgtcttct	catgctccgt	gatgcatgag	gctctgcaca	accactacac	gcagaagagc	1320
ctctccctgt	ctccgggtgg	cggcggaggc	tccggaggcg	gaggatctgg	gggaggcgga	1380
agtagcccg	gccagggcac	ccagagcgag	aacagctgca	cccacttccc	cggcaacctg	1440
cccaacatgc	tgcgggacct	gagggacgcc	ttcagcagag	tgaaaacctt	cttccagatg	1500
aaggaccagc	tggacaacct	gctgctgaaa	gagagcctgc	tggaagattt	caagggctac	1560
ctgggctgtc	agggcctgag	cgagatgata	cagttctacc	tggaagaagt	gatgccccag	1620
gccgagaacc	aggacccccga	catcaaggcc	cacgtgaaca	gcctgggcca	gaacctgaaa	1680
accctgcggc	tgagactgag	gcgggtccac	agatttctgc	cctgcgagaa	caagagcaag	1740
gccgtggaac	aggtgaagaa	cgccttcaac	aagctgcagg	aaaagggcat	ctacaaggcc	1800
atgtccgagt	tcgacatctt	catcaactac	atcgaagctt	acatgaccat	gaagatcaga	1860
aacggcggag	gcggatctgg	cggcgggtga	agtggaggcg	gaggatctgg	gggaggcgga	1920
agtagcccg	gccagggcac	ccagagcgag	aacagctgca	cccacttccc	cggcaacctg	1980
cccaacatgc	tgcgggacct	gagggacgcc	ttcagcagag	tgaaaacctt	cttccagatg	2040
aaggaccagc	tggacaacct	gctgctgaaa	gagagcctgc	tggaagattt	caagggctac	2100
ctgggctgtc	agggcctgag	cgagatgata	cagttctacc	tggaagaagt	gatgccccag	2160
gccgagaacc	aggacccccga	catcaaggcc	cacgtgaaca	gcctgggcca	gaacctgaaa	2220
accctgcggc	tgagactgag	gcgggtccac	agatttctgc	cctgcgagaa	caagagcaag	2280
gccgtggaac	aggtgaagaa	cgccttcaac	aagctgcagg	aaaagggcat	ctacaaggcc	2340
atgtccgagt	tcgacatctt	catcaactac	atcgaggcct	acatgacaat	gaaaatccgc	2400
aat						2403

<210> 245
 <211> 627
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> 4G8 Fab HC-Fc hole (LALA P329G)-IL-10M1
 <400> 245

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

eo1f-seq1

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

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

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
195 200 205

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
210 215 220

Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

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

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

eo1f-seq1

Val 305 Leu Thr Val Leu His 310 Gln Asp Trp Leu Asn 315 Gly Lys Glu Tyr Lys 320
 Cys Lys Val Ser Asn 325 Lys Ala Leu Gly Ala 330 Pro Ile Glu Lys Thr 335 Ile
 Ser Lys Ala Lys 340 Gly Gln Pro Arg Glu 345 Pro Gln Val Cys Thr 350 Leu Pro
 Pro Ser Arg 355 Asp Glu Leu Thr Lys 360 Asn Gln Val Ser Leu 365 Ser Cys Ala
 Val 370 Lys Gly Phe Tyr Pro Ser 375 Asp Ile Ala Val Glu 380 Trp Glu Ser Asn
 Gly 385 Gln Pro Glu Asn Asn 390 Tyr Lys Thr Thr Pro 395 Pro Val Leu Asp Ser 400
 Asp Gly Ser Phe Phe 405 Leu Val Ser Lys Leu 410 Thr Val Asp Lys Ser 415 Arg
 Trp Gln Gln Gly 420 Asn Val Phe Ser Cys 425 Ser Val Met His Glu 430 Ala Leu
 His Asn His 435 Tyr Thr Gln Lys Ser 440 Leu Ser Leu Ser Pro 445 Gly Gly Gly
 Gly 450 Gly Ser Gly Gly Gly Gly 455 Ser Gly Gly Gly Gly 460 Ser Ser Pro Gly
 Gln 465 Gly Thr Gln Ser Glu 470 Asn Ser Cys Thr His 475 Phe Pro Gly Asn Leu 480
 Pro Asn Met Leu Arg 485 Asp Leu Arg Asp Ala 490 Phe Ser Arg Val Lys 495 Thr
 Phe Phe Gln Met 500 Lys Asp Gln Leu Asp 505 Asn Leu Leu Leu Lys 510 Glu Ser
 Leu Leu Glu 515 Asp Phe Lys Gly Tyr 520 Leu Gly Cys Gln Ala 525 Leu Ser Glu
 Met Ile 530 Gln Phe Tyr Leu Glu 535 Glu Val Met Pro Gln 540 Ala Glu Asn Gln
 Asp 545 Pro Asp Ile Lys Ala 550 His Val Asn Ser Leu 555 Gly Glu Asn Leu Lys 560
 Thr Leu Arg Leu Arg 565 Leu Arg Arg Cys His 570 Arg Phe Leu Pro Cys 575 Glu

eolf-seq1

Asn Gly Gly Gly Ser Gly Gly Lys Ser Lys Ala Val Glu Gln Val Lys
580 585 590

Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser
595 600 605

Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys
610 615 620

Ile Arg Asn
625

<210> 246
<211> 1881
<212> DNA
<213> Artificial Sequence

<220>
<223> 4G8 Fab HC-Fc hole (LALA P329G)-IL-10M1

<400> 246
gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt cacctttagc agttatgcc a tgagctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggtgg 300
ctgggtaatt ttgactactg gggccaagga accctgggtca ccgtctcgag tgctagcacc 360
aagggcccat cggctcttccc cctggcacc tcctccaaga gcacctctgg gggcacagcg 420
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540
tccttcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 660
gacaaaactc acacatgccc accgtgcccc gcacctgaag ctgcaggggg accgtcagtc 720
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 780
tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 840
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 900
cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 960
tgcaaggctt ccaacaaagc cctcggcgcc cccatcgaga aaaccatctc caaagccaaa 1020
gggcagcccc gagaaccaca ggtgtgcacc ctgcccccat cccgggatga gctgaccaag 1080
aaccagggtca gcctctctgt cgcagtcaaa ggcttctatc ccagcgacat cgccgtggag 1140
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1200
gacggctcct tcttctctgt gagcaagctc accgtggaca agagcaggtg gcagcagggg 1260

eolf-seq1

aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 1320
ctctccctgt ctccgggtgg cggcggaggc tccggaggcg gaggaagtgg cggcgggtggc 1380
agctctccag gccagggcac ccagagcgag aacagctgca cccacttccc cggcaacctg 1440
cccaacatgc tgcgggacct gagggacgcc ttcagcagag tgaaaacctt cttccagatg 1500
aaggaccagc tggacaacct gctgctgaaa gagagcctgc tggaagattt caagggctac 1560
ctgggctgtc aggccctgag cgagatgatc cagttctacc tggaagaagt gatgccccag 1620
gccgagaacc aggaccccgga catcaaggcc cacgtgaaca gcctgggcga gaacctgaaa 1680
accctgcggc tgagactgcg gcggtgccac agatttctgc cctgcgagaa cggcggaggc 1740
tctggcggaa agtccaaggc cgtggaacag gtgaagaacg ccttcaacaa gctgcaggaa 1800
aagggcatct acaaggccat gagcgagttc gacatcttca tcaactacat cgaagcttac 1860
atgacaatga agatacgaaa c 1881

<210> 247
<211> 366
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-2 qm-Fc knob (LALA P329G) (IL-2 N-terminal)

<400> 247

Ala Pro Ala Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
1 5 10 15

Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
20 25 30

Asn Pro Lys Leu Thr Arg Met Leu Thr Ala Lys Phe Ala Met Pro Lys
35 40 45

Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
50 55 60

Pro Leu Glu Glu Val Leu Asn Gly Ala Gln Ser Lys Asn Phe His Leu
65 70 75 80

Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
85 90 95

Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
100 105 110

Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
115 120 125

Ile Ser Thr Leu Thr Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr
130 135 140

eolf-seq1

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
145 150 155 160

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
165 170 175

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
180 185 190

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
195 200 205

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
210 215 220

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
225 230 235 240

Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
245 250 255

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
260 265 270

Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
275 280 285

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
290 295 300

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

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
325 330 335

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
340 345 350

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
355 360 365

<210> 248
<211> 1098
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-2 qm-Fc knob (LALA P329G) (IL-2 N-terminal)

<400> 248
gctcctgcct cctccagcac caagaaaacc cagctccagc tggaacatct cctgctggat
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eolf-seq1

ctgcagatga tcctgaacgg catcaacaac tacaagaacc ccaagctgac ccggatgctg 120
accgccaagt tcgcatgcc caagaaggcc accgagctga aacatctgca gtgcctggaa 180
gaggaactga agcctctgga agaggtgctg aacggcgccc agtccaagaa cttccacctg 240
aggcctcggg acctgatctc caacatcaac gtgatcgtgc tggaactgaa gggctccgag 300
acaaccttca tgtgcgagta cgccgacgag acagctacca tcgtggaatt tctgaaccgg 360
tggtacacct tcgcccagtc catcatctcc accctgacct ccggtggtgg cggatccgac 420
aaaactcaca catgcccacc gtgcccagca cctgaagctg caggggggacc gtcagtcttc 480
ctcttccccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 540
gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 600
gtggaggtgc ataatgcca gacaaagccg cgggaggagc agtacaacag cacgtaccgt 660
gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 720
aaggtctcca acaaagccct cggcgccccc atcgagaaaa ccatctccaa agccaaaggg 780
cagccccgag aaccacaggt gtacaccctg ccccatgcc gggatgagct gaccaagaac 840
caggtcagcc tgtggtgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 900
gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 960
ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1020
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1080
tccctgtctc cgggtaaa 1098

<210> 249
<211> 384
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-7-Fc knob (LALA P329G) (IL-7 N-terminal)
<400> 249

Asp Cys Asp Ile Glu Gly Lys Asp Gly Lys Gln Tyr Glu Ser Val Leu
1 5 10 15

Met Val Ser Ile Asp Gln Leu Leu Asp Ser Met Lys Glu Ile Gly Ser
20 25 30

Asn Cys Leu Asn Asn Glu Phe Asn Phe Phe Lys Arg His Ile Cys Asp
35 40 45

Ala Asn Lys Glu Gly Met Phe Leu Phe Arg Ala Ala Arg Lys Leu Arg
50 55 60

Gln Phe Leu Lys Met Asn Ser Thr Gly Asp Phe Asp Leu His Leu Leu
65 70 75 80

Lys Val Ser Glu Gly Thr Thr Ile Leu ^{eolf-seq1} Leu Asn Cys Thr Gly Gln Val
 85 90 95
 Lys Gly Arg Lys Pro Ala Ala Leu Gly Glu Ala Gln Pro Thr Lys Ser
 100 105 110
 Leu Glu Glu Asn Lys Ser Leu Lys Glu Gln Lys Lys Leu Asn Asp Leu
 115 120 125
 Cys Phe Leu Lys Arg Leu Leu Gln Glu Ile Lys Thr Cys Trp Asn Lys
 130 135 140
 Ile Leu Met Gly Thr Lys Glu His Gly Gly Gly Gly Ser Asp Lys Thr
 145 150 155 160
 His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
 165 170 175
 Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 180 185 190
 Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
 195 200 205
 Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 210 215 220
 Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
 225 230 235 240
 Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 245 250 255
 Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr
 260 265 270
 Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 275 280 285
 Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys
 290 295 300
 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 305 310 315 320
 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 325 330 335
 Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 340 345 350

eolf-seq1
 Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 355 360 365

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 370 375 380

<210> 250
 <211> 1152
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IL-7-Fc knob (LALA P329G) (IL-7 N-terminal)

<400> 250
 gattgtgata ttgaaggtaa agatggcaaa caatatgaga gtgttctaata ggtcagcatc 60
 gatcaattat tggacagcat gaaagaaatt ggtagcaatt gcctgaataa tgaatttaac 120
 ttttttaaaa gacatatctg tgatgctaata aaggaaggta tgtttttatt ccgtgctgct 180
 cgcaagttga ggcaatttct taaaatgaat agcactggtg attttgatct ccacttatta 240
 aaagtttcag aaggcacaac aatactgttg aactgcactg gccagggttaa aggaagaaaa 300
 ccagctgccc tgggtgaagc ccaaccaaca aagagtttg aagaaaataa atctttaaag 360
 gaacagaaaa aactgaatga cttgtgtttc cttaaagagac tattacaaga gataaaaaact 420
 tgttggaata aaattttgat gggcactaaa gaacacggtg gtggcggatc cgacaaaact 480
 cacacatgcc caccgtgccc agcacctgaa gctgcagggg gaccgtcagt cttcctcttc 540
 cccccaaaac ccaaggacac cctcatgata tcccggaccc ctgagggtcac atgcgtggtg 600
 gtggacgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag 660
 gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtggtc 720
 agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc 780
 tccaacaaag ccctcggcgc ccccatcgag aaaaccatct ccaaagccaa agggcagccc 840
 cgagaaccac aggtgtacac cctgccccca tgccgggatg agctgaccaa gaaccaggtc 900
 agcctgtggt gcctgggtcaa aggcttctat ccagcgaca tcgccgtgga gtgggagagc 960
 aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacgggtcc 1020
 ttcttctctt acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 1080
 tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 1140
 tctccgggta aa 1152

<210> 251
 <211> 398
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IFN-a-Fc knob (LALA P329G) (IFN-a N-terminal)

<400> 251

eolf-seq1

Ser Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu
 1 5 10 15

Met Leu Leu Ala Gln Met Arg Lys Ile Ser Leu Phe Ser Cys Leu Lys
 20 25 30

Asp Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe
 35 40 45

Gln Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile
 50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr
 65 70 75 80

Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
 85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
 100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
 115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
 130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
 145 150 155 160

Ser Leu Arg Ser Lys Glu Gly Gly Gly Gly Ser Asp Lys Thr His Thr
 165 170 175

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
 180 185 190

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 195 200 205

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
 210 215 220

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 225 230 235 240

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 245 250 255

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 260 265 270

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

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 290 295 300

Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
 305 310 315 320

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

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

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 355 360 365

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 370 375 380

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 385 390 395

<210> 252
 <211> 1194
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IFN-a-Fc knob (LALA P329G) (IFN-a N-terminal)

<400> 252
 agctgtgacc tgcctcagac acacagcctg ggcagccggc ggaccctgat gctgctggcc 60
 cagatgcgga agatcagcct gttcagctgc ctgaaggacc ggcacgactt cggcttcct 120
 caggaagagt tcggcaacca gttccagaag gccgagacaa tccccgtgct gcacgagatg 180
 atccagcaga ttttcaacct gttcagcacc aaggacagca gcgccgcctg ggacgagaca 240
 ctgctggaca agttctacac cgagctgtac cagcagctga acgacctgga agcctgctg 300
 atccagggcg tgggcgtgac cgagacaccc ctgatgaagg aagatagcat cctggccgtg 360
 cggaagtatt tccagcggat caccctgtac ctgaaagaga agaagtacag cccctgcgcc 420
 tgggaggtcg tgcgggccga gatcatgcgg agcttcagcc tgagcaccaa cctgcaggaa 480
 agcctgcgga gcaaagaggg tggcggcgga tccgacaaaa ctcacacatg cccaccgtgc 540
 ccagcacctg aagctgcagg gggaccgtca gtcttcctct tcccccaaa acccaaggac 600
 accctcatga tctcccggac ccctgaggtc acatgcgtgg tggcggacgt gagccacgaa 660
 gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 720
 aagccgcggg aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg 780
 caccaggact ggctgaatgg caaggagtac aagtgcagg tctccaacaa agccctcggc 840

eolf-seq1

gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac 900
accctgcccc catgccggga tgagctgacc aagaaccagg tcagcctgtg gtgcctggtc 960
aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 1020
aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag 1080
ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat 1140
gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg taaa 1194

<210> 253
<211> 593
<212> PRT
<213> Artificial sequence

<220>
<223> 28H1 Fab HC-Fc (LALA P329G)-IL-2 qm
<400> 253

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser His
20 25 30

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

Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp Ser Val Lys
50 55 60

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

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

Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

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

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
130 135 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145 150 155 160

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
165 170 175

eolf-seq1
 Gly Leu Tyr Ser₁₈₀ Leu Ser Ser Val₁₈₅ Val Thr Val Pro Ser Ser₁₉₀ Ser Leu
 Gly Thr Gln₁₉₅ Thr Tyr Ile Cys Asn₂₀₀ Val Asn His Lys Pro₂₀₅ Ser Asn Thr
 Lys Val₂₁₀ Asp Lys Lys Val₂₁₅ Glu Pro Lys Ser Cys Asp₂₂₀ Lys Thr His Thr
 Cys₂₂₅ Pro Pro Cys Pro Ala₂₃₀ Pro Glu Ala Ala Gly₂₃₅ Gly Pro Ser Val Phe₂₄₀
 Leu Phe Pro Pro Lys₂₄₅ Pro Lys Asp Thr Leu₂₅₀ Met Ile Ser Arg Thr₂₅₅ Pro
 Glu Val Thr Cys₂₆₀ Val Val Val Asp Val₂₆₅ Ser His Glu Asp Pro₂₇₀ Glu Val
 Lys Phe Asn₂₇₅ Trp Tyr Val Asp Gly₂₈₀ Val Glu Val His Asn₂₈₅ Ala Lys Thr
 Lys Pro₂₉₀ Arg Glu Glu Gln Tyr₂₉₅ Asn Ser Thr Tyr Arg₃₀₀ Val Val Ser Val
 Leu₃₀₅ Thr Val Leu His Gln₃₁₀ Asp Trp Leu Asn Gly₃₁₅ Lys Glu Tyr Lys Cys₃₂₀
 Lys Val Ser Asn₃₂₅ Lys Ala Leu Gly Ala Pro₃₃₀ Ile Glu Lys Thr Ile₃₃₅ Ser
 Lys Ala Lys Gly₃₄₀ Gln Pro Arg Glu Pro₃₄₅ Gln Val Tyr Thr Leu₃₅₀ Pro Pro
 Ser Arg Asp₃₅₅ Glu Leu Thr Lys Asn₃₆₀ Gln Val Ser Leu Thr₃₆₅ Cys Leu Val
 Lys Gly₃₇₀ Phe Tyr Pro Ser Asp₃₇₅ Ile Ala Val Glu Trp₃₈₀ Glu Ser Asn Gly
 Gln₃₈₅ Pro Glu Asn Asn Tyr₃₉₀ Lys Thr Thr Pro Pro₃₉₅ Val Leu Asp Ser Asp₄₀₀
 Gly Ser Phe Phe₄₀₅ Leu Tyr Ser Lys Leu Thr₄₁₀ Val Asp Lys Ser Arg₄₁₅ Trp
 Gln Gln Gly Asn₄₂₀ Val Phe Ser Cys Ser₄₂₅ Val Met His Glu Ala₄₃₀ Leu His
 Asn His Tyr₄₃₅ Thr Gln Lys Ser Leu₄₄₀ Ser Leu Ser Pro Gly₄₄₅ Gly Gly Gly

eolf-seq1

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Pro Ala Ser
 450 455 460

Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp
 465 470 475 480

Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu
 485 490 495

Thr Arg Met Leu Thr Ala Lys Phe Ala Met Pro Lys Lys Ala Thr Glu
 500 505 510

Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu
 515 520 525

Val Leu Asn Gly Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp
 530 535 540

Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu
 545 550 555 560

Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu
 565 570 575

Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu
 580 585 590

Thr

<210> 254
 <211> 1779
 <212> DNA
 <213> Artificial sequence

<220>
 <223> 28H1 Fab HC-Fc (LALA P329G)-IL-2 qm

<400> 254	
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tcttgcgccg cctccggctt caccttctcc tcccacgcca tgtcctgggt ccgacaggct	120
cctggcaaag gcctggaatg ggtgtccgcc atctgggcct ccggcggagca gtactacgcc	180
gactctgtga agggccggtt caccatctcc cgggacaact ccaagaacac cctgtacctg	240
cagatgaact ccctgcgggc cgaggacacc gccgtgtact actgtgcaa gggctggctg	300
ggcaacttcg actactgggg acagggcacc ctggtcaccg tgtccagcgc tagcaccaag	360
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc	420
ctgggctgcc tgggtcaagga ctacttcccc gaaccgggtga cgggtgctgt gaactcaggc	480
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc	540
ctcagcagcg tgggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac	600

eolf-seq1

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gtgaatcaca agcccagcaa caccaaggtg gacaagaaaag ttgagcccaa atcttgtgac      660
aaaactcaca catgcccacc gtgcccagca cctgaagctg caggggggacc gtcagtcttc      720
ctcttccccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc      780
gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc      840
gtggaggtgc ataatgcaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt      900
gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc      960
aaggtctcca acaaagccct cggcgccccc atcgagaaaa ccatctccaa agccaaaggg    1020
cagccccgag aaccacaggt gtacaccctg ccccatcccc gggatgagct gaccaagaac    1080
caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg    1140
gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac    1200
ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac    1260
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc    1320
tcctgtctc cgggtggcgg cggaggctcc ggaggcggag gttctggcgg aggtggctcc    1380
gcacctgcct caagttctac aaagaaaaca cagctacaac tggagcattt actgctggat    1440
ttacagatga ttttgaatgg aattaataat tacaagaatc caaaactcac caggatgctc    1500
acagccaagt ttgccatgcc caagaaggcc acagaactga aacatcttca gtgtctagaa    1560
gaagaactca aacctctgga ggaagtgcta aatggcgctc aaagcaaaaa ctttcactta    1620
agaccaggg acttaatcag caatatcaac gtaatagttc tggaactaaa gggatctgaa    1680
acaacattca tgtgtgaata tgctgatgag acagcaacca ttgtagaatt tctgaacaga    1740
tggtattacct ttgcccagag catcatctca aactgact                                1779

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<210> 255

<211> 473

<212> PRT

<213> Artificial Sequence

<220>

<223> Murine IL-2R-beta-Fc(hole) fusion protein

<400> 255

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Phe Pro Leu Leu Leu Leu Trp Phe Pro Gly Ala Arg Cys Ala Val Lys
20 25 30

Asn Cys Ser His Leu Glu Cys Phe Tyr Asn Ser Arg Ala Asn Val Ser
35 40 45

Cys Met Trp Ser His Glu Glu Ala Leu Asn Val Thr Thr Cys His Val
50 55 60

eolf-seq1
 His Ala Lys Ser Asn Leu Arg His Trp Asn Lys Thr Cys Glu Leu Thr
 65 70 75 80
 Leu Val Arg Gln Ala Ser Trp Ala Cys Asn Leu Ile Leu Gly Ser Phe
 85 90 95
 Pro Glu Ser Gln Ser Leu Thr Ser Val Asp Leu Leu Asp Ile Asn Val
 100 105 110
 Val Cys Trp Glu Glu Lys Gly Trp Arg Arg Val Lys Thr Cys Asp Phe
 115 120 125
 His Pro Phe Asp Asn Leu Arg Leu Val Ala Pro His Ser Leu Gln Val
 130 135 140
 Leu His Ile Asp Thr Gln Arg Cys Asn Ile Ser Trp Lys Val Ser Gln
 145 150 155 160
 Val Ser His Tyr Ile Glu Pro Tyr Leu Glu Phe Glu Ala Arg Arg Arg
 165 170 175
 Leu Leu Gly His Ser Trp Glu Asp Ala Ser Val Leu Ser Leu Lys Gln
 180 185 190
 Arg Gln Gln Trp Leu Phe Leu Glu Met Leu Ile Pro Ser Thr Ser Tyr
 195 200 205
 Glu Val Gln Val Arg Val Lys Ala Gln Arg Asn Asn Thr Gly Thr Trp
 210 215 220
 Ser Pro Trp Ser Gln Pro Leu Thr Phe Arg Thr Arg Pro Ala Asp Pro
 225 230 235 240
 Met Lys Glu Gly Ala Gln 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

eolf-seq1

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 Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu
 370 375 380

Thr Lys Asn Gln Val Ser Leu Ser Cys Ala 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

Val 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
 465 470

<210> 256
 <211> 1422
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Murine IL-2R-beta-Fc(hole) fusion protein

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<400> 256
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ctgctctggt tcccagggtgc cagggtgtgca gtgaaaaact gttcccatct tgaatgcttc      120
tacaactcaa gagccaatgt ctcttgcattg tggagccatg aagaggctct gaatgtcaca      180
acctgccacg tccatgccaa gtcgaacctg cgacactgga acaaaacctg tgagctaact      240
cttgtgagggc aggcattcctg ggcctgcaac ctgatacctg ggtcgttccc agagtcccag      300
tacttgacct ccgtggacct ccttgacata aatgtgggtgt gctgggaaga gaaggggttg      360
cgtagggtaa agacctgcga cttccatccc ttgacaacc ttcgcctggt ggccccctcat      420
tccttccaag ttctgcacat tgataccag agatgtaaca taagctggaa ggtctcccag      480
gtctctcact acattgaacc atacttgga tttgaggccc gtagacgtct tctgggccac      540
agctgggagg atgcatccgt attaagcctc aagcagagac agcagtggt cttcttgagg      600
atgctgatcc ctagtacctc atatgaggtc cagggtgagg tcaaagctca acgaaacaat      660
accgggacct ggagtccctg gagccagccc ctgacctttc ggacaaggcc agcagatccc      720

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eolf-seq1

atgaaggagg gagctcagga caaaactcac acatgcccac cgtgcccagc acctgaactc 780
ctgggggggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 840
cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtaag 900
ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 960
cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 1020
aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1080
accatctcca aagccaaagg gcagccccga gaaccacagg tgtgcaccct gcccccatcc 1140
cgggatgagc tgaccaagaa ccaggtcagc ctctcgtgcg cagtcaaagg cttctatccc 1200
agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1260
cctcccgtgc tggactccga cggctccttc ttctcgtga gcaagctcac cgtggacaag 1320
agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcattgaggc tctgcacaac 1380
cactacacgc agaagagcct ctccctgtct ccgggtaaat ga 1422

<210> 257
<211> 500
<212> PRT
<213> Artificial Sequence

<220>
<223> Murine IL-2R-gamma-Fc(knob) fusion protein
<400> 257

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Phe Pro Leu Leu Leu Trp Phe Pro Gly Ala Arg Cys Trp Ser Ser
20 25 30

Lys Val Leu Met Ser Ser Ala Asn Glu Asp Ile Lys Ala Asp Leu Ile
35 40 45

Leu Thr Ser Thr Ala Pro Glu His Leu Ser Ala Pro Thr Leu Pro Leu
50 55 60

Pro Glu Val Gln Cys Phe Val Phe Asn Ile Glu Tyr Met Asn Cys Thr
65 70 75 80

Trp Asn Ser Ser Ser Glu Pro Gln Ala Thr Asn Leu Thr Leu His Tyr
85 90 95

Arg Tyr Lys Val Ser Asp Asn Asn Thr Phe Gln Glu Cys Ser His Tyr
100 105 110

Leu Phe Ser Lys Glu Ile Thr Ser Gly Cys Gln Ile Gln Lys Glu Asp
115 120 125

eolf-seq1
 Ile Gln Leu Tyr Gln Thr Phe Val Val Gln Leu Gln Asp Pro Gln Lys
 130 135 140
 Pro Gln Arg Arg Ala Val Gln Lys Leu Asn Leu Gln Asn Leu Val Ile
 145 150 155 160
 Pro Arg Ala Pro Glu Asn Leu Thr Leu Ser Asn Leu Ser Glu Ser Gln
 165 170 175
 Leu Glu Leu Arg Trp Lys Ser Arg His Ile Lys Glu Arg Cys Leu Gln
 180 185 190
 Tyr Leu Val Gln Tyr Arg Ser Asn Arg Asp Arg Ser Trp Thr Glu Leu
 195 200 205
 Ile Val Asn His Glu Pro Arg Phe Ser Leu Pro Ser Val Asp Glu Leu
 210 215 220
 Lys Arg Tyr Thr Phe Arg Val Arg Ser Arg Tyr Asn Pro Ile Cys Gly
 225 230 235 240
 Ser Ser Gln Gln Trp Ser Lys Trp Ser Gln Pro Val His Trp Gly Ser
 245 250 255
 His Thr Val Glu Glu Asn Pro Ser Leu Phe Ala Leu Glu Ala Gly Ala
 260 265 270
 Gln Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 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

eolf-seq1

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

Ser Leu Trp 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> 258
<211> 1503
<212> DNA
<213> Artificial Sequence

<220>
<223> Murine IL-2R-gamma-Fc(knob) fusion protein

<400> 258
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gaagacatca aagctgattt gatcctgact tctacagccc ctgaacacct cagtgtcctt 180
actctgcccc ttccagaggt tcagtgtttt gtgttcaaca tagagtacat gaattgcact 240
tggaatagca gttctgagcc tcaggcaacc aacctcacgc tgcactatag gtacaaggta 300
tctgataata atacattcca ggagtgcagt cactatttgt tctccaaaga gattacttct 360
ggctgtcaga tacaaaaaga agatatccag ctctaccaga catttggtgt ccagctccag 420
gacccccaga aaccccagag gcgagctgta cagaagctaa acctacagaa tcttgtgatc 480
ccacgggctc cagaaaatct aacactcagc aatctgagtg aatcccagct agagctgaga 540
tggaagagca gacatattaa agaacgctgt ttacaatact tgggtgcagta ccggagcaac 600
agagatcgaa gctggacgga actaatagtg aatcatgaac ctagattctc cctgcctagt 660
gtggatgagc tgaaacggta cacatttcgg gttcggagcc gctataaccc aatctgtgga 720
agtttctaac agtggagtaa atggagccag cctgtccact gggggagtca tactgtagag 780
gagaatcctt ccttgtttgc actggaagct ggagctcagg acaaaactca cacatgccca 840
ccgtgcccag cacctgaact cctgggggga ccgtcagtct tcctcttccc cccaaaaccc 900
aaggacaccc tcatgatctc ccggacccct gaggtcacat gcgtgggtgg ggacgtgagc 960

eof-seq1

cacgaagacc ctgagggtcaa gttcaactgg tacgtggacg gcgaggaggt gcataatgcc 1020
aagacaaagc cgcgaggagga gcagtacaac agcacgtacc gtgtgggtcag cgtcctcacc 1080
gtcctgcacc aggactggct gaatggcaag gaggacaagt gcaagggtctc caacaaagcc 1140
ctcccagccc ccatcgagaa aaccatctcc aaagccaaag ggcagccccg agaaccacag 1200
gtgtacacccc tgcccccatg ccgggatgag ctgaccaaga accagggtcag cctgtgggtgc 1260
ctgggtcaaag gcttctatcc cagcgacatc gccgtggagt gggagagcaa tgggcagccg 1320
gagaacaact acaagaccac gcctcccgtg ctggactccg acggctcctt cttcctctac 1380
agcaagctca ccgtggacaa gaggagggtg caggagggga acgtcttctc atgctccgtg 1440
atgcatgagg ctctgcacaa ccactacacg cagaagagcc tctccctgtc tccgggtaaa 1500
tga 1503

<210> 259
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<223> Murine IL-2R alpha subunit + Avi-tag + His-tag
<400> 259

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15
Val His Ser Glu Leu Cys Leu Tyr Asp Pro Pro Glu Val Pro Asn Ala
20 25 30
Thr Phe Lys Ala Leu Ser Tyr Lys Asn Gly Thr Ile Leu Asn Cys Glu
35 40 45
Cys Lys Arg Gly Phe Arg Arg Leu Lys Glu Leu Val Tyr Met Arg Cys
50 55 60
Leu Gly Asn Ser Trp Ser Ser Asn Cys Gln Cys Thr Ser Asn Ser His
65 70 75 80
Asp Lys Ser Arg Lys Gln Val Thr Ala Gln Leu Glu His Gln Lys Glu
85 90 95
Gln Gln Thr Thr Thr Asp Met Gln Lys Pro Thr Gln Ser Met His Gln
100 105 110
Glu Asn Leu Thr Gly His Cys Arg Glu Pro Pro Pro Trp Lys His Glu
115 120 125
Asp Ser Lys Arg Ile Tyr His Phe Val Glu Gly Gln Ser Val His Tyr
130 135 140

eolf-seq1

Glu Cys Ile Pro Gly Tyr Lys Ala Leu Gln Arg Gly Pro Ala Ile Ser
 145 150 155 160

Ile Cys Lys Met Lys Cys Gly Lys Thr Gly Trp Thr Gln Pro Gln Leu
 165 170 175

Thr Cys Val Asp Glu Gln Leu Tyr Phe Gln Gly Gly Ser Gly Leu Asn
 180 185 190

Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu Ala Arg Ala His
 195 200 205

His His His His His
 210

<210> 260
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Murine IL-2R alpha subunit + Avi-tag + His-tag

<400> 260
 atgggatgga gctgtatcat cctcttcttg gtagcaacag ctaccggtgt gcattccgaa 60
 ctgtgtctgt atgacccacc cgagggtcccc aatgccacat tcaaagccct ctctacaag 120
 aacggcacca tcctaaactg tgaatgcaag agagggtttcc gaagactaaa ggaattggtc 180
 tatatgcgtt gcttaggaaa ctcttgagagc agcaactgcc agtgcaccag caactcccat 240
 gacaaatcga gaaagcaagt tacagctcaa cttgaacacc agaaagagca acaaaccaca 300
 acagacatgc agaagccaac acagtctatg caccaagaga accttacagg tcactgcagg 360
 gagccacctc cttggaaaca tgaagattcc aagagaatct atcatttcgt ggaaggacag 420
 agtgttcact acgagtgtat tccgggatac aaggctctac agagaggtcc tgctattagc 480
 atctgcaaga tgaagtgtgg gaaaacgggg tggactcagc cccagctcac atgtgtcgac 540
 gaacagttat attttcaggg cggtcagggc ctgaacgaca tcttcgaggc ccagaagatc 600
 gagtggcacg aggctcgagc tcaccacat caccatcact ga 642

<210> 261
 <211> 480
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Cynomolgous IL-2R-beta-Fc(knob) fusion protein + Avi-tag

<400> 261

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15

Val His Ser Ala Val Asn Gly Thr Ser Arg Phe Thr Cys Phe Tyr Asn
 20 25 30

eo1f-seq1

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

Asp Thr Ser Cys Gln Val His Ala Trp Pro Asp Arg Arg Arg Trp Asn
50 55 60

Gln Thr Cys Glu Leu Leu Pro Val Ser Gln Ala Ser Trp Ala Cys Asn
65 70 75 80

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

Val Thr Leu Arg Val Met Cys Arg Glu Gly Val Arg Trp Arg Met Met
100 105 110

Ala Ile Gln Asp Phe Lys Pro Phe Glu Asn Leu Arg Leu Met Ala Pro
115 120 125

Ile Ser Leu Gln Val Val His Val Glu Thr His Arg Cys Asn Ile Ser
130 135 140

Trp Lys Ile Ser Gln Ala Ser His Tyr Phe Glu Arg His Leu Glu Phe
145 150 155 160

Glu Ala Arg Thr Leu Ser Pro Gly His Thr Trp Glu Glu Ala Pro Leu
165 170 175

Met Thr Leu Lys Gln Lys Gln Glu Trp Ile Cys Leu Glu Thr Leu Thr
180 185 190

Pro Asp Thr Gln Tyr Glu Phe Gln Val Arg Val Lys Pro Leu Gln Gly
195 200 205

Glu Phe Thr Thr Trp Ser Pro Trp Ser Gln Pro Leu Ala Phe Arg Thr
210 215 220

Lys Pro Ala Ala Leu Gly Lys Asp Thr Gly Ala Gln Asp Lys Thr His
225 230 235 240

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

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

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

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

eolf-seq1

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

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

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

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

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

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

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

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

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

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

Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu
465 470 475 480

<210> 262
<211> 1443
<212> DNA
<213> Artificial Sequence

<220>
<223> Cynomolgous IL-2R-beta-Fc(knob) fusion protein + Avi-tag

<400> 262
atgggatgga gctgtatcat cctcttcttg gtagcaacag ctaccggtgt gcattccgcg 60
gtcaacggca cttcccggtt cacatgcttc tacaactcga gagccaacat ctctgtgtc 120
tgagagccaag atggggctct gcaggacact tcctgccaag tccacgcctg gccggacaga 180
cggcgggtgga accaaacctg tgagctgctc cctgtgagtc aagcatcctg ggcctgcaac 240
ctgatcctcg gaacccaga ttctcagaaa ctgaccgcag tggatatcgt caccctgagg 300
gtgatgtgcc gtgaaggggt gcgatggagg atgatggcca tccaggactt caaacccctt 360
gagaaccttc gcctgatggc ccccatctcc ctccaagtcg tccacgtgga gaccacaga 420

eolf-seq1

tgcaacataa gctggaaaat ctcccaagcc tcccactact ttgaaagaca cctggagttt 480
gaggcccgga cgctgtcccc aggccacacc tgggaggagg cccccctgat gaccctcaag 540
cagaagcagg aatggatctg cctggagacg ctcaccccag acaccagta tgagtttcag 600
gtgcgggtca agcctctgca aggcgagttc acgacctgga gcccctggag ccagcccctg 660
gccttcagga caaagcctgc agcccttggg aaggacaccg gagctcagga caaaactcac 720
acatgcccac cgtgcccagc acctgaactc ctgggggggac cgtcagtctt cctcttcccc 780
ccaaaacca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg 840
gacgtgagcc acgaagaccc tgaggtaag ttcaactggg acgtggacgg cgtggagggtg 900
cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 960
gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 1020
aacaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 1080
gaaccacagg tgtacaccct gcccccatgc cgggatgagc tgaccaagaa ccaggtcagc 1140
ctgtggtgcc tgggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 1200
gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1260
ttcctctaca gcaagctcac cgtggacaag agcagggtggc agcaggggaa cgtcttctca 1320
tgctccgtga tgcattgagg tctgcacaac cactacacgc agaagagcct ctccctgtct 1380
ccgggtaaat ccggaggcct gaacgacatc ttcgaggccc agaagattga atggcacgag 1440
tga 1443

<210> 263

<211> 489

<212> PRT

<213> Artificial Sequence

<220>

<223> Cynomolgous IL-2R-gamma-Fc(hole) fusion protein

<400> 263

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

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

Ala Thr Thr Asp Phe Phe Leu Thr Ser Met Pro Thr Asp Ser Leu Ser
35 40 45

Val Ser Thr Leu Pro Leu Pro Glu Val Gln Cys Phe Val Phe Asn Val
50 55 60

Glu Tyr Met Asn Cys Thr Trp Asn Ser Ser Ser Glu Pro Gln Pro Thr
65 70 75 80

Asn Leu Thr Leu His Tyr Trp Tyr Lys eolf-seq1
 85 90 95 Val
 Gln Lys Cys Ser His Tyr Leu Phe Ser Glu Glu Ile Thr Ser Gly Cys
 100 105 110
 Gln Leu Gln Lys Lys Glu Ile His Leu Tyr Gln Thr Phe Val Val Gln
 115 120 125
 Leu Gln Asp Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln Met Leu Lys
 130 135 140
 Leu Gln Asn Leu Val Ile Pro Trp Ala Pro Glu Asn Leu Thr Leu Arg
 145 150 155 160
 Lys Leu Ser Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn Arg Phe Leu
 165 170 175
 Asn His Cys Leu Glu His Leu Val Gln Tyr Arg Thr Asp Trp Asp His
 180 185 190
 Ser Trp Thr Glu Gln Ser Val Asp Tyr Arg His Lys Phe Ser Leu Pro
 195 200 205
 Ser Val Asp Gly Gln Lys Arg Tyr Thr Phe Arg Val Arg Ser Arg Phe
 210 215 220
 Asn Pro Leu Cys Gly Ser Ala Gln His Trp Ser Glu Trp Ser His Pro
 225 230 235 240
 Ile His Trp Gly Ser Asn Ser Ser Lys Glu Asn Pro Phe Leu Phe Ala
 245 250 255
 Leu Glu Ala Gly Ala Gln Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 260 265 270
 Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 275 280 285
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 290 295 300
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 305 310 315 320
 Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 325 330 335
 Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 340 345 350

eolf-seq1

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

Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
370 375 380

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

Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro
405 410 415

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

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

Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
450 455 460

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

Lys Ser Leu Ser Leu Ser Pro Gly Lys
485

<210> 264
<211> 1470
<212> DNA
<213> Artificial Sequence

<220>
<223> Cynomolgous IL-2R-gamma-Fc(hole) fusion protein

<400> 264
atgggatgga gctgtatcat cctcttcttg gtagcaacag ctaccggtgt gcattccctg 60
aacacgacaa ttctgacgcc caatgggaat gaagacgcca caactgattt cttcctgacc 120
tctatgccca ctgactccct cagtgtttcc actctgcccc tcccagaggt tcagtgtttt 180
gtgttcaatg tcgagtacat gaattgcact tggaacagca gctctgagcc ccagcctacc 240
aacctcactc tgcattattg gtacaagaat tcggataatg ataaagtcca gaagtgcagc 300
cactatctat tctctgaaga aatcatttct ggctgtcagt tgcaaaaaaa ggagatccac 360
ctctaccaa cgtttgttgt tcagctccag gaccacggg aaccaggag acaggccaca 420
cagatgctaa aactgcagaa tctggtgatc ccctgggctc cggagaacct aacacttcgc 480
aaactgagtg aatcccagct agaactgaac tggaacaaca gattcttgaa cactgtttg 540
gagcacttgg tgcagtaccg gactgactgg gaccacagct ggactgaaca atcagtggat 600
tatagacata agttctcctt gcctagtgtg gatgggcaga aacgctacac gtttcgtgtc 660
cggagccgct ttaaccact ctgtggaagt gctcagcatt ggagtgaatg gagccacca 720

eof-seq1

atccactggg ggagcaatag ttcaaaagag aatcctttcc tgtttgcatt ggaagccgga 780
gctcaggaca aaactcacac atgcccaccg tgcccagcac ctgaactcct ggggggaccg 840
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gaccctgag 900
gtcacatgcg tgggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 960
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 1020
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 1080
tacaagtgca aggtctccaa caaagccctc ggcgccccca tcgagaaaac catctccaaa 1140
gccaaagggc agccccgaga accacagggtg tgcaccctgc ccccatcccg ggatgagctg 1200
accaagaacc aggtcagcct ctcgtgcgca gtcaaaggct tctatcccag cgacatcgcc 1260
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1320
gactccgacg gctccttctt cctcgtgagc aagctcaccg tggacaagag caggtggcag 1380
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1440
aagagcctct ccctgtctcc gggtaaatga 1470

<210> 265
<211> 217
<212> PRT
<213> Artificial sequence

<220>
<223> Cynomolgous IL-2R alpha subunit + Avi-tag + His-tag
<400> 265

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Glu Leu Cys Asp Asp Asp Pro Pro Lys Ile Thr His Ala Thr Phe Lys
20 25 30

Ala Met Ala Tyr Lys Glu Gly Thr Met Leu Asn Cys Glu Cys Lys Arg
35 40 45

Gly Phe Arg Arg Ile Lys Ser Gly Ser Pro Tyr Met Leu Cys Thr Gly
50 55 60

Asn Ser Ser His Ser Ser Trp Asp Asn Gln Cys Gln Cys Thr Ser Ser
65 70 75 80

Ala Ala Arg Asn Thr Thr Lys Gln Val Thr Pro Gln Pro Glu Glu Gln
85 90 95

Lys Glu Arg Lys Thr Thr Glu Met Gln Ser Gln Met Gln Leu Ala Asp
100 105 110

Gln Val Ser Leu Pro Gly His Cys Arg Glu Pro Pro Pro Trp Glu Asn
115 120 125

eolf-seq1

Glu Ala Thr Glu Arg Ile Tyr His Phe Val Val Gly Gln Thr Val Tyr
130 135 140

Tyr Gln Cys Val Gln Gly Tyr Arg Ala Leu His Arg Gly Pro Ala Glu
145 150 155 160

Ser Val Cys Lys Met Thr His Gly Lys Thr Arg Trp Thr Gln Pro Gln
165 170 175

Leu Ile Cys Thr Gly Glu Val Asp Glu Gln Leu Tyr Phe Gln Gly Gly
180 185 190

Ser Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu
195 200 205

Ala Arg Ala His His His His His His
210 215

<210> 266
<211> 654
<212> DNA
<213> Artificial Sequence

<220>
<223> Cynomolgous IL-2R alpha subunit + Avi-tag + His-tag

<400> 266
atgggatgga gctgtatcat cctcttcttg gtagcaacag ctaccggtga gctctgtgac 60
gatgaccgc caaaaatcac acatgccaca ttcaaagcca tggcctacaa ggaaggaacc 120
atgttgaact gtgaatgcaa gagagggttc cgcagaataa aaagcgggtc accctatatg 180
ctctgtacag gaaactctag ccaactcgcc tgggacaacc aatgtcaatg cacaagctct 240
gctgctcgga acacaacaaa acaagtgaca cctcaacctg aagaacagaa agaaagaaaa 300
accacagaaa tgcaaagtca aatgcagctg gcggaaccaag tgagccttcc aggtcactgc 360
agggaacctc caccgtggga aaatgaagcc acagaaagaa tttatcattt cgtggtgggg 420
cagacggttt actaccagtg cgtccaggga tacagggtc tacacagagg tcctgctgag 480
agcgtctgca aaatgacca cggaagaca agatggaccc agccccagct catatgcaca 540
ggtgaagtcg acgaacagtt atatcttcag ggcggctcag gcctgaacga catcttcgag 600
gccagaaga tcgagtggca cgaggctcga gctcaccacc atcaccatca ctga 654

<210> 267
<211> 474
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IL-10R1-Fc fusion + Avi-tag

<400> 267

eolf-seq1

His Gly Thr Glu Leu Pro Ser Pro Pro Ser Val Trp Phe Glu Ala Glu
 1 5 10 15

Phe Phe His His Ile Leu His Trp Thr Pro Ile Pro Asn Gln Ser Glu
 20 25 30

Ser Thr Cys Tyr Glu Val Ala Leu Leu Arg Tyr Gly Ile Glu Ser Trp
 35 40 45

Asn Ser Ile Ser Asn Cys Ser Gln Thr Leu Ser Tyr Asp Leu Thr Ala
 50 55 60

Val Thr Leu Asp Leu Tyr His Ser Asn Gly Tyr Arg Ala Arg Val Arg
 65 70 75 80

Ala Val Asp Gly Ser Arg His Ser Asn Trp Thr Val Thr Asn Thr Arg
 85 90 95

Phe Ser Val Asp Glu Val Thr Leu Thr Val Gly Ser Val Asn Leu Glu
 100 105 110

Ile His Asn Gly Phe Ile Leu Gly Lys Ile Gln Leu Pro Arg Pro Lys
 115 120 125

Met Ala Pro Ala Asn Asp Thr Tyr Glu Ser Ile Phe Ser His Phe Arg
 130 135 140

Glu Tyr Glu Ile Ala Ile Arg Lys Val Pro Gly Asn Phe Thr Phe Thr
 145 150 155 160

His Lys Lys Val Lys His Glu Asn Phe Ser Leu Leu Thr Ser Gly Glu
 165 170 175

Val Gly Glu Phe Cys Val Gln Val Lys Pro Ser Val Ala Ser Arg Ser
 180 185 190

Asn Lys Gly Met Trp Ser Lys Glu Glu Cys Ile Ser Leu Thr Arg Gln
 195 200 205

Tyr Phe Thr Val Thr Asn Val Asp Glu Gln Leu Tyr Phe Gln Gly Gly
 210 215 220

Ser Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 225 230 235 240

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 245 250 255

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 260 265 270

eolf-seq1

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
275 280 285

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
290 295 300

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
305 310 315 320

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
325 330 335

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
340 345 350

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
355 360 365

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
370 375 380

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
405 410 415

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
435 440 445

Ser Leu Ser Leu Ser Pro Gly Gly Gly Ser Gly Gly Leu Asn Asp Ile
450 455 460

Phe Glu Ala Gln Lys Ile Glu Trp His Glu
465 470

<210> 268
<211> 1422
<212> DNA
<213> Artificial Sequence

<220>
<223> Human IL-10R1-Fc fusion + Avi-tag

<400> 268	
catgggacag agctgcccag ccctccgtct gtgtggtttg aagcagaatt tttccaccac	60
atcctccact ggacacccat cccaaatcag tctgaaagta cctgctatga agtggcactc	120
ctgaggtatg gaatagagtc ctggaactcc atctccaact gtagccagac cctgtcctat	180
gaccttaccg cagtgacctt ggacctgtac cacagcaatg gctaccgggc cagagtgcgg	240

eolf-seq1

gctgtggacg gcagccggca ctccaactgg accgtcacca acacccgctt ctctgtggat 300
gaagtgactc tgacagttgg cagtgtgaac ctagagatcc acaatggctt catcctcggg 360
aagattcagc taccagggcc caagatggcc cccgcaaatg acacatatga aagcatcttc 420
agtcacttcc gagagtatga gattgccatt cgcaagggtgc cgggaaactt cacgttcaca 480
cacaagaaag taaaacatga aaacttcagc ctcctaacct ctggagaagt gggagagttc 540
tgtgtccagg tgaaccatc tgtcgcttcc cgaagtaaca aggggatgtg gtctaaagag 600
gagtgcattc cctcaccag gcagtatttc accgtgacca acgtcgacga acagttatat 660
tttcagggcg gctcacccaa atctgcagac aaaactcaca catgcccacc gtgcccagca 720
cctgaactcc tgggggggacc gtcagtcttc ctcttcccc caaaacccaa ggacaccctc 780
atgatctccc ggaccctga ggtcacatgc gtggtggtgg acgtgagcca cgaagaccct 840
gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgcca gacaaagccg 900
cgggaggagc agtacaacag cacgtaccgt gtggtcagcg tcctcaccgt cctgcaccag 960
gactggctga atggcaagga gtacaagtgc aaggctcca acaaagccct cccagcccc 1020
atcgagaaaa ccatctcaa agccaaaggg cagccccgag aaccacaggt gtacaccctg 1080
cccccatccc gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc 1140
ttctatccca gcgacatcg cgtggagtgg gagagcaatg ggcagccgga gaacaactac 1200
aagaccacgc ctcccgctg ggactccgac ggctccttct tcctctacag caagctcacc 1260
gtggacaaga gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct 1320
ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtggcgg gtccggaggc 1380
ctgaacgaca tcttcgaggc ccagaagatt gaatggcacg ag 1422

<210> 269
<211> 593
<212> PRT
<213> Artificial Sequence

<220>
<223> 28H1 Fab HC-Fc knob (LALA P329G)-IL-2 qm (2)

<400> 269

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser His
20 25 30

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

Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp Ser Val Lys
50 55 60

eolf-seq1
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
 65 70 75 80
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
 115 120 125
 Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
 130 135 140
 Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
 145 150 155 160
 Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
 165 170 175
 Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
 180 185 190
 Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
 195 200 205
 Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
 210 215 220
 Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
 225 230 235 240
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 245 250 255
 Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
 260 265 270
 Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 275 280 285
 Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 290 295 300
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 305 310 315 320
 Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser
 325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 340 345 350
 Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val
 355 360 365
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 370 375 380
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 385 390 395 400
 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 405 410 415
 Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 420 425 430
 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
 435 440 445
 Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Pro Ala Ser
 450 455 460
 Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp
 465 470 475 480
 Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu
 485 490 495
 Thr Arg Met Leu Thr Ala Lys Phe Ala Met Pro Lys Lys Ala Thr Glu
 500 505 510
 Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu
 515 520 525
 Val Leu Asn Gly Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp
 530 535 540
 Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu
 545 550 555 560
 Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu
 565 570 575
 Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu
 580 585 590
 Thr

eolf-seq1

<210> 270
 <211> 1779
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 28H1 Fab HC-Fc knob (LALA P329G)-IL-2 qm (2)

<400> 270
 gaagtgcagc tgctggaatc cggcggaggc ctggtgcagc ctggcggatc tctgagactg 60
 tcctgcgccg cctccggctt caccttctcc tcccacgcca tgtcctgggt ccgacaggct 120
 cctggcaaag gcctggaatg ggtgtccgcc atctgggcct ccggcgagca gtactacgcc 180
 gactctgtga agggccggtt caccatctcc cgggacaact ccaagaacac cctgtacctg 240
 cagatgaact ccctgcgggc cgaggacacc gccgtgtact actgtgcca gggctggctg 300
 ggcaacttcg actactgggg acagggcacc ctggtcaccg tgtccagcgc tagcaccaag 360
 ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420
 ctgggctgcc tgggtcaagga ctacttcccc gaaccggtga cgggtgcgtg gaactcaggc 480
 gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc 540
 ctcagcagcg tgggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 600
 gtgaatcaca agcccagcaa caccaagggtg gacaagaaaag ttgagcccaa atcttgtgac 660
 aaaactcaca catgcccacc gtgcccagca cctgaagctg caggggggacc gtcagtcttc 720
 ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 780
 gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840
 gtggaggtgc ataatgcca gacaaagccg cgggaggagc agtacaacag cacgtaccgt 900
 gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960
 aagggtctcca acaaagccct cggcgccccc atcgagaaaa ccatctccaa agccaaaggg 1020
 cagccccgag aaccacaggt gtacaccctg ccccatgcc gggatgagct gaccaagaac 1080
 caggctcagc tgtggtgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1140
 gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200
 ggctccttct tcctctacag caagctcacc gtggacaaga gcagggtggca gcaggggaac 1260
 gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1320
 tccctgtctc cgggtggcgg cggaggctcc ggaggcggag gttctggcgg aggtggctcc 1380
 gcacctgcct caagttctac aaagaaaaca cagctacaac tggagcattt actgctggat 1440
 ttacagatga ttttgaatgg aattaataat tacaagaatc ccaaactcac caggatgctc 1500
 acagccaagt ttgccatgcc caagaaggcc acagaactga aacatcttca gtgtctagaa 1560
 gaagaactca aacctctgga ggaagtgcta aatggcgctc aaagcaaaaa ctttcactta 1620
 agaccaggg acttaatcag caatatcaac gtaatagttc tggaactaaa gggatctgaa 1680
 acaacattca tgtgtgaata tgctgatgag acagcaacca ttgtagaatt tctgaacaga 1740
 tggattacct ttgcccgaag catcatctca acactgact 1779

eolf-seq1

<210> 271
 <211> 594
 <212> PRT
 <213> Artificial sequence

<220>
 <223> 4B9 Fab HC-Fc knob (LALA P329G)-IL-2 qm (2)
 <400> 271

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

Ser Ala Ile Ile Gly Ser Gly Ala Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

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

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 195 200 205

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
 210 215 220

eolf-seq1
 Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
 225 230 235 240
 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 245 250 255
 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
 260 265 270
 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 275 280 285
 Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
 290 295 300
 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 305 310 315 320
 Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile
 325 330 335
 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
 340 345 350
 Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu
 355 360 365
 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 370 375 380
 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
 385 390 395 400
 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
 405 410 415
 Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
 420 425 430
 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly
 435 440 445
 Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Pro Ala
 450 455 460
 Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu
 465 470 475 480
 Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys
 485 490 495

eolf-seq1

Leu Thr Arg Met Leu Thr Ala Lys Phe Ala Met Pro Lys Lys Ala Thr
500 505 510

Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu
515 520 525

Glu Val Leu Asn Gly Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg
530 535 540

Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser
545 550 555 560

Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val
565 570 575

Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr
580 585 590

Leu Thr

<210> 272
<211> 1782
<212> DNA
<213> Artificial Sequence

<220>
<223> 4B9 Fab HC-Fc knob (LALA P329G)-IL-2 qm (2)

<400> 272

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cctggcaagg gactggaatg ggtgtccgcc atcatcggct ctggcgccag cacctactac	180
gccgacagcg tgaagggccg gttcaccatc agccgggaca acagcaagaa caccctgtac	240
ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcgc caagggatgg	300
ttcggcggct tcaactactg gggacagggc accctgggtca cagtgtccag cgctagcacc	360
aagggcccat cggctcttccc cctggcacc cctccaaga gcacctctgg gggcacagcg	420
gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca	480
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac	540
tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc	600
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	660
gacaaaactc acacatgccc accgtgccc gcacctgaag ctgcaggggg accgtcagtc	720
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca	780
tgcgtggtgg tggacgtgag ccacgaagac cctgagggtca agttcaactg gtacgtggac	840
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac	900
cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag	960

eolf-seq1

tgcaaggtct ccaacaaagc cctcggcgcc cccatcgaga aaaccatctc caaagccaaa 1020
 gggcagcccc gagaaccaca ggtgtacacc ctgcccccat gccgggatga gctgaccaag 1080
 aaccaggtca gcctgtggtg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 1140
 tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1200
 gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 1260
 aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 1320
 ctctccctgt ctccgggtgg cggcggaggc tccggaggcg gaggttctgg cggaggtggc 1380
 tccgcacctg cctcaagttc tacaagaaa acacagctac aactggagca tttactgctg 1440
 gatttacaga tgattttgaa tggaattaat aattacaaga atcccaaact caccaggatg 1500
 ctacacagcca agtttgccat gccaagaag gccacagaac tgaaacatct tcagtgtcta 1560
 gaagaagaac tcaaacctct ggaggaagtg ctaaatggcg ctcaaagcaa aaactttcac 1620
 ttaagaccca gggacttaat cagcaatatc aacgtaatag ttctggaact aaagggatct 1680
 gaaacaacat tcatgtgtga atatgctgat gagacagcaa ccattgtaga atttctgaac 1740
 agatggatta cctttgcca aagcatcatc tcaacactga ct 1782

<210> 273
 <211> 594
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 4B9 Fab HC-Fc knob (LALA P329G)-IL-2 wt
 <400> 273

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ala Ile Ile Gly Ser Gly Ala Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

eolf-seq1
 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 115 120 125
 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 130 135 140
 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 145 150 155 160
 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 165 170 175
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 180 185 190
 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 195 200 205
 Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
 210 215 220
 Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
 225 230 235 240
 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 245 250 255
 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
 260 265 270
 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 275 280 285
 Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
 290 295 300
 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 305 310 315 320
 Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile
 325 330 335
 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
 340 345 350
 Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu
 355 360 365
 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 370 375 380

eolf-seq1

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

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly
435 440 445

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Pro Thr
450 455 460

Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu
465 470 475 480

Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys
485 490 495

Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr
500 505 510

Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu
515 520 525

Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg
530 535 540

Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser
545 550 555 560

Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val
565 570 575

Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr
580 585 590

Leu Thr

<210> 274
<211> 1782
<212> DNA
<213> Artificial Sequence

<220>
<223> 4B9 Fab HC-Fc knob (LALA P329G)-IL-2 wt

<400> 274
gaggtgcagc tgctcgaaag cggcggagga ctggtgcagc ctggcggcag cctgagactg 60
tcttgcgccg ccagcggctt caccttcagc agctacgccca tgagctgggt ccgccaggcc 120
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eolf-seq1

cctggcaagg gactggaatg ggtgtccgcc atcatcggct ctggcgccag cacctactac	180
gccgacagcg tgaagggccg gttcaccatc agccgggaca acagcaagaa caccctgtac	240
ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcgc caagggatgg	300
ttcggcggct tcaactactg gggacagggc accctgggtca cagtgtccag cgctagcacc	360
aagggcccat cgggtctttcc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	420
gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca	480
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac	540
tccttcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc	600
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	660
gacaaaactc acacatgccc accgtgccc a gcacctgaag ctgcaggggg accgtcagtc	720
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca	780
tgctgtggtg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac	840
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac	900
cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag	960
tgcaaggtct ccaacaaagc cctcggcgcc cccatcgaga aaaccatctc caaagccaaa	1020
gggcagcccc gagaaccaca ggtgtacacc ctgcccccat gccgggatga gctgaccaag	1080
aaccagggtca gcctgtggtg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag	1140
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc	1200
gacggctcct tcttctctca cagcaagctc accgtggaca agagcagggtg gcagcagggg	1260
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc	1320
ctctccctgt ctccgggtgg cggcggaggc tccggaggcg gaggttctgg aggcggaggc	1380
tccgcaccta cttcaagttc taaaaagaaa acacagctac aactggagca tttactgctg	1440
gatttacaga tgattttgaa tggaattaat aattacaaga atcccaaact caccaggatg	1500
ctcacattta agttttacat gccaagaag gccacagaac tgaaacatct tcagtgtcta	1560
gaagaagaac tcaaacctct ggaggaagtg ctaaatttag ctcaaagcaa aaactttcac	1620
ttaagaccca gggacttaat cagcaatatc aacgtaatag ttctggaact aaagggatct	1680
gaaacaacat tcatgtgtga atatgctgat gagacagcaa ccattgtaga atttctgaac	1740
agatggatta cctttgccc aagcatcatc tcaacactga ct	1782

<210> 275
 <211> 599
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CH1A1A 98/99 2F1 Fab HC-Fc knob (LALA P329G)-IL-2 qm

<400> 275

eolf-seq1
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Glu Phe
 20 25 30
 Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Trp Ile Asn Thr Lys Thr Gly Glu Ala Thr Tyr Val Glu Glu Phe
 50 55 60
 Lys Gly Arg Val Thr Phe Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Trp Asp Phe Ala Tyr Tyr Val Glu Ala Met Asp Tyr Trp Gly
 100 105 110
 Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125
 Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
 130 135 140
 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 145 150 155 160
 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 165 170 175
 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 180 185 190
 Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 195 200 205
 Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
 210 215 220
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 225 230 235 240
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 245 250 255
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 260 265 270

eolf-seq1

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
450 455 460

Gly Gly Ala Pro Ala Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
465 470 475 480

Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn
485 490 495

Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Ala Lys Phe Ala Met
500 505 510

Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu
515 520 525

Leu Lys Pro Leu Glu Glu Val Leu Asn Gly Ala Gln Ser Lys Asn Phe
530 535 540

eolf-seq1

His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu
545 550 555 560

Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu
565 570 575

Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln
580 585 590

Ser Ile Ile Ser Thr Leu Thr
595

<210> 276
<211> 1797
<212> DNA
<213> Artificial Sequence

<220>
<223> CH1A1A 98/99 2F1 Fab HC-Fc knob (LALA P329G)-IL-2 qm

<400> 276

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tcctgcaagg	ccagcggcta	caccttcacc	gagttcggca	tgaactgggt	ccgacaggct	120
ccaggccagg	gcctcgaatg	gatgggctgg	atcaacacca	agaccggcga	ggccacctac	180
gtggaagagt	tcaagggcag	agtgaccttc	accacggaca	ccagcaccag	caccgcctac	240
atggaactgc	ggagcctgag	aagcgacgac	accgccgtgt	actactgcg	cagatgggac	300
ttcgctatt	acgtggaagc	catggactac	tggggccagg	gcaccaccgt	gaccgtgtct	360
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ggcggaacag	ccgccctggg	ctgcctggtc	aaggactact	tccccgagcc	cgtagacagt	480
tcctggaaca	gcggagccct	gaccagcggc	gtgcacacct	ttccagccgt	gctgcagagc	540
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acctacatct	gcaacgtgaa	ccacaagccc	agcaacacca	aggtggacaa	gaaggtggag	660
cccaagagct	gcgacaagac	ccacacctgt	cccccttgct	ctgcccctga	gctgctgggc	720
ggacccagcg	tgttcctgtt	ccccccaaag	cccaaggaca	ccctgatgat	cagccggacc	780
cccgaagtga	cctgcgtggg	ggtggacgtg	tcccacgagg	accctgaagt	gaagttcaat	840
tggtacgtgg	acggcgtgga	ggtgcacaat	gccaagacca	agccccggga	ggaacagtac	900
aacagcacct	accgggtggg	gtccgtgctg	accgtgctgc	accaggactg	gctgaacggc	960
aaagagtaca	agtgcaaggt	ctccaacaag	gccctgcctg	ccccatcga	gaaaaccatc	1020
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gagctgacca	agaaccaggt	gtccctgtgg	tgtctgggtca	agggcttcta	ccccagcgat	1140
atcgccgtgg	agtgggagag	caacggccag	cctgagaaca	actacaagac	cacccccctt	1200
gtgctggaca	gcgacggcag	cttcttcctg	tactccaaac	tgaccgtgga	caagagccgg	1260
tggcagcagg	gcaacgtgtt	cagctgcagc	gtgatgcacg	aggccctgca	caaccactac	1320

eof-seq1

acccagaagt ccctgagcct gagccccggc aagtccggag gcggaggctc cggcggcgga 1380
 ggttctggcg gaggtggcgc tcctgcctcc tccagcacca agaaaaccca gctccagctg 1440
 gaacatctcc tgctggatct gcagatgata ctgaacggca tcaacaacta caagaacccc 1500
 aagctgaccc ggatgctgac cgccaagttc gccatgcccc agaaggccac cgagctgaaa 1560
 catctgcagt gcctggaaga ggaactgaag cctctggaag aggtgctgaa cggcgccccag 1620
 tccaagaact tccacctgag gcctcgggac ctgatctcca acatcaacgt gatcgtgctg 1680
 gaactgaagg gctccgagac aaccttcatg tgcgagtacg ccgacgagac agctaccatc 1740
 gtggaatttc tgaaccggtg gatcaccttc gcccagtcca tcatctccac cctgacc 1797

<210> 277
 <211> 598
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CH1A1A 98/99 2F1 Fab HC-Fc knob (LALA P329G)-IL-2 qm (2)
 <400> 277

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

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

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

Gly Trp Ile Asn Thr Lys Thr Gly Glu Ala Thr Tyr Val Glu Glu Phe
 50 55 60

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

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

Ala Arg Trp Asp Phe Ala Tyr Tyr Val Glu Ala Met Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125

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

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
 210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
 225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 245 250 255

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

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
 325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 340 345 350

Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 355 360 365

Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430

eolf-seq1

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
450 455 460

Ser Ala Pro Ala Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu
465 470 475 480

His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr
485 490 495

Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Ala Lys Phe Ala Met Pro
500 505 510

Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu
515 520 525

Lys Pro Leu Glu Glu Val Leu Asn Gly Ala Gln Ser Lys Asn Phe His
530 535 540

Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu
545 550 555 560

Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr
565 570 575

Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser
580 585 590

Ile Ile Ser Thr Leu Thr
595

<210> 278
<211> 1794
<212> DNA
<213> Artificial sequence

<220>
<223> CH1A1A 98/99 2F1 Fab HC-Fc knob (LALA P329G)-IL-2 qm (2)

<400> 278
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ccaggccagg gcctcgaatg gatgggctgg atcaacacca agaccggcga ggccacctac 180
gtggaagagt tcaagggcag agtgaccttc accacggaca ccagcaccag caccgcctac 240
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agcgctagca ccaagggccc atcggcttc cccctggcac cctcctccaa gagcacctct 420
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacgggtg 480

eolf-seq1

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tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc      540
tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcaccacag      600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag      660
cccaaattct gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg      720
ggaccgtcag tcttcctctt ccccccaaaa cccaaggaca ccctcatgat ctcccgacc      780
cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac      840
tggtacgtgg acggcgtgga ggtgcataat gccaaagacaa agccgcggga ggagcagtac      900
aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc      960
aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg ccccatcga gaaaaccatc     1020
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atgccgggat     1080
gagctgacca agaaccaggt cagcctgtgg tgcttggtca aaggcttcta tcccagcgac     1140
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc     1200
gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg     1260
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac     1320
acgcagaaga gcctctccct gtctccgggt ggcggcggag gctccggagg cggaggttct     1380
ggcggaggtg gctccgcacc tgcctcaagt tctacaaaga aaacacagct acaactggag     1440
catttactgc tggatttaca gatgattttg aatggaatta ataattacaa gaatcccaaa     1500
ctcaccagga tgctcacagc caagtttgcc atgcccaga aggccacaga actgaaacat     1560
cttcagtgtc tagaagaaga actcaaacct ctggaggaag tgctaaatgg cgctcaaagc     1620
aaaaactttc acttaagacc cagggactta atcagcaata tcaacgtaat agttctggaa     1680
ctaaagggat ctgaaacaac attcatgtgt gaatatgctg atgagacagc aaccattgta     1740
gaatttctga acagatggat tacctttgcc caaagcatca tctcaacact gact          1794

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<210> 279
 <211> 598
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CH1A1A 98/99 2F1 Fab HC-Fc knob (LALA P329G)-IL-2 wt
 <400> 279

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

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

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

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Gly Trp Ile Asn Thr Lys Thr Gly Glu Ala Thr Tyr Val Glu Glu Phe
50 55 60

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

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

Ala Arg Trp Asp Phe Ala Tyr Tyr Val Glu Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

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

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

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

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
 325 330 335 eolf-seq1
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 340 345 350
 Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 355 360 365
 Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 385 390 395 400
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 405 410 415
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 435 440 445
 Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 450 455 460
 Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu
 465 470 475 480
 His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr
 485 490 495
 Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro
 500 505 510
 Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu
 515 520 525
 Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His
 530 535 540
 Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu
 545 550 555 560
 Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr
 565 570 575
 Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser
 580 585 590

eolf-seq1

Ile Ile Ser Thr Leu Thr
595

<210> 280
<211> 1794
<212> DNA
<213> Artificial Sequence

<220>
<223> CH1A1A 98/99 2F1 Fab HC-Fc knob (LALA P329G)-IL-2 wt

<400> 280
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ccaggccagg gcctcgaatg gatgggctgg atcaacacca agaccggcga ggccacctac 180
gtggaagagt tcaagggcag agtgaccttc accacggaca ccagcaccag caccgcctac 240
atggaactgc ggagcctgag aagcgacgac accgccgtgt actactgctc cagatgggac 300
ttcgcttatt acgtggaagc catggactac tggggccagg gcaccaccgt gaccgtgtct 360
agcgctagca ccaagggccc atcggctctc cccctggcac cctcctcaa gagcacctct 420
gggggacacg cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacgggtg 480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540
tcaggactct actccctcag cagcgtgggt accgtgccct ccagcagctt gggcaccag 600
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gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1260
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1320
acgcagaaga gcctctccct gtctccgggt ggcggcggag gctccggagg cggaggttct 1380
ggaggcggag gctccgcacc tacttcaagt tctacaaaga aaacacagct acaactggag 1440
catttactgc tggatttaca gatgattttg aatggaatta ataattacaa gaatcccaaa 1500
ctcaccagga tgctcacatt taagttttac atgcccaga aggccacaga actgaaacat 1560
cttcagtgtc tagaagaaga actcaaacct ctggaggaag tgctaaattt agctcaaagc 1620
aaaaactttc acttaagacc cagggactta atcagcaata tcaacgtaat agttctggaa 1680

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ctaaagggat ctgaaacaac attcatgtgt gaatatgctg atgagacagc aaccattgta 1740
gaatttctga acagatggat tacctttgcc caaagcatca tctcaacact gact 1794

<210> 281
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1A 98/99 2F1 Fab HC-Fc hole (LALA P329G)

<400> 281

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

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

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

Gly Trp Ile Asn Thr Lys Thr Gly Glu Ala Thr Tyr Val Glu Glu Phe
50 55 60

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

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

Ala Arg Trp Asp Phe Ala Tyr Tyr Val Glu Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

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

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

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

<210> 282
 <211> 1353
 <212> DNA
 <213> Artificial Sequence

eolf-seq1

<220>

<223> CH1A1A 98/99 2F1 Fab HC-Fc hole (LALA P329G)

<400> 282

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caggtgcagc tgggtgcagtc tggcgccgaa gtgaagaaac ctggagctag tgtgaaggtag      60
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ccaggccagg gcctcgaatg gatgggctgg atcaacacca agaccggcga ggccacctac      180
gtggaagagt tcaagggcag agtgaccttc accacggaca ccagcaccag caccgcctac      240
atggaactgc ggagcctgag aagcgacgac accgccgtgt actactgcg cagatgggac      300
ttcgctatt acgtggaagc catggactac tggggccagg gcaccaccgt gaccgtgtct      360
agcgctagca ccaagggccc ctccgtgttc cccctggccc ccagcagcaa gagcaccagc      420
ggcggcacag ccgctctggg ctgcctggtc aaggactact tccccgagcc cgtgaccgtg      480
tcctggaaca gcggagccct gacctccggc gtgcacacct tccccgccgt gctgcagagt      540
tctggcctgt atagcctgag cagcgtggtc accgtgcctt ctagcagcct gggcacccag      600
acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggag      660
cccaagagct gcgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg      720
ggaccgtcag tcttcctctt cccccaaaaa cccaaggaca ccctcatgat ctcccggacc      780
cctgaggtca catgcgtggg ggtggacgtg agccacgaag accctgaggt caagttcaac      840
tggtacgtgg acggcgaggg ggtgcataat gccaagacaa agccgcggga ggagcagtag      900
aacagcacgt accgtgtggg cagcgtcctc accgtcctgc accaggactg gctgaatggc      960
aaggagtaca agtgcaaggc ctccaacaaa gccctcggcg ccccatcga gaaaaccatc     1020
tccaaagcca aagggcagcc ccgagaacca cagggtgtgca ccctgcccc atccccggat     1080
gagctgacca agaaccaggc cagcctctcg tgcgcagtca aaggcttcta tcccagcgac     1140
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc     1200
gtgctggact ccgacggctc cttcttcctc gtgagcaagc tcaccgtgga caagagcagg     1260
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac     1320
acgcagaaga gcctctccct gtctccgggt aaa                                  1353

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<210> 283

<211> 215

<212> PRT

<213> Artificial Sequence

<220>

<223> CH1A1A 98/99 2F1 Fab LC

<400> 283

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

eof-seq1

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

Tyr Ser Ala Ser Tyr Arg Lys Arg 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 His Gln Tyr Tyr Thr Tyr Pro Leu
85 90 95

Phe Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

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

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

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 284
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> CH1A1A 98/99 2F1 Fab LC

<400> 284
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gggaaagcac ctaagctcct gatctattcg gcatcctacc gcaaaagggg agtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagatttcg caacttacta ctgtcaccaa tattacacct atcctctatt cacgtttggc 300
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cagggcacca agctcgagat caagcgtacg gtggctgcac catctgtctt catcttcccc 360
ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420
tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480
caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcacctg 540
acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600
ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 645

<210> 285
<211> 598
<212> PRT
<213> Artificial sequence

<220>
<223> 2B10 Fab HC-Fc knob (LALA P329G)-IL-2 qm
<400> 285

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

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

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

Ala Arg Leu Tyr Gly Tyr Ala Tyr Tyr Gly Ala Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

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

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 180 185 eolf-seq1 190
 Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 195 200 205
 Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
 210 215 220
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
 225 230 235 240
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 245 250 255
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 260 265 270
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 275 280 285
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 290 295 300
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 305 310 315 320
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
 325 330 335
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 340 345 350
 Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 355 360 365
 Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 385 390 395 400
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 405 410 415
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 435 440 445

eolf-seq1
 Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 450 455 460
 Ser Ala Pro Ala Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu
 465 470 475 480
 His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr
 485 490 495
 Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Ala Lys Phe Ala Met Pro
 500 505 510
 Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu
 515 520 525
 Lys Pro Leu Glu Glu Val Leu Asn Gly Ala Gln Ser Lys Asn Phe His
 530 535 540
 Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu
 545 550 555 560
 Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr
 565 570 575
 Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser
 580 585 590
 Ile Ile Ser Thr Leu Thr
 595

<210> 286
 <211> 1794
 <212> DNA
 <213> Artificial sequence

<220>
 <223> 2B10 Fab HC-Fc knob (LALA P329G)-IL-2 qm

<400> 286
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 gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
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 ggttacgctt actacggtgc ttttgactac tggggccaag ggaccaccgt gaccgtctcc 360
 tcagctagca ccaagggccc atcgggtcttc cccctggcac cctcctcaa gagcacctct 420
 gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480
 tcgtggaact caggcgcctt gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540
 tcaggactct actccctcag cagcgtgggtg accgtgccct ccagcagctt gggcacccag 600

eolf-seq1

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 cccaaatctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720
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 aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960
 aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg ccccatcga gaaaaccatc 1020
 tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atgccgggat 1080
 gagctgacca agaaccaggt cagcctgtgg tgcctgggtca aaggcttcta tcccagcgac 1140
 atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc 1200
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 tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1320
 acgcagaaga gcctctccct gtctccgggt ggcggcggag gctccggagg cggaggttct 1380
 ggcggagggtg gctccgcacc tgcctcaagt tctacaaaga aaacacagct acaactggag 1440
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 ctaaagggat ctgaaacaac attcatgtgt gaatatgctg atgagacagc aaccattgta 1740
 gaatttctga acagatggat tacctttgcc caagcatca tctcaacact gact 1794

<210> 287
 <211> 451
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 2B10 Fab HC-Fc hole (LALA P329G)

<400> 287

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

eolf-seq1
 Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Leu Tyr Gly Tyr Ala Tyr Tyr Gly Ala Phe Asp Tyr Trp Gly
 100 105 110
 Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125
 Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
 130 135 140
 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 145 150 155 160
 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 165 170 175
 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 180 185 190
 Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 195 200 205
 Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
 210 215 220
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
 225 230 235 240
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 245 250 255
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 260 265 270
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 275 280 285
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 290 295 300
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 305 310 315 320
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile
 325 330 335

eolf-seq1

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 288
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> 2B10 Fab HC-Fc hole (LALA P329G)

<400> 288
caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagactgtac 300
ggttacgctt actacggtgc ttttgactac tggggccaag ggaccaccgt gaccgtctcc 360
tcagctagca ccaagggccc ctccgtgttc cccctggccc ccagcagcaa gagcaccagc 420
ggcggcacag ccgctctggg ctgcctggtc aaggactact tccccgagcc cgtgaccgtg 480
tcctggaaca gcggagccct gacctccggc gtgcacacct tccccgccgt gctgcagagt 540
tctggcctgt atagcctgag cagcgtggtc accgtgcctt ctagcagcct gggcaccag 600
acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggag 660
cccaagagct gcgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccgacc 780
cctgaggtca catgcgtggg ggtggacgtg agccacgaag accctgaggt caagttcaac 840

eof-seq1

tggtacgtgg acggcgtgga ggtgcataat gccaaagacaa agccgcggga ggagcagtac	900
aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc	960
aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg ccccatcga gaaaaccatc	1020
tccaaagcca aagggcagcc ccgagaacca caggtgtgca ccctgcccc atcccgggat	1080
gagctgacca agaaccaggt cagcctctcg tgcgcagtca aaggcttcta tcccagcgac	1140
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc	1200
gtgctggact ccgacggctc cttcttcctc gtgagcaagc tcaccgtgga caagagcagg	1260
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac	1320
acgcagaaga gcctctccct gtctccgggt aaa	1353

<210> 289
 <211> 592
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DP47GS Fab HC-Fc knob (LALA P329G)-IL-2 qm
 <400> 289

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

Ser Leu Arg	Leu Ser Cys Ala Ala	Ser Gly Phe Thr Phe	Ser Ser Tyr
20	25	30	

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

Ser Ala Ile	Ser Gly Ser Gly Gly	Ser Thr Tyr Tyr	Ala Asp Ser Val
50	55	60	

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

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

Ala Lys Gly	Ser Gly Phe Asp Tyr	Trp Gly Gln Gly Thr	Leu Val Thr
100	105	110	

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

Ser Ser	Lys Ser Thr Ser	Gly Gly Thr Ala Ala	Leu Gly Cys	Leu Val
130	135	140		

Lys Asp Tyr Phe Pro	Glu Pro Val Thr Val	Ser Trp Asn Ser Gly	Ala
145	150	155	160

eo1f-seq1

Leu Thr Ser Gly Val₁₆₅ His Thr Phe Pro Ala₁₇₀ Val Leu Gln Ser Ser₁₇₅ Gly
 Leu Tyr Ser Leu₁₈₀ Ser Ser Val Val₁₈₅ Thr Val Pro Ser Ser Ser₁₉₀ Leu Gly
 Thr Gln Thr₁₉₅ Tyr Ile Cys Asn Val₂₀₀ Asn His Lys Pro Ser₂₀₅ Asn Thr Lys
 Val Asp₂₁₀ Lys Lys Val Glu Pro₂₁₅ Lys Ser Cys Asp Lys₂₂₀ Thr His Thr Cys
 Pro₂₂₅ Pro Cys Pro Ala Pro₂₃₀ Glu Ala Ala Gly Gly₂₃₅ Pro Ser Val Phe Leu₂₄₀
 Phe Pro Pro Lys Pro₂₄₅ Lys Asp Thr Leu Met₂₅₀ Ile Ser Arg Thr Pro₂₅₅ Glu
 Val Thr Cys Val₂₆₀ Val Val Asp Val₂₆₅ Ser His Glu Asp Pro Glu₂₇₀ Val Lys
 Phe Asn Trp₂₇₅ Tyr Val Asp Gly Val₂₈₀ Glu Val His Asn Ala₂₈₅ Lys Thr Lys
 Pro Arg₂₉₀ Glu Glu Gln Tyr Asn₂₉₅ Ser Thr Tyr Arg Val₃₀₀ Val Ser Val Leu
 Thr Val₃₀₅ Leu His Gln Asp₃₁₀ Trp Leu Asn Gly Lys₃₁₅ Glu Tyr Lys Cys Lys₃₂₀
 Val Ser Asn Lys Ala₃₂₅ Leu Gly Ala Pro Ile₃₃₀ Glu Lys Thr Ile Ser₃₃₅ Lys
 Ala Lys Gly Gln₃₄₀ Pro Arg Glu Pro Gln₃₄₅ Val Tyr Thr Leu Pro₃₅₀ Pro Cys
 Arg Asp Glu₃₅₅ Leu Thr Lys Asn Gln Val Ser Leu Trp Cys₃₆₅ Leu Val Lys
 Gly Phe₃₇₀ Tyr Pro Ser Asp Ile₃₇₅ Ala Val Glu Trp Glu₃₈₀ Ser Asn Gly Gln
 Pro Glu Asn Asn Tyr Lys₃₉₀ Thr Thr Pro Pro Val₃₉₅ Leu Asp Ser Asp Gly₄₀₀
 Ser Phe Phe Leu Tyr₄₀₅ Ser Lys Leu Thr Val₄₁₀ Asp Lys Ser Arg Trp₄₁₅ Gln
 Gln Gly Asn Val₄₂₀ Phe Ser Cys Ser Val₄₂₅ Met His Glu Ala Leu₄₃₀ His Asn

eolf-seq1

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
435 440 445

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Pro Ala Ser Ser
450 455 460

Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu
465 470 475 480

Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr
485 490 495

Arg Met Leu Thr Ala Lys Phe Ala Met Pro Lys Lys Ala Thr Glu Leu
500 505 510

Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
515 520 525

Leu Asn Gly Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu
530 535 540

Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr
545 550 555 560

Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe
565 570 575

Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
580 585 590

<210> 290
<211> 1776
<212> DNA
<213> Artificial Sequence

<220>
<223> DP47GS Fab HC-Fc knob (LALA P329G)-IL-2 qm

<400> 290
gaggtgcaat tgttgagtc tgggggaggc ttgttacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcagct attagtggta gtgggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggcagc 300
ggatttgact actggggcca aggaaccctg gtcaccgtct cgagtgctag caccaagggc 360
ccatcgggtct tccccctggc accctcctcc aagagcacct ctggggggcac agcggccctg 420
ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgctgtggaa ctcaggcgcc 480
ctgaccagcg gcgtgcacac cttccccggct gtcctacagt cctcaggact ctactccctc 540
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eof-seq1

agcagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg 600
aatcacaagc ccagcaacac caaggtggac aagaaaagttg agcccaaadc ttgtgacaaa 660
actcacacat gcccaccgtg cccagcacct gaagctgcag ggggaccgtc agtcttcctc 720
ttccccccaa aaccaagga caccctcatg atctcccga cccctgaggt cacatgcgtg 780
gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 840
gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg 900
gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgaag 960
gtctccaaca aagccctcgg cgcccccatc gagaaaacca tctccaaagc caaagggcag 1020
ccccgagaac cacaggtgta caccctgccc ccatgccggg atgagctgac caagaaccag 1080
gtcagcctgt ggtgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 1140
agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1200
tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1260
ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc 1320
ctgtctccgg gtggcggcgg aggtctccga ggcgagggtt ctggcggagg tggctccgca 1380
cctgcctcaa gttctacaaa gaaaacacag ctacaactgg agcatttact gctggattta 1440
cagatgattt tgaatggaat taataattac aagaatccca aactcaccag gatgctcaca 1500
gccaaagttt ccatgccccaa gaaggccaca gaactgaaac atcttcagt tctagaagaa 1560
gaactcaaac ctctggagga agtgctaaat ggcgctcaaa gcaaaaaactt tcacttaaga 1620
cccagggact taatcagcaa tatcaacgta atagttctgg aactaaagg atctgaaaca 1680
acattcatgt gtgaatatgc tgatgagaca gcaaccattg tagaatttct gaacagatgg 1740
attacctttg cccaaagcat catctcaaca ctgact 1776

<210> 291
<211> 592
<212> PRT
<213> Artificial Sequence

<220>
<223> DP47GS Fab HC-Fc knob (LALA P329G)-IL-2 wt (2)
<400> 291

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

eolf-seq1

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

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

Ala Lys Gly Ser Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

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

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
130 135 140

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
145 150 155 160

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
165 170 175

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
180 185 190

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
195 200 205

Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

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

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
275 280 285

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys
325 330 335

eo1f-seq1

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Cys
340 345 350

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu Val Lys
355 360 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
370 375 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385 390 395 400

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
405 410 415

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly
435 440 445

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Pro Thr Ser Ser
450 455 460

Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu
465 470 475 480

Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr
485 490 495

Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu
500 505 510

Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
515 520 525

Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu
530 535 540

Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr
545 550 555 560

Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe
565 570 575

Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
580 585 590

<210> 292
<211> 1776

eolf-seq1

<212> DNA

<213> Artificial Sequence

<220>

<223> DP47GS Fab HC-Fc knob (LALA P329G)-IL-2 wt (2)

<400> 292

gaggtgcaat tgttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc	60
tcctgtgcag cctccggatt cacctttagc agttatgccca tgagctgggt ccgccaggct	120
ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggcagc	300
ggatttgact actggggcca aggaaccctg gtcaccgtct cgagtgctag caccaagggc	360
ccatcggctt tccccctggc accctcctcc aagagcacct ctggggggcac agcggccctg	420
ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgctgtggaa ctcaggcgcc	480
ctgaccagcg gcgtgcacac cttccccggct gtcctacagt cctcaggact ctactccctc	540
agcagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg	600
aatcacaagc ccagcaacac caaggtggac aagaaaagttg agcccaaadc ttgtgacaaa	660
actcacacat gcccaccgtg cccagcacct gaagctgcag ggggaccgtc agtcttcctc	720
ttcccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg	780
gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg	840
gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg	900
gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgaag	960
gtctccaaca aagccctcgg cggcccatc gagaaaacca tctccaaagc caaagggcag	1020
ccccgagaac cacaggtgta caccctgccc ccatgccggg atgagctgac caagaaccag	1080
gtcagcctgt ggtgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag	1140
agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc	1200
tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc	1260
ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc	1320
ctgtctccgg gtggcggcgg aggtctccga ggcggagggt ctggaggcgg aggtctccga	1380
cctacttcaa gttctacaaa gaaaacacag ctacaactgg agcatttact gctggattta	1440
cagatgattt tgaatggaat taataattac aagaatccca aactcaccag gatgctcaca	1500
tttaagtttt acatgcccga gaaggccaca gaactgaaac atcttcagtg tctagaagaa	1560
gaactcaaac ctctggagga agtgctaaat ttagctcaaa gcaaaaactt tcacttaaga	1620
cccagggact taatcagcaa tatcaacgta atagtctctg aactaaaggg atctgaaaca	1680
acattcatgt gtgaatatgc tgatgagaca gcaaccattg tagaatttct gaacagatgg	1740
attacctttg cccaaagcat catctcaaca ctgact	1776

eof-seq1

<210> 293
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CH1A1A 98/99 2F1; VL

<400> 293

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

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

Tyr Ser Ala Ser Tyr Arg Lys Arg 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 His Gln Tyr Tyr Thr Tyr Pro Leu
 85 90 95

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

<210> 294
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CH1A1A 98/99 2F1; VL

<400> 294

gatatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtgggaga cagagtcacc	60
atcacttgca aggccagtc ggctgtgggt acgtatgttg cgtggtatca gcagaaacca	120
gggaaagcac ctaagctcct gatctattcg gcatcctacc gcaaaagggg agtcccatca	180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagatttcg caacttacta ctgtcaccaa tattacacct atcctctatt cacgtttggc	300
cagggcacca agctcgagat caag	324

<210> 295
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CH1A1A 98/99 2F1; VH

eof-seq1

<400> 295

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

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

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

Gly Trp Ile Asn Thr Lys Thr Gly Glu Ala Thr Tyr Val Glu Glu Phe
50 55 60

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

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

Ala Arg Trp Asp Phe Ala Tyr Tyr Val Glu Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 296

<211> 363

<212> DNA

<213> Artificial sequence

<220>

<223> CH1A1A 98/99 2F1; VH

<400> 296

caggtgcagc tgggtgcagtc tggcgccgaa gtgaagaaac ctggagctag tgtgaagggtg	60
tcctgcaagg ccagcggcta caccttcacc gagttcggca tgaactgggt cgcacaggct	120
ccaggccagg gcctcgaatg gatgggctgg atcaacacca agaccggcga ggccacctac	180
gtggaagagt tcaagggcag agtgaccttc accacggaca ccagcaccag caccgcctac	240
atggaactgc ggagcctgag aagcgacgac accgccgtgt actactgcdc cagatgggac	300
ttgcctatt acgtggaagc catggactac tggggccagg gcaccaccgt gaccgtgtct	360
agc	363

<210> 297

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> DP47GS VL

<400> 297

eolf-seq1

Glu Ile Val 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

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

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

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

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

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

<210> 298
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DP47GS VL

<400> 298
 gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcttgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180
 gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcaccgct gacgttcggc 300
 caggggacca aagtggaaat caaa 324

<210> 299
 <211> 115
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DP47GS VH

<400> 299
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Gly Ser Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110
 Val Ser Ser
 115

<210> 300
 <211> 345
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DP47GS VH

<400> 300
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