SEQUENCE LISTING

<110> Roche Glycart AG

<120> Interleukin-10 fusion proteins and uses thereof

<130> 31135

<150> EP 12179709.6
<151> 2012-08-08

<160> 89

<170> PatentIn version 3.5

<210> 1
<211> 160
<212> PRT
<213> Homo sapiens

<400> 1

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

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

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

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

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

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

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

Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe
        115                 120                 125

Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp
    130                 135                 140

Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn
145                 150                 155                 160
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<210> 2
<211> 480
<212> DNA
<213> Homo sapiens

<400> 2

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aacatgctgc gggacctgag ggacgccttc agcagagtga aaaccttctt ccagatgaag 120

gaccagctgg acaacctgct gctgaaagag agcctgctgg aagatttcaa gggctacctg 180

ggctgtcagg ccctgagcga gatgatccag ttctacctgg aagaagtgat gccccaggcc 240

gagaaccagg accccgacat caaggcccac gtgaacagcc tgggcgagaa cctgaaaacc 300

ctgcggctga gactgcggcg gtgccacaga tttctgccct gcgagaacaa gagcaaggcc 360

gtggaacagg tgaagaacgc cttcaacaag ctgcaggaaa agggcatcta caaggccatg 420

tccgagttcg acatcttcat caactacatc gaggcctaca tgacaatgaa aatccgcaat 480

<210> 3
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> scIL-10

<400> 3

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

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

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

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

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

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

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

Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe
115 120 125

Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp
130 135 140

Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn
145 150 155 160

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

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                165                 170                 175

Gly Gly Gly Ser Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys
            180                 185                 190

Thr His Phe Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp
        195                 200                 205

Ala Phe Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp
    210                 215                 220

Asn Leu Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu
225                 230                 235                 240

Gly Cys Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val
                245                 250                 255

Met Pro Gln Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn
            260                 265                 270

Ser Leu Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys
        275                 280                 285

His Arg Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val
    290                 295                 300

Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met
305                 310                 315                 320

Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met
                325                 330                 335

Lys Ile Arg Asn
            340


<210>  4
<211>  1020
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  scIL-10

<400>  4
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gaccagctgg acaacctgct gctgaaagag agcctgctgg aagatttcaa gggctacctg      180

ggctgtcagg ccctgagcga gatgatccag ttctacctgg aagaagtgat gccccaggcc      240

gagaaccagg accccgacat caaggcccac gtgaacagcc tgggcgagaa cctgaaaacc      300

ctgcggctga gactgcggcg gtgccacaga tttctgccct gcgagaacaa gagcaaggcc      360
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gtggaacagg tgaagaacgc cttcaacaag ctgcaggaaa agggcatcta caaggccatg 420

tccgagttcg acatcttcat caactacatc gaagcttaca tgaccatgaa gatcagaaac 480

ggcggaggcg gatctggcgg cggtggaagt ggaggcggag gatctggggg aggcggaagt 540

agcccgggcc agggcaccca gagcgagaac agctgcaccc acttccccgg caacctgccc 600

aacatgctgc gggacctgag ggacgccttc agcagagtga aaaccttctt ccagatgaag 660

gaccagctgg acaacctgct gctgaaagag agcctgctgg aagatttcaa gggctacctg 720

ggctgtcagg ccctgagcga gatgatccag ttctacctgg aagaagtgat gccccaggcc 780

gagaaccagg accccgacat caaggcccac gtgaacagcc tgggcgagaa cctgaaaacc 840

ctgcggctga gactgcggcg gtgccacaga tttctgccct gcgagaacaa gagcaaggcc 900

gtggaacagg tgaagaacgc cttcaacaag ctgcaggaaa agggcatcta caaggccatg 960

tccgagttcg acatcttcat caactacatc gaggcctaca tgacaatgaa aatccgcaat 1020

<210> 5
<211> 166
<212> PRT
<213> Artificial Sequence

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

<400> 5

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

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

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

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

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

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

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

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

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

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


Thr Met Lys Ile Arg Asn
                165


<210>  6
<211>  498
<212>  DNA
<213>  Artificial Sequence

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

<400>  6
tctccaggcc agggcaccca gagcgagaac agctgcaccc acttccccgg caacctgccc       60

aacatgctgc gggacctgag ggacgccttc agcagagtga aaaccttctt ccagatgaag      120

gaccagctgg acaacctgct gctgaaagag agcctgctgg aagatttcaa gggctacctg      180

ggctgtcagg ccctgagcga gatgatccag ttctacctgg aagaagtgat gccccaggcc      240

gagaaccagg accccgacat caaggcccac gtgaacagcc tgggcgagaa cctgaaaacc      300

ctgcggctga gactgcggcg gtgccacaga tttctgccct gcgagaacgg cggaggctct      360

ggcggaaagt ccaaggccgt ggaacaggtg aagaacgcct tcaacaagct gcaggaaaag      420

ggcatctaca aggccatgag cgagttcgac atcttcatca actacatcga agcttacatg      480

acaatgaaga tacgaaac                                                    498


<210>  7
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  4G8 IgG - IL-10 (LC)

<400>  7

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
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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> 8
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> 4G8 IgG - IL-10 (LC)

<400> 8
gagatcgtgc tgacccagtc ccccggcacc ctgtctctga gccctggcga gagagccacc 60

ctgtcctgca gagcctccca gtccgtgtcc cggtcctacc tcgcctggta tcagcagaag 120

cccggccagg cccctcggct gctgatcatc ggcgcctcta ccagagccac cggcatccct 180

gaccggttct ccggctctgg ctccggcacc gacttcaccc tgaccatctc ccggctggaa 240

cccgaggact tcgccgtgta ctactgccag cagggccagg tcatccctcc caccttggc 300

cagggcacca aggtggaaat caagcgtacg gtggccgctc cctccgtgtt catcttccca 360

ccctccgacg agcagctgaa gtccggcacc gcctccgtcg tgtgcctgct gaacaacttc 420

taccccgcg 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> 9

<211> 626
<212> PRT
<213> Artificial Sequence

<220>
<223> 4G8 IgG - IL-10 (HC P329G LALA + IL-10)

<400> 9

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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 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
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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 Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
        355                 360                 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    370                 375                 380

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

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
                405                 410                 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
            420                 425                 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly
        435                 440                 445

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
    450                 455                 460

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

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

Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu
            500                 505                 510
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Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys
515 520 525

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

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

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

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

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

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

Arg Asn
625

<210> 10
<211> 1878
<212> DNA
<213> Artificial Sequence

<220>
<223> 4G8 IgG - IL-10 (HC P329G LALA + IL-10)

<400> 10
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tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggtgg 300

ctgggtaatt ttgactactg gggccaagga accctggtca ccgtctcgag tgctagcacc 360

aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600

aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 660

gacaaaactc acacatgccc accgtgccca gcacctgaag ctgcaggggg accgtcagtc 720

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 780

tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 840

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 900

cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 960

tgcaaggtct ccaacaaagc cctcggcgcc cccatcgaga aaaccatctc caaagccaaa 1020

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aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 1140

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1200

gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 1260

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ttccccggca acctgcccaa catgctgcgg gacctgaggg acgccttcag cagagtgaaa 1500

accttcttcc agatgaagga ccagctggac aacctgctgc tgaaagagag cctgctggaa 1560

gatttcaagg gctacctggg ctgtcaggcc ctgagcgaga tgatccagtt ctacctggaa 1620

gaagtgatgc cccaggccga gaaccaggac cccgacatca aggcccacgt gaacagcctg 1680

ggcgagaacc tgaaaaccct gcggctgaga ctgcggcggt gccacagatt tctgccctgc 1740

gagaacaaga gcaaggccgt ggaacaggtg aagaacgcct tcaacaagct gcaggaaaag 1800

ggcatctaca aggccatgtc cgagttcgac atcttcatca actacatcga agcttacatg 1860

acaatgaaaa tccgcaat 1878

<210> 11
<211> 801
<212> PRT
<213> Artificial Sequence

<220>
<223> 4G8 IgG - scIL-10 (HC hole P329G LALA + scIL-10)

<400> 11

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225                 230                 235                 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                 250                 255

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

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
    290                 295                 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305                 310                 315                 320

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

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro
            340                 345                 350
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```
Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala
        355                 360                 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    370                 375                 380

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

Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg
                405                 410                 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
            420                 425                 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly
        435                 440                 445

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Pro Gly
    450                 455                 460

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

Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg Val Lys Thr
                485                 490                 495

Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu Lys Glu Ser
            500                 505                 510

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

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

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

Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu Pro Cys Glu
                565                 570                 575

Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe Asn Lys Leu
            580                 585                 590

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

Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn Gly Gly Gly
    610                 615                 620
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```
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
625                 630                 635                 640

Ser Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe
                645                 650                 655

Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser
            660                 665                 670

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

Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln
    690                 695                 700

Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln
705                 710                 715                 720

Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly
                725                 730                 735

Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe
            740                 745                 750

Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala
        755                 760                 765

Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe
    770                 775                 780

Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg
785                 790                 795                 800

Asn
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<210> 12
<211> 2403
<212> DNA
<213> Artificial Sequence

<220>
<223> 4G8 IgG - scIL-10 (HC hole P329G LALA + scIL-10)

<400> 12

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tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct      120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac      180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat      240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggtgg      300
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ctgggtaatt ttgactactg gggccaagga accctggtca ccgtctcgag tgctagcacc      360
aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg      420
gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca      480
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac      540
tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc      600
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt      660
gacaaaactc acacatgccc accgtgccca gcacctgaag ctgcaggggg accgtcagtc      720
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca      780
tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac      840
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac      900
cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag      960
tgcaaggtct ccaacaaagc cctcggcgcc cccatcgaga aaaccatctc caaagccaaa     1020
gggcagcccc gagaaccaca ggtgtgcacc ctgcccccat cccgggatga gctgaccaag     1080
aaccaggtca gcctctcgtg cgcagtcaaa ggcttctatc ccagcgacat cgccgtggag     1140
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc     1200
gacggctcct tcttcctcgt gagcaagctc accgtggaca agagcaggtg gcagcagggg     1260
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc     1320
ctctccctgt ctccgggtgg cggcggaggc tccggaggcg gaggatctgg gggaggcgga     1380
agtagcccgg gccagggcac ccagagcgag aacagctgca cccacttccc cggcaacctg     1440
cccaacatgc tgcgggacct gagggacgcc ttcagcagag tgaaaacctt cttccagatg     1500
aaggaccagc tggacaacct gctgctgaaa gagagcctgc tggaagattt caagggctac     1560
ctgggctgtc aggccctgag cgagatgatc cagttctacc tggaagaagt gatgccccag     1620
gccgagaacc aggaccccga catcaaggcc cacgtgaaca gcctgggcga gaacctgaaa     1680
accctgcggc tgagactgcg gcggtgccac agatttctgc cctgcgagaa caagagcaag     1740
gccgtggaac aggtgaagaa cgccttcaac aagctgcagg aaaagggcat ctacaaggcc     1800
atgtccgagt tcgacatctt catcaactac atcgaagctt acatgaccat gaagatcaga     1860
aacggcggag gcggatctgg cggcggtgga agtggaggcg gaggatctgg gggaggcgga     1920
agtagcccgg gccagggcac ccagagcgag aacagctgca cccacttccc cggcaacctg     1980
cccaacatgc tgcgggacct gagggacgcc ttcagcagag tgaaaacctt cttccagatg     2040
aaggaccagc tggacaacct gctgctgaaa gagagcctgc tggaagattt caagggctac     2100
ctgggctgtc aggccctgag cgagatgatc cagttctacc tggaagaagt gatgccccag     2160
gccgagaacc aggaccccga catcaaggcc cacgtgaaca gcctgggcga gaacctgaaa     2220
accctgcggc tgagactgcg gcggtgccac agatttctgc cctgcgagaa caagagcaag     2280
gccgtggaac aggtgaagaa cgccttcaac aagctgcagg aaaagggcat ctacaaggcc     2340
```

atgtccgagt tcgacatctt catcaactac atcgaggcct acatgacaat gaaaatccgc 2400

aat 2403

<210> 13
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> 4G8 IgG - scIL-10 (HC knob P329G LALA)

<400> 13

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

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

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

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

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

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

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

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

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

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

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

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

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

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His

210 215 220

Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

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

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

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

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Cys Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Trp Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

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

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 14
<211> 1341
<212> DNA
<213> Artificial Sequence

<220>
<223> 4G8 IgG - scIL-10 (HC knob P329G LALA)

<400> 14

gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggtgg 300

ctgggtaatt ttgactactg gggccaagga accctggtca ccgtctcgag tgctagcacc 360

aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600

aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 660

gacaaaactc acacatgccc accgtgccca gcacctgaag ctgcaggggg accgtcagtc 720

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 780

tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 840

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 900

cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 960

tgcaaggtct ccaacaaagc cctcggcgcc cccatcgaga aaaccatctc caaagccaaa 1020

gggcagcccc gagaaccaca ggtgtacacc ctgcccccat gccgggatga gctgaccaag 1080

aaccaggtca gcctgtggtg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 1140

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1200

gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 1260

aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 1320

ctctccctgt ctccgggtaa a 1341

<210> 15
<211> 627
<212> PRT
<213> Artificial Sequence

<220>
<223> 4G8 IgG -IL-10M1 (HC hole P329G LALA + IL-10M1)

<400> 15

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

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

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

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

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

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

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

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

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

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

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

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

Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225                 230                 235                 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                 250                 255

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

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
    290                 295                 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305                 310                 315                 320
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Cys Lys Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile
                325                 330                 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Cys Thr Leu Pro
            340                 345                 350

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Ser Cys Ala
        355                 360                 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    370                 375                 380

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

Asp Gly Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg
                405                 410                 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
            420                 425                 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly
        435                 440                 445

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Pro Gly
    450                 455                 460

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

Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg Val Lys Thr
                485                 490                 495

Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu Lys Glu Ser
            500                 505                 510

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

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

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

Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu Pro Cys Glu
                565                 570                 575

Asn Gly Gly Gly Ser Gly Gly Lys Ser Lys Ala Val Glu Gln Val Lys
            580                 585                 590
```

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

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

Ile Arg Asn
625

<210> 16
<211> 1881
<212> DNA
<213> Artificial Sequence

<220>
<223> 4G8 IgG -IL-10M1 (HC hole P329G LALA + IL-10M1)

<400> 16
gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggtgg 300

ctgggtaatt ttgactactg gggccaagga accctggtca ccgtctcgag tgctagcacc 360

aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600

aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 660

gacaaaactc acacatgccc accgtgccca gcacctgaag ctgcaggggg accgtcagtc 720

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 780

tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 840

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 900

cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 960

tgcaaggtct ccaacaaagc cctcggcgcc cccatcgaga aaaccatctc caaagccaaa 1020

gggcagcccc gagaaccaca ggtgtgcacc ctgcccccat cccgggatga gctgaccaag 1080

aaccaggtca gcctctcgtg cgcagtcaaa ggcttctatc ccagcgacat cgccgtggag 1140

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1200

gacggctcct tcttcctcgt gagcaagctc accgtggaca agagcaggtg gcagcagggg 1260

aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 1320

ctctccctgt ctccgggtgg cggcggaggc tccggaggcg gaggaagtgg cggcggtggc 1380

agctctccag gccagggcac ccagagcgag aacagctgca cccacttccc cggcaacctg 1440

cccaacatgc tgcgggacct gagggacgcc ttcagcagag tgaaaacctt cttccagatg 1500

aaggaccagc tggacaacct gctgctgaaa gagagcctgc tggaagattt caagggctac 1560

ctgggctgtc aggccctgag cgagatgatc cagttctacc tggaagaagt gatgccccag 1620

gccgagaacc aggaccccga catcaaggcc cacgtgaaca gcctgggcga gaacctgaaa 1680

accctgcggc tgagactgcg gcggtgccac agatttctgc cctgcgagaa cggcggaggc 1740

tctggcggaa agtccaaggc cgtggaacag gtgaagaacg ccttcaacaa gctgcaggaa 1800

aagggcatct acaaggccat gagcgagttc gacatcttca tcaactacat cgaagcttac 1860

atgacaatga agatacgaaa c 1881

<210> 17
<211> 627
<212> PRT
<213> Artificial Sequence

<220>
<223> 4G8 IgG -(IL-10M1)2 (HC P329G LALA + IL-10M1)

<400> 17

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

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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 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 Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
        355                 360                 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    370                 375                 380

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

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
                405                 410                 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
            420                 425                 430
```

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly
435 440 445

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Pro Gly
450 455 460

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

Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg Val Lys Thr
485 490 495

Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu Lys Glu Ser
500 505 510

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

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

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

Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu Pro Cys Glu
565 570 575

Asn Gly Gly Gly Ser Gly Gly Lys Ser Lys Ala Val Glu Gln Val Lys
580 585 590

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

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

Ile Arg Asn
625

<210> 18
<211> 1881
<212> DNA
<213> Artificial Sequence

<220>
<223> 4G8 IgG -(IL-10M1)2 (HC P329G LALA + IL-10M1)

<400> 18
gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggtgg 300

ctgggtaatt ttgactactg gggccaagga accctggtca ccgtctcgag tgctagcacc 360

aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600

aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 660

gacaaaactc acacatgccc accgtgccca gcacctgaag ctgcaggggg accgtcagtc 720

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 780

tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 840

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 900

cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 960

tgcaaggtct ccaacaaagc cctcggcgcc cccatcgaga aaaccatctc caaagccaaa 1020

gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag 1080

aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 1140

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1200

gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 1260

aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 1320

ctctccctgt ctccgggtgg cggcggaggc tccggaggcg gaggaagtgg cggcggtggc 1380

agctctccag gccagggcac ccagagcgag aacagctgca cccacttccc cggcaacctg 1440

cccaacatgc tgcgggacct gagggacgcc ttcagcagag tgaaaacctt cttccagatg 1500

aaggaccagc tggacaacct gctgctgaaa gagagcctgc tggaagattt caagggctac 1560

ctgggctgtc aggccctgag cgagatgatc cagttctacc tggaagaagt gatgccccag 1620

gccgagaacc aggaccccga catcaaggcc cacgtgaaca gcctgggcga gaacctgaaa 1680

accctgcggc tgagactgcg gcggtgccac agatttctgc cctgcgagaa cggcggaggc 1740

tctggcggaa agtccaaggc cgtggaacag gtgaagaacg ccttcaacaa gctgcaggaa 1800

aagggcatct acaaggccat gagcgagttc gacatcttca tcaactacat cgaagcttac 1860

atgacaatga agatacgaaa c 1881

<210> 19
<211> 396
<212> PRT
<213> Artificial Sequence

<220>
<223> 4G8 Fab - IL-10 (HC + IL-10)

<400> 19

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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 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 Gly Gly Gly
    210                 215                 220

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Pro Gly Gln
225                 230                 235                 240

Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro Gly Asn Leu Pro
                245                 250                 255

Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg Val Lys Thr Phe
            260                 265                 270
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Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu Lys Glu Ser Leu
        275                 280                 285

Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala Leu Ser Glu Met
    290                 295                 300

Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala Glu Asn Gln Asp
305                 310                 315                 320

Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly Glu Asn Leu Lys Thr
                325                 330                 335

Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu Pro Cys Glu Asn
            340                 345                 350

Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe Asn Lys Leu Gln
        355                 360                 365

Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp Ile Phe Ile Asn
    370                 375                 380

Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn
385                 390                 395


<210>  20
<211>  1188
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  4G8 Fab - IL-10 (HC + IL-10)

<400>  20
gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc       60

tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct      120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac      180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat      240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggtgg      300

ctgggtaatt ttgactactg gggccaagga accctggtca ccgtctcgag tgctagcacc      360

aagggcccca gcgtgtttcc tctggccccc agcagcaaga gcacaagcgg cggaacagcc      420

gccctgggct gcctggtgaa ggactacttc cccgagcccg tgaccgtgtc ttggaacagc      480

ggagccctga ccagcggcgt gcacaccttt ccagccgtgc tgcagagcag cggcctgtac      540

agcctgagca gcgtggtgac cgtgcctagc agcagcctgg gcacccagac ctacatctgc      600

aacgtgaacc acaagcccag caacaccaag gtggacaaga aggtggagcc caagagctgt      660

gatggcggcg gaggctccgg aggcggagga tctgggggag gcggaagtag cccgggccag      720

ggcacccaga gcgagaacag ctgcacccac ttccccggca acctgcccaa catgctgcgg      780
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gacctgaggg acgccttcag cagagtgaaa accttcttcc agatgaagga ccagctggac 840

aacctgctgc tgaaagagag cctgctggaa gatttcaagg gctacctggg ctgtcaggcc 900

ctgagcgaga tgatccagtt ctacctggaa gaagtgatgc cccaggccga gaaccaggac 960

cccgacatca aggcccacgt gaacagcctg ggcgagaacc tgaaaaccct gcggctgaga 1020

ctgcggcggt gccacagatt tctgccctgc gagaacaaga gcaaggccgt ggaacaggtg 1080

aagaacgcct tcaacaagct gcaggaaaag ggcatctaca aggccatgtc cgagttcgac 1140

atcttcatca actacatcga agcttacatg acaatgaaaa tccgcaat 1188

<210> 21
<211> 812
<212> PRT
<213> Artificial Sequence

<220>
<223> 4G8 Fab - scIL-10 - Fab (HC + scIL-10 + HC)

<400> 21

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

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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 Gly Gly Gly
    210                 215                 220

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Pro Gly Gln
225                 230                 235                 240

Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro Gly Asn Leu Pro
                245                 250                 255

Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg Val Lys Thr Phe
            260                 265                 270

Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu Lys Glu Ser Leu
        275                 280                 285

Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala Leu Ser Glu Met
    290                 295                 300

Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala Glu Asn Gln Asp
305                 310                 315                 320

Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly Glu Asn Leu Lys Thr
                325                 330                 335

Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu Pro Cys Glu Asn
            340                 345                 350

Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe Asn Lys Leu Gln
        355                 360                 365

Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp Ile Phe Ile Asn
    370                 375                 380

Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn Gly Gly Gly Gly
385                 390                 395                 400

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                405                 410                 415

Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro
            420                 425                 430

Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg
        435                 440                 445
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Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu
    450                 455                 460

Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala
465                 470                 475                 480

Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala
                485                 490                 495

Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly Glu
            500                 505                 510

Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu
        515                 520                 525

Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe
    530                 535                 540

Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp
545                 550                 555                 560

Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn
                565                 570                 575

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
            580                 585                 590

Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        595                 600                 605

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala
    610                 615                 620

Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
625                 630                 635                 640

Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
                645                 650                 655

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            660                 665                 670

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        675                 680                 685

Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
    690                 695                 700

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
705                 710                 715                 720
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Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
                725                 730                 735

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
            740                 745                 750

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
        755                 760                 765

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
    770                 775                 780

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
785                 790                 795                 800

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
                805                 810


<210>  22
<211>  2436
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  4G8 Fab - scIL-10 - Fab (HC + scIL-10 + HC)

<400>  22
gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc       60

tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct      120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac      180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat      240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggtgg      300

ctgggtaatt ttgactactg gggccaagga accctggtca ccgtctcgag tgctagcacc      360

aagggcccca gcgtgtttcc tctggccccc agcagcaaga gcacaagcgg cggaacagcc      420

gccctgggct gcctggtgaa ggactacttc cccgagcccg tgaccgtgtc ttggaacagc      480

ggagccctga ccagcggcgt gcacaccttt ccagccgtgc tgcagagcag cggcctgtac      540

agcctgagca gcgtggtgac cgtgcctagc agcagcctgg gcacccagac ctacatctgc      600

aacgtgaacc acaagcccag caacaccaag gtggacaaga aggtggagcc caagagctgt      660

gatggcggcg gaggctccgg aggcggagga tctgggggag gcggaagtag cccgggccag      720

ggcacccaga gcgagaacag ctgcacccac ttccccggca acctgcccaa catgctgcgg      780

gacctgaggg acgccttcag cagagtgaaa accttcttcc agatgaagga ccagctggac      840

aacctgctgc tgaaagagag cctgctggaa gatttcaagg gctacctggg ctgtcaggcc      900

ctgagcgaga tgatccagtt ctacctggaa gaagtgatgc cccaggccga gaaccaggac      960

cccgacatca aggcccacgt gaacagcctg ggcgagaacc tgaaaaccct gcggctgaga     1020
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ctgcggcggt gccacagatt tctgccctgc gagaacaaga gcaaggccgt ggaacaggtg 1080

aagaacgcct tcaacaagct gcaggaaaag ggcatctaca aggccatgtc cgagttcgac 1140

atcttcatca actacatcga agcttacatg accatgaaga tcagaaacgg cggaggcgga 1200

tctggcggcg gtggaagtgg aggcggagga tctgggggag gcggaagtag cccgggccag 1260

ggcacccaga gcgagaacag ctgcacccac ttccccggca acctgcccaa catgctgcgg 1320

gacctgaggg acgccttcag cagagtgaaa accttcttcc agatgaagga ccagctggac 1380

aacctgctgc tgaaagagag cctgctggaa gatttcaagg gctacctggg ctgtcaggcc 1440

ctgagcgaga tgatccagtt ctacctggaa gaagtgatgc cccaggccga gaaccaggac 1500

cccgacatca aggcccacgt gaacagcctg ggcgagaacc tgaaaaccct gcggctgaga 1560

ctgcggcggt gccacagatt tctgccctgc gagaacaaga gcaaggccgt ggaacaggtg 1620

aagaacgcct tcaacaagct gcaggaaaag ggcatctaca aggccatgtc cgagttcgac 1680

atcttcatca actacatcga ggcctacatg acaatgaaaa tccgcaatgg cgggggagga 1740

tcaggtggag ggggcagcgg tggtggagga tccgaggtgc aattgttgga gtctggggga 1800

ggcttggtac agcctggggg gtccctgaga ctctcctgtg cagcctccgg attcaccttt 1860

agcagttatg ccatgagctg ggtccgccag gctccaggga aggggctgga gtgggtctca 1920

gctattagtg gtagtggtgg tagcacatac tacgcagact ccgtgaaggg ccggttcacc 1980

atctccagag acaattccaa gaacacgctg tatctgcaga tgaacagcct gagagccgag 2040

gacacggccg tatattactg tgcgaaaggg tggctgggta attttgacta ctggggccaa 2100

ggaaccctgg tcaccgtctc gagtgctagc accaagggcc catcggtctt ccccctggca 2160

ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 2220

ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 2280

ttcccggctg tcctacagtc ctcaggactc tactccctca gcagcgtggt gaccgtgccc 2340

tccagcagct tgggcaccca gacctacatc tgcaacgtga atcacaagcc cagcaacacc 2400

aaggtggata agaaagttga gcccaaatct tgtgac 2436

<210> 23
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> 4G8 Fab -IL-10M1 - Fab (HC + IL-10M1 + HC)

<400> 23

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

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

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

35 40 45

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

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

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

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

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

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

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

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

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

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

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Pro Gly Gln
225 230 235 240

Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro Gly Asn Leu Pro
245 250 255

Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg Val Lys Thr Phe
260 265 270

Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu Lys Glu Ser Leu
275 280 285

Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala Leu Ser Glu Met
290 295 300

Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala Glu Asn Gln Asp

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305                 310                 315                 320

Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly Glu Asn Leu Lys Thr
                325                 330                 335

Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu Pro Cys Glu Asn
            340                 345                 350

Gly Gly Gly Ser Gly Gly Lys Ser Lys Ala Val Glu Gln Val Lys Asn
        355                 360                 365

Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu
    370                 375                 380

Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile
385                 390                 395                 400

Arg Asn Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                405                 410                 415

Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
            420                 425                 430

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser
        435                 440                 445

Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
    450                 455                 460

Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser
465                 470                 475                 480

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
                485                 490                 495

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
            500                 505                 510

Cys Ala Lys Gly Trp Leu Gly Asn Phe Asp Tyr Trp Gly Gln Gly Thr
        515                 520                 525

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
    530                 535                 540

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
545                 550                 555                 560

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
                565                 570                 575

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
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580 585 590

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
595 600 605

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
610 615 620

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
625 630 635

<210> 24
<211> 1914
<212> DNA
<213> Artificial Sequence

<220>
<223> 4G8 Fab -IL-10M1 - Fab (HC + IL-10M1 + HC)

<400> 24
gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggtgg 300

ctgggtaatt ttgactactg gggccaagga accctggtca ccgtctcgag tgctagcacc 360

aagggcccca gcgtgtttcc tctggccccc agcagcaaga gcacaagcgg cggaacagcc 420

gccctgggct gcctggtgaa ggactacttc cccgagcccg tgaccgtgtc ttggaacagc 480

ggagccctga ccagcggcgt gcacaccttt ccagccgtgc tgcagagcag cggcctgtac 540

agcctgagca gcgtggtgac cgtgcctagc agcagcctgg gcacccagac ctacatctgc 600

aacgtgaacc acaagcccag caacaccaag gtggacaaga aggtggagcc caagagctgt 660

gatggcggcg gaggctccgg aggcggagga agtggcggag gcggcagcag cccaggccag 720

ggcacccagt ctgagaacag ctgcacccac ttcccaggca acctgcctaa catgcttcga 780

gatctccgag atgccttcag cagagtgaag actttctttc aaatgaagga tcagctggac 840

aacttgttgt taaaggagtc cttgctggag gactttaagg gttacctggg ttgccaagcc 900

ttgtctgaga tgatccagtt ttacctggag gaggtgatgc cccaagctga gaaccaagac 960

ccagacatca aggcgcatgt gaactccctg ggggagaacc tgaagaccct caggctgagg 1020

ctacggcgct gtcatcgatt tcttccctgt gaaaacggcg gaggctctgg aggcaagagc 1080

aaggccgtgg agcaggtgaa gaacgccttt aataagctcc aagagaaagg catctacaaa 1140

gccatgagtg agtttgacat cttcatcaac tacatagaag cttacatgac aatgaagata 1200

cgaaacggcg gcggaggctc cggtggcgga ggaagtggcg gaggaggatc cgaggtgcaa 1260

ttgttggagt ctgggggagg cttggtacag cctgggggt ccctgagact ctcctgtgca 1320

gcctccggat tcacctttag cagttatgcc atgagctggg tccgccaggc tccagggaag 1380

gggctggagt gggtctcagc tattagtggt agtggtggta gcacatacta cgcagactcc 1440

gtgaagggcc ggttcaccat ctccagagac aattccaaga acacgctgta tctgcagatg 1500

aacagcctga gagccgagga cacggccgta tattactgtg cgaaagggtg gctgggtaat 1560

tttgactact ggggccaagg aaccctggtc accgtctcga gtgctagcac caagggccca 1620

tcggtcttcc ccctggcacc ctcctccaag agcacctctg ggggcacagc ggccctgggc 1680

tgcctggtca aggactactt ccccgaaccg gtgacggtgt cgtggaactc aggcgccctg 1740

accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcagc 1800

agcgtggtga ccgtgccctc cagcagcttg ggcacccaga cctacatctg caacgtgaat 1860

cacaagccca gcaacaccaa ggtggataag aaagttgagc ccaaatcttg tgac 1914

<210> 25
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> 4B9 IgG - IL-10 (LC)

<400> 25

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

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

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

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

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

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

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

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

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

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser

145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 26
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> 4B9 IgG - IL-10 (LC)

<400> 26
gagatcgtgc tgacccagtc ccccggcacc ctgtctctga gccctggcga gagagccacc 60

ctgtcctgca gagcctccca gtccgtgacc tcctcctacc tcgcctggta tcagcagaag 120

cccggccagg cccctcggct gctgatcaac gtgggcagtc ggagagccac cggcatccct 180

gaccggttct ccggctctgg ctccggcacc gacttcaccc tgaccatctc ccggctggaa 240

cccgaggact tcgccgtgta ctactgccag cagggcatca tgctgccccc cacctttggc 300

cagggcacca aggtggaaat caagcgtacg gtggccgctc cctccgtgtt catcttccca 360

ccctccgacg agcagctgaa gtccggcacc gcctccgtcg tgtgcctgct gaacaacttc 420

taccccgcg 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> 27
<211> 626
<212> PRT
<213> Artificial Sequence

<220>
<223> 4B9 IgG - IL-10 (HC P329G LALA + IL-10)

<400> 27

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

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

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

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

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

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

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

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

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

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

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

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

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

Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225                 230                 235                 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                 250                 255

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

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
    290                 295                 300
```

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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 Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
        355                 360                 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    370                 375                 380

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

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
                405                 410                 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
            420                 425                 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly
        435                 440                 445

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
    450                 455                 460

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

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

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

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

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

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

Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg
                565                 570                 575
```

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

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

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

Arg Asn
625

<210> 28
<211> 1878
<212> DNA
<213> Artificial Sequence

<220>
<223> 4B9 IgG - IL-10 (HC P329G LALA + IL-10)

<400> 28
gaggtgcagc tgctcgaaag cggcggagga ctggtgcagc ctggcggcag cctgagactg 60

tcttgcgccg ccagcggctt caccttcagc agctacgcca tgagctgggt ccgccaggcc 120

cctggcaagg gactggaatg ggtgtccgcc atcatcggct ctggcgccag cacctactac 180

gccgacagcg tgaagggccg gttcaccatc agccgggaca acagcaagaa caccctgtac 240

ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcgc caagggatgg 300

ttcggcggct tcaactactg gggacagggc accctggtca cagtgtccag cgctagcacc 360

aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600

aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 660

gacaaaactc acacatgccc accgtgccca gcacctgaag ctgcaggggg accgtcagtc 720

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 780

tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 840

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 900

cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 960

tgcaaggtct ccaacaaagc cctcggcgcc cccatcgaga aaaccatctc caaagccaaa 1020

gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag 1080

aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 1140

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1200

gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 1260

aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 1320

ctctccctgt ctccgggtgg cggaggggga tctggaggtg gcggctccgg aggcggagga 1380

tctgggggag gcggaagtag cccgggccag ggcacccaga gcgagaacag ctgcacccac 1440

ttccccggca acctgcccaa catgctgcgg gacctgaggg acgccttcag cagagtgaaa 1500

accttcttcc agatgaagga ccagctggac aacctgctgc tgaaagagag cctgctggaa 1560

gatttcaagg gctacctggg ctgtcaggcc ctgagcgaga tgatccagtt ctacctggaa 1620

gaagtgatgc cccaggccga gaaccaggac cccgacatca aggcccacgt gaacagcctg 1680

ggcgagaacc tgaaaaccct gcggctgaga ctgcggcggt gccacagatt tctgccctgc 1740

gagaacaaga gcaaggccgt ggaacaggtg aagaacgcct tcaacaagct gcaggaaaag 1800

ggcatctaca aggccatgtc cgagttcgac atcttcatca actacatcga agcttacatg 1860

acaatgaaaa tccgcaat 1878

<210> 29
<211> 627
<212> PRT
<213> Artificial Sequence

<220>
<223> 4B9 IgG -(IL-10M1)2 (HC P329G LALA + IL-10M1)

<400> 29

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225                 230                 235                 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                 250                 255

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

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 Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
        355                 360                 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    370                 375                 380

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

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
                405                 410                 415
```

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Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
            420                 425                 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly
        435                 440                 445

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Pro Gly
    450                 455                 460

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

Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg Val Lys Thr
                485                 490                 495

Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu Lys Glu Ser
            500                 505                 510

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

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

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

Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu Pro Cys Glu
                565                 570                 575

Asn Gly Gly Gly Ser Gly Gly Lys Ser Lys Ala Val Glu Gln Val Lys
            580                 585                 590

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

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

Ile Arg Asn
625
```

<210> 30
<211> 1881
<212> DNA
<213> Artificial Sequence

<220>
<223> 4B9 IgG -(IL-10M1)2 (HC P329G LALA + IL-10M1)

<400> 30
gaggtgcagc tgctcgaaag cggcggagga ctggtgcagc ctggcggcag cctgagactg 60

tcttgcgccg ccagcggctt caccttcagc agctacgcca tgagctgggt ccgccaggcc 120

cctggcaagg gactggaatg ggtgtccgcc atcatcggct ctggcgccag cacctactac 180

gccgacagcg tgaagggccg gttcaccatc agccgggaca acagcaagaa caccctgtac 240

ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcgc caagggatgg 300

ttcggcggct tcaactactg gggacagggc accctggtca cagtgtccag cgctagcacc 360

aagggcccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 420

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 480

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 540

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 600

aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 660

gacaaaactc acacatgccc accgtgccca gcacctgaag ctgcaggggg accgtcagtc 720

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 780

tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 840

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 900

cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 960

tgcaaggtct ccaacaaagc cctcggcgcc cccatcgaga aaaccatctc caaagccaaa 1020

gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag 1080

aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 1140

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 1200

gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 1260

aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 1320

ctctccctgt ctccgggtgg cggcggaggc tccggaggcg gaggaagtgg cggcggtggc 1380

agctctccag gccagggcac ccagagcgag aacagctgca cccacttccc cggcaacctg 1440

cccaacatgc tgcgggacct gagggacgcc ttcagcagag tgaaaacctt cttccagatg 1500

aaggaccagc tggacaacct gctgctgaaa gagagcctgc tggaagattt caagggctac 1560

ctgggctgtc aggccctgag cgagatgatc cagttctacc tggaagaagt gatgccccag 1620

gccgagaacc aggaccccga catcaaggcc cacgtgaaca gcctgggcga gaacctgaaa 1680

accctgcggc tgagactgcg gcggtgccac agatttctgc cctgcgagaa cggcggaggc 1740

tctggcggaa agtccaaggc cgtggaacag gtgaagaacg ccttcaacaa gctgcaggaa 1800

aagggcatct acaaggccat gagcgagttc gacatcttca tcaactacat cgaagcttac 1860

atgacaatga agatacgaaa c 1881

<210> 31
<211> 396
<212> PRT
<213> Artificial Sequence

<220>
<223> 4B9 Fab - IL-10 (HC + IL-10)

<400> 31

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Pro Gly Gln
225                 230                 235                 240

Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro Gly Asn Leu Pro
                245                 250                 255
```

```
Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg Val Lys Thr Phe
            260                 265                 270

Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu Lys Glu Ser Leu
        275                 280                 285

Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala Leu Ser Glu Met
    290                 295                 300

Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala Glu Asn Gln Asp
305                 310                 315                 320

Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly Glu Asn Leu Lys Thr
                325                 330                 335

Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu Pro Cys Glu Asn
            340                 345                 350

Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe Asn Lys Leu Gln
        355                 360                 365

Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp Ile Phe Ile Asn
    370                 375                 380

Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn
385                 390                 395


<210>  32
<211>  1188
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  4B9 Fab - IL-10 (HC + IL-10)

<400>  32
gaggtgcagc tgctcgaaag cggcggagga ctggtgcagc ctggcggcag cctgagactg       60

tcttgcgccg ccagcggctt caccttcagc agctacgcca tgagctgggt ccgccaggcc      120

cctggcaagg gactggaatg ggtgtccgcc atcatcggct ctggcgccag cacctactac      180

gccgacagcg tgaagggccg gttcaccatc agccgggaca acagcaagaa caccctgtac      240

ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcgc caagggatgg      300

ttcggcggct tcaactactg gggacagggc accctggtca cagtgtccag cgctagcacc      360

aagggcccca gcgtgtttcc tctggccccc agcagcaaga gcacaagcgg cggaacagcc      420

gccctgggct gcctggtgaa ggactacttc cccgagcccg tgaccgtgtc ttggaacagc      480

ggagccctga ccagcggcgt gcacaccttt ccagccgtgc tgcagagcag cggcctgtac      540

agcctgagca gcgtggtgac cgtgcctagc agcagcctgg gcacccagac ctacatctgc      600

aacgtgaacc acaagcccag caacaccaag gtggacaaga aggtggagcc caagagctgt      660
```

gatggcggcg gaggctccgg aggcggagga tctgggggag gcggaagtag cccgggccag 720

ggcacccaga gcgagaacag ctgcacccac ttccccggca acctgcccaa catgctgcgg 780

gacctgaggg acgccttcag cagagtgaaa accttcttcc agatgaagga ccagctggac 840

aacctgctgc tgaaagagag cctgctggaa gatttcaagg gctacctggg ctgtcaggcc 900

ctgagcgaga tgatccagtt ctacctggaa gaagtgatgc cccaggccga gaaccaggac 960

cccgacatca aggcccacgt gaacagcctg ggcgagaacc tgaaaaccct gcggctgaga 1020

ctgcggcggt gccacagatt tctgccctgc gagaacaaga gcaaggccgt ggaacaggtg 1080

aagaacgcct tcaacaagct gcaggaaaag ggcatctaca aggccatgtc cgagttcgac 1140

atcttcatca actacatcga agcttacatg acaatgaaaa tccgcaat 1188

<210> 33
<211> 812
<212> PRT
<213> Artificial Sequence

<220>
<223> 4B9 Fab - scIL-10 - Fab (HC + IL-10 + HC)

<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 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 Gly Gly Gly
    210                 215                 220

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Pro Gly Gln
225                 230                 235                 240

Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro Gly Asn Leu Pro
                245                 250                 255

Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg Val Lys Thr Phe
            260                 265                 270

Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu Lys Glu Ser Leu
        275                 280                 285

Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala Leu Ser Glu Met
    290                 295                 300

Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala Glu Asn Gln Asp
305                 310                 315                 320

Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly Glu Asn Leu Lys Thr
                325                 330                 335

Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu Pro Cys Glu Asn
            340                 345                 350

Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe Asn Lys Leu Gln
        355                 360                 365

Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp Ile Phe Ile Asn
    370                 375                 380

Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn Gly Gly Gly Gly
385                 390                 395                 400

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                405                 410                 415

Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro
            420                 425                 430
```

```
Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg
        435                 440                 445

Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu
    450                 455                 460

Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala
465                 470                 475                 480

Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala
                485                 490                 495

Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly Glu
            500                 505                 510

Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu
        515                 520                 525

Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe
    530                 535                 540

Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp
545                 550                 555                 560

Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn
                565                 570                 575

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
            580                 585                 590

Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
        595                 600                 605

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala
    610                 615                 620

Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
625                 630                 635                 640

Ala Ile Ile Gly Ser Gly Ala Ser Thr Tyr Tyr Ala Asp Ser Val Lys
                645                 650                 655

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
            660                 665                 670

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
        675                 680                 685

Lys Gly Trp Phe Gly Gly Phe Asn Tyr Trp Gly Gln Gly Thr Leu Val
    690                 695                 700
```

```
Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
705                 710                 715                 720

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
                725                 730                 735

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
            740                 745                 750

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
        755                 760                 765

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
    770                 775                 780

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
785                 790                 795                 800

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
                805                 810
```

<210> 34
<211> 2436
<212> DNA
<213> Artificial Sequence

<220>
<223> 4B9 Fab - scIL-10 - Fab (HC + IL-10 + HC)

<400> 34

```
gaggtgcagc tgctcgaaag cggcggagga ctggtgcagc ctggcggcag cctgagactg       60

tcttgcgccg ccagcggctt caccttcagc agctacgcca tgagctgggt ccgccaggcc      120

cctggcaagg gactggaatg ggtgtccgcc atcatcggct ctggcgccag cacctactac      180

gccgacagcg tgaagggccg gttcaccatc agccgggaca acagcaagaa caccctgtac      240

ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcgc caagggatgg      300

ttcggcggct tcaactactg gggacagggc accctggtca cagtgtccag cgctagcacc      360

aagggcccca gcgtgtttcc tctggccccc agcagcaaga gcacaagcgg cggaacagcc      420

gccctgggct gcctggtgaa ggactacttc cccgagcccg tgaccgtgtc ttggaacagc      480

ggagccctga ccagcggcgt gcacaccttt ccagccgtgc tgcagagcag cggcctgtac      540

agcctgagca gcgtggtgac cgtgcctagc agcagcctgg gcacccagac ctacatctgc      600

aacgtgaacc acaagcccag caacaccaag gtggacaaga aggtggagcc caagagctgt      660

gatggcggcg gaggctccgg aggcggagga tctgggggag gcggaagtag cccgggccag      720

ggcacccaga gcgagaacag ctgcacccac ttccccggca acctgcccaa catgctgcgg      780

gacctgaggg acgccttcag cagagtgaaa accttcttcc agatgaagga ccagctggac      840

aacctgctgc tgaaagagag cctgctggaa gatttcaagg gctacctggg ctgtcaggcc      900
```

ctgagcgaga tgatccagtt ctacctggaa gaagtgatgc cccaggccga gaaccaggac 960

cccgacatca aggcccacgt gaacagcctg ggcgagaacc tgaaaaccct gcggctgaga 1020

ctgcggcggt gccacagatt tctgccctgc gagaacaaga gcaaggccgt ggaacaggtg 1080

aagaacgcct tcaacaagct gcaggaaaag ggcatctaca aggccatgtc cgagttcgac 1140

atcttcatca actacatcga agcttacatg accatgaaga tcagaaacgg cggaggcgga 1200

tctggcggcg gtggaagtgg aggcggagga tctgggggag gcggaagtag cccgggccag 1260

ggcacccaga gcgagaacag ctgcacccac ttccccggca acctgcccaa catgctgcgg 1320

gacctgaggg acgccttcag cagagtgaaa accttcttcc agatgaagga ccagctggac 1380

aacctgctgc tgaaagagag cctgctggaa gatttcaagg gctacctggg ctgtcaggcc 1440

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cccgacatca aggcccacgt gaacagcctg ggcgagaacc tgaaaaccct gcggctgaga 1560

ctgcggcggt gccacagatt tctgccctgc gagaacaaga gcaaggccgt ggaacaggtg 1620

aagaacgcct tcaacaagct gcaggaaaag ggcatctaca aggccatgtc cgagttcgac 1680

atcttcatca actacatcga ggcctacatg acaatgaaaa tccgcaatgg cgggggagga 1740

tcaggtggag ggggcagcgg tggtggagga tccgaggtgc aattgctcga aagcggcgga 1800

ggactggtgc agcctggcgg cagcctgaga ctgtcttgcg ccgccagcgg tttcaccttc 1860

agcagctacg ccatgagctg ggtccgccag gcccctggca agggactgga atgggtgtcc 1920

gccatcatcg gctctggcgc cagcacctac tacgccgaca gcgtgaaggg ccggttcacc 1980

atcagccggg acaacagcaa gaacaccctg tacctgcaga tgaacagcct gcgggccgag 2040

gacaccgccg tgtactactg cgccaaggga tggttcggcg gcttcaacta ctggggacag 2100

ggcaccctgg tcacagtgtc cagcgctagc accaagggcc catcggtctt cccctggca 2160

ccctcctcca agagcacctc tgggggcaca gcggccctgg gctgcctggt caaggactac 2220

ttccccgaac cggtgacggt gtcgtggaac tcaggcgccc tgaccagcgg cgtgcacacc 2280

ttcccggctg tcctacagtc ctcaggactc tactccctca gcagcgtggt gaccgtgccc 2340

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aaggtggata agaaagttga gcccaaatct tgtgac 2436

<210> 35
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Leader peptide

<400> 35

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

Val His Ser

<210> 36
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Leader peptide

<400> 36
atgggctggt cctgcatcat cctgtttctg gtcgccacag ccaccggcgt gcactct 57

<210> 37
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> HCDR1 (1)

<400> 37

Ser Tyr Ala Met Ser
1 5

<210> 38
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> HCDR1 (1)

<400> 38
agttatgcca tgagc 15

<210> 39
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> HCDR1 (2)

<400> 39

Ser His Ala Met Ser
1 5

<210> 40
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> HCDR1 (2)

<400> 40
agtcatgcta tgagc 15

<210> 41

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

<220>
<223> HCDR2 (1)

<400> 41

Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

<210> 42
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> HCDR2 (1)

<400> 42
gctattagtg gtagtggtgg tagcacatac tacgcagact ccgtgaag 48

<210> 43
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> HCDR2 (2)

<400> 43

Ala Ile Ile Gly Ser Gly Ala Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

<210> 44
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> HCDR2 (2)

<400> 44
gccatcatcg gctctggcgc cagcacctac tacgccgaca gcgtgaag 48

<210> 45
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> HCDR2 (3)

<400> 45

Ala Ile Trp Ala Ser Gly Glu Gln Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

<210> 46
<211> 45
<212> DNA

<213> Artificial Sequence

<220>
<223> HCDR2 (3)

<400> 46
gctatttggg ctagtgggga gcaatactac gcagactccg tgaag 45

<210> 47
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> HCDR3 (1)

<400> 47

Tyr Cys Ala Lys Gly Trp Phe Gly
1 5

<210> 48
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> HCDR3 (1)

<400> 48
tactgcgcca agggatggtt cggc 24

<210> 49
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> HCDR3 (2)

<400> 49

Tyr Cys Ala Lys Gly Trp Leu Gly
1 5

<210> 50
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> HCDR3 (2)

<400> 50
tactgtgcga aagggtggct gggt 24

<210> 51
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> LCDR1 (1)

<400> 51

Arg Ala Ser Gln Ser Val Thr Ser Ser Tyr Leu
1 5 10

<210> 52
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> LCDR1 (1)

<400> 52
agagcctccc agtccgtgac ctcctcctac ctc 33

<210> 53
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> LCDR1 (2)

<400> 53

Arg Ala Ser Gln Ser Val Ser Arg Ser Tyr Leu
1 5 10

<210> 54
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> LCDR1 (2)

<400> 54
agagcctccc agtccgtgtc ccggtcctac ctc 33

<210> 55
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> LCDR2 (1)

<400> 55

Asn Val Gly Ser Arg Arg Ala
1 5

<210> 56
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> LCDR2 (1)

<400> 56

aacgtgggca gtcggagagc c 21

<210> 57
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> LCDR2 (2)

<400> 57

Ile Gly Ala Ser Thr Arg Ala
1 5

<210> 58
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> LCDR2 (2)

<400> 58
atcggcgcct ctaccagagc c 21

<210> 59
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> LCDR3 (1)

<400> 59

Cys Gln Gln Gly Ile Met Leu Pro Pro
1 5

<210> 60
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> LCDR3 (1)

<400> 60
tgccagcagg gcatcatgct gcccccc 27

<210> 61
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> LCDR3 (2)

<400> 61

Cys Gln Gln Gly Gln Val Ile Pro Pro
1 5

<210> 62
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> LCDR3 (2)

<400> 62
tgccagcagg gccaggtcat ccctccc 27

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

<220>
<223> 4G8; 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 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> 64
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> 4G8; VH

<400> 64
gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggtgg 300

ctgggtaatt ttgactactg gggccaagga accctggtca ccgtctcgag t 351

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

<220>
<223> 4G8; 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 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> 66
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 4G8; VL

<400> 66
gagatcgtgc tgacccagtc ccccggcacc ctgtctctga gccctggcga gagagccacc 60

ctgtcctgca gagcctccca gtccgtgtcc cggtcctacc 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 caag 324

<210> 67
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> 4B9; 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

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> 68
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> 4B9; VH

<400> 68
gaggtgcagc tgctcgaaag cggcggagga ctggtgcagc ctggcggcag cctgagactg 60

tcttgcgccg ccagcggctt caccttcagc agctacgcca tgagctgggt ccgccaggcc 120

cctggcaagg gactggaatg ggtgtccgcc atcatcggct ctggcgccag cacctactac 180

gccgacagcg tgaagggccg gttcaccatc agccgggaca acagcaagaa caccctgtac 240

ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcgc caagggatgg 300

ttcggcggct tcaactactg gggacagggc accctggtca cagtgtccag c 351

<210> 69
<211> 108
<212> PRT

<213> Artificial Sequence

<220>
<223> 4B9; VL

<400> 69

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val 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> 70
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 4B9; VL

<400> 70
gagatcgtgc tgacccagtc ccccggcacc ctgtctctga gccctggcga gagagccacc 60

ctgtcctgca gagcctccca gtccgtgacc tcctcctacc tcgcctggta tcagcagaag 120

cccggccagg cccctcggct gctgatcaac gtgggcagtc ggagagccac cggcatccct 180

gaccggttct ccggctctgg ctccggcacc gacttcaccc tgaccatctc ccggctggaa 240

cccgaggact tcgccgtgta ctactgccag cagggcatca tgctgccccc cacctttggc 300

cagggcacca aggtggaaat caag 324

<210> 71
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> 28H1; 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 His
20 25 30

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

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

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

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

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

Thr Val Ser Ser
115

<210> 72
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<223> 28H1; VH

<400> 72
gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctccggatt cacctttagc agtcatgcta tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct atttgggcta gtggggagca atactacgca 180

gactccgtga agggccggtt caccatctcc agagacaatt ccaagaacac gctgtatctg 240

cagatgaaca gcctgagagc cgaggacacg gccgtatatt actgtgcgaa agggtggctg 300

ggtaattttg actactgggg ccaaggaacc ctggtcaccg tctcgagt 348

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

<220>
<223> 28H1; 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 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> 74
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> 28H1; VL

<400> 74
gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcttgca gggccagtca gagtgttagc cgcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatcatt ggggcctcca ccagggccac tggcatccca 180

gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagggtcagg ttattccccc tacgttcggc 300

caggggacca aagtggaaat caaa 324

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

<220>
<223> 3F2; VH

<400> 75

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

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

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

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

50 55 60

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

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

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

Val Thr Val Ser Ser
115

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

<220>
<223> 3F2; VH

<400> 76
gaggtgcaat tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctccggatt cacctttagc agttatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagggtgg 300

tttggtggtt ttaactactg gggccaagga accctggtca ccgtctcgag t 351

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

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

<400> 77

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val 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> 78
<211> 324
<212> DNA
<213> Artificial Sequence

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

<400> 78
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 cagggtatta tgcttccccc gacgttcggc 300

caggggacca aagtggaaat caaa 324

<210> 79
<211> 330
<212> PRT
<213> Homo sapiens

<400> 79

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

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

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

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

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

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

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

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Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
        115                 120                 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
    130                 135                 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145                 150                 155                 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
                165                 170                 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
            180                 185                 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        195                 200                 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
    210                 215                 220

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

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

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
            260                 265                 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
        275                 280                 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
    290                 295                 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305                 310                 315                 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330
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<210> 80
<211> 107
<212> PRT
<213> Homo sapiens

<400> 80

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

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

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

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

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

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

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

<210> 81
<211> 748
<212> PRT
<213> Artificial Sequence

<220>
<223> Human FAP ectodomain+poly-lys-tag+his6-tag

<400> 81

Arg Pro Ser Arg Val His Asn Ser Glu Glu Asn Thr Met Arg Ala Leu
1 5 10 15

Thr Leu Lys Asp Ile Leu Asn Gly Thr Phe Ser Tyr Lys Thr Phe Phe
20 25 30

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

Asn Ile Val Leu Tyr Asn Ile Glu Thr Gly Gln Ser Tyr Thr Ile Leu
50 55 60

Ser Asn Arg Thr Met Lys Ser Val Asn Ala Ser Asn Tyr Gly Leu Ser
65 70 75 80

Pro Asp Arg Gln Phe Val Tyr Leu Glu Ser Asp Tyr Ser Lys Leu Trp
85 90 95

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

Glu Phe Val Arg Gly Asn Glu Leu Pro Arg Pro Ile Gln Tyr Leu Cys
115 120 125

Trp Ser Pro Val Gly Ser Lys Leu Ala Tyr Val Tyr Gln Asn Asn Ile
130 135 140

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Tyr Leu Lys Gln Arg Pro Gly Asp Pro Pro Phe Gln Ile Thr Phe Asn
145                 150                 155                 160

Gly Arg Glu Asn Lys Ile Phe Asn Gly Ile Pro Asp Trp Val Tyr Glu
                165                 170                 175

Glu Glu Met Leu Ala Thr Lys Tyr Ala Leu Trp Trp Ser Pro Asn Gly
            180                 185                 190

Lys Phe Leu Ala Tyr Ala Glu Phe Asn Asp Thr Asp Ile Pro Val Ile
        195                 200                 205

Ala Tyr Ser Tyr Tyr Gly Asp Glu Gln Tyr Pro Arg Thr Ile Asn Ile
    210                 215                 220

Pro Tyr Pro Lys Ala Gly Ala Lys Asn Pro Val Val Arg Ile Phe Ile
225                 230                 235                 240

Ile Asp Thr Thr Tyr Pro Ala Tyr Val Gly Pro Gln Glu Val Pro Val
                245                 250                 255

Pro Ala Met Ile Ala Ser Ser Asp Tyr Tyr Phe Ser Trp Leu Thr Trp
            260                 265                 270

Val Thr Asp Glu Arg Val Cys Leu Gln Trp Leu Lys Arg Val Gln Asn
        275                 280                 285

Val Ser Val Leu Ser Ile Cys Asp Phe Arg Glu Asp Trp Gln Thr Trp
    290                 295                 300

Asp Cys Pro Lys Thr Gln Glu His Ile Glu Glu Ser Arg Thr Gly Trp
305                 310                 315                 320

Ala Gly Gly Phe Phe Val Ser Thr Pro Val Phe Ser Tyr Asp Ala Ile
                325                 330                 335

Ser Tyr Tyr Lys Ile Phe Ser Asp Lys Asp Gly Tyr Lys His Ile His
            340                 345                 350

Tyr Ile Lys Asp Thr Val Glu Asn Ala Ile Gln Ile Thr Ser Gly Lys
        355                 360                 365

Trp Glu Ala Ile Asn Ile Phe Arg Val Thr Gln Asp Ser Leu Phe Tyr
    370                 375                 380

Ser Ser Asn Glu Phe Glu Glu Tyr Pro Gly Arg Arg Asn Ile Tyr Arg
385                 390                 395                 400

Ile Ser Ile Gly Ser Tyr Pro Pro Ser Lys Lys Cys Val Thr Cys His
                405                 410                 415
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Leu Arg Lys Glu Arg Cys Gln Tyr Tyr Thr Ala Ser Phe Ser Asp Tyr
            420                 425                 430

Ala Lys Tyr Tyr Ala Leu Val Cys Tyr Gly Pro Gly Ile Pro Ile Ser
        435                 440                 445

Thr Leu His Asp Gly Arg Thr Asp Gln Glu Ile Lys Ile Leu Glu Glu
    450                 455                 460

Asn Lys Glu Leu Glu Asn Ala Leu Lys Asn Ile Gln Leu Pro Lys Glu
465                 470                 475                 480

Glu Ile Lys Lys Leu Glu Val Asp Glu Ile Thr Leu Trp Tyr Lys Met
                485                 490                 495

Ile Leu Pro Pro Gln Phe Asp Arg Ser Lys Lys Tyr Pro Leu Leu Ile
            500                 505                 510

Gln Val Tyr Gly Gly Pro Cys Ser Gln Ser Val Arg Ser Val Phe Ala
        515                 520                 525

Val Asn Trp Ile Ser Tyr Leu Ala Ser Lys Glu Gly Met Val Ile Ala
    530                 535                 540

Leu Val Asp Gly Arg Gly Thr Ala Phe Gln Gly Asp Lys Leu Leu Tyr
545                 550                 555                 560

Ala Val Tyr Arg Lys Leu Gly Val Tyr Glu Val Glu Asp Gln Ile Thr
                565                 570                 575

Ala Val Arg Lys Phe Ile Glu Met Gly Phe Ile Asp Glu Lys Arg Ile
            580                 585                 590

Ala Ile Trp Gly Trp Ser Tyr Gly Gly Tyr Val Ser Ser Leu Ala Leu
        595                 600                 605

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

Ser Ser Trp Glu Tyr Tyr Ala Ser Val Tyr Thr Glu Arg Phe Met Gly
625                 630                 635                 640

Leu Pro Thr Lys Asp Asp Asn Leu Glu His Tyr Lys Asn Ser Thr Val
                645                 650                 655

Met Ala Arg Ala Glu Tyr Phe Arg Asn Val Asp Tyr Leu Leu Ile His
            660                 665                 670

Gly Thr Ala Asp Asp Asn Val His Phe Gln Asn Ser Ala Gln Ile Ala
        675                 680                 685
```

Lys Ala Leu Val Asn Ala Gln Val Asp Phe Gln Ala Met Trp Tyr Ser
690 695 700

Asp Gln Asn His Gly Leu Ser Gly Leu Ser Thr Asn His Leu Tyr Thr
705 710 715 720

His Met Thr His Phe Leu Lys Gln Cys Phe Ser Leu Ser Asp Gly Lys
725 730 735

Lys Lys Lys Lys Lys Gly His His His His His His
740 745

<210> 82
<211> 2244
<212> DNA
<213> Artificial Sequence

<220>
<223> Human FAP ectodomain+poly-lys-tag+his6-tag

<400> 82
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attttaaatg gaacattttc ttataaaaca ttttttccaa actggatttc aggacaagaa 120

tatcttcatc aatctgcaga taacaatata gtactttata atattgaaac aggacaatca 180

tataccattt tgagtaatag aaccatgaaa agtgtgaatg cttcaaatta cggcttatca 240

cctgatcggc aatttgtata tctagaaagt gattattcaa agctttggag atactcttac 300

acagcaacat attacatcta tgaccttagc aatggagaat ttgtaagagg aaatgagctt 360

cctcgtccaa ttcagtattt atgctggtcg cctgttggga gtaaattagc atatgtctat 420

caaaacaata tctatttgaa acaaagacca ggagatccac cttttcaaat aacatttaat 480

ggaagagaaa ataaaatatt taatggaatc ccagactggg tttatgaaga ggaaatgctt 540

gctacaaaat atgctctctg gtggtctcct aatggaaaat ttttggcata tgcggaattt 600

aatgatacgg atataccagt tattgcctat tcctattatg gcgatgaaca atatcctaga 660

acaataaata ttccataccc aaaggctgga gctaagaatc ccgttgttcg gatatttatt 720

atcgatacca cttaccctgc gtatgtaggt ccccaggaag tgcctgttcc agcaatgata 780

gcctcaagtg attattattt cagttggctc acgtgggtta ctgatgaacg agtatgtttg 840

cagtggctaa aaagagtcca gaatgtttcg gtcctgtcta tatgtgactt cagggaagac 900

tggcagacat gggattgtcc aaagacccag gagcatatag aagaaagcag aactggatgg 960

gctggtggat tctttgtttc aacaccagtt ttcagctatg atgccatttc gtactacaaa 1020

atatttagtg acaaggatgg ctacaaacat attcactata tcaaagacac tgtggaaaat 1080

gctattcaaa ttacaagtgg caagtgggag gccataaata tattcagagt aacacaggat 1140

tcactgtttt attctagcaa tgaatttgaa gaataccctg gaagaagaaa catctacaga 1200

attagcattg gaagctatcc tccaagcaag aagtgtgtta cttgccatct aaggaaagaa 1260

aggtgccaat attacacagc aagtttcagc gactacgcca agtactatgc acttgtctgc 1320

tacggcccag gcatccccat ttccaccctt catgatggac gcactgatca agaaattaaa 1380

atcctggaag aaaacaagga attggaaaat gctttgaaaa atatccagct gcctaaagag 1440

gaaattaaga aacttgaagt agatgaaatt actttatggt acaagatgat tcttcctcct 1500

caatttgaca gatcaaagaa gtatcccttg ctaattcaag tgtatggtgg tccctgcagt 1560

cagagtgtaa ggtctgtatt tgctgttaat tggatatctt atcttgcaag taaggaaggg 1620

atggtcattg ccttggtgga tggtcgagga acagctttcc aaggtgacaa actcctctat 1680

gcagtgtatc gaaagctggg tgtttatgaa gttgaagacc agattacagc tgtcagaaaa 1740

ttcatagaaa tgggtttcat tgatgaaaaa agaatagcca tatggggctg gtcctatgga 1800

ggatacgttt catcactggc ccttgcatct ggaactggtc ttttcaaatg tggtatagca 1860

gtggctccag tctccagctg ggaatattac gcgtctgtct acacagagag attcatgggt 1920

ctcccaacaa aggatgataa tcttgagcac tataagaatt caactgtgat ggcaagagca 1980

gaatatttca gaaatgtaga ctatcttctc atccacggaa cagcagatga taatgtgcac 2040

tttcaaaact cagcacagat tgctaaagct ctggttaatg cacaagtgga tttccaggca 2100

atgtggtact ctgaccagaa ccacggctta tccggcctgt ccacgaacca cttatacacc 2160

cacatgaccc acttcctaaa gcagtgtttc tctttgtcag acggcaaaaa gaaaaagaaa 2220

aagggccacc accatcacca tcac 2244

<210> 83
<211> 749
<212> PRT
<213> Artificial Sequence

<220>
<223> Murine FAP ectodomain+poly-lys-tag+his6-tag

<400> 83

Arg Pro Ser Arg Val Tyr Lys Pro Glu Gly Asn Thr Lys Arg Ala Leu
1 5 10 15

Thr Leu Lys Asp Ile Leu Asn Gly Thr Phe Ser Tyr Lys Thr Tyr Phe
20 25 30

Pro Asn Trp Ile Ser Glu Gln Glu Tyr Leu His Gln Ser Glu Asp Asp
35 40 45

Asn Ile Val Phe Tyr Asn Ile Glu Thr Arg Glu Ser Tyr Ile Ile Leu
50 55 60

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

Pro Asp Arg Gln Phe Val Tyr Leu Glu Ser Asp Tyr Ser Lys Leu Trp
85 90 95

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

Glu Phe Val Arg Gly Tyr Glu Leu Pro Arg Pro Ile Gln Tyr Leu Cys
        115                 120                 125

Trp Ser Pro Val Gly Ser Lys Leu Ala Tyr Val Tyr Gln Asn Asn Ile
    130                 135                 140

Tyr Leu Lys Gln Arg Pro Gly Asp Pro Pro Phe Gln Ile Thr Tyr Thr
145                 150                 155                 160

Gly Arg Glu Asn Arg Ile Phe Asn Gly Ile Pro Asp Trp Val Tyr Glu
                165                 170                 175

Glu Glu Met Leu Ala Thr Lys Tyr Ala Leu Trp Trp Ser Pro Asp Gly
            180                 185                 190

Lys Phe Leu Ala Tyr Val Glu Phe Asn Asp Ser Asp Ile Pro Ile Ile
        195                 200                 205

Ala Tyr Ser Tyr Tyr Gly Asp Gly Gln Tyr Pro Arg Thr Ile Asn Ile
    210                 215                 220

Pro Tyr Pro Lys Ala Gly Ala Lys Asn Pro Val Val Arg Val Phe Ile
225                 230                 235                 240

Val Asp Thr Thr Tyr Pro His His Val Gly Pro Met Glu Val Pro Val
                245                 250                 255

Pro Glu Met Ile Ala Ser Ser Asp Tyr Tyr Phe Ser Trp Leu Thr Trp
            260                 265                 270

Val Ser Ser Glu Arg Val Cys Leu Gln Trp Leu Lys Arg Val Gln Asn
        275                 280                 285

Val Ser Val Leu Ser Ile Cys Asp Phe Arg Glu Asp Trp His Ala Trp
    290                 295                 300

Glu Cys Pro Lys Asn Gln Glu His Val Glu Glu Ser Arg Thr Gly Trp
305                 310                 315                 320

Ala Gly Gly Phe Phe Val Ser Thr Pro Ala Phe Ser Gln Asp Ala Thr
                325                 330                 335

Ser Tyr Tyr Lys Ile Phe Ser Asp Lys Asp Gly Tyr Lys His Ile His
            340                 345                 350

Tyr Ile Lys Asp Thr Val Glu Asn Ala Ile Gln Ile Thr Ser Gly Lys
        355                 360                 365
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Trp Glu Ala Ile Tyr Ile Phe Arg Val Thr Gln Asp Ser Leu Phe Tyr
    370                 375                 380

Ser Ser Asn Glu Phe Glu Gly Tyr Pro Gly Arg Arg Asn Ile Tyr Arg
385                 390                 395                 400

Ile Ser Ile Gly Asn Ser Pro Pro Ser Lys Lys Cys Val Thr Cys His
                405                 410                 415

Leu Arg Lys Glu Arg Cys Gln Tyr Tyr Thr Ala Ser Phe Ser Tyr Lys
            420                 425                 430

Ala Lys Tyr Tyr Ala Leu Val Cys Tyr Gly Pro Gly Leu Pro Ile Ser
        435                 440                 445

Thr Leu His Asp Gly Arg Thr Asp Gln Glu Ile Gln Val Leu Glu Glu
    450                 455                 460

Asn Lys Glu Leu Glu Asn Ser Leu Arg Asn Ile Gln Leu Pro Lys Val
465                 470                 475                 480

Glu Ile Lys Lys Leu Lys Asp Gly Gly Leu Thr Phe Trp Tyr Lys Met
                485                 490                 495

Ile Leu Pro Pro Gln Phe Asp Arg Ser Lys Lys Tyr Pro Leu Leu Ile
            500                 505                 510

Gln Val Tyr Gly Gly Pro Cys Ser Gln Ser Val Lys Ser Val Phe Ala
        515                 520                 525

Val Asn Trp Ile Thr Tyr Leu Ala Ser Lys Glu Gly Ile Val Ile Ala
    530                 535                 540

Leu Val Asp Gly Arg Gly Thr Ala Phe Gln Gly Asp Lys Phe Leu His
545                 550                 555                 560

Ala Val Tyr Arg Lys Leu Gly Val Tyr Glu Val Glu Asp Gln Leu Thr
                565                 570                 575

Ala Val Arg Lys Phe Ile Glu Met Gly Phe Ile Asp Glu Glu Arg Ile
            580                 585                 590

Ala Ile Trp Gly Trp Ser Tyr Gly Gly Tyr Val Ser Ser Leu Ala Leu
        595                 600                 605

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

Ser Ser Trp Glu Tyr Tyr Ala Ser Ile Tyr Ser Glu Arg Phe Met Gly
625                 630                 635                 640
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Leu Pro Thr Lys Asp Asp Asn Leu Glu His Tyr Lys Asn Ser Thr Val
                645                 650                 655

Met Ala Arg Ala Glu Tyr Phe Arg Asn Val Asp Tyr Leu Leu Ile His
            660                 665                 670

Gly Thr Ala Asp Asp Asn Val His Phe Gln Asn Ser Ala Gln Ile Ala
        675                 680                 685

Lys Ala Leu Val Asn Ala Gln Val Asp Phe Gln Ala Met Trp Tyr Ser
    690                 695                 700

Asp Gln Asn His Gly Ile Leu Ser Gly Arg Ser Gln Asn His Leu Tyr
705                 710                 715                 720

Thr His Met Thr His Phe Leu Lys Gln Cys Phe Ser Leu Ser Asp Gly
                725                 730                 735

Lys Lys Lys Lys Lys Lys Gly His His His His His His
            740                 745


<210>  84
<211>  2247
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Murine FAP ectodomain+poly-lys-tag+his6-tag

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attttaaatg gaacattctc atataaaaca tattttccca actggatttc agaacaagaa      120

tatcttcatc aatctgagga tgataacata gtattttata atattgaaac aagagaatca      180

tatatcattt tgagtaatag caccatgaaa agtgtgaatg ctacagatta tggtttgtca      240

cctgatcggc aatttgtgta tctagaaagt gattattcaa agctctggcg atattcatac      300

acagcgacat actacatcta cgaccttcag aatggggaat ttgtaagagg atacgagctc      360

cctcgtccaa ttcagtatct atgctggtcg cctgttggga gtaaattagc atatgtatat      420

caaaacaata tttatttgaa acaaagacca ggagatccac cttttcaaat aacttatact      480

ggaagagaaa atagaatatt taatggaata ccagactggg tttatgaaga ggaaatgctt      540

gccacaaaat atgctctttg gtggtctcca gatggaaaat ttttggcata tgtagaattt      600

aatgattcag atataccaat tattgcctat tcttattatg gtgatggaca gtatcctaga      660

actataaata ttccatatcc aaaggctggg gctaagaatc cggttgttcg tgtttttatt      720

gttgacacca cctaccctca ccacgtgggc ccaatggaag tgccagttcc agaaatgata      780

gcctcaagtg actattattt cagctggctc acatgggtgt ccagtgaacg agtatgcttg      840

cagtggctaa aaagagtgca gaatgtctca gtcctgtcta tatgtgattt cagggaagac      900
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tggcatgcat gggaatgtcc aaagaaccag gagcatgtag aagaaagcag aacaggatgg 960

gctggtggat tctttgtttc gacaccagct tttagccagg atgccacttc ttactacaaa 1020

atatttagcg acaaggatgg ttacaaacat attcactaca tcaaagacac tgtggaaaat 1080

gctattcaaa ttacaagtgg caagtgggag gccatatata tattccgcgt aacacaggat 1140

tcactgtttt attctagcaa tgaatttgaa ggttaccctg gaagaagaaa catctacaga 1200

attagcattg gaaactctcc tccgagcaag aagtgtgtta cttgccatct aaggaaagaa 1260

aggtgccaat attacacagc aagtttcagc tacaaagcca agtactatgc actcgtctgc 1320

tatggccctg gcctccccat ttccaccctc catgatggcc gcacagacca agaaatacaa 1380

gtattagaag aaaacaaaga actggaaaat tctctgagaa atatccagct gcctaaagtg 1440

gagattaaga agctcaaaga cgggggactg actttctggt acaagatgat tctgcctcct 1500

cagtttgaca gatcaaagaa gtacccttg ctaattcaag tgtatggtgg tccttgtagc 1560

cagagtgtta agtctgtgtt tgctgttaat tggataactt atctcgcaag taaggagggg 1620

atagtcattg ccctggtaga tggtcggggc actgctttcc aaggtgacaa attcctgcat 1680

gccgtgtatc gaaaactggg tgtatatgaa gttgaggacc agctcacagc tgtcagaaaa 1740

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gtggctccag tctccagctg ggaatattac gcatctatct actcagagag attcatgggc 1920

ctcccaacaa aggacgacaa tctcgaacac tataaaaatt caactgtgat ggcaagagca 1980

gaatatttca gaaatgtaga ctatcttctc atccacggaa cagcagatga taatgtgcac 2040

tttcagaact cagcacagat tgctaaagct ttggttaatg cacaagtgga tttccaggcg 2100

atgtggtact ctgaccagaa ccatggtata ttatctgggc gctcccagaa tcatttatat 2160

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aaaaagggcc accaccatca ccatcac 2247

<210> 85
<211> 748
<212> PRT
<213> Artificial Sequence

<220>
<223> Cynomolgus FAP ectodomain+poly-lys-tag+his6-tag

<400> 85

Arg Pro Pro Arg Val His Asn Ser Glu Glu Asn Thr Met Arg Ala Leu
1 5 10 15

Thr Leu Lys Asp Ile Leu Asn Gly Thr Phe Ser Tyr Lys Thr Phe Phe
20 25 30

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

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Asn Ile Val Leu Tyr Asn Ile Glu Thr Gly Gln Ser Tyr Thr Ile Leu
    50                  55                  60

Ser Asn Arg Thr Met Lys Ser Val Asn Ala Ser Asn Tyr Gly Leu Ser
65                  70                  75                  80

Pro Asp Arg Gln Phe Val Tyr Leu Glu Ser Asp Tyr Ser Lys Leu Trp
                85                  90                  95

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

Glu Phe Val Arg Gly Asn Glu Leu Pro Arg Pro Ile Gln Tyr Leu Cys
        115                 120                 125

Trp Ser Pro Val Gly Ser Lys Leu Ala Tyr Val Tyr Gln Asn Asn Ile
    130                 135                 140

Tyr Leu Lys Gln Arg Pro Gly Asp Pro Pro Phe Gln Ile Thr Phe Asn
145                 150                 155                 160

Gly Arg Glu Asn Lys Ile Phe Asn Gly Ile Pro Asp Trp Val Tyr Glu
                165                 170                 175

Glu Glu Met Leu Ala Thr Lys Tyr Ala Leu Trp Trp Ser Pro Asn Gly
            180                 185                 190

Lys Phe Leu Ala Tyr Ala Glu Phe Asn Asp Thr Asp Ile Pro Val Ile
        195                 200                 205

Ala Tyr Ser Tyr Tyr Gly Asp Glu Gln Tyr Pro Arg Thr Ile Asn Ile
    210                 215                 220

Pro Tyr Pro Lys Ala Gly Ala Lys Asn Pro Phe Val Arg Ile Phe Ile
225                 230                 235                 240

Ile Asp Thr Thr Tyr Pro Ala Tyr Val Gly Pro Gln Glu Val Pro Val
                245                 250                 255

Pro Ala Met Ile Ala Ser Ser Asp Tyr Tyr Phe Ser Trp Leu Thr Trp
            260                 265                 270

Val Thr Asp Glu Arg Val Cys Leu Gln Trp Leu Lys Arg Val Gln Asn
        275                 280                 285

Val Ser Val Leu Ser Ile Cys Asp Phe Arg Glu Asp Trp Gln Thr Trp
    290                 295                 300

Asp Cys Pro Lys Thr Gln Glu His Ile Glu Glu Ser Arg Thr Gly Trp
305                 310                 315                 320
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Ala Gly Gly Phe Phe Val Ser Thr Pro Val Phe Ser Tyr Asp Ala Ile
                325                 330                 335

Ser Tyr Tyr Lys Ile Phe Ser Asp Lys Asp Gly Tyr Lys His Ile His
            340                 345                 350

Tyr Ile Lys Asp Thr Val Glu Asn Ala Ile Gln Ile Thr Ser Gly Lys
        355                 360                 365

Trp Glu Ala Ile Asn Ile Phe Arg Val Thr Gln Asp Ser Leu Phe Tyr
    370                 375                 380

Ser Ser Asn Glu Phe Glu Asp Tyr Pro Gly Arg Arg Asn Ile Tyr Arg
385                 390                 395                 400

Ile Ser Ile Gly Ser Tyr Pro Pro Ser Lys Lys Cys Val Thr Cys His
                405                 410                 415

Leu Arg Lys Glu Arg Cys Gln Tyr Tyr Thr Ala Ser Phe Ser Asp Tyr
            420                 425                 430

Ala Lys Tyr Tyr Ala Leu Val Cys Tyr Gly Pro Gly Ile Pro Ile Ser
        435                 440                 445

Thr Leu His Asp Gly Arg Thr Asp Gln Glu Ile Lys Ile Leu Glu Glu
    450                 455                 460

Asn Lys Glu Leu Glu Asn Ala Leu Lys Asn Ile Gln Leu Pro Lys Glu
465                 470                 475                 480

Glu Ile Lys Lys Leu Glu Val Asp Glu Ile Thr Leu Trp Tyr Lys Met
                485                 490                 495

Ile Leu Pro Pro Gln Phe Asp Arg Ser Lys Lys Tyr Pro Leu Leu Ile
            500                 505                 510

Gln Val Tyr Gly Gly Pro Cys Ser Gln Ser Val Arg Ser Val Phe Ala
        515                 520                 525

Val Asn Trp Ile Ser Tyr Leu Ala Ser Lys Glu Gly Met Val Ile Ala
    530                 535                 540

Leu Val Asp Gly Arg Gly Thr Ala Phe Gln Gly Asp Lys Leu Leu Tyr
545                 550                 555                 560

Ala Val Tyr Arg Lys Leu Gly Val Tyr Glu Val Glu Asp Gln Ile Thr
                565                 570                 575

Ala Val Arg Lys Phe Ile Glu Met Gly Phe Ile Asp Glu Lys Arg Ile
            580                 585                 590
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Ala Ile Trp Gly Trp Ser Tyr Gly Gly Tyr Val Ser Ser Leu Ala Leu
        595                 600                 605

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

Ser Ser Trp Glu Tyr Tyr Ala Ser Val Tyr Thr Glu Arg Phe Met Gly
625                 630                 635                 640

Leu Pro Thr Lys Asp Asp Asn Leu Glu His Tyr Lys Asn Ser Thr Val
                645                 650                 655

Met Ala Arg Ala Glu Tyr Phe Arg Asn Val Asp Tyr Leu Leu Ile His
            660                 665                 670

Gly Thr Ala Asp Asp Asn Val His Phe Gln Asn Ser Ala Gln Ile Ala
        675                 680                 685

Lys Ala Leu Val Asn Ala Gln Val Asp Phe Gln Ala Met Trp Tyr Ser
    690                 695                 700

Asp Gln Asn His Gly Leu Ser Gly Leu Ser Thr Asn His Leu Tyr Thr
705                 710                 715                 720

His Met Thr His Phe Leu Lys Gln Cys Phe Ser Leu Ser Asp Gly Lys
                725                 730                 735

Lys Lys Lys Lys Lys Gly His His His His His His
            740                 745
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<210> 86
<211> 2244
<212> DNA
<213> Artificial Sequence

<220>
<223> Cynomolgus FAP ectodomain+poly-lys-tag+his6-tag (DNA)

<400> 86

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tatcttcatc aatctgcaga taacaatata gtactttata atattgaaac aggacaatca      180

tataccattt tgagtaacag aaccatgaaa agtgtgaatg cttcaaatta tggcttatca      240

cctgatcggc aatttgtata tctagaaagt gattattcaa agctttggag atactcttac      300

acagcaacat attacatcta tgaccttagc aatggagaat ttgtaagagg aaatgagctt      360

cctcgtccaa ttcagtattt atgctggtcg cctgttggga gtaaattagc atatgtctat      420

caaaacaata tctatttgaa acaaagacca ggagatccac cttttcaaat aacatttaat      480

ggaagagaaa ataaaatatt taatggaatc ccagactggg tttatgaaga ggaaatgctt      540
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gctacaaaat atgctctctg gtggtctcct aatggaaaat ttttggcata tgcggaattt 600

aatgatacag atataccagt tattgcctat tcctattatg gcgatgaaca atatcccaga 660

acaataaata ttccataccc aaaggccgga gctaagaatc cttttgttcg gatatttatt 720

atcgatacca cttaccctgc gtatgtaggt ccccaggaag tgcctgttcc agcaatgata 780

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tggcagacat gggattgtcc aaagacccag gagcatatag aagaaagcag aactggatgg 960

gctggtggat tctttgtttc aacaccagtt ttcagctatg atgccatttc atactacaaa 1020

atatttagtg acaaggatgg ctacaaacat attcactata tcaaagacac tgtggaaaat 1080

gctattcaaa ttacaagtgg caagtgggag gccataaata tattcagagt aacacaggat 1140

tcactgtttt attctagcaa tgaatttgaa gattaccctg gaagaagaaa catctacaga 1200

attagcattg gaagctatcc tccaagcaag aagtgtgtta cttgccatct aaggaaagaa 1260

aggtgccaat attacacagc aagtttcagc gactacgcca agtactatgc acttgtctgc 1320

tatggcccag gcatccccat ttccaccctt catgacggac gcactgatca agaaattaaa 1380

atcctggaag aaaacaagga attggaaaat gctttgaaaa atatccagct gcctaaagag 1440

gaaattaaga aacttgaagt agatgaaatt actttatggt acaagatgat tcttcctcct 1500

caatttgaca gatcaaagaa gtatcccttg ctaattcaag tgtatggtgg tccctgcagt 1560

cagagtgtaa ggtctgtatt tgctgttaat tggatatctt atcttgcaag taaggaaggg 1620

atggtcattg ccttggtgga tggtcgggga acagctttcc aaggtgacaa actcctgtat 1680

gcagtgtatc gaaagctggg tgtttatgaa gttgaagacc agattacagc tgtcagaaaa 1740

ttcatagaaa tgggtttcat tgatgaaaaa agaatagcca tatggggctg gtcctatgga 1800

ggatatgttt catcactggc ccttgcatct ggaactggtc ttttcaaatg tgggatagca 1860

gtggctccag tctccagctg ggaatattac gcgtctgtct acacagagag attcatgggt 1920

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gaatatttca gaaatgtaga ctatcttctc atccacggaa cagcagatga taatgtgcac 2040

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atgtggtact ctgaccagaa ccacggctta tccggcctgt ccacgaacca cttatacacc 2160

cacatgaccc acttcctaaa gcagtgtttc tctttgtcag acggcaaaaa gaaaaagaaa 2220

aagggccacc accatcacca tcac 2244

<210> 87
<211> 474
<212> PRT
<213> Artificial Sequence

<220>
<223> Human IL-10R1-Fc fusion + Avi-tag

<400> 87

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His Gly Thr Glu Leu Pro Ser Pro Pro Ser Val Trp Phe Glu Ala Glu
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Phe Phe His His Ile Leu His Trp Thr Pro Ile Pro Asn Gln Ser Glu
            20                  25                  30

Ser Thr Cys Tyr Glu Val Ala Leu Leu Arg Tyr Gly Ile Glu Ser Trp
        35                  40                  45

Asn Ser Ile Ser Asn Cys Ser Gln Thr Leu Ser Tyr Asp Leu Thr Ala
    50                  55                  60

Val Thr Leu Asp Leu Tyr His Ser Asn Gly Tyr Arg Ala Arg Val Arg
65                  70                  75                  80

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

Phe Ser Val Asp Glu Val Thr Leu Thr Val Gly Ser Val Asn Leu Glu
            100                 105                 110

Ile His Asn Gly Phe Ile Leu Gly Lys Ile Gln Leu Pro Arg Pro Lys
        115                 120                 125

Met Ala Pro Ala Asn Asp Thr Tyr Glu Ser Ile Phe Ser His Phe Arg
    130                 135                 140

Glu Tyr Glu Ile Ala Ile Arg Lys Val Pro Gly Asn Phe Thr Phe Thr
145                 150                 155                 160

His Lys Lys Val Lys His Glu Asn Phe Ser Leu Leu Thr Ser Gly Glu
                165                 170                 175

Val Gly Glu Phe Cys Val Gln Val Lys Pro Ser Val Ala Ser Arg Ser
            180                 185                 190

Asn Lys Gly Met Trp Ser Lys Glu Glu Cys Ile Ser Leu Thr Arg Gln
        195                 200                 205

Tyr Phe Thr Val Thr Asn Val Asp Glu Gln Leu Tyr Phe Gln Gly Gly
    210                 215                 220

Ser Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
225                 230                 235                 240

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
                245                 250                 255

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
            260                 265                 270
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Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
        275                 280                 285

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
    290                 295                 300

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
305                 310                 315                 320

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
                325                 330                 335

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
            340                 345                 350

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
        355                 360                 365

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
    370                 375                 380

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

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
                405                 410                 415

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

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
        435                 440                 445

Ser Leu Ser Leu Ser Pro Gly Gly Gly Ser Gly Gly Leu Asn Asp Ile
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Phe Glu Ala Gln Lys Ile Glu Trp His Glu
465                 470


<210>  88
<211>  1422
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Human IL-1OR1-Fc fusion + Avi-tag

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ctgaggtatg gaatagagtc ctggaactcc atctccaact gtagccagac cctgtcctat      180
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gaagtgactc tgacagttgg cagtgtgaac ctagagatcc acaatggctt catcctcggg 360

aagattcagc tacccaggcc caagatggcc cccgcaaatg acacatatga aagcatcttc 420

agtcacttcc gagagtatga gattgccatt cgcaaggtgc cgggaaactt cacgttcaca 480

cacaagaaag taaaacatga aaacttcagc ctcctaacct ctggagaagt gggagagttc 540

tgtgtccagg tgaaaccatc tgtcgcttcc cgaagtaaca aggggatgtg gtctaaagag 600

gagtgcatct ccctcaccag gcagtatttc accgtgacca acgtcgacga acagttatat 660

tttcagggcg gctcacccaa atctgcagac aaaactcaca catgcccacc gtgcccagca 720

cctgaactcc tgggggggacc gtcagtcttc ctcttccccc caaaacccaa ggacaccctc 780

atgatctccc ggacccctga ggtcacatgc gtggtggtgg acgtgagcca cgaagaccct 840

gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgccaa gacaaagccg 900

cgggaggagc agtacaacag cacgtaccgt gtggtcagcg tcctcaccgt cctgcaccag 960

gactggctga atggcaagga gtacaagtgc aaggtctcca acaaagccct cccagccccc 1020

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cccccatccc gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc 1140

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<210> 89
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> HCDR Kabat (1)

<400> 89
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