

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

[illegible]

eolf-seq1

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

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

<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

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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

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

eolf-seq1

<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

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

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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

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

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Thr Ser

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

<220>
 <223> leader sequence

<400> 8

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

<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

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20

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

<220>
 <223> leader sequence

<400> 12
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 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
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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
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 <212> DNA
 <213> Artificial Sequence

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<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

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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	

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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 ggcgggtggaa 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 ctgggaaaac tcccaagcct cccactactt tgaaagacac 480
 ctggagttcg agggccggac gctgtcccca ggccacacct gggaggaggc ccccctgctg 540
 actctcaagc agaagcagga atggatctgc ctggagacgc tcaccccaga caccagtat 600
 gagtttcagg tgcgggtcaa gcctctgcaa ggcgagttca cgacctggag cccctggagc 660
 cagcccctgg ccttcagaac aaagcctgca gcccttgga aggacaccgg agctcaggac 720
 aaaactcaca catgccacc gtgccagca cctgaactcc tggggggacc gtcagtcttc 780
 ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 840
 gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 900
 gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 960
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 aaggtctcca acaaagccct cccagcccc atcgagaaaa ccatctcaa agccaaaggg 1080
 cagccccgag aaccacaggt gtgcaccctg ccccatccc gggatgagct gaccaagaac 1140
 caggtcagcc tctcgtgcgc agtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1200
 gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1260

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ggctccttct tcctcgtgag caagctcacc gtggacaaga gcaggtggca gcaggggaac	1320
gtcttctcat 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

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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

eo1f-seq1

435

440

445

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

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

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

<210> 20
<211> 1479
<212> DNA
<213> Artificial Sequence

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

<400> 20
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gtggggctga acacgacaat tctgacgccc aatgggaatg aagacaccac agctgatttc 120
ttcctgacca ctatgcccac tgactccctc agtgtttcca ctctgcccct cccagagggt 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 agagaacct 480
acattcaca aactgagtga atcccagcta gaactgaact ggaacaacag attcttgaac 540
cactgttttg agcacttggt gcagtaccgg actgactggg accacagctg gactgaacaa 600
tcagtggatt atagacataa gttctccttg cctagtgtgg atgggcagaa acgctacacg 660
tttcgtgttc ggagccgctt taaccactc tgtggaagtg ctcagcattg gagtgaatgg 720
agccaccaa tccactgggg gagcaatact tcaaaagaga atcctttcct gtttgcattg 780
gaagccggag ctcaggacaa aactcacaca tgcccaccgt gccagcacc tgaactcctg 840
gggggaccgt cagtcttcct cttccccca aaacccaagg acaccctcat gatctcccgg 900
accctgagg tcacatgctt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 960
aactggtacg tggacggcgt ggaggtgcat aatgccaaaga caaagccgcg ggaggagcag 1020
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1080
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1140
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatgccgg 1200

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gatgagctga ccaagaacca ggtcagcctg tgggtgcctgg 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 ggtaaatga 1479

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

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<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

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

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```

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

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

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```

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

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```

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

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

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

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

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

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

<210> 22
 <211> 660
 <212> DNA
 <213> Artificial Sequence

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

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 gaaggaacca tgttgaactg tgaatgcaag agagggttcc gcagaataaa aagcgggtca 180
 ctctatatgc tctgtacagg aaactctagc cactcgtcct gggacaacca atgtcaatgc 240
 acaagctctg ccaactcggaa cacaacgaaa caagtgcacac ctcaacctga agaacagaaa 300
 gaaaggaaaa ccacagaaat gcaaagtcca atgcagccag tggaccaagc gagccttcca 360
 ggtcactgca gggaacctcc accatgggaa aatgaagcca cagagagaat ttatcatttc 420
 gtgggtggggc agatggttta ttatcagtgc gtccagggat acagggtctc acacagaggt 480
 cctgctgaga gcgtctgcaa aatgaccac gggaagacaa ggtggacca gccccagctc 540
 atatgcacag gtgtcgacga acagttatat tttcagggcg gctcaggcct gaacgacatc 600
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<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

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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

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

<220>
<223> 2B10; VL

<400> 24
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atcacctgcc gggcaagtca gggcattaga aatgatttag gctggtacca gcagaagcca 120
gggaaagccc ctaagcgcct gatctatgct gcatccagtt tgcagagtgg cgtcccatca 180
aggttcagcg gcggtggatc cgggacagag ttactctca ccatcagcag cttgcagcct 240
gaagattttg ccacctatta ctgcttgag 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
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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

<400> 26
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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> 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

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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
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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
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 tca 363

<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

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35

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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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cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcgtccca 180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta ttactgtcag cagggtcagt atactcccc caggttcggc 300
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

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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
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 cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180
 gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgtg ttactgtcag cagggtcagt atactcccc cacgttcggc 300
 caggggacca aagtggaaat caaa 324

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

<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

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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
gagggtgcaat tggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt cacctttagc agttatgccca tgagctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag 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

<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

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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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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

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
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60

50

55

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

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

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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
gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcttgca gggccagtca gagtgttacc agtagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatcaat gtgggctccc gtagggccac tggcatccca 180
gacaggttca gtggcagtggt atccggggaca 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

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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
gaggtgcaat tggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt cacctttagc agttatgccca tgagctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cgcgtgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300
tttggtggtt 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

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

<220>
<223> 3D9, VL

<400> 44
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 cagggtcagc ttattccccc 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 eolf-seq1 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> 46
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> 3D9, VH

<400> 46
gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt cacctttagc agttatgcta tgagctgggt ccgccagact 120
ccagggaagg ggctggagtg ggtctcagct attggtgtta gtactggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggttg 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
<212> DNA
<213> Artificial Sequence

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

<400> 48
gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt cacctttagc agttatgcta tgagctgggt ccgccaggct 120
ccaggaagg ggctggagtg ggtctcagct attggtgtta gtactggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggttg 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

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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
gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcttgca gggccagtca gagtgttagc cgcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatcatt ggggcctcca ccagggccac 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

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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
gaggtgcaat tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt cacctttagc agttatgccca tgagctgggt ccgccaggct 120
ccagggaagg 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> 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
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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 gagtgtagc agcaattact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggcgcctaca tcagggccac tggcatccca 180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta ttactgtcag cagggtcagg ttattccccc tacgttcggc 300
caggggacca aagtggaaat caaa 324

<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
gagggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt cacctttagc agttatgcc a tgagctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcagct attagtggta gtgggtgtag 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

<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

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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
gacagggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg ttactgtcag caggggtcagg 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

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

eolf-seq1

Val Thr Val Ser Ser
115

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

<220>
<223> 4D6; VH

<400> 60
gaggtgcaat tgttggagtc 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 gaaaggggtgg 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

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
Page 37

eolf-seq1

100

105

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

<220>
 <223> 2C6; VL

<400> 62
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 ctctcttgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120
 cctggccagg ctccaggct 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
 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

eo1f-seq1

Val Thr Val Ser Ser
115

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

<220>
<223> 2C6; VH

<400> 64
gaggtgcaat tggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatc cacctttagc agttatgcc a tgagctgggt ccgccaggct 120
ccagggaagg 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

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

eolf-seq1

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

<220>
<223> 5H5; VL

<400> 66
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ctctcttgca gggccagtca gagtgtagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta 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
Thr Val Ser Ser
115

eolf-seq1

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

<220>
<223> 5H5; VH

<400> 68
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tcctgtgcag cctccggatt cacctttagc agttatacca tgagctgggt ccgccggtct 120
ccagggaagg ggctggagtg ggtctcagct attagtgggt gtggtaggac atactacgca 180
gactccgtga agggccggtt caccatctcc agagacaatt ccaagaacac gctgtatctg 240
cagatgaaca gcctgagagc cgaggacacg gccgtatatt actgtgcgaa 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

eof-seq1

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

<220>
 <223> 2C4; VL

<400> 70
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 ctctcttgca gggccagtca gagtgttagc agtaactact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatctat ggtgcctcca ttagggccac tggcatccca 180
 gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgtg ttactgtcag cagggtaatc agattcccc tacgttcggt 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

eolf-seq1

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

<220>
<223> 2C4; VH

<400> 72
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tcctgtgcag cctccggatt cacccttagc agttatgccca tgagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcagct attagcggtg gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggttg 300
tttacgcctt ttgactactg gggccaagga accctggtca 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

eof-seq1

<213> Artificial Sequence

<220>

<223> 2D9; VL

<400> 74

gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
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 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> 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

eof-seq1

<212> DNA
<213> Artificial Sequence

<220>
<223> 2D9; VH

<400> 76
gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt caccttttagc agttatgccca tgagctgggt ccgccaggct 120
ccagggaagg 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> 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

eolf-seq1

<220>

<223> 4B8; VL

<400> 78

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

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<210> 79

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> 4B8; VH

<400> 79

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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 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

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<210> 80

<211> 351

<212> DNA

<213> Artificial Sequence

eof-seq1

<220>
 <223> 4B8; VH
 <400> 80
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 tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120
 ccagggaagg 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> 81
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 7A1; VL

<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

eolf-seq1

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<400> 82
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 agattcccc tacgttcggc      300
caggggacca aagtggaaat caaa                                           324

```

```

<210> 83
<211> 117
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> 7A1; VH

```

```

<400> 83

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```

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 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>

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eof-seq1

<223> 7A1; VH

<400> 84
gaggtgcaat tgttgagtc 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 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

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

eolf-seq1

gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc	60
ctctcttgca gggccagtca gagtgtagc agcagctact tagcctggta ccagcagaaa	120
cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatcca	180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag	240
cctgaagatt ttgcagtgtg 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

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

eof-seq1

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<400> 88
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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 gaaagggttg      300
ctgggtcctt ttgactactg gggccaagga accctgggtca ccgtctcgag t              351

```

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

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```

<220>
<223> 13E8; VL

```

<400> 89

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

```

```

<220>
<223> 13E8; VL

```

```

<400> 90
gaaatcggtg taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc      60

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eolf-seq1

ctctcttgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa	120
cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca	180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag	240
cctgaagatt ttgcagtgtg 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

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

<220>
 <223> 13E8; VH

<400> 92

gaggtgcaat tgttggagtc tggggggaggc ttggtacagc ctgggggggtc cctgagactc	60
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eof-seq1

tcctgtgcag cctccggatt cacctttagc agttatgcc	tgagctgggt ccgccaggct	120
ccagggaagg ggctggagtg ggtctcagct attagtggta	gtgggtggtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca	attccaagaa cacgctgtat	240
ctgcagatga acagcctgag agccgaggac acggccgtat	attactgtgc gaaagggttg	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

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

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

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

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65

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

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

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

<220>
 <223> 14C10; VL

<400> 94

gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc	60
ctctcttgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa	120

eolf-seq1

cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca	180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag	240
cctgaagatt ttgcagtgtg ttactgtcag cagggtcata ttattcccc gacgttcggc	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 tggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc	60
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tcctgtgcag cctccggatt cacctttagc agttatgccg tgagctgggt ccgccaggct	120
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eof-seq1

ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggttag 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 gagtgtagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180

eolf-seq1

gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag	240
cctgaagatt ttgcagtgtg ttactgtcag caggggtctga atattccctc gacgttcggc	300
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 tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc	60
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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 gaaagggttg 300
ttgggtccgt ttgactactg gggccaagga accctgggtca ccgtctcgag t 351
```

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

```
<220>
<223> 19G1; VL
```

```
<400> 101
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```
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
```

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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
```

eolf-seq1

cctgaagatt ttgcagtgtg ttactgtcag cagggtatta tgcttcccc	gacgttcggc	300
caggggacca aagtggaaat caaa		324

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

<220>
 <223> 19G1; VH

<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 tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc	60
tcctgtgcag cctccggatt cacccttagc agttatgcga tgagctgggt ccgccaggct	120
ccaggggaagg ggctggagtg ggtctcagcg attattagta gtggtggtct cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240

eolf-seq1

```
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtgg      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
```

```
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
```

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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

<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

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

ccagggaagg ggctggagtg ggtctcagct attattggga gtggtagtcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtgg 300

eof-seq1

tttggtggtt ttaactactg gggccaagga accctggtca 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

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 gagtggtacc 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

eolf-seq1

<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

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
gagggtcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt cacctttagc agttatgcta tgagctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcagct attattggta gtggtgctag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300
tttggtggtt ttaactactg gggccaagga accctgggtca ccgtctcgtc c 351

eolf-seq1

<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

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

<220>
<223> 5B8; VL

<400> 114

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 cagggtatta tgcttcccc gacgttcggc	300
caggggacca aagtggaaat caaa	324

<210> 115

eolf-seq1

<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
<212> DNA
<213> Artificial Sequence

<220>
<223> 5B8; VH

<400> 116

gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc	60
tcctgtgcag cctccggatt cacctttagc agttatgcta tgagctgggt ccgccaggct	120
ccagggaagg ggctggagtg ggtctcagct atttggggtg gtggtcgtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggtgg	300
tttggtggtt ttaactactg gggccaagga accctgggtca ccgtctcgtc c	351

eo1f-seq1

<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
 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

eof-seq1

<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 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 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
115

<210> 120

<211> 351

<212> DNA

<213> Artificial Sequence

<220>

<223> 5F1; VH

<400> 120

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

<210> 121

<211> 108

eof-seq1

<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
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<213> Artificial Sequence

<220>
<223> 14B3; VL

<400> 122

gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc	60
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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> 123
<211> 117
<212> PRT
<213> Artificial Sequence

eolf-seq1

<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

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ccagggaagg ggctggagtg ggtctcagct attttggcta gtggtgcat cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cagctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300

tttggtggtt ttaactactg gggccaagga accctgggtca ccgtctcgtc c 351

<210> 125

<211> 108

<212> PRT

<213> Artificial Sequence

eolf-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

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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 cagggtatta tgcttcccc gacgttcggc 300

caggggacca aagtggaaat caaa 324

<210> 127

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> 16F1; VH

eolf-seq1

<400> 127

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 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 tgttggagtc tgggggaggc ttgttacagc ctgggggggtc cctgagactc 60

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ccagggaagg ggctggagtg ggtctcaggt attattggtg gtggtggtat cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggtgg 300

tttggtggtt ttaactactg gggccaagga accctgggtca ccgtctcgtc c 351

<210> 129

<211> 108

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<213> Artificial Sequence

<220>

eof-seq1

<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

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
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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 ttgcagtgta ttactgtcag caggggtatta tgcttcccc gacgttcggc 300
caggggacca aagtggaaat caaa 324

<210> 131

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> 16F8; VH

<400> 131

eo1f-seq1

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

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
gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt cacctttagc agttatgcc a tgagctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcagct attcttggt a gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggtgg 300
tttggtggtt ttaactactg gggccaagga accctgggtca ccgtctcgtc c 351

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

<220>
<223> 03C9; VL

eolf-seq1

<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

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

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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> 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

eolf-seq1

1	5	10	15
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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

Val Thr Val Ser Ser
 115

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

<220>
 <223> O3C9; VH

<400> 136 gaggtgcaat tggtggagtc tgggggagggc ttggtacagc ctgggggggtc cctgagactc tcctgtgcag cctccggatt cacctttagc agttttgcca tgagctgggt ccgtcagtct ccagggaagg ggctggagtg ggtctcagct attattggta gtggtagtaa cacatactac gcagactccg tgaagggccg gttcaccatc tcagagaca attccaagaa cacgctgtat ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg tttggtggtt ttaactactg gggccaagga accctgggtca ccgtctcgtc c	60 120 180 240 300 351
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<210> 137
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> O2D7; VL

<400> 137

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 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
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> O2D7; VL

<400> 138
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 ctctcttgca gggccagtca gagtgttacc 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

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 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>
<223> O2D7; VH

<400> 140
gagggtgcaat tgttgaggatc 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
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

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
100 105

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

<220>
<223> 28H1; VL

<400> 142
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ctctcttgca gggccagtca gagtgttagc cgcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatcatt ggggcctcca ccagggccac tggcatccca 180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg ttactgtcag cagggtcagg ttattcccc 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
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[illegible]

eolf-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> 146
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 22A3; VL

<400> 146
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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 ttgcagtgta ttactgtcag caggggtatta tgcttcccc gacgttcggc 300
 caggggacca aagtggaaat caaa 324

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

<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

eo1f-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 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 tggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120
 ccagggaagg ggctggagtg ggtctcagct attattggta gtggtagtat cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300
 tttgttggtt ttaactactg gggccaagga accctgggtca ccgtctcgag t 351

<210> 149
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 29B11; VL

<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

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> 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 cagggtatta 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

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
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eolf-seql															
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													

eolf-seq1

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

<220>
 <223> 23C10; VL

<400> 154
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 cctggccagg ctcccaggct cctcatcatt ggggcctcca ccagggccac tggcatccca 180
 gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgtg 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

eolf-seq1

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

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
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tcctgtgcag cctccggatt caccttttagc agttctgccca tgagctgggt cgcaggct 120
ccagggaagg ggctggagtg ggtctcagct attagtacta atggtaatta tacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggtgg 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

eo1f-seq1

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

<220>
<223> 2B10_C3B6; VL

<400> 158
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gggaaagccc ctaagcgcct gatctatgct gcatccagtt tgcagagtgg cgtcccatca 180
aggttcagcg gcagtggatc cgggacagag ttactctca ccatcagcag cttgcagcct 240
gaagattttg ccacctatta ctgcttgtag 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

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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> 160
<211> 363
<212> DNA
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<220>
<223> 2B10_C3B6; VH

<400> 160
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tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
cctggacaag ggctcgagtg gatgggagct atcatccccga tccttggtat cgcaaactac 180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagactgtac 300
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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

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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

<220>
<223> 2B10_6A12; VL

<400> 162
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gggaaagccc ctaagcgcct gatctatgct gcatccagtt tgcagagtgg cgtcccatca 180
aggttcagcg gcagtggatc cgggacagag ttactctca 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
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60

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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
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<212> DNA
<213> Artificial Sequence

<220>
<223> 2B10_6A12; VH

<400> 164
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tcctgcaagg cctccggagg cacattcagc agctatgcta taagctgggt gcgacaggcc 120
cctggacaag ggctcgagtg gatgggagtg atcatcccta tccttggtac cgcaaactac 180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagactgtac 300
ggttacgctt actacgggtgc 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

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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
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gggaaagccc ctaagcgcct gatctatgat tcgtccagtt tgcagagtgg cgtcccatca 180
aggttcagcg gcggtggatc cgggacagag ttactctca ccatcagcag cttgcagcct 240
gaagattttg ccacctatta ctgcttgtag 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

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60

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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
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<220>
<223> 2B10_C3A6; VH

<400> 168
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cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180
gcacagaagt tccagggcag gggtcaccatt actgcagaca aatccacgag cacagcctac 240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagactgtac 300
ggttacgctt actacgggtgc 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

eo1f-seq1

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
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gggaaagccc ctaagcgcct gatctatgat gcttacagct tgcagagtgg cgtcccatca 180
aggttcagcg gcggtggatc cgggacagag ttactctca ccatcagcag cttgcagcct 240
gaagattttg ccacctatta ctgcttgcat aatgggtctgc agcccgcgac gtttggccag 300
ggcaccaaag tcgagatcaa g 321

<210> 171
<211> 121
<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
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60

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55

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

<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

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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
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gggaaagccc ctaagcgcct gatctatgat gcttacagct tgcagagtgg cgtcccatca 180
aggttcagcg gcggtggatc cgggacagag ttactctca ccatcagcag cttgcagcct 240
gaagattttg ccacctatta ctgcttgtag aatgggtctgc agcccgcgac gtttggccag 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

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
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60

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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
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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_O7D8; VL

<400> 177

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 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

eolf-seq1

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_07D8; VL

<400> 178
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gggaaagccc ctaagcgcct gatctatgat gtgtccagtt tgcagagtgg cgtcccatca 180
aggttcagcg gcggtggatc cgggacagag ttactctca 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_07D8; 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

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

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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
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cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180
gcacagaagt tccagggcag gggtcaccatt actgcagaca aatccacgag cacagcctac 240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagactgtac 300
ggttacgctt actacgggtgc 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

eo1f-seq1

Tyr Asp 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

<210> 182
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> 2B10_O1F7; VL

<400> 182
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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_O1F7; 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
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60

50

55

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> 184
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> 2B10_O1F7; VH

<400> 184
cagggtgcaat 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

eo1f-seq1

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

<210> 186
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> 2B10_6H10; VL

<400> 186
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gggaaagccc ctaagcgcct gatccaggct gctaccagtt tgcagagtgg cgtcccatca 180
aggttcagcg gcggtggatc cgggacagag ttactctca ccatcagcag cttgcagcct 240
gaagattttg ccacctatta ctgcttgtag 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

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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> 188
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> 2B10_6H10; VH

<400> 188
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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

eo1f-seq1

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>
<223> CH1A1A; VL

<400> 190
gatatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtgggaga cagagtcacc 60
atcacttgca aggccagtc ggctgtgggt acgtatgttg cgtgggtatca 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

eof-seq1
60

50

55

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
cagggtgcagc 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
atggaactgc ggagcctgag aagcgacgac accgccgtgt actactgcgc cagatgggac 300
ttcgccattt 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

eolf-seq1

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

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val

eolf-seq1
300

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 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> 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 cctccggcctt caccttctcc tcccacgcca tgtcctgggt ccgacaggct	120
cctggcaaag 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
ggcccctccg tgttccccct ggcccccagc agcaagagca ccagcggcgg cacagccgct	420
ctgggctgcc tgggtcaagga ctacttcccc gagcccgtga ccgtgtcctg gaacagcgga	480

eof-seq1

gccctgacct ccggcgtgca caccttcccc gccgtgctgc agagttcttg cctgtatagc 540
 ctgagcagcg tggtcaccgt gccttctagc agcctgggca cccagacct catctgcaac 600
 gtgaaccaca agcccagcaa caccaaggtg gacaagaagg tggagcccaa gagctgcgac 660
 aaaactcaca catgcccacc gtgcccagca cctgaagctg cagggggacc gtcagtcttc 720
 ctcttcccccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 780
 gtgggtggtg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840
 gtggaggtgc ataatgcaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 900
 gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960
 aaggtctcca acaaagccct cggcgcccc atcgagaaaa ccatctccaa agccaaaggg 1020
 cagccccgag aaccacaggt gtgcaccctg ccccatccc gggatgagct gaccaagaac 1080
 caggctagcc tctcgtgctg agtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1140
 gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200
 ggctccttct tcctcgtgag caagctcacc gtggacaaga gcagggtggc 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

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

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

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
 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

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<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 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 cgggtgctgt gaactcaggc 480
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc 540
ctcagcagcg tggtgaccgt gccctccagc agcttgggca ccagaccta catctgcaac 600
gtgaatcaca agcccagcaa caccaagggt gacaagaaag ttgagcccaa atcttgtgac 660
aaaactcaca catgcccacc gtgcccagca cctgaagctg cagggggacc 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
aaggctctca acaaagccct cggcgcccc atcgagaaaa ccatctccaa agccaaaggg 1020
cagccccgag aaccacaggt gtacaccctg ccccatgcc gggatgagct gaccaagaac 1080
caggctagcc 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 aggtggcgct 1380
cctgcctcct ccagcaccaa gaaaaccag ctccagctgg aacatctcct gctggatctg 1440
cagatgatcc tgaacggcat caacaactac aagaacccca agctgacccg gatgctgacc 1500
gccaagtctg ccatgccc aaaggccacc gagctgaaac atctgcagt cctggaagag 1560
gaactgaagc ctctggaaga ggtgctgaac ggcgcccagt ccaagaactt ccacctgagg 1620

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cctcgggacc tgatctccaa catcaacgtg atcgtgctgg aactgaaggg ctccgagaca 1680
accttcatgt gcgagtacgc cgacgagaca gctaccatcg tggaatttct gaaccggtgg 1740
atcaccttcg cccagtccat catctccacc ctgacc 1776

<210> 197
<211> 592
<212> PRT
<213> Artificial Sequence

<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

eolf-seql

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

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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

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
tcctgcgccg cctccggctt caccttctcc tcccacgcca tgtcctgggt ccgacaggct 120
cctggcaaaag gcctggaatg ggtgtccgcc atctgggcct ccggcgagca 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

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ctgggctgcc	tgggtcaagga	ctacttcccc	gaaccggtga	cggtgtcgtg	gaactcaggc	480
gccctgacca	gcggcgtgca	caccttcccc	gctgtcctac	agtcctcagg	actctactcc	540
ctcagcagcg	tgggtgaccgt	gccctccagc	agcttgggca	cccagaccta	catctgcaac	600
gtgaatcaca	agcccagcaa	caccaaggtg	gacaagaaa	ttgagcccaa	atcttgtgac	660
aaaactcaca	catgcccacc	gtgcccagca	cctgaagctg	cagggggacc	gtcagtcttc	720
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	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	gcaggtggca	gcaggggaac	1260
gtcttctcat	gctccgtgat	gcatgaggct	ctgcacaacc	actacacgca	gaagagcctc	1320
tccctgtctc	cgggtggcgg	cggaggctcc	ggaggcggag	gttctggcgg	aggtggcgct	1380
cctacatcct	ccagcaccaa	gaaaacccag	ctccagctgg	aacatctcct	gctggatctg	1440
cagatgatcc	tgaacggcat	caacaactac	aagaacccca	agctgaccgc	gatgctgacc	1500
ttcaagttct	acatgcccc	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

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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

eolf-seq1

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
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
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
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

eolf-seq1

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
 gactctgtga agggccggtt caccatctcc cgggacaact ccaagaacac cctgtacctg 240
 cagatgaact ccctgcgggc cgaggacacc gccgtgtact actgtgccaa gggctggctg 300
 ggcaacttcg actactgggg acagggcacc ctggtcaccg tgtccagcgc tagcaccaag 360
 ggccccatcg tcttccccct ggacacctcc tccaagagca cctctggggg cacagcggcc 420
 ctgggctgcc tgggtcaagga ctacttcccc gaaccgggtga cgggtgcgtg gaactcaggc 480
 gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc 540
 ctcagcagcg tggtgaccgt gccctccagc agcttgggca ccagaccta catctgcaac 600
 gtgaatcaca agcccagcaa caccaagggt gacaagaaa ttgagcccaa atcttgtgac 660
 aaaactcaca catgcccacc gtgcccagca cctgaagctg cagggggacc gtcagtcttc 720
 ctcttcccc caaaacccaa ggacacctc atgatctccc ggaccttga ggtcacatgc 780
 gtggtggtgg acgtgagcca cgaagacctt gaggtcaagt tcaactggta cgtggacggc 840
 gtggagggtgc ataattgcaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 900
 gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960
 aaggtctcca acaaagccct cggcgcccc atcgagaaaa ccatctccaa agccaaaggg 1020
 cagccccgag aaccacagggt gtacacctg ccccatgcc gggatgagct gaccaagaac 1080
 caggtcagcc tgtggtgcct ggtcaaaggc ttctatccca gcgacatcg cgtggagtgg 1140
 gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200
 ggctccttct tcctctacag caagctcacc gtggacaaga gcagggtggc gcaggggaac 1260

eolf-seq1

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gtctttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1320
tccctgtctc cgggttccgg cggcggaggc tccggaggcg gaggttctgg cggagggtggc 1380
aactgggtga atgtaataag tgatttgaaa aaaattgaag atcttattca atctatgcat 1440
attgatgcta ctttatatac ggaaagtgat gttcacccca gttgcaaagt aacagcaatg 1500
aagtgctttc tcttggagtt acaagttatt tcacttgcgt ccggagatgc aagtattcat 1560
gatacagtag aaaatctgat catcctagca aacaacagtt tgtcttctaa tggggctgta 1620
acagaatctg gatgcaaaga atgtgaggaa ctggaggaaa aaaatattaa agaatttttg 1680
cagagttttg tacatattgt ccaaattgtt atcaacactt ct 1722

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<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

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

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

eolf-seq1

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 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 gaaaggggtg 300
ctgggtaatt ttgactactg gggccaagga accctgggtca ccgtctcgag tgctagcacc 360
aagggcccct ccgtgttccc cctggccccc agcagcaaga gcaccagcgg cggcacagcc 420
gctctgggct gcctgggtcaa ggactacttc cccgagcccc tgaccgtgtc ctggaacagc 480
ggagccctga cctccggcgt gcacaccttc cccgccgtgc tgcagagttc tggcctgtat 540
agcctgagca gcgtgggtcac cgtgccttct agcagcctgg gcacccagac ctacatctgc 600
aacgtgaacc acaagcccag caacaccaag gtggacaaga aggtggagcc caagagctgc 660
gacaaaaactc acacatgccc accgtgcccc gcacctgaag ctgcaggggg accgtcagtc 720
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 780
tgcgtggtgg tggacgtgag ccacgaagac cctgagggtca agttcaactg gtacgtggac 840
ggcgtggagg tgcataatgc caagacaaag ccgcggggagg agcagtacaa cagcacgtac 900
cgtgtgggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 960
tgcaagggtct 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 agagcagggtg gcagcagggg 1260

eolf-seq1

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

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

eolf-seq1

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
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

eolf-seq1

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 tgttggagtc 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 gaaaggggtgg 300
ctgggtaatt ttgactactg gggccaagga accctgggtca ccgtctcgag tgctagcacc 360

eolf-seq1

aagggcccat	cggtcttccc	cctggcaccc	tcctccaaga	gcacctctgg	gggcacagcg	420
gccctgggct	gcctgggtcaa	ggactacttc	cccgaaccgg	tgacggtgtc	gtggaactca	480
ggcgccctga	ccagcggcgt	gcacaccttc	ccggctgtcc	tacagtcctc	aggactctac	540
tccctcagca	gcgtgggtgac	cgtgccctcc	agcagcttgg	gcacccagac	ctacatctgc	600
aacgtgaatc	acaagcccag	caacaccaag	gtggacaaga	aagttgagcc	caaatcttgt	660
gacaaaactc	acacatgccc	accgtgcca	gcacctgaag	ctgcaggggg	accgtcagtc	720
ttcctcttcc	ccccaaaacc	caaggacacc	ctcatgatct	cccggacccc	tgaggtcaca	780
tgcgtgggtg	tggacgtgag	ccacgaagac	cctgaggtca	agttcaactg	gtacgtggac	840
ggcgtggagg	tgcataatgc	caagacaaa	ccgcgggagg	agcagtacaa	cagcacgtac	900
cgtgtgggtca	gcgtcctcac	cgtcctgcac	caggactggc	tgaatggcaa	ggagtacaag	960
tgcaaggtct	ccaacaaagc	cctcggcgcc	cccctcgaga	aaacctctc	caaagccaaa	1020
gggcagcccc	gagaaccaca	ggtgtacacc	ctgcccccat	gccgggatga	gctgaccaag	1080
aaccagggtca	gcctgtgggtg	cctgggtcaaa	ggcttctatc	ccagcgacat	cgccgtggag	1140
tgggagagca	atgggcagcc	ggagaacaac	tacaagacca	cgcctcccgt	gctggactcc	1200
gacggctcct	tcttctctta	cagcaagctc	accgtggaca	agagcagggtg	gcagcagggg	1260
aacgtcttct	catgctccgt	gatgcatgag	gctctgcaca	accactacac	gcagaagagc	1320
ctctccctgt	ctccgggttg	cggcggaggc	tccggaggcg	gaggttcttg	cggagggtggc	1380
gctctgcct	cctccagcac	caagaaaacc	cagctccagc	tggaacatct	cctgctggat	1440
ctgcagatga	tcctgaacgg	catcaacaac	tacaagaacc	ccaagctgac	ccggatgctg	1500
accgccaaagt	tcgccatgcc	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
 gagatcgtgc tgacccagtc ccccggcacc ctgtctctga gccctggcga gagagccacc

60

eolf-seq1

ctgtcctgca gagcctccca gtccgtgtcc cggtcctacc tcgcctggta tcagcagaag	120
cccggccagg cccctcggct gctgatcatc ggcgccctcta ccagagccac cggcatccct	180
gaccggttct ccggctctgg ctccggcacc gacttcaccc tgaccatctc ccggctggaa	240
cccgaggact tcgccgtgta ctactgccag cagggccagg tcatccctcc cacctttggc	300
cagggcacca aggtggaaat caagcgtacg gtggctgcac catctgtctt catcttcccg	360
ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc	420
tatcccagag aggccaaaagt acagtggaaag 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> 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 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

eolf-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 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

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 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> 208
<211> 1341
<212> DNA
<213> Artificial Sequence

<220>
<223> 4B9 Fab HC-Fc hole (LALA P329G)

<400> 208
gagggtgcagc tgctcgaaaag cggcggagga ctggtgcagc ctggcggcag cctgagactg 60
tcttgcgccg ccagcggcctt 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
aagggccccct ccgtgttccc cctggcccc 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
aacgtgaacc acaagcccag caacaccaag gtggacaaga aggtggagcc caagagctgc 660
gacaaaactc acacatgccc accgtgccca gcacctgaag ctgcaggggg accgtcagtc 720
ttcctcttcc ccccaaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 780
tgcgtgggtg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 840
ggcgtggagg tgcataatgc caagacaaaag ccgcgggagg agcagtacaa cagcacgtac 900
cgtgtgggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 960
tgcaagggtct ccaacaaagc cctcggcgcc cccatcgaga aaaccatctc caaagccaaa 1020
gggcagcccc gagaaccaca ggtgtgcacc ctgcccccat cccgggatga gctgaccaag 1080
aaccaggtca gcctctcgtg cgcagtcaaa ggcttctatc ccagcgacat cgccgtggag 1140

eof-seq1

tgaggagagca 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

<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

eo1f-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 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

eolf-seq1

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> 210
<211> 1779
<212> DNA
<213> Artificial Sequence

<220>
<223> 4B9 Fab HC-Fc knob (LALA P329G)-IL-2 qm

<400> 210	
gagggtgcagc tgctcgaaag cggcggagga ctggtgcagc ctggcggcag cctgagactg	60
tcttgcgccg ccagcggtt cacttcagc agctacgcca tgagctgggt ccgccaggcc	120
cctggcaagg gactggaatg ggtgtccgcc atcatcggct ctggcgccag cacctactac	180
gccgacagcg tgaagggccg gttcaccatc agccgggaca acagcaagaa caccctgtac	240

eolf-seq1

ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcgc caagggatgg	300
ttcggcggct tcaactactg gggacagggc accctgggtca cagtgtccag cgctagcacc	360
aagggcccat cgggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	420
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca	480
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac	540
tcctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcaccagac ctacatctgc	600
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	660
gacaaaactc acacatgccc accgtgcccga gcacctgaag ctgcaggggg accgtcagtc	720
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca	780
tgcgtgggtg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac	840
ggcgtggagg tgcataatgc caagacaaaag ccgcgggagg agcagtacaa cagcacgtac	900
cgtgtgggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag	960
tgcaagggtct ccaacaaaagc cctcggcgcc cccatcgaga aaaccatctc caaagccaaa	1020
gggcagcccc gagaaccaca ggtgtacacc ctgcccccat gccgggatga gctgaccaag	1080
aaccagggtca gcctgtgggt cctgggtcaaa 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 ctccgggtgg cggcggaggc tccggaggcg gaggttctgg cggagggtggc	1380
gctcctgcct cctccagcac caagaaaacc cagctccagc tggaacatct cctgctggat	1440
ctgcagatga tcctgaacgg catcaacaac tacaagaacc ccaagctgac ccggatgctg	1500
accgccaagt tcgccatgcc caagaaggcc accgagctga aacatctgca gtgcctggaa	1560
gaggaaactga agcctctgga agagggtgctg aacggcgccc agtccaagaa cttccacctg	1620
aggcctcggg acctgatctc caacatcaac gtgatcgtgc tggaactgaa gggctccgag	1680
acaaccttca tgtgagagta 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

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 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

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

eolf-seq1

```

<400> 212
gagatcgtgc tgacccagtc ccccggcacc ctgtctctga gccctggcga gagagccacc      60
ctgtcctgca gagcctccca gtccgtgacc tcctcctacc tcgcctggta tcagcagaag      120
cccggccagg cccctcggct gctgatcaac gtgggcagtc ggagagccac cggcatccct      180
gaccggttct ccggctctgg ctccggcacc gacttcaccc tgaccatctc ccggctggaa      240
cccgaggact tcgccgtgta ctactgccag cagggcatca tgctgcccc cacttttggc      300
cagggcacca aggtggaaat caagcgtacg gtggccgctc cctccgtgtt catcttccca      360
ccctccgacg agcagctgaa gtccggcacc gcctccgctc tgtgcctgct gaacaacttc      420
taccctcgcg aggccaaggt gcagtggaag gtggacaacg ccctgcagtc cggcaactcc      480
caggaatccg tcaccgagca ggactccaag gacagcacct actccctgtc ctccaccctg      540
accctgtcca aggccgacta cgagaagcac aaggtgtacg cctgcgaagt gacccaccag      600
ggcctgtcca gcccgtgac caagtccttc aaccggggcg agtgc                        645

```

```

<210> 213
<211> 446
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> L19 Fab HC-Fc hole (LALA P329G)

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```

<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

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eolf-seq1

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 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

eof-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 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 caccttttagc agtttttcga tgagctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcatct atttccggtg gttcgggtac cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaccgttt 300
ccgtattttg actactgggg ccagggaacc ctggtcaccg tctcgagtgc tagcaccaag 360
ggccccctccg tgttccccct ggcccccagc agcaagagca ccagcggcgg cacagccgct 420
ctgggctgcc tgggtcaagga ctacttcccc gagcccgtga ccgtgtcctg gaacagcgga 480
gccctgacct ccggcgtgca caccttcccc gccgtgctgc agagtcttgg cctgtatagc 540
ctgagcagcg tggtcaccgt gccttctagc agcctgggca cccagaccta catctgcaac 600
gtgaaccaca agcccagcaa caccaagggtg gacaagaagg tggagcccaa gagctgcgac 660
aaaactcaca catgcccacc gtgcccagca cctgaagctg cagggggacc gtcagtcttc 720
ctcttcccc caaaaccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 780
gtgggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840
gtggagggtgc ataattgcaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 900
gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960
aaggctctcca acaaagccct cggcgccccc atcgagaaaa ccatctccaa agccaaaggg 1020

eolf-seq1

```

cagccccgag aaccacaggt gtgcaccctg ccccatccc gggatgagct gaccaagaac      1080
caggtcagcc tctcgtgctg 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> 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

```

```

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145          150          155          160

```

eo1f-seq1

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

eolf-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
gagggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttagc agtttttcga tgagctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcatct atttccggtg gttcgggtac cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

eolf-seq1

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaccgttt	300
ccgtatttttg actactgggg ccaggggaacc ctggtcaccg tctcgagtgc tagcaccaag	360
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc	420
ctgggctgcc tgggtcaagga ctacttcccc gaaccggtga cgggtgctgtg gaactcaggc	480
gccctgacca gcggcgtgca caccctcccc gctgtcctac agtcctcagg actctactcc	540
ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac	600
gtgaatcaca agcccagcaa caccaagggtg gacaagaaaag 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
aagggtctcca acaaagccct cggcgccccc atcgagaaaa ccatctccaa agccaaaggg	1020
cagccccgag aaccacaggt gtacaccctg ccccatgcc gggatgagct gaccaagaac	1080
caggctagcc 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 aggtggcgct	1380
cctgcctcct ccagcaccaa gaaaacccag ctccagctgg aacatctcct gctggatctg	1440
cagatgatcc tgaacggcat caacaactac aagaacccca agctgaccgc gatgctgacc	1500
gccaagtctg ccatgcccga 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

<210> 217
 <211> 215
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> L19 Fab LC

<400> 217

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 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

eolf-seq1

```

<400> 218
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc      60
ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa      120
cctggccagg ctcccaggct cctcatctat tatgcatcca gcagggccac tggcatccca      180
gacagggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag      240
cctgaagatt ttgcagtgta ttactgtcag cagacgggtc gtattcctcc gacgttcggc      300
caagggacca aggtggaaat caaacgtacg gtggctgcac catctgtctt catcttcccg      360
ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc      420
tatccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggttaactcc      480
caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg      540
acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag      600
ggcctgagct cgcccgtcac aaagagcttc aacagggggag 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

```

eolf-seq1
 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
 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

eolf-seq1

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

<220>
<223> DP47 GS Fab HC-Fc hole (LALA P329G)

<400> 220
gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt caccttttagc agttatgcc a tgagctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtgtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggcagc 300
ggatttgact actggggcca aggaaccctg gtcaccgtct cgagtgtag caccaagggc 360
ccctccgtgt tccccctggc cccagcagc aagagcacca gcggcggcac agccgctctg 420
ggctgcctgg tcaaggacta cttccccgag cccgtgaccg tgtcctggaa cagcggagcc 480
ctgacctccg gcgtgcacac cttccccgcc gtgtgcaga gttctggcct gtatagcctg 540
agcagcgtgg tcaccgtgcc ttctagcagc ctgggcaccc agacctacat ctgcaacgtg 600
aaccacaagc ccagcaacac caaggtggac aagaagggtg agcccaagag ctgcgacaaa 660
actcacacat gccaccgtg cccagcacct gaagctgcag ggggaccgtc agtcttcctc 720
ttcccccaa aaccaagga caccctcatg atctcccga cccctgaggt cacatgcgtg 780
gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 840
gaggtgcata atgccaagac aaagccgcg gaggagcagt acaacagcac gtaccgtgtg 900
gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgaag 960
gtctccaaca aagccctcgg cgccccatc gagaaaacca tctccaaagc caaagggcag 1020

eolf-seq1

```

ccccgagaac cacaggtgtg caccctgccc ccatcccggg atgagctgac caagaaccag      1080
gtcagcctct cgtgcgcagt caaaggcttc tatcccagcg acatcgccgt ggagtgggag      1140
agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc      1200
tccttcttcc tcgtgagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc      1260
ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc      1320
ctgtctccgg gtaaa                                                    1335

```

```

<210> 221
<211> 591
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> DP47 GS Fab HC-Fc knob (LALA P329G)-IL-2 qm

```

```

<400> 221

```

```

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 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
 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

eolf-seq1

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

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

<400> 222
gaggtgcaat tgttgaggatc 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

eolf-seq1

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggcagc	300
ggatttgact actggggcca aggaaccctg gtcaccgtct cgagtgctag caccaagggc	360
ccatcggctct 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 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 caagtgcag	960
gtctccaaca aagccctcgg cgtccccatc 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 tggcgctcct	1380
gcctcctcca gcaccaagaa aaccagctc cagctggaac atctcctgct ggatctgcag	1440
atgatcctga acggcatcaa caactacaag aacccaagc tgaccggat gctgaccgcc	1500
aagttcgcca tgccaagaa ggccaccgag ctgaaacatc tgcagtgcct ggaagaggaa	1560
ctgaagcctc tggaagaggt gctgaacggc gcccagtcca agaacttcca cctgaggcct	1620
cgggacctga tctccaacat caacgtgatc gtgctggaac tgaagggtc 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

eolf-seq1

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

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

eo1f-seq1

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
 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

eolf-seq1

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
gaggtgcaat tggtggagtc 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 gaaaggcagc 300
ggatttgact actggggcca aggaaccctg gtcaccgtct cgagtgttag caccaagggc 360
ccatcgggtct tccccctggc accctcctcc aagagcacct ctggggggcac agcggccctg 420
ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgctgtggaa ctcaggcgcc 480
ctgaccagcg gcgtgcacac cttcccggtc gtcctacagt cctcaggact ctactccctc 540
agcagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg 600
aatcacaagc ccagcaacac caagggtggac 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

eolf-seq1

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 aggctccgga ggcggagggt ctggcggagg tggcgctcct	1380
acatcctcca gcaccaagaa aaccagctc cagctggaac atctcctgct ggatctgcag	1440
atgatcctga acggcatcaa caactacaag aacccaagc tgaccgggat gctgaccttc	1500
aagttctaca tgccaagaa ggccaccgag ctgaaacatc tgcagtgcct ggaagaggaa	1560
ctgaagcctc tggaagaggt gctgaacctg gccagtgcca agaacttcca cctgaggcct	1620
cgggacctga tctcaacat caacgtgatc gtgctggaac tgaagggctc cgagacaacc	1680
ttcatgtgcg agtacgccga cgagacagct accatcgtag 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

eolf-seq1

Leu 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> 226
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> DP47GS Fab LC

<400> 226
gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcttgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180
gacagggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg 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 aacagggggag agtgt 645

eolf-seq1

<210> 227
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<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

eolf-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 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

eof-seq1

<210> 228
 <211> 1353
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CH1A1A Fab HC-Fc hole (wt)

<400> 228
 cagggtgcagc 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 actactgctc cagatgggac 300
 ttgcctatt 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 gggcaccag 600
 acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaagggtggag 660
 cccaagagct gcgacaagac ccacacctgt cccccttgct ctgcccctga gctgctgggc 720
 ggaccagcgt tgttctgtt cccccaaag cccaaggaca ccctgatgat cagccggacc 780
 cccgaagtga cctgcgtggt ggtggacgtg tcccacgagg accctgaagt gaagttcaat 840
 tgggtacgtg acggcgtgga ggtgcacaaat gccaaagacca 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 gtgatgcagc aggccctgca caaccactac 1320
 acccagaagt ccctgagcct gagccccggc aag 1353

<210> 229
 <211> 599
 <212> PRT
 <213> Artificial Sequence

<220>

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<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

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

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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

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 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

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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
<212> DNA
<213> Artificial Sequence

<220>
<223> CH1A1A Fab HC-Fc knob (wt)-IL-2 qm

<400> 230
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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 actactgcmc cagatggggac 300
ttgcctatt 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 gggcaccacg 600
acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggag 660
cccaagagct gcgacaagac ccacacctgt ccccttggtc ctgcccctga gctgctgggc 720

eolf-seq1

ggacccagcg tgttcctggt ccccccaaag cccaaggaca ccctgatgat cagccggacc	780
cccgaagtga cctgcgtggt ggtggacgtg tcccacgagg accctgaagt gaagttcaat	840
tggtacgtgg acggcgtgga ggtgcacaat gccaagacca agccccggga ggaacagtac	900
aacagcacct accgggtggt gtccgtgctg accgtgctgc accaggactg gctgaacggc	960
aaagagtaca agtgcaaggt ctccaacaag gccctgcctg ccccatcga gaaaaccatc	1020
agcaaggcca agggccagcc cagagaacct cagggtgata ccctgcccc ctgcagagat	1080
gagctgacca agaaccaggt gtccctgtgg tgtctggtca agggcttcta cccagcgat	1140
atcgccgtgg agtgggagag caacggccag cctgagaaca actacaagac cccccccct	1200
gtgctggaca gcgacggcag cttcttcctg tactccaaac tgaccgtgga caagagccgg	1260
tggcagcagg gcaacgtgtt cagctgcagc gtgatgcacg aggccctgca caaccactac	1320
accagaagt ccctgagcct gagccccggc aagtccggag gcggaggctc cggcggcgga	1380
ggttctggcg gaggtggcgc tcctgcctcc tccagacca agaaaacca gctccagctg	1440
gaacatctcc tgctggatct gcagatgatc ctgaacggca tcaacaacta caagaacccc	1500
aagctgaccc ggatgctgac cgccaagttc gccatgcccc agaaggccac cgagctgaaa	1560
catctgcagt gcctggaaga ggaactgaag cctctggaag aggtgctgaa cggcgcccag	1620
tccaagaact tccacctgag gcctcgggac ctgatctcca acatcaacgt gatcgtgctg	1680
gaactgaagg gctccgagac aaccttcatg tgcgagtacg ccgacgagac agctaccatc	1740
gtggaatttc tgaaccggtg gatcaccttc gccagtgcca tcatctccac cctgacc	1797

<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

eolf-seq1

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
<212> DNA
<213> Artificial Sequence

<220>
<223> 2F1 Fab LC

<400> 232
gatatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtgggaga cagagtcacc 60
atcacttgca aggccagtc ggctgtgggt acgtatgttg cgtggtatca 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 caagcgtacg gtggctgcac catctgtctt catcttcccg 360
ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420

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tatcccagag aggccaaaagt 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> 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

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

eo1f-seq1

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 ggctcgagt gatgggagg atcatcccta tctttggtac agcaaaactac 180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagactgtac 300
ggttacgctt actacgggtgc ttttgactac tggggccaag ggaccaccgt gaccgtctcc 360
tcagctagca ccaagggccc atcggctctc cccctggcac cctcctccaa gagcacctct 420
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacgggtg 480
tcgtggaact caggcgcctt gaccagcggc gtgcacacct tcccggtgt cctacagtcc 540
tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcaccag 600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag 660
cccaaattctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 780
cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840
tggtacgtgg acggcgtgga ggtgcataat gccaagacaa 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 tgcctggtca aaggcttcta tcccagcgac 1140
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1200
gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1260
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1320
acgcagaaga gcctctccct gtctccgggt aaa 1353

eolf-seq1

<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

eo1f-seq1

Ser 465 Ser Pro Gly Gln Gly 470 Thr Gln Ser Glu Asn 475 Ser Cys Thr His Phe 480

Pro Gly Asn Leu Pro 485 Asn Met Leu Arg Asp 490 Leu Arg Asp Ala Phe 495 Ser

Arg Val Lys Thr 500 Phe Phe Gln Met Lys 505 Asp Gln Leu Asp Asn 510 Leu Leu

Leu Lys Glu 515 Ser Leu Leu Glu Asp 520 Phe Lys Gly Tyr Leu 525 Gly Cys Gln

Ala Leu 530 Ser Glu Met Ile Gln 535 Phe Tyr Leu Glu Glu 540 Val Met Pro Gln

Ala 545 Glu Asn Gln Asp Pro 550 Asp Ile Lys Ala His 555 Val Asn Ser Leu Gly 560

Glu Asn Leu Lys Thr 565 Leu Arg Leu Arg Leu 570 Arg Arg Cys His Arg 575 Phe

Leu Pro Cys Glu 580 Asn Lys Ser Lys Ala 585 Val Glu Gln Val Lys 590 Asn Ala

Phe Asn Lys 595 Leu Gln Glu Lys Gly 600 Ile Tyr Lys Ala Met 605 Ser Glu Phe

Asp Ile 610 Phe Ile Asn Tyr Ile 615 Glu Ala Tyr Met Thr 620 Met Lys Ile Arg

Asn 625 Gly Gly Gly Gly Gly Ser 630 Gly Gly Gly Gly Ser 635 Gly Gly Gly Gly Ser 640

Gly Gly Gly Gly Ser 645 Ser Pro Gly Gln Gly 650 Thr Gln Ser Glu Asn 655 Ser

Cys Thr His Phe 660 Pro Gly Asn Leu Pro 665 Asn Met Leu Arg Asp 670 Leu Arg

Asp Ala Phe 675 Ser Arg Val Lys Thr 680 Phe Phe Gln Met Lys 685 Asp Gln Leu

Asp Asn 690 Leu Leu Leu Lys Glu 695 Ser Leu Leu Glu Asp 700 Phe Lys Gly Tyr

Leu Gly Cys Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu

eolfs-seql															
705				710				715				720			
Val	Met	Pro	Gln	Ala 725	Glu	Asn	Gln	Asp	Pro 730	Asp	Ile	Lys	Ala	His 735	Val
Asn	Ser	Leu	Gly 740	Glu	Asn	Leu	Lys	Thr 745	Leu	Arg	Leu	Arg	Leu 750	Arg	Arg
Cys	His	Arg 755	Phe	Leu	Pro	Cys	Glu 760	Asn	Lys	Ser	Lys	Ala 765	Val	Glu	Gln
Val	Lys 770	Asn	Ala	Phe	Asn	Lys 775	Leu	Gln	Glu	Lys	Gly 780	Ile	Tyr	Lys	Ala
Met 785	Ser	Glu	Phe	Asp	Ile 790	Phe	Ile	Asn	Tyr	Ile 795	Glu	Ala	Tyr	Met	Thr 800
Met	Lys	Ile	Arg	Asn 805											

eof-seq1

tggtacgtgg	acggcgtgga	ggtgcataat	gccaaagacaa	agccgcggga	ggagcagtac	900
aacagcacgt	accgtgtggt	cagcgtcctc	accgtcctgc	accaggactg	gctgaatggc	960
aaggagtaca	agtgcaaggt	ctccaacaaa	gccctcggcg	cccccatcga	gaaaaccatc	1020
tccaaagcca	aagggcagcc	ccgagaacca	caggtgtgca	ccctgcccc	atcccgggat	1080
gagctgacca	agaaccaggt	cagcctctcg	tgcgcagtca	aaggcttcta	tcccagcgac	1140
atcgccgtgg	agtgggagag	caatgggcag	ccggagaaca	actacaagac	cacgcctccc	1200
gtgctggact	ccgacggctc	cttcttcctc	gtgagcaagc	tcaccgtgga	caagagcagg	1260
tggcagcagg	ggaacgtctt	ctcatgctcc	gtgatgcatg	aggctctgca	caaccactac	1320
acgcagaaga	gcctctccct	gtctccgggt	ggcggcggag	gctccggagg	cggaggatct	1380
gggggaggcg	gaagtagccc	gggccagggc	accagagcg	agaacagctg	caccacttc	1440
cccggcaacc	tgcccaacat	gctgcgggac	ctgagggacg	ccttcagcag	agtgaaaacc	1500
ttcttccaga	tgaaggacca	gctggacaac	ctgctgctga	aagagagcct	gctggaagat	1560
ttcaagggct	acctgggctg	tcaggccctg	agcgagatga	tccagttcta	cctggaagaa	1620
gtgatgcccc	aggccgagaa	ccaggacccc	gacatcaagg	cccacgtgaa	cagcctgggc	1680
gagaacctga	aaaccctgcg	gctgagactg	cggcggtgcc	acagatttct	gccctgcgag	1740
aacaagagca	aggccgtgga	acaggtgaag	aacgccttca	acaagctgca	ggaaaagggc	1800
atctacaagg	ccatgtccga	gttcgacatc	ttcatcaact	acatcgaagc	ttacatgacc	1860
atgaagatca	gaaacggcgg	aggcggatct	ggcggcggtg	gaagtggagg	cggaggatct	1920
gggggaggcg	gaagtagccc	gggccagggc	accagagcg	agaacagctg	caccacttc	1980
cccggcaacc	tgcccaacat	gctgcgggac	ctgagggacg	ccttcagcag	agtgaaaacc	2040
ttcttccaga	tgaaggacca	gctggacaac	ctgctgctga	aagagagcct	gctggaagat	2100
ttcaagggct	acctgggctg	tcaggccctg	agcgagatga	tccagttcta	cctggaagaa	2160
gtgatgcccc	aggccgagaa	ccaggacccc	gacatcaagg	cccacgtgaa	cagcctgggc	2220
gagaacctga	aaaccctgcg	gctgagactg	cggcggtgcc	acagatttct	gccctgcgag	2280
aacaagagca	aggccgtgga	acaggtgaag	aacgccttca	acaagctgca	ggaaaagggc	2340
atctacaagg	ccatgtccga	gttcgacatc	ttcatcaact	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

eo1f-seq1

<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

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

eolf-seq1
 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 Asn₂₉₀ 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 Gly Ala Pro₃₃₅ Ile
 Glu Lys Thr Ile₃₄₀ Ser Lys Ala Lys Gly₃₄₅ Gln Pro Arg Glu Pro₃₅₀ Gln Val
 Cys Thr Leu₃₅₅ Pro Pro Ser Arg Asp₃₆₀ Glu Leu Thr Lys Asn₃₆₅ Gln Val Ser
 Leu Ser₃₇₀ Cys Ala Val Lys Gly₃₇₅ Phe Tyr Pro Ser Asp₃₈₀ Ile Ala Val Glu
 Trp₃₈₅ Glu Ser Asn Gly Gln₃₉₀ Pro Glu Asn Asn Tyr₃₉₅ Lys Thr Thr Pro₄₀₀
 Val Leu Asp Ser Asp₄₀₅ Gly Ser Phe Phe Leu₄₁₀ Val Ser Lys Leu Thr₄₁₅ Val
 Asp Lys Ser Arg₄₂₀ Trp Gln Gln Gly Asn₄₂₅ Val Phe Ser Cys Ser₄₃₀ Val Met
 His Glu Ala₄₃₅ Leu His Asn His Tyr₄₄₀ Thr Gln Lys Ser Leu₄₄₅ Ser Leu Ser
 Pro Gly₄₅₀ Gly Gly Gly Gly Ser₄₅₅ Gly Gly Gly Gly Ser₄₆₀ Gly Gly Gly Gly
 Ser₄₆₅ Ser Pro Gly Gln Gly₄₇₀ Thr Gln Ser Glu Asn₄₇₅ Ser Cys Thr His Phe₄₈₀
 Pro Gly Asn Leu Pro₄₈₅ Asn Met Leu Arg Asp₄₉₀ Leu Arg Asp Ala Phe₄₉₅ Ser

eolf-seq1

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

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
cagggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
cctggacaag ggctcgagtg gatggggagg atcatcccta tctttggtac agcaaaactac 180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagactgtac 300
ggttacgctt actacgggtgc ttttgactac tggggccaag ggaccaccgt gaccgtctcc 360
tcagctagca ccaagggccc atcgggtctt cccctggcac cctcctccaa gagcacctct 420
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540

eolf-seq1

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcaccag	600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag	660
cccaaactct gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg	720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc	780
cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac	840
tggtacgtgg acggcgtgga ggtgcataat gccaagacaa 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 ggcggcggag gctccggagg cggaggaagt	1380
ggcggcgggtg gcagctctcc aggccagggc acccagagcg agaacagctg caccacttc	1440
cccggcaacc tgcccaacat gctgcgggac ctgagggacg ccttcagcag agtgaaaacc	1500
ttcttccaga tgaaggacca gctggacaac ctgctgctga aagagagcct gctggaagat	1560
ttcaagggct acctgggctg tcaggccctg agcgagatga tccagttcta cctggaagaa	1620
gtgatgcccc aggccgagaa ccaggacccc gacatcaagg ccacgtgaa 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

eof-seq1

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

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 tgaccagtc tccatcctcc ctgtctgcat ctgtcggaga ccgggtcacc 60

atcacctgcc gggcaagtca gggcattaga aatgatttag gctggtacca gcagaagcca 120

eolf-seq1

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gggaaagccc ctaagcgcct gatctatgct gcatccagtt tgcagagtgg cgtcccatca      180
aggttcagcg gcggtggatc cgggacagag ttactctca ccatcagcag cttgcagcct      240
gaagattttg ccacctatta ctgcttgagc aatgggtctgc agcccgcgac gtttggccag      300
ggcaccaaag tcgagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcc      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 aggggagagt gt                        642

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<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

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

eolf-seq1

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 Lys
 435 440 445

<210> 242
 <211> 1341
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 4G8 Fab HC-Fc knob (LALA P329G)

<400> 242
 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 gaaaggggtg 300
 ctgggtaatt ttgactactg gggccaagga accctgggtca cctgtctcgag tgctagcacc 360
 aagggcccat cggctcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420
 gccctgggct gcctgtgcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca 480
 ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540
 tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600
 aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 660
 gacaaaaactc acacatgccc accgtgcccc gcacctgaag ctgcaggggg accgtcagtc 720
 ttctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 780
 tgcgtggtgg tggacgtgag ccacgaagac cctgagggtca agttcaactg gtacgtggac 840
 ggcgtggagg tgcataatgc caagacaaaag ccgcgggagg agcagtacaa cagcacgtac 900
 cgtgtgggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 960
 tgcaaggctc ccaacaaagc cctcggcgcc cccatcgaga aaaccatctc caaagccaaa 1020
 gggcagcccc gagaaccaca ggtgtacacc ctgcccccat gccgggatga gctgaccaag 1080
 aaccagggtca gcctgtggtg cctgggtcaaa ggcttctatc ccagcgacat cgccgtggag 1140

eolf-seq1

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc	1200
gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg 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

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

eo1f-seq1

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

eolf-seq1

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
gagggtgcaat 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 gaaaggggtg 300
ctgggtaatt ttgactactg gggccaagga accctgggtca ccgtctcgag tgctagcacc 360
aagggcccat cggctcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420
gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540
tcctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600

eol-f-seq1						
aacgtgaatc	acaagcccag	caacaccaag	gtggacaaga	aaagttgagcc	caaattcttgt	660
gacaaaactc	acacatgccc	accgtgccc	gcacctgaag	ctgcaggggg	accgtcagtc	720
ttcctcttcc	ccccaaaacc	caaggacacc	ctcatgatct	cccggacccc	tgaggtcaca	780
tgctgtggtg	tggacgtgag	ccacgaagac	cctgaggtca	agttcaactg	gtacgtggac	840
ggcgtggagg	tgcataatgc	caagacaaaag	ccgcgggagg	agcagtacaa	cagcacgtac	900
cgtgtggtca	gcgtcctcac	cgctctgcac	caggactggc	tgaatggcaa	ggagtacaag	960
tgcaagggtct	ccaacaaaagc	cctcggcgcc	cccattcgaga	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	tcttcctcgt	gagcaagctc	accgtggaca	agagcaggtg	gcagcagggg	1260
aacgtcttct	catgctccgt	gatgcatgag	gctctgcaca	accactacac	gcagaagagc	1320
ctctccctgt	ctccgggtgg	cggcggaggc	tccggaggcg	gaggatctgg	gggaggcgga	1380
agtagcccgg	gccagggcac	ccagagcgag	aacagctgca	cccacttccc	cggcaacctg	1440
cccaacatgc	tgccgggacct	gagggacgcc	ttcagcagag	tgaaaacctt	cttcagatg	1500
aaggaccagc	tggacaacct	gctgctgaaa	gagagcctgc	tggaagattt	caagggctac	1560
ctgggctgtc	aggccctgag	cgagatgata	cagttctacc	tggaagaagt	gatgccccag	1620
gccgagaacc	aggaccccga	catcaaggcc	cacgtgaaca	gcctgggcga	gaacctgaaa	1680
accctgcggc	tgagactgcg	gcggtgccac	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
agtagcccgg	gccagggcac	ccagagcgag	aacagctgca	cccacttccc	cggcaacctg	1980
cccaacatgc	tgccgggacct	gagggacgcc	ttcagcagag	tgaaaacctt	cttcagatg	2040
aaggaccagc	tggacaacct	gctgctgaaa	gagagcctgc	tggaagattt	caagggctac	2100
ctgggctgtc	aggccctgag	cgagatgata	cagttctacc	tggaagaagt	gatgccccag	2160
gccgagaacc	aggaccccga	catcaaggcc	cacgtgaaca	gcctgggcga	gaacctgaaa	2220
accctgcggc	tgagactgcg	gcggtgccac	agatttctgc	cctgcgagaa	caagagcaag	2280
gccgtggaac	aggtgaagaa	cgccttcaac	aagctgcagg	aaaagggcat	ctacaaggcc	2340
atgtccgagt	tcgacatctt	catcaactac	atcgaggcct	acatgacaat	gaaaatccgc	2400
aat						2403

eolf-seq1

<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

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
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eolf-seq1

210		215		220
Thr 225	Cys	Pro	Pro	Cys
		Pro 230	Ala	Pro
			Glu	Ala
			Ala 235	Gly
			Gly	Pro
			Ser	Val 240
Phe	Leu	Phe	Pro	Pro
		Pro 245	Lys	Pro
			Lys	Asp
			Thr 250	Leu
			Met	Ile
			Ser	Arg 255
Pro	Glu	Val	Thr 260	Cys
		Val	Val	Val
			Asp 265	Val
			Ser	His
			Glu	Asp 270
Val	Lys	Phe 275	Asn	Trp
			Tyr	Val
			Asp 280	Gly
			Val	Glu
			Val	His 285
			Asn	Ala
			Lys	
Thr 290	Lys	Pro	Arg	Glu
			Glu	Gln 295
			Tyr	Asn
			Ser	Thr
			Tyr 300	Arg
			Val	Val
			Ser	
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
			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	Lys 370	Gly	Phe	Tyr
			Pro	Ser
			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	Arg 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
Gly 450	Ser	Gly	Gly	Gly
			Gly 455	Ser
			Gly	Gly
			Gly 460	Ser
			Ser	Pro
			Gly	

eolf-seq1

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 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 tgttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt cacccttagc agttatgcc a tgagctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300

eol-f-seq1

ctgggtaatt ttgactactg gggccaagga accctgggtca ccgctctcgag tgctagcacc	360
aagggcccat cgggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	420
gccctgggct gcctgggtcaa 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 accgtgcccga gcacctgaag ctgcaggggg accgtcagtc	720
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca	780
tgctgtggtg tggaagtgtg ccacgaagac cctgagggtca agttcaactg gtacgtggac	840
ggcgtggagg tgcataatgc caagacaaaag ccgcgggagg agcagtacaa cagcacgtac	900
cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag	960
tgcaagggtc ccaacaaagc cctcggcgcc cccatcgaga aaaccatctc caaagccaaa	1020
gggcagcccc gagaaccaca ggtgtgcacc ctgcccccat cccgggatga gctgaccaag	1080
aaccagggtc gcctctcgtg cgcagtcaaa ggcttctatc ccagcgacat cgccgtggag	1140
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc	1200
gacggctcct tcttcctcgt gagcaagctc accgtggaca agagcagggtg gcagcagggg	1260
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc	1320
ctctccctgt ctccgggtg cggcggaggc tccggaggcg gaggaagtgg cggcgggtggc	1380
agctctccag gccagggcac ccagagcgag aacagctgca cccacttccc cggcaacctg	1440
cccaacatgc tgcgggacct gagggacgcc ttcagcagag tgaaaaacctt cttccagatg	1500
aaggaccagc tggacaacct gctgctgaaa gagagcctgc tggaaagattt caagggctac	1560
ctgggctgtc aggccctgag cgagatgatc cagttctacc tggaagaagt gatgccccag	1620
gccgagaacc aggaccccga catcaaggcc cacgtgaaca gcctgggcca gaacctgaaa	1680
accctgcggc tgagactgcg gcggtgccac agatttctgc cctgcgagaa cggcggaggc	1740
tctggcggaa agtccaaggc cgtggaacag gtgaagaacg ccttcaacaa gctgcaggaa	1800
aagggcatct acaaggccat gagcgagttc gacatcttca tcaactacat cgaagcttac	1860
atgacaatga agatacga c	1881

<210> 247
 <211> 366
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IL-2 qm-Fc knob (LALA P329G) (IL-2 N-terminal)

eo1f-seq1

<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

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

eolfs-seq1															
245								250				255			
Lys	Ala	Lys	Gly 260	Gln	Pro	Arg	Glu	Pro 265	Gln	Val	Tyr	Thr	Leu 270	Pro	Pro
Cys	Arg	Asp 275	Glu	Leu	Thr	Lys	Asn 280	Gln	Val	Ser	Leu	Trp 285	Cys	Leu	Val
Lys	Gly 290	Phe	Tyr	Pro	Ser	Asp 295	Ile	Ala	Val	Glu	Trp 300	Glu	Ser	Asn	Gly
Gln 305	Pro	Glu	Asn	Asn	Tyr 310	Lys	Thr	Thr	Pro	Pro 315	Val	Leu	Asp	Ser	Asp 320
Gly	Ser	Phe	Phe	Leu 325	Tyr	Ser	Lys	Leu	Thr 330	Val	Asp	Lys	Ser	Arg 335	Trp
Gln	Gln	Gly	Asn 340	Val	Phe	Ser	Cys	Ser 345	Val	Met	His	Glu	Ala 350	Leu	His
Asn	His	Tyr 355	Thr	Gln	Lys	Ser	Leu 360	Ser	Leu	Ser	Pro	Gly 365	Lys		

<210>	248
<211>	1098
<212>	DNA
<213>	Artificial Sequence

<400>	248						
gctcctgcct	cctccagcac	caagaaaacc	cagctccagc	tggaacatct	cctgctggat		60
ctgcagatga	tcctgaacgg	catcaacaac	tacaagaacc	ccaagctgac	ccggatgctg		120
accgccaagt	tcgccatgcc	caagaaggcc	accgagctga	aacatctgca	gtgcctggaa		180
gaggaactga	agcctctgga	agagggtgctg	aacggcgccc	agtccaagaa	cttccacctg		240
aggcctcggg	acctgatctc	caacatcaac	gtgatcgtgc	tggaactgaa	gggctccgag		300
acaaccttca	tgtgcgagta	cgccgacgag	acagctacca	tcgtggaatt	tctgaaccgg		360
tggtatcacct	tcgcccagtc	catcatctcc	accctgacct	ccggtggtgg	cggatccgac		420
aaaactcaca	catgcccacc	gtgcccagca	cctgaagctg	caggggggacc	gtcagtcttc		480
ctcttccccc	caaaacccaa	ggacaccctc	atgatctccc	ggacccctga	gttcacatgc		540
gtgggtggtgg	acgtgagcca	cgaagaccct	gagggtcaagt	tcaactggta	cgtggacggc		600
gtggaggtgc	ataatgccaa	gacaaagccg	cgggagggagc	agtacaacag	cacgtaccgt		660
gtgggtcagcg	tcctcaccgt	cctgcaccag	gactggctga	atggcgaagga	gtacaagtgc		720

eolf-seq1

```

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

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<210> 249
<211> 384
<212> PRT
<213> Artificial Sequence

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```

<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

```

```

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 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	eolf-seql										160				
	155														
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		
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

eolf-seq1

<220>

<223> IL-7-Fc knob (LALA P329G) (IL-7 N-terminal)

<400> 250

gattgtgata ttgaaggtaa agatggcaaa caatatgaga gtgttctaataat ggtcagcatc	60
gatcaattat tggacagcat gaaagaaatt ggtagcaatt gcctgaataa tgaatttaac	120
tttttttaaaa gacatatctg tgatgctaataa aaggaaggta tgttttttatt ccgtgctgct	180
cgcaagttga ggcaatttct taaaatgaat agcactgggtg attttgatct ccacttatta	240
aaagtttcag aaggcacaac aatactgttg aactgcactg gccagggttaa aggaagaaaa	300
ccagctgccc tgggtgaagc ccaaccaaca aagagtttgg aagaaaaataa atcttttaaag	360
gaacagaaaa aactgaatga cttgtgtttc ctaaagagac tattacaaga gataaaaaact	420
tggttgaata aaattttgat gggcactaaa gaacacgggtg gtggcggatc cgacaaaact	480
cacacatgcc caccgtgccc agcacctgaa gctgcagggg gaccgtcagt cttcctcttc	540
cccccaaaac ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtgggtg	600
gtggacgtga gccacgaaga ccctgagggtc aagttcaact ggtacgtgga cggcgtggag	660
gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtggtc	720
agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaagggtc	780
tccaacaaag ccctcggcgc ccccatcgag aaaaccatct ccaaagccaa agggcagccc	840
cgagaaccac aggtgtacac cctgccccca tgccgggatg agctgaccaa gaaccaggtc	900
agcctgtggt gcctgggtcaa aggcttctat cccagcgaca tcgccgtgga gtgggagagc	960
aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc	1020
ttcttctctc 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

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		

eo1f-seq1

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

eolf-seq1

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 cggcttccct 120
caggaagagt tcggcaacca gttccagaag gccgagacaa tccccgtgct gcacgagatg 180
atccagcaga ttttcaacct gttcagcacc aaggacagca gcgccgcctg ggacgagaca 240
ctgctggaca agttctacac cgagctgtac cagcagctga acgacctgga agcctgcgtg 300
atccagggcg tgggcgtgac cgagacaccc ctgatgaagg aagatagcat cctggccgtg 360
cggaagtatt tccagcggat caccctgtac ctgaaagaga agaagtacag cccctgcgcc 420
tgaggaggtcg tgcgggccga gatcatgcgg agcttcagcc tgagcaccaa cctgcaggaa 480
agcctgcgga gcaaagaggg tgggtggcga tccgacaaaa ctacacatg cccaccgtgc 540
ccagcacctg aagctgcagg gggaccgtca gtcttctct tcccccaaa acccaaggac 600
accctcatga tctcccgga cctgaggtc acatgcgtgg tgggtggacgt gagccacgaa 660
gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 720

eolf-seq1

aagccgcggg aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg	780
caccaggact ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctcggc	840
gccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac	900
accctgcccc catgccggga tgagctgacc aagaaccagg tcagcctgtg gtgcctggtc	960
aaaggcttct atcccagcga catcgccgtg gagtggggaga gcaatgggca gccggagaac	1020
aactacaaga ccacgcctcc cgtgctggac tccgacggct ctttcttcct 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

eolf-seq1

Val 145	Lys	Asp	Tyr	Phe	Pro 150	Glu	Pro	Val	Thr	Val 155	Ser	Trp	Asn	Ser	Gly 160
Ala	Leu	Thr	Ser	Gly 165	Val	His	Thr	Phe	Pro 170	Ala	Val	Leu	Gln	Ser 175	Ser
Gly	Leu	Tyr	Ser 180	Leu	Ser	Ser	Val	Val 185	Thr	Val	Pro	Ser	Ser 190	Ser	Leu
Gly	Thr	Gln 195	Thr	Tyr	Ile	Cys	Asn 200	Val	Asn	His	Lys	Pro 205	Ser	Asn	Thr
Lys	Val 210	Asp	Lys	Lys	Val	Glu 215	Pro	Lys	Ser	Cys	Asp 220	Lys	Thr	His	Thr
Cys 225	Pro	Pro	Cys	Pro	Ala 230	Pro	Glu	Ala	Ala	Gly 235	Gly	Pro	Ser	Val	Phe 240
Leu	Phe	Pro	Pro	Lys 245	Pro	Lys	Asp	Thr	Leu 250	Met	Ile	Ser	Arg	Thr 255	Pro
Glu	Val	Thr	Cys 260	Val	Val	Val	Asp	Val 265	Ser	His	Glu	Asp	Pro 270	Glu	Val
Lys	Phe	Asn 275	Trp	Tyr	Val	Asp	Gly 280	Val	Glu	Val	His	Asn 285	Ala	Lys	Thr
Lys	Pro 290	Arg	Glu	Glu	Gln	Tyr 295	Asn	Ser	Thr	Tyr	Arg 300	Val	Val	Ser	Val
Leu 305	Thr	Val	Leu	His	Gln 310	Asp	Trp	Leu	Asn	Gly 315	Lys	Glu	Tyr	Lys	Cys 320
Lys	Val	Ser	Asn	Lys 325	Ala	Leu	Gly	Ala	Pro 330	Ile	Glu	Lys	Thr	Ile 335	Ser
Lys	Ala	Lys	Gly 340	Gln	Pro	Arg	Glu	Pro 345	Gln	Val	Tyr	Thr	Leu 350	Pro	Pro
Ser	Arg	Asp 355	Glu	Leu	Thr	Lys	Asn 360	Gln	Val	Ser	Leu	Thr 365	Cys	Leu	Val
Lys	Gly 370	Phe	Tyr	Pro	Ser	Asp 375	Ile	Ala	Val	Glu	Trp 380	Glu	Ser	Asn	Gly
Gln 385	Pro	Glu	Asn	Asn	Tyr 390	Lys	Thr	Thr	Pro	Pro 395	Val	Leu	Asp	Ser	Asp 400

eo1f-seq1

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

<210> 254
<211> 1779
<212> DNA
<213> Artificial Sequence

<220>
<223> 28H1 Fab HC-Fc (LALA P329G)-IL-2 qm

<400> 254
gaagtgcagc tgctggaatc cggcggaggc ctggtgcagc ctggcggatc tctgagactg

eof-seq1

tcctgcgccg cctccggctt caccttctcc tcccacgcca tgtcctgggt ccgacaggct	120
cctggcaaaag gcctggaatg ggtgtccgcc atctgggcct ccggcgagca 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 tggtaagga ctacttcccc gaaccggtga cgggtgctg gaactcaggc	480
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc	540
ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagacct catctgcaac	600
gtgaatcaca agcccagcaa caccaagggt gacaagaaag ttgagccaa atcttgtgac	660
aaaactcaca catgcccacc gtgcccagca cctgaagctg cagggggacc gtcagtcttc	720
ctcttcccc caaaaccaa 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
aagggtctca acaaagccct cggcgcccc atcgagaaaa ccatctcaa agccaaaggg	1020
cagccccgag aaccacaggt gtacaccctg ccccatccc gggatgagct gaccaagaac	1080
caggtcagcc tgacctgcct 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 caaaactcac caggatgctc	1500
acagccaagt ttgccatgcc caagaaggcc acagaactga aacatcttca gtgtctagaa	1560
gaagaactca aacctctgga ggaagtgcta aatggcgctc aaagcaaaaa ctttactta	1620
agaccaggg acttaatcag caatatcaac gtaatagttc tggaactaaa gggatctgaa	1680
acaacattca tgtgtgaata tgctgatgag acagcaacca ttgtagaatt tctgaacaga	1740
tggattacct ttgcccaaag catcatctca acactgact	1779

<210> 255
 <211> 473
 <212> PRT

eo1f-seq1

<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 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

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

eolf-seq1

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

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

eof-seq1

<210> 256
 <211> 1422
 <212> DNA
 <213> Artificial Sequence

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

<400> 256
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 ctgctctggt tcccagggtgc cagggtgtgca gtgaaaaact gttcccatct tgaatgcttc 120
 tacaactcaa gagccaatgt ctcttgcatg tggagccatg aagaggctct gaatgtcaca 180
 acctgccacg tccatgccaa gtcgaacctg cgacactgga acaaaacctg tgagctaact 240
 cttgtgaggc aggcattcctg ggcctgcaac ctgatcctcg ggtcgttccc agagtcccag 300
 tctactgacct ccgtggacct ccttgacata aatgtggtgt gctgggaaga gaaggggttg 360
 cgtagggtaa agacctgcga cttccatccc tttgacaacc ttcgcctggt ggcccccat 420
 tccctccaag ttctgcacat tgatacccag agatgtaaca taagctggaa ggtctcccag 480
 gtctctcact acattgaacc atacttgga tttgaggccc gtagacgtct tctgggccac 540
 agctgggagg atgcatccgt attaacctc aagcagagac agcagtggtt cttcttgagg 600
 atgctgatcc ctagtacctc atatgaggtc cagggtgagg tcaaagctca acgaaacaat 660
 accgggacct ggagtccctg gagccagccc ctgacctttc ggacaaggcc agcagatccc 720
 atgaaggagg gagctcagga caaaactcac acatgcccac cgtgcccagc acctgaactc 780
 ctgggggggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 840
 cggaccccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgagggtcaag 900
 ttcaactggt acgtggacgg cgtggagggt cataatgcc agacaaagcc gcgggaggag 960
 cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 1020
 aatggcaagg agtacaagt caaggctctc aacaaagccc tcccagcccc catcgagaaa 1080
 accatctcca aagccaaagg gcagccccga gaaccacagg tgtgcaccct gccccatcc 1140
 cgggatgagc tgaccaagaa ccaggtcagc ctctcgtgcg cagtcaaagg cttctatccc 1200
 agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1260
 cctcccgtgc tggactccga cggctccttc ttcctcgtga gcaagctcac cgtggacaag 1320
 agcagggtggc agcaggggaa cgtcttctca tgctccgtga tgcattgagg tctgcacaac 1380
 cactacacgc agaagagcct ctccctgtct ccgggtaaat ga 1422

<210> 257
 <211> 500
 <212> PRT
 <213> Artificial Sequence

eo1f-seq1

<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 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

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									eo1f-seq1									240
					230				235									
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			
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

eo1f-seq1

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
 atggacatga ggggtccccgc tcagctcctg ggcctcctgc tgctctgggt cccctcctg 60
 ctgctctggt tcccaggtgc caggtgttgg agttccaagg tcctcatgtc cagtgcgaat 120
 gaagacatca aagctgattt gatcctgact tctacagccc ctgaacacct cagtgtcctt 180
 actctgcccc ttccagaggt tcagtgtctt gtgttcaaca tagagtacat gaattgcact 240
 tggaatagca gttctgagcc tcaggcaacc aacctcacgc tgactatag gtacaaggta 300
 tctgataata atacattcca ggagtgcagt cactatttgt tctccaaaga gattacttct 360
 ggctgtcaga tacaaaaaga agatatccag ctctaccaga catttggtgt ccagctccag 420
 gacccccaga aaccccagag gcgagctgta cagaagctaa acctacagaa tcttgatgac 480
 ccacgggctc cagaaaatct aacactcagc aatctgagtg aatcccagct agagctgaga 540
 tggaaaagca gacatattaa agaacgctgt ttacaatact tgggtgcagta ccggagcaac 600
 agagatcgaa gctggacgga actaatagt aatcatgaac ctagattctc cctgcctagt 660
 gtggatgagc tgaaacggtg cacatttcgg gttcggagcc gctataaccc aatctgtgga 720
 agttctcaac agtggagtaa atggagccag cctgtccact gggggagtca tactgtagag 780
 gagaatcctt ccttgtttgc actggaagct ggagctcagg acaaaactca cacatgcccc 840
 ccgtgcccag cacctgaact cctgggggga ccgtcagtct tcctcttccc cccaaaaccc 900
 aaggacaccc tcatgatctc ccggacccct gaggtcacat gcgtggtggt ggacgtgagc 960
 cacgaagacc ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt gcataatgcc 1020
 aagacaaagc cgcgaggaga gcagtacaac agcacgtacc gtgtggtcag cgtcctcacc 1080
 gtcctgcacc aggactggct gaatggcaag gagtacaagt gcaagggtct caacaaagcc 1140
 ctcccagccc ccatcgagaa aaccatctcc aaagccaaag ggcagccccg agaaccacag 1200
 gtgtacaccc tgcccccatg ccgggatgag ctgaccaaga accaggtcag cctgtggtgc 1260
 ctggtcaaag gcttctatcc cagcgacatc gccgtggagt gggagagcaa tgggcagccg 1320
 gagaacaact acaagaccac gcctcccgtg ctggactccg acggctcctt cttcctctac 1380

eolf-seq1

agcaagctca ccgtaggacaa gagcaggtgg cagcagggga 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

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

eolf-seq1

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 ggaattgggtc 180
tatatgcgtt gcttaggaaa ctctggagc agcaactgcc agtgcaccag caactcccat 240
gacaaatcga gaaagcaagt tacagctcaa cttgaacacc agaaagagca acaaaccaca 300
acagacatgc agaagccaac acagtctatg caccaagaga accttacagg tcaactgcagg 360
gagccacctc cttggaaaca tgaagattcc aagagaatct atcatttcgt ggaaggacag 420
agtgttcact acgagtgtat tccgggatac aaggctctac agagagggtcc tgctattagc 480
atctgcaaga tgaagtgtgg gaaaacgggg tggactcagc cccagctcac atgtgtcgac 540
gaacagttat attttcaggg cggtcaggc ctgaacgaca tcttcgaggc ccagaagatc 600
gagtggcacg aggtctgagc 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

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

eo1f-seq1

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
tggagccaag atggggctct gcaggacact tcctgccaag tccacgcctg gccggacaga	180
cggcggtgga accaaacctg tgagctgctc cctgtgagtc aagcatcctg ggcctgcaac	240

eolf-seq1

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ctgatcctcg gaaccccaga ttctcagaaa ctgaccgcag tggatatcgt caccctgagg 300
gtgatgtgcc gtgaaggggt gcgatggagg atgatggcca tccaggactt caaacccctt 360
gagaaccttc gcctgatggc ccccatctcc ctccaagtcg tccacgtgga gaccacaga 420
tgcaacataa gctggaaaaat 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
acatgccac cgctgccagc acctgaactc ctggggggac cgtcagtcct cctcttcccc 780
ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg 840
gacgtgagcc acgaagaccc tgaggtaag ttcaactggt acgtggacgg cgtggagggtg 900
cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 960
gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 1020
aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 1080
gaaccacagg tgtacaccct gccccatgc cgggatgagc tgaccaagaa ccaggtcagc 1140
ctgtggtgcc tggtaaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 1200
gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1260
ttccttaca gcaagctcac cgtggacaag agcaggtygc agcaggggaa cgtcttctca 1320
tgctccgtga tgcattgagg tctgcacaac cactacacgc agaagagcct ctccctgtct 1380
ccgggtaaat ccggaggcct gaacgacatc ttcgaggccc agaagattga atggcacgag 1440
tga 1443

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<210> 263
 <211> 489
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Cynomolgous IL-2R-gamma-Fc(hole) fusion protein
 <400> 263

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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 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

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eolf-seq1

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 Asn Ser Asp Asn Asp Lys Val
85 90 95
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

eolf-seq1

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

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
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aacacgacaa ttctgacgcc caatgggaat gaagacgcc caactgattt cttcctgacc 120

eolf-seq1

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tctatgccca ctgactccct cagtgtttcc actctgcccc tcccagaggt tcagtgtttt 180
gtgttcaatg tcgagtacat gaattgcact tggaacagca gctctgagcc ccagcctacc 240
aacctcactc tgcattattg gtacaagaat tcggataatg ataaagtcca gaagtgcagc 300
cactatctat tctctgaaga aatcacttct ggctgtcagt tgcaaaaaaa ggagatccac 360
ctctacaaaa cgtttgttgt tcagctccag gacccacggg aacccaggag acaggccaca 420
cagatgctaa aactgcagaa tctggtgatc ccctgggctc cggagaacct aacacttcgc 480
aaactgagtg aatcccagct agaactgaac tggaacaaca gattcttgaa ccactgtttg 540
gagcacttgg tgcagtaccg gactgactgg gaccacagct ggactgaaca atcagtggat 600
tatagacata agttctcctt gcctagtgtg gatgggcaga aacgctacac gtttcgtgtc 660
cggagccgct ttaaccact ctgtggaagt gctcagcatt ggagtgaatg gagccacca 720
atccactggg ggagcaatag ttcaaaagag aatcctttcc tgtttgcatt ggaagccgga 780
gctcaggaca aaactcacac atgcccaccg tgcccagcac ctgaactcct ggggggaccg 840
tcagtcttcc tcttcccccc aaaaccaag 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 accacaggtg tgcaccctgc ccccatcccc ggatgagctg 1200
accaagaacc aggtcagcct ctcgtgcgca gtcaaaggct tctatcccag cgacatcgcc 1260
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1320
gactccgacg gtccttctt cctcgtgagc aagctcaccg tggacaagag caggtggcag 1380
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1440
aagagcctct ccctgtctcc gggtaaatga 1470

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<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

eo1f-seq1

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

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

gatgacccgc caaaaatcac acatgccaca ttcaaagcca tggcctacaa ggaaggaacc 120

eof-seq1

atgttgaact gtgaatgcaa gagaggtttc cgcagaataa aaagcgggtc accctatatg 180
 ctctgtacag gaaactctag ccactcgtcc tgggacaacc aatgtcaatg cacaagctct 240
 gctgctcgga acacaacaaa acaagtgaca cctcaacctg aagaacagaa agaaagaaaa 300
 accacagaaa tgcaaagtca aatgcagctg gcggaccaag tgagccttcc aggtcactgc 360
 agggaaacctc caccgtggga aaatgaagcc acagaaagaa tttatcattt cgtggtgggg 420
 cagacggttt actaccagtg cgtccaggga tacagggtc tacacagagg tcctgctgag 480
 agcgtctgca aaatgacca cggaagaca agatggacct agccccagct catatgcaca 540
 ggtgaagtcg acgaacagtt atattttcag ggcggctcag gcctgaacga catcttcgag 600
 gcccaagaaga 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

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

eolff-seql															
130				135				140							
Glu 145	Tyr	Glu	Ile	Ala	Ile 150	Arg	Lys	Val	Pro	Gly 155	Asn	Phe	Thr	Phe	Thr 160
His	Lys	Lys	Val	Lys 165	His	Glu	Asn	Phe	Ser 170	Leu	Leu	Thr	Ser	Gly 175	Glu
Val	Gly	Glu	Phe 180	Cys	Val	Gln	Val	Lys 185	Pro	Ser	Val	Ala	Ser 190	Arg	Ser
Asn	Lys	Gly 195	Met	Trp	Ser	Lys	Glu 200	Glu	Cys	Ile	Ser	Leu 205	Thr	Arg	Gln
Tyr	Phe 210	Thr	Val	Thr	Asn	Val 215	Asp	Glu	Gln	Leu	Tyr 220	Phe	Gln	Gly	Gly
Ser 225	Pro	Lys	Ser	Ala	Asp 230	Lys	Thr	His	Thr	Cys 235	Pro	Pro	Cys	Pro	Ala 240
Pro	Glu	Leu	Leu	Gly 245	Gly	Pro	Ser	Val	Phe 250	Leu	Phe	Pro	Pro	Lys 255	Pro
Lys	Asp	Thr	Leu 260	Met	Ile	Ser	Arg	Thr 265	Pro	Glu	Val	Thr	Cys 270	Val	Val
Val	Asp	Val 275	Ser	His	Glu	Asp	Pro 280	Glu	Val	Lys	Phe	Asn 285	Trp	Tyr	Val
Asp	Gly 290	Val	Glu	Val	His	Asn 295	Ala	Lys	Thr	Lys	Pro 300	Arg	Glu	Glu	Gln
Tyr 305	Asn	Ser	Thr	Tyr	Arg 310	Val	Val	Ser	Val	Leu 315	Thr	Val	Leu	His	Gln 320
Asp	Trp	Leu	Asn	Gly 325	Lys	Glu	Tyr	Lys	Cys 330	Lys	Val	Ser	Asn	Lys 335	Ala
Leu	Pro	Ala	Pro 340	Ile	Glu	Lys	Thr	Ile 345	Ser	Lys	Ala	Lys	Gly 350	Gln	Pro
Arg	Glu	Pro 355	Gln	Val	Tyr	Thr	Leu 360	Pro	Pro	Ser	Arg	Asp 365	Glu	Leu	Thr
Lys	Asn 370	Gln	Val	Ser	Leu	Thr 375	Cys	Leu	Val	Lys	Gly 380	Phe	Tyr	Pro	Ser

eolf-seq1

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
 ctgaggatatg gaatagagtc ctggaactcc atctccaact gtagccagac cctgtcctat 180
 gaccttaccg cagtgaacct ggacctgtac cacagcaatg gctaccgggc cagagtgcgg 240
 gctgtggacg gcagccggca ctccaactgg accgtcacca acacccgctt ctctgtggat 300
 gaagtgactc tgacagttgg cagtgtgaac ctagagatcc acaatggctt catcctcggg 360
 aagattcagc taccagggcc caagatggcc cccgcaaagc acacatatga aagcatcttc 420
 agtcacttcc gagagtatga gattgccatt cgcaagggtgc cgggaaactt cacgttcaca 480
 cacaagaaag taaaacatga aaacttcagc ctctaacct ctggagaagt gggagagttc 540
 tgtgtccagg tgaaaccatc tgtcgcttcc cgaagtaaca aggggatgtg gtctaaagag 600
 gagtgcattc ccctcaccag gcagtatttc accgtgacca acgtcgacga acagttatat 660
 tttcaggggc gtcacccaa atctgcagac aaaactcaca catgcccacc gtgcccagca 720
 cctgaactcc tgggggggacc gtcagtcttc ctcttcccc caaaaccaa ggacaccctc 780
 atgatctccc ggaccctga ggtcacatgc gtggtggtgg acgtgagcca cgaagaccct 840
 gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgcaa gacaaagccg 900

eolf-seq1

cgggaggagc agtacaacag cacgtaccgt gtggtcagcg tcctcaccgt cctgcaccag	960
gactggctga atggcaagga gtacaagtgc aaggtctcca acaaagccct cccagcccc	1020
atcgagaaaa ccatctcaa agccaaaggg cagccccgag aaccacaggt gtacaccctg	1080
cccccatccc gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc	1140
ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac	1200
aagaccacgc ctcccggtgt 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

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

eolf-seq1

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
Page 215

385		390	eolf-seq1										400		
			395												
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

<210> 270
 <211> 1779
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 28H1 Fab HC-Fc knob (LALA P329G)-IL-2 qm (2)

eof-seq1

```

<400> 270
gaagtgcagc tgctggaatc cggcggaggc ctggtgcagc ctggcggatc tctgagactg      60
tcctgcgccg cctccggcctt caccttctcc tcccacgccca tgtcctgggt ccgacaggct      120
cctggcaaag 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 ggacacctcc tccaagagca cctctggggg cacagcggcc      420
ctgggctgcc tgggtcaagga ctacttcccc gaaccgggtga cgggtgcgtg gaactcaggc      480
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc      540
ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac      600
gtgaatcaca agcccagcaa caccaagggtg gacaagaaaag ttgagcccaa atcttgtgac      660
aaaactcaca catgcccacc gtgcccagca cctgaagctg cagggggacc gtcagtcttc      720
ctcttcccc caaaaccaa ggacacctc atgatctccc ggaccctga ggtcacatgc      780
gtggtggtgg acgtgagcca cgaagacctt gaggtcaagt tcaactggta cgtggacggc      840
gtggagggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt      900
gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc      960
aaggctctca acaaagccct cggcgccccc atcgagaaaa ccatctccaa agccaaaggg     1020
cagccccgag aaccacaggt gtacaccctg ccccatgcc gggatgagct gaccaagaac     1080
caggtcagcc tgtggtgcct ggtcaaaggc ttctatcca gcgacatcg cgtggagtgg     1140
gagagcaatg ggagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac     1200
ggctccttct tcctctacag caagctcacc gtggacaaga gcagggtggca gcaggggaac     1260
gtcttctcat gtcctgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc     1320
tcctgtctc 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 ctttactta     1620
agaccaggg acttaatcag caatatcaac gtaatagttc tggaactaaa gggatctgaa     1680
acaacattca tgtgtgaata tgctgatgag acagcaacca ttgtagaatt tctgaacaga     1740
tggattacct ttgccc aaag catcatctca acactgact                                1779

```

<210> 271

eolf-seq1

<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

e0lf-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

eolf-seq1
475

465 470 480

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 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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tcttgcgccg ccagcggctt caccttcagc agctacgcca 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
aagggcccat cggctctccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	420
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca	480
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac	540
tccttcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc	600

eolf-seq1

```

aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt      660
gacaaaaactc acacatgccc accgtgcccga gcacctgaag ctgcagggggg accgtcagtc      720
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca      780
tgcgtggttg tggacgtgag ccacgaagac cctgagggtca agttcaactg gtacgtggac      840
ggcgtggagg tgcataatgc caagacaaaag ccgcggggagg agcagtacaa cagcacgtac      900
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 cgctcccgt gctggactcc     1200
gacggctcct tcttcttcta cagcaagctc accgtggaca agagcagggtg gcagcagggg     1260
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc     1320
ctctccctgt ctccgggttg cggcggaggc tccggaggcg gaggttcttg cggagggtgg     1380
tccgcacctg cctcaagttc taaaaagaaa acacagctac aactggagca ttactgctg     1440
gatttacaga tgattttgaa tggaattaat aattacaaga atcccaaact caccaggatg     1500
ctcacagcca agtttgccat gcccaagaag gccacagaac tgaaacatct tcagtgtcta     1560
gaagaagaac tcaaacctct ggaggaagtg ctaaattggcg ctcaaagcaa aaactttcac     1620
ttaagaccca gggacttaat cagcaatatc aacgtaatag ttctggaact aaagggatct     1680
gaaacaacat tcatgtgtga atatgctgat gagacagcaa ccattgtaga atttctgaac     1740
agatggatta cctttgcccc 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

```

eolf-seq1

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
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

eolf-seq1

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 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

eo1f-seq1

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	tgctcgaag	cggcggagga	ctggtgcagc	ctggcggcag	cctgagactg		60
tcttgcgccc	ccagcggctt	caccttcagc	agctacgcc	tgagctgggt	ccgccaggcc		120
cctggcaagg	gactggaatg	ggtgtccgcc	atcatcggct	ctggcggccag	cacctactac		180
gccgacagcg	tgaagggccg	gttcaccatc	agccgggaca	acagcaagaa	caccctgtac		240
ctgcagatga	acagcctgcg	ggccgaggac	accgccgtgt	actactgctc	caagggatgg		300
ttcggcggct	tcaactactg	gggacagggc	accctggtca	cagtgtccag	cgctagcacc		360
aagggcccat	cggtcttccc	cctggcaccc	tcctccaaga	gcacctctgg	gggcacagcg		420
gccctgggct	gcctggtcaa	ggactacttc	cccgaaccgg	tgacggtgtc	gtggaactca		480
ggcgccctga	ccagcggcgt	gcacaccttc	ccggctgtcc	tacagtcctc	aggactctac		540
tcctctagca	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
tgctgtgtgg	tggacgtgag	ccacgaagac	cctgaggtca	agttcaactg	gtacgtggac		840
ggcgtggagg	tgcataatgc	caagacaaag	ccgcggggagg	agcagtacaa	cagcacgtac		900
cgtgtggtca	gcgtcctcac	cgtcctgcac	caggactggc	tgaatggcaa	ggagtacaag		960
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

eolf-seq1

```

gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg      1260
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc      1320
ctctccctgt ctccgggtgg cggcggaggc tccggaggcg gaggttctgg aggcggaggc      1380
tccgcaccta cttcaagttc tacaaagaaa acacagctac aactggagca tttactgctg      1440
gattttacaga tgattttgaa tggaattaat aattacaaga atcccaaact caccaggatg      1500
ctcacattta agttttacat gcccaagaag 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 cctttgcca aagcatcatc tcaacactga ct                          1782

```

```

<210> 275
<211> 599
<212> PRT
<213> Artificial Sequence

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```

<220>
<223> CH1A1A 98/99 2F1 Fab HC-Fc knob (LALA P329G)-IL-2 qm

```

```

<400> 275

```

```

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

```

eo1f-seq1

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
 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

eolf-seq1

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> 276
<211> 1797
<212> DNA
<213> Artificial Sequence

eof-seq1

<220>

<223> CH1A1A 98/99 2F1 Fab HC-Fc knob (LALA P329G)-IL-2 qm

<400> 276

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	actactgcg	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	ctgcccctga	gctgctgggc	720
ggaccagcg	tgctcctgtt	ccccccaaag	cccaaggaca	ccctgatgat	cagccggacc	780
cccgaagtga	cctgcgtggt	ggtggacgtg	tcccacgagg	accctgaagt	gaagttcaat	840
tggtacgtgg	acggcgtgga	ggtgcacaat	gccaagacca	agccccggga	ggaacagtac	900
aacagcacct	accgggtggt	gtccgtgctg	accgtgctgc	accaggactg	gctgaacggc	960
aaagagtaca	agtgcaaggt	ctccaacaag	gccctgcctg	cccccatcga	gaaaaccatc	1020
agcaaggcca	agggccagcc	cagagaaccc	cagggtgtaca	ccctgcccc	ctgcagagat	1080
gagctgacca	agaaccaggt	gtccctgtgg	tgtctgggtca	agggtttcta	ccccagcgat	1140
atcgccgtgg	agtgaggag	caacggccag	cctgagaaca	actacaagac	cacccccct	1200
gtgctggaca	gcgacggcag	cttcttcctg	tactccaaac	tgaccgtgga	caagagccgg	1260
tggcagcagg	gcaacgtgtt	cagctgcagc	gtgatgcacg	aggccctgca	caaccactac	1320
accagaagt	ccctgagcct	gagccccggc	aagtccggag	gcggaggctc	cggcggcgga	1380
ggttctggcg	gaggtggcgc	tcctgcctcc	tccagacca	agaaaaccca	gctccagctg	1440
gaacatctcc	tgctggatct	gcagatgatc	ctgaacggca	tcaacaacta	caagaacccc	1500
aagctgaccc	ggatgctgac	cgccaagttc	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	tgaaccggtg	gatcaccttc	gcccagtcca	tcattctccac	cctgacc	1797

eolf-seq1

<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

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
 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

eo1f-seq1

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
caggtgcagc tgggtgcagtc tggcgccgaa gtgaagaaac ctggagctag tgtgaaggtg 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 actactgcmc cagatgggac 300
ttgcctatt acgtggaagc catggactac tggggccagg gcaccaccgt gaccgtgtct 360
agcgctagca ccaagggccc atcggctctc cccctggcac cctcctccaa gagcacctct 420
gggggacacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480

eolf-seq1

tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc	540
tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag	600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag	660
cccaaattctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg	720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc	780
cctgagggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac	840
tggtagctgg 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 tgccctggta 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
ggcggagggtg gctccgcacc tgctcaagt tctacaaaga aaacacagct acaactggag	1440
cattttactgc tggattttaca gatgattttg aatggaatta ataattacaa gaatcccaaa	1500
ctcaccagga tgctcacagc caagtttgcc atgcccaaga aggccacaga actgaaacat	1560
cttcagtgtc tagaagaaga actcaaacct ctggaggaag tgctaaatgg cgctcaaagc	1620
aaaaactttc acttaagacc cagggactta atcagcaata tcaacgtaat agttctggaa	1680
ctaaagggat ctgaaacaac attcatgtgt gaatatgctg atgagacagc aaccattgta	1740
gaattttctga acagatggat tacctttgcc caaagcatca tctcaacact gact	1794

<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		

eolf-seq1

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

eo1f-seq1

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 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

eolf-seq1

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> 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
cagggtgcagc 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 actactgcmc cagatgggac 300
ttcgcctatt acgtggaagc catggactac tggggccagg gcaccaccgt gaccgtgtct 360
agcgctagca ccaagggccc atcggtcttc cccctggcac cctcctcaa gagcacctct 420
gggggcacag cggccctggg ctgcctggtc 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
cccaaattct gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720
ggaccgtcag tcttctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 780
cctgagggtca catgcgtggg ggtggacgtg agccacgaag accctgaggt caagttcaac 840
tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 900
aacagcacgt accgtgtggg cagcgtcctc accgtcctgc accaggactg gctgaatggc 960
aaggagtaca agtgcaaggt ctccaacaaa gccctcggcg ccccatcga gaaaaccatc 1020
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atgccgggat 1080

eolf-seq1

gagctgacca agaaccaggt cagcctgtgg tgcctgggtca aaggcttcta tcccagcgac	1140
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc	1200
gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg	1260
tggcagcagg ggaacgtctt ctcattgctcc gtgatgcatg aggctctgca caaccactac	1320
acgcagaaga gcctctccct gtctccgggt ggcggcggag gctccggagg cggagggttct	1380
ggaggcggag gctccgcacc tacttcaagt tctacaaaga aaacacagct acaactggag	1440
catttactgc tggatttaca gatgattttg aatggaatta ataattacaa gaatcccaaa	1500
ctcaccagga tgctcacatt taagttttac atgccaaga aggccacaga actgaaacat	1560
cttcagtgtc tagaagaaga actcaaacct ctggaggaag tgctaaattt agctcaaagc	1620
aaaaactttc acttaagacc cagggactta atcagcaata tcaacgtaat agttctggaa	1680
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

eolf-seq1

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

<220>
<223> CH1A1A 98/99 2F1 Fab HC-Fc hole (LALA P329G)

<400> 282
cagggtgcagc 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
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 gggcaccacag 600
acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggag 660
cccaagagct gcgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg 720
ggaccgtcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 780
cctgagggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840
tggtacgtgg acggcgtgga ggtgcataat gccaaagacaa agccgcggga ggagcagtac 900

eolf-seq1

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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 cacgcctccc      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

```

```

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

```

eolf-seq1

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
gatatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtgggaga cagagtcacc 60
atcacttgca aggccagtg gcgtgtgggt acgtatgttg cgtggatatca gcagaaacca 120
gggaaagcac ctaagctcct gatctattcg gcacccctacc gcaaaagggg agtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
gaagatttcg caacttacta ctgtcaccaa tattacacct atcctctatt cacgtttggc 300
cagggcacca agctcgagat caagcgtacg gtggctgcac catctgtctt catcttcccg 360
ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420
tatcccagag aggccaaaagt acagtggaag gtggataacg ccctccaatc gggtaaactcc 480
caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540
acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt caccatcag 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

eolf-seq1

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

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

eo1f-seq1

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 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

eolf-seq1

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	
cagggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc	60
tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc	120
cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaaactac	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
gggggacacag cggccctggg ctgcctgggtc aaggactact tccccgaacc ggtgacgggtg	480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc	540
tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag	600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag	660
cccaaattctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg	720
ggaccgtcag tcttcctctt cccccaaaaa cccaaggaca ccctcatgat ctcccggacc	780
cctgaggtca catgcgtgggt ggtggacgtg agccacgaag accctgaggt caagttcaac	840

eolf-seq1

tggtacgtgg acggcggtgga 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 tgcctgggtca aaggcttcta tcccagcgac	1140
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc	1200
gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg	1260
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac	1320
acgcagaaga gcctctccct gtctccgggt gccggcggag gctccggagg cggaggttct	1380
ggcggagggtg gctccgcacc tgcctcaagt tctacaaaga aaacacagct acaactggag	1440
catttactgc tggatttaca gatgatattg aatggaatta ataattacaa gaatcccaaa	1500
ctcaccagga tgctcacagc caagtttgcc atgcccaaga 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

<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

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

Met Glu Leu Ser Ser₈₅ Leu Arg Ser Glu Asp₉₀ Thr Ala Val Tyr Tyr₉₅ Cys
 Ala Arg Leu Tyr₁₀₀ Gly Tyr Ala Tyr Tyr₁₀₅ Gly Ala Phe 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
 Ala 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 Ala Ala Gly₂₄₀
 Gly Pro Ser Val Phe₂₄₅ Leu Phe Pro Pro Lys₂₅₀ Pro Lys Asp Thr Leu Met₂₅₅
 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 Asn₂₉₀ Ala Lys Thr Lys Pro₂₉₅ Arg Glu Glu Gln Tyr₃₀₀ Asn Ser Thr Tyr
 Arg Val₃₀₅ 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 Gly Ala Pro₃₃₅ Ile

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 ggctcgagt gatgggagg atcatcccta tctttggtac agcaaaactac 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

eolf-seq1

```

cccaagagct gcgacaaaac tcacacatgc ccaccgtgcc cagcacctga agctgcaggg      720
ggaccgtcag tcttcctctt ccccccaaaa cccaaggaca ccctcatgat ctcccggacc      780
cctgagggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac      840
tggtacgtgg acggcgtgga ggtgcataat gccaagacaa 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

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<210> 289
<211> 592
<212> PRT
<213> Artificial Sequence

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<220>
<223> DP47GS Fab HC-Fc knob (LALA P329G)-IL-2 qm

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```

<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

```

eo1f-seq1

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
 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

eolf-seq1

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 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

eof-seq1

<220>

<223> DP47GS Fab HC-Fc knob (LALA P329G)-IL-2 qm

<400> 290

gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc	60
tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct	120
ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac	180
gcagactccg tgaaggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggcagc	300
ggatttgact actggggcca aggaaccctg gtcaccgtct cgagtgctag caccaagggc	360
ccatcggtct tccccctggc accctctctc aagagcacct ctggggggcac agcgccctg	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 atctcccga cccctgaggt cacatgcgtg	780
gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg	840
gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg	900
gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcag	960
gtctccaaca aagccctcgg cgtcccatc 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 aggtccgga ggcgagggtt ctggcggagg tggctccgca	1380
cctgcctcaa gttctacaaa gaaaacacag ctacaactgg agcatttact gctggattta	1440
cagatgattt tgaatggaat taataattac aagaatccca aactcaccag gatgctcaca	1500
gccaagtttg ccatgcccaa gaaggccaca gaactgaaac atcttcagtg tctagaagaa	1560
gaactcaaac ctctggagga agtgctaaat ggcgctcaaa gcaaaaaactt tacttaaga	1620
cccagggact taatcagcaa tatcaacgta atagtcttg aactaaagg atctgaaaca	1680
acattcatgt gtgaatatgc tgatgagaca gcaaccattg tagaatttct gaacagatgg	1740
attacctttg cccaaagcat catctcaaca ctgact	1776

eolf-seq1

<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

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

eolf-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 Ser 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> 292
<211> 1776
<212> DNA
<213> Artificial Sequence

<220>
<223> DP47GS Fab HC-Fc knob (LALA P329G)-IL-2 wt (2)

<400> 292
gaggtgcaat tgttgaggatc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt cacctttagc agttatgcc ttagctgggt 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 cgagtgttag caccaagggc 360
ccatcggtct 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

eolf-seq1

aatcacaagc ccagcaacac caaggtggac aagaaaagttg agcccaaatc ttgtgacaaa	660
actcacacat gcccaccgtg cccagcacct gaagctgcag ggggaccgtc agtcttcctc	720
ttcccccaa aaccaagga caccctcatg atctcccga cccctgaggt cacatgcgtg	780
gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg	840
gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg	900
gtcagcgccc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgaag	960
gtctccaaca aagccctcgg cgccccatc 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 aggctccgga ggcggagggt ctggaggcgg aggctccgca	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 gcaaaaaactt tcacttaaga	1620
cccagggact taatcagcaa tatcaacgta atagttctgg aactaaaggg atctgaaaca	1680
acattcatgt gtgaatatgc tgatgagaca gcaaccattg tagaatttct gaacagatgg	1740
attacctttg cccaaagcat catctcaaca ctgact	1776

<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			

eolf-seq1

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
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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> 295
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1A 98/99 2F1; VH

<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

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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

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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 actactgcgc cagatgggac 300
ttcgctatt acgtggaagc catggactac tggggccagg gcaccaccgt gaccgtgtct 360
agc 363

<210> 297
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> DP47GS VL

<400> 297

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

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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
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 cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180
 gacagggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgta 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

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
115

<210> 300
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
<223> DP47GS VH

<400> 300
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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 cgagt 345