SEQUENCE LISTING

<110> Genentech, Inc.

<120> DOSING FOR TREATMENT WITH IL-22 Fc FUSION PROTEINS

<130> 50474-173WO2

<150> US 62/633,534
<151> 2018-02-21

<160> 80

<170> PatentIn version 3.5

<210> 1
<211> 495
<212> DNA
<213> Homo sapiens

<220>
<223> Human IL-22

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cgcaccttca tgctggctaa ggaggctagc ttggctgata acaacacaga cgttcgtctc 180

attggggaga aactgttcca cggagtcagt atgagtgagc gctgctatct gatgaagcag 240

gtgctgaact tcacccttga agaagtgctg ttccctcaat ctgataggtt ccagccttat 300

atgcaggagg tggtgccctt cctggccagg ctcagcaaca ggctaagcac atgtcatatt 360

gaaggtgatg acctgcatat ccagaggaat gtgcaaaagc tgaaggacac agtgaaaaag 420

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agaaatgcct gcatt 495

<210> 2
<211> 165
<212> PRT
<213> Homo sapiens

<220>
<223> Human IL-22

<400> 2
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1 5 10 15

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Val His Ser Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn
            20                  25                  30

Phe Gln Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu
        35                  40                  45

Ala Ser Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys
    50                  55                  60

Leu Phe His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln
65                  70                  75                  80

Val Leu Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg
                85                  90                  95

Phe Gln Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser
            100                 105                 110

Asn Arg Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln
        115                 120                 125

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

Gly Glu Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu
145                 150                 155                 160

Arg Asn Ala Cys Ile
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<210> 3
<211> 438
<212> DNA
<213> Homo sapiens

<220>
<223> IL-22 DNA (mature)

<400> 3
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ctcattgggg agaaactgtt ccacggagtc agtatgagtg agcgctgcta tctgatgaag 180

caggtgctga acttcaccct tgaagaagtg ctgttccctc aatctgatag gttccagcct 240

tatatgcagg aggtggtgcc cttcctggcc aggctcagca acaggctaag cacatgtcat 300

attgaaggtg atgacctgca tatccagagg aatgtgcaaa agctgaagga cacagtgaaa 360

aagcttggag agagtggaga gatcaaagca attggagaac tggatttgct gtttatgtct 420

ctgagaaatg cctgcatt 438

<210> 4
<211> 146
<212> PRT
<213> Homo sapiens

<220>
<223> IL-22 (mature)

<400> 4
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1 5 10 15

Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser Leu
20 25 30

Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe His
35 40 45

Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu Asn
50 55 60

Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln Pro
65 70 75 80

Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg Leu
85 90 95

Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn Val
100 105 110

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

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

Cys Ile
145

<210> 5
<211> 57
<212> DNA
<213> Homo sapiens

<220>
<223> IL-22 leader sequence

<400> 5
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<210> 6
<211> 19
<212> PRT
<213> Homo sapiens

<220>
<223> IL-22 leader sequence

<400> 6
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser

<210> 7
<211> 1128
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> IL-22 Fc fusion IgG4 (minus C-terminal Lys) N297G

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aaccgcacct tcatgctggc taaggaggct agcttggctg ataacaacac agacgttcgt 120

ctcattgggg agaaactgtt ccacggagtc agtatgagtg agcgctgcta tctgatgaag 180

caggtgctga acttcaccct tgaagaagtg ctgttccctc aatctgatag gttccagcct 240

tatatgcagg aggtggtgcc cttcctggcc aggctcagca acaggctaag cacatgtcat 300

attgaaggtg atgacctgca tatccagagg aatgtgcaaa agctgaagga cacagtgaaa 360

aagcttggag agagtggaga gatcaaagca attggagaac tggatttgct gtttatgtct 420

ctgagaaatg cctgcattcg cgttgagtcc aaatatggtc ccccatgccc accatgccca 480

gcacctgagt tcctgggggg accatcagtc ttcctgttcc ccccaaaacc caaggacact 540

ctcatgatct cccggacccc tgaggtcacg tgcgtggtgg tggacgtgag ccaggaagac 600

cccgaggtcc agttcaactg gtacgtggat ggcgtggagg tgcataatgc caagacaaag 660

ccgcgggagg agcagttcgg aagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 720

caggactggc tgaacggcaa ggagtacaag tgcaaggtct ccaacaaagg cctcccgtcc 780

tccatcgaga aaaccatctc caaagccaaa gggcagcccc gagagccaca ggtgtacacc 840

ctgcccccat cccaggagga gatgaccaag aaccaggtca gcctgacctg cctggtcaaa 900

ggcttctacc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 960

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaggcta 1020

accgtggaca agagcaggtg gcaggagggg aatgtcttct catgctccgt gatgcatgag 1080

gctctgcaca accactacac acagaagagc ctctccctgt ctctgggt 1128

<210> 8
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> IL-22 Fc fusion IgG4 (minus C-terminal Lys) N297G

<400> 8
Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln Gln
1 5 10 15

Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser Leu

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            20                  25                  30

Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe His
        35                  40                  45

Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu Asn
    50                  55                  60

Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln Pro
65                  70                  75                  80

Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg Leu
                85                  90                  95

Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn Val
            100                 105                 110

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

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

Cys Ile Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
145                 150                 155                 160

Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                165                 170                 175

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            180                 185                 190

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
        195                 200                 205

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    210                 215                 220

Gln Phe Gly Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
225                 230                 235                 240
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Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
245 250 255

Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
260 265 270

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
275 280 285

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
290 295 300

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
305 310 315 320

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
325 330 335

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

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
355 360 365

Lys Ser Leu Ser Leu Ser Leu Gly
370 375

<210> 9
<211> 1128
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> IL-22 Fc fusion IgG4 (minus C-terminal Lys) N297A

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aaccgcacct tcatgctggc taaggaggct agcttggctg ataacaacac agacgttcgt 120

ctcattgggg agaaactgtt ccacggagtc agtatgagtg agcgctgcta tctgatgaag 180

caggtgctga acttcaccct tgaagaagtg ctgttccctc aatctgatag gttccagcct 240

tatatgcagg aggtggtgcc cttcctggcc aggctcagca acaggctaag cacatgtcat 300

attgaaggtg atgacctgca tatccagagg aatgtgcaaa agctgaagga cacagtgaaa 360

aagcttggag agagtggaga gatcaaagca attggagaac tggatttgct gtttatgtct 420

ctgagaaatg cctgcattcg cgttgagtcc aaatatggtc ccccatgccc accatgccca 480

gcacctgagt tcctgggggg accatcagtc ttcctgttcc ccccaaaacc caaggacact 540

ctcatgatct cccggacccc tgaggtcacg tgcgtggtgg tggacgtgag ccaggaagac 600

cccgaggtcc agttcaactg gtacgtggat ggcgtggagg tgcataatgc caagacaaag 660

ccgcgggagg agcagttcgc tagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 720

caggactggc tgaacggcaa ggagtacaag tgcaaggtct ccaacaaagg cctcccgtcc 780

tccatcgaga aaaccatctc caaagccaaa gggcagcccc gagagccaca ggtgtacacc 840

ctgcccccat cccaggagga gatgaccaag aaccaggtca gcctgacctg cctggtcaaa 900

ggcttctacc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 960

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaggcta 1020

accgtggaca agagcaggtg gcaggagggg aatgtcttct catgctccgt gatgcatgag 1080

gctctgcaca accactacac acagaagagc ctctccctgt ctctgggt 1128

<210> 10
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> IL-22 Fc fusion IgG4 (minus C-terminal Lys) N297A

<400> 10
Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln Gln
1 5 10 15

Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser Leu
20 25 30

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Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe His
        35                  40                  45

Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu Asn
    50                  55                  60

Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln Pro
65                  70                  75                  80

Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg Leu
                85                  90                  95

Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn Val
            100                 105                 110

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

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

Cys Ile Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
145                 150                 155                 160

Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                165                 170                 175

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            180                 185                 190

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
        195                 200                 205

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    210                 215                 220

Gln Phe Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
225                 230                 235                 240
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Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                245                 250                 255

Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            260                 265                 270

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
        275                 280                 285

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    290                 295                 300

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
305                 310                 315                 320

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                325                 330                 335

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

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        355                 360                 365

Lys Ser Leu Ser Leu Ser Leu Gly
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<210> 11
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> IL-22 Fc fusion IgG1 (minus C-terminal Lys) N297G

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ctcattgggg agaaactgtt ccacggagtc agtatgagtg agcgctgcta tctgatgaag 180

caggtgctga acttcaccct tgaagaagtg ctgttccctc aatctgatag gttccagcct 240

tatatgcagg aggtggtgcc cttcctggcc aggctcagca acaggctaag cacatgtcat 300

attgaaggtg atgacctgca tatccagagg aatgtgcaaa agctgaagga cacagtgaaa 360

aagcttggag agagtggaga gatcaaagca attggagaac tggatttgct gtttatgtct 420

ctgagaaatg cctgcattga gcccaaatct agtgacaaaa ctcacacatg cccaccgtgc 480

ccagcacctg aactcctggg gggaccgtca gtcttcctct tcccccaaa acccaaggac 540

accctcatga tctcccggac ccctgaggtc acatgcgtgg tggtggacgt gagccacgaa 600

gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 660

aagccgcggg aggagcagta cggaagcacg taccgtgtgg tcagcgtcct caccgtcctg 720

caccaggact ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca 780

gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac 840

accctgcccc catcccggga gagatgacc aagaaccagg tcagcctgac ctgcctggtc 900

aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 960

aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag 1020

ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat 1080

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<210> 12
<211> 377
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> IL-22 Fc fusion IgG1 (minus C-terminal Lys) N297G

<400> 12
Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln Gln
1 5 10 15

Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser Leu
20 25 30

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Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe His
        35                  40                  45

Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu Asn
    50                  55                  60

Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln Pro
65                  70                  75                  80

Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg Leu
                85                  90                  95

Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn Val
            100                 105                 110

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

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

Cys Ile Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys
145                 150                 155                 160

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
                165                 170                 175

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
            180                 185                 190

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
        195                 200                 205

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
    210                 215                 220

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

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
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245 250 255

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
260 265 270

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
275 280 285

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
290 295 300

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
305 310 315 320

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
325 330 335

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
340 345 350

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
355 360 365

Gln Lys Ser Leu Ser Leu Ser Pro Gly
370 375

<210> 13
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> IL-22 Fc fusion IgG1 (minus C-terminal Lys) N297A

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aaccgcacct tcatgctggc taaggaggct agcttggctg ataacaacac agacgttcgt 120

ctcattgggg agaaactgtt ccacggagtc agtatgagtg agcgctgcta tctgatgaag 180

caggtgctga acttcaccct tgaagaagtg ctgttccctc aatctgatag gttccagcct 240

tatatgcagg aggtggtgcc cttcctggcc aggctcagca acaggctaag cacatgtcat 300

attgaaggtg atgacctgca tatccagagg aatgtgcaaa agctgaagga cacagtgaaa 360

aagcttggag agagtggaga gatcaaagca attggagaac tggatttgct gtttatgtct 420

ctgagaaatg cctgcattga gcccaaatct agtgacaaaa ctcacacatg cccaccgtgc 480

ccagcacctg aactcctggg gggaccgtca gtcttcctct tcccccaaa acccaaggac 540

accctcatga tctcccggac ccctgaggtc acatgcgtgg tggtggacgt gagccacgaa 600

gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 660

aagccgcggg aggagcagta cgctagcacg taccgtgtgg tcagcgtcct caccgtcctg 720

caccaggact ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca 780

gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac 840

accctgcccc catcccggga gagatgacc aagaaccagg tcagcctgac ctgcctggtc 900

aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 960

aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag 1020

ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat 1080

gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg t 1131

<210> 14
<211> 377
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> IL-22 Fc fusion IgG1 (minus C-terminal Lys) N297A

<400> 14
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1 5 10 15

Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser Leu
20 25 30

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Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe His
        35                  40                  45

Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu Asn
    50                  55                  60

Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln Pro
65                  70                  75                  80

Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg Leu
                85                  90                  95

Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn Val
            100                 105                 110

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

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

Cys Ile Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys
145                 150                 155                 160

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
                165                 170                 175

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
            180                 185                 190

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
        195                 200                 205

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
    210                 215                 220

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

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
                245                 250                 255
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Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
            260                 265                 270

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
        275                 280                 285

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
    290                 295                 300

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
305                 310                 315                 320

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
                325                 330                 335

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
            340                 345                 350

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
        355                 360                 365

Gln Lys Ser Leu Ser Leu Ser Pro Gly
    370                 375
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<210> 15
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> IL-22 Fc fusion IgG4 (full) N297G

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ctcattgggg agaaactgtt ccacggagtc agtatgagtg agcgctgcta tctgatgaag 180

caggtgctga acttcaccct tgaagaagtg ctgttccctc aatctgatag gttccagcct 240

tatatgcagg aggtggtgcc cttcctggcc aggctcagca acaggctaag cacatgtcat 300

attgaaggtg atgacctgca tatccagagg aatgtgcaaa agctgaagga cacagtgaaa 360

aagcttggag agagtggaga gatcaaagca attggagaac tggatttgct gtttatgtct 420

ctgagaaatg cctgcattcg cgttgagtcc aaatatggtc ccccatgccc accatgccca 480

gcacctgagt tcctgggggg accatcagtc ttcctgttcc ccccaaaacc caaggacact 540

ctcatgatct cccggacccc tgaggtcacg tgcgtggtgg tggacgtgag ccaggaagac 600

cccgaggtcc agttcaactg gtacgtggat ggcgtggagg tgcataatgc caagacaaag 660

ccgcgggagg agcagttcgg aagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 720

caggactggc tgaacggcaa ggagtacaag tgcaaggtct ccaacaaagg cctcccgtcc 780

tccatcgaga aaaccatctc caaagccaaa gggcagcccc gagagccaca ggtgtacacc 840

ctgcccccat cccaggagga gatgaccaag aaccaggtca gcctgacctg cctggtcaaa 900

ggcttctacc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 960

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaggcta 1020

accgtggaca agagcaggtg gcaggagggg aatgtcttct catgctccgt gatgcatgag 1080

gctctgcaca accactacac acagaagagc ctctccctgt ctctgggtaa a 1131

<210> 16
<211> 377
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> IL-22 Fc fusion IgG4 (full) N297G

<400> 16
Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln Gln
1 5 10 15

Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser Leu
20 25 30

Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe His

```
        35                  40                  45

Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu Asn
    50                  55                  60

Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln Pro
65                  70                  75                  80

Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg Leu
                85                  90                  95

Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn Val
            100                 105                 110

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

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

Cys Ile Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
145                 150                 155                 160

Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                165                 170                 175

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            180                 185                 190

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
        195                 200                 205

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    210                 215                 220

Gln Phe Gly Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
225                 230                 235                 240

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                245                 250                 255
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Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
260 265 270

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
275 280 285

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
290 295 300

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
305 310 315 320

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
325 330 335

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

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
355 360 365

Lys Ser Leu Ser Leu Ser Leu Gly Lys
370 375

<210> 17
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> IL-22 Fc fusion IgG4 (full) N297A

<400> 17
gcgcccatca gctcccactg caggcttgac aagtccaact tccagcagcc ctatatcacc 60

aaccgcacct tcatgctggc taaggaggct agcttggctg ataacaacac agacgttcgt 120

ctcattgggg agaaactgtt ccacggagtc agtatgagtg agcgctgcta tctgatgaag 180

caggtgctga acttcaccct tgaagaagtg ctgttccctc aatctgatag gttccagcct 240

tatatgcagg aggtggtgcc cttcctggcc aggctcagca acaggctaag cacatgtcat 300

attgaaggtg atgacctgca tatccagagg aatgtgcaaa agctgaagga cacagtgaaa 360

aagcttggag agagtggaga gatcaaagca attggagaac tggatttgct gtttatgtct 420

ctgagaaatg cctgcattcg cgttgagtcc aaatatggtc ccccatgccc accatgccca 480

gcacctgagt tcctgggggg accatcagtc ttcctgttcc ccccaaaacc caaggacact 540

ctcatgatct cccggacccc tgaggtcacg tgcgtggtgg tggacgtgag ccaggaagac 600

cccgaggtcc agttcaactg gtacgtggat ggcgtggagg tgcataatgc caagacaaag 660

ccgcgggagg agcagttcgc tagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 720

caggactggc tgaacggcaa ggagtacaag tgcaaggtct ccaacaaagg cctcccgtcc 780

tccatcgaga aaaccatctc caaagccaaa gggcagcccc gagagccaca ggtgtacacc 840

ctgcccccat cccaggagga gatgaccaag aaccaggtca gcctgacctg cctggtcaaa 900

ggcttctacc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 960

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaggcta 1020

accgtggaca agagcaggtg gcaggagggg aatgtcttct catgctccgt gatgcatgag 1080

gctctgcaca accactacac acagaagagc ctctccctgt ctctgggtaa a 1131

<210> 18
<211> 377
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> IL-22 Fc fusion IgG4 (full) N297A

<400> 18
Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln Gln
1 5 10 15

Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser Leu
20 25 30

Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe His
35 40 45

```
Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu Asn
    50                  55                  60

Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln Pro
65                  70                  75                  80

Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg Leu
                85                  90                  95

Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn Val
            100                 105                 110

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

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

Cys Ile Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
145                 150                 155                 160

Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                165                 170                 175

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            180                 185                 190

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
        195                 200                 205

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    210                 215                 220

Gln Phe Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
225                 230                 235                 240

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                245                 250                 255
```

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Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            260                 265                 270

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
        275                 280                 285

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    290                 295                 300

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
305                 310                 315                 320

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                325                 330                 335

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

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        355                 360                 365

Lys Ser Leu Ser Leu Ser Leu Gly Lys
    370                 375
```

<210> 19
<211> 1134
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> IL-22 Fc fusion IgG1 (full) N297G

<400> 19
gcgcccatca gctcccactg caggcttgac aagtccaact tccagcagcc ctatatcacc 60

aaccgcacct tcatgctggc taaggaggct agcttggctg ataacaacac agacgttcgt 120

ctcattgggg agaaactgtt ccacggagtc agtatgagtg agcgctgcta tctgatgaag 180

caggtgctga acttcaccct tgaagaagtg ctgttccctc aatctgatag gttccagcct 240

tatatgcagg aggtggtgcc cttcctggcc aggctcagca acaggctaag cacatgtcat 300

attgaaggtg atgacctgca tatccagagg aatgtgcaaa agctgaagga cacagtgaaa 360

aagcttggag agagtggaga gatcaaagca attggagaac tggatttgct gtttatgtct 420

ctgagaaatg cctgcattga gcccaaatct agtgacaaaa ctcacacatg cccaccgtgc 480

ccagcacctg aactcctggg gggaccgtca gtcttcctct tcccccaaa acccaaggac 540

accctcatga tctcccggac ccctgaggtc acatgcgtgg tggtggacgt gagccacgaa 600

gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 660

aagccgcggg aggagcagta cggaagcacg taccgtgtgg tcagcgtcct caccgtcctg 720

caccaggact ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca 780

gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac 840

accctgcccc catcccggga gagatgacc aagaaccagg tcagcctgac ctgcctggtc 900

aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 960

aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag 1020

ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat 1080

gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg taaa 1134

<210> 20
<211> 378
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> IL-22 Fc fusion IgG1 (full) N297G

<400> 20
Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln Gln
1 5 10 15

Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser Leu
20 25 30

Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe His
35 40 45

```
Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu Asn
    50                  55                  60

Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln Pro
65                  70                  75                  80

Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg Leu
                85                  90                  95

Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn Val
            100                 105                 110

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

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

Cys Ile Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys
145                 150                 155                 160

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
                165                 170                 175

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
            180                 185                 190

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
        195                 200                 205

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
    210                 215                 220

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

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
                245                 250                 255

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

260 265 270

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
275 280 285

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
290 295 300

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
305 310 315 320

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
325 330 335

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
340 345 350

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
355 360 365

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
370 375

<210> 21
<211> 1134
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> IL-22 Fc fusion IgG1 (full) N297A

<400> 21
gcgcccatca gctcccactg caggcttgac aagtccaact tccagcagcc ctatatcacc 60

aaccgcacct tcatgctggc taaggaggct agcttggctg ataacaacac agacgttcgt 120

ctcattgggg agaaactgtt ccacggagtc agtatgagtg agcgctgcta tctgatgaag 180

caggtgctga acttcaccct tgaagaagtg ctgttccctc aatctgatag gttccagcct 240

tatatgcagg aggtggtgcc cttcctggcc aggctcagca acaggctaag cacatgtcat 300

attgaaggtg atgacctgca tatccagagg aatgtgcaaa agctgaagga cacagtgaaa 360

aagcttggag agagtggaga gatcaaagca attggagaac tggatttgct gtttatgtct 420

ctgagaaatg cctgcattga gcccaaatct agtgacaaaa ctcacacatg cccaccgtgc 480

ccagcacctg aactcctggg gggaccgtca gtcttcctct tccccccaaa acccaaggac 540

accctcatga tctcccggac ccctgaggtc acatgcgtgg tggtggacgt gagccacgaa 600

gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 660

aagccgcggg aggagcagta cgctagcacg taccgtgtgg tcagcgtcct caccgtcctg 720

caccaggact ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca 780

gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac 840

accctgcccc catcccggga agagatgacc aagaaccagg tcagcctgac ctgcctggtc 900

aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 960

aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag 1020

ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat 1080

gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg taaa 1134

<210> 22
<211> 378
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> IL-22 Fc fusion IgG1 (full) N297A

<400> 22
Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln Gln
1 5 10 15

Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser Leu
20 25 30

Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe His
35 40 45

```
Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu Asn
    50                  55                  60

Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln Pro
65                  70                  75                  80

Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg Leu
                85                  90                  95

Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn Val
            100                 105                 110

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

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

Cys Ile Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys
145                 150                 155                 160

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
                165                 170                 175

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
            180                 185                 190

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
        195                 200                 205

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
    210                 215                 220

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

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
                245                 250                 255

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
            260                 265                 270
```

```
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
        275                 280                 285


Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
    290                 295                 300


Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
305                 310                 315                 320


Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
                325                 330                 335


Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
            340                 345                 350


Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
        355                 360                 365


Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
    370                 375


<210> 23
<211> 1128
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<220>
<223> IL-22 Fc fusion IgG4 (wt N297, minus Lys)

<400> 23
gcgcccatca gctcccactg caggcttgac aagtccaact tccagcagcc ctatatcacc       60

aaccgcacct tcatgctggc taaggaggct agcttggctg ataacaacac agacgttcgt      120

ctcattgggg agaaactgtt ccacggagtc agtatgagtg agcgctgcta tctgatgaag      180

caggtgctga acttcaccct tgaagaagtg ctgttccctc aatctgatag gttccagcct      240

tatatgcagg aggtggtgcc cttcctggcc aggctcagca acaggctaag cacatgtcat      300

attgaaggtg atgacctgca tatccagagg aatgtgcaaa agctgaagga cacagtgaaa      360
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aagcttggag agagtggaga gatcaaagca attggagaac tggatttgct gtttatgtct 420

ctgagaaatg cctgcattcg cgttgagtcc aaatatggtc ccccatgccc accatgccca 480

gcacctgagt tcctgggggg accatcagtc ttcctgttcc ccccaaaacc caaggacact 540

ctcatgatct cccggacccc tgaggtcacg tgcgtggtgg tggacgtgag ccaggaagac 600

cccgaggtcc agttcaactg gtacgtggat ggcgtggagg tgcataatgc caagacaaag 660

ccgcgggagg agcagttcaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 720

caggactggc tgaacggcaa ggagtacaag tgcaaggtct ccaacaaagg cctcccgtcc 780

tccatcgaga aaaccatctc caaagccaaa gggcagcccc gagagccaca ggtgtacacc 840

ctgcccccat cccaggagga gatgaccaag aaccaggtca gcctgacctg cctggtcaaa 900

ggcttctacc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 960

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaggcta 1020

accgtggaca agagcaggtg gcaggagggg aatgtcttct catgctccgt gatgcatgag 1080

gctctgcaca accactacac acagaagagc ctctccctgt ctctgggt 1128

<210> 24
<211> 376
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> IL-22 Fc fusion IgG4 (wt N297, minus Lys)

<400> 24
Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln Gln
1 5 10 15

Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser Leu
20 25 30

Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe His
35 40 45

Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu Asn

```
    50                  55                  60

Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln Pro
65                  70                  75                  80

Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg Leu
                85                  90                  95

Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn Val
            100                 105                 110

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

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

Cys Ile Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
145                 150                 155                 160

Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                165                 170                 175

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            180                 185                 190

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
        195                 200                 205

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    210                 215                 220

Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
225                 230                 235                 240

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                245                 250                 255

Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            260                 265                 270
```

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
        275   280   285

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
    290   295   300

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
305   310   315   320

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                325   330   335

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

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
        355   360   365

Lys Ser Leu Ser Leu Ser Leu Gly
    370   375

<210> 25
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<220>
<223> IL-22 Fc fusion IgG1 (wt N297, minus Lys)

<400> 25
gcgcccatca gctcccactg caggcttgac aagtccaact tccagcagcc ctatatcacc 60

aaccgcacct tcatgctggc taaggaggct agcttggctg ataacaacac agacgttcgt 120

ctcattgggg agaaactgtt ccacggagtc agtatgagtg agcgctgcta tctgatgaag 180

caggtgctga acttcaccct tgaagaagtg ctgttccctc aatctgatag gttccagcct 240

tatatgcagg aggtggtgcc cttcctggcc aggctcagca acaggctaag cacatgtcat 300

attgaaggtg atgacctgca tatccagagg aatgtgcaaa agctgaagga cacagtgaaa 360

aagcttggag agagtggaga gatcaaagca attggagaac tggatttgct gtttatgtct 420

ctgagaaatg cctgcattga gcccaaatct agtgacaaaa ctcacacatg cccaccgtgc 480

ccagcacctg aactcctggg gggaccgtca gtcttcctct tccccccaaa acccaaggac 540

accctcatga tctcccggac ccctgaggtc acatgcgtgg tggtggacgt gagccacgaa 600

gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 660

aagccgcggg aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg 720

caccaggact ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca 780

gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac 840

accctgcccc catcccggga agagatgacc aagaaccagg tcagcctgac ctgcctggtc 900

aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 960

aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag 1020

ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat 1080

gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg t 1131

<210> 26
<211> 377
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> IL-22 Fc fusion IgG1 (wt N297, minus Lys)

<400> 26
Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln Gln
1 5 10 15

Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser Leu
20 25 30

Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe His
35 40 45

Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu Asn
50 55 60

```
Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln Pro
65                  70                  75                  80

Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg Leu
                85                  90                  95

Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn Val
            100                 105                 110

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

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

Cys Ile Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys
145                 150                 155                 160

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
                165                 170                 175

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
            180                 185                 190

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
        195                 200                 205

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
    210                 215                 220

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

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
                245                 250                 255

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
            260                 265                 270
```

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
275 280 285

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
290 295 300

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
305 310 315 320

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
325 330 335

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
340 345 350

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
355 360 365

Gln Lys Ser Leu Ser Leu Ser Pro Gly
370 375

<210> 27
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<220>
<223> IL-22 Fc fusion IgG4 (N297 wt)

<400> 27
gcgcccatca gctcccactg caggcttgac aagtccaact tccagcagcc ctatatcacc 60

aaccgcacct tcatgctggc taaggaggct agcttggctg ataacaacac agacgttcgt 120

ctcattgggg agaaactgtt ccacggagtc agtatgagtg agcgctgcta tctgatgaag 180

caggtgctga acttcaccct tgaagaagtg ctgttccctc aatctgatag gttccagcct 240

tatatgcagg aggtggtgcc cttcctggcc aggctcagca acaggctaag cacatgtcat 300

attgaaggtg atgacctgca tatccagagg aatgtgcaaa agctgaagga cacagtgaaa 360

aagcttggag agagtggaga gatcaaagca attggagaac tggatttgct gtttatgtct 420

ctgagaaatg cctgcattcg cgttgagtcc aaatatggtc ccccatgccc accatgccca 480

gcacctgagt tcctgggggg accatcagtc ttcctgttcc ccccaaaacc caaggacact 540

ctcatgatct cccggacccc tgaggtcacg tgcgtggtgg tggacgtgag ccaggaagac 600

cccgaggtcc agttcaactg gtacgtggat ggcgtggagg tgcataatgc caagacaaag 660

ccgcgggagg agcagttcaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 720

caggactggc tgaacggcaa ggagtacaag tgcaaggtct ccaacaaagg cctcccgtcc 780

tccatcgaga aaaccatctc caaagccaaa gggcagcccc gagagccaca ggtgtacacc 840

ctgcccccat cccaggagga gatgaccaag aaccaggtca gcctgacctg cctggtcaaa 900

ggcttctacc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 960

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta cagcaggcta 1020

accgtggaca agagcaggtg gcaggagggg aatgtcttct catgctccgt gatgcatgag 1080

gctctgcaca accactacac acagaagagc ctctccctgt ctctgggtaa a 1131

<210> 28
<211> 377
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> IL-22 Fc fusion IgG4 (N297 wt)

<400> 28
Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln Gln
1 5 10 15

Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser Leu
20 25 30

Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe His
35 40 45

Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu Asn
50 55 60

```
Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln Pro
65                  70                  75                  80

Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg Leu
                85                  90                  95

Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn Val
            100                 105                 110

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

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

Cys Ile Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
145                 150                 155                 160

Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                165                 170                 175

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            180                 185                 190

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
        195                 200                 205

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    210                 215                 220

Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
225                 230                 235                 240

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
                245                 250                 255

Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
            260                 265                 270

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
```

275 280 285

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
290 295 300

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
305 310 315 320

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
325 330 335

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

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
355 360 365

Lys Ser Leu Ser Leu Ser Leu Gly Lys
370 375

<210> 29
<211> 1134
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<223> IL-22 Fc fusion IgG1 (N297 wt)

<400> 29
gcgcccatca gctcccactg caggcttgac aagtccaact tccagcagcc ctatatcacc 60

aaccgcacct tcatgctggc taaggaggct agcttggctg ataacaacac agacgttcgt 120

ctcattgggg agaaactgtt ccacggagtc agtatgagtg agcgctgcta tctgatgaag 180

caggtgctga acttcaccct tgaagaagtg ctgttccctc aatctgatag gttccagcct 240

tatatgcagg aggtggtgcc cttcctggcc aggctcagca acaggctaag cacatgtcat 300

attgaaggtg atgacctgca tatccagagg aatgtgcaaa agctgaagga cacagtgaaa 360

aagcttggag agagtggaga gatcaaagca attggagaac tggatttgct gtttatgtct 420

ctgagaaatg cctgcattga gcccaaatct agtgacaaaa ctcacacatg cccaccgtgc 480

ccagcacctg aactcctggg gggaccgtca gtcttcctct tccccccaaa acccaaggac 540

accctcatga tctcccggac ccctgaggtc acatgcgtgg tggtggacgt gagccacgaa 600

gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 660

aagccgcggg aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg 720

caccaggact ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca 780

gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac 840

accctgcccc catcccggga gagatgacc aagaaccagg tcagcctgac ctgcctggtc 900

aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 960

aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag 1020

ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat 1080

gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg taaa 1134

<210> 30
<211> 378
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> IL-22 Fc fusion IgG1 (N297 wt)

<400> 30
Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln Gln
1 5 10 15

Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser Leu
20 25 30

Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe His
35 40 45

Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu Asn
50 55 60

```
Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln Pro
65                  70                  75                  80

Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg Leu
                85                  90                  95

Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn Val
            100                 105                 110

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

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

Cys Ile Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys
145                 150                 155                 160

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
                165                 170                 175

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
            180                 185                 190

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
        195                 200                 205

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
    210                 215                 220

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

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
                245                 250                 255

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
            260                 265                 270

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
        275                 280                 285
```

```
Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
    290                 295                 300


Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
305                 310                 315                 320


Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
                325                 330                 335


Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
            340                 345                 350


Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
        355                 360                 365


Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
    370                 375


<210> 31
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      hinge peptide

<400> 31
Cys Pro Pro Cys Pro
1               5


<210> 32
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      linker peptide

<400> 32
Asp Lys Thr His Thr
1               5
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<210> 33
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
linker peptide

<400> 33
Glu Pro Lys Ser Cys Asp Lys Thr His Thr
1 5 10

<210> 34
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
linker peptide

<400> 34
Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
1 5 10

<210> 35
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
linker peptide

<400> 35
Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
1 5 10

<210> 36
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
linker peptide

<400> 36
Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
1 5 10

<210> 37
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
linker peptide

<400> 37
Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
1 5 10

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

<220>
<223> Description of Artificial Sequence: Synthetic
linker peptide

<400> 38
Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
1 5 10 15

<210> 39
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
linker peptide

<400> 39
Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
1 5 10 15

<210> 40
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
linker peptide

<400> 40

Glu Pro Lys Ser Ser Asp Lys Thr His Thr
1 5 10

<210> 41
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic linker peptide

<400> 41
Gly Gly Gly Asp Lys Thr His Thr
1 5

<210> 42
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic linker (IgG3) peptide

<400> 42
Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr
1 5 10

<210> 43
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic linker peptide

<400> 43
Ser Lys Tyr Gly Pro Pro
1 5

<210> 44
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic linker peptide

<400> 44
Arg Val Glu Ser Lys Tyr Gly Pro Pro
1   5

<210> 45
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      linker peptide

<400> 45
Gly Gly Ser
1

<210> 46
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      linker peptide

<400> 46
Gly Gly Gly Ser
1

<210> 47
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      linker peptide

<400> 47
Gly Gly Gly Gly Ser
1   5

<210> 48
<211> 146
<212> PRT
<213> Pan troglodytes

<400> 48

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Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Ser Phe Gln Gln
1               5                   10                  15


Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser Leu
            20                  25                  30


Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe His
        35                  40                  45


Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu Asn
    50                  55                  60


Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln Pro
65                  70                  75                  80


Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg Leu
                85                  90                  95


Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn Val
            100                 105                 110


Gln Lys Leu Lys Asp Thr Val Lys Lys Leu Gly Glu Asn Gly Glu Ile
        115                 120                 125


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


Cys Ile
145


<210> 49
<211> 146
<212> PRT
<213> Pongo abelii

<400> 49
Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln Gln
1               5                   10                  15


Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser Leu
            20                  25                  30
```

Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe Arg
        35   40   45

Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu Asn
    50   55   60

Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln Pro
65   70   75   80

Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg Leu
                85   90   95

Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn Val
            100   105   110

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

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

Cys Ile
145

<210> 50
<211> 146
<212> PRT
<213> Mus musculus

<400> 50
Leu Pro Val Asn Thr Arg Cys Lys Leu Glu Val Ser Asn Phe Gln Gln
1   5   10   15

Pro Tyr Ile Val Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser Leu
            20   25   30

Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe Arg
        35   40   45

Gly Val Ser Ala Lys Asp Gln Cys Tyr Leu Met Lys Gln Val Leu Asn
    50   55   60

```
Phe Thr Leu Glu Asp Val Leu Leu Pro Gln Ser Asp Arg Phe Gln Pro
65                  70                  75                  80


Tyr Met Gln Glu Val Val Pro Phe Leu Thr Lys Leu Ser Asn Gln Leu
                85                  90                  95


Ser Ser Cys His Ile Ser Gly Asp Asp Gln Asn Ile Gln Lys Asn Val
            100                 105                 110


Arg Arg Leu Lys Glu Thr Val Lys Lys Leu Gly Glu Ser Gly Glu Ile
        115                 120                 125


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


Cys Val
145


<210> 51
<211> 146
<212> PRT
<213> Canis familiaris

<400> 51
Leu Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln Gln
1               5                   10                  15


Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser Leu
            20                  25                  30


Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe His
        35                  40                  45


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


Phe Thr Leu Glu Glu Val Leu Leu Pro Gln Ser Asp Arg Phe Gln Pro
65                  70                  75                  80


Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Lys Leu
                85                  90                  95
```

Ser Gln Cys His Ile Glu Asn Asp Asp Gln His Ile Gln Arg Asn Val
100 105 110

Gln Lys Leu Lys Asp Thr Val Gln Lys Leu Gly Glu Asn Gly Glu Ile
115 120 125

Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ala Leu Arg Asn Ala
130 135 140

Cys Val
145

<210> 52
<211> 94
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
IL-22 Fc fusion protein IgG1 forward primer

<400> 52
ttgaattcca ccatgggatg gtcatgtatc atccttttc tagtagcaac tgcaactgga 60

gtacattcag cgcccatcag ctcccactgc aggc 94

<210> 53
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
IL-22 Fc fusion IgG1 reverse primer

<400> 53
aggtcgactc atttacccgg agacagggag agg 33

<210> 54
<211> 94
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
IL-22 Fc fusion IgG4 forward primer

<400> 54

ttgaattcca ccatgggatg gtcatgtatc atccttttttc tagtagcaac tgcaactgga 60

gtacattcag cgcccatcag ctcccactgc aggc 94

<210> 55
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
IL-22 Fc fusion IgG4 reverse primer

<400> 55
aggtcgactt atttacccag agacagggag agg 33

<210> 56
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
IgG1 N297G forward primer

<400> 56
gcgggaggag cagtacggaa gcacgtaccg tgtgg 35

<210> 57
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
IgG1 N297G reverse primer

<400> 57
ccacacggta cgtgcttccg tactgctcct cccgc 35

<210> 58
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
IgG4 N297G forward primer

<400> 58

acaaagccgc gggaggagca gttcggaagc acgtaccgtg tggtcagcgt c 51

<210> 59
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
IgG4 N297G reverse primer

<400> 59
gacgctgacc acacggtacg tgcttccgaa ctgctcctcc cgcggctttg t 51

<210> 60
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<223> IL-22 Fc fusion IgG2a

<400> 60
Met Ala Val Leu Gln Lys Ser Met Ser Phe Ser Leu Met Gly Thr Leu
1 5 10 15

Ala Ala Ser Cys Leu Leu Leu Ile Ala Leu Trp Ala Gln Glu Ala Asn
20 25 30

Ala Leu Pro Val Asn Thr Arg Cys Lys Leu Glu Val Ser Asn Phe Gln
35 40 45

Gln Pro Tyr Ile Val Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser
50 55 60

Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe
65 70 75 80

Arg Gly Val Ser Ala Lys Asp Gln Cys Tyr Leu Met Lys Gln Val Leu
85 90 95

Asn Phe Thr Leu Glu Asp Val Leu Leu Pro Gln Ser Asp Arg Phe Gln

```
            100                 105                 110

Pro Tyr Met Gln Glu Val Val Pro Phe Leu Thr Lys Leu Ser Asn Gln
        115                 120                 125

Leu Ser Ser Cys His Ile Ser Gly Asp Asp Gln Asn Ile Gln Lys Asn
    130                 135                 140

Val Arg Arg Leu Lys Glu Thr Val Lys Lys Leu Gly Glu Ser Gly Glu
145                 150                 155                 160

Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn
                165                 170                 175

Ala Cys Val Ala Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys
            180                 185                 190

Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro
        195                 200                 205

Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr
    210                 215                 220

Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser
225                 230                 235                 240

Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His
                245                 250                 255

Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile
            260                 265                 270

Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn
        275                 280                 285

Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys
    290                 295                 300

Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu
305                 310                 315                 320
```

Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe
325 330 335

Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu
340 345 350

Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr
355 360 365

Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg
370 375 380

Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His
385 390 395 400

Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
405 410

<210> 61
<211> 372
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<223> IL-22 IgG1 fusion knob (T366W) minus Lys

<400> 61
Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln Gln
1 5 10 15

Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser Leu
20 25 30

Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe His
35 40 45

Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu Asn
50 55 60

```
Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln Pro
65                  70                  75                  80

Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg Leu
                85                  90                  95

Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn Val
            100                 105                 110

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

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

Cys Ile Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
145                 150                 155                 160

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                165                 170                 175

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

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        195                 200                 205

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    210                 215                 220

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
225                 230                 235                 240

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                245                 250                 255

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            260                 265                 270

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        275                 280                 285
```

Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
290 295 300

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

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
325 330 335

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
340 345 350

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
355 360 365

Leu Ser Pro Gly
370

<210> 62
<211> 226
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<223> Monomeric Fc hole

<400> 62
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15

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

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

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

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

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

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

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

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

Leu Ser Cys Ala 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 Val 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
225
```

<210> 63
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
linker peptide

<400> 63
Gly Gly Gly Ser Thr His Thr
1 5

<210> 64
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
linker peptide

<400> 64
Asp Lys Lys Val Glu Pro Lys Ser Ser Asp Lys Thr His Thr
1 5 10

<210> 65
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
linker peptide

<400> 65
Lys Val Asp Lys Lys Val Glu Pro Lys Ser Ser Asp Lys Thr His Thr
1 5 10 15

<210> 66
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
linker peptide

<400> 66
Lys Lys Val Glu Pro Lys Ser Ser Asp Lys Thr His Thr
1 5 10

<210> 67
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

linker peptide

<400> 67
Val Glu Pro Lys Ser Ser Asp Lys Thr His Thr
1 5 10

<210> 68
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
linker peptide

<400> 68
Lys Val Glu Pro Lys Ser Ser Asp Lys Thr His Thr
1 5 10

<210> 69
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
linker peptide

<400> 69
Val Asp Lys Lys Val Glu Pro Lys Ser Ser Asp Lys Thr His Thr
1 5 10 15

<210> 70
<211> 1152
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (58)..(597)

<400> 70
cttcagaaca ggttctcctt ccccagtcac cagttgctcg agttagaatt gtctgca 57

atg gcc gcc ctg cag aaa tct gtg agc tct ttc ctt atg ggg acc ctg 105
Met Ala Ala Leu Gln Lys Ser Val Ser Ser Phe Leu Met Gly Thr Leu
1 5 10 15

gcc acc agc tgc ctc ctt ctc ttg gcc ctc ttg gta cag gga gga gca 153
Ala Thr Ser Cys Leu Leu Leu Leu Ala Leu Leu Val Gln Gly Gly Ala

```
            20                  25                  30

gct gcg ccc atc agc tcc cac tgc agg ctt gac aag tcc aac ttc cag        201
Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln
        35                  40                  45

cag ccc tat atc acc aac cgc acc ttc atg ctg gct aag gag gct agc        249
Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser
    50                  55                  60

ttg gct gat aac aac aca gac gtt cgt ctc att ggg gag aaa ctg ttc        297
Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe
65                  70                  75                  80

cac gga gtc agt atg agt gag cgc tgc tat ctg atg aag cag gtg ctg        345
His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu
                85                  90                  95

aac ttc acc ctt gaa gaa gtg ctg ttc cct caa tct gat agg ttc cag        393
Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln
            100                 105                 110

cct tat atg cag gag gtg gtg ccc ttc ctg gcc agg ctc agc aac agg        441
Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg
        115                 120                 125

cta agc aca tgt cat att gaa ggt gat gac ctg cat atc cag agg aat        489
Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn
    130                 135                 140

gtg caa aag ctg aag gac aca gtg aaa aag ctt gga gag agt gga gag        537
Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu Gly Glu Ser Gly Glu
145                 150                 155                 160

atc aaa gca att gga gaa ctg gat ttg ctg ttt atg tct ctg aga aat        585
Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn
                165                 170                 175

gcc tgc att tga ccagagcaaa gctgaaaaat gaataactaa ccccctttcc           637
Ala Cys Ile


ctgctagaaa taacaattag atgccccaaa gcgatttttt ttaaccaaaa ggaagatggg     697

aagccaaact ccatcatgat gggtggattc caaatgaacc cctgcgttag ttacaaagga     757

aaccaatgcc acttttgttt ataagaccag aaggtagact ttctaagcat agatatttat     817

tgataacatt tcattgtaac tggtgttcta tacacagaaa acaatttatt ttttaaataa     877

ttgtcttttt ccataaaaaa gattactttc cattccttta ggggaaaaaa cccctaaata     937

gcttcatgtt tccataatca gtactttata tttataaatg tatttattat tattataaga     997
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ctgcatttta tttatatcat tttattaata tggatttatt tatagaaaca tcattcgata 1057

ttgctacttg agtgtaaggc taatattgat atttatgaca ataattatag agctataaca 1117

tgtttatttg acctcaataa acacttggat atccc 1152

<210> 71
<211> 179
<212> PRT
<213> Homo sapiens

<400> 71
Met Ala Ala Leu Gln Lys Ser Val Ser Ser Phe Leu Met Gly Thr Leu
1 5 10 15

Ala Thr Ser Cys Leu Leu Leu Leu Ala Leu Leu Val Gln Gly Gly Ala
20 25 30

Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln
35 40 45

Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser
50 55 60

Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe
65 70 75 80

His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu
85 90 95

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

Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg
115 120 125

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

Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu Gly Glu Ser Gly Glu
145 150 155 160

Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn

165 170 175

Ala Cys Ile

<210> 72
<211> 1236
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 72
atggctgtcc tgcagaaatc tatgagtttt tcccttatgg ggactttggc cgccagctgc 60

ctgcttctca ttgccctgtg ggcccaggag gcaaatgcgc tgcccgtcaa cacccggtgc 120

aagcttgagg tgtccaactt ccagcagcca tacatcgtca accgcacctt tatgctggcc 180

aaggaggcca gccttgcaga taacaacaca gatgtccggc tcatcgggga gaaactgttc 240

cgaggagtca gtgctaagga tcagtgctac ctgatgaagc aggtgctcaa cttcaccctg 300

gaagacgttc tgctccccca gtcagacagg ttccagccct acatgcagga ggtggtgcct 360

ttcctgacca aactcagcaa tcagctcagc tcctgtcaca tcagcggtga cgaccagaac 420

atccagaaga atgtcagaag gctgaaggag acagtgaaaa agcttggaga gagtggagag 480

atcaaggcga ttggggaact ggacctgctg tttatgtctc tgagaaatgc ttgcgtcgct 540

cgaggaccca caatcaagcc ctgtcctcca tgcaaatgcc cagcacctaa cctcttgggt 600

ggaccatccg tcttcatctt ccctccaaag atcaaggatg tactcatgat ctccctgagc 660

cccatagtca catgtgtggt ggtggatgtg agcgaggatg acccagatgt ccagatcagc 720

tggtttgtga acaacgtgga agtacacaca gctcagacac aaacccatag agaggattac 780

aacagtactc tacgcgtggt cagtgccctc cccatccagc accaggactg gatgagtggc 840

aaggagttca aatgcaaggt caacaacaaa gacctcccag cgcccatcga gagaaccatc 900

tcaaaaccca aagggtcagt aagagctcca caggtatatg tcttgcctcc accagaagaa 960

gagatgacta agaaacaggt cactctgacc tgcatggtca cagacttcat gcctgaagac 1020

atttacgtgg agtggaccaa caacgggaaa acagagctaa actacaagaa cactgaacca 1080

gtcctggact ctgatggttc ttacttcatg tacagcaagc tgagagtgga aaagaagaac 1140

tgggtggaaa gaaatagcta ctcctgttca gtggtccacg agggtctgca caatcaccac 1200

acgactaaga gcttctcccg gactccgggt aaatga 1236

<210> 73
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 73

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

Ala Ala Ser Cys Leu Leu Leu Ile Ala Leu Trp Ala Gln Glu Ala Asn
20 25 30

Ala Leu Pro Val Asn Thr Arg Cys Lys Leu Glu Val Ser Asn Phe Gln
35 40 45

Gln Pro Tyr Ile Val Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser
50 55 60

Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe
65 70 75 80

Arg Gly Val Ser Ala Lys Asp Gln Cys Tyr Leu Met Lys Gln Val Leu
85 90 95

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

Pro Tyr Met Gln Glu Val Val Pro Phe Leu Thr Lys Leu Ser Asn Gln
115 120 125

Leu Ser Ser Cys His Ile Ser Gly Asp Asp Gln Asn Ile Gln Lys Asn
130 135 140

Val Arg Arg Leu Lys Glu Thr Val Lys Lys Leu Gly Glu Ser Gly Glu
145 150 155 160

```
Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn
                165                 170                 175

Ala Cys Val Ala Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys
            180                 185                 190

Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro
        195                 200                 205

Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr
    210                 215                 220

Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser
225                 230                 235                 240

Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His
                245                 250                 255

Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile
            260                 265                 270

Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn
        275                 280                 285

Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys
    290                 295                 300

Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu
305                 310                 315                 320

Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe
                325                 330                 335

Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu
            340                 345                 350

Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr
        355                 360                 365

Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg
```

370 375 380

Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His
385 390 395 400

Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
405 410

<210> 74
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 74
aggtccattc agatgctggt 20

<210> 75
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 75
taggtgtggt tgacgtggag 20

<210> 76
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 76
ccaccccaca ctcacaccgg 20

<210> 77
<211> 177
<212> PRT
<213> Homo sapiens

<400> 77

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Met Lys Leu Gln Cys Val Ser Leu Trp Leu Leu Gly Thr Ile Leu Ile
1               5                  10                  15

Leu Cys Ser Val Asp Asn His Gly Leu Arg Arg Cys Leu Ile Ser Thr
            20                  25                  30

Asp Met His His Ile Glu Glu Ser Phe Gln Glu Ile Lys Arg Ala Ile
        35                  40                  45

Gln Ala Lys Asp Thr Phe Pro Asn Val Thr Ile Leu Ser Thr Leu Glu
    50                  55                  60

Thr Leu Gln Ile Ile Lys Pro Leu Asp Val Cys Cys Val Thr Lys Asn
65                  70                  75                  80

Leu Leu Ala Phe Tyr Val Asp Arg Val Phe Lys Asp His Gln Glu Pro
                85                  90                  95

Asn Pro Lys Ile Leu Arg Lys Ile Ser Ser Ile Ala Asn Ser Phe Leu
            100                 105                 110

Tyr Met Gln Lys Thr Leu Arg Gln Cys Gln Glu Gln Arg Gln Cys His
        115                 120                 125

Cys Arg Gln Glu Ala Thr Asn Ala Thr Arg Val Ile His Asp Asn Tyr
    130                 135                 140

Asp Gln Leu Glu Val His Ala Ala Ala Ile Lys Ser Leu Gly Glu Leu
145                 150                 155                 160

Asp Val Phe Leu Ala Trp Ile Asn Lys Asn His Glu Val Met Ser Ser
                165                 170                 175

Ala
```

<210> 78
<211> 176
<212> PRT
<213> Homo sapiens

<400> 78

```
Met Lys Ala Ser Ser Leu Ala Phe Ser Leu Leu Ser Ala Ala Phe Tyr
1               5                   10                  15

Leu Leu Trp Thr Pro Ser Thr Gly Leu Lys Thr Leu Asn Leu Gly Ser
            20                  25                  30

Cys Val Ile Ala Thr Asn Leu Gln Glu Ile Arg Asn Gly Phe Ser Glu
        35                  40                  45

Ile Arg Gly Ser Val Gln Ala Lys Asp Gly Asn Ile Asp Ile Arg Ile
    50                  55                  60

Leu Arg Arg Thr Glu Ser Leu Gln Asp Thr Lys Pro Ala Asn Arg Cys
65                  70                  75                  80

Cys Leu Leu Arg His Leu Leu Arg Leu Tyr Leu Asp Arg Val Phe Lys
                85                  90                  95

Asn Tyr Gln Thr Pro Asp His Tyr Thr Leu Arg Lys Ile Ser Ser Leu
            100                 105                 110

Ala Asn Ser Phe Leu Thr Ile Lys Lys Asp Leu Arg Leu Cys His Ala
        115                 120                 125

His Met Thr Cys His Cys Gly Glu Glu Ala Met Lys Lys Tyr Ser Gln
    130                 135                 140

Ile Leu Ser His Phe Glu Lys Leu Glu Pro Gln Ala Ala Val Val Lys
145                 150                 155                 160

Ala Leu Gly Glu Leu Asp Ile Leu Leu Gln Trp Met Glu Glu Thr Glu
                165                 170                 175
```

<210> 79
<211> 207
<212> PRT
<213> Homo sapiens

<400> 79

```
Met Asn Phe Gln Gln Arg Leu Gln Ser Leu Trp Thr Leu Ala Ser Arg
1               5                   10                  15
```

```
Pro Phe Cys Pro Pro Leu Leu Ala Thr Ala Ser Gln Met Gln Met Val
            20                  25                  30

Val Leu Pro Cys Leu Gly Phe Thr Leu Leu Leu Trp Ser Gln Val Ser
        35                  40                  45

Gly Ala Gln Gly Gln Glu Phe His Phe Gly Pro Cys Gln Val Lys Gly
    50                  55                  60

Val Val Pro Gln Lys Leu Trp Glu Ala Phe Trp Ala Val Lys Asp Thr
65                  70                  75                  80

Met Gln Ala Gln Asp Asn Ile Thr Ser Ala Arg Leu Leu Gln Gln Glu
                85                  90                  95

Val Leu Gln Asn Val Ser Asp Ala Glu Ser Cys Tyr Leu Val His Thr
            100                 105                 110

Leu Leu Glu Phe Tyr Leu Lys Thr Val Phe Lys Asn Tyr His Asn Arg
        115                 120                 125

Thr Val Glu Val Arg Thr Leu Lys Ser Phe Ser Thr Leu Ala Asn Asn
    130                 135                 140

Phe Val Leu Ile Val Ser Gln Leu Gln Pro Ser Gln Glu Asn Glu Met
145                 150                 155                 160

Phe Ser Ile Arg Asp Ser Ala His Arg Arg Phe Leu Leu Phe Arg Arg
                165                 170                 175

Ala Phe Lys Gln Leu Asp Val Glu Ala Ala Leu Thr Lys Ala Leu Gly
            180                 185                 190

Glu Val Asp Ile Leu Leu Thr Trp Met Gln Lys Phe Tyr Lys Leu
        195                 200                 205
```

<210> 80
<211> 171
<212> PRT
<213> Homo sapiens

<400> 80

```
Met Leu Val Asn Phe Ile Leu Arg Cys Gly Leu Leu Leu Val Thr Leu
1               5                  10                  15

Ser Leu Ala Ile Ala Lys His Lys Gln Ser Ser Phe Thr Lys Ser Cys
            20                  25                  30

Tyr Pro Arg Gly Thr Leu Ser Gln Ala Val Asp Ala Leu Tyr Ile Lys
        35                  40                  45

Ala Ala Trp Leu Lys Ala Thr Ile Pro Glu Asp Arg Ile Lys Asn Ile
    50                  55                  60

Arg Leu Leu Lys Lys Lys Thr Lys Lys Gln Phe Met Lys Asn Cys Gln
65                  70                  75                  80

Phe Gln Glu Gln Leu Leu Ser Phe Phe Met Glu Asp Val Phe Gly Gln
                85                  90                  95

Leu Gln Leu Gln Gly Cys Lys Lys Ile Arg Phe Val Glu Asp Phe His
            100                 105                 110

Ser Leu Arg Gln Lys Leu Ser His Cys Ile Ser Cys Ala Ser Ser Ala
        115                 120                 125

Arg Glu Met Lys Ser Ile Thr Arg Met Lys Arg Ile Phe Tyr Arg Ile
    130                 135                 140

Gly Asn Lys Gly Ile Tyr Lys Ala Ile Ser Glu Leu Asp Ile Leu Leu
145                 150                 155                 160

Ser Trp Ile Lys Lys Leu Leu Glu Ser Ser Gln
                165                 170
```