

eolf-seq1
SEQUENCE LISTING

<110> Roche Glycart AG

<120> Mutant Interleukin-2 Polypeptides

<130> 27307

<150> EP 11153964.9

<151> 2011-02-10

<150> EP 11164237.7

<151> 2011-04-29

<160> 324

<170> PatentIn version 3.5

<210> 1

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<212> PRT

<213> Homo sapiens

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

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

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

Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
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Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser Ile
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Ile Ser Thr Leu Thr
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<223> wild-type human IL-2

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gaagaactca aacctctgga ggaagtgcta aatttagctc aaagcaaaaa ctttcactta      240
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<223> wild-type human IL-2 (C125A)

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

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

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

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

Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
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115    120    125

Ile Ser Thr Leu Thr
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gaagaactca aacctctgga ggaagtgcta aatttagctc aaagcaaaaa ctttactta	240
agaccaggg acttaatcag caatatcaac gtaatagttc tggaactaaa gggatctgaa	300
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gaggaactga agcctctgga agagggtgctg aacctggccc agagcaagaa cttccacctg	240
aggcccaggg acctgatcag caacatcaac gtgatcgtgc tggaactgaa gggcagcgag	300
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<210> 7

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

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

Pro Leu Glu Glu Val Leu Asn 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
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Ile Ser Thr Leu Thr
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 gaagaactca aacctctgga ggaagtgcta aatggcgctc aaagcaaaaa ctttcaactta 240
 agaccaggg acttaatcag caatatcaac gtaatagttc tggaactaaa gggatctgaa 300
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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 Tyr Met Pro Lys
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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
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Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
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Ile Ser Thr Leu Thr
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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	
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 115 120 125

Ile Ser Thr Leu Thr
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 agaccaggg acttaatcag caatatcaac gtaatagttc tggaactaaa gggatctgaa 300
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aggcccaggg acctgatcag caacatcaac gtgatcgtgc tggaactgaa gggcagcgag	300
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			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				
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65					70					75					80
Arg	Pro	Arg	Asp	Leu	Ile	Ser	Asn	Ile	Asn	Val	Ile	Val	Leu	Glu	Leu
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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
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accgccaagt tcgccatgcc caagaaggcc accgagctga aacatctgca gtgcctggaa	180
gaggaactga agcctctgga agagggtgctg aacggcgccc agtccaagaa cttccacctg	240
aggcctcggg acctgatctc caacatcaac gtgatcgtgc tggaactgaa gggctccgag	300
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<223> 2B10; VL

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20 25 30

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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

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

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<223> 2B10; VL

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gggaaagccc ctaagcgct gatctatgct gcatccagtt tgcagagtgg cgtcccatca 180

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<223> 2B10(GS); VL

<400> 25

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

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

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

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
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<210> 26
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gggaaagccc ctaagcgcct gatctatgct gcatccagtt tgcagagtgg cgtcccatca 180
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<223> 2B10; VH

<400> 27

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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
caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
tcttgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
cctggacaag ggctcgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac 240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagactgtac 300
ggttacgctt actacgggtgc ttttgactac tggggccaag ggaccaccgt gaccgtctcc 360
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
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val 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 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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ctctcttgca gggccagtca gagggttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcgtccca 180
gacaggttca gtggcagtg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgt ttactgtcag cagggtcagt atactcccc cacgttcggc 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

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
Page 14

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

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

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

<400> 32
gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
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cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgt ttactgtcag cagggtcagt atactcccc caggttcggc 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

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

eof-seq1

115

<210> 34
 <211> 351
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 2F11; VH

<400> 34
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 tcctgtgcag cctccggatt caccttttagc 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
 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

eolf-seq1

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

<220>
 <223> 2F11(MT); VH

<400> 36
 gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctccggatt caccttttagc agttatgccca tgagctgggt ccgccaggct 120
 ccaggaagg 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
 50 55 60
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Gly Ile Met Leu Pro
 85 90 95
 Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

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

<220>
 <223> 3F2; VL

<400> 38

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gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt atccagggga 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

<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

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 gagtggtacc agtagctact tagcctggta ccagcagaaa	120
cctggccagg ctcccaggct cctcatcaat gtgggctccc gtagggccac tggcatccca	180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag	240

eolf-seq1

cctgaagatt ttgcagtgtg 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

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 tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt caccttttagc agttatgccca tgagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gtccaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300
tttggtggtt ttaactactg gggccaagga accctgggtca ccgtctcgag t 351

eolf-seq1

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

<220>
 <223> 3D9, VL

<400> 43

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

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

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

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

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

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

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 gagtgtagc 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

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<400> 45

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

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

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

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

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

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

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

Val Thr Val Ser Ser
115

<210> 46

<211> 351

<212> DNA

<213> Artificial Sequence

<220>

<223> 3D9, VH

<400> 46

gaggtgcaat tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctccggatt caccttttagc 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
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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
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 tcctgtgcag cctccggatt caccttttagc agttatgcta tgagctgggt ccgccaggct 120
 ccaggggaagg 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
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20

25

30

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

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

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

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

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

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

<220>
<223> 4G8; VL

<400> 50
gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcttgca gggccagtca gagtggttagc cgcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatcatt ggggcctcca ccagggccac tggcatccca 180
gacaggttca gtggcagtggtg 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
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60

50

55

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

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

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

Val Thr Val Ser Ser
115

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

<220>
<223> 4G8; VH

<400> 52
gaggtgcaat tgttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt cacctttagc agttatgcc a tgagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300
ctgggtaatt ttgactactg gggccaagga accctgggtca ccgtctcgag t 351

<210> 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
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100 105 eolf-seql 110

Val Thr Val Ser Ser
115

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

<220>
<223> 4B3; VH

<400> 56
gaggtgcaat tgttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt cacctttagc agttatgcc a tgagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtagtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggtag 300
ctgggtaatt ttgactactg gggccaagga accctgggtca ccgtctcag 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

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

<210> 58

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

<220>
 <223> 4D6; VL

<400> 58
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 ctctcttgca gggccagtca gagggttagc agcaactact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatccag ggcgcctcca gcagggccac tggcatccca 180
 gacaggttca gtggcagtggt atccgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgtg ttactgtcag cagggtcagg ttattcccc tacgttcggc 300
 caggggacca aagtggaaat caaa 324

<210> 59
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 4D6; VH

<400> 59

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

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

eo1f-seq1

<220>

<223> 4D6; VH

<400> 60

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

<210> 61

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> 2C6; VL

<400> 61

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

<210> 62

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> 2C6; VL

<400> 62

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

eolf-seq1

cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatcca	180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag caggctggag	240
cctgaagatt ttgcagtgtg ttactgtcag caggggtcagc 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

Val Thr Val Ser Ser
115

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

<220>
 <223> 2C6; VH

<400> 64

gaggtgcaat tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc	60
tcctgtgcag cctccggatc caccttttagc agttatgccg tgagctgggt ccgccaggct	120
ccaggggaagg ggctggagtg ggtctcagct attagtggga gtgctgggta tacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240

eolf-seq1

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggttgg	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			

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

<220>
 <223> 5H5; VL

<400> 66

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

<210> 67
 <211> 116
 <212> PRT

eolf-seql

<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

<210> 68

<211> 348

<212> DNA

<213> Artificial Sequence

<220>

<223> 5H5; VH

<400> 68

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tcctgtgcag cctccggatt caccttttagc agttatacca tgagctgggt ccgccgggtct 120

ccaggggaagg 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

eo1f-seq1

<400> 69

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

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

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

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

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

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

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

<210> 70

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> 2C4; VL

<400> 70

gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc	60
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cctggccagg ctcccaggct cctcatctat ggtgcctcca ttagggccac tggcatccca	180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag	240
cctgaagatt ttgcagtgta 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
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20

25

30

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

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

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

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

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

Val Thr Val Ser Ser
115

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

<220>
<223> 2C4; VH

<400> 72
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tcctgtgcag cctccggatt cacctttagc agttatgcc a tgagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcagct attagcggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggttg 300
tttacgcctt ttgactactg gggccaagga accctgggtca ccgtctcgag t 351

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

<220>
<223> 2D9; VL

<400> 73

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

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

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

40

45

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

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

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

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

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

<220>
<223> 2D9; VL

<400> 74
gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcttgca gggccagtca gagggttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgt ttactgtcag cagggtaatc agattcccc 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
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85

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90

95

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

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

<220>
<223> 4B8; VL

<400> 78
gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcttgca gggccagtca gagggttagc agcagctact tagcctggta ccagcagaaa 120
cctggccagg ctccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg ttactgtcag cagggtcagg ttattccccc tacgttcggc 300
caggggacca aagtggaaat caaa 324

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

<220>
<223> 4B8; VH

<400> 79

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

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

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

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

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

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

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

Val Thr Val Ser Ser

eof-seq1

115

<210> 80
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> 4B8; VH

<400> 80
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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> 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

eolf-seql

<220>

<223> 7A1; VL

<400> 82

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

<210> 83

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> 7A1; VH

<400> 83

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

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

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

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

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

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

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

Val Thr Val Ser Ser
115

<210> 84

<211> 351

<212> DNA

<213> Artificial Sequence

<220>

<223> 7A1; VH

<400> 84

eolf-seq1

gaggtgcaat tgttgagtc tgggggaggc ttggtacagc ctgggggggc cctgagactc	60
tcctgtgcag cctccggatt caccttttagc agttatgccca tgagctgggt ccgccaggct	120
ccaggggaagg ggctggagtg ggtctcagct attagtggta gtgggtggtag 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

gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc	60
ctctcttgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa	120
cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca	180
gacaggttca gtggcagtg atccgggaca gacttcactc tcaccatcag cagactggag	240

eolf-seq1

cctgaagatt ttgcagtgtg ttactgtcag cagggtcagc ttattcccc 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

<400> 88

gaggtgcaat tggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc	60
tcctgtgcag cctccggatt cacctttagc agttatgccg tgagctgggt ccgccaggct	120
ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggttg	300
ctgggtcctt ttgactactg gggccaagga accctggtca ccgtctcgag t	351

eolf-seq1

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

<220>
<223> 13E8; VL

<400> 89

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

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

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

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

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

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

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

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

<220>
<223> 13E8; VL

<400> 90

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

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

<220>
<223> 13E8; VH

eo1f-seq1

<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 tgttgagatc tgggggagggc 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 gaaaggttgg 300

ttgggtccgt ttgactactg gggccaagga accctgggtca ccgtctcgag t 351

<210> 93

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> 14C10; VL

<400> 93

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly

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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 tgttggagtc 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 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
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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 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
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cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta ttactgtcag caggggtctga atattccctc gacgttcggc 300
caggggacca aagtggaaat caaa 324

<210> 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
Page 45

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
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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 gaaaggttgg 300
ttgggtccgt ttgactactg gggccaagga accctgggtca ccgtctcgag t 351

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

<220>
<223> 19G1; VL

<400> 101

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

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

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

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

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

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

Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
Page 46

100 eolf-seql
105

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

<220>
<223> 19G1; VL

<400> 102
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ctctcttgca gggccagtca gagggttacc agtagctact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatcaat gtgggctccc gtagggccac tggcatccca 180
gacaggttca gtggcagtggt atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtta ttactgtcag caggggtatta tgcttccccc 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

eof-seq1

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

<220>
 <223> 19G1; VH

<400> 104
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 tcctgtgcag cctccggatt cacctttagc agttatgcga tgagctgggt ccgccaggct 120
 ccagggaagg ggctggagtg ggtctcagcg attattagta gtggtggtct cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300
 tttggtggtt ttaactactg gggccaagga accctggtca 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

eolf-seq1

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

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

<220>
 <223> 20G8; VH

<400> 107

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

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

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

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 tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctccggatt caccttttagc agttatgcaa tgagctgggt ccgccaggct 120

eolf-seq1

ccaggggaagg ggctggagtg ggtctcagct attattggga gtggtagtcg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg	300
tttgggtggtt ttaactactg gggccaagga accctgggtca ccgtctcgtc c	351

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

<220>
 <223> 4B9; VL

<400> 109

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

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

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

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

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
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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

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

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

<210> 113
<211> 108
<212> PRT

eolf-seql

<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
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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> 115

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> 5B8; VH

<400> 115

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
Page 52

eo1f-seq1

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
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cctggccagg ctcccaggct cctcatcaat gtgggctccc gtagggccac tggcatccca 180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg ttactgtcag caggggtatta tgcttcccc gacgttcggc 300
caggggacca aagtggaaat caaa 324

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

<220>
<223> 5F1; VH

<400> 119

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 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
Page 54

colf-seq1
60

50

55

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 tgttgagatc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt caccttttagc agttatgcta tgagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcagct attattagta gtgggggctag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300
tttggtgggt ttaactactg gggccaagga accctgggtca ccgtctcgtc c 351

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

<220>
<223> 14B3; VL

<400> 121

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

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

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

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

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
Page 55

eolf-seql

100 105 110

Val Thr Val Ser Ser
115

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

<220>
<223> 14B3; VH

<400> 124
gaggtgcaat tggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt caccttttagc agttatgcta tgagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcagct attttggtc gtggtgcat cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggtgg 300
tttggtggtt ttaactactg gggccaagga accctggtca ccgtctcgtc c 351

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

<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

eolf-seq1

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

<220>
 <223> 16F1; VL

<400> 126
 gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcttgca gggccagtca gagtgttacc agtagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatcaat gtgggctccc gtagggccac tggcatccca 180
 gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgtg ttactgtcag caggggtatta tgcttcccc gacgttcggc 300
 caggggacca aagtggaaat caaa 324

<210> 127
 <211> 117
 <212> PRT
 <213> Artificial sequence

<220>
 <223> 16F1; VH

<400> 127

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

eolf-seq1

<220>

<223> 16F1; VH

<400> 128

gaggtgcaat tgttgagtc tgggggaggc ttggtacagc ctgggggggc cctgagactc 60
tcctgtgcag cctccggatt caccttttagc agttatgcta tgagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcaggt attattggta gtgggtggat cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300
tttggtggtt ttaactactg gggccaagga accctgggtca ccgtctcgtc c 351

<210> 129

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> 16F8; VL

<400> 129

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

<210> 130

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> 16F8; VL

<400> 130

gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcttgca gggccagtca gagtgttacc agtagctact tagcctggta ccagcagaaa 120

eolf-seq1

cctggccagg ctcccaggct cctcatcaat gtgggctccc gtagggccac tggcatccca	180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag	240
cctgaagatt ttgcagtgta ttactgtcag caggggtatta tgcttcccc caggttcggc	300
caggggacca aagtggaaat caaa	324

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

<220>
 <223> 16F8; VH

<400> 131

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

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

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

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

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 tggttgagtc tgggggaggc ttgttacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctccggatt cacctttagc agttatgcc a tgagctgggt ccgccaggct 120

ccaggggaagg ggctggagtg ggtctcagct attcttggtg gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

eolf-seql

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtgg	300
tttggtggtt ttaactactg gggccaagga accctgggtca ccgtctcgtc c	351

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

<220>
 <223> o3C9; VL

<400> 133

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

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

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

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

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

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
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 <213> Artificial Sequence

<220>
 <223> o3C9; VL

<400> 134

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> 135
 <211> 117
 <212> PRT

eo1f-seq1

<213> Artificial Sequence

<220>

<223> O3C9; VH

<400> 135

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

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

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

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

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

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

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

Val Thr Val Ser Ser
115

<210> 136

<211> 351

<212> DNA

<213> Artificial Sequence

<220>

<223> O3C9; VH

<400> 136

gaggtgcaat tgttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctccggatt cacctttagc agttttgcc tggagctgggt ccgtcagtct 120

ccaggggaagg ggctggagtg ggtctcagct attattggta gtggtagtaa cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300

tttgggtggtt ttaactactg gggccaagga accctgggtca ccgtctcgtc c 351

<210> 137

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> O2D7; VL

eolf-seq1

<400> 137

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

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

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

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

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

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

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

<210> 138

<211> 324

<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 gtaggggccac tggcacccca 180

gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgtg ttactgtcag caggctatta tgcttcctcc gacgttcggc 300

caggggacca aagtggaaat caaa 324

<210> 139

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> O2D7; VH

<400> 139

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
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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
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tcctgtgcag cctccggatt caccttttagc agttatgcc a tgagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcagct attagtggta gtgggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtgg 300
tttggtggtt ttaactactg gggccaagga accctgggtca ccgtctcgtc c 351

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

<220>
<223> 28H1; VL

<400> 141

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

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

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
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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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cctggccagg ctcccaggct cctcatcatt ggggcctcca ccaggggccac tggcatccca 180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta 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
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
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65 70 75 80

100 105 110 115

120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200

205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300

305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400

405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500

505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600

605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700

705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800

805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900

905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995 1000

1005 1010 1015 1020 1025 1030 1035 1040 1045 1050 1055 1060 1065 1070 1075 1080 1085 1090 1095 1100

1105 1110 1115 1120 1125 1130 1135 1140 1145 1150 1155 1160 1165 1170 1175 1180 1185 1190 1195 1200

1205 1210 1215 1220 1225 1230 1235 1240 1245 1250 1255 1260 1265 1270 1275 1280 1285 1290 1295 1300

1305 1310 1315 1320 1325 1330 1335 1340 1345 1350 1355 1360 1365 1370 1375 1380 1385 1390 1395 1400

1405 1410 1415 1420 1425 1430 1435 1440 1445 1450 1455 1460 1465 1470 1475 1480 1485 1490 1495 1500

1505 1510 1515 1520 1525 1530 1535 1540 1545 1550 1555 1560 1565 1570 1575 1580 1585 1590 1595 1600

1605 1610 1615 1620 1625 1630 1635 1640 1645 1650 1655 1660 1665 1670 1675 1680 1685 1690 1695 1700

1705 1710 1715 1720 1725 1730 1735 1740 1745 1750 1755 1760 1765 1770 1775 1780 1785 1790 1795 1800

1805 1810 1815 1820 1825 1830 1835 1840 1845 1850 1855 1860 1865 1870 1875 1880 1885 1890 1895 1900

1905 1910 1915 1920 1925 1930 1935 1940 1945 1950 1955 1960 1965 1970 1975 1980 1985 1990 1995 2000

2005 2010 2015 2020 2025 2030 2035 2040 2045 2050 2055 2060 2065 2070 2075 2080 2085 2090 2095 2100

2105 2110 2115 2120 2125 2130 2135 2140 2145 2150 2155 2160 2165 2170 2175 2180 2185 2190 2195 2200

2205 2210 2215 2220 2225 2230 2235 2240 2245 2250 2255 2260 2265 2270 2275 2280 2285 2290 2295 2300

2305 2310 2315 2320 2325 2330 2335 2340 2345 2350 2355 2360 2365 2370 2375 2380 2385 2390 2395 2400

2405 2410 2415 2420 2425 2430 2435 2440 2445 2450 2455 2460 2465 2470 2475 2480 2485 2490 2495 2500

2505 2510 2515 2520 2525 2530 2535 2540 2545 2550 2555 2560 2565 2570 2575 2580 2585 2590 2595 2600

2605 2610 2615 2620 2625 2630 2635 2640 2645 2650 2655 2660 2665 2670 2675 2680 2685 2690 2695 2700

2705 2710 2715 2720 2725 2730 2735 2740 2745 2750 2755 2760 2765 2770 2775 2780 2785 2790 2795 2800

2805 2810 2815 2820 2825 2830 2835 2840 2845 2850 2855 2860 2865 2870 2875 2880 2885 2890 2895 2900

2905 2910 2915 2920 2925 2930 2935 2940 2945 2950 2955 2960 2965 2970 2975 2980 2985 2990 2995 3000

3005 3010 3015 3020 3025 3030 3035 3040 3045 3050 3055 3060 3065 3070 3075 3080 3085 3090 3095 3100

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3205 3210 3215 3220 3225 3230 3235 3240 3245 3250 3255 3260 3265 3270 3275 3280 3285 3290 3295 3300

3305 3310 3315 3320 3325 3330 3335 3340 3345 3350 3355 3360 3365 3370 3375 3380 3385 3390 3395 3400

3405 3410 3415 3420 3425 3430 3435 3440 3445 3450 3455 3460 3465 3470 3475 3480 3485 3490 3495 3500

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3605 3610 3615 3620 3625 3630 3635 3640 3645 3650 3655 3660 3665 3670 3675 3680 3685 3690 3695 3700

3705 3710 3715 3720 3725 3730 3735 3740 3745 3750 3755 3760 3765 3770 3775 3780 3785 3790 3795 3800

3805 3810 3815 3820 3825 3830 3835 3840 3845 3850 3855 3860 3865 3870 3875 3880 3885 3890 3895 3900

3905 3910 3915 3920 3925 3930 3935 3940 3945 3950 3955 3960 3965 3970 3975 3980 3985 3990 3995 4000

4005 4010 4015 4020 4025 4030 4035 4040 4045 4050 4055 4060 4065 4070 4075 4080 4085 4090 4095 4100

4105 4110 4115 4120 4125 4130 4135 4140 4145 4150 4155 4160 4165 4170 4175 4180 4185 4190

85

eolf-seql
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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cctggccagg ctcccaggct cctcatcaat gtgggctccc gtagggccac tggcatccca 180
gacaggttca gtggcagtggt atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg 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

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

eof-seq1

115

<210> 148
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> 22A3; VH

<400> 148
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tcctgtgcag cctccggatt caccttttagc agttatgccca tgagctgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcagct attattggta gtggtagtat cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300
tttgggtggtt 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

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

eolf-seq1

<220>

<223> 29B11; VL

<400> 150

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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 caggttcggc      300
caggggacca aagtggaaat caaa                                           324

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<210> 151

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> 29B11; VH

<400> 151

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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 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

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<210> 152

<211> 351

<212> DNA

<213> Artificial Sequence

<220>

<223> 29B11; VH

<400> 152

eolf-seq1

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tcctgtgcag cctccggatt caccttttagc agttatgcta tgagctgggt ccgccaggct	120
ccaggggaagg ggctggagtg ggtctcagct attattggta gtgggtggtat cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtgg	300
tttggtggtt ttaactactg gggccaagga accctgggtca ccgtctcgag t	351

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

<220>
 <223> 23C10; VL

<400> 153

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

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

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

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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ctctcttgca gggccagtca gagtgttagc cgagctact tagcctggta ccagcagaaa	120
cctggccagg ctcccaggct cctcatcatt ggggcctcca ccagggccac tggcatccca	180
gacaggttca gtggcagtg atccgggaca gacttcactc tcaccatcag cagactggag	240

eolf-seq1

cctgaagatt ttgcagtgtg ttactgtcag caggggtcagg ttattcccc 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

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

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

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

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

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

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 agttctgccg tgagctgggt ccgccaggct	120
ccaggggaagg 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

eo1f-seq1

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

<220>
 <223> 2B10_C3B6; VL

<400> 157

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 1 5 10 15

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

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

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

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

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

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

<210> 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 ttcactctca ccatcagcag cttgcagcct 240
 gaagattttg ccacctatta ctgcttgag aatggtctgc agcccgcgac gtttggccag 300
 ggcaccaaag tcgagatcaa g 321

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

<220>
 <223> 2B10_C3B6; VH

eolf-seq1

<400> 159

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

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

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

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

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 160

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> 2B10_C3B6; VH

<400> 160

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cctggacaag ggctcgagtg gatgggagct atcatcccga tccttgggtat cgcaaactac	180
gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac	240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagactgtac	300
ggttacgctt actacggtgc ttttgactac tggggccaag ggaccaccgt gaccgtctcc	360
tca	363

<210> 161

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> 2B10_6A12; VL

<400> 161

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

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

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

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

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

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

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

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

<220>
<223> 2B10_6A12; VL

<400> 162
gatatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtcggaga ccgggtcacc 60
atcacctgcc gggcaagtca gggcattaga aatgatttag gctggtacca gcagaagcca 120
gggaaagccc ctaagcgcct gatctatgct gcatccagtt tgcagagtgg cgtcccatca 180
aggttcagcg gcagtggatc cgggacagag ttactctca ccatcagcag cttgcagcct 240
gaagattttg ccacctatta ctgcttcag 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

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

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

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

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

<220>
<223> 2B10_6A12; VH

<400> 164
caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
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
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35

40

45

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

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

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

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

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

<220>
<223> 2B10_C3A6; VL

<400> 166
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atcacctgcc gggcaagtca gggcattcgt aatgttttag gctggtacca gcagaagcca 120
gggaaagccc ctaagcgcct gatctatgat tcgtccagtt tgcagagtgg cgtcccatca 180
aggttcagcg gcggtggatc cgggacagag ttcactctca ccatcagcag cttgcagcct 240
gaagattttg ccacctatta ctgcttgcat aatgggtctgc agcccgcgac gtttggccag 300
ggcaccaaag tcgagatcaa g 321

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

<220>
<223> 2B10_C3A6; VH

<400> 167

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

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

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

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

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
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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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atcacctgcc gggcaagtca ggggattcgt aatgttttag gctggtacca gcagaagcca 120
gggaaagccc ctaagcgcct gatctatgat gcttacagct tgcagagtgg cgtcccatca 180
aggttcagcg gcggtggatc cgggacagag ttactctca ccatcagcag cttgcagcct 240
gaagattttg ccacctatta ctgcttgag 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
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

eof-seq1

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

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

eof-seq1

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

<220>
 <223> 2B10_D1A2_VD; VL

<400> 174
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 atcacctgcc gggcaagtca ggggattcgt aatgatttag gctggtagca gcagaagcca 120
 gggaaagccc ctaagcgcct gatctatgat gcttacagct tgcagagtgg cgtcccatca 180
 aggttcagcg gcggtggatc cgggacagag ttactctca ccatcagcag cttgcagcct 240
 gaagattttg ccacctatta ctgcttgag 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
 50 55 60
 Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Leu Tyr Gly Tyr Ala Tyr Tyr Gly Ala Phe Asp Tyr Trp Gly
 100 105 110
 Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

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

eof-seq1

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

<210> 178

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> 2B10_O7D8; VL

<400> 178

gatatccaga	tgaccagtc	tccatcctcc	ctgtctgcat	ctgtcggaga	ccgggtcacc	60
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eolf-seq1

atcacctgcc gggcaagtca gagcattcgt aatgttttag gctggtacca gcagaagcca	120
gggaaagccc ctaagcgcct gatctatgat gtgtccagtt tgcagagtgg cgtcccatca	180
aggttcagcg gcggtggatc cgggacagag ttcaactctca ccatcagcag cttgcagcct	240
gaagattttg ccacctatta ctgcttgagc 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
 50 55 60

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 180
 <211> 363
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 2B10_07D8; VH

<400> 180

caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc	60
tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc	120
cctggacaag ggctcgagtg gatggggagg atcatcccta tctttggtac agcaaactac	180

eolf-seq1

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gcacagaagt tccagggcag ggtcaccatt actgcagaca aatccacgag cacagcctac      240
atggagctga gcagcctgag atctgaggac accgccgtgt attactgtgc gagactgtac      300
ggttacgctt actacggtgc ttttgactac tggggccaag ggaccaccgt gaccgtctcc      360
tca                                                                    363

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<210> 181
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 2B10_O1F7; VL

<400> 181

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

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

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

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

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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gatatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtcggaga ccgggtcacc      60
atcacctgcc gggcaagtca gggcattcgt aatgttttag gctggtacca gcagaagcca      120
gggaaagccc ctaagcgcct gatctatgat gcgtccagtt tgcagagtgg cgtcccatca      180
aggttcagcg gcggtggatc cgggacagag ttactctca ccatcagcag cttgcagcct      240
gaagattttg ccacctatta ctgcctgcag aatgggtctgc agcccgcgac gtttggccag      300
ggcaccaaag tcgagatcaa g                                                                    321

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eo1f-seq1

<210> 183
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 2B10_01F7; VH

<400> 183

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

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

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

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

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

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

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_01F7; VH

<400> 184

caggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc	60
tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc	120
cctggacaag ggctcgagt 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

eo1f-seq1

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

<220>
<223> 2B10_6H10; VL

<400> 185

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

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

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

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

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

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

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

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

<220>
<223> 2B10_6H10; VL

<400> 186

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtcggaga ccgggtcacc	60
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gggaaagccc ctaagcgcct gatccaggct gctaccagtt tgcagagtgg cgtcccatca	180
aggttcagcg gcggtggatc cgggacagag ttcactctca ccatcagcag cttgcagcct	240
gaagattttg ccacctatta ctgcttgag aatgggtctgc agcccgcgac gtttggccag	300
ggcaccaaag tcgagatcaa g	321

<210> 187
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> 2B10_6H10; VH

<400> 187

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

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

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

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

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 188
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> 2B10_6H10; VH

<400> 188
caggtgcaat tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
tcctgcaagg cctccggagg cacattcagc agctacgcta taagctgggt gcgacaggcc 120
cctggacaag ggctcgagt gatgggaggg 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
tca 363

<210> 189
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> MHLG1; VH

<400> 189

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
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eolf-seq1

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

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

Tyr Ser Ala Ser Tyr Arg Tyr Thr 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 Gln Gln Tyr Asn Ser Tyr Pro Leu
85 90 95

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

<210> 192
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> KV9; VL

<400> 192
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atcacctgca aggccagtca gaatgtggat actaacgtgg cttggtacca gcagaagcca 120
gggcaggcac ctaggcctct gatctattcg gcatcctacc ggtacactgg cgtcccatca 180
aggttcagcg gcagtggatc cgggacagag ttcactctca caatctcaag cctgcaacct 240
gaagatttcg caacttacta ctgtcaacag tacaatagtt accctctgac gttcggcgga 300
ggtaccaagg tggagatcaa gcgtacg 327

<210> 193
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> MHLG; VH

<400> 193

Glu Val Gln Leu Val 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 Asn Tyr
20 25 30

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

eo1f-seq1

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

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

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

Tyr Cys Thr Thr Tyr Gly Asn Tyr Val Gly His Tyr Phe Asp His Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 194
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> MHLG; VH

<400> 194
gaagtgcagc tgggtggagtc tggaggaggc ttggtccagc ctggcgggctc cctgcggctc 60
tcctgtgcag cctccggatt cacatttagc aactattgga tgaactgggt gcggcaggct 120
cctggaaagg gcctcgagtg ggtggccgag atcagattga aatccaataa cttcgggaaga 180
tattacgctg caagcgtgaa gggccggttc accatcagca gagatgattc caagaacacg 240
ctgtacctgc agatgaacag cctgaagacc gaggatacgg ccgtgtatta ctgtaccaca 300
tacggcaact acgttgggca ctacttcgac cactggggcc aagggaccac cgtcaccgctc 360
tccagt 366

<210> 195
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> KV1; VL

<400> 195

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

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

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

Tyr Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro Ser Arg Phe Ser Gly
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60

50

55

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 Gln Gln Tyr Asn Ser Tyr Pro Leu
85 90 95

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

<210> 196
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> KV1; VL

<400> 196
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atcacctgca gggccagtca gaatgtggat actaacttag cttggtacca gcagaagcca 120
gggaaagcac ctaagctcct gatctattcg gcatcctacc gttacactgg cgtcccatca 180
aggttcagcg gcagtggatc cgggacagag ttactctca caatctcaag cctgcaacct 240
gaagatttcg caacttacta ctgtcaacag tacaatagtt accctctgac gttcggcgga 300
ggtaccaagg tggagatcaa gcgtacggtg 330

<210> 197
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> KV7; VL

<400> 197

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1 5 10 15

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

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

Tyr Ser Ala Ser Tyr Arg Tyr Thr 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 Gln Gln Tyr Asn Ser Tyr Pro Leu
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90

95

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

<210> 198
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> KV7; VL

<400> 198
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gggaaagcac ctaagcctct gatctattcg gcatcctacc ggtacactgg cgtcccatca 180
aggttcagcg gcagtggatc cgggacagag ttcactctca caatctcaag cctgcaacct 240
gaagatttcg caacttacta ctgtcaacag tacaatagtt accctctgac gttcggcgga 300
ggtaccaagg tggagatcaa gcgtacggtg 330

<210> 199
<211> 603
<212> PRT
<213> Artificial Sequence

<220>
<223> L19 Fab-IL2 qm-Fab (heavy chain cytokine fusion construct)

<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 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
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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
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Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Ser	Gly	Gly	Gly
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Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ala	Pro	Ala	Ser	Ser
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Ser	Thr	Lys	Lys	Thr	Gln	Leu	Gln	Leu	Glu	His	Leu	Leu	Leu	Asp	Leu
				245					250					255	
Gln	Met	Ile	Leu	Asn	Gly	Ile	Asn	Asn	Tyr	Lys	Asn	Pro	Lys	Leu	Thr
			260					265					270		
Arg	Met	Leu	Thr	Ala	Lys	Phe	Ala	Met	Pro	Lys	Lys	Ala	Thr	Glu	Leu
		275					280					285			
Lys	His	Leu	Gln	Cys	Leu	Glu	Glu	Glu	Leu	Lys	Pro	Leu	Glu	Glu	Val
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Leu	Asn	Gly	Ala	Gln	Ser	Lys	Asn	Phe	His	Leu	Arg	Pro	Arg	Asp	Leu
305					310					315					320
Ile	Ser	Asn	Ile	Asn	Val	Ile	Val	Leu	Glu	Leu	Lys	Gly	Ser	Glu	Thr
				325					330					335	
Thr	Phe	Met	Cys	Glu	Tyr	Ala	Asp	Glu	Thr	Ala	Thr	Ile	Val	Glu	Phe
			340					345					350		
Leu	Asn	Arg	Trp	Ile	Thr	Phe	Ala	Gln	Ser	Ile	Ile	Ser	Thr	Leu	Thr
		355					360					365			
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Glu
	370					375					380				
Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser

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385				390				395				400			
Leu	Arg	Leu	Ser	Cys 405	Ala	Ala	Ser	Gly	Phe 410	Thr	Phe	Ser	Ser	Phe 415	Ser
Met	Ser	Trp	Val 420	Arg	Gln	Ala	Pro	Gly 425	Lys	Gly	Leu	Glu	Trp 430	Val	Ser
Ser	Ile	Ser 435	Gly	Ser	Ser	Gly	Thr 440	Thr	Tyr	Tyr	Ala	Asp 445	Ser	Val	Lys
Gly	Arg 450	Phe	Thr	Ile	Ser	Arg 455	Asp	Asn	Ser	Lys	Asn 460	Thr	Leu	Tyr	Leu
Gln 465	Met	Asn	Ser	Leu	Arg 470	Ala	Glu	Asp	Thr	Ala 475	Val	Tyr	Tyr	Cys	Ala 480
Lys	Pro	Phe	Pro	Tyr 485	Phe	Asp	Tyr	Trp	Gly 490	Gln	Gly	Thr	Leu	Val 495	Thr
Val	Ser	Ser	Ala 500	Ser	Thr	Lys	Gly	Pro 505	Ser	Val	Phe	Pro	Leu 510	Ala	Pro
Ser	Ser	Lys 515	Ser	Thr	Ser	Gly	Gly 520	Thr	Ala	Ala	Leu	Gly 525	Cys	Leu	Val
Lys	Asp 530	Tyr	Phe	Pro	Glu	Pro 535	Val	Thr	Val	Ser	Trp 540	Asn	Ser	Gly	Ala
Leu 545	Thr	Ser	Gly	Val	His 550	Thr	Phe	Pro	Ala	Val 555	Leu	Gln	Ser	Ser	Gly 560
Leu	Tyr	Ser	Leu	Ser 565	Ser	Val	Val	Thr	Val 570	Pro	Ser	Ser	Ser	Leu 575	Gly
Thr	Gln	Thr	Tyr 580	Ile	Cys	Asn	Val	Asn 585	His	Lys	Pro	Ser	Asn 590	Thr	Lys
Val	Asp	Lys 595	Lys	Val	Glu	Pro	Lys 600	Ser	Cys	Asp					

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ccgtattttg	actactgggg	ccaggggaacc	ctggtcaccg	tctcgagtgc	tagcaccaag	360
ggcccatcgg	tcttccccct	ggcaccctcc	tccaagagca	cctctggggg	cacagcggcc	420
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caaagcatca	tctcaacact	gacttccggc	ggaggaggat	ccggcggagg	tggctctggc	1140
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tcttgtgac						1809

<210> 201
 <211> 215
 <212> PRT
 <213> Artificial sequence

<220>
 <223> L19 light chain

<400> 201

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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 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> 202
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> L19 light chain

<400> 202
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60

eolf-seq1

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cctggccagg ctcccaggct cctcatctat tatgcatcca gcagggccac tggcatccca	180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag	240
cctgaagatt ttgcagtgtg ttactgtcag cagacgggtc gtattcctcc gacgttcggc	300
caagggacca aggtggaaat caaacgtacg gtggctgcac catctgtctt catcttcccg	360
ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc	420
tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc	480
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acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag	600
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<210> 203
 <211> 641
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> F16 scFv-IL2 qm-scFv

<400> 203

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

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

Thr Val Ser Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 115 120 125

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

Gly Gln Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr
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145				150				eolf-seql 155				160			
Tyr	Ala	Ser	Trp	Tyr 165	Gln	Gln	Lys	Pro	Gly 170	Gln	Ala	Pro	Val	Leu 175	Val
Ile	Tyr	Gly	Lys 180	Asn	Asn	Arg	Pro	Ser 185	Gly	Ile	Pro	Asp	Arg 190	Phe	Ser
Gly	Ser	Ser 195	Ser	Gly	Asn	Thr	Ala 200	Ser	Leu	Thr	Ile	Thr 205	Gly	Ala	Gln
Ala	Glu 210	Asp	Glu	Ala	Asp	Tyr 215	Tyr	Cys	Asn	Ser	Ser 220	Val	Tyr	Thr	Met
Pro 225	Pro	Val	Val	Phe	Gly 230	Gly	Gly	Thr	Lys	Leu 235	Thr	Val	Leu	Gly	Ser 240
Ser	Ser	Ser	Gly	Ser 245	Ser	Ser	Ser	Gly	Ser 250	Ser	Ser	Ser	Gly	Ala 255	Pro
Ala	Ser	Ser	Ser 260	Thr	Lys	Lys	Thr	Gln 265	Leu	Gln	Leu	Glu	His 270	Leu	Leu
Leu	Asp	Leu 275	Gln	Met	Ile	Leu	Asn 280	Gly	Ile	Asn	Asn	Tyr 285	Lys	Asn	Pro
Lys	Leu 290	Thr	Arg	Met	Leu	Thr 295	Ala	Lys	Phe	Ala	Met 300	Pro	Lys	Lys	Ala
Thr 305	Glu	Leu	Lys	His	Leu 310	Gln	Cys	Leu	Glu	Glu 315	Glu	Leu	Lys	Pro	Leu 320
Glu	Glu	Val	Leu	Asn 325	Gly	Ala	Gln	Ser	Lys 330	Asn	Phe	His	Leu	Arg 335	Pro
Arg	Asp	Leu	Ile 340	Ser	Asn	Ile	Asn	Val 345	Ile	Val	Leu	Glu	Leu 350	Lys	Gly
Ser	Glu	Thr 355	Thr	Phe	Met	Cys	Glu 360	Tyr	Ala	Asp	Glu	Thr 365	Ala	Thr	Ile
Val	Glu 370	Phe	Leu	Asn	Arg	Trp 375	Ile	Thr	Phe	Ala	Gln 380	Ser	Ile	Ile	Ser
Thr 385	Leu	Thr	Ser	Gly	Gly 390	Gly	Gly	Ser	Gly	Gly 395	Gly	Gly	Ser	Gly	Gly 400
Gly	Gly	Ser	Ser	Glu 405	Leu	Thr	Gln	Asp	Pro 410	Ala	Val	Ser	Val	Ala 415	Leu
Gly	Gln	Thr	Val	Arg	Ile	Thr	Cys	Gln	Gly	Asp	Ser	Leu	Arg	Ser	Tyr

eol f-seq1						
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ccaggggaagg	ggctggagtg	ggtctcagct	attagtggta	gtggtggtag	cacatactac	180
gcagactccg	tgaagggccg	gttcaccatc	tccagagaca	attccaagaa	cacgctgtat	240
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aatgcttttg	actactgggg	ccaggggaacc	ctggtcaccg	tgtcgagagg	tggaggcggt	360
tcaggcggag	gtggctcttg	cggtggcgga	tcgtctgagc	tgactcagga	ccctgctgtg	420
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tccttgacca	tcactggggc	tcaggcggaa	gatgaggctg	actattactg	taactcctct	660
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tcctcatcgg	gtagtagctc	ttccggctca	tcgtcctccg	gagcacctgc	ctcaagttct	780
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ggaattaata	attacaagaa	tcccaaactc	accaggatgc	tcacagccaa	gtttgccatg	900
cccaagaagg	ccacagaact	gaaacatctt	cagtgtctag	aagaagaact	caaacctctg	960
gaggaagtgc	taaatggcgc	tcaaagcaaa	aactttcact	taagaccag	ggacttaatc	1020
agcaatatca	acgtaatatg	tctggaacta	aagggatctg	aaacaacatt	catgtgtgaa	1080
tatgctgatg	agacagcaac	cattgtagaa	tttctgaaca	gatggattac	ctttgccc	1140
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tccaagaaca	cgctgtatct	gcaaatgaac	agcctgagag	ccgaggacac	ggccgtatat	1860
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tcg						1923

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<211> 603
 <212> PRT
 <213> Artificial sequence

<220>
 <223> F16 Fab-IL2 qm-Fab (heavy chain cytokine fusion construct)

<400> 205

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 20 25 30

Gly 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 His Asn Ala 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 Ser Ser Ser Ser
 210 215 220

Gly Ser Ser Ser Ser Gly Ser Ser Ser Ser Gly Ala Pro Ala Ser Ser
 225 230 235 240

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Ser Thr Lys Lys Thr 245 Gln Leu Gln Leu Glu 250 His Leu Leu Leu Asp 255 Leu

Gln Met Ile Leu 260 Asn Gly Ile Asn Asn 265 Tyr Lys Asn Pro Lys 270 Leu Thr

Arg Met Leu 275 Thr Ala Lys Phe Ala 280 Met Pro Lys Lys Ala 285 Thr Glu Leu

Lys His 290 Leu Gln Cys Leu Glu 295 Glu Glu Leu Lys Pro 300 Leu Glu Glu Val

Leu 305 Asn Gly Ala Gln Ser 310 Lys Asn Phe His Leu 315 Arg Pro Arg Asp Leu 320

Ile Ser Asn Ile Asn 325 Val Ile Val Leu Glu 330 Leu Lys Gly Ser Glu 335 Thr

Thr Phe Met Cys 340 Glu Tyr Ala Asp Glu 345 Thr Ala Thr Ile Val 350 Glu Phe

Leu Asn Arg 355 Trp Ile Thr Phe Ala 360 Gln Ser Ile Ile Ser 365 Thr Leu Thr

Ser Gly 370 Gly Gly Gly Ser Gly 375 Gly Gly Gly Ser Gly 380 Gly Gly Gly Glu

Val 385 Gln Leu Leu Glu Ser 390 Gly Gly Gly Leu Val 395 Gln Pro Gly Gly Ser 400

Leu Arg Leu Ser Cys 405 Ala Ala Ser Gly Phe 410 Thr Phe Ser Arg Tyr 415 Gly

Met Ser Trp Val 420 Arg Gln Ala Pro Gly 425 Lys Gly Leu Glu Trp 430 Val Ser

Ala Ile Ser 435 Gly Ser Gly Gly Ser 440 Thr Tyr Tyr Ala Asp 445 Ser Val Lys

Gly Arg 450 Phe Thr Ile Ser Arg 455 Asp Asn Ser Lys Asn 460 Thr Leu Tyr Leu

Gln Met Asn Ser Leu Arg 470 Ala Glu Asp Thr Ala 475 Val Tyr Tyr Cys Ala 480

Lys Ala His Asn Ala 485 Phe Asp Tyr Trp Gly 490 Gln Gly Thr Leu Val 495 Thr

Val Ser Ser Ala 500 Ser Thr Lys Gly Pro 505 Ser Val Phe Pro Leu 510 Ala Pro

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Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
515 520 525

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
530 535 540

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
545 550 555 560

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
565 570 575

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
580 585 590

Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
595 600

<210> 206
<211> 1809
<212> DNA
<213> Artificial Sequence

<220>
<223> F16 Fab-IL2 qm-Fab (heavy chain cytokine fusion construct)

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ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagcgcac 300
aatgcttttg actactgggg ccaggggaacc ctggtcaccg tgctcagtg tagcaccaag 360
ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420
ctgggctgcc tgggtcaagga ctacttcccc gaaccgggtga cgggtgtcgtg gaactcaggc 480
gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc 540
ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 600
gtgaatcaca agcccagcaa caccaagggtg gataagaaa ttgagcccaa atcttgtgac 660
tcttcctcat cgggtagtag ctcttcgggc tcatcgtcct ccggagcacc tgcctcaagt 720
tctacaaaga aaacacagct acaactggag catttactgc tggatttaca gatgattttg 780
aatggaatta ataattacaa gaatcccaaa ctcaccagga tgctcacagc caagtttgcc 840
atgcccaaga agggcacaga actgaaacat cttcagtgtc tagaagaaga actcaaact 900
ctggaggaag tgctaaatgg cgctcaaagc aaaaactttc acttaagacc cagggactta 960
atcagcaata tcaacgtaat agttctggaa ctaaagggat ctgaaacaac attcatgtgt 1020

eolf-seq1

gaatatgctg atgagacagc aaccattgta gaatttctga acagatggat tacctttgcc	1080
caaagcatca tctcaacact gacttccggc ggaggaggga gcggcggagg tggctctggc	1140
ggtggcggag aggtgcaatt gttggagtct gggggaggct tggtagagcc tgggggggtcc	1200
ctgagactct cctgtgcagc ctctggattc acctttagcc ggtatggat gagctgggtc	1260
cgccaggctc caggggaagg gctggagtgg gtctcagcta ttagtggtag tggtggtagc	1320
acatactacg cagactccgt gaagggccgg ttcaccatct ccagagacaa ttccaagaac	1380
acgctgtatc tgcaaatgaa cagcctgaga gccgaggaca cggccgtata ttactgtgcg	1440
aaagcgcata atgcttttga ctactggggc cagggaaacc tggtcaccgt gtcgagtgtc	1500
agcaccaagg gcccacggt cttccccctg gcaccctcct ccaagagcac ctctgggggc	1560
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg	1620
aactcaggcg ccctgaccag cggcgtgcac accttccccg ctgtcctaca gtcctcagga	1680
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac	1740
atctgcaacg tgaatcacaa gccagcaac accaaggtgg acaagaaagt tgagcccaaa	1800
tcttgtgac	1809

<210> 207
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> F16 light chain

<400> 207

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

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

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

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

Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
 65 70 75 80

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

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys
 100 105 110

Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln

eolf-seq1

115	120	125
Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly		
130	135	140
Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly		
145	150	155
Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala		
165	170	175
Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser		
180	185	190
Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val		
195	200	205
Ala Pro Thr Glu Cys Ser		
210		

<210> 208
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> F16 light chain

<400>	208		60
		tcttctgagc tgactcagga ccctgctgtg tctgtggcct tgggacagac agtcaggatc	
		acatgccaaag gagacagcct cagaagctat tatgcaagct ggtaccagca gaagccagga	120
		caggcccctg tacttgatcat ctatggtaaa aacaaccggc cctcagggat cccagaccga	180
		ttctctggct ccagctcagg aaacacagct tccttgacca tcaactggggc tcaggcggaa	240
		gatgaggctg actattactg taactcctct gtttatacta tgccgcccgt ggtattcggc	300
		ggagggacca agctgaccgt cctaggtcaa cccaaggctg ccccagcgt gaccctgttc	360
		ccccccagca gcgaggaact gcaggccaac aaggccaccc tggctctgcct gatcagcgac	420
		ttctacccag gcgccgtgac cgtggcctgg aaggccgaca gcagccccgt gaaggccggc	480
		gtggagacca ccacccccag caagcagagc aacaacaagt acgccgccag cagctacctg	540
		agcctgaccc ccgagcagtg gaagagccac aggtcctaca gctgccaggt gaccacagag	600
		ggcagcaccg tggagaaaac cgtggccccc accgagtgca gc	642

<210> 209
 <211> 605
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 3F2 Fab-IL2 qm-Fab (heavy chain cytokine fusion construct)

<400> 209

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 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 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 Ser Gly Gly
 210 215 220
 Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Ala Ser
 225 230 235 240
 Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp
 245 250 255
 Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu
 260 265 270

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

eolf-seq1

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
545 550 555 560

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
565 570 575

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
580 585 590

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
595 600 605

<210> 210
<211> 1815
<212> DNA
<213> Artificial Sequence

<220>
<223> 3F2 Fab-IL2 qm-Fab (heavy chain cytokine fusion construct)

<400> 210
gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt caccttttagc agttatgccca tgagctgggt ccgccaggct 120
ccaggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggtgg 300
tttggtggtt ttaactactg gggccaagga accctgggtca ccgtctcgag tgctagcacc 360
aaggggcccat cggtcttccc cctggcacc cctccaaga gcacctctgg gggcacagcg 420
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca 480
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540
tcctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600
aacgtgaatc acaagcccag caacaccaag gtggataaga aagttgagcc caaatcttgt 660
gactccggcg gaggagggag cggcggaggt ggctccggag gtggcggagc acctgcctca 720
agttctacaa agaaaacaca gctacaactg gagcatttac tgctggattt acagatgatt 780
ttgaatggaa ttaataatta caagaatccc aaactcacca ggatgctcac agccaagttt 840
gccatgcca agaaggccac agaactgaaa catcttcagt gtctagaaga agaactcaaa 900
cctctggagg aagtgtctaaa tggcgtctca agcaaaaact ttcacttaag acccagggac 960
ttaatcagca atatcaacgt aatagttctg gaactaaagg gatctgaaac aacattcatg 1020
tgtgaatatg ctgatgagac agcaaccatt gtagaatttc tgaacagatg gattaccttt 1080
gcccaaagca tcattctaac actgacttcc ggcggaggag gatccggcgg aggtggctct 1140
ggcgggtggcg gagaggtgca attggtggag tctgggggag gcttggtaca gcctgggggg 1200
tcctgagac tctcctgtgc agcctccgga ttcaccttta gcagttatgc catgagctgg 1260

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gtccgccagg ctccagggaa ggggctggag tgggtctcag ctattagtgg tagtggtggt	1320
agcacatact acgcagactc cgtgaagggc cggttcacca tctccagaga caattccaag	1380
aacacgctgt atctgcagat gaacagcctg agagccgagg acacggccgt atattactgt	1440
gcgaaagggg ggtttggtgg ttttaactac tggggccaag gaaccctggt caccgtctcg	1500
agtgctagca ccaagggccc atcgggtcttc cccctggcac cctcctccaa gagcacctct	1560
gggggacacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg	1620
tcgtggaact caggcgcctt gaccagcggc gtgcacacct tcccggctgt cctacagtcc	1680
tcaggactct actccctcag cagcgtgggt accgtgccct ccagcagctt gggcaccacg	1740
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggataa gaaagttgag	1800
cccaaattctt gtgac	1815

<210> 211

<211> 605

<212> PRT

<213> Artificial Sequence

<220>

<223> 4G8 Fab-IL2 qm-Fab (heavy chain cytokine fusion construct)

<400> 211

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	eolf-seql										155	160				
Gly	Ala	Leu	Thr	Ser ₁₆₅	Gly	Val	His	Thr	Phe ₁₇₀	Pro	Ala	Val	Leu	Gln ₁₇₅	Ser	
Ser	Gly	Leu	Tyr ₁₈₀	Ser	Leu	Ser	Ser	Val ₁₈₅	Val	Thr	Val	Pro	Ser ₁₉₀	Ser	Ser	
Leu	Gly	Thr ₁₉₅	Gln	Thr	Tyr	Ile	Cys ₂₀₀	Asn	Val	Asn	His	Lys ₂₀₅	Pro	Ser	Asn	
Thr	Lys ₂₁₀	Val	Asp	Lys	Lys	Val ₂₁₅	Glu	Pro	Lys	Ser	Cys ₂₂₀	Asp	Ser	Gly	Gly	
Gly ₂₂₅	Gly	Ser	Gly	Gly	Gly ₂₃₀	Gly	Ser	Gly	Gly	Gly ₂₃₅	Gly	Ala	Pro	Ala	Ser ₂₄₀	
Ser	Ser	Thr	Lys	Lys ₂₄₅	Thr	Gln	Leu	Gln	Leu ₂₅₀	Glu	His	Leu	Leu	Leu ₂₅₅	Asp	
Leu	Gln	Met	Ile ₂₆₀	Leu	Asn	Gly	Ile	Asn ₂₆₅	Asn	Tyr	Lys	Asn	Pro ₂₇₀	Lys	Leu	
Thr	Arg	Met ₂₇₅	Leu	Thr	Ala	Lys	Phe ₂₈₀	Ala	Met	Pro	Lys	Lys ₂₈₅	Ala	Thr	Glu	
Leu	Lys ₂₉₀	His	Leu	Gln	Cys	Leu ₂₉₅	Glu	Glu	Glu	Leu	Lys ₃₀₀	Pro	Leu	Glu	Glu	
Val ₃₀₅	Leu	Asn	Gly	Ala	Gln ₃₁₀	Ser	Lys	Asn	Phe	His ₃₁₅	Leu	Arg	Pro	Arg	Asp ₃₂₀	
Leu	Ile	Ser	Asn	Ile ₃₂₅	Asn	Val	Ile	Val	Leu ₃₃₀	Glu	Leu	Lys	Gly	Ser ₃₃₅	Glu	
Thr	Thr	Phe	Met ₃₄₀	Cys	Glu	Tyr	Ala	Asp ₃₄₅	Glu	Thr	Ala	Thr	Ile ₃₅₀	Val	Glu	
Phe	Leu	Asn ₃₅₅	Arg	Trp	Ile	Thr	Phe ₃₆₀	Ala	Gln	Ser	Ile	Ile ₃₆₅	Ser	Thr	Leu	
Thr	Ser ₃₇₀	Gly	Gly	Gly	Gly	Ser ₃₇₅	Gly	Gly	Gly	Gly	Ser ₃₈₀	Gly	Gly	Gly	Gly	
Glu ₃₈₅	Val	Gln	Leu	Leu	Glu ₃₉₀	Ser	Gly	Gly	Gly	Leu ₃₉₅	Val	Gln	Pro	Gly	Gly ₄₀₀	
Ser	Leu	Arg	Leu	Ser ₄₀₅	Cys	Ala	Ala	Ser	Gly ₄₁₀	Phe	Thr	Phe	Ser	Ser ₄₁₅	Tyr	
Ala	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	

eo1f-seq1

420 425 430

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
435 440 445

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
450 455 460

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
465 470 475 480

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

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
500 505 510

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
515 520 525

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
530 535 540

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
545 550 555 560

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
565 570 575

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
580 585 590

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
595 600 605

<210> 212
<211> 1815
<212> DNA
<213> Artificial Sequence

<220>
<223> 4G8 Fab-IL2 qm-Fab (heavy chain cytokine fusion construct)

<400> 212

gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc	60
tcctgtgcag cctccggatt caccttttagc agttatgccca tgagctgggt ccgccaggct	120
ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg	300
ctgggtaatt ttgactactg gggccaagga accctgggtca ccgtctcgag tgctagcacc	360

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aagggcccat	cggtcttccc	cctggcacc	tcctccaaga	gcacctctgg	gggcacagcg	420
gccctgggct	gcctgggtcaa	ggactacttc	cccgaaccgg	tgacgggtgtc	gtggaactca	480
ggcgccctga	ccagcggcgt	gcacaccttc	ccggctgtcc	tacagtcctc	aggactctac	540
tccctcagca	gcgtgggtgac	cgtgccctcc	agcagcttgg	gcacccagac	ctacatctgc	600
aacgtgaatc	acaagcccag	caacaccaag	gtggataaga	aagttgagcc	caaatcttgt	660
gactccggcg	gaggagggag	cggcggaggt	ggctccggag	gtggcggagc	acctgcctca	720
agttctacaa	agaaaacaca	gctacaactg	gagcatttac	tgctggattt	acagatgatt	780
ttgaatggaa	ttaataatta	caagaatccc	aaactcacca	ggatgctcac	agccaagttt	840
gccatgccc	agaaggccac	agaactgaaa	catcttcagt	gtctagaaga	agaactcaaa	900
cctctggagg	aagtgtctaaa	tggcgtctca	agcaaaaact	ttcacttaag	acccagggac	960
ttaatcagca	atatcaacgt	aatagtcttg	gaactaaagg	gatctgaaac	aacattcatg	1020
tgtgaatatg	ctgatgagac	agcaaccatt	gtagaatttc	tgaacagatg	gattaccttt	1080
gccc aaagca	tcattctaac	actgacttcc	ggcggaggag	gatccggcgg	aggtggctct	1140
ggcgggtggc	gagaggtgca	attgtttggag	tctgggggag	gcttggtaca	gcctgggggg	1200
tccctgagac	tctcctgtgc	agcctccgga	ttcaccttta	gcagttatgc	catgagctgg	1260
gtccgccagg	ctccagggaa	ggggctggag	tgggtctcag	ctattagtgg	tagtggtggt	1320
agcacatact	acgcagactc	cgtgaagggc	cggttcacca	tctccagaga	caattccaag	1380
aacacgtgt	atctgcagat	gaacagcctg	agagccgagg	acacggccgt	atattactgt	1440
gcgaaaggg	ggctgggtaa	ttttgactac	tggggccaag	gaaccctgg	caccgtctcg	1500
agtgtagca	ccaaggggcc	atcgggtctt	cccctggcac	cctcctccaa	gagcacctct	1560
gggggcacag	cggccctggg	ctgcctggtc	aaggactact	tccccgaacc	ggtgacggtg	1620
tcgtggaact	caggcgcct	gaccagcggc	gtgcacacct	tcccggctgt	cctacagtcc	1680
tcaggactct	actccctcag	cagcgtgggt	accgtgccct	ccagcagctt	gggcacccag	1740
acctacatct	gcaacgtgaa	tcacaagccc	agcaacacca	aggtggataa	gaaagttgag	1800
cccaaattct	gtgac					1815

<210> 213
 <211> 605
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 3D9 Fab-IL2 qm-Fab (heavy chain cytokine fusion construct)

<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 Tyr
 20 25 30

eo1f-seq1

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

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

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

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

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

Val Thr Val Ser Ser 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 Ser Gly Gly
210 215 220

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Ala Ser
225 230 235 240

Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp
245 250 255

Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu
260 265 270

Thr Arg Met Leu Thr Ala Lys Phe Ala Met Pro Lys Lys Ala Thr Glu
275 280 285

Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu
290 295 300

co1f-seq1

Val 305 Leu Asn Gly Ala Gln 310 Ser Lys Asn Phe 315 His Leu Arg Pro Arg Asp 320
Leu Ile Ser Asn Ile 325 Asn Val Ile Val Leu 330 Glu Leu Lys Gly Ser 335 Glu
Thr Thr Phe Met 340 Cys Glu Tyr Ala Asp 345 Glu Thr Ala Thr Ile 350 Val Glu
Phe Leu Asn 355 Arg Trp Ile Thr Phe 360 Ala Gln Ser Ile Ile 365 Ser Thr Leu
Thr Ser 370 Gly Gly Gly Gly Ser 375 Gly Gly Gly Gly Ser 380 Gly Gly Gly Gly
Glu 385 Val Gln Leu Leu Glu 390 Ser Gly Gly Gly Leu 395 Val Gln Pro Gly Gly 400
Ser Leu Arg Leu 405 Ser Cys Ala Ala Ser Gly 410 Phe Thr Phe Ser Ser 415 Tyr
Ala Met Ser 420 Trp Val Arg Gln Thr Pro 425 Gly Lys Gly Leu Glu 430 Trp Val
Ser Ala Ile 435 Gly Val Ser Thr Gly 440 Ser Thr Tyr Tyr Ala 445 Asp Ser Val
Lys Gly 450 Arg Phe Thr Ile Ser 455 Arg Asp Asn Ser Lys 460 Asn Thr Leu Tyr
Leu 465 Gln Met Asn Ser 470 Leu Arg Ala Glu Asp Thr 475 Ala Val Tyr Tyr Cys 480
Ala Lys Gly Trp 485 Leu Gly Pro Phe Asp Tyr 490 Trp Gly Gln Gly Thr 495 Leu
Val Thr Val 500 Ser Ser Ala Ser Thr Lys 505 Gly Pro Ser Val Phe 510 Pro Leu
Ala Pro Ser 515 Ser Lys Ser Thr Ser 520 Gly Gly Thr Ala Ala 525 Leu Gly Cys
Leu Val 530 Lys Asp Tyr Phe Pro 535 Glu Pro Val Thr Val 540 Ser Trp Asn Ser
Gly 545 Ala Leu Thr Ser Gly 550 Val His Thr Phe Pro 555 Ala Val Leu Gln Ser 560
Ser Gly Leu Tyr Ser 565 Leu Ser Ser Val Val 570 Thr Val Pro Ser Ser 575 Ser

eolf-seq1

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
580 585 590

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
595 600 605

<210> 214
<211> 1815
<212> DNA
<213> Artificial Sequence

<220>
<223> 3D9 Fab-IL2 qm-Fab (heavy chain cytokine fusion construct)

<400> 214
gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctccggatt caccttttagc agttatgcta tgagctgggt ccgccagact 120
ccagggaagg ggctggagtg ggtctcagct attggtgtta gtactggtag cacatactac 180
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gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca 480
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gccc aaagca tcatctcaac actgacttcc ggcggaggag gatccggcgg aggtggctct 1140
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agcacatact acgcagactc cgtgaagggc cggttcacca tctccagaga caattccaag 1380
aacacgctgt atctgcagat gaacagcctg agagccgagg acacggccgt atattactgt 1440
gcgaaagggt ggctgggtcc ttttgactac tggggccaag gaaccctggt caccgtctcg 1500

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agtgctagca ccaagggccc atcgggtcttc cccctggcac cctcctccaa gagcacctct	1560
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tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggtgt cctacagtcc	1680
tcaggactct actccctcag cagcgtgggtg accgtgccct ccagcagctt gggcaccag	1740
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggataa gaaagttgag	1800
cccaaattctt gtgac	1815

<210> 215
 <211> 605
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 2F11 Fab-IL2 qm-Fab (heavy chain cytokine fusion construct)

<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 Tyr
 20 25 30

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

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

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

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

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

Val Thr Val Ser Ser 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

190

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

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460

450

455

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
465 470 475 480

Ala Lys Trp Arg Trp Met Met Phe Asp Tyr Trp Gly Gln Gly Thr Leu
485 490 495

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
500 505 510

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
515 520 525

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
530 535 540

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
545 550 555 560

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
565 570 575

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
580 585 590

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
595 600 605

<210> 216
<211> 1815
<212> DNA
<213> Artificial Sequence

<220>
<223> 2F11 Fab-IL2 qm-Fab (heavy chain cytokine fusion construct)

<400> 216
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tcctgtgcag cctccggatt caccttttagc agttatgccca tgagctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac accgccgtat attactgtgc gaaatggaga 300
tggtatgatgt ttgactactg gggccaagga accctgggtca ccgtctcgag tgctagcacc 360
aagggcccat cggctcttccc cctggcacc tcctccaaga gcacctctgg gggcacagcg 420
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca 480
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540
tcctcagca gcgtggtgac cgtgccctcc agcagcttgg gcaccagac ctacatctgc 600

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aacgtgaatc acaagcccag caacaccaag gtggataaga aagttgagcc caaatcttgt	660
gactccggcg gaggagggag cggcggaggt ggctccggag gtggcggagc acctgcctca	720
agttctacaa agaaaacaca gctacaactg gagcatttac tgctggattt acagatgatt	780
ttgaatggaa ttaataatta caagaatccc aaactcacca ggatgctcac agccaagttt	840
gccatgcccc agaaggccac agaactgaaa catcttcagt gtctagaaga agaactcaaa	900
cctctggagg aagtgctaaa tggcgctcaa agcaaaaact ttcacttaag acccagggac	960
ttaatcagca atatcaacgt aatagttctg gaactaaagg gatctgaaac aacattcatg	1020
tgtgaatatg ctgatgagac agcaaccatt gtagaatttc tgaacagatg gattaccttt	1080
gccc aaagca tcatctcaac actgacttcc ggcggaggag gatccggcgg aggtggctct	1140
ggcggtggcg gagaggtgca attgttggag tctgggggag gcttggtaca gcctgggggg	1200
tccctgagac tctcctgtgc agcctccgga ttcaccttta gcagttatgc catgagctgg	1260
gtccgccagg ctccaggga ggggctggag tgggtctcag ctattagtgg tagtggtggg	1320
agcacatact acgcagactc cgtgaagggc cggttcacca tctccagaga caattccaag	1380
aacacgtgt atctgcagat gaacagcctg agagccgagg acaccgccgt atattactgt	1440
gcgaaatgga gatggatgat gtttgactac tggggccaag gaaccctggg caccgtctcg	1500
agtgctagca ccaagggccc atcgggtctt cccctggcac cctcctcca gagcacctct	1560
gggggcacag cggccctggg ctgcctgggc aaggactact tccccgaacc ggtgacgggtg	1620
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggtgt cctacagtcc	1680
tcaggactct actccctcag cagcgtgggt accgtgccct ccagcagctt gggcaccag	1740
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cccaaattct gtgac	1815

<210> 217
 <211> 605
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 4B3 Fab-IL2 qm-Fab (heavy chain cytokine fusion construct)
 <400> 217

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
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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 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 Ser Gly Gly
 210 215 220
 Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Ala Ser
 225 230 235 240
 Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp
 245 250 255
 Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu
 260 265 270
 Thr Arg Met Leu Thr Ala Lys Phe Ala Met Pro Lys Lys Ala Thr Glu
 275 280 285
 Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu
 290 295 300
 Val Leu Asn Gly Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp
 305 310 315 320
 Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu
 325 330 335

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Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu
340 345 350

Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu
355 360 365

Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
370 375 380

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
385 390 395 400

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
405 410 415

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
420 425 430

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
435 440 445

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
450 455 460

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
465 470 475 480

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

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
500 505 510

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
515 520 525

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
530 535 540

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
545 550 555 560

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
565 570 575

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
580 585 590

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
595 600 605

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<210> 218
<211> 1815
<212> DNA
<213> Artificial Sequence

<220>
<223> 4B3 Fab-IL2 qm-Fab (heavy chain cytokine fusion construct)

<400> 218
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gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
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gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca 480
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540
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aacgtgaatc acaagcccag caacaccaag gtggataaga aagttgagcc caaatcttgt 660
gactccggcg gaggagggag cggcggaggt ggctccggag gtggcggagc acctgcctca 720
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gccc aaagca tcatctcaac actgacttcc ggcggaggag gatccggcgg aggtggctct 1140
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agtgctagca ccaagggccc atcggctctc cccctggcac cctcctccaa gagcacctct 1560
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tcgtggaact caggcgcctt gaccagcggc gtgcacacct tcccggctgt cctacagtcc 1680
tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcaccacg 1740

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acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggataa gaaagttgag 1800
cccaaattctt gtgac 1815

<210> 219
<211> 603
<212> PRT
<213> Artificial Sequence

<220>
<223> 28H1 Fab-IL2 qm-Fab (heavy chain cytokine fusion construct)
<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 His
20 25 30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp Ser Val Lys
50 55 60
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95
Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110
Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
115 120 125
Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
130 135 140
Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145 150 155 160
Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
165 170 175
Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
180 185 190
Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
195 200 205
Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Ser Gly Gly Gly

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220

210

215

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Ala Ser Ser
225 230 235 240

Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu
245 250 255

Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr
260 265 270

Arg Met Leu Thr Ala Lys Phe Ala Met Pro Lys Lys Ala Thr Glu Leu
275 280 285

Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
290 295 300

Leu Asn Gly Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu
305 310 315 320

Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr
325 330 335

Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe
340 345 350

Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
355 360 365

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Glu
370 375 380

Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
385 390 395 400

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser His Ala
405 410 415

Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
420 425 430

Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp Ser Val Lys Gly
435 440 445

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
450 455 460

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys
465 470 475 480

Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
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Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
500 505 510

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
515 520 525

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
530 535 540

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
545 550 555 560

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
565 570 575

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
580 585 590

Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
595 600

<210> 220
<211> 1809
<212> DNA
<213> Artificial Sequence

<220>
<223> 28H1 Fab-IL2 qm-Fab (heavy chain cytokine fusion construct)

<400> 220
gaagtgcagc tgctggaatc cggcggaggc ctggtgcagc ctggcggatc tctgagactg 60
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cctggcaaag gcctggaatg ggtgtccgcc atctgggcct ccggcgagca gtactacgcc 180
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ggcaacttcg actactgggg acagggcacc ctggtcaccg tgtccagcgc tagcaccaag 360
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ctgggctgcc tgggtcaagga ctacttcccc gagcccgtga ccgtgtcctg gaactctggc 480
gccctgacca gcggcgcca cacctttcca gccgtgctgc agtcctccgg cctgtactcc 540
ctgtcctccg tcgtgaccgt gccctccagc tctctgggca cccagaccta catctgcaac 600
gtgaaccaca agccctcaa caccaagggt gacaagaagg tggaacccaa gtcctgcgac 660
agtgggtgggg gaggatctgg tggcggagggt tctggcggag gtggcgctcc tgcctcctcc 720
agcaccaaga aaaccagct ccagctggaa catctcctgc tggatctgca gatgatcctg 780
aacggcatca acaactacaa gaacccaag ctgacccgga tgctgaccgc caagttcgcc 840

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ctggaagagg tgctgaacgg cgcccagttc aagaacttcc acctgaggcc tcgggacctg	960
atctccaaca tcaacgtgat cgtgctggaa ctgaagggct ccgagacaac cttcatgtgc	1020
gagtacgccg acgagacagc taccatcgtg gaatttctga accggtggat caccttcgcc	1080
cagtccatca tctccaccct gacctccggt ggtggcggat ccgggggagg gggttctggc	1140
ggaggcggag aagtgcagct gctggaatcc ggcggaggcc tggcgcagcc tggcggatct	1200
ctgagactgt cctgcgccgc ctccggcttc accttctcct ccacgccat gtcctgggtc	1260
cgacaggctc caggcaaggg cctggaatgg gtgtccgcca tctgggcctc cggcgagcag	1320
tactacgccg actctgtgaa gggccggttc accatctccc gggacaactc caagaacacc	1380
ctgtacctgc agatgaactc cctgcgggcc gaggacaccg ccgtgtacta ctgtgccaag	1440
ggctggctgg gcaacttcga ctactggggc cagggcaccc tggtcaccgt gtcctccgcc	1500
tctaccaagg gcccctccgt gttccctctg gcccctcca gcaagtctac ctctggcggc	1560
accgccgtc tgggctgcct ggtcaaggac tacttccccg agcccgtgac cgtgtcctgg	1620
aactctggcg ccctgaccag cggcgtgcac acctttccag ccgtgctgca gtcctccggc	1680
ctgtactccc tgtcctccgt cgtgaccgtg ccctccagct ctctgggcac ccagacctac	1740
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tcctgcgac	1809

<210> 221
 <211> 605
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 29B11 Fab-IL2 qm-Fab (heavy chain cytokine fusion construct)

<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 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

eo1f-seq1

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

Val Thr Val Ser Ser 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 Ser Gly Gly
210 215 220

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Ala Ser
225 230 235 240

Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp
245 250 255

Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu
260 265 270

Thr Arg Met Leu Thr Ala Lys Phe Ala Met Pro Lys Lys Ala Thr Glu
275 280 285

Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu
290 295 300

Val Leu Asn Gly Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp
305 310 315 320

Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu
325 330 335

Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu
340 345 350

Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu
355 360 365

eo1f-seq1

Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
370 375 380

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
385 390 400

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
405 410 415

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
420 425 430

Ser Ala Ile Ile Gly Ser Gly Gly Ile Thr Tyr Tyr Ala Asp Ser Val
435 440 445

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
450 455 460

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
465 470 475 480

Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu
485 490 495

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
500 505 510

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
515 520 525

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
530 535 540

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
545 550 555 560

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
565 570 575

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
580 585 590

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
595 600 605

<210> 222

<211> 1815

<212> DNA

<213> Artificial sequence

<220>

<223> 29B11 Fab-IL2 qm-Fab (heavy chain cytokine fusion construct)

eof-seq1

<400> 222
gaagtgcagc tgctggaatc cggcggaggc ctggtgcagc ctggcggatc tctgagactg 60
tcctgcgccg cctccggctt caccttctcc tcctacgcca tgtcctgggt ccgacaggct 120
cctggcaaag gcctggaatg ggtgtccgcc atcatcggct ccggcggcat cacctactac 180
gccgactctg tgaaggggccg gttcaccatc tcccgggaca actccaagaa caccctgtac 240
ctgcagatga actccctgcg ggccgaggac accgccgtgt actactgtgc caagggctgg 300
ttcggaggct tcaactactg gggacagggc accctgggtca ccgtgtccag cgctagcacc 360
aagggaccct ccgtgttccc cctggccccc tcagcaagt ctacctctgg cggcaccgcc 420
gctctgggct gcctggtcaa ggactacttc cccgagcccg tgaccgtgtc ctggaactct 480
ggcgccctga ccagcggcgt ccacaccttt ccagccgtgc tgcagtcctc cggcctgtac 540
tcctgtctct ccgtcgtgac cgtgccctcc agctctctgg gcaccagac ctacatctgc 600
aacgtgaacc acaagccctc caacaccaag gtggacaaga aggtggaacc caagtcctgc 660
gacagtgggtg ggggaggatc tgggtggcga ggttctggcg gaggtggcg tctgcctcc 720
tccagcacca agaaaacca gctccagctg gaacatctcc tgctggatct gcagatgatc 780
ctgaacggca tcaacaacta caagaacccc aagctgaccc ggatgctgac cgccaagttc 840
gccatgccc aagaggccac cgagctgaaa catctgcagt gcctggaaga ggaactgaag 900
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gcccagtcca tcatctccac cctgacctcc ggtggtggcg gatccggggg aggggggttct 1140
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tctctgagac tgtcctgcgc cgcctccggc ttcaccttct cctcctatgc catgtcctgg 1260
gtccgacagg ctccaggcaa gggcctggaa tgggtgtccg ccatcatcgg ctccggcggc 1320
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aacaccctgt acctgcagat gaactccctg cgggccgagg acaccgccgt gtactactgt 1440
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tccgcctcta ccaagggcc ctccgtgttc cctctggccc cctccagcaa gtctacctct 1560
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tcctggaact ctggcgccct gaccagcggc gtgcacacct ttccagccgt gctgcagtcc 1680
tccggcctgt actccctgtc ctccgtcgtg accgtgccct ccagctctct gggcaccag 1740
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cccaagtcct gcgac 1815

<210> 223
<211> 605
<212> PRT

eolf-seq1

<213> Artificial Sequence

<220>

<223> 19G1 Fab-IL2 qm-Fab (heavy chain cytokine fusion construct)

<400> 223

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

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

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

Ser Ala Ile 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 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 Ser Gly Gly
210 215 220

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Ala Ser
225 230 235 240

Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp
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515

520

525

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
530 535 540

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
545 550 555 560

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
565 570 575

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
580 585 590

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
595 600 605

<210> 224
<211> 1815
<212> DNA
<213> Artificial sequence

<220>
<223> 19G1 Fab-IL2 qm-Fab (heavy chain cytokine fusion construct)

<400> 224
gaggtgcagc tgctcgaaag cggcggagga ctggtgcagc ctggcggcag cctgagactg 60
tcttgcgccg ccagcggcctt caccttcagc agctacgcca tgagctgggt ccgccaggcc 120
cctggcaagg gactggaatg ggtgtccgcc atcatcagct ctggcggcct gacctactac 180
gccgacagcg tgaagggccg gttcaccatc agccgggaca acagcaagaa caccctgtac 240
ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcgc caagggatgg 300
ttcggcggct tcaactactg gggacagggc accctgggtca cagtgtccag cgctagcacc 360
aagggaccca gcgtgtttccc cctggccccc agcagcaaga gcacatctgg cggaacagcc 420
gccctgggct gcctggtcaa agactacttc cccgagcccc tgaccgtgtc ctggaacagc 480
ggagccctga ccagcggcgt gcacaccttt ccagccgtgc tgcagagcag cggcctgtac 540
agcctgagca gcgtggtcac cgtgcctagc tctagcctgg gcacccagac ctacatctgc 600
aacgtgaacc acaagcccag caacaccaag gtggacaaga aggtggaacc caagagctgc 660
gactccggcg gaggcggatc tggcgggtga ggctccggag gcggaggcgc tcctgccagc 720
agctccacca agaaaacca gctccagctg gaacatctgc tgctggatct gcagatgatc 780
ctgaacggca tcaacaacta caagaacccc aagctgaccc ggatgctgac cgccaagtgc 840
gccatgccc aagaaggccac cgaactgaaa catctgcagt gcctggaaga ggaactgaag 900
cctctggaag aggtgctgaa cggcggccag agcaagaact tccacctgag gcccagggac 960
ctgatcagca acatcaacgt gatcgtgctg gaactgaagg gcagcgagac aaccttcatg 1020
tgcgagtacg ccgacgagac agccaccatc gtggaatttc tgaaccggtg gatcaccttc 1080

eof-seq1

gcccagagca tcacagcac cctgacaagc ggaggcggcg gatccggcgg aggcggatct 1140
 ggcggaggag gcgaggcca gctgctcgaa agcggcggag gactggtgca gcctggcggc 1200
 agcctgagac tgtcttgccg cgccagcggc ttcacctca gcagctacgc catgagctgg 1260
 gtccgccagg cccctggcaa gggactggaa tgggtgtccg ccatcatcag ctctggcggc 1320
 ctgacctact acgccgacag cgtgaagggc cgggtcacca tcagccggga caacagcaag 1380
 aacaccctgt acctgcagat gaacagcctg cggggccgagg acaccgccgt gtactactgc 1440
 gccaaaggat gggtcggcgg cttcaactac tggggacagg gcaccctggg cacagtgtcc 1500
 agcggcagca ccaaggggcc cagcgtgttc cccctggccc ccagcagcaa gagcacatct 1560
 ggcggaacag ccgccctggg ctgcctgggc aaagactact tccccgagcc cgtgaccgtg 1620
 tcctggaaca gcggagccct gaccagcggc gtgcacacct ttccagccgt gctgcagagc 1680
 agcggcctgt acagcctgag cagcgtgggc accgtgccta gctctagcct gggcaccag 1740
 acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggaa 1800
 cccaagagct gcgac 1815

<210> 225

<211> 605

<212> PRT

<213> Artificial Sequence

<220>

<223> 20G8 Fab-IL2 qm-Fab (heavy chain cytokine fusion construct)

<400> 225

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

eo1f-seq1

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
130 135 140

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

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
195 200 205

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Ser Gly Gly
210 215 220

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ala Pro Ala Ser
225 230 235 240

Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp
245 250 255

Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu
260 265 270

Thr Arg Met Leu Thr Ala Lys Phe Ala Met Pro Lys Lys Ala Thr Glu
275 280 285

Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu
290 295 300

Val Leu Asn Gly Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp
305 310 315 320

Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu
325 330 335

Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu
340 345 350

Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu
355 360 365

Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
370 375 380

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
385 390 395 400

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
405 410 415

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
420 425 430

Ser Ala Ile Ile Gly Ser Gly Ser Arg Thr Tyr Tyr Ala Asp Ser Val
435 440 445

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
450 455 460

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
465 470 475 480

Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu
485 490 495

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
500 505 510

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
515 520 525

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
530 535 540

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
545 550 555 560

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
565 570 575

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
580 585 590

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
595 600 605

<210> 226

<211> 1815

<212> DNA

<213> Artificial Sequence

<220>

<223> 20G8 Fab-IL2 qm-Fab (heavy chain cytokine fusion construct)

<400> 226

gaggtgcagc tgctcgaaag cggcggagga ctggtgcagc ctggcggcag cctgagactg 60

tcttgcgccg ccagcggctt caccttcagc agctacgcca tgagctgggt ccgccaggcc 120

cctggcaagg gactggaatg ggtgtccgcc atcatcggct ctggcagccg gacctactac 180

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gccgacagcg tgaagggccg gttcaccatc agccggggaca acagcaagaa caccctgtac	240
ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcgc caagggatgg	300
ttcggcggct tcaactactg gggacagggc accctgggtca cagtgtccag cgctagcacc	360
aagggaccca gcgtgttccc cctggccccc agcagcaaga gcacatctgg cggaacagcc	420
gccctgggct gcctgggtcaa agactacttc cccgagcccc tgaccgtgtc ctggaacagc	480
ggagccctga ccagcggcgt gcacaccttt ccagccgtgc tgcagagcag cggcctgtac	540
agcctgagca gcgtgggtcac cgtgcctagc tctagcctgg gcacccagac ctacatctgc	600
aacgtgaacc acaagcccag caacaccaag gtggacaaga aggtggaacc caagagctgc	660
gactccggcg gaggcggatc tggcgggtga ggctccggag gcggaggcgc tcctgccagc	720
agctccacca agaaaacca gctccagctg gaacatctgc tgctggatct gcagatgac	780
ctgaacggca tcaacaacta caagaacccc aagctgaccc ggatgctgac cgccaagtgc	840
gccatgcca agaaggccac cgaactgaaa catctgcagt gcctggaaga ggaactgaag	900
cctctggaag aggtgctgaa cggcgcccag agcaagaact tccacctgag gcccagggac	960
ctgatcagca acatcaacgt gatcgtgctg gaactgaagg gcagcgagac aaccttcatg	1020
tgcgagtacg ccgacgagac agccaccatc gtggaatttc tgaaccggtg gatcaccttc	1080
gcccagagca tcatcagcac cctgacaagc ggaggcggcg gatccggcgg aggcggatct	1140
ggcggaggag gcgaggtcca gctgctcgaa agcggcggag gactggtgca gcctggcggc	1200
agcctgagac tgtcttgccg cgccagcggc ttcaccttca gcagctacgc catgagctgg	1260
gtccgccagg cccctggcaa gggactggaa tgggtgtccg ccatcatcgg ctctggcagc	1320
cggacctact acgccgacag cgtgaagggc cgggttacca tcagccggga caacagcaag	1380
aacaccctgt acctgcagat gaacagcctg cgggccgagg acaccgccgt gtactactgc	1440
gccaagggat gggttcggcg cttcaactac tggggacagg gcaccctggt cacagtgtcc	1500
agcgccagca ccaagggccc cagcgtgttc cccctggccc ccagcagcaa gagcacatct	1560
ggcggaaacag ccgccctggg ctgcctggtc aaagactact tccccgagcc cgtgaccgtg	1620
tcctggaaca gcggagccct gaccagcggc gtgcacacct ttccagccgt gctgcagagc	1680
agcggcctgt acagcctgag cagcgtggtc accgtgccta gctctagcct gggcacccag	1740
acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggaa	1800
cccaagagct gcgac	1815

<210> 227
 <211> 605
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 4B9 Fab-IL2 qm-Fab (heavy chain cytokine fusion construct)

<400> 227

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

eol f-seq1															
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	Ser	Gly	Gly
	210					215					220				
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ala	Pro	Ala	Ser
225					230					235					240
Ser	Ser	Thr	Lys	Lys	Thr	Gln	Leu	Gln	Leu	Glu	His	Leu	Leu	Leu	Asp
				245					250					255	
Leu	Gln	Met	Ile	Leu	Asn	Gly	Ile	Asn	Asn	Tyr	Lys	Asn	Pro	Lys	Leu
			260					265					270		
Thr	Arg	Met	Leu	Thr	Ala	Lys	Phe	Ala	Met	Pro	Lys	Lys	Ala	Thr	Glu

eolf-seq1

275

280

285

Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu
 290 295 300

Val Leu Asn Gly Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp
 305 310 315 320

Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu
 325 330 335

Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu
 340 345 350

Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu
 355 360 365

Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 370 375 380

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 385 390 395 400

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 405 410 415

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 420 425 430

Ser Ala Ile Ile Gly Ser Gly Ala Ser Thr Tyr Tyr Ala Asp Ser Val
 435 440 445

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 450 455 460

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 465 470 475 480

Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu
 485 490 495

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 500 505 510

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 515 520 525

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 530 535 540

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
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eol f-seq1															
545				550				555				560			
Ser	Gly	Leu	Tyr	Ser ₅₆₅	Leu	Ser	Ser	Val	Val ₅₇₀	Thr	Val	Pro	Ser	Ser ₅₇₅	Ser
Leu	Gly	Thr	Gln ₅₈₀	Thr	Tyr	Ile	Cys	Asn ₅₈₅	Val	Asn	His	Lys	Pro ₅₉₀	Ser	Asn
Thr	Lys	Val ₅₉₅	Asp	Lys	Lys	Val	Glu ₆₀₀	Pro	Lys	Ser	Cys	Asp ₆₀₅			

<400>	228						
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cctggcaagg	gactggaatg	ggtgtccgcc	atcatcggct	ctggcgccag	cacctactac		180
gccgacagcg	tgaagggccg	gttcaccatc	agccgggaca	acagcaagaa	caccctgtac		240
ctgcagatga	acagcctgcg	ggccgaggac	accgccgtgt	actactgcgc	caagggatgg		300
ttcggcggt	tcaactactg	gggacagggc	accctgggtca	cagtgtccag	cgctagcacc		360
aagggaccca	gcgtgttccc	cctggccccc	agcagcaaga	gcacatctgg	cggaacagcc		420
gccctgggct	gcctgggtcaa	agactacttc	cccagagccc	tgaccgtgtc	ctggaacagc		480
ggagccctga	ccagcggcgt	gcacaccttt	ccagccgtgc	tgcagagcag	cggcctgtac		540
agcctgagca	gcgtgggtcac	cgtgcctagc	tctagcctgg	gcaccagac	ctacatctgc		600
aacgtgaacc	acaagcccag	caacaccaag	gtggacaaga	aggtggaacc	caagagctgc		660
gactccggcg	gaggcggatc	tggcgggtga	ggctccggag	gcggaggcgc	tcctgccagc		720
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ctgaacggca	tcaacaacta	caagaacccc	aagctgaccc	ggatgctgac	cgccaagttc		840
gccatgccc	agaaggccac	cgaactgaaa	catctgcagt	gcctggaaga	ggaactgaag		900
cctctggaag	aggtgctgaa	cggcgcccag	agcaagaact	tccacctgag	gcccagggac		960
ctgatcagca	acatcaacgt	gatcgtgctg	gaactgaagg	gcagcgagac	aaccttcatg		1020
tgcgagtacg	ccgacgagac	agccaccatc	gtggaatttc	tgaaccggtg	gatcaccttc		1080
gccagagca	tcatcagcac	cctgacaagc	ggaggcggcg	gatccggcgg	aggcggatct		1140
ggcggaggag	gcgaggtcca	gctgctcgaa	agcggcggag	gactggtgca	gcctggcggc		1200
agcctgagac	tgtcttgcg	cgccagcggc	ttcaccttca	gcagctacgc	catgagctgg		1260
gtccgccagg	cccctggcaa	gggactggaa	tgggtgtccg	ccatcatcgg	ctctggcgcc		1320

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agcacctact acgccgacag cgtgaagggc cggttcacca tcagccggga caacagcaag	1380
aacaccctgt acctgcagat gaacagcctg cgggccgagg acaccgccgt gtactactgc	1440
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agcgccagca ccaagggccc cagcgtgttc cccctggccc ccagcagcaa gagcacatct	1560
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tcctggaaca gcggagccct gaccagcggc gtgcacacct ttccagccgt gctgcagagc	1680
agcggcctgt acagcctgag cagcgtgggc accgtgccta gctctagcct gggcacccag	1740
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cccaagagct gcgac	1815

<210> 229
 <211> 605
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 14B3 Fab-IL2 qm-Fab (heavy chain cytokine fusion construct)

<400> 229

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 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

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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 Ser Gly Gly
210 215 220

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Ala Ser
225 230 235 240

Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp
245 250 255

Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu
260 265 270

Thr Arg Met Leu Thr Ala Lys Phe Ala Met Pro Lys Lys Ala Thr Glu
275 280 285

Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu
290 295 300

Val Leu Asn Gly Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp
305 310 315 320

Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu
325 330 335

Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu
340 345 350

Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu
355 360 365

Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
370 375 380

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
385 390 395 400

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
405 410 415

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
420 425 430

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Ser Ala Ile Leu Ala Ser Gly Ala Ile Thr Tyr Tyr Ala Asp Ser Val
435 440 445

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
450 455 460

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
465 470 475 480

Ala Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu
485 490 495

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
500 505 510

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
515 520 525

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
530 535 540

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
545 550 555 560

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
565 570 575

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
580 585 590

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
595 600 605

<210> 230

<211> 1815

<212> DNA

<213> Artificial Sequence

<220>

<223> 14B3 Fab-IL2 qm-Fab (heavy chain cytokine fusion construct)

<400> 230

gaggtgcagc tgctcgaaag cggcggagga ctggtgcagc ctggcggcag cctgagactg 60

tcttgcgccg ccagcggctt caccttcagc agctacgcca tgagctgggt ccgccaggcc 120

cctggcaagg gactggaatg ggtgtccgcc atcctggcct ctggcgccat cacctactac 180

gccgacagcg tgaagggccg gttcaccatc agccgggaca acagcaagaa caccctgtac 240

ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcgc caagggatgg 300

ttcggcggct tcaactactg gggacagggc accctgggtca cagtgtccag cgctagcacc 360

aagggaccca gcgtgttccc cctggccccc agcagcaaga gcacatctgg cggaacagcc 420

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gccctgggct gcctggtcaa agactacttc cccgagcccg tgaccgtgtc ctggaacagc      480
ggagccctga ccagcggcgt gcacaccttt ccagccgtgc tgcagagcag cggcctgtac      540
agcctgagca gcggtggtcac cgtgcctagc tctagcctgg gcacccagac ctacatctgc      600
aacgtgaacc acaagcccag caacaccaag gtggacaaga aggtggaacc caagagctgc      660
gactccggcg gaggcggatc tggcgggtgga ggctccggag gcggaggcgc tcctgccagc      720
agctccacca agaaaacca gctccagctg gaacatctgc tgctggatct gcagatgatc      780
ctgaacggca tcaacaacta caagaacccc aagctgaccc ggatgctgac cgccaagtgc      840
gccatgcccc agaaggccac cgaactgaaa catctgcagt gcctggaaga ggaactgaag      900
cctctggaag aggtgctgaa cggcgcccag agcaagaact tccacctgag gcccagggac      960
ctgatcagca acatcaacgt gatcgtgctg gaactgaagg gcagcgagac aaccttcatg     1020
tgcgagtacg ccgacgagac agccaccatc gtggaatttc tgaaccggtg gatcaccttc     1080
gccagagca tcatcagcac cctgacaagc ggaggcggcg gatccggcgg aggcggatct     1140
ggcggaggag gcgaggtcca gctgctcgaa agcggcggag gactggtgca gcctggcggc     1200
agcctgagac tgtcttgccg cgccagcggc ttcaccttca gcagctacgc catgagctgg     1260
gtccgccagg cccctggcaa gggactggaa tgggtgtccg ccatcctggc ctctggcgcc     1320
atcacctact acgccgacag cgtgaagggc cggttcacca tcagccggga caacagcaag     1380
aacaccctgt acctgcagat gaacagcctg cgggccgagg acaccgccgt gtactactgc     1440
gccaagggat ggttcggcgg cttcaactac tggggacagg gcaccctggt cacagtgtcc     1500
agcggcagca ccaagggccc cagcgtgttc cccctggccc ccagcagcaa gagcacatct     1560
ggcggaaacag ccgccctggg ctgcctggtc aaagactact tccccgagcc cgtgaccgtg     1620
tcctggaaca gcggagccct gaccagcggc gtgcacacct ttccagccgt gctgcagagc     1680
agcggcctgt acagcctgag cagcgtggtc accgtgccta gctctagcct gggcacccag     1740
acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggaa     1800
cccaagagct gcgac                                     1815

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<210> 231
 <211> 215
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 3F2 light chain

<400> 231

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
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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> 232
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> 3F2 light chain

<400> 232
gagatcgtgc tgaccagtc 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

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ccctccgacg agcagctgaa gtccggcacc gcctccgtcg tgtgcctgct gaacaacttc	420
tacccccgcg aggccaaggt gcagtggaag gtggacaacg ccctgcagtc cggcaactcc	480
caggaatccg tcaccgagca ggactccaag gacagcacct actccctgtc ctccaccctg	540
accctgtcca aggccgacta cgagaagcac aaggtgtacg cctgcgaagt gacccaccag	600
ggcctgtcca gccccgtgac caagtccttc aaccggggcg agtgc	645

<210> 233
 <211> 215
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 4G8 light chain

<400> 233

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

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

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

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

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

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

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

eo1f-seq1

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> 234
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> 4G8 light chain

<400> 234
gagatcgtgc tgaccagtc ccccggcacc ctgtctctga gccctggcga gagagccacc 60
ctgtcctgca gagcctccca gtccgtgtcc cggctcctacc tcgcctggta tcagcagaag 120
cccggccagg cccctcggct gctgatcatc ggcgcctcta ccagagccac cggcatccct 180
gaccggttct ccggctctgg ctccggcacc gacttcaccc tgaccatctc ccggctggaa 240
cccgaggact tcgccgtgta ctactgccag cagggccagg tcatccctcc cacctttggc 300
cagggcacca aggtggaaat caagcgtacg gtggccgctc cctccgtgtt catcttccca 360
ccctccgacg agcagctgaa gtccggcacc gcctccgctg tgtgcctgct gaacaacttc 420
tacccccgcg aggccaaagg gcagtggaag gtggacaacg ccctgcagtc cggcaactcc 480
caggaatccg tcaccgagca ggactccaag gacagcacct actccctgtc ctccaccctg 540
accctgtcca aggccgacta cgagaagcac aaggtgtacg cctgcgaagt gaccaccag 600
ggcctgtcca gccccgtgac caagtccttc aaccggggcg agtgc 645

<210> 235
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> 3D9 light chain

<400> 235

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
Page 145

								eolf-seq1																
65				70								75								80				
Pro	Glu	Asp	Phe	Ala ₈₅	Val	Tyr	Tyr	Cys	Gln ₉₀	Gln	Gly	Gln	Leu	Ile ₉₅	Pro									
Pro	Thr	Phe	Gly ₁₀₀	Gln	Gly	Thr	Lys	Val ₁₀₅	Glu	Ile	Lys	Arg	Thr ₁₁₀	Val	Ala									
Ala	Pro	Ser ₁₁₅	Val	Phe	Ile	Phe	Pro ₁₂₀	Pro	Ser	Asp	Glu	Gln ₁₂₅	Leu	Lys	Ser									
Gly	Thr ₁₃₀	Ala	Ser	Val	Val	Cys ₁₃₅	Leu	Leu	Asn	Asn	Phe ₁₄₀	Tyr	Pro	Arg	Glu									
Ala ₁₄₅	Lys	Val	Gln	Trp	Lys ₁₅₀	Val	Asp	Asn	Ala	Leu ₁₅₅	Gln	Ser	Gly	Asn	Ser ₁₆₀									
Gln	Glu	Ser	Val	Thr ₁₆₅	Glu	Gln	Asp	Ser	Lys ₁₇₀	Asp	Ser	Thr	Tyr	Ser ₁₇₅	Leu									
Ser	Ser	Thr	Leu ₁₈₀	Thr	Leu	Ser	Lys	Ala ₁₈₅	Asp	Tyr	Glu	Lys	His ₁₉₀	Lys	Val									
Tyr	Ala	Cys ₁₉₅	Glu	Val	Thr	His	Gln ₂₀₀	Gly	Leu	Ser	Ser	Pro ₂₀₅	Val	Thr	Lys									
Ser	Phe ₂₁₀	Asn	Arg	Gly	Glu	Cys ₂₁₅																		

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt

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645

<210> 237
 <211> 215
 <212> PRT
 <213> Artificial sequence

<220>
 <223> 2F11 light chain

<400> 237

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

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

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

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

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

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

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

eolf-seql

<210> 238
 <211> 645
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 2F11 light chain

<400> 238
 gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
 ctctcttgca gggccagtca gagggttagc agcagctact tagcctggta ccagcagaaa 120
 cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180
 gacaggttca gtggcagtggt atccgggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagtgtta ttactgtcag caggggtcagt atactcccc cacgttcggc 300
 caggggacca aagtggaaat caaacgtacg gtggctgcac catctgtctt catcttcccg 360
 ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420
 tatcccagag aggccaaagt acagtggag gtggataacg cctccaatc gggtaactcc 480
 caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540
 acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt caccatcag 600
 ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 645

<210> 239
 <211> 215
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 4B3 light chain

<400> 239

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

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

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

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

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

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

Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
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eolf-seql

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> 240
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> 4B3 light chain

<400> 240
gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcttgca gggccagtca gagtgttagc agcaattact tagcctggta ccagcagaaa 120
cctggccagg ctcccaggct cctcatctat ggcgcctaca tcagggccac tggcatccca 180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgtg ttactgtcag caggggtcagg ttattccccc tacgttcggc 300
caggggacca aagtggaaat caaacgtacg gtggctgcac catctgtctt catcttcccg 360
ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420
tatcccagag aggccaaagt acagtggaag gtggataacg cctccaatc gggtaactcc 480
caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540
acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600
ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 645

<210> 241
<211> 613
<212> PRT
<213> Artificial Sequence

eo1f-seq1

<220>

<223> 2B10 Fab-IL2 qm-Fab (heavy chain cytokine fusion construct)

<400> 241

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 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ala Pro Ala Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
245 250 255

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Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
 260 265 270
 Asn Pro Lys Leu Thr Arg Met Leu Thr Ala Lys Phe Ala Met Pro Lys
 275 280 285
 Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
 290 295 300
 Pro Leu Glu Glu Val Leu Asn Gly Ala Gln Ser Lys Asn Phe His Leu
 305 310 315 320
 Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
 325 330 335
 Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
 340 345 350
 Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
 355 360 365
 Ile Ser Thr Leu Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 370 375 380
 Gly Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys
 385 390 395 400
 Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr
 405 410 415
 Phe Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly
 420 425 430
 Leu Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr
 435 440 445
 Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr
 450 455 460
 Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
 465 470 475 480
 Val Tyr Tyr Cys Ala Arg Leu Tyr Gly Tyr Ala Tyr Tyr Gly Ala Phe
 485 490 495
 Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
 500 505 510
 Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
 515 520 525

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Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
530 535 540

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
545 550 555 560

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

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
580 585 590

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
595 600 605

Pro Lys Ser Cys Asp
610

<210> 242
<211> 1839
<212> DNA
<213> Artificial Sequence

<220>
<223> 2B10 Fab-IL2 qm-Fab (heavy chain cytokine fusion construct)

<400> 242
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
tcagctagca ccaagggccc atcgggtcttc cccctggcac cctcctccaa gagcacctct 420
ggggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacgggtg 480
tcgtggaaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540
tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcaccag 600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggataa gaaagttgag 660
cccaaactct gtgactccgg cggaggaggg agcggcggag gtggctccgg aggtggcgga 720
gcacctgcct caagttctac aaagaaaaca cagctacaac tggagcattt actgctggat 780
ttacagatga ttttgaatgg aattaataat tacaagaatc ccaaactcac caggatgctc 840
acagccaagt ttgccatgcc caagaaggcc acagaactga aacatcttca gtgtctagaa 900
gaagaactca aacctctgga ggaagtgcta aatggcgctc aaagcaaaaa ctttactta 960
agaccaggg acttaatcag caatatcaac gtaatagttc tggaactaaa gggatctgaa 1020

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acaacattca tgtgtgaata tgctgatgag acagcaacca ttgtagaatt tctgaacaga	1080
tggattacct ttgcccaaag catcatctca aactgactt ccggcggagg aggatccggc	1140
ggaggtggct ctggcgggtg cggacaggtg caattggtgc agtctggggc tgaggtgaag	1200
aagcctgggt cctcggtgaa ggtctcctgc aaggcctccg gaggcacatt cagcagctac	1260
gctataagct ggggtgcgaca ggcccctgga caagggctcg agtggatggg agggatcatc	1320
cctatctttg gtacagcaaa ctacgcacag aagttccagg gcaggggtcac cattactgca	1380
gacaaatcca cgagcacagc ctacatggag ctgagcagcc tgagatctga ggacaccgcc	1440
gtgtattact gtgcgagact gtacggttac gcttactacg gtgcttttga ctactggggc	1500
caagggacca ccgtgaccgt ctctcagct agcaccaagg gcccatcggc cttccccctg	1560
gcaccctcct ccaagagcac ctctgggggc acagcggccc tgggctgcct ggtcaaggac	1620
tacttccccg aaccggtgac ggtgtcgtgg aactcaggcg ccctgaccag cggcgtgcac	1680
accttccccg ctgtcctaca gtcctcagga ctctactccc tcagcagcgt ggtgaccgtg	1740
ccctccagca gcttgggcac ccagacctac atctgcaacg tgaatcacia gccagcaac	1800
accaaggtgg ataagaaagt tgagcccaaa tcttgtgac	1839

<210> 243
 <211> 613
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> C3B6 Fab-IL2 qm-Fab (heavy chain cytokine fusion construct)
 <400> 243

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

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

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

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

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
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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	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly
225					230					235					240
Ala	Pro	Ala	Ser	Ser	Ser	Thr	Lys	Lys	Thr	Gln	Leu	Gln	Leu	Glu	His
				245					250					255	
Leu	Leu	Leu	Asp	Leu	Gln	Met	Ile	Leu	Asn	Gly	Ile	Asn	Asn	Tyr	Lys
			260					265					270		
Asn	Pro	Lys	Leu	Thr	Arg	Met	Leu	Thr	Ala	Lys	Phe	Ala	Met	Pro	Lys
		275					280					285			
Lys	Ala	Thr	Glu	Leu	Lys	His	Leu	Gln	Cys	Leu	Glu	Glu	Glu	Leu	Lys
	290					295					300				
Pro	Leu	Glu	Glu	Val	Leu	Asn	Gly	Ala	Gln	Ser	Lys	Asn	Phe	His	Leu
305					310					315					320
Arg	Pro	Arg	Asp	Leu	Ile	Ser	Asn	Ile	Asn	Val	Ile	Val	Leu	Glu	Leu
				325					330					335	
Lys	Gly	Ser	Glu	Thr	Thr	Phe	Met	Cys	Glu	Tyr	Ala	Asp	Glu	Thr	Ala
			340					345					350		
Thr	Ile	Val	Glu	Phe	Leu	Asn	Arg	Trp	Ile	Thr	Phe	Ala	Gln	Ser	Ile
	355						360					365			
Ile	Ser	Thr	Leu	Thr	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
	370					375					380				
Gly	Gly	Gly	Gly	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys

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tcctgcaagg	cctccggagg	cacattcagc	agctacgcta	taagctgggt	gcgacaggcc	120
cctggacaag	ggctcgagtg	gatgggagct	atcatcccga	tccttggtat	cgaaaactac	180
gcacagaagt	tccagggcag	ggtcaccatt	actgcagaca	aatccacgag	cacagcctac	240
atggagctga	gcagcctgag	atctgaggac	accgccgtgt	attactgtgc	gagactgtac	300
ggttacgctt	actacggtgc	ttttgactac	tggggccaag	ggaccaccgt	gaccgtctcc	360
tcagctagca	ccaagggccc	atcggctctt	cccctggcac	cctcctccaa	gagcacctct	420
gggggcacag	cggccctggg	ctgcctgggt	aaggactact	tccccgaacc	ggtgacggtg	480
tcgtggaact	caggcgccct	gaccagcggc	gtgcacacct	tcccggtgt	cctacagtcc	540
tcaggactct	actccctcag	cagcgtgggt	accgtgccct	ccagcagctt	gggcacccag	600
acctacatct	gcaacgtgaa	tcacaagccc	agcaacacca	aggtggataa	gaaagttgag	660
cccaaattct	gtgactccgg	cggaggaggg	agcggcggag	gtggctccgg	aggtggcgga	720
gcacctgcct	caagttctac	aaagaaaaca	cagctacaac	tggagcattt	actgctggat	780
ttacagatga	ttttgaatgg	aattaataat	tacaagaatc	ccaaactcac	caggatgctc	840
acagccaagt	ttgccatgcc	caagaaggcc	acagaactga	aacatcttca	gtgtctagaa	900
gaagaactca	aacctctgga	ggaagtgcta	aatggcgctc	aaagcaaaaa	ctttcactta	960
agaccagggg	acttaatcag	caatatcaac	gtaatagttc	tggaaactaaa	gggatctgaa	1020
acaacattca	tgtgtgaata	tgtgatgag	acagcaacca	ttgtagaatt	tctgaacaga	1080
tggattacct	ttgccccaaag	catcatctca	acactgactt	ccggcggagg	aggatccggc	1140
ggaggtggct	ctggcggtgg	cggacagggt	caattgggtgc	agtctggggc	tgaggtgaag	1200
aagcctgggt	cctcggtgaa	ggtctcctgc	aaggcctccg	gaggcacatt	cagcagctac	1260
gctataagct	gggtgcgaca	ggccccctgga	caagggctcg	agtggatggg	agctatcatc	1320
ccgatccttg	gtatcgcaaa	ctacgcacag	aagttccagg	gcagggtcac	cattactgca	1380
gacaaatcca	cgagcacagc	ctacatggag	ctgagcagcc	tgagatctga	ggacaccgcc	1440
gtgtattact	gtgcgagact	gtacggttac	gcttactacg	gtgcttttga	ctactggggc	1500
caagggacca	ccgtgaccgt	ctcctcagct	agcaccaagg	gcccacgggt	cttccccctg	1560
gcaccctcct	ccaagagcac	ctctgggggc	acagcggccc	tgggctgcct	ggtcaaggac	1620
tacttccccg	aaccggtgac	ggtgtcgtgg	aactcaggcg	ccctgaccag	cggcgtgcac	1680
accttccccg	ctgtcctaca	gtcctcagga	ctctactccc	tcagcagcgt	ggtgaccgtg	1740
ccctccagca	gcttgggcac	ccagacctac	atctgcaacg	tgaatcacia	gccagcaac	1800
accaaggtgg	ataagaaagt	tgagcccaaa	tcttgtgac			1839

<210> 245
 <211> 613
 <212> PRT
 <213> Artificial Sequence

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<220>

<223> 6A12 Fab-IL2 qm-Fab (heavy chain cytokine fusion construct)

<400> 245

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

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

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

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

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

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

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

Gln Gly Thr Thr Val Thr Val Ser Ser 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 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ala Pro Ala Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
245 250 255

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Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
 260 265 270
 Asn Pro Lys Leu Thr Arg Met Leu Thr Ala Lys Phe Ala Met Pro Lys
 275 280 285
 Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
 290 295 300
 Pro Leu Glu Glu Val Leu Asn Gly Ala Gln Ser Lys Asn Phe His Leu
 305 310 315 320
 Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
 325 330 335
 Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
 340 345 350
 Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
 355 360 365
 Ile Ser Thr Leu Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 370 375 380
 Gly Gly Gly Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys
 385 390 395 400
 Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr
 405 410 415
 Phe Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly
 420 425 430
 Leu Glu Trp Met Gly Val Ile Ile Pro Ile Leu Gly Thr Ala Asn Tyr
 435 440 445
 Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr
 450 455 460
 Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
 465 470 475 480
 Val Tyr Tyr Cys Ala Arg Leu Tyr Gly Tyr Ala Tyr Tyr Gly Ala Phe
 485 490 495
 Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
 500 505 510
 Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
 515 520 525

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Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
530 535 540

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
545 550 555 560

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

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
580 585 590

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
595 600 605

Pro Lys Ser Cys Asp
610

<210> 246
<211> 1839
<212> DNA
<213> Artificial Sequence

<220>
<223> 6A12 Fab-IL2 qm-Fab (heavy chain cytokine fusion construct)

<400> 246	
cagggtgcaat tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc	60
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
tcagctagca ccaagggccc atcgggtctt cccctggcac cctcctccaa gagcacctct	420
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacgggtg	480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc	540
tcaggactct actccctcag cagcgtgggt accgtgccct ccagcagctt gggcacccag	600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggataa gaaagttgag	660
cccaaactct gtgactccgg cggaggaggg agcggcggag gtggctccgg aggtggcgga	720
gcacctgcct caagttctac aaagaaaaca cagctacaac tggagcattt actgctggat	780
ttacagatga ttttgaatgg aattaataat tacaagaatc ccaaactcac caggatgctc	840
acagccaagt ttgccatgcc caagaaggcc acagaactga aacatcttca gtgtctagaa	900
gaagaactca aacctctgga ggaagtgcta aatggcgctc aaagcaaaaa ctttcactta	960
agaccaggg acttaatcag caatatcaac gtaatagttc tggaactaaa gggatctgaa	1020

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acaacattca tgtgtgaata tgctgatgag acagcaacca ttgtagaatt tctgaacaga 1080
 tggattacct ttgcccaaag catcatctca aactgactt ccggcggagg aggatccggc 1140
 ggaggtggct ctggcgggtg cggacaggtg caattggtgc agtctggggc tgaggtgaag 1200
 aagcctgggt cctcggtgaa ggtctcctgc aaggcctccg gaggcacatt cagcagctat 1260
 gctataagct ggggtgcgaca ggcccctgga caagggctcg agtggatggg agtgatcatc 1320
 cctatccttg gtaccgcaaa ctacgcacag aagtccagg gcagggtcac cattactgca 1380
 gacaaatcca cgagcacagc ctacatggag ctgagcagcc tgagatctga ggacaccgcc 1440
 gtgtattact gtgcgagact gtacggttac gcttactacg gtgcttttga ctactggggc 1500
 caagggacca ccgtgaccgt ctctcagct agcaccaagg gcccatcggc cttccccctg 1560
 gcaccctcct ccaagagcac ctctgggggc acagcggccc tgggctgcct ggtcaaggac 1620
 tacttccccg aaccggtgac ggtgtcgtgg aactcaggcg ccctgaccag cggcgtgcac 1680
 accttccccg ctgtcctaca gtcctcagga ctctactccc tcagcagcgt ggtgaccgtg 1740
 ccctccagca gcttgggcac ccagacctac atctgcaacg tgaatcacia gccagcaac 1800
 accaaggtgg ataagaaagt tgagcccaaa tcttgtgac 1839

<210> 247
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 2B10 light chain
 <400> 247

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
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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> 248
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> 2B10 light chain

<400> 248
gatatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtcggaga ccgggtcacc 60
atcacctgcc gggcaagtca gggcattaga aatgatttag gctggtacca gcagaagcca 120
gggaaagccc ctaagcgcct gatctatgct gcatccagtt tgacagagtgg cgtcccatca 180
aggttcagcg gcagtggatc cgggacagag ttcactctca ccatcagcag cttgcagcct 240
gaagattttg ccacctatta ctgcttgagc aatgggtctgc agcccgcgac gtttgccag 300
ggcaccaaag tcgagatcaa gcgtacggtg gctgcacat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttggtg 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

<210> 249
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> D1A2 light chain

<400> 249

eolf-seql

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

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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 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> 250
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> D1A2 light chain

<400> 250
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60

eolf-seq1

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gggaaagccc ctaagcgcct gatctatgat gcttacagct tgcagagtgg cgtcccatca	180
aggttcagcg gcggtggatc cgggacagag ttcaacttca 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

<210> 251
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> o7D8 light chain

<400> 251

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			

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	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
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

eo1f-seq1

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

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

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

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

Tyr Cys Thr Thr Tyr Gly Asn Tyr Val Gly His Tyr Phe Asp His Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125

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

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

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
180 185 190

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

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
210 215 220

Cys Asp Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
225 230 235 240

Gly Ala Pro Ala Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu
245 250 255

His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr
260 265 270

Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Ala Lys Phe Ala Met Pro
275 280 285

Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu
290 295 300

eo1f-seq1

Lys Pro Leu Glu Glu Val Leu Asn Gly Ala Gln Ser Lys Asn Phe His
 305 310 315 320
 Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu
 325 330 335
 Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr
 340 345 350
 Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser
 355 360 365
 Ile Ile Ser Thr Leu Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 370 375 380
 Ser Gly Gly Gly Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
 385 390 395 400
 Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
 405 410 415
 Thr Phe Ser Asn Tyr Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys
 420 425 430
 Gly Leu Glu Trp Val Ala Glu Ile Arg Leu Lys Ser Asn Asn Phe Gly
 435 440 445
 Arg Tyr Tyr Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
 450 455 460
 Asp Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu
 465 470 475 480
 Asp Thr Ala Val Tyr Tyr Cys Thr Thr Tyr Gly Asn Tyr Val Gly His
 485 490 495
 Tyr Phe Asp His Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
 500 505 510
 Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
 515 520 525
 Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
 530 535 540
 Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
 545 550 555 560
 Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
 565 570 575

eolf-seq1

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
580 585 590

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
595 600 605

Val Glu Pro Lys Ser Cys Asp
610 615

<210> 254
<211> 1845
<212> DNA
<213> Artificial Sequence

<220>
<223> MHLG1 Fab-IL2 qm-Fab (heavy chain cytokine fusion construct)

<400> 254
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tcctgtgcag cctccggatt cacatttagc aactattgga tgaactgggt gcggcaggct 120
cctggaaagg gcctcgagtg ggtggccgag atcagattga aatccaataa cttcgggaaga 180
tattacgctg caagcgtgaa gggccggttc accatcagca gagatgattc caagaacacg 240
ctgtacctgc agatgaacag cctgaagacc gaggatacgg ccgtgtatta ctgtaccaca 300
tacggcaact acgttgggca ctacttcgac cactggggcc aagggaccac cgtcaccgtc 360
tccagtgcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 420
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 480
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca cttcccggc tgtcctacag 540
tcctcaggac tctactcct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 600
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaagggtgga taagaaagtt 660
gagcccaaat cttgtgactc cggcggagga gggagcggcg gaggtggctc cggagggtggc 720
ggagcacctg cctcaagttc taaaagaaa acacagctac aactggagca tttactgctg 780
gatttacaga tgattttgaa tggaattaat aattacaaga atcccaaact caccaggatg 840
ctcacagcca agtttgccat gcccaagaag gccacagaac tgaaacatct tcagtgtcta 900
gaagaagaac tcaaacctct ggaggaagtg ctaaatggcg ctcaaagcaa aaactttcac 960
ttaagacca gggacttaat cagcaatatc aacgtaatag ttctggaact aaagggatct 1020
gaaacaacat tcatgtgtga atatgtgtat gagacagcaa ccattgtaga atttctgaac 1080
agatggatta cttttgcca aagcatcatc tcaacactga cttccggcgg aggaggatcc 1140
ggcggagggtg gctctggcgg tggcggagaa gtgcagctgg tggagtctgg aggaggcttg 1200
gtcaagcctg gcgggtccct gcggctctcc tgtgcagcct ccggattcac atttagcaac 1260
tattggatga actgggtgcg gcaggctcct ggaaagggcc tcgagtgggt ggccgagatc 1320
agattgaaat ccaataactt cggaagatat tacgctgcaa gcgtgaaggg ccggttcacc 1380

eof-seq1

atcagcagag atgattccaa gaacacgctg tacctgcaga tgaacagcct gaagaccgag 1440
gatacggccg tgtattactg taccacatac ggcaactacg ttgggcacta cttcgaccac 1500
tggggccaag ggaccaccgt caccgtctcc agtgctagca ccaagggccc atcgggtcttc 1560
cccctggcac cctcctccaa gagcacctct gggggcacag cggccctggg ctgcctggtc 1620
aaggactact tccccgaacc ggtgacggtg tcgtggaact caggcgccct gaccagcggc 1680
gtgcacacct tcccggtgtg cctacagtcc tcaggactct actccctcag cagcgtggtg 1740
accgtgccct ccagcagctt gggcaccag acctacatct gcaacgtgaa tcacaagccc 1800
agcaacacca aggtggataa gaaagttgag cccaaatctt gtgac 1845

<210> 255
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> kv9 light chain

<400> 255

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

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

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

Tyr Ser Ala Ser Tyr Arg Tyr Thr 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 Gln Gln Tyr Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gly 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
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	eolf-seq1							
	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>	256							
<211>	642							
<212>	DNA							
<213>	Artificial Sequence							
<220>								
<223>	KV9 light chain							
<400>	256							
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gggcaggcac ctaggcctct gatctattcg gcatcctacc ggtaccttg cgccccatca	180							
aggttcagcg gcagtggatc cgggacagag ttactcttca caatctcaag cctgcaacct	240							
gaagatttcg caacttacta ctgtcaacag tacaatagtt accctctgac gttcggcgga	300							
ggtaccaagg tggagatcaa gcgtacggtg gctgcacCAT ctgtcttcat cttcccGCCA	360							
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat	420							
cccagagagg ccaaagtaca gtggaaggTg gataacGccc tccaatCggg taactCCCag	480							
gagagtgtCa cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg	540							
ctgagCAAag cagactacGa gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc	600							
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagT gt	642							
<210>	257							
<211>	615							
<212>	PRT							
<213>	Artificial Sequence							
<220>								
<223>	MHLG Fab-IL2 qm-Fab (heavy chain cytokine fusion construct)							
<400>	257							
Glu Val Gln Leu Val 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 Asn Tyr								
20 25 30								
Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val								
35 40 45								

eo1f-seq1

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

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

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

Tyr Cys Thr Thr Tyr Gly Asn Tyr Val Gly His Tyr Phe Asp His Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125

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

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

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
180 185 190

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

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
210 215 220

Cys Asp Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
225 230 235 240

Gly Ala Pro Ala Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu
245 250 255

His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr
260 265 270

Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Ala Lys Phe Ala Met Pro
275 280 285

Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu
290 295 300

Lys Pro Leu Glu Glu Val Leu Asn Gly Ala Gln Ser Lys Asn Phe His
305 310 315 320

eolf-seq1

Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu
325 330 335

Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr
340 345 350

Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser
355 360 365

Ile Ile Ser Thr Leu Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
370 375 380

Ser Gly Gly Gly Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
385 390 395 400

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
405 410 415

Thr Phe Ser Asn Tyr Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys
420 425 430

Gly Leu Glu Trp Val Ala Glu Ile Arg Leu Lys Ser Asn Asn Phe Gly
435 440 445

Arg Tyr Tyr Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
450 455 460

Asp Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu
465 470 475 480

Asp Thr Ala Val Tyr Tyr Cys Thr Thr Tyr Gly Asn Tyr Val Gly His
485 490 495

Tyr Phe Asp His Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
500 505 510

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
515 520 525

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
530 535 540

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
545 550 555 560

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
565 570 575

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
580 585 590

eo1f-seq1

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
595 600 605

Val Glu Pro Lys Ser Cys Asp
610 615

<210> 258

<211> 1845

<212> DNA

<213> Artificial Sequence

<220>

<223> MHLG Fab-IL2 qm-Fab (heavy chain cytokine fusion construct)

<400> 258

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cctggaaagg gcctcgagtg ggtggccgag atcagattga aatccaataa cttcgggaaga	180
tattacgctg caagcgtgaa gggccggttc accatcagca gagatgattc caagaacacg	240
ctgtacctgc agatgaacag cctgaagacc gaggatacgg ccgtgtatta ctgtaccaca	300
tacggcaact acgttgggca ctacttcgac cactggggcc aagggaccac cgtcaccgtc	360
tccagtgcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc	420
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg	480
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag	540
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc	600
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaagggtgga taagaaagtt	660
gagcccaaat cttgtgactc cggcggagga gggagcggcg gaggtggctc cggaggtggc	720
ggagcacctg cctcaagttc taaaagaaa acacagctac aactggagca tttactgctg	780
gatttacaga tgattttgaa tggaattaat aattacaaga atcccaaact caccaggatg	840
ctcacagcca agtttgccat gcccaagaag gccacagaac tgaaacatct tcagtgtcta	900
gaagaagaac tcaaacctct ggaggaagtg ctaaattggcg ctcaaagcaa aaactttcac	960
ttaagacca gggacttaat cagcaatatc aacgtaatag ttctggaact aaagggatct	1020
gaaacaacat tcatgtgtga atatgctgat gagacagcaa ccattgtaga atttctgaac	1080
agatggatta cctttgcca aagcatcatc tcaacactga cttccggcgg aggaggatcc	1140
ggcggagggtg gctctggcgg tggcggagaa gtgcagctgg tggagtctgg aggaggcttg	1200
gtccagcctg gcgggtccct gcggctctcc tgtgcagcct ccggattcac atttagcaac	1260
tattggatga actgggtgcg gcaggctcct ggaaagggcc tcgagtgggt ggccgagatc	1320
agattgaaat ccaataactt cggaagatat tacgctgcaa gcgtgaaggg ccggttcacc	1380
atcagcagag atgattccaa gaacacgctg tacctgcaga tgaacagcct gaagaccgag	1440
gatacggccg tgtattactg taccacatac ggcaactacg ttgggcacta cttcgaccac	1500

eolf-seq1

tggggccaag ggaccaccgt caccgtctcc agtgctagca ccaagggccc atcgggtcttc	1560
cccctggcac cctcctccaa gagcacctct gggggcacag cggccctggg ctgcctggtc	1620
aaggactact tccccgaacc ggtgacggtg tcgtggaact caggcgccct gaccagcggc	1680
gtgcacacct tcccggctgt cctacagtcc tcaggactct actccctcag cagcgtggtg	1740
accgtgccct ccagcagctt gggcacccag acctacatct gcaacgtgaa tcacaagccc	1800
agcaacacca aggtggataa gaaagttgag cccaaatctt gtgac	1845

<210> 259
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KV1 light chain

<400> 259

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

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

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

Tyr	Ser	Ala	Ser	Tyr	Arg	Tyr	Thr	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	Gln	Gln	Tyr	Asn	Ser	Tyr	Pro	Leu
				85					90					95	

Thr	Phe	Gly	Gly	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
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

eo1f-seq1

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> 260
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> kv1 light chain

<400> 260
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atcacctgca gggccagtca gaatgtggat actaacttag cttggtacca gcagaagcca 120
gggaaagcac ctaagctcct gatctattcg gcatcctacc gttacactgg cgtcccatca 180
aggttcagcg gcagtggatc cgggacagag ttcaacttca caatctcaag cctgcaacct 240
gaagatttcg caacttacta ctgtcaacag tacaatagtt accctctgac gttcggcgga 300
ggtaccaagg tggagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 261
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> kv7 light chain

<400> 261

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

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

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

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

eolf-seq1

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 Gln Gln Tyr Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gly 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> 262
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> KV7 light chain

<400> 262
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atcacctgca aggccagtca gaatgtggat actaacgtgg cttggtacca gcagaagcca 120
gggaaagcac ctaagcctct gatctattcg gcatcctacc ggtacactgg cgtcccatca 180
aggttcagcg gcagtggatc cgggacagag ttactctca caatctcaag cctgcaacct 240
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ggtaccaagg tggagatcaa gcgtacgggtg gctgcacat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

eolf-seq1

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
 ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 263
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> leader sequence

<400> 263

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

Ala His Ser

<210> 264
 <211> 57
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> leader sequence

<400> 264
 atggactgga cctggagaat cctcttcttg gtggcagcag ccacaggagc ccactcc 57

<210> 265
 <211> 57
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> leader sequence

<400> 265
 atggactgga cctggaggat cctcttcttg gtggcagcag ccacaggagc ccactcc 57

<210> 266
 <211> 22
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> leader sequence

<400> 266

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

Phe Pro Gly Ala Arg Cys
 20

<210> 267
 <211> 66
 <212> DNA

<213> Artificial Sequence

<220>

<223> leader sequence

<400> 267

atggacatga ggggtccccgc tcagctcctg ggcctcctgc tgctctgggt cccaggtgcc 60

aggtgt 66

<210> 268

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> leader sequence

<400> 268

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

Val His Ser

<210> 269

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> leader sequence

<400> 269

atgggatgga gctgtatcat cctcttcttg gtagcaacag ctaccgggtg gcattcc 57

<210> 270

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> leader sequence

<400> 270

atgggctggt cctgcatcat cctgtttctg gtggctaccg ccactggagt gcattcc 57

<210> 271

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> leader sequence

<400> 271

atgggctggt cctgcatcat cctgtttctg gtcgccacag ccaccggcgt gcactct 57

<210> 272

<211> 20

<212> PRT

eolf-seq1

<213> Artificial Sequence

<220>

<223> leader sequence

<400> 272

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
 1 5 10 15

Val Thr Asn Ser
 20

<210> 273

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> leader sequence

<400> 273

atgtacagga tgcaactcct gtcttgcatc gcactaagtc ttgcacttgt cacaacagt 60

<210> 274

<211> 466

<212> PRT

<213> Artificial Sequence

<220>

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

<400> 274

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly 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

eolf-seq1

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

eo1f-seq1

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

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

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

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

Gly Lys
465

<210> 275
<211> 1401
<212> DNA
<213> Artificial Sequence

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

<400> 275
atggacatga ggggtccccgc tcagctcctg ggcctcctgc tgctctgggt cccaggtgcc 60
aggtgtgcgg tgaatggcac ttcccagttc acatgcttct acaactcgag agccaacatc 120
tcctgtgtct ggagccaaga tggggctctg caggacactt cctgccaaagt 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
accacagat gcaacataag ctgggaaatc 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 gcccttggga aggacaccgg agctcaggac 720
aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc 780
ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 840
gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 900
gtggaggtgc ataatgcca gacaaagccg cgggaggagc agtacaacag cacgtaccgt 960
gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1020
aaggtctcca acaaagccct ccagcccc atcgagaaaa ccatctcaa agccaaaggg 1080
cagccccgag aaccacaggt gtgcaccctg ccccatccc gggatgagct gaccaagaac 1140

eolf-seq1

caggtcagcc tctcgtgcgc agtcaaaggc ttctatccca gcgacatcgc cgtggagtgg	1200
gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac	1260
ggctccttct tctcgtgag caagctcacc gtggacaaga gcaggtggca gcaggggaac	1320
gtctttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc	1380
tccctgtctc cgggtaaata a	1401

<210> 276
 <211> 492
 <212> PRT
 <213> Artificial Sequence

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

<400> 276

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

eo1f-seq1

Trp Asp His Ser Trp Thr Glu Gln Ser Val Asp Tyr Arg His Lys Phe
195 200 205

Ser Leu Pro Ser Val Asp Gly Gln Lys Arg Tyr Thr Phe Arg Val Arg
210 215 220

Ser Arg Phe Asn Pro Leu Cys Gly Ser Ala Gln His Trp Ser Glu Trp
225 230 235 240

Ser His Pro Ile His Trp Gly Ser Asn Thr Ser Lys Glu Asn Pro Phe
245 250 255

Leu Phe Ala Leu Glu Ala Gly Ala Gln Asp Lys Thr His Thr Cys Pro
260 265 270

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

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

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

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

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

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

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

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

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

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

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

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

eof-seq1

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> 277
<211> 1479
<212> DNA
<213> Artificial Sequence

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

<400> 277
atgttgaagc catcattacc attcacatcc ctcttattcc tgcagctgcc cctgctggga 60
gtggggctga acacgacaat tctgacgccc aatgggaatg aagacaccac agctgatttc 120
ttcctgacca ctatgccac tgactccctc agtgtttcca ctctgcccct cccagaggtt 180
cagtgttttg tgttcaatgt cgagtacatg aattgcactt ggaacagcag ctctgagccc 240
cagcctacca acctcactct gcattattgg tacaagaact cggataatga taaagtccag 300
aagtgcagcc actatctatt ctctgaagaa atcacttctg gctgtcagtt gcaaaaaaag 360
gagatccacc tctaccaaac atttgttggt cagctccagg acccacggga acccaggaga 420
caggccacac agatgctaaa actgcagaat ctggtgatcc cctgggctcc agagaaccta 480
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 ctgagcattg gagtgaatgg 720
agccaccaa tccactggg gagcaatact tcaaaagaga atcctttcct gtttgattg 780
gaagccggag ctgaggacaa aactcacaca tgcccaccgt gccagcacc tgaactcctg 840
gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 900
accctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 960
aactggtacg tggacggcgt ggagggtcat aatgccaaaga caaagccgcg ggaggagcag 1020
tacaacagca cgtaccgtgt ggtcagcgtc ctaccgtcc tgcaccagga ctggctgaat 1080
ggcaaggagt acaagtcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1140
atctccaaag ccaaagggca gccccgagaa ccacagggtgt acaccctgcc cccatgccgg 1200
gatgagctga ccaagaacca ggtcagcctg tggcgcctgg tcaaaggctt ctatcccagc 1260
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1320
cccgtgctgg actccgacgg ctcttcttc ctctacagca agctcaccgt ggacaagagc 1380
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1440
tacacgcaga agagcctctc cctgtctccg ggtaaata 1479

eo1f-seq1

<210> 278
 <211> 219
 <212> PRT
 <213> Artificial Sequence

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

<400> 278

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 279

eolf-seq1

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

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

<400> 279
atgggatgga gctgtatcat cctcttcttg gtagcaacag ctaccgggtg gcattccgag 60
ctctgtgacg atgacccgcc agagatccca cacgccacat tcaaagccat ggcctacaag 120
gaaggaacca tgttgaactg tgaatgcaag agagggttcc gcagaataaa aagcgggtca 180
ctctatatgc tctgtacagg aaactctagc cactcgtcct gggacaacca atgtcaatgc 240
acaagctctg ccactcggaa cacaacgaaa caagtgcacac ctcaacctga agaacagaaa 300
gaaaggaaaa ccacagaaat gcaaagtcca atgcagccag tggaccaagc gagccttcca 360
ggtcactgca gggaaacctcc accatgggaa aatgaagcca cagagagaat ttatcatttc 420
gtggtggggc agatggttta ttatcagtgc gtccagggat acagggctct acacagaggt 480
cctgctgaga gcgtctgcaa aatgaccac ggggaagaca ggtggacca gccccagctc 540
atatgcacag gtgtcgacga acagttatat tttcagggcg gctcaggcct gaacgacatc 600
ttcgaggccc agaagatcga gtggcacgag gctcgagctc accaccatca ccatcactga 660

<210> 280
<211> 473
<212> PRT
<213> Artificial Sequence

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

<400> 280

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

eo1f-seq1

Val Cys Trp Glu Glu Lys Gly Trp Arg Arg Val Lys Thr Cys Asp Phe
115 120 125

His Pro Phe Asp Asn Leu Arg Leu Val Ala Pro His Ser Leu Gln Val
130 135 140

Leu His Ile Asp Thr Gln Arg Cys Asn Ile Ser Trp Lys Val Ser Gln
145 150 155 160

Val Ser His Tyr Ile Glu Pro Tyr Leu Glu Phe Glu Ala Arg Arg Arg
165 170 175

Leu Leu Gly His Ser Trp Glu Asp Ala Ser Val Leu Ser Leu Lys Gln
180 185 190

Arg Gln Gln Trp Leu Phe Leu Glu Met Leu Ile Pro Ser Thr Ser Tyr
195 200 205

Glu Val Gln Val Arg Val Lys Ala Gln Arg Asn Asn Thr Gly Thr Trp
210 215 220

Ser Pro Trp Ser Gln Pro Leu Thr Phe Arg Thr Arg Pro Ala Asp Pro
225 230 235 240

Met Lys Glu Gly Ala Gln Asp Lys Thr His Thr Cys Pro Pro Cys Pro
245 250 255

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

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

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

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

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

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

eolf-seq1

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

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

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

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

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

Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470

<210> 281
<211> 1422
<212> DNA
<213> Artificial Sequence

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

<400> 281
atggacatga ggggtccccgc tcagctcctg ggcctcctgc tgctctgggt cccctcctg 60
ctgctctggt tcccagggtgc cagggtgtgca gtgaaaaact gttcccatct tgaatgcttc 120
tacaactcaa gagccaatgt ctcttgcattg tggagccattg aagaggctct gaatgtcaca 180
acctgccacg tccatgccaa gtcgaacctg cgacactgga acaaacctg tgagctaact 240
cttgtgaggc aggcattcctg ggcctgcaac ctgattcctg ggctcgttccc agagtccacg 300
tcaactgacct ccgtggacct ccttgacata aatgtgggtg gctgggaaga gaagggttgg 360
cgtagggtaa agacctgcga cttccatccc ttgacaacc ttcgcctggt ggccccctcat 420
tccctccaag ttctgcacat tgataccag agatgtaaca taagctggaa ggtctcccag 480
gtctctcact acattgaacc atacttgga tttgaggccc gtagacgtct tctggggcac 540
agctgggagg atgcatccgt attaacctc aagcagagac agcagtggct cttcttggag 600
atgctgatcc ctatgacctc atatgagggtc cagggtgagg tcaaagctca acgaaacaat 660
accgggacct ggagtccctg gagccagccc ctgacctttc ggacaaggcc agcagatccc 720
atgaaggagg gagctcagga caaaactcac acatgcccac cgtgcccagc acctgaactc 780
ctgggggggac cgtcagttct cctcttcccc ccaaaacca aggacaccct catgatctcc 840
cggacccttg aggtcacatg cgtggtggtg gacgtgagcc acgaagacct tgagggtcaag 900
ttcaactggt acgtggacgg cgtggagggtg cataatgcca agacaaagcc gcgggaggag 960
cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 1020

eolf-seq1

aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa	1080
accatctcca aagccaaagg gcagccccga gaaccacagg tgtgcaccct gcccccatcc	1140
cgggatgagc tgaccaagaa ccaggtcagc ctctcgtgcg cagtcaaagg cttctatccc	1200
agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg	1260
cctcccgtgc tggactccga cggctccttc ttcctcgtga gcaagctcac cgtggacaag	1320
agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcattgaggc tctgcacaac	1380
cactacacgc agaagagcct ctccctgtct ccgggtaaat ga	1422

<210> 282
 <211> 500
 <212> PRT
 <213> Artificial Sequence

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

<400> 282

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

Phe Pro Leu Leu Leu Trp Phe Pro Gly Ala Arg Cys Trp Ser Ser
 20 25 30

Lys Val Leu Met Ser Ser Ala Asn Glu Asp Ile Lys Ala Asp Leu Ile
 35 40 45

Leu Thr Ser Thr Ala Pro Glu His Leu Ser Ala Pro Thr Leu Pro Leu
 50 55 60

Pro Glu Val Gln Cys Phe Val Phe Asn Ile Glu Tyr Met Asn Cys Thr
 65 70 75 80

Trp Asn Ser Ser Ser Glu Pro Gln Ala Thr Asn Leu Thr Leu His Tyr
 85 90 95

Arg Tyr Lys Val Ser Asp Asn Asn Thr Phe Gln Glu Cys Ser His Tyr
 100 105 110

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

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

eo1f-seq1

Leu Glu Leu Arg Trp Lys Ser Arg His Ile Lys Glu Arg Cys Leu Gln
180 185 190

Tyr Leu Val Gln Tyr Arg Ser Asn Arg Asp Arg Ser Trp Thr Glu Leu
195 200 205

Ile Val Asn His Glu Pro Arg Phe Ser Leu Pro Ser Val Asp Glu Leu
210 215 220

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

Ser Ser Gln Gln Trp Ser Lys Trp Ser Gln Pro Val His Trp Gly Ser
245 250 255

His Thr Val Glu Glu Asn Pro Ser Leu Phe Ala Leu Glu Ala Gly Ala
260 265 270

Gln Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
275 280 285

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

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

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

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

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

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

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

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

eo1f-seq1

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

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

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

Ser Pro Gly Lys
500

<210> 283
<211> 1503
<212> DNA
<213> Artificial Sequence

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

<400> 283
atggacatga ggggtccccgc tcagctcctg ggcctcctgc tgctctggtt cccctcctg 60
ctgctctggt tcccagggtgc cagggtgttg agttccaagg tcctcatgtc cagtgcgaat 120
gaagacatca aagctgattt gatcctgact tctacagccc ctgaacacct cagtgtcctt 180
actctgcccc ttccagaggt tcagtgttt gtgttcaaca tagagtacat gaattgcact 240
tggaatagca gttctgagcc tcaggcaacc aacctcacgc tgcactatag gtacaaggta 300
tctgataata atacattcca ggagtgcagt cactatttgt tctccaaaga gattacttct 360
ggctgtcaga tacaaaaaga agatatccag ctctaccaga ctttgttgt ccagctccag 420
gacccccaga aaccccagag gcgagctgta cagaagctaa acctacagaa tcttgtgatc 480
ccacgggctc cagaaaatct aacactcagc aatctgagtg aatcccagct agagctgaga 540
tggaagagca gacatatata agaacgctgt ttacaatact tgggtgcagta ccggagcaac 600
agagatcgaa gctggacgga actaatagt aatcatgaac ctgattctc cctgcctagt 660
gtggatgagc tgaaacggta cacatttcgg gttcggagcc gctataacc aatctgtgga 720
agtttctaac agtggagtaa atggagccag cctgtccact gggggagtca tactgtagag 780
gagaatcctt ccttgtttgc actggaagct ggagctcagg acaaaactca cacatgccca 840
ccgtgcccag cacctgaact cctgggggga ccgtcagtct tcctcttccc cccaaaaccc 900
aaggacaccc tcatgatctc ccggacccct gaggtcacat gcgtggtggt ggacgtgagc 960
cacgaagacc ctgagggtcaa gttcaactgg tacgtggacg gcgtggaggt gcataatgcc 1020
aagacaaagc cgcgaggagga gcagtacaac agcacgtacc gtgtggtcag cgtcctcacc 1080
gtcctgcacc aggactggct gaatggcaag gagtacaagt gcaaggcttc caacaaagcc 1140
ctcccagccc ccatcgagaa aaccatctcc aaagccaaag ggcagccccg agaaccacag 1200
gtgtacaccc tgcccccatg ccgggatgag ctgaccaaga accaggtcag cctgtggtgc 1260

eolf-seq1

ctgggtcaaag gcttctatcc cagcgacatc gccgtggagt gggagagcaa tgggcagccg	1320
gagaacaact acaagaccac gcctcccgtg ctggactccg acggctcctt cttcctctac	1380
agcaagctca ccgtggacaa gagcaggtgg cagcagggga acgtcttctc atgctccgtg	1440
atgcatgagg ctctgcacaa ccactacacg cagaagagcc tctccctgtc tccgggtaaa	1500
tga	1503

<210> 284
 <211> 213
 <212> PRT
 <213> Artificial Sequence

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

<400> 284

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

eo1f-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> 285
<211> 642
<212> DNA
<213> Artificial Sequence

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

<400> 285
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ctgtgtctgt atgacccacc cgagggtcccc aatgccacat tcaaagccct ctctacaag 120
aacggcacca tcctaaactg tgaatgcaag agagggttcc gaagactaaa ggaattgggtc 180
tatatgcgtt gcttaggaaa ctcttgagagc 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 agagaggtcc tgctattagc 480
atctgcaaga tgaagtgtgg gaaaacgggg tggactcagc cccagctcac atgtgtcgac 540
gaacagttat attttcaggg cggtcagggc ctgaacgaca tcttcgaggc ccagaagatc 600
gagtggcacg aggtctgagc tcaccacat caccatcact ga 642

<210> 286
<211> 480
<212> PRT
<213> Artificial Sequence

<220>
<223> Cynomolgous IL-2R-beta-Fc(knob) fusion protein + Avi-tag

<400> 286

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

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
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															eolf-seql									
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													
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									

eolf-seql

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
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> 287
 <211> 1443
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Cynomolgous IL-2R-beta-Fc(knob) fusion protein + Avi-tag

<400>	287	
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	gtcaacggca cttcccgggt cacatgcttc tacaactcga gagccaacat ctctgtgtc	120
	tggagccaag atggggctct gcaggacact tcctgccaag tccacgcctg gccggacaga	180
	cggcgggtgga accaaacctg tgagctgctc cctgtgagtc aagcatcctg ggcctgcaac	240
	ctgatcctcg gaaccccgaga ttctcagaaa ctgaccgcag tggatatcgt caccctgagg	300
	gtgatgtgcc gtgaaggggt gcgatggagg atgatggcca tccaggactt caaaccttt	360
	gagaaccttc gcctgatggc ccccatctcc ctccaagtcg tccacgtgga gaccacaga	420
	tgcaacataa gctggaaaat ctcccaagcc tccactact ttgaaagaca cctggagttt	480
	gaggcccgga cgctgtcccc aggccacacc tgggaggagg cccccctgat gaccctcaag	540
	cagaagcagg aatggatctg cctggagacg ctacccccag acaccagta tgagtttcag	600
	gtgcgggtca agcctctgca aggcgagttc acgacctgga gccctggag ccagcccctg	660
	gccttcagga caaagcctgc agcccttggg aaggacaccg gagctcagga caaaactcac	720

eolf-seq1

acatgcccac cgtgcccagc acctgaactc ctgggggggac cgtcagtctt cctcttcccc	780
ccaaaaccca aggacaccct catgatctcc cggacccttg aggtcacatg cgtggtggtg	840
gacgtgagcc acgaagaccc tgagggtcaag 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 gcccccatgc cgggatgagc tgaccaagaa ccaggtcagc	1140
ctgtggtgcc tgggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat	1200
gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc	1260
ttcctctaca gcaagctcac cgtggacaag agcagggtggc agcaggggaa cgtcttctca	1320
tgctccgtga tgcattgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct	1380
ccgggtaaat ccggaggcct gaacgacatc ttcgagggcc agaagattga atggcacgag	1440
tga	1443

<210> 288
 <211> 489
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Cynomolgous IL-2R-gamma-Fc(hole) fusion protein
 <400> 288

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

eo1f-seq1

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

eo1f-seq1

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> 289
<211> 1470
<212> DNA
<213> Artificial Sequence

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

<400> 289
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aacacgacaa ttctgacgcc caatgggaat gaagacgcca caactgattt cttcctgacc 120
tctatgccca ctgactccct cagtgtttcc actctgcccc tcccagaggt tcagtgtttt 180
gtgttcaatg tcgagtacat gaattgcact tggaacagca gctctgagcc ccagcctacc 240
aacctcactc tgcattattg gtacaagaat tcggataatg ataaagtcca gaagtgcagc 300
cactatctat tctctgaaga aatcacttct ggctgtcagt tgcaaaaaaaaa ggagatccac 360
ctctaccaa cgtttgttgt tcagctccag gaccacggg aaccaggag acaggccaca 420
cagatgctaa aactgcagaa tctggtgatc ccctgggctc cggagaacct aacacttcgc 480
aaactgagt aatcccagct agaactgaac tggaacaaca gattcttgaa cactgtttg 540
gagcacttg 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 aaaacccaag gacaccctca tgatctcccg gacccttag 900
gtcacatgcg tgggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 960
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 1020

eolf-seq1

acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag	1080
tacaagtgca aggtctccaa caaagccctc ccagcccca tcgagaaaac catctccaaa	1140
gccaaagggc agccccgaga accacaggtg tgcaccctgc ccccatcccg ggatgagctg	1200
accaagaacc aggtcagcct ctcgtgcgca gtcaaaggct tctatcccag cgacatcgcc	1260
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg	1320
gactccgacg gctccttctt cctcgtgagc aagctcaccg tggacaagag caggtggcag	1380
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag	1440
aagagcctct ccctgtctcc gggtaaata	1470

<210> 290
 <211> 217
 <212> PRT
 <213> Artificial Sequence

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

<400> 290

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

Glu Leu Cys Asp Asp Asp Pro Pro Lys Ile Thr His Ala Thr Phe Lys
 20 25 30

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

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

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

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

Lys Glu Arg Lys Thr Thr Glu Met Gln Ser Gln Met Gln Leu Ala Asp
 100 105 110

Gln Val Ser Leu Pro Gly His Cys Arg Glu Pro Pro Pro Trp Glu Asn
 115 120 125

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

eolf-seq1
 tggattacct ttgcccacaaag catcatctca acactgact 399

<210> 293
 <211> 399
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IL-2 mutant L72G (C125A) (4)

<400> 293
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 ttacagatga ttttgaatgg aattaataat tacaagaatc ccaaactcac caggatgctc 120
 acatttaagt tttacatgcc caagaaggcc acagaactga aacatcttca gtgtctagaa 180
 gaagaactca aacctctgga ggaagtgcta aatggcgctc aaagcaaaaa ctttcactta 240
 agaccaggg acttaatcag caatatcaac gtaatagttc tggaactaaa gggatctgaa 300
 acaacattca tgtgtgaata tgctgatgag acagcaacca ttgtagaatt tctgaacaga 360
 tggattacct ttgcccacaaag catcatctca acactgact 399

<210> 294
 <211> 399
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IL-2 mutant L72G / F42A (C125A) (4)

<400> 294
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 ttacagatga ttttgaatgg aattaataat tacaagaatc ccaaactcac caggatgctc 120
 acagccaagt tttacatgcc caagaaggcc acagaactga aacatcttca gtgtctagaa 180
 gaagaactca aacctctgga ggaagtgcta aatggcgctc aaagcaaaaa ctttcactta 240
 agaccaggg acttaatcag caatatcaac gtaatagttc tggaactaaa gggatctgaa 300
 acaacattca tgtgtgaata tgctgatgag acagcaacca ttgtagaatt tctgaacaga 360
 tggattacct ttgcccacaaag catcatctca acactgact 399

<210> 295
 <211> 399
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IL-2 triple mutant F42A / Y45A / L72G (C125A) (4)

<400> 295
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 ttacagatga ttttgaatgg aattaataat tacaagaatc ccaaactcac caggatgctc 120
 acagccaagt ttgcatgcc caagaaggcc acagaactga aacatcttca gtgtctagaa 180
 gaagaactca aacctctgga ggaagtgcta aatggcgctc aaagcaaaaa ctttcactta 240

eolf-seq1

agaccaggg acttaatcag caatatcaac gtaatagttc tggaactaaa gggatctgaa	300
acaacattca tgtgtgaata tgctgatgag acagcaacca ttgtagaatt tctgaacaga	360
tggtattacct ttgcccaaag catcatctca acactgact	399

<210> 296
 <211> 399
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IL-2 quadruple mutant T3A / F42A /Y45A /L72G (C125A) (4)

<400> 296	
gcacctgcct caagttctac aaagaaaaca cagctacaac tggagcattt actgctggat	60
ttacagatga ttttgaatgg aattaataat tacaagaatc ccaaactcac caggatgctc	120
acagccaagt ttgccatgcc caagaaggcc acagaactga aacatcttca gtgtctagaa	180
gaagaactca aacctctgga ggaagtgcta aatggcgctc aaagcaaaaa ctttactta	240
agaccaggg acttaatcag caatatcaac gtaatagttc tggaactaaa gggatctgaa	300
acaacattca tgtgtgaata tgctgatgag acagcaacca ttgtagaatt tctgaacaga	360
tggtattacct ttgcccaaag catcatctca acactgact	399

<210> 297
 <211> 593
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 28H1 Fab heavy chain-Fc (knob)-IL-2 qm

<400> 297

Glu Val Gln Leu	Leu Glu Ser Gly Gly	Gly Leu Val Gln Pro Gly Gly
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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
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

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 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

eo1f-seq1

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
435 440 445

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Pro Ala Ser
450 455 460

Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp
465 470 475 480

Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu
485 490 495

Thr Arg Met Leu Thr Ala Lys Phe Ala Met Pro Lys Lys Ala Thr Glu
500 505 510

Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu
515 520 525

Val Leu Asn Gly Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp
530 535 540

Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu
545 550 555 560

Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu
565 570 575

Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu
580 585 590

Thr

<210> 298
<211> 1779
<212> DNA
<213> Artificial Sequence

<220>
<223> 28H1 Fab heavy chain-Fc (knob)-IL-2 qm

<400> 298
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eolf-seq1

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gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc	960
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caggtcagcc tgtggtgcct ggtcaaaggc ttctatcca gcgacatcg cgtggagtgg	1140
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<210> 299

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<223> 28H1 Fab heavy chain-Fc (hole)

<400> 299

eo1f-seq1

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

eo1f-seq1

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

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> 300
<211> 1338
<212> DNA
<213> Artificial Sequence

<220>
<223> 28H1 Fab heavy chain-Fc (hole)

<400> 300
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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
ggcccctccg tgttccccct ggccccccagc agcaagagca ccagcggcgg cacagccgct 420

eolf-seq1

ctgggctgcc tgggtcaagga ctacttcccc gagcccgtga ccgtgtcctg gaacagcgga	480
gccctgacct ccggcggtgca caccttcccc gccgtgctgc agagtctctgg cctgtatagc	540
ctgagcagcg tgggtaccgt gccttctagc agcctgggca cccagaccta catctgcaac	600
gtgaaccaca agcccagcaa caccaagggtg gacaagaagg tggagcccaa gagctgcgac	660
aaaactcaca catgcccacc gtgcccagca cctgaagctg caggggggacc gtcagtcttc	720
ctcttcccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc	780
gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc	840
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gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc	960
aaggtctcca acaaagccct cggcgccccc atcgagaaaa ccatctccaa agccaaaggg	1020
cagccccgag aaccacaggt gtgcaccctg ccccatcccc gggatgagct gaccaagaac	1080
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tcctgtctc cgggtaaa	1338

<210> 301
 <211> 594
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 4B9 Fab heavy chain-Fc (knob)-IL-2 qm
 <400> 301

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
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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
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eolf-seql

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	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

eolf-seq1
380

370

375

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

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly
435 440 445

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Pro Ala
450 455 460

Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu
465 470 475 480

Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys
485 490 495

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> 302
<211> 1782
<212> DNA
<213> Artificial Sequence

<220>
<223> 4B9 Fab heavy chain-Fc (knob)-IL-2 qm

<400> 302

eolf-seq1						
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cctggcaagg	gactggaatg	ggtgtccgcc	atcatcggct	ctggcggcag	cacctactac	180
gccgacagcg	tgaagggccg	gttcaccatc	agccgggaca	acagcaagaa	caccctgtac	240
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gaagaagaac	tcaaacctct	ggaggaagtg	ctaaatggcg	ctcaaagcaa	aaactttcac	1620
ttaagacca	gggacttaat	cagcaatatc	aacgtaatag	ttctggaact	aaagggatct	1680
gaaacaacat	tcatgtgtga	atatgctgat	gagacagcaa	ccattgtaga	atttctgaac	1740
agatggatta	cctttgccca	aagcatcatc	tcaacactga	ct		1782

<210> 303

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> 4B9 Fab heavy chain-Fc (hole)

eo1f-seq1

<400> 303

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

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

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

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

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

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

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

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
130 135 140

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

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
195 200 205

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
210 215 220

Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
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eo1f-seq1

260 265 270

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro
340 345 350

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

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

Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 304
<211> 1341
<212> DNA
<213> Artificial Sequence

<220>
<223> 4B9 Fab heavy chain-Fc (hole)

<400> 304
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gccgacagcg tgaagggccg gttcaccatc agccgggaca acagcaagaa caccctgtac 240
ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcgc caagggatgg 300
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eolf-seq1

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gacaaaactc acacatgccc accgtgcccc gcacctgaag ctgcaggggg accgtcagtc      720
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tgcgtgggtg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac      840
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac      900
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aaccaggtca gcctctcgtg cgcagtcaaa ggcttctatc ccagcgacat cgccgtggag     1140
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gacggctcct tcttctcgtg gagcaagctc accgtggaca agagcagggtg gcagcagggg     1260
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ctctccctgt ctccgggtaa a                                             1341

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<210> 305
 <211> 592
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DP47GS Fab heavy chain-Fc (knob)-IL-2 qm

<400> 305

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

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

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
130 135 140

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

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
165 170 175

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
180 185 190

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
195 200 205

Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

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

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
275 280 285

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys
325 330 335

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

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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> 306
<211> 1776
<212> DNA
<213> Artificial sequence

<220>
<223> DP47GS Fab heavy chain-Fc (knob)-IL-2 qm

<400> 306
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eolf-seq1						
tcctgtgcag	cctccggatt	caccttttagc	agttatgcc	tgagctgggt	ccgccaggct	120
ccaggggaagg	ggctggagtg	ggtctcagct	attagtggta	gtggtggtag	cacatactac	180
gcagactccg	tgaagggccg	gttcaccatc	tccagagaca	attccaagaa	cacgctgtat	240
ctgcagatga	acagcctgag	agccgaggac	acggccgtat	attactgtgc	gaaaggcagc	300
ggatttgact	actggggcca	aggaaccctg	gtcaccgtct	cgagtgctag	caccaagggc	360
ccatcgggtct	tccccctggc	accctcctcc	aagagcacct	ctggggggcac	agcggccctg	420
ggctgcctgg	tcaaggacta	cttccccgaa	ccggtgacgg	tgctcgtggaa	ctcaggcgcc	480
ctgaccagcg	gcgtgcacac	cttcccggct	gtcctacagt	cctcaggact	ctactccctc	540
agcagcgtgg	tgaccgtgcc	ctccagcagc	ttgggcaccc	agacctacat	ctgcaacgtg	600
aatcacaagc	ccagcaacac	caaggtggac	aagaaagttg	agcccaaatc	ttgtgacaaa	660
actcacacat	gcccaccgtg	cccagcacct	gaagctgcag	ggggaccgtc	agtcttcctc	720
ttccccccaa	aacccaagga	caccctcatg	atctcccgga	cccctgaggt	cacatgcgtg	780
gtggtggacg	tgagccacga	agaccctgag	gtcaagttca	actggtacgt	ggacggcgtg	840
gaggtgcata	atgccaagac	aaagccgcgg	gaggagcagt	acaacagcac	gtaccgtgtg	900
gtcagcgtcc	tcaccgtcct	gcaccaggac	tggctgaatg	gcaaggagta	caagtgcgaag	960
gtctccaaca	aagccctcgg	cgcccccatc	gagaaaacca	tctccaaagc	caaagggcag	1020
ccccgagaac	cacaggtgta	caccctgccc	ccatgccggg	atgagctgac	caagaaccag	1080
gtcagcctgt	ggtgcctggt	caaaggcttc	tatcccagcg	acatcgccgt	ggagtgggag	1140
agcaatgggc	agccggagaa	caactacaag	accacgcctc	ccgtgctgga	ctccgacggc	1200
tcctttcttc	tctacagcaa	gctcaccgtg	gacaagagca	ggtggcagca	ggggaacgtc	1260
ttctcatgct	ccgtgatgca	tgaggctctg	cacaaccact	acacgcagaa	gagcctctcc	1320
ctgtctccgg	gtggcggcgg	aggctccgga	ggcggagggt	ctggcggagg	tggctccgca	1380
cctgcctcaa	gttctacaaa	gaaaacacag	ctacaactgg	agcattttact	gctggattta	1440
cagatgatgtt	tgaatggaat	taataattac	aagaatccca	aactcaccag	gatgctcaca	1500
gccaaagtttg	ccatgcccaa	gaaggccaca	gaactgaaac	atcttcagtg	tctagaagaa	1560
gaactcaaac	ctctggagga	agtgcataat	ggcgctcaaa	gcaaaaactt	tcacttaaga	1620
cccagggact	taatcagcaa	tatcaacgta	atagttcttg	aactaaaggg	atctgaaaca	1680
acattcatgt	gtgaatatgc	tgatgagaca	gcaaccattg	tagaatttct	gaacagatgg	1740
attacctttg	cccaaagcat	catctcaaca	ctgact			1776

<210> 307
 <211> 445
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DP47GS Fab heavy chain-Fc (hole)

<400> 307

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

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Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
275 280 285

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys
325 330 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser
340 345 350

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys
355 360 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
370 375 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385 390 395 400

Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
405 410 415

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 308
<211> 1335
<212> DNA
<213> Artificial Sequence

<220>
<223> DP47GS Fab heavy chain-Fc (hole)

<400> 308
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ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggcagc 300
ggatttgact actggggcca aggaaccctg gtcaccgtct cgagtgttag caccaagggc 360
ccctccgtgt tccccctggc cccagcagc aagagcacca gcggcggcac agccgctctg 420

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ggctgcctgg tcaaggacta cttccccgag cccgtgaccg tgtcctggaa cagcggagcc	480
ctgacctccg gcgtgcacac cttccccgcc gtgtgcaga gttctggcct gtatagcctg	540
agcagcgtgg tcaccgtgcc ttctagcagc ctgggcaccc agacctacat ctgcaacgtg	600
aaccacaagc ccagcaacac caaggtggac aagaaggtgg agcccaagag ctgcgacaaa	660
actcacacat gcccaccgtg cccagcacct gaagctgcag ggggaccgtc agtcttcctc	720
ttcccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg	780
gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg	840
gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg	900
gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgaag	960
gtctccaaca aagccctcgg cgccccatc gagaaaacca tctccaaagc caaagggcag	1020
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> 309
 <211> 215
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DP47GS light chain

<400> 309

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

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

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

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

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

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

Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala

eolf-seql

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
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> 310
 <211> 645
 <212> DNA
 <213> Artificial sequence

<220>
 <223> DP47GS light chain

<400> 310	
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ctctcttgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa	120
cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca	180
gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag	240
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcaccgct gacgttcggc	300
caggggacca aagtggaaat caaacgtacg gtggctgcac catctgtctt catcttcccg	360
ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc	420
tatcccagag aggccaaagt acagtggaag gtggataacg cctccaatc gggtaactcc	480
caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg	540
acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag	600
ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt	645

<210> 311
 <211> 108
 <212> PRT
 <213> Artificial sequence

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<220>

<223> CH1A1A; VL

<400> 311

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

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

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

Tyr Ser Ala Ser Tyr Arg Lys Arg Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

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

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

<210> 312

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> CH1A1A; VL

<400> 312

gatatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtgggaga cagagtcacc	60
atcacttgca aggccagtg gcgtgtgggt 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> 313

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> CH1A1A; VH

<400> 313

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

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

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

Gly Trp Ile Asn Thr Lys Thr Gly Glu Ala Thr Tyr Val Glu Glu Phe
50 55 60

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

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

Ala Arg Trp Asp Phe Ala Tyr Tyr Val Glu Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 314
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> CH1A1A; VH

<400> 314
caggtgcagc tgggtgcagtc tggcgccgaa gtgaagaaac ctggagctag tgtgaagggtg 60
tcctgcaagg ccagcggcta caccttcacc gagttcggca tgaactgggt cgcacaggct 120
ccaggccagg gcctcgaatg gatgggctgg atcaacacca agaccggcga ggccacctac 180
gtggaagagt tcaagggcag agtgaccttc accacggaca ccagcaccag caccgcctac 240
atggaactgc ggagcctgag aagcgacgac accgccgtgt actactgcgc cagatgggac 300
ttcgctatt acgtggaagc catggactac tggggccagg gcaccaccgt gaccgtgtct 360
agc 363

<210> 315
<211> 594
<212> PRT
<213> Artificial Sequence

<220>
<223> 4G8 Fab heavy chain-Fc (knob)-IL-2 qm

<400> 315

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

565

eolf-seq1
570

575

Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr
580 585 590

Leu Thr

<210> 316
<211> 1782
<212> DNA
<213> Artificial Sequence

<220>
<223> 4G8 Fab heavy chain-Fc (knob)-IL-2 qm

<400> 316
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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 gaaaggggtg 300
ctgggtaatt ttgactactg gggccaagga accctgggtca ccgtctcgag tgctagcacc 360
aagggcccat cggctcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420
gccctgggct gcctgggtcaa ggactacttc cccgaaccgg tgacgggtgtc gtggaactca 480
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540
tcctctagca gcgtgggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 660
gacaaaactc acacatgccc accgtgccc a gcacctgaag ctgcaggggg accgtcagtc 720
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 780
tgctgtgggtg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 840
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 900
cgtgtgggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 960
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gggcagcccc gagaaccaca ggtgtacacc ctgcccccat gccgggatga gctgaccaag 1080
aaccaggatca gcctgtggtg cctgggtcaaa ggcttctatc ccagcgacat cgccgtggag 1140
tgaggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1200
gacggctcct tcttctctta cagcaagctc accgtggaca agagcagggtg gcagcagggg 1260
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 1320
ctctccctgt ctccgggtg cggcggaggc tccggaggcg gaggttcttg cgagggtggc 1380
tccgcacctg cctcaagttc taaaagaaa acacagctac aactggagca ttactgctg 1440

eolf-seq1

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 cctttgccca aagcatcatc tcaacactga ct	1782

<210> 317
 <211> 447
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 4G8 Fab heavy chain-Fc (hole)

<400> 317

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

eolf-seql

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
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
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
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

eo1f-seq1

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

<220>
 <223> 4G8 Fab heavy chain-Fc (hole)

<400> 318
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 tcctgtgcag cctccggatt cacctttagc agttatgcc a tgagctgggt ccgccaggct 120
 ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggggtg 300
 ctgggtaatt ttgactactg gggccaagga accctgggtca ccgtctcgag tgctagcacc 360
 aagggcccct ccgtgttccc cctggccccc agcagcaaga gcaccagcgg cggcacagcc 420
 gctctgggct gcctggtcaa ggactacttc cccgagcccg tgaccgtgtc ctggaacagc 480
 ggagccctga cctccggcgt gcacaccttc cccgccgtgc tgcagagttc tggcctgtat 540
 agcctgagca gcgtggtcac cgtgccttct agcagcctgg gcaccagac ctacatctgc 600
 aacgtgaacc acaagcccag caacaccaag gtggacaaga aggtggagcc caagagctgc 660
 gacaaaactc acacatgccc accgtgcccc gcacctgaag ctgcaggggg accgtcagtc 720
 ttctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 780
 tgcgtggtgg tggacgtgag ccacgaagac cctgagggtca agttcaactg gtacgtggac 840
 ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 900
 cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 960
 tgcaaggtct ccaacaaagc cctcggcgcc cccatcgaga aaaccatctc caaagccaaa 1020
 gggcagcccc gagaaccaca ggtgtgcacc ctgcccccat cccgggatga gctgaccaag 1080
 aaccagggtca gcctctcgtg cgcagtcaaa ggcttctatc ccagcgacat cgccgtggag 1140
 tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1200
 gacggctcct tcttctcgt gagcaagctc accgtggaca agagcagggtg gcagcagggg 1260
 aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 1320
 ctctccctgt ctccgggtaa a 1341

<210> 319
 <211> 600
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CH1A1A Fab heavy chain-Fc (knob)-IL-2 qm

<400> 319

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

eo1f-seq1

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

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

Gly Trp Ile Asn Thr Lys Thr Gly Glu Ala Thr Tyr Val Glu Glu Phe
50 55 60

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

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

Ala Arg Trp Asp Phe Ala Tyr Tyr Val Glu Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

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

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

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

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

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

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

eof-seq1

Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp
565 570 575

Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala
580 585 590

Gln Ser Ile Ile Ser Thr Leu Thr
595 600

<210> 320
<211> 1800
<212> DNA
<213> Artificial sequence

<220>
<223> CH1A1A Fab heavy chain-Fc (knob)-IL-2 qm

<400> 320
caggtgcagc tgggtgcagtc tggcgccgaa gtgaagaaac ctggagctag tgtgaagggtg 60
tcctgcaagg ccagcggcta caccttcacc gagttcggca tgaactgggt ccgacaggct 120
ccaggccagg gcctcgaatg gatgggctgg atcaacacca agaccggcga ggccacctac 180
gtggaagagt tcaagggcag agtgaccttc accacggaca ccagcaccag caccgcctac 240
atggaactgc ggagcctgag aagcgacgac accgccgtgt actactgcg cagatgggac 300
ttcgctatt acgtggaagc catggactac tggggccagg gcaccaccgt gaccgtgtct 360
agcgctagca ccaagggccc aagcgtgttc cctctggccc ccagcagcaa gagcacaagc 420
ggcgaacag 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 gaaggtggag 660
cccaagagct gcgacaagac ccacacctgt cccccttgtc ctgccccctga gctgctgggc 720
ggacccagcg tgttcctggt ccccccaaag cccaaggaca ccctgatgat cagccggacc 780
cccgaagtga cctgcgtggg ggtggacgtg tcccacgagg accctgaagt gaagttcaat 840
tggtacgtgg acggcgtgga ggtgcacaat gccaagacca agccccggga ggaacagtac 900
aacagcacct accgggtggg gtccgtgctg accgtgctgc accaggactg gctgaacggc 960
aaagagtaca agtgcaaggc ctccaacaag gccctgcctg ccccatcga gaaaaccatc 1020
agcaaggcca agggccagcc cagagaaccc cagggtgata ccctgcccc ctgcagagat 1080
gagctgacca agaaccaggg gtccctgtgg tgtctgggtc agggcttcta cccagcgat 1140
atcgccgtgg agtgggagag caacggccag cctgagaaca actacaagac cccccccct 1200
gtgctggaca gcgacggcag cttcttcctg tactccaaac tgaccgtgga caagagccgg 1260
tggcagcagg gcaacgtggt cagctgcagc gtgatgcacg aggccctgca caaccactac 1320
accagaagt ccctgagcct gagccccggc aagtccggag gcggaggctc cggcggcgga 1380

eolf-seq1

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ggttctggcg gaggtggctc cgcacctgcc tcaagttcta caaagaaaac acagctacaa      1440
ctggagcatt tactgctgga tttacagatg attttgaatg gaattaataa ttacaagaat      1500
cccaaactca ccaggatgct cacagccaag tttgccatgc ccaagaaggc cacagaactg      1560
aaacatcttc agtgtctaga agaagaactc aaacctctgg aggaagtgct aaatggcgct      1620
caaagcaaaa actttcactt aagacccagg gacttaatca gcaatatcaa cgtaatagtt      1680
ctggaactaa agggatctga aacaacattc atgtgtgaat atgctgatga gacagcaacc      1740
attgtagaat ttctgaacag atggattacc tttgccc aaa gcatcatctc aacactgact      1800

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<210> 321
 <211> 451
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CH1A1A Fab heavy chain-Fc (hole)

<400> 321

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

eolf-seql

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

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

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

eo1f-seq1

Pro Gly Lys
450

<210> 322
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> CH1A1A Fab heavy chain-Fc (hole)

<400> 322
caggtgcagc tgggtgcagtc tggcgccgaa gtgaagaaac ctggagctag tgtgaagggtg 60
tcctgcaagg ccagcggcta caccttcacc gagttcggca tgaactgggt ccgacaggct 120
ccaggccagg gcctcgaatg gatgggctgg atcaacacca agaccggcga ggccacctac 180
gtggaagagt tcaagggcag agtgaccttc accacggaca ccagcaccag caccgcctac 240
atggaactgc ggagcctgag aagcgacgac accgccgtgt actactgcgc 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 gaaggtggag 660
cccaagagct gcgacaagac ccacacctgt ccccttgtc ctgcccctga gctgctgggc 720
ggacccagcg tgttcctgtt cccccaaaag cccaaggaca ccctgatgat cagccggacc 780
cccgaagtga cctgcgtggt ggtggacgtg tcccacgagg accctgaagt gaagttcaat 840
tggtacgtgg acggcgtgga ggtgcacaat gccaaagacca agccccggga ggaacagtac 900
aacagcacct accgggtggt gtccgtgctg accgtgctgc accaggactg gctgaacggc 960
aaagagtaca agtgcaaggt ctccaacaag gccctgcctg ccccatcga gaaaaccatc 1020
agcaaggcca agggccagcc cagagaacct caggtgtgca ccctgcccc cagcagagat 1080
gagctgacca agaaccagggt gtccctgagc tgtgccgtca agggcttcta cccagcgat 1140
atcgccgtgg agtgggagag caacggccag cctgagaaca actacaagac cccccccct 1200
gtgctggaca gcgacggcag cttcttcctg gtgtccaaac tgaccgtgga caagagccgg 1260
tggcagcagg gcaacgtgtt cagctgcagc gtgatgcacg aggccctgca caaccactac 1320
accagaagt ccctgagcct gagccccggc aag 1353

<210> 323
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1A1A light chain

co1f-seq1

<400> 323

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

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<210> 324

<211> 645

<212> DNA

<213> Artificial sequence

<220>

<223> CH1A1A light chain

<400> 324

eolf-seq1						
gatatccaga	tgacccagtc	tccatcctcc	ctgtctgcat	ctgtgggaga	cagagtcacc	60
atcacttgca	aggccagtc	ggctgtgggt	acgtatgttg	cgtgggatca	gcagaaacca	120
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aggttcagtg	gcagtggatc	tgggacagat	ttcactctca	ccatcagcag	tctgcaacct	240
gaagatttcg	caacttacta	ctgtcaccaa	tattacacct	atcctctatt	cacgtttggc	300
cagggcacca	agctcgagat	caagcgtacg	gtggctgcac	catctgtcct	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	cacccatcag	600
ggcctgagct	cgcccgtcac	aaagagcttc	aacaggggag	agtgt		645