eolf-seql

SEQUENCE LISTING

<110> F. Hoffmann-La Roche AG

<120> Interleukin-2 fusion proteins and uses thereof

<130> 31142

<150> US 61/936564
<151> 2014-02-06

<160> 66

<170> PatentIn version 3.5

<210> 1
<211> 133
<212> PRT
<213> Homo sapiens

<400> 1

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

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

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

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

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

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

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

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

Ile Ser Thr Leu Thr
130

<210> 2
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> Wild-type human IL-2

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ttacagatga ttttgaatgg aattaataat tacaagaatc ccaaactcac caggatgctc 120

acatttaagt tttacatgcc caagaaggcc acagaactga aacatcttca gtgtctagaa 180

gaagaactca aacctctgga ggaagtgcta aatttagctc aaagcaaaaa ctttcactta 240

agacccaggg acttaatcag caatatcaac gtaatagttc tggaactaaa gggatctgaa 300

acaacattca tgtgtgaata tgctgatgag acagcaacca ttgtagaatt tctgaacaga 360

tggattacct tttgtcaaag catcatctca acactgact 399

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

<220>
<223> Wild-type human IL-2 (C125A)

<400> 3

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

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

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

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

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

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

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

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

Ile Ser Thr Leu Thr
130

<210> 4
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> Wild-type human IL-2 (C125A) (1)

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ctgcagatga tcctgaacgg catcaacaac tacaagaacc ccaagctgac ccggatgctg 120

accttcaagt tctacatgcc caagaaggcc accgagctga aacatctgca gtgcctggaa 180

gaggaactga agcctctgga agaggtgctg aacctggccc agtccaagaa cttccacctg 240

aggcctcggg acctgatctc caacatcaac gtgatcgtgc tggaactgaa gggctccgag 300

acaaccttca tgtgcgagta cgccgacgag acagctacca tcgtggaatt tctgaaccgg 360

tggatcacct tcgcccagtc catcatctcc accctgacc 399

<210> 5
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> Wild-type human IL-2 (C125A) (2)

<400> 5
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ttacagatga ttttgaatgg aattaataat tacaagaatc ccaaactcac caggatgctc 120

acatttaagt tttacatgcc caagaaggcc acagaactga aacatcttca gtgtctagaa 180

gaagaactca aacctctgga ggaagtgcta aatttagctc aaagcaaaaa ctttcactta 240

agacccaggg acttaatcag caatatcaac gtaatagttc tggaactaaa gggatctgaa 300

acaacattca tgtgtgaata tgctgatgag acagcaacca ttgtagaatt tctgaacaga 360

tggattacct ttgcccaaag catcatctca acactgact 399

<210> 6
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> Wild-type human IL-2 (C125A) (3)

<400> 6
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ctgcagatga tcctgaacgg catcaacaac tacaagaacc ccaagctgac ccggatgctg 120

accttcaagt tctacatgcc caagaaggcc accgaactga aacatctgca gtgcctggaa 180

gaggaactga agcctctgga agaggtgctg aacctggccc agagcaagaa cttccacctg 240

aggcccaggg acctgatcag caacatcaac gtgatcgtgc tggaactgaa gggcagcgag 300

acaaccttca tgtgcgagta cgccgacgag acagccacca tcgtggaatt tctgaaccgg 360

tggatcacct tcgcccagag catcatcagc accctgaca 399

<210> 7
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> Wild-type IL-2 (C125A) (4)

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acatttaagt tttacatgcc caagaaggcc acagaactga aacatcttca gtgtctagaa 180

gaagaactca aacctctgga ggaagtgcta aatttagctc aaagcaaaaa ctttcactta 240

agacccaggg acttaatcag caatatcaac gtaatagttc tggaactaaa gggatctgaa 300

acaacattca tgtgtgaata tgctgatgag acagcaacca ttgtagaatt tctgaacaga 360

tggattacct ttgcccaaag catcatctca acactgact 399

<210> 8
<211> 227
<212> PRT
<213> Homo sapiens

<400> 8

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

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

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

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        35                  40                  45

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

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

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

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

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

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

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

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

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

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

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

Pro Gly Lys
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225

<210> 9
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> DP47GS VH

<400> 9

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

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

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

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

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

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

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

Val Ser Ser
115

<210> 10
<211> 345
<212> DNA

<213> Artificial Sequence

<220>
<223> DP47GS VH

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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

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ggatttgact actggggcca aggaaccctg gtcaccgtct cgagt 345

<210> 11
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> DP47GS VL

<400> 11

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

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

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

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

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

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

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

<210> 12
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> DP47GS VL

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ctctcttgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccgct gacgttcggc 300

caggggacca aagtggaaat caaa 324

<210> 13
<211> 592
<212> PRT
<213> Artificial Sequence

<220>
<223> DP47GS HC(Fc knob,P329G LALA)-IL2

<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

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

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

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

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

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

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

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

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

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

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

Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
    210                 215                 220
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Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu
225                 230                 235                 240


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


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


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


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


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


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


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


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


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


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


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

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Pro Thr Ser Ser
    450                 455                 460

Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu
465                 470                 475                 480

Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr
                485                 490                 495

Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu
            500                 505                 510

Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
        515                 520                 525

Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu
    530                 535                 540

Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr
545                 550                 555                 560

Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe
                565                 570                 575

Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
            580                 585                 590
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<210> 14
<211> 1776
<212> DNA

<213> Artificial Sequence

<220>
<223> DP47GS HC(Fc knob,P329G LALA)-IL2

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ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggcagc 300

ggatttgact actggggcca aggaaccctg gtcaccgtct cgagtgctag caccaagggc 360

ccatcggtct tccccctggc accctcctcc aagagcacct ctgggggcac agcggccctg 420

ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc 480

ctgaccagcg gcgtgcacac cttcccggct gtcctacagt cctcaggact ctactccctc 540

agcagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg 600

aatcacaagc ccagcaacac caaggtggac aagaaagttg agcccaaatc ttgtgacaaa 660

actcacacat gcccaccgtg cccagcacct gaagctgcag ggggaccgtc agtcttcctc 720

ttccccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg 780

gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 840

gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg 900

gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag 960

gtctccaaca aagccctcgg cgcccccatc gagaaaacca tctccaaagc caaagggcag 1020

ccccgagaac cacaggtgta caccctgccc ccatgccggg atgagctgac caagaaccag 1080

gtcagcctgt ggtgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 1140

agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1200

tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1260

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ctgtctccgg gtggcggcgg aggctccgga ggcggaggtt ctggaggcgg aggctccgca 1380

cctacttcaa gttctacaaa gaaaacacag ctacaactgg agcatttact gctggattta 1440

cagatgattt tgaatggaat taataattac aagaatccca aactcaccag gatgctcaca 1500

tttaagtttt acatgcccaa gaaggccaca gaactgaaac atcttcagtg tctagaagaa 1560

gaactcaaac ctctggagga agtgctaaat ttagctcaaa gcaaaaactt tcacttaaga 1620

cccagggact taatcagcaa tatcaacgta atagttctgg aactaaaggg atctgaaaca 1680

acattcatgt gtgaatatgc tgatgagaca gcaaccattg tagaatttct gaacagatgg 1740

attacctttg cccaaagcat catctcaaca ctgact 1776

<210> 15
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> DP47GS HC(Fc hole, P329G LALA)

<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

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

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

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

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

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

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

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

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

Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu
225                 230                 235                 240

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

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
            260                 265                 270
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Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        275                 280                 285

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

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

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

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

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

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

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

Ser Phe Phe Leu Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                405                 410                 415

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

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445
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<210> 16
<211> 1335
<212> DNA

<213> Artificial Sequence

<220>
<223> DP47GS HC(Fc hole, P329G LALA)

<400> 16
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ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcagatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaggcagc 300

ggatttgact actggggcca aggaaccctg gtcaccgtct cgagtgctag caccaagggc 360

ccctccgtgt tccccctggc ccccagcagc aagagcacca gcggcggcac agccgctctg 420

ggctgcctgg tcaaggacta cttccccgag cccgtgaccg tgtcctggaa cagcggagcc 480

ctgacctccg gcgtgcacac cttccccgcc gtgctgcaga gttctggcct gtatagcctg 540

agcagcgtgg tcaccgtgcc ttctagcagc ctgggcaccc agacctacat ctgcaacgtg 600

aaccacaagc ccagcaacac caaggtggac aagaaggtgg agcccaagag ctgcgacaaa 660

actcacacat gcccaccgtg cccagcacct gaagctgcag ggggaccgtc agtcttcctc 720

ttcccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg 780

gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 840

gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg 900

gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag 960

gtctccaaca aagccctcgg cgcccccatc gagaaaacca tctccaaagc caaagggcag 1020

ccccgagaac cacaggtgtg caccctgccc ccatcccggg atgagctgac caagaaccag 1080

gtcagcctct cgtgcgcagt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 1140

agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1200

tccttcttcc tcgtgagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1260

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<210> 17
<211> 592
<212> PRT
<213> Artificial Sequence

<220>
<223> DP47GS HC (Fc wt, P329G LALA)-IL2

<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 Ser Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

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

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val

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    130                 135                 140

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

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

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

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

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

Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu
225                 230                 235                 240

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

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

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

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

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

Val Ser Asn Lys Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys
```

```
                325                 330                 335

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

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

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

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

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

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

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

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Pro Thr Ser Ser
    450                 455                 460

Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu
465                 470                 475                 480

Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr
                485                 490                 495

Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu
            500                 505                 510

Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
```

eolf-seql

515 520 525

Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu
530 535 540

Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr
545 550 555 560

Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe
565 570 575

Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
580 585 590

<210> 18
<211> 1776
<212> DNA
<213> Artificial Sequence

<220>
<223> DP47GS HC (Fc wt, P329G LALA)-IL2

<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 gaaaggcagc 300

ggatttgact actggggcca aggaaccctg gtcaccgtct cgagtgctag caccaagggc 360

ccatcggtct tcccctggc accctcctcc aagagcacct ctgggggcac agcggccctg 420

ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc 480

ctgaccagcg gcgtgcacac cttcccggct gtcctacagt cctcaggact ctactccctc 540

agcagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg 600

aatcacaagc ccagcaacac caaggtggac aagaaagttg agcccaaatc ttgtgacaaa 660

actcacacat gcccaccgtg cccagcacct gaagctgcag ggggaccgtc agtcttcctc 720

ttccccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg 780

gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 840

gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg 900

gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag 960

gtctccaaca aagccctcgg cgcccccatc gagaaaacca tctccaaagc caaagggcag 1020

ccccgagaac cacaggtgta caccctgccc ccatcccggg atgagctgac caagaaccag 1080

gtcagcctga cctgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 1140

agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1200

tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1260

ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc 1320

ctgtctccgg gtggcggcgg aggctccgga ggcggaggtt ctggaggcgg aggctccgca 1380

cctacttcaa gttctacaaa gaaaacacag ctacaactgg agcatttact gctggattta 1440

cagatgattt tgaatggaat taataattac aagaatccca aactcaccag gatgctcaca 1500

tttaagtttt acatgcccaa gaaggccaca gaactgaaac atcttcagtg tctagaagaa 1560

gaactcaaac ctctggagga agtgctaaat ttagctcaaa gcaaaaactt tcacttaaga 1620

cccagggact taatcagcaa tatcaacgta atagttctgg aactaaaggg atctgaaaca 1680

acattcatgt gtgaatatgc tgatgagaca gcaaccattg tagaatttct gaacagatgg 1740

attacctttg cccaaagcat catctcaaca ctgact 1776

<210> 19
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> DP47GS LC

<400> 19

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


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


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


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


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


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


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


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
```

eolf-seql

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> 20
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> DP47GS LC

<400> 20
gaaatcgtgt taacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcttgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggagcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg atccgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccgct gacgttcggc 300

caggggacca aagtggaaat caaacgtacg gtggctgcac catctgtctt catcttcccg 360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 420

tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600

ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgt 645

<210> 21
<211> 466
<212> PRT
<213> Artificial Sequence

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

<400> 21

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


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


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


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


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


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


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


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


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


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


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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Lys
465
```

<210> 22
<211> 1401
<212> DNA
<213> Artificial Sequence

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

<400> 22

```
atggacatga gggtccccgc tcagctcctg ggcctcctgc tgctctggtt cccaggtgcc       60

aggtgtgcgg tgaatggcac ttcccagttc acatgcttct acaactcgag agccaacatc      120

tcctgtgtct ggagccaaga tggggctctg caggacactt cctgccaagt ccatgcctgg      180

ccggacagac ggcggtggaa ccaaacctgt gagctgctcc ccgtgagtca agcatcctgg      240

gcctgcaacc tgatcctcgg agccccagat tctcagaaac tgaccacagt tgacatcgtc      300
```

accctgaggg tgctgtgccg tgaggggtg cgatggaggg tgatggccat ccaggacttc 360

aagccctttg agaaccttcg cctgatggcc cccatctccc tccaagttgt ccacgtggag 420

acccacagat gcaacataag ctgggaaatc tcccaagcct cccactactt tgaaagacac 480

ctggagttcg aggcccggac gctgtcccca ggccacacct gggaggaggc ccccctgctg 540

actctcaagc agaagcagga atggatctgc ctggagacgc tcaccccaga cacccagtat 600

gagtttcagg tgcgggtcaa gcctctgcaa ggcgagttca cgacctggag cccctggagc 660

cagcccctgg ccttcagaac aaagcctgca gcccttggga aggacaccgg agctcaggac 720

aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc 780

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 840

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 900

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 960

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 1020

aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggg 1080

cagccccgag aaccacaggt gtgcaccctg cccccatccc gggatgagct gaccaagaac 1140

caggtcagcc tctcgtgcgc agtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1200

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1260

ggctccttct tcctcgtgag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1320

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1380

tccctgtctc cgggtaaatg a 1401

<210> 23
<211> 492
<212> PRT
<213> Artificial Sequence

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

<400> 23

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

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

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

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

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

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

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

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

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

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

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

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

```
Trp Asp His Ser Trp Thr Glu Gln Ser Val Asp Tyr Arg His Lys Phe
        195                 200                 205

Ser Leu Pro Ser Val Asp Gly Gln Lys Arg Tyr Thr Phe Arg Val Arg
    210                 215                 220

Ser Arg Phe Asn Pro Leu Cys Gly Ser Ala Gln His Trp Ser Glu Trp
225                 230                 235                 240

Ser His Pro Ile His Trp Gly Ser Asn Thr Ser Lys Glu Asn Pro Phe
                245                 250                 255

Leu Phe Ala Leu Glu Ala Gly Ala Gln Asp Lys Thr His Thr Cys Pro
            260                 265                 270

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

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

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

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

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

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

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

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


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


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


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


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


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


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

<210> 24
<211> 1479
<212> DNA
<213> Artificial Sequence

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

<400> 24

```
atgttgaagc catcattacc attcacatcc ctcttattcc tgcagctgcc cctgctggga       60

gtggggctga acacgacaat tctgacgccc aatgggaatg aagacaccac agctgatttc      120

ttcctgacca ctatgcccac tgactccctc agtgtttcca ctctgcccct cccagaggtt      180

cagtgttttg tgttcaatgt cgagtacatg aattgcactt ggaacagcag ctctgagccc      240

cagcctacca acctcactct gcattattgg tacaagaact cggataatga taaagtccag      300
```

aagtgcagcc actatctatt ctctgaagaa atcacttctg gctgtcagtt gcaaaaaaag 360

gagatccacc tctaccaaac atttgttgtt cagctccagg acccacggga acccaggaga 420

caggccacac agatgctaaa actgcagaat ctggtgatcc cctgggctcc agagaaccta 480

acacttcaca aactgagtga atcccagcta gaactgaact ggaacaacag attcttgaac 540

cactgtttgg agcacttggt gcagtaccgg actgactggg accacagctg gactgaacaa 600

tcagtggatt atagacataa gttctccttg cctagtgtgg atgggcagaa acgctacacg 660

tttcgtgttc ggagccgctt taacccactc tgtggaagtg ctcagcattg gagtgaatgg 720

agccacccaa tccactgggg gagcaatact tcaaaagaga atcctttcct gtttgcattg 780

gaagccggag ctcaggacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 840

gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 900

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 960

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 1020

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 1080

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 1140

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatgccgg 1200

gatgagctga ccaagaacca ggtcagcctg tggtgcctgg tcaaaggctt ctatcccagc 1260

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1320

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1380

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1440

tacacgcaga agagcctctc cctgtctccg ggtaaatga 1479

<210> 25
<211> 219
<212> PRT
<213> Artificial Sequence

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

<400> 25

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


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


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


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


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


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


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


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


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


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


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


Gln Pro Gln Leu Ile Cys Thr Gly Val Asp Glu Gln Leu Tyr Phe Gln
```

eolf-seql

180 185 190

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

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

<210> 26
<211> 660
<212> DNA
<213> Artificial Sequence

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

<400> 26
atgggatgga gctgtatcat cctcttcttg gtagcaacag ctaccggtgt gcattccgag 60

ctctgtgacg atgacccgcc agagatccca cacgccacat tcaaagccat ggcctacaag 120

gaaggaacca tgttgaactg tgaatgcaag agaggtttcc gcagaataaa aagcgggtca 180

ctctatatgc tctgtacagg aaactctagc cactcgtcct gggacaacca atgtcaatgc 240

acaagctctg ccactcggaa cacaacgaaa caagtgacac ctcaacctga agaacagaaa 300

gaaaggaaaa ccacagaaat gcaaagtcca atgcagccag tggaccaagc gagccttcca 360

ggtcactgca gggaacctcc accatgggaa aatgaagcca cagagagaat ttatcatttc 420

gtggtggggc agatggttta ttatcagtgc gtccagggat acagggctct acacagaggt 480

cctgctgaga gcgtctgcaa aatgacccac gggaagacaa ggtggaccca gccccagctc 540

atatgcacag gtgtcgacga acagttatat tttcagggcg gctcaggcct gaacgacatc 600

ttcgaggccc agaagatcga gtggcacgag gctcgagctc accaccatca ccatcactga 660

<210> 27
<211> 473
<212> PRT
<213> Artificial Sequence

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

<400> 27

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


Phe Pro Leu Leu Leu Leu Trp Phe Pro Gly Ala Arg Cys Ala Val Lys
            20                  25                  30


Asn Cys Ser His Leu Glu Cys Phe Tyr Asn Ser Arg Ala Asn Val Ser
        35                  40                  45


Cys Met Trp Ser His Glu Glu Ala Leu Asn Val Thr Thr Cys His Val
    50                  55                  60


His Ala Lys Ser Asn Leu Arg His Trp Asn Lys Thr Cys Glu Leu Thr
65                  70                  75                  80


Leu Val Arg Gln Ala Ser Trp Ala Cys Asn Leu Ile Leu Gly Ser Phe
                85                  90                  95


Pro Glu Ser Gln Ser Leu Thr Ser Val Asp Leu Leu Asp Ile Asn Val
            100                 105                 110


Val Cys Trp Glu Glu Lys Gly Trp Arg Arg Val Lys Thr Cys Asp Phe
        115                 120                 125


His Pro Phe Asp Asn Leu Arg Leu Val Ala Pro His Ser Leu Gln Val
    130                 135                 140


Leu His Ile Asp Thr Gln Arg Cys Asn Ile Ser Trp Lys Val Ser Gln
145                 150                 155                 160


Val Ser His Tyr Ile Glu Pro Tyr Leu Glu Phe Glu Ala Arg Arg Arg
                165                 170                 175
```

```
Leu Leu Gly His Ser Trp Glu Asp Ala Ser Val Leu Ser Leu Lys Gln
            180                 185                 190

Arg Gln Gln Trp Leu Phe Leu Glu Met Leu Ile Pro Ser Thr Ser Tyr
        195                 200                 205

Glu Val Gln Val Arg Val Lys Ala Gln Arg Asn Asn Thr Gly Thr Trp
    210                 215                 220

Ser Pro Trp Ser Gln Pro Leu Thr Phe Arg Thr Arg Pro Ala Asp Pro
225                 230                 235                 240

Met Lys Glu Gly Ala Gln Asp Lys Thr His Thr Cys Pro Pro Cys Pro
                245                 250                 255

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
            260                 265                 270

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

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

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

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

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

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

```
Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu
    370                 375                 380

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

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

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

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

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

Lys Ser Leu Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 28
<211> 1422
<212> DNA
<213> Artificial Sequence

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

<400> 28

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atggacatga gggtccccgc tcagctcctg ggcctcctgc tgctctggtt ccccctcctg       60

ctgctctggt tcccaggtgc caggtgtgca gtgaaaaact gttcccatct tgaatgcttc      120

tacaactcaa gagccaatgt ctcttgcatg tggagccatg aagaggctct gaatgtcaca      180

acctgccacg tccatgccaa gtcgaacctg cgacactgga acaaaacctg tgagctaact      240

cttgtgaggc aggcatcctg ggcctgcaac ctgatcctcg ggtcgttccc agagtcccag      300
```

tcactgacct ccgtggacct ccttgacata aatgtggtgt gctgggaaga gaagggttgg 360

cgtagggtaa agacctgcga cttccatccc tttgacaacc ttcgcctggt ggcccctcat 420

tccctccaag ttctgcacat tgatacccag agatgtaaca taagctggaa ggtctcccag 480

gtctctcact acattgaacc atacttggaa tttgaggccc gtagacgtct tctgggccac 540

agctgggagg atgcatccgt attaagcctc aagcagagac agcagtggct cttcttggag 600

atgctgatcc ctagtacctc atatgaggtc caggtgaggg tcaaagctca acgaaacaat 660

accgggacct ggagtccctg gagccagccc ctgacctttc ggacaaggcc agcagatccc 720

atgaaggagg gagctcagga caaaactcac acatgcccac cgtgcccagc acctgaactc 780

ctgggggggac cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc 840

cggacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 900

ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 960

cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 1020

aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 1080

accatctcca aagccaaagg gcagccccga gaaccacagg tgtgcaccct gcccccatcc 1140

cgggatgagc tgaccaagaa ccaggtcagc ctctcgtgcg cagtcaaagg cttctatccc 1200

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 1260

cctcccgtgc tggactccga cggctccttc ttcctcgtga gcaagctcac cgtggacaag 1320

agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 1380

cactacacgc agaagagcct ctccctgtct ccgggtaaat ga 1422

<210> 29
<211> 500
<212> PRT
<213> Artificial Sequence

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

<400> 29

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

Phe Pro Leu Leu Leu Leu Trp Phe Pro Gly Ala Arg Cys Trp Ser Ser
            20                  25                  30

Lys Val Leu Met Ser Ser Ala Asn Glu Asp Ile Lys Ala Asp Leu Ile
        35                  40                  45

Leu Thr Ser Thr Ala Pro Glu His Leu Ser Ala Pro Thr Leu Pro Leu
    50                  55                  60

Pro Glu Val Gln Cys Phe Val Phe Asn Ile Glu Tyr Met Asn Cys Thr
65                  70                  75                  80

Trp Asn Ser Ser Ser Glu Pro Gln Ala Thr Asn Leu Thr Leu His Tyr
                85                  90                  95

Arg Tyr Lys Val Ser Asp Asn Asn Thr Phe Gln Glu Cys Ser His Tyr
            100                 105                 110

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

Ile Gln Leu Tyr Gln Thr Phe Val Val Gln Leu Gln Asp Pro Gln Lys
    130                 135                 140

Pro Gln Arg Arg Ala Val Gln Lys Leu Asn Leu Gln Asn Leu Val Ile
145                 150                 155                 160

Pro Arg Ala Pro Glu Asn Leu Thr Leu Ser Asn Leu Ser Glu Ser Gln
                165                 170                 175

Leu Glu Leu Arg Trp Lys Ser Arg His Ile Lys Glu Arg Cys Leu Gln
            180                 185                 190
```

```
Tyr Leu Val Gln Tyr Arg Ser Asn Arg Asp Arg Ser Trp Thr Glu Leu
        195                 200                 205

Ile Val Asn His Glu Pro Arg Phe Ser Leu Pro Ser Val Asp Glu Leu
    210                 215                 220

Lys Arg Tyr Thr Phe Arg Val Arg Ser Arg Tyr Asn Pro Ile Cys Gly
225                 230                 235                 240

Ser Ser Gln Gln Trp Ser Lys Trp Ser Gln Pro Val His Trp Gly Ser
                245                 250                 255

His Thr Val Glu Glu Asn Pro Ser Leu Phe Ala Leu Glu Ala Gly Ala
            260                 265                 270

Gln Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
        275                 280                 285

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

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

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

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

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

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

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


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


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


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


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


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


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


Ser Pro Gly Lys
            500
```

<210> 30
<211> 1503
<212> DNA
<213> Artificial Sequence

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

<400> 30

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atggacatga gggtccccgc tcagctcctg ggcctcctgc tgctctggtt ccccctcctg       60

ctgctctggt tcccaggtgc caggtgttgg agttccaagg tcctcatgtc cagtgcgaat      120

gaagacatca aagctgattt gatcctgact tctacagccc ctgaacacct cagtgctcct      180
```

actctgcccc ttccagaggt tcagtgcttt gtgttcaaca tagagtacat gaattgcact 240

tggaatagca gttctgagcc tcaggcaacc aacctcacgc tgcactatag gtacaaggta 300

tctgataata atacattcca ggagtgcagt cactatttgt tctccaaaga gattacttct 360

ggctgtcaga tacaaaaaga agatatccag ctctaccaga catttgttgt ccagctccag 420

gacccccaga aaccccagag gcgagctgta cagaagctaa acctacagaa tcttgtgatc 480

ccacgggctc cagaaaatct aacactcagc aatctgagtg aatcccagct agagctgaga 540

tggaaaagca gacatattaa agaacgctgt ttacaatact tggtgcagta ccggagcaac 600

agagatcgaa gctggacgga actaatagtg aatcatgaac ctagattctc cctgcctagt 660

gtggatgagc tgaaacggta cacatttcgg gttcggagcc gctataaccc aatctgtgga 720

agttctcaac agtggagtaa atggagccag cctgtccact gggggagtca tactgtagag 780

gagaatcctt ccttgtttgc actggaagct ggagctcagg acaaaactca cacatgccca 840

ccgtgcccag cacctgaact cctgggggga ccgtcagtct tcctcttccc cccaaaaccc 900

aaggacaccc tcatgatctc ccggacccct gaggtcacat gcgtggtggt ggacgtgagc 960

cacgaagacc ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt gcataatgcc 1020

aagacaaagc cgcgggagga gcagtacaac agcacgtacc gtgtggtcag cgtcctcacc 1080

gtcctgcacc aggactggct gaatggcaag gagtacaagt gcaaggtctc caacaaagcc 1140

ctcccagccc ccatcgagaa aaccatctcc aaagccaaag ggcagccccg agaaccacag 1200

gtgtacaccc tgcccccatg ccgggatgag ctgaccaaga accaggtcag cctgtggtgc 1260

ctggtcaaag gcttctatcc cagcgacatc gccgtggagt gggagagcaa tgggcagccg 1320

gagaacaact acaagaccac gcctcccgtg ctggactccg acggctcctt cttcctctac 1380

agcaagctca ccgtggacaa gagcaggtgg cagcagggga acgtcttctc atgctccgtg 1440

atgcatgagg ctctgcacaa ccactacacg cagaagagcc tctccctgtc tccgggtaaa 1500

tga 1503

<210> 31

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

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

<400> 31

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

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

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

Cys Lys Arg Gly Phe Arg Arg Leu Lys Glu Leu Val Tyr Met Arg Cys
50 55 60

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

Asp Lys Ser Arg Lys Gln Val Thr Ala Gln Leu Glu His Gln Lys Glu
85 90 95

Gln Gln Thr Thr Thr Asp Met Gln Lys Pro Thr Gln Ser Met His Gln
100 105 110

Glu Asn Leu Thr Gly His Cys Arg Glu Pro Pro Pro Trp Lys His Glu
115 120 125

Asp Ser Lys Arg Ile Tyr His Phe Val Glu Gly Gln Ser Val His Tyr
130 135 140

Glu Cys Ile Pro Gly Tyr Lys Ala Leu Gln Arg Gly Pro Ala Ile Ser
145 150 155 160

```
Ile Cys Lys Met Lys Cys Gly Lys Thr Gly Trp Thr Gln Pro Gln Leu
                165                 170                 175


Thr Cys Val Asp Glu Gln Leu Tyr Phe Gln Gly Gly Ser Gly Leu Asn
            180                 185                 190


Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu Ala Arg Ala His
        195                 200                 205


His His His His His
    210


<210>  32
<211>  642
<212>  DNA
<213>  Artificial Sequence

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

<400>  32
atgggatgga gctgtatcat cctcttcttg gtagcaacag ctaccggtgt gcattccgaa       60

ctgtgtctgt atgacccacc cgaggtcccc aatgccacat tcaaagccct ctcctacaag      120

aacggcacca tcctaaactg tgaatgcaag agaggtttcc gaagactaaa ggaattggtc      180

tatatgcgtt gcttaggaaa ctcctggagc agcaactgcc agtgcaccag caactcccat      240

gacaaatcga gaaagcaagt tacagctcaa cttgaacacc agaaagagca acaaaccaca      300

acagacatgc agaagccaac acagtctatg caccaagaga accttacagg tcactgcagg      360

gagccacctc cttggaaaca tgaagattcc aagagaatct atcatttcgt ggaaggacag      420

agtgttcact acgagtgtat tccgggatac aaggctctac agagaggtcc tgctattagc      480

atctgcaaga tgaagtgtgg gaaaacgggg tggactcagc cccagctcac atgtgtcgac      540

gaacagttat attttcaggg cggctcaggc ctgaacgaca tcttcgaggc ccagaagatc      600

gagtggcacg aggctcgagc tcaccaccat caccatcact ga                         642
```

<210> 33
<211> 480
<212> PRT
<213> Artificial Sequence

<220>
<223> Cynomolgous IL-2R-beta-Fc(knob) fusion protein + Avi-tag

<400> 33

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

Val His Ser Ala Val Asn Gly Thr Ser Arg Phe Thr Cys Phe Tyr Asn
20 25 30

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

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

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

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

Val Thr Leu Arg Val Met Cys Arg Glu Gly Val Arg Trp Arg Met Met
100 105 110

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

Ile Ser Leu Gln Val Val His Val Glu Thr His Arg Cys Asn Ile Ser
130 135 140

Trp Lys Ile Ser Gln Ala Ser His Tyr Phe Glu Arg His Leu Glu Phe

```
145                 150                 155                 160

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

Met Thr Leu Lys Gln Lys Gln Glu Trp Ile Cys Leu Glu Thr Leu Thr
            180                 185                 190

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

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

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

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

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

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

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

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

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

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
```

eolf-seql

340 345 350

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

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

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

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

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

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

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

Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu
465 470 475 480

<210> 34
<211> 1443
<212> DNA
<213> Artificial Sequence

<220>
<223> Cynomolgous IL-2R-beta-Fc(knob) fusion protein + Avi-tag

<400> 34
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gtcaacggca cttcccggtt cacatgcttc tacaactcga gagccaacat ctcctgtgtc 120

tggagccaag atggggctct gcaggacact tcctgccaag tccacgcctg gccggacaga 180

cggcggtgga accaaacctg tgagctgctc cctgtgagtc aagcatcctg ggcctgcaac 240

ctgatcctcg gaaccccaga ttctcagaaa ctgaccgcag tggatatcgt caccctgagg 300

gtgatgtgcc gtgaaggggt gcgatggagg atgatggcca tccaggactt caaacccttt 360

gagaaccttc gcctgatggc ccccatctcc ctccaagtcg tccacgtgga gacccacaga 420

tgcaacataa gctggaaaat ctcccaagcc tcccactact ttgaaagaca cctggagttt 480

gaggcccgga cgctgtcccc aggccacacc tgggaggagg ccccccctgat gaccctcaag 540

cagaagcagg aatggatctg cctggagacg ctcaccccag acacccagta tgagtttcag 600

gtgcgggtca agcctctgca aggcgagttc acgacctgga gcccctggag ccagcccctg 660

gccttcagga caaagcctgc agcccttggg aaggacaccg gagctcagga caaaactcac 720

acatgcccac cgtgcccagc acctgaactc ctgggggggac cgtcagtctt cctcttcccc 780

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg 840

gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 900

cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 960

gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 1020

aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 1080

gaaccacagg tgtacaccct gcccccatgc cgggatgagc tgaccaagaa ccaggtcagc 1140

ctgtggtgcc tggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 1200

gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1260

ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1320

tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1380

ccgggtaaat ccggaggcct gaacgacatc ttcgaggccc agaagattga atggcacgag 1440

tga 1443

<210> 35

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

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

<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 Leu Asn Thr Thr Ile Leu Thr Pro Asn Gly Asn Glu Asp
20 25 30

Ala Thr Thr Asp Phe Phe Leu Thr Ser Met Pro Thr Asp Ser Leu Ser
35 40 45

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

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

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

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

Gln Leu Gln Lys Lys Glu Ile His Leu Tyr Gln Thr Phe Val Val Gln
115 120 125

Leu Gln Asp Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln Met Leu Lys
130 135 140

Leu Gln Asn Leu Val Ile Pro Trp Ala Pro Glu Asn Leu Thr Leu Arg
145 150 155 160

```
Lys Leu Ser Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn Arg Phe Leu
                165                 170                 175

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

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

Ser Val Asp Gly Gln Lys Arg Tyr Thr Phe Arg Val Arg Ser Arg Phe
    210                 215                 220

Asn Pro Leu Cys Gly Ser Ala Gln His Trp Ser Glu Trp Ser His Pro
225                 230                 235                 240

Ile His Trp Gly Ser Asn Ser Ser Lys Glu Asn Pro Phe Leu Phe Ala
                245                 250                 255

Leu Glu Ala Gly Ala Gln Asp Lys Thr His Thr Cys Pro Pro Cys Pro
            260                 265                 270

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

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

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
305                 310                 315                 320

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

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
            340                 345                 350
```

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

Ala Leu Gly Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
    370                 375                 380

Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu
385                 390                 395                 400

Thr Lys Asn Gln Val Ser Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro
                405                 410                 415

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

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

Val Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
    450                 455                 460

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

Lys Ser Leu Ser Leu Ser Pro Gly Lys
                485
```

<210> 36
<211> 1470
<212> DNA
<213> Artificial Sequence

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

<400> 36
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aacacgacaa ttctgacgcc caatgggaat gaagacgcca caactgattt cttcctgacc 120

tctatgccca ctgactccct cagtgtttcc actctgcccc tcccagaggt tcagtgtttt 180

gtgttcaatg tcgagtacat gaattgcact tggaacagca gctctgagcc ccagcctacc 240

aacctcactc tgcattattg gtacaagaat tcggataatg ataaagtcca gaagtgcagc 300

cactatctat tctctgaaga aatcacttct ggctgtcagt tgcaaaaaaa ggagatccac 360

ctctaccaaa cgtttgttgt tcagctccag gacccacggg aacccaggag acaggccaca 420

cagatgctaa aactgcagaa tctggtgatc ccctgggctc cggagaacct aacacttcgc 480

aaactgagtg aatcccagct agaactgaac tggaacaaca gattcttgaa ccactgtttg 540

gagcacttgg tgcagtaccg gactgactgg gaccacagct ggactgaaca atcagtggat 600

tatagacata agttctcctt gcctagtgtg gatgggcaga aacgctacac gtttcgtgtc 660

cggagccgct ttaacccact ctgtggaagt gctcagcatt ggagtgaatg gagccaccca 720

atccactggg ggagcaatag ttcaaaagag aatcctttcc tgtttgcatt ggaagccgga 780

gctcaggaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 840

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 900

gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 960

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 1020

acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 1080

tacaagtgca aggtctccaa caaagccctc ggcgccccca tcgagaaaac catctccaaa 1140

gccaaagggc agccccgaga accacaggtg tgcaccctgc ccccatcccg ggatgagctg 1200

accaagaacc aggtcagcct ctcgtgcgca gtcaaaggct tctatcccag cgacatcgcc 1260

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1320

gactccgacg gctccttctt cctcgtgagc aagctcaccg tggacaagag caggtggcag 1380

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1440

aagagcctct ccctgtctcc gggtaaatga 1470

<210> 37
<211> 217
<212> PRT
<213> Artificial Sequence

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

<400> 37

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


Glu Leu Cys Asp Asp Asp Pro Pro Lys Ile Thr His Ala Thr Phe Lys
            20                  25                  30


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


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


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


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


Lys Glu Arg Lys Thr Thr Glu Met Gln Ser Gln Met Gln Leu Ala Asp
            100                 105                 110


Gln Val Ser Leu Pro Gly His Cys Arg Glu Pro Pro Pro Trp Glu Asn
        115                 120                 125


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


Tyr Gln Cys Val Gln Gly Tyr Arg Ala Leu His Arg Gly Pro Ala Glu
```

eolf-seql

145 150 155 160

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

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

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

Ala Arg Ala His His His His His His
210 215

<210> 38
<211> 654
<212> DNA
<213> Artificial Sequence

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

<400> 38
atgggatgga gctgtatcat cctcttcttg gtagcaacag ctaccggtga gctctgtgac 60

gatgacccgc caaaaatcac acatgccaca ttcaaagcca tggcctacaa ggaaggaacc 120

atgttgaact gtgaatgcaa gagaggtttc cgcagaataa aaagcgggtc accctatatg 180

ctctgtacag gaaactctag ccactcgtcc tgggacaacc aatgtcaatg cacaagctct 240

gctgctcgga acacaacaaa acaagtgaca cctcaacctg aagaacagaa agaaagaaaa 300

accacagaaa tgcaaagtca aatgcagctg gcggaccaag tgagccttcc aggtcactgc 360

agggaacctc caccgtggga aaatgaagcc acagaaagaa tttatcattt cgtggtgggg 420

cagacggttt actaccagtg cgtccaggga tacagggctc tacacagagg tcctgctgag 480

agcgtctgca aaatgaccca cgggaagaca agatggaccc agccccagct catatgcaca 540

ggtgaagtcg acgaacagtt atattttcag ggcggctcag gcctgaacga catcttcgag 600

gcccagaaga tcgagtggca cgaggctcga gctcaccacc atcaccatca ctga 654

<210> 39
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> leader sequence

<400> 39

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

Ala His Ser

<210> 40
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> leader sequence

<400> 40
atggactgga cctggagaat cctcttcttg gtggcagcag ccacaggagc ccactcc 57

<210> 41
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> leader sequence

<400> 41
atggactgga cctggaggat cctcttcttg gtggcagcag ccacaggagc ccactcc 57

<210> 42
<211> 22
<212> PRT

<213> Artificial Sequence

<220>
<223> leader sequence

<400> 42

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

Phe Pro Gly Ala Arg Cys
20

<210> 43
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> leader sequence

<400> 43
atggacatga gggtccccgc tcagctcctg ggcctcctgc tgctctggtt cccaggtgcc 60

aggtgt 66

<210> 44
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> leader sequence

<400> 44

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

Val His Ser

<210> 45

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

<220>
<223> leader sequence

<400> 45
atgggatgga gctgtatcat cctcttcttg gtagcaacag ctaccggtgt gcattcc 57

<210> 46
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> leader sequence

<400> 46
atgggctggt cctgcatcat cctgtttctg gtggctaccg ccactggagt gcattcc 57

<210> 47
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> leader sequence

<400> 47
atgggctggt cctgcatcat cctgtttctg gtcgccacag ccaccggcgt gcactct 57

<210> 48
<211> 592
<212> PRT
<213> Artificial Sequence

<220>
<223> DP47GS HC(Fc knob,P329G LALA)-IL2 N88D

<400> 48

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu
225                 230                 235                 240

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu
465                 470                 475                 480

Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr
                485                 490                 495

Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu
            500                 505                 510

Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
        515                 520                 525

Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu
    530                 535                 540

Ile Ser Asp Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr
545                 550                 555                 560

Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe
                565                 570                 575

Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
            580                 585                 590
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<210> 49
<211> 1776
<212> DNA
<213> Artificial Sequence

<220>
<223> DP47GS HC(Fc knob,P329G LALA)-IL2 N88D

<400> 49
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 gaaaggcagc 300

ggatttgact actggggcca aggaaccctg gtcaccgtct cgagtgctag caccaagggc 360

ccatcggtct tccccctggc accctcctcc aagagcacct ctgggggcac agcggccctg 420

ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc 480

ctgaccagcg gcgtgcacac cttcccggct gtcctacagt cctcaggact ctactccctc 540

agcagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg 600

aatcacaagc ccagcaacac caaggtggac aagaaagttg agcccaaatc ttgtgacaaa 660

actcacacat gcccaccgtg cccagcacct gaagctgcag ggggaccgtc agtcttcctc 720

ttccccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg 780

gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 840

gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg 900

gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag 960

gtctccaaca aagccctcgg cgcccccatc gagaaaacca tctccaaagc caaagggcag 1020

ccccgagaac cacaggtgta caccctgccc ccatgccggg atgagctgac caagaaccag 1080

gtcagcctgt ggtgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 1140

agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1200

tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1260

ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc 1320

ctgtctccgg gtggcggcgg aggctccgga ggcggaggtt ctggaggcgg aggctccgca 1380

cctgcctcaa gttctacaaa gaaaacacag ctacaactgg agcatttact gctggattta 1440

cagatgattt tgaatggaat taataattac aagaatccca aactcaccag gatgctcaca 1500

tttaagtttt acatgcccaa gaaggccaca gaactgaaac atcttcagtg tctagaagaa 1560

gaactcaaac ctctggagga agtgctaaat ttagctcaaa gcaaaaactt tcacttaaga 1620

cccagggact taatcagcga tatcaacgta atagttctgg aactaaaggg atctgaaaca 1680

acattcatgt gtgaatatgc tgatgagaca gcaaccattg tagaatttct gaacagatgg 1740

attacctttg cccaaagcat catctcaaca ctgact 1776

<210> 50
<211> 592
<212> PRT
<213> Artificial Sequence

<220>
<223> DP47GS HC(Fc wt,P329G LALA)-IL2 N88D

<400> 50

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu
225                 230                 235                 240

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

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

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

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

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

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

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

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

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

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

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

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

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

```
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Pro Ala Ser Ser
    450                 455                 460


Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu
465                 470                 475                 480


Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr
                485                 490                 495


Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu
            500                 505                 510


Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
        515                 520                 525


Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu
    530                 535                 540


Ile Ser Asp Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr
545                 550                 555                 560


Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe
                565                 570                 575


Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
            580                 585                 590
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<210> 51
<211> 1776
<212> DNA
<213> Artificial Sequence

<220>
<223> DP47GS HC(Fc wt,P329G LALA)-IL2 N88D

<400> 51
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 gaaaggcagc 300

ggatttgact actggggcca aggaaccctg gtcaccgtct cgagtgctag caccaagggc 360

ccatcggtct tccccctggc accctcctcc aagagcacct ctgggggcac agcggccctg 420

ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc 480

ctgaccagcg gcgtgcacac cttcccggct gtcctacagt cctcaggact ctactccctc 540

agcagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg 600

aatcacaagc ccagcaacac caaggtggac aagaaagttg agcccaaatc ttgtgacaaa 660

actcacacat gcccaccgtg cccagcacct gaagctgcag ggggaccgtc agtcttcctc 720

ttcccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg 780

gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 840

gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg 900

gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag 960

gtctccaaca aagccctcgg cgcccccatc gagaaaacca tctccaaagc caaagggcag 1020

ccccgagaac cacaggtgta caccctgccc ccatcccggg atgagctgac caagaaccag 1080

gtcagcctga cctgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 1140

agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1200

tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1260

ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc 1320

ctgtctccgg gtggcggcgg aggctccgga ggcggaggtt ctggaggcgg aggctccgca 1380

cctgcctcaa gttctacaaa gaaaacacag ctacaactgg agcatttact gctggattta 1440

cagatgattt tgaatggaat taataattac aagaatccca aactcaccag gatgctcaca 1500

tttaagtttt acatgcccaa gaaggccaca gaactgaaac atcttcagtg tctagaagaa 1560

gaactcaaac ctctggagga agtgctaaat ttagctcaaa gcaaaaactt tcacttaaga 1620

cccagggact taatcagcga tatcaacgta atagttctgg aactaaaggg atctgaaaca 1680

acattcatgt gtgaatatgc tgatgagaca gcaaccattg tagaatttct gaacagatgg 1740

attacctttg cccaaagcat catctcaaca ctgact 1776

<210> 52
<211> 592
<212> PRT
<213> Artificial Sequence

<220>
<223> DP47GS HC(Fc wt, P329G LALA)-IL2 E95A

<400> 52

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu
225                 230                 235                 240

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

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

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

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

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


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


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


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


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


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


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


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


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


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


Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu
465                 470                 475                 480


Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr
                485                 490                 495
```

```
Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu
            500                 505                 510

Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
        515                 520                 525

Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu
    530                 535                 540

Ile Ser Asn Ile Asn Val Ile Val Leu Pro Leu Lys Gly Ser Glu Thr
545                 550                 555                 560

Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe
                565                 570                 575

Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
            580                 585                 590
```

<210> 53
<211> 1776
<212> DNA
<213> Artificial Sequence

<220>
<223> DP47GS HC(Fc wt, P329G LALA)-IL2 E95A

<400> 53

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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 gaaaggcagc      300

ggatttgact actggggcca aggaaccctg gtcaccgtct cgagtgctag caccaagggc      360

ccatcggtct tccccctggc accctcctcc aagagcacct ctgggggcac agcggccctg      420
```

ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc 480

ctgaccagcg gcgtgcacac cttcccggct gtcctacagt cctcaggact ctactccctc 540

agcagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg 600

aatcacaagc ccagcaacac caaggtggac aagaaagttg agcccaaatc ttgtgacaaa 660

actcacacat gcccaccgtg cccagcacct gaagctgcag ggggaccgtc agtcttcctc 720

ttcccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg 780

gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 840

gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg 900

gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag 960

gtctccaaca aagccctcgg cgcccccatc gagaaaacca tctccaaagc caaagggcag 1020

ccccgagaac cacaggtgta caccctgccc ccatcccggg atgagctgac caagaaccag 1080

gtcagcctga cctgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 1140

agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1200

tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1260

ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc 1320

ctgtctccgg gtggcggcgg aggctccgga ggcggaggtt ctggaggcgg aggctccgca 1380

cctgcctcaa gttctacaaa gaaaacacag ctacaactgg agcatttact gctggattta 1440

cagatgattt tgaatggaat taataattac aagaatccca aactcaccag gatgctcaca 1500

tttaagtttt acatgcccaa gaaggccaca gaactgaaac atcttcagtg tctagaagaa 1560

gaactcaaac ctctggagga agtgctaaat ttagctcaaa gcaaaaactt tcacttaaga 1620

cccagggact taatcagcaa tatcaacgta atagttctgc cactaaaggg atctgaaaca 1680

acattcatgt gtgaatatgc tgatgagaca gcaaccattg tagaatttct gaacagatgg 1740

attacctttg cccaaagcat catctcaaca ctgact 1776

<210> 54

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<223> FOXP3 forward primer

<400> 54
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<210> 56
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<223> CTLA-4 forward primer

<400> 56
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<210> 57
<211> 45
<212> DNA
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<220>
<223> CTLA-4 reverse primer

<400> 57
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<210> 58

<211> 133
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<220>
<223> IL-2 N88D T3A C125A

<400> 58

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1               5                   10                  15


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


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


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


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


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


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


Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ala Gln Ser Ile
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Ile Ser Thr Leu Thr
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<211> 399
<212> DNA

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acatttaagt tttacatgcc caagaaggcc acagaactga aacatcttca gtgtctagaa 180

gaagaactca aacctctgga ggaagtgcta aatttagctc aaagcaaaaa ctttcactta 240

agacccaggg acttaatcag cgatatcaac gtaatagttc tggaactaaa gggatctgaa 300

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tggattacct ttgcccaaag catcatctca acactgact 399

<210> 60
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<220>
<223> IL-2 N88D

<400> 60

Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His
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Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys
20 25 30

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

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

Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu

eolf-seql

65 70 75 80

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

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

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

Ile Ser Thr Leu Thr
130

<210> 61
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-2 N88D

<400> 61
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acatttaagt tttacatgcc caagaaggcc acagaactga aacatcttca gtgtctagaa 180

gaagaactca aacctctgga ggaagtgcta aatttagctc aaagcaaaaa ctttcactta 240

agacccaggg acttaatcag cgatatcaac gtaatagttc tggaactaaa gggatctgaa 300

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<210> 62
<211> 133
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<220>
<223> IL-2 N88D C125A

<400> 62

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1               5                   10                  15


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


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


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


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


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


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


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


Ile Ser Thr Leu Thr
    130
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<210> 63
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-2 N88D C125A

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acatttaagt tttacatgcc caagaaggcc acagaactga aacatcttca gtgtctagaa 180

gaagaactca aacctctgga ggaagtgcta aatttagctc aaagcaaaaa ctttcactta 240

agacccaggg acttaatcag cgatatcaac gtaatagttc tggaactaaa gggatctgaa 300

acaacattca tgtgtgaata tgctgatgag acagcaacca ttgtagaatt tctgaacaga 360

tggattacct ttgcccaaag catcatctca acactgact 399

<210> 64
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-2 N88D T3A

<400> 64

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

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

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

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

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

Arg Pro Arg Asp Leu Ile Ser Asp Ile Asn Val Ile Val Leu Glu Leu

eolf-seql

85 90 95

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

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

Ile Ser Thr Leu Thr
130

<210> 65
<211> 399
<212> DNA
<213> Artificial Sequence

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<223> IL-2 N88D T3A

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acatttaagt tttacatgcc caagaaggcc acagaactga aacatcttca gtgtctagaa 180

gaagaactca aacctctgga ggaagtgcta aatttagctc aaagcaaaaa ctttcactta 240

agacccaggg acttaatcag cgatatcaac gtaatagttc tggaactaaa gggatctgaa 300

acaacattca tgtgtgaata tgctgatgag acagcaacca ttgtagaatt tctgaacaga 360

tggattacct tttgtcaaag catcatctca acactgact 399

<210> 66
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<220>
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<400> 66

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1               5                   10                  15
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