SEQUENCE LISTING

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<120> FGF21 Mutants and Uses Thereof

<130> A-1429-WO-PCT2

<160> 165

<170> PatentIn version 3.5

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<220>
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1               5                  10                  15

gtg ctg gct ggt ctt ctg ctg gga gcc tgc cag gca cac ccc atc cct          96
Val Leu Ala Gly Leu Leu Leu Gly Ala Cys Gln Ala His Pro Ile Pro
            20                  25                  30

gac tcc agt cct ctc ctg caa ttc ggg ggc caa gtc cgg cag cgg tac         144
Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln Arg Tyr
        35                  40                  45

ctc tac aca gat gat gcc cag cag aca gaa gcc cac ctg gag atc agg         192
Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His Leu Glu Ile Arg
    50                  55                  60

gag gat ggg acg gtg ggg ggc gct gct gac cag agc ccc gaa agt ctc         240
Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser Pro Glu Ser Leu
65                  70                  75                  80

ctg cag ctg aaa gcc ttg aag ccg gga gtt att caa atc ttg gga gtc         288
Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu Gly Val
                85                  90                  95

aag aca tcc agg ttc ctg tgc cag cgg cca gat ggg gcc ctg tat gga         336
Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly Ala Leu Tyr Gly
            100                 105                 110

tcg ctc cac ttt gac cct gag gcc tgc agc ttc cgg gag ctg ctt ctt         384
Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu Leu Leu
        115                 120                 125

gag gac gga tac aat gtt tac cag tcc gaa gcc cac ggc ctc ccg ctg         432
Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu Pro Leu
    130                 135                 140

cac ctg cca ggg aac aag tcc cca cac cgg gac cct gca ccc cga gga         480
His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro Ala Pro Arg Gly
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145                 150                 155                 160

cca gct cgc ttc ctg cca cta cca ggc ctg ccc ccc gca ccc ccg gag        528
Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro Ala Pro Pro Glu
                165                 170                 175

cca ccc gga atc ctg gcc ccc cag ccc ccc gat gtg ggc tcc tcg gac        576
Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp Val Gly Ser Ser Asp
            180                 185                 190

cct ctg agc atg gtg gga cct tcc cag ggc cga agc ccc agc tac gct        624
Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg Ser Pro Ser Tyr Ala
        195                 200                 205

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Val Leu Ala Gly Leu Leu Leu Gly Ala Cys Gln Ala His Pro Ile Pro
            20                  25                  30

Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln Arg Tyr
        35                  40                  45

Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His Leu Glu Ile Arg
    50                  55                  60

Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser Pro Glu Ser Leu
65                  70                  75                  80

Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu Gly Val
                85                  90                  95

Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly Ala Leu Tyr Gly
            100                 105                 110

Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu Leu Leu
        115                 120                 125

Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu Pro Leu
    130                 135                 140

His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro Ala Pro Arg Gly
145                 150                 155                 160

Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro Ala Pro Pro Glu
                165                 170                 175
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Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp Val Gly Ser Ser Asp
            180                 185                 190

Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg Ser Pro Ser Tyr Ala
        195                 200                 205

Ser
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<210> 3
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<213> Homo sapiens

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

cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca gaa gcc cac          96
Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His
            20                  25                  30

ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct gac cag agc         144
Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser
        35                  40                  45

ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga gtt att caa         192
Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln
    50                  55                  60

atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg cca gat ggg         240
Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly
65                  70                  75                  80

gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc agc ttc cgg         288
Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg
                85                  90                  95

gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc gaa gcc cac         336
Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His
            100                 105                 110

ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac cgg gac cct         384
Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro
        115                 120                 125

gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc ctg ccc ccc         432
Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro
    130                 135                 140

gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc ccc gat gtg         480
Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp Val
145                 150                 155                 160

ggc tcc tcg gac cct ctg agc atg gtg gga cct tcc cag ggc cga agc         528
Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg Ser
                165                 170                 175
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ccc agc tac gct tcc tga 546
Pro Ser Tyr Ala Ser
180

<210> 4
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<213> Homo sapiens

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His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val
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Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His
20 25 30

Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser
35 40 45

Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln
50 55 60

Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly
65 70 75 80

Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg
85 90 95

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

Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro
115 120 125

Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro
130 135 140

Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp Val
145 150 155 160

Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg Ser
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Pro Ser Tyr Ala Ser
180

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Met Asp Ser Asp Glu Thr Gly Phe Glu His Ser Gly Leu Trp Val Ser
1               5                  10                  15

gtg ctg gct ggt ctt ctg ctg gga gcc tgc cag gca cac ccc atc cct          96
Val Leu Ala Gly Leu Leu Leu Gly Ala Cys Gln Ala His Pro Ile Pro
            20                  25                  30

gac tcc agt cct ctc ctg caa ttc ggg ggc caa gtc cgg cag cgg tac         144
Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln Arg Tyr
        35                  40                  45

ctc tac aca gat gat gcc cag cag aca gaa gcc cac ctg gag atc agg         192
Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His Leu Glu Ile Arg
    50                  55                  60

gag gat ggg acg gtg ggg ggc gct gct gac cag agc ccc gaa agt ctc         240
Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser Pro Glu Ser Leu
65                  70                  75                  80

ctg cag ctg aaa gcc ttg aag ccg gga gtt att caa atc ttg gga gtc         288
Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu Gly Val
                85                  90                  95

aag aca tcc agg ttc ctg tgc cag cgg cca gat ggg gcc ctg tat gga         336
Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly Ala Leu Tyr Gly
            100                 105                 110

tcg ctc cac ttt gac cct gag gcc tgc agc ttc cgg gag ctg ctt ctt         384
Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu Leu Leu
        115                 120                 125

gag gac gga tac aat gtt tac cag tcc gaa gcc cac ggc ctc ccg ctg         432
Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu Pro Leu
    130                 135                 140

cac ctg cca ggg aac aag tcc cca cac cgg gac cct gca ccc cga gga         480
His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro Ala Pro Arg Gly
145                 150                 155                 160

cca gct cgc ttc ctg cca cta cca ggc ctg ccc ccc gca ctc ccg gag         528
Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro Ala Leu Pro Glu
                165                 170                 175

cca ccc gga atc ctg gcc ccc cag ccc ccc gat gtg ggc tcc tcg gac         576
Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp Val Gly Ser Ser Asp
            180                 185                 190

cct ctg agc atg gtg gga cct tcc cag ggc cga agc ccc agc tac gct         624
Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg Ser Pro Ser Tyr Ala
        195                 200                 205

tcc tga                                                                 630
Ser
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<213> Homo sapiens

<400> 6

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Val Leu Ala Gly Leu Leu Leu Gly Ala Cys Gln Ala His Pro Ile Pro
            20                  25                  30

Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln Arg Tyr
        35                  40                  45

Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His Leu Glu Ile Arg
    50                  55                  60

Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser Pro Glu Ser Leu
65                  70                  75                  80

Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu Gly Val
                85                  90                  95

Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly Ala Leu Tyr Gly
            100                 105                 110

Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu Leu Leu
        115                 120                 125

Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu Pro Leu
    130                 135                 140

His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro Ala Pro Arg Gly
145                 150                 155                 160

Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro Ala Leu Pro Glu
                165                 170                 175

Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp Val Gly Ser Ser Asp
            180                 185                 190

Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg Ser Pro Ser Tyr Ala
        195                 200                 205

Ser
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<210> 7
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<213> Homo sapiens

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

cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca gaa gcc cac          96
Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His
            20                  25                  30

ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct gac cag agc         144
Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser
        35                  40                  45

ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga gtt att caa         192
Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln
    50                  55                  60

atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg cca gat ggg         240
Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly
65                  70                  75                  80

gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc agc ttc cgg         288
Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg
                85                  90                  95

gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc gaa gcc cac         336
Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His
            100                 105                 110

ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac cgg gac cct         384
Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro
        115                 120                 125

gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc ctg ccc ccc         432
Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro
    130                 135                 140

gca ctc ccg gag cca ccc gga atc ctg gcc ccc cag ccc ccc gat gtg         480
Ala Leu Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp Val
145                 150                 155                 160

ggc tcc tcg gac cct ctg agc atg gtg gga cct tcc cag ggc cga agc         528
Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg Ser
                165                 170                 175

ccc agc tac gct tcc tga                                                546
Pro Ser Tyr Ala Ser
            180


<210>  8
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<213>  Homo sapiens

<400>  8

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1               5                  10                  15


Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His
            20                  25                  30


Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser
        35                  40                  45


Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln
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```
    50                  55                  60

Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly
65                  70                  75                  80

Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg
                85                  90                  95

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

Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro
        115                 120                 125

Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro
    130                 135                 140

Ala Leu Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp Val
145                 150                 155                 160

Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg Ser
                165                 170                 175

Pro Ser Tyr Ala Ser
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<212> DNA
<213> Homo sapiens

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1               5                   10                  15

gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg        96
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
```

```
atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac        144
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg        192
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60

cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg tac        240
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65                  70                  75                  80

cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc        288
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc        336
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110

gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg        384
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125

tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc agc        432
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag        480
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160

tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc        528
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg        576
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190

gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg        624
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205

cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct        672
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220

ccg ggt aaa                                                            681
Pro Gly Lys
225
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<210> 11
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<213> Homo sapiens

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Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
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Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
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Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45

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

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

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

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

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

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

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
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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<210> 13
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
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<400> 13
tagtgagctc gaattcttag gaagcgtagc tgg 33

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

<220>
<223> PCR primer

<400> 14
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<210> 15
<211> 34
<212> DNA
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<220>
<223> PCR primer

<400> 15
catatgtata tctccttctt aaagttaaac aaaa 34

<210> 16
<211> 34
<212> DNA
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<220>
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aaaacaaatt gaaattcttc ctctatatgt atac 34

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

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<223> sense strand from a portion of an FGF21 expression construct

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att 63

<210> 18
<211> 63
<212> DNA
<213> Artificial

<220>
<223> antisense strand from a portion of an FGF21 expression construct

<400> 18
aaaacaaatt gaaattcttc ctctatatgt atacgtaggt taaggtctaa gaagaggtaa 60

taa 63

<210> 19
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 19
aggaggaata acatatggac aaaactcaca catg 34

<210> 20
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<220>
<223> PCR primer

<400> 20
ggatccacca ccaccgctac cac 23

<210> 21
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<212> DNA
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<400> 21
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<210> 22
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<400> 22
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<210> 23
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<213> Artificial Sequence

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<210> 25
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<210> 26
<211> 30
<212> DNA
<213> Artificial

<220>
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<400> 26
agcctgggag actcgtacca ccttggaagg 30

<210> 27
<211> 50
<212> DNA
<213> artificial

<220>
<223> antisense strand from a portion of an FGF21 expression construct

<400> 27
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<210> 28
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<212> PRT
<213> Artificial Sequence

<220>
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<210> 29
<211> 4
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<220>
<223> G4 Linker

<400> 29

Gly Gly Gly Gly
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<210> 30
<211> 5
<212> PRT
<213> Artificial

<220>
<223> G5 Linker

<400> 30

Gly Gly Gly Gly Gly
1 5

<210> 31
<211> 15
<212> PRT
<213> Artificial

<220>
<223> (G4S)3 Linker

<400> 31

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 32
<211> 8
<212> PRT
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<220>
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<400> 32

Gly Gly Gly Lys Gly Gly Gly Gly
1 5

<210> 33
<211> 8
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<213> Artificial

<220>
<223> G3NGSG2 Linker

<400> 33

Gly Gly Gly Asn Gly Ser Gly Gly
1 5

<210> 34
<211> 8
<212> PRT
<213> Artificial

<220>
<223> G3CG4 linker

<400> 34

Gly Gly Gly Cys Gly Gly Gly Gly
1 5

<210> 35
<211> 5
<212> PRT
<213> Artificial

<220>
<223> GPNG2 Linker

<400> 35

Gly Pro Asn Gly Gly
1 5

<210> 36
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> FGF21 RG

<220>
<221> CDS
<222> (1)..(549)

<400> 36
atg cat cca att cca gat tct tct cca tta tta caa ttc ggg ggc caa 48
Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1 5 10 15

gtc cgg cag cgt tac ctc tac aca gat gat gcc cag cag aca gaa gcc 96
Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
20 25 30

cac ctg gag atc agg gag gac ggg acg gtg ggg ggt gct gct gac cag 144
His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
35 40 45

agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg ggt gtt att 192
Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
50 55 60

caa atc ttg ggt gtc aag aca tcc agg ttc ctg tgc cag cgg cca gat 240
Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp
65 70 75 80

ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc agc ttc 288
Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe
85 90 95

cgt gag cgt ctt ctt gag gac ggt tac aat gtt tac cag tcc gaa gcc 336
Arg Glu Arg Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
100 105 110

cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac cgt gac 384
His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
115 120 125

cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc ctg ccc 432
Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro

```
    130                 135                 140

ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc ccc gat        480
Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145                 150                 155                 160

gtg ggc tcc tcg gac cct ctg agc atg gtg ggt ggt tcc cag ggc cga        528
Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Gly Ser Gln Gly Arg
                165                 170                 175

agc ccc agc tac gct tcc taa                                        549
Ser Pro Ser Tyr Ala Ser
            180


<210>  37
<211>  182
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  37

Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1               5                   10                  15

Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
            20                  25                  30

His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
        35                  40                  45

Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
    50                  55                  60

Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp
65                  70                  75                  80

Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe
                85                  90                  95

Arg Glu Arg Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
            100                 105                 110

His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
        115                 120                 125

Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro
    130                 135                 140

Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145                 150                 155                 160

Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Gly Ser Gln Gly Arg
                165                 170                 175
```

```
Ser Pro Ser Tyr Ala Ser
            180


<210>  38
<211>  546
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  FGF21 RGE


<220>
<221>  CDS
<222>  (1)..(546)

<400>  38
cat cca att cca gat tct tct cca tta tta caa ttc ggg ggc caa gtc          48
His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val
1               5                   10                  15

cgg cag cgt tac ctc tac aca gat gat gcc cag cag aca gaa gcc cac          96
Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His
            20                  25                  30

ctg gag atc agg gag gac ggg acg gtg ggg ggt gct gct gac cag agc         144
Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser
        35                  40                  45

ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg ggt gtt att caa         192
Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln
    50                  55                  60

atc ttg ggt gtc aag aca tcc agg ttc ctg tgc cag cgg cca gat ggg         240
Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly
65                  70                  75                  80

gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc agc ttc cgt         288
Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg
                85                  90                  95

gag cgt ctt ctt gag gac ggt tac aat gtt tac cag tcc gaa gcc cac         336
Glu Arg Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His
            100                 105                 110

ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac cgt gac cct         384
Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro
        115                 120                 125

gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc ctg ccc ccc         432
Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro
    130                 135                 140

gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc ccc gat gtg         480
Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp Val
145                 150                 155                 160

ggc tcc tcg gac cct ctg agc atg gtg ggt ggt tcc cag ggc cga agc         528
Gly Ser Ser Asp Pro Leu Ser Met Val Gly Gly Ser Gln Gly Arg Ser
                165                 170                 175

ccc agc tac gaa tcc taa                                                 546
Pro Ser Tyr Glu Ser
            180
```

<210> 39
<211> 181
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 39

```
His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val
1               5                  10                  15

Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His
            20                  25                  30

Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser
        35                  40                  45

Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln
    50                  55                  60

Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly
65                  70                  75                  80

Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg
                85                  90                  95

Glu Arg Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His
            100                 105                 110

Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro
        115                 120                 125

Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro
    130                 135                 140

Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp Val
145                 150                 155                 160

Gly Ser Ser Asp Pro Leu Ser Met Val Gly Gly Ser Gln Gly Arg Ser
                165                 170                 175

Pro Ser Tyr Glu Ser
            180
```

<210> 40
<211> 1272
<212> DNA
<213> Artificial Sequence

<220>
<223> WT21-L15-Fc

<220>

<221> CDS
<222> (1)..(1272)

<400> 40

```
atg cat cca att cca gat tct tct cca tta tta caa ttc ggg ggc caa          48
Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1               5                  10                  15

gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca gaa gcc          96
Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
            20                  25                  30

cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct gac cag         144
His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
        35                  40                  45

agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga gtt att         192
Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
    50                  55                  60

caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg cca gat         240
Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp
65                  70                  75                  80

ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc agc ttc         288
Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe
                85                  90                  95

cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc gaa gcc         336
Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
            100                 105                 110

cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac cgg gac         384
His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
        115                 120                 125

cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc ctg cca         432
Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro
    130                 135                 140

ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc ccc gat         480
Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145                 150                 155                 160

gtg ggc tcc tcg gac cct ctg agc atg gtg gga cct tcc cag ggc cga         528
Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
                165                 170                 175

agc ccc agc tac gct tcc ggt gga ggt ggt ggt tct ggt ggt ggt agc         576
Ser Pro Ser Tyr Ala Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser
            180                 185                 190

ggt ggt ggt gga tcc gac aaa act cac aca tgc cca ccg tgc cca gca         624
Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
        195                 200                 205

cct gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc         672
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
    210                 215                 220

aag gac acc ctc atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg         720
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
225                 230                 235                 240

gtg gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg         768
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
                245                 250                 255
```

```
gac ggc gtg gag gtg cat aat gcc aag aca aag ccg cgt gag gag cag        816
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
            260                 265                 270

tac aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag        864
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
        275                 280                 285

gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc        912
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
    290                 295                 300

ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc        960
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
305                 310                 315                 320

cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc       1008
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
                325                 330                 335

aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc       1056
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
            340                 345                 350

gac atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac       1104
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
        355                 360                 365

aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tat       1152
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
    370                 375                 380

agc aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc       1200
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
385                 390                 395                 400

tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag       1248
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
                405                 410                 415

agc ctc tcc ctg tct ccg ggt aaa                                      1272
Ser Leu Ser Leu Ser Pro Gly Lys
            420
```

<210> 41
<211> 424
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 41

```
Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1               5                   10                  15

Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
            20                  25                  30

His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
        35                  40                  45

Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
```

50 55 60

Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp
65 70 75 80

Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe
85 90 95

Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
100 105 110

His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
115 120 125

Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro
130 135 140

Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145 150 155 160

Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
165 170 175

Ser Pro Ser Tyr Ala Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser
180 185 190

Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
195 200 205

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
210 215 220

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
225 230 235 240

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
245 250 255

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
260 265 270

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
275 280 285

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
290 295 300

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
305 310 315 320

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr

325 330 335

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
340 345 350

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
355 360 365

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
370 375 380

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
385 390 395 400

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
405 410 415

Ser Leu Ser Leu Ser Pro Gly Lys
420

<210> 42
<211> 1275
<212> DNA
<213> Artificial

<220>
<223> Fc L15 RG

<220>
<221> CDS
<222> (1)..(1275)

<400> 42

```
atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg          48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                   10                  15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc          96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc         144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag         192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg         240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat         288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc         336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110
```

```
atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag        384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc        432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg        480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct        528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc        576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg        624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg        672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

tct ccg ggt aaa ggt gga ggt ggt ggt tct ggt ggt ggt agc ggt ggt        720
Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

ggt gga tcc cat cca att cca gat tct tct cca tta tta caa ttc ggg        768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggc caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca        816
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

gaa gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct        864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga        912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg        960
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc       1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

agc ttc cgg gag cgt ctt ctt gag gac gga tac aat gtt tac cag tcc       1056
Ser Phe Arg Glu Arg Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac       1104
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

cgg gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc       1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380
```

```
ctg ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc       1200
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg gga ggt tcc cag       1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Gly Ser Gln
                405                 410                 415

ggc cga agc ccc agc tac gct tcc taa                                  1275
Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 43
<211> 424
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 43

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

Ser Phe Arg Glu Arg Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Gly Ser Gln
                405                 410                 415

Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 44
<211> 1275
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc-(G4S)3-RG

<220>
<221> CDS
<222> (1)..(1275)

<400> 44

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atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg          48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                  10                  15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc          96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc         144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag         192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg         240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat         288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc         336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag         384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc         432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg         480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct         528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc         576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg         624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg         672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

tct ccg ggt aaa ggt ggt ggt ggt tcc ggt ggc ggc ggc tct ggt ggt         720
Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
```

```
225                 230                 235                 240

ggt ggc agc cat ccg atc ccg gac tct tct ccg ctg ctg cag ttc ggt  768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggt cag gtt cgt cag cgt tac ctg tac acc gac gac gcg cag cag acc  816
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

gag gcg cac ctg gag atc cgt gaa gac ggt acc gtt ggt ggt gcg gcc  864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

gac cag tct ccg gaa tct ctg ctg cag ctg aaa gcc ctg aaa ccg ggt  912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt atc cag atc ctg ggc gtt aaa acc tct cgt ttc ctg tgc cag cgt  960
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

ccg gac ggc gcc ctg tac ggt tct ctg cac ttc gac ccg gag gcg tgc 1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

tct ttt cgt gaa cgt ctg ctc gaa gac ggt tac aac gtt tac cag tct 1056
Ser Phe Arg Glu Arg Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gag gcg cac ggt ctg ccg ctg cac ctg ccg ggt aac aaa tct ccg cac 1104
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

cgt gac ccg gcg cca cgt ggt cct gcg cgt ttc ctg cca ctg ccg ggc 1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

ctg ccg cct gcg cct cct gaa ccg cct ggt atc ctg gct ccg cag ccg 1200
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

cca gac gtt ggt tct tct gac ccg ctg tct atg gtt ggt ggc tct cag 1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Gly Ser Gln
                405                 410                 415

ggt cgt tct ccg tct tac gcc tct taa                             1275
Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 45
<211> 424
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 45

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300
```

```
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

Ser Phe Arg Glu Arg Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Gly Ser Gln
                405                 410                 415

Gly Arg Ser Pro Ser Tyr Ala Ser
            420


<210>  46
<211>  1275
<212>  DNA
<213>  Artificial

<220>
<223>  Fc-(G4S)3-RGE


<220>
<221>  CDS
<222>  (1)..(1275)

<400>  46
atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg          48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                   10                  15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc          96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc         144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag         192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg         240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat         288
```

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

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc        336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag        384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc        432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg        480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct        528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc        576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg        624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg        672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

tct ccg ggt aaa ggt ggt ggt ggt tct ggt ggt ggt ggt agc ggt ggt        720
Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

ggt ggt tcc cat cca att cca gat tct tct cca tta tta caa ttc ggg        768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggc caa gtc cgg cag cgt tac ctc tac aca gat gat gcc cag cag aca        816
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

gaa gcc cac ctg gag atc agg gag gac ggg acg gtg ggg ggt gct gct        864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg ggt        912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt att caa atc ttg ggt gtc aag aca tcc agg ttc ctg tgc cag cgg        960
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc       1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

agc ttc cgt gag cgt ctt ctt gag gac ggt tac aat gtt tac cag tcc       1056
Ser Phe Arg Glu Arg Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac       1104
```

```
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

cgt gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc       1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

ctg ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc       1200
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg ggt ggt tcc cag       1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Gly Ser Gln
                405                 410                 415

ggc cga agc ccc agc tac gaa tcc taa                                  1275
Gly Arg Ser Pro Ser Tyr Glu Ser
            420


<210>  47
<211>  424
<212>  PRT
<213>  Artificial

<220>
<223>  Synthetic Construct

<400>  47

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


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


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


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


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


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


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


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


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


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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

Ser Phe Arg Glu Arg Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Gly Ser Gln
                405                 410                 415

Gly Arg Ser Pro Ser Tyr Glu Ser
            420
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<210> 48
<211> 1275
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc-L15-WT21

<220>
<221> CDS
<222> (1)..(1275)

<400> 48

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atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg          48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                  10                  15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc          96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc         144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag         192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg         240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat         288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc         336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag         384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc         432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg         480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct         528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc         576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg         624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205
```

```
atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg        672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

tct ccg ggt aaa ggt gga ggt ggt ggt tct ggt ggt ggt agc ggt ggt        720
Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

ggt gga tcc cat cca att cca gat tct tct cca tta tta caa ttc ggg        768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggc caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca        816
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

gaa gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct        864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga        912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg        960
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc       1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

agc ttc cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc       1056
Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac       1104
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

cgg gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc       1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

ctg ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc       1200
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg gga cct tcc cag       1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln
                405                 410                 415

ggc cga agc ccc agc tac gct tcc taa                                  1275
Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 49
<211> 424
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 49

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Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
```

```
1               5                   10                  15

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
```

```
        275                 280                 285

Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln
                405                 410                 415

Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 50
<211> 1275
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc-L15-G170E

<220>
<221> CDS
<222> (1)..(1275)

<400> 50

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atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg          48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                   10                  15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc          96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc         144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag         192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60
```

```
gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg        240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat        288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc        336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag        384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc        432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg        480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct        528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc        576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg        624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg        672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

tct ccg ggt aaa ggt gga ggt ggt ggt tct ggt ggt ggt agc ggt ggt        720
Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

ggt gga tcc cat cca att cca gat tct tct cca tta tta caa ttc ggg        768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggc caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca        816
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

gaa gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct        864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga        912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg        960
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc       1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335
```

```
agc ttc cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc       1056
Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac       1104
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

cgg gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc       1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

ctg ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc       1200
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg gaa cct tcc cag       1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Glu Pro Ser Gln
                405                 410                 415

ggc cga agc ccc agc tac gct tcc taa                                  1275
Gly Arg Ser Pro Ser Tyr Ala Ser
            420
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<210> 51
<211> 424
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 51

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400
```

```
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Glu Pro Ser Gln
                405                 410                 415


Gly Arg Ser Pro Ser Tyr Ala Ser
            420


<210>  52
<211>  1275
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Fc-L15-P171A


<220>
<221>  CDS
<222>  (1)..(1275)

<400>  52
atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg          48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                   10                  15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc          96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc         144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag         192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg         240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat         288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc         336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag         384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc         432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg         480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct         528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc         576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
```

```
            180                 185                 190

gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg        624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg        672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

tct ccg ggt aaa ggt gga ggt ggt ggt tct ggt ggt ggt agc ggt ggt        720
Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

ggt gga tcc cat cca att cca gat tct tct cca tta tta caa ttc ggg        768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggc caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca        816
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

gaa gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct        864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga        912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg        960
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc       1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

agc ttc cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc       1056
Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac       1104
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

cgg gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc       1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

ctg ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc       1200
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg gga gct tcc cag       1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Ala Ser Gln
                405                 410                 415

ggc cga agc ccc agc tac gct tcc taa                                  1275
Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 53
<211> 424
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 53

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255
```

```
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Ala Ser Gln
                405                 410                 415

Gly Arg Ser Pro Ser Tyr Ala Ser
            420


<210>  54
<211>  1275
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Fc-L15-S172L


<220>
<221>  CDS
<222>  (1)..(1275)

<400>  54
atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg          48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                   10                  15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc          96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc         144
```

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

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag        192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg        240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat        288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc        336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag        384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc        432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg        480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct        528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc        576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg        624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg        672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

tct ccg ggt aaa ggt gga ggt ggt ggt tct ggt ggt ggt agc ggt ggt        720
Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

ggt gga tcc cat cca att cca gat tct tct cca tta tta caa ttc ggg        768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggc caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca        816
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

gaa gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct        864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga        912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg        960
```

```
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc       1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

agc ttc cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc       1056
Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac       1104
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

cgg gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc       1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

ctg ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc       1200
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg gga cct ctg cag       1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Leu Gln
                405                 410                 415

ggc cga agc ccc agc tac gct tcc taa                                  1275
Gly Arg Ser Pro Ser Tyr Ala Ser
            420
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<210> 55
<211> 424
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 55

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380
```

```
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Leu Gln
                405                 410                 415

Gly Arg Ser Pro Ser Tyr Ala Ser
            420
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<210> 56
<211> 1275
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc-L15-RGE

<220>
<221> CDS
<222> (1)..(1275)

<400> 56

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atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg          48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                   10                  15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc          96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc         144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag         192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg         240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat         288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc         336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag         384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc         432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg         480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160
```

```
gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct          528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc          576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg          624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg          672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

tct ccg ggt aaa ggt ggt ggt ggt ggt tct ggt ggt ggt agc ggt ggt          720
Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

ggt ggt tcc cat cca att cca gat tct tct cca tta tta caa ttc ggg          768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggc caa gtc cgg cag cgt tac ctc tac aca gat gat gcc cag cag aca          816
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

gaa gcc cac ctg gag atc agg gag gac ggg acg gtg ggg ggt gct gct          864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg ggt          912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt att caa atc ttg ggt gtc aag aca tcc agg ttc ctg tgc cag cgg          960
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc         1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

agc ttc cgt gag cgt ctt ctt gag gac ggt tac aat gtt tac cag tcc         1056
Ser Phe Arg Glu Arg Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac         1104
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

cgt gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc         1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

ctg ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc         1200
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg ggt ggt tcc cag         1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Gly Ser Gln
                405                 410                 415

ggc cga agc ccc agc tac gaa tcc taa                                    1275
Gly Arg Ser Pro Ser Tyr Glu Ser
            420
```

<210> 57
<211> 424
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 57

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
```

225 230 235 240

Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
245 250 255

Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
260 265 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
275 280 285

Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
290 295 300

Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305 310 315 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
325 330 335

Ser Phe Arg Glu Arg Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
340 345 350

Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
355 360 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
370 375 380

Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385 390 395 400

Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Gly Ser Gln
405 410 415

Gly Arg Ser Pro Ser Tyr Glu Ser
420

<210> 58
<211> 1275
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc-L15-G170E P171A S172L

<220>
<221> CDS
<222> (1)..(1275)

<400> 58
atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg 48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1 5 10 15

```
ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc          96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc         144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag         192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg         240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat         288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc         336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag         384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc         432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg         480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct         528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc         576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg         624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg         672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

tct ccg ggt aaa ggt gga ggt ggt ggt tct ggt ggt ggt agc ggt ggt         720
Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

ggt gga tcc cat cca att cca gat tct tct cca tta tta caa ttc ggg         768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggc caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca         816
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

gaa gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct         864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285
```

```
gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga        912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg        960
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc       1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

agc ttc cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc       1056
Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac       1104
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

cgg gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc       1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

ctg ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc       1200
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg gaa gct ctg cag       1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Glu Ala Leu Gln
                405                 410                 415

ggc cga agc ccc agc tac gct tcc taa                                  1275
Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 59
<211> 424
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 59

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350
```

```
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Glu Ala Leu Gln
                405                 410                 415

Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 60
<211> 1275
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc-L15-G151A

<220>
<221> CDS
<222> (1)..(1275)

<400> 60

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atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg          48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                   10                  15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc          96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc         144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag         192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg         240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat         288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc         336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag         384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc         432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
```

```
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg        480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct        528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc        576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg        624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg        672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

tct ccg ggt aaa ggt gga ggt ggt ggt tct ggt ggt ggt agc ggt ggt        720
Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

ggt gga tcc cat cca att cca gat tct tct cca tta tta caa ttc ggg        768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggc caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca        816
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

gaa gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct        864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga        912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg        960
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc       1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

agc ttc cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc       1056
Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac       1104
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

cgg gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc       1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

ctg ccc ccc gca ccc ccg gag cca ccc gca atc ctg gcc ccc cag ccc       1200
Leu Pro Pro Ala Pro Pro Glu Pro Pro Ala Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg gga cct tcc cag       1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln
```

405 410 415

ggc cga agc ccc agc tac gct tcc taa 1275
Gly Arg Ser Pro Ser Tyr Ala Ser
420

<210> 61
<211> 424
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 61

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

Leu Pro Pro Ala Pro Pro Glu Pro Pro Ala Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln
                405                 410                 415

Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 62
<211> 1275
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc-L15-G170E P171A

<220>
<221> CDS

<222> (1)..(1275)

<400> 62

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atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg          48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                  10                  15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc          96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc         144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag         192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg         240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat         288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc         336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag         384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc         432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg         480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct         528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc         576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg         624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg         672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

tct ccg ggt aaa ggt gga ggt ggt ggt tct ggt ggt ggt agc ggt ggt         720
Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

ggt gga tcc cat cca att cca gat tct tct cca tta tta caa ttc ggg         768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggc caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca         816
```

```
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

gaa gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct        864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga        912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg        960
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc       1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

agc ttc cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc       1056
Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac       1104
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

cgg gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc       1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

ctg ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc       1200
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg gaa gct tcc cag       1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Glu Ala Ser Gln
                405                 410                 415

ggc cga agc ccc agc tac gct tcc taa                                  1275
Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 63
<211> 424
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 63

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335
```

```
Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Glu Ala Ser Gln
                405                 410                 415

Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 64
<211> 1275
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc-L15-P150A G151A I152V

<220>
<221> CDS
<222> (1)..(1275)

<400> 64

```
atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg          48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                   10                  15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc          96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc         144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag         192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg         240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat         288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc         336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110
```

```
atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag        384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc        432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg        480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct        528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc        576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg        624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg        672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

tct ccg ggt aaa ggt gga ggt ggt ggt tct ggt ggt ggt agc ggt ggt        720
Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

ggt gga tcc cat cca att cca gat tct tct cca tta tta caa ttc ggg        768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggc caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca        816
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

gaa gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct        864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga        912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg        960
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc       1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

agc ttc cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc       1056
Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac       1104
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

cgg gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc       1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380
```

```
ctg ccc ccc gca ccc ccg gag cca gcc gca gtt ctg gcc ccc cag ccc       1200
Leu Pro Pro Ala Pro Pro Glu Pro Ala Ala Val Leu Ala Pro Gln Pro
385                 390                 395                 400

ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg gga cct tcc cag       1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln
                405                 410                 415

ggc cga agc ccc agc tac gct tcc taa                                   1275
Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 65
<211> 424
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 65

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

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

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

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

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

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

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

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

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

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

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

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
```

180 185 190

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225 230 235 240

Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
245 250 255

Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
260 265 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
275 280 285

Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
290 295 300

Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305 310 315 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
325 330 335

Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
340 345 350

Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
355 360 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
370 375 380

Leu Pro Pro Ala Pro Pro Glu Pro Ala Ala Val Leu Ala Pro Gln Pro
385 390 395 400

Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln
405 410 415

Gly Arg Ser Pro Ser Tyr Ala Ser
420

<210> 66
<211> 1275
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc-L15-G170E S172L

<220>
<221> CDS
<222> (1)..(1275)

<400> 66

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atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg          48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                  10                  15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc          96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc         144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag         192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg         240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat         288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc         336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag         384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc         432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg         480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct         528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc         576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg         624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg         672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

tct ccg ggt aaa ggt gga ggt ggt ggt tct ggt ggt ggt agc ggt ggt         720
Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240
```

```
ggt gga tcc cat cca att cca gat tct tct cca tta tta caa ttc ggg        768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggc caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca        816
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

gaa gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct        864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga        912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg        960
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc       1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

agc ttc cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc       1056
Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac       1104
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

cgg gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc       1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

ctg ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc       1200
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg gaa cct ctg cag       1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Glu Pro Leu Gln
                405                 410                 415

ggc cga agc ccc agc tac gct tcc taa                                  1275
Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 67
<211> 424
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 67

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300
```

```
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Glu Pro Leu Gln
                405                 410                 415

Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 68
<211> 1275
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc-L15-G170A

<220>
<221> CDS
<222> (1)..(1275)

<400> 68

```
atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg          48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                   10                  15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc          96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc         144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag         192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg         240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat         288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
```

```
                    85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc        336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag        384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc        432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg        480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct        528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc        576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg        624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg        672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

tct ccg ggt aaa ggt gga ggt ggt ggt tct ggt ggt ggt agc ggt ggt        720
Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

ggt gga tcc cat cca att cca gat tct tct cca tta tta caa ttc ggg        768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggc caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca        816
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

gaa gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct        864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga        912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg        960
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc       1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

agc ttc cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc       1056
Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac       1104
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
```

```
        355                 360                 365

cgg gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc       1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

ctg ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc       1200
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg gct cct tcc cag       1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Ala Pro Ser Gln
                405                 410                 415

ggc cga agc ccc agc tac gct tcc taa                                  1275
Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 69
<211> 424
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 69

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Ala Pro Ser Gln
                405                 410                 415

Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 70
<211> 1275
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc-L15-G170C

<220>
<221> CDS
<222> (1)..(1275)

<400> 70

```
atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg          48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                  10                  15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc          96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc         144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag         192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg         240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat         288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc         336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag         384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc         432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg         480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct         528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc         576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg         624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg         672
```

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

tct ccg ggt aaa ggt gga ggt ggt ggt tct ggt ggt ggt agc ggt ggt        720
Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

ggt gga tcc cat cca att cca gat tct tct cca tta tta caa ttc ggg        768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggc caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca        816
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

gaa gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct        864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga        912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg        960
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc       1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

agc ttc cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc       1056
Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac       1104
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

cgg gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc       1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

ctg ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc       1200
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg tgc cct tcc cag       1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Cys Pro Ser Gln
                405                 410                 415

ggc cga agc ccc agc tac gct tcc taa                                  1275
Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 71
<211> 424
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 71

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285
```

```
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Cys Pro Ser Gln
                405                 410                 415

Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 72
<211> 1275
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc-L15-G170D

<220>
<221> CDS
<222> (1)..(1275)

<400> 72

```
atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg          48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                   10                  15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc          96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc         144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag         192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60
```

```
gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg        240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat        288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc        336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag        384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc        432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg        480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct        528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc        576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg        624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg        672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

tct ccg ggt aaa ggt gga ggt ggt ggt tct ggt ggt ggt agc ggt ggt        720
Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

ggt gga tcc cat cca att cca gat tct tct cca tta tta caa ttc ggg        768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggc caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca        816
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

gaa gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct        864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga        912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg        960
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc       1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335
```

```
agc ttc cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc       1056
Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac       1104
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

cgg gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc       1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

ctg ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc       1200
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg gac cct tcc cag       1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Asp Pro Ser Gln
                405                 410                 415

ggc cga agc ccc agc tac gct tcc taa                                  1275
Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 73
<211> 424
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 73

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

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

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

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

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

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

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

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

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
```

130 135 140

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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225 230 235 240

Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
245 250 255

Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
260 265 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
275 280 285

Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
290 295 300

Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305 310 315 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
325 330 335

Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
340 345 350

Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
355 360 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
370 375 380

Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385 390 395 400

Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Asp Pro Ser Gln

405 410 415

Gly Arg Ser Pro Ser Tyr Ala Ser
420

<210> 74
<211> 1275
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc-L15-G170N

<220>
<221> CDS
<222> (1)..(1275)

<400> 74

```
atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg          48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                   10                  15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc          96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc         144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag         192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg         240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat         288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc         336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag         384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc         432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg         480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct         528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc         576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190
```

```
gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg        624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg        672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

tct ccg ggt aaa ggt gga ggt ggt ggt tct ggt ggt ggt agc ggt ggt        720
Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

ggt gga tcc cat cca att cca gat tct tct cca tta tta caa ttc ggg        768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggc caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca        816
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

gaa gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct        864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga        912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg        960
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc       1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

agc ttc cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc       1056
Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac       1104
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

cgg gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc       1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

ctg ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc       1200
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg aac cct tcc cag       1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Asn Pro Ser Gln
                405                 410                 415

ggc cga agc ccc agc tac gct tcc taa                                  1275
Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 75
<211> 424
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 75

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255
```

```
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Asn Pro Ser Gln
                405                 410                 415

Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 76
<211> 1275
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc-L15-G170S

<220>
<221> CDS
<222> (1)..(1275)

<400> 76

```
atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg          48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                   10                  15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc          96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc         144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
```

```
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag        192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg        240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat        288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc        336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag        384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc        432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg        480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct        528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc        576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg        624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg        672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

tct ccg ggt aaa ggt gga ggt ggt ggt tct ggt ggt ggt agc ggt ggt        720
Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

ggt gga tcc cat cca att cca gat tct tct cca tta tta caa ttc ggg        768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggc caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca        816
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

gaa gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct        864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga        912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg        960
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
```

```
305                 310                 315                 320

cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc       1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

agc ttc cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc       1056
Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac       1104
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

cgg gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc       1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

ctg ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc       1200
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg tcc cct tcc cag       1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Ser Pro Ser Gln
                405                 410                 415

ggc cga agc ccc agc tac gct tcc taa                                  1275
Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 77
<211> 424
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 77

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380
```

```
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Ser Pro Ser Gln
                405                 410                 415

Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 78
<211> 1275
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc-L15-P171E

<220>
<221> CDS
<222> (1)..(1275)

<400> 78

```
atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg          48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                   10                  15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc          96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc         144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag         192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg         240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat         288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc         336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag         384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc         432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg         480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct         528
```

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

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc        576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg        624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg        672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

tct ccg ggt aaa ggt gga ggt ggt ggt tct ggt ggt ggt agc ggt ggt        720
Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

ggt gga tcc cat cca att cca gat tct tct cca tta tta caa ttc ggg        768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggc caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca        816
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

gaa gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct        864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga        912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg        960
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc       1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

agc ttc cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc       1056
Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac       1104
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

cgg gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc       1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

ctg ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc       1200
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg gga gaa tcc cag       1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Glu Ser Gln
                405                 410                 415

ggc cga agc ccc agc tac gct tcc taa                                  1275
Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 79
<211> 424
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 79

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240
```

```
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Glu Ser Gln
                405                 410                 415

Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 80
<211> 1275
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc-L15-P171H

<220>
<221> CDS
<222> (1)..(1275)

<400> 80

```
atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg        48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                   10                  15
```

```
ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc          96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc         144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag         192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg         240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat         288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc         336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag         384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc         432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg         480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct         528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc         576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg         624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg         672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

tct ccg ggt aaa ggt gga ggt ggt ggt tct ggt ggt ggt agc ggt ggt         720
Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

ggt gga tcc cat cca att cca gat tct tct cca tta tta caa ttc ggg         768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggc caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca         816
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

gaa gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct         864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285
```

```
gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga        912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg        960
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc       1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

agc ttc cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc       1056
Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac       1104
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

cgg gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc       1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

ctg ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc       1200
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg gga cac tcc cag       1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly His Ser Gln
                405                 410                 415

ggc cga agc ccc agc tac gct tcc taa                                  1275
Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 81
<211> 424
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 81

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

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

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

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

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

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
```

85 90 95

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

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

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

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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225 230 235 240

Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
245 250 255

Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
260 265 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
275 280 285

Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
290 295 300

Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305 310 315 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
325 330 335

Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
340 345 350

Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His

```
        355                 360                 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly His Ser Gln
                405                 410                 415

Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 82
<211> 1275
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc-L15-P171Q

<220>
<221> CDS
<222> (1)..(1275)

<400> 82

```
atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg          48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                   10                  15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc          96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc         144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag         192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg         240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat         288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc         336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag         384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc         432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140
```

```
agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg        480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct        528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc        576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg        624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg        672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

tct ccg ggt aaa ggt gga ggt ggt ggt tct ggt ggt ggt agc ggt ggt        720
Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

ggt gga tcc cat cca att cca gat tct tct cca tta tta caa ttc ggg        768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggc caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca        816
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

gaa gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct        864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga        912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg        960
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc       1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

agc ttc cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc       1056
Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac       1104
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

cgg gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc       1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

ctg ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc       1200
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg gga cag tcc cag       1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Gln Ser Gln
                405                 410                 415
```

```
ggc cga agc ccc agc tac gct tcc taa                                    1275
Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 83
<211> 424
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 83

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Gln Ser Gln
                405                 410                 415

Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 84
<211> 1275
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc-L15-P171T

<220>
<221> CDS
<222> (1)..(1275)

<400> 84

```
atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg          48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                  10                  15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc          96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc         144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag         192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg         240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat         288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc         336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag         384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc         432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg         480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct         528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc         576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg         624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg         672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

tct ccg ggt aaa ggt gga ggt ggt ggt tct ggt ggt ggt agc ggt ggt         720
Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

ggt gga tcc cat cca att cca gat tct tct cca tta tta caa ttc ggg         768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggc caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca         816
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
```

```
            260                 265                 270

gaa gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct        864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga        912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg        960
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc       1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

agc ttc cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc       1056
Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac       1104
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

cgg gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc       1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

ctg ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc       1200
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg gga act tcc cag       1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Thr Ser Gln
                405                 410                 415

ggc cga agc ccc agc tac gct tcc taa                                  1275
Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 85
<211> 424
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 85

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335
```

```
Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Thr Ser Gln
                405                 410                 415

Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 86
<211> 1275
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc-L15-P171Y

<220>
<221> CDS
<222> (1)..(1275)

<400> 86

```
atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg          48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                   10                  15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc          96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc         144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag         192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg         240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat         288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc         336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag         384
```

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

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc        432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg        480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct        528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc        576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg        624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg        672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

tct ccg ggt aaa ggt gga ggt ggt ggt tct ggt ggt ggt agc ggt ggt        720
Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

ggt gga tcc cat cca att cca gat tct tct cca tta tta caa ttc ggg        768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggc caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca        816
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

gaa gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct        864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga        912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg        960
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc       1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

agc ttc cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc       1056
Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac       1104
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

cgg gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc       1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

ctg ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc       1200
```

```
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg gga tac tcc cag      1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Tyr Ser Gln
                405                 410                 415

ggc cga agc ccc agc tac gct tcc taa                                  1275
Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 87
<211> 424
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 87

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Tyr Ser Gln
                405                 410                 415

Gly Arg Ser Pro Ser Tyr Ala Ser
            420
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<210> 88
<211> 1275
<212> DNA
<213> Artificial Sequence

<220>

<223> Fc-L15-P171G

<220>
<221> CDS
<222> (1)..(1275)

<400> 88

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atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg          48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                  10                  15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc          96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc         144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag         192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg         240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat         288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc         336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag         384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc         432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg         480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct         528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc         576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg         624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg         672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

tct ccg ggt aaa ggt gga ggt ggt ggt tct ggt ggt ggt agc ggt ggt         720
Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240
```

```
ggt gga tcc cat cca att cca gat tct tct cca tta tta caa ttc ggg        768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggc caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca        816
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

gaa gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct        864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga        912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg        960
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc       1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

agc ttc cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc       1056
Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac       1104
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

cgg gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc       1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

ctg ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc       1200
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg gga ggt tcc cag       1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Gly Ser Gln
                405                 410                 415

ggc cga agc ccc agc tac gct tcc taa                                  1275
Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 89
<211> 424
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 89

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

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
```

35 40 45

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225 230 235 240

Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
245 250 255

Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
260 265 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
275 280 285

Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
290 295 300

Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg

305 310 315 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
325 330 335

Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
340 345 350

Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
355 360 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
370 375 380

Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385 390 395 400

Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Gly Ser Gln
405 410 415

Gly Arg Ser Pro Ser Tyr Ala Ser
420

<210> 90
<211> 1275
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc-L15-P171S

<220>
<221> CDS
<222> (1)..(1275)

<400> 90
atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg 48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1 5 10 15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc 96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
20 25 30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc 144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
35 40 45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag 192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
50 55 60

gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg 240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65 70 75 80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat 288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
85 90 95

```
ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc        336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag        384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc        432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg        480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct        528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc        576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg        624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg        672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

tct ccg ggt aaa ggt gga ggt ggt ggt tct ggt ggt ggt agc ggt ggt        720
Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

ggt gga tcc cat cca att cca gat tct tct cca tta tta caa ttc ggg        768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggc caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca        816
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

gaa gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct        864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga        912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg        960
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc       1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

agc ttc cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc       1056
Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac       1104
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365
```

```
cgg gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc       1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

ctg ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc       1200
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg gga tct tcc cag       1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Ser Ser Gln
                405                 410                 415

ggc cga agc ccc agc tac gct tcc taa                                  1275
Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 91
<211> 424
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 91

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Ser Ser Gln
                405                 410                 415

Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 92
<211> 1275
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc-L15-P171W

<220>
<221> CDS
<222> (1)..(1275)

<400> 92

```
atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg          48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                  10                  15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc          96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc         144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag         192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg         240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat         288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc         336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag         384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc         432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg         480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct         528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc         576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg         624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg         672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
```

```
    210                 215                 220

tct ccg ggt aaa ggt gga ggt ggt ggt tct ggt ggt ggt agc ggt ggt        720
Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

ggt gga tcc cat cca att cca gat tct tct cca tta tta caa ttc ggg        768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggc caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca        816
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

gaa gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct        864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga        912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg        960
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc       1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

agc ttc cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc       1056
Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac       1104
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

cgg gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc       1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

ctg ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc       1200
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg gga tgg tcc cag       1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Trp Ser Gln
                405                 410                 415

ggc cga agc ccc agc tac gct tcc taa                                  1275
Gly Arg Ser Pro Ser Tyr Ala Ser
            420


<210>  93
<211>  424
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  93

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285
```

```
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Trp Ser Gln
                405                 410                 415

Gly Arg Ser Pro Ser Tyr Ala Ser
            420
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<210> 94
<211> 1275
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc-L15-P171C

<220>
<221> CDS
<222> (1)..(1275)

<400> 94

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atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg         48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                   10                  15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc         96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc        144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag        192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg        240
```

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

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat        288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc        336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag        384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc        432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg        480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct        528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc        576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg        624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg        672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

tct ccg ggt aaa ggt gga ggt ggt ggt tct ggt ggt ggt agc ggt ggt        720
Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

ggt gga tcc cat cca att cca gat tct tct cca tta tta caa ttc ggg        768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggc caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca        816
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

gaa gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct        864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga        912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg        960
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc       1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

agc ttc cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc       1056
```

```
Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac      1104
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

cgg gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc      1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

ctg ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc      1200
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg gga tgc tcc cag      1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Cys Ser Gln
                405                 410                 415

ggc cga agc ccc agc tac gct tcc taa                                 1275
Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 95
<211> 424
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 95

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Cys Ser Gln
                405                 410                 415
```

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Gly Arg Ser Pro Ser Tyr Ala Ser
            420


<210>  96
<211>  1275
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Fc-L15-A45K G170E


<220>
<221>  CDS
<222>  (1)..(1275)

<400>  96
atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg          48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                  10                  15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc          96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc         144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag         192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg         240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat         288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc         336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag         384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc         432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg         480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct         528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc         576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190
```

```
gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg        624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg        672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

tct ccg ggt aaa ggt gga ggt ggt ggt tct ggt ggt ggt agc ggt ggt        720
Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

ggt gga tcc cat cca att cca gat tct tct cca tta tta caa ttc ggg        768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggc caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca        816
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

gaa gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct aaa        864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Lys
        275                 280                 285

gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga        912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg        960
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc       1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

agc ttc cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc       1056
Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac       1104
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

cgg gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc       1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

ctg ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc       1200
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg gaa cct tcc cag       1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Glu Pro Ser Gln
                405                 410                 415

ggc cga agc ccc agc tac gct tcc taa                                  1275
Gly Arg Ser Pro Ser Tyr Ala Ser
            420
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<210> 97
<211> 424
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 97

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
```

260 265 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Lys
275 280 285

Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
290 295 300

Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305 310 315 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
325 330 335

Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
340 345 350

Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
355 360 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
370 375 380

Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385 390 395 400

Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Glu Pro Ser Gln
405 410 415

Gly Arg Ser Pro Ser Tyr Ala Ser
420

<210> 98
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> FGF21 A45K

<220>
<221> CDS
<222> (1)..(549)

<400> 98
atg cat cca att cca gat tct tct cca tta tta caa ttc ggg ggc caa 48
Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1 5 10 15

gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca gaa gcc 96
Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
20 25 30

cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct aaa gac cag 144
His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Lys Asp Gln
35 40 45

```
agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga gtt att        192
Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
    50                  55                  60

caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg cca gat        240
Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp
65                  70                  75                  80

ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc agc ttc        288
Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe
                85                  90                  95

cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc gaa gcc        336
Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
            100                 105                 110

cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac cgg gac        384
His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
        115                 120                 125

cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc ctg ccc        432
Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro
    130                 135                 140

ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc ccc gat        480
Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145                 150                 155                 160

gtg ggc tcc tcg gac cct ctg agc atg gtg gga cct tcc cag ggc cga        528
Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
                165                 170                 175

agc ccc agc tac gct tcc taa                                           549
Ser Pro Ser Tyr Ala Ser
            180
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<210> 99
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 99

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Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1               5                   10                  15

Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
            20                  25                  30

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

Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
    50                  55                  60

Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp
65                  70                  75                  80
```

```
Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe
                85                  90                  95

Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
            100                 105                 110

His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
        115                 120                 125

Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro
    130                 135                 140

Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145                 150                 155                 160

Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
                165                 170                 175

Ser Pro Ser Tyr Ala Ser
            180
```

<210> 100
<211> 1260
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc-L15-FGF21 6-181 G170E

<220>
<221> CDS
<222> (1)..(1260)

<400> 100

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atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg          48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                   10                  15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc          96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc         144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag         192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg         240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat         288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc         336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
```

```
            100                 105                 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag        384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc        432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg        480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct        528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc        576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg        624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg        672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

tct ccg ggt aaa ggt gga ggt ggt ggt tct ggt ggt ggt agc ggt ggt        720
Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

ggt gga tcc tct tct cca tta tta caa ttc ggt ggt caa gtc cgg cag        768
Gly Gly Ser Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln
                245                 250                 255

cgg tac ctc tac aca gat gat gcc cag cag aca gaa gcc cac ctg gag        816
Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His Leu Glu
            260                 265                 270

atc agg gag gat ggg acg gtg ggg ggc gct gct gac cag agc ccc gaa        864
Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser Pro Glu
        275                 280                 285

agt ctc ctg cag ctg aaa gcc ttg aag ccg gga gtt att caa atc ttg        912
Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu
    290                 295                 300

gga gtc aag aca tcc agg ttc ctg tgc cag cgg cca gat ggg gcc ctg        960
Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly Ala Leu
305                 310                 315                 320

tat gga tcg ctc cac ttt gac cct gag gcc tgc agc ttc cgg gag ctg       1008
Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu
                325                 330                 335

ctt ctt gag gac gga tac aat gtt tac cag tcc gaa gcc cac ggc ctc       1056
Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu
            340                 345                 350

ccg ctg cac ctg cca ggg aac aag tcc cca cac cgg gac cct gca ccc       1104
Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro Ala Pro
        355                 360                 365

cga gga cca gct cgc ttc ctg cca cta cca ggc ctg ccc ccc gca ccc       1152
Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro Ala Pro
```

```
    370                 375                 380

ccg gag cca ccc gga atc ctg gcc ccc cag ccc ccc gat gtg ggc tcc       1200
Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp Val Gly Ser
385                 390                 395                 400

tcg gac cct ctg agc atg gtg gaa cct tcc cag ggc cga agc ccc agc       1248
Ser Asp Pro Leu Ser Met Val Glu Pro Ser Gln Gly Arg Ser Pro Ser
                405                 410                 415

tac gct tcc taa                                                      1260
Tyr Ala Ser
```

<210> 101
<211> 419
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 101

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

Gly Gly Ser Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln
                245                 250                 255

Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His Leu Glu
            260                 265                 270

Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser Pro Glu
        275                 280                 285

Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu
    290                 295                 300

Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly Ala Leu
305                 310                 315                 320

Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu
                325                 330                 335

Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu
            340                 345                 350

Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro Ala Pro
        355                 360                 365

Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro Ala Pro
    370                 375                 380

Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp Val Gly Ser
385                 390                 395                 400

Ser Asp Pro Leu Ser Met Val Glu Pro Ser Gln Gly Arg Ser Pro Ser
                405                 410                 415

Tyr Ala Ser
```

<210> 102
<211> 1275
<212> DNA

<213> Artificial Sequence

<220>
<223> Fc-L15-A45K P171G

<220>
<221> CDS
<222> (1)..(1275)

<400> 102

```
atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg          48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                  10                  15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc          96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc         144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag         192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg         240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat         288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc         336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag         384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc         432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg         480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct         528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc         576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg         624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg         672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

tct ccg ggt aaa ggt gga ggt ggt ggt tct ggt ggt ggt agc ggt ggt         720
```

```
Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

ggt gga tcc cat cca att cca gat tct tct cca tta tta caa ttc ggg        768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggc caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca        816
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

gaa gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct aaa        864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Lys
        275                 280                 285

gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga        912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg        960
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc       1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

agc ttc cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc       1056
Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac       1104
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

cgg gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc       1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

ctg ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc       1200
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg gga ggt tcc cag       1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Gly Ser Gln
                405                 410                 415

ggc cga agc ccc agc tac gct tcc taa                                  1275
Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 103
<211> 424
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 103

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Lys
        275                 280                 285

Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300
```

```
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Gly Ser Gln
                405                 410                 415

Gly Arg Ser Pro Ser Tyr Ala Ser
            420
```

<210> 104
<211> 1320
<212> DNA
<213> Artificial Sequence

<220>
<223> FGF21-(G3)-Fc; 28 AA signal sequence removed during processing

<220>
<221> CDS
<222> (1)..(1320)

<400> 104

```
atg gac tcg gac gag acc ggg ttc gag cac tca gga ctg tgg gtt tct         48
Met Asp Ser Asp Glu Thr Gly Phe Glu His Ser Gly Leu Trp Val Ser
1               5                   10                  15

gtg ctg gct ggt ctt ctg ctg gga gcc tgc cag gca cac ccc atc cct         96
Val Leu Ala Gly Leu Leu Leu Gly Ala Cys Gln Ala His Pro Ile Pro
            20                  25                  30

gac tcc agt cct ctc ctg caa ttc ggg ggc caa gtc cgg cag cgg tac        144
Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln Arg Tyr
        35                  40                  45

ctc tac aca gat gat gcc cag cag aca gaa gcc cac ctg gag atc agg        192
Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His Leu Glu Ile Arg
    50                  55                  60

gag gat ggg acg gtg ggg ggc gct gct gac cag agc ccc gaa agt ctc        240
Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser Pro Glu Ser Leu
65                  70                  75                  80
```

```
ctg cag ctg aaa gcc ttg aag ccg gga gtt att caa atc ttg gga gtc        288
Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu Gly Val
                85                  90                  95

aag aca tcc agg ttc ctg tgc cag cgg cca gat ggg gcc ctg tat gga        336
Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly Ala Leu Tyr Gly
            100                 105                 110

tcg ctc cac ttt gac cct gag gcc tgc agc ttc cgg gag ctg ctt ctt        384
Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu Leu Leu
        115                 120                 125

gag gac gga tac aat gtt tac cag tcc gaa gcc cac ggc ctc ccg ctg        432
Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu Pro Leu
    130                 135                 140

cac ctg cca ggg aac aag tcc cca cac cgg gac cct gca ccc cga gga        480
His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro Ala Pro Arg Gly
145                 150                 155                 160

cca gct cgc ttc ctg cca cta cca ggc ctg cca ccc gca ccc ccg gag        528
Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro Ala Pro Pro Glu
                165                 170                 175

cca ccc gga atc ctg gcc ccc cag ccc ccc gat gtg ggc tcc tcg gac        576
Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp Val Gly Ser Ser Asp
            180                 185                 190

cct ctg agc atg gtg gga cct tcc cag ggc cga agc ccc agc tac gct        624
Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg Ser Pro Ser Tyr Ala
        195                 200                 205

tcc ggt gga ggt gac aaa act cac aca tgc cca ccg tgc cca gca cct        672
Ser Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
    210                 215                 220

gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag        720
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
225                 230                 235                 240

gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg        768
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
                245                 250                 255

gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac        816
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
            260                 265                 270

ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac        864
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
        275                 280                 285

aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac        912
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
    290                 295                 300

tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc        960
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
305                 310                 315                 320

cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga       1008
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
                325                 330                 335

gaa cca cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag       1056
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
            340                 345                 350
```

```
aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac       1104
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
        355                 360                 365

atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag       1152
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
    370                 375                 380

acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tat agc       1200
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
385                 390                 395                 400

aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca       1248
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
                405                 410                 415

tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc       1296
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
            420                 425                 430

ctc tcc ctg tct ccg ggt aaa tga                                      1320
Leu Ser Leu Ser Pro Gly Lys
        435
```

<210> 105
<211> 439
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 105

```
Met Asp Ser Asp Glu Thr Gly Phe Glu His Ser Gly Leu Trp Val Ser
1               5                   10                  15

Val Leu Ala Gly Leu Leu Leu Gly Ala Cys Gln Ala His Pro Ile Pro
            20                  25                  30

Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln Arg Tyr
        35                  40                  45

Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His Leu Glu Ile Arg
    50                  55                  60

Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser Pro Glu Ser Leu
65                  70                  75                  80

Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu Gly Val
                85                  90                  95

Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly Ala Leu Tyr Gly
            100                 105                 110

Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu Leu Leu
        115                 120                 125

Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu Pro Leu
```

130 135 140

His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro Ala Pro Arg Gly
145 150 155 160

Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro Ala Pro Pro Glu
165 170 175

Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp Val Gly Ser Ser Asp
180 185 190

Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg Ser Pro Ser Tyr Ala
195 200 205

Ser Gly Gly Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
210 215 220

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
225 230 235 240

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
245 250 255

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
260 265 270

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
275 280 285

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
290 295 300

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
305 310 315 320

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
325 330 335

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

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
355 360 365

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

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
385 390 395 400

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

405 410 415

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
420 425 430

Leu Ser Leu Ser Pro Gly Lys
435

<210> 106
<211> 1245
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc-G5-FGF21

<220>
<221> CDS
<222> (1)..(1245)

<400> 106

```
atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg          48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                  10                  15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc          96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc         144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag         192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg         240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat         288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc         336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag         384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc         432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg         480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct         528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175
```

```
ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc        576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg        624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg        672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

tct ccg ggt aaa ggt ggc gga ggg ggt cat cca att cca gat tct tct        720
Ser Pro Gly Lys Gly Gly Gly Gly Gly His Pro Ile Pro Asp Ser Ser
225                 230                 235                 240

cca tta tta caa ttc ggg ggc caa gtc cgg cag cgg tac ctc tac aca        768
Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr
                245                 250                 255

gat gat gcc cag cag aca gaa gcc cac ctg gag atc agg gag gat ggg        816
Asp Asp Ala Gln Gln Thr Glu Ala His Leu Glu Ile Arg Glu Asp Gly
            260                 265                 270

acg gtg ggg ggc gct gct gac cag agc ccc gaa agt ctc ctg cag ctg        864
Thr Val Gly Gly Ala Ala Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu
        275                 280                 285

aaa gcc ttg aag ccg gga gtt att caa atc ttg gga gtc aag aca tcc        912
Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu Gly Val Lys Thr Ser
    290                 295                 300

agg ttc ctg tgc cag cgg cca gat ggg gcc ctg tat gga tcg ctc cac        960
Arg Phe Leu Cys Gln Arg Pro Asp Gly Ala Leu Tyr Gly Ser Leu His
305                 310                 315                 320

ttt gac cct gag gcc tgc agc ttc cgg gag ctg ctt ctt gag gac gga       1008
Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly
                325                 330                 335

tac aat gtt tac cag tcc gaa gcc cac ggc ctc ccg ctg cac ctg cca       1056
Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu Pro Leu His Leu Pro
            340                 345                 350

ggg aac aag tcc cca cac cgg gac cct gca ccc cga gga cca gct cgc       1104
Gly Asn Lys Ser Pro His Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg
        355                 360                 365

ttc ctg cca cta cca ggc ctg ccc ccc gca ccc ccg gag cca ccc gga       1152
Phe Leu Pro Leu Pro Gly Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly
    370                 375                 380

atc ctg gcc ccc cag ccc ccc gat gtg ggc tcc tcg gac cct ctg agc       1200
Ile Leu Ala Pro Gln Pro Pro Asp Val Gly Ser Ser Asp Pro Leu Ser
385                 390                 395                 400

atg gtg gga cct tcc cag ggc cga agc ccc agc tac gct tcc taa           1245
Met Val Gly Pro Ser Gln Gly Arg Ser Pro Ser Tyr Ala Ser
                405                 410
```

<210> 107
<211> 414
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 107

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly His Pro Ile Pro Asp Ser Ser
225                 230                 235                 240

Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr
                245                 250                 255
```

```
Asp Asp Ala Gln Gln Thr Glu Ala His Leu Glu Ile Arg Glu Asp Gly
            260                 265                 270

Thr Val Gly Gly Ala Ala Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu
        275                 280                 285

Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu Gly Val Lys Thr Ser
    290                 295                 300

Arg Phe Leu Cys Gln Arg Pro Asp Gly Ala Leu Tyr Gly Ser Leu His
305                 310                 315                 320

Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly
                325                 330                 335

Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu Pro Leu His Leu Pro
            340                 345                 350

Gly Asn Lys Ser Pro His Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg
        355                 360                 365

Phe Leu Pro Leu Pro Gly Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly
    370                 375                 380

Ile Leu Ala Pro Gln Pro Pro Asp Val Gly Ser Ser Asp Pro Leu Ser
385                 390                 395                 400

Met Val Gly Pro Ser Gln Gly Arg Ser Pro Ser Tyr Ala Ser
                405                 410
```

<210> 108
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> FGF21 L99R

<220>
<221> CDS
<222> (1)..(549)

<400> 108

```
atg cat cca att cca gat tct tct cca tta tta caa ttc ggg ggc caa          48
Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1               5                   10                  15

gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca gaa gcc          96
Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
            20                  25                  30

cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct gac cag         144
His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
        35                  40                  45

agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga gtt att         192
Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
```

```
    50                  55                  60

caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg cca gat        240
Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp
65                  70                  75                  80

ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc agc ttc        288
Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe
                85                  90                  95

cgg gag ctg cgt ctt gag gac gga tac aat gtt tac cag tcc gaa gcc        336
Arg Glu Leu Arg Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
            100                 105                 110

cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac cgg gac        384
His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
        115                 120                 125

cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc ctg ccc        432
Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro
    130                 135                 140

ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc ccc gat        480
Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145                 150                 155                 160

gtg ggc tcc tcg gac cct ctg agc atg gtg gga cct tcc cag ggc cga        528
Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
                165                 170                 175

agc ccc agc tac gct tcc taa                                           549
Ser Pro Ser Tyr Ala Ser
            180
```

<210> 109
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 109

```
Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1               5                   10                  15

Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
            20                  25                  30

His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
        35                  40                  45

Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
    50                  55                  60

Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp
65                  70                  75                  80

Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe
                85                  90                  95
```

```
Arg Glu Leu Arg Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
            100                 105                 110

His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
        115                 120                 125

Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro
    130                 135                 140

Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145                 150                 155                 160

Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
                165                 170                 175

Ser Pro Ser Tyr Ala Ser
            180
```

<210> 110
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> FGF21 L99D

<220>
<221> CDS
<222> (1)..(549)

<400> 110

```
atg cat cca att cca gat tct tct cca tta tta caa ttc ggg ggc caa          48
Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1               5                   10                  15

gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca gaa gcc          96
Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
            20                  25                  30

cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct gac cag         144
His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
        35                  40                  45

agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga gtt att         192
Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
    50                  55                  60

caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg cca gat         240
Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp
65                  70                  75                  80

ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc agc ttc         288
Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe
                85                  90                  95

cgg gag ctg gac ctt gag gac gga tac aat gtt tac cag tcc gaa gcc         336
Arg Glu Leu Asp Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
            100                 105                 110

cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac cgg gac         384
```

```
His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
        115                 120                 125

cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc ctg ccc        432
Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro
    130                 135                 140

ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc ccc gat        480
Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145                 150                 155                 160

gtg ggc tcc tcg gac cct ctg agc atg gtg gga cct tcc cag ggc cga        528
Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
                165                 170                 175

agc ccc agc tac gct tcc taa                                           549
Ser Pro Ser Tyr Ala Ser
            180


<210>  111
<211>  182
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  111

Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1               5                   10                  15

Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
            20                  25                  30

His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
        35                  40                  45

Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
    50                  55                  60

Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp
65                  70                  75                  80

Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe
                85                  90                  95

Arg Glu Leu Asp Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
            100                 105                 110

His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
        115                 120                 125

Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro
    130                 135                 140

Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145                 150                 155                 160
```

```
Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
                165                 170                 175

Ser Pro Ser Tyr Ala Ser
            180


<210>  112
<211>  549
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  FGF21 A111T


<220>
<221>  CDS
<222>  (1)..(549)

<400>  112
atg cat cca att cca gat tct tct cca tta tta caa ttc ggg ggc caa         48
Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1               5                   10                  15

gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca gaa gcc         96
Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
            20                  25                  30

cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct gac cag        144
His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
        35                  40                  45

agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga gtt att        192
Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
    50                  55                  60

caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg cca gat        240
Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp
65                  70                  75                  80

ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc agc ttc        288
Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe
                85                  90                  95

cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc gaa acc        336
Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Thr
            100                 105                 110

cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac cgg gac        384
His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
        115                 120                 125

cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc ctg ccc        432
Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro
    130                 135                 140

ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc ccc gat        480
Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145                 150                 155                 160

gtg ggc tcc tcg gac cct ctg agc atg gtg gga cct tcc cag ggc cga        528
Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
                165                 170                 175
```

agc ccc agc tac gct tcc taa 549
Ser Pro Ser Tyr Ala Ser
180

<210> 113
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 113

Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1 5 10 15

Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
20 25 30

His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
35 40 45

Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
50 55 60

Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp
65 70 75 80

Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe
85 90 95

Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Thr
100 105 110

His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
115 120 125

Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro
130 135 140

Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145 150 155 160

Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
165 170 175

Ser Pro Ser Tyr Ala Ser
180

<210> 114
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> FGF21 A129D

<220>
<221> CDS
<222> (1)..(549)

<400> 114

```
atg cat cca att cca gat tct tct cca tta tta caa ttc ggg ggc caa          48
Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1               5                  10                  15

gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca gaa gcc          96
Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
            20                  25                  30

cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct gac cag         144
His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
        35                  40                  45

agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga gtt att         192
Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
    50                  55                  60

caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg cca gat         240
Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp
65                  70                  75                  80

ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc agc ttc         288
Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe
                85                  90                  95

cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc gaa gcc         336
Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
            100                 105                 110

cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac cgg gac         384
His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
        115                 120                 125

cct gac ccc cga gga cca gct cgc ttc ctg cca cta cca ggc ctg ccc         432
Pro Asp Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro
    130                 135                 140

ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc ccc gat         480
Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145                 150                 155                 160

gtg ggc tcc tcg gac cct ctg agc atg gtg gga cct tcc cag ggc cga         528
Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
                165                 170                 175

agc ccc agc tac gct tcc taa                                             549
Ser Pro Ser Tyr Ala Ser
            180
```

<210> 115
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 115

Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1 5 10 15

Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
20 25 30

His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
35 40 45

Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
50 55 60

Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp
65 70 75 80

Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe
85 90 95

Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
100 105 110

His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
115 120 125

Pro Asp Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro
130 135 140

Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145 150 155 160

Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
165 170 175

Ser Pro Ser Tyr Ala Ser
180

<210> 116
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> FGF21 A129Q

<220>
<221> CDS
<222> (1)..(549)

<400> 116
atg cat cca att cca gat tct tct cca tta tta caa ttc ggg ggc caa 48
Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1 5 10 15

gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca gaa gcc 96
Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala

```
            20                  25                  30

cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct gac cag        144
His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
        35                  40                  45

agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga gtt att        192
Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
    50                  55                  60

caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg cca gat        240
Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp
65                  70                  75                  80

ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc agc ttc        288
Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe
                85                  90                  95

cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc gaa gcc        336
Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
            100                 105                 110

cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac cgg gac        384
His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
        115                 120                 125

cct cag ccc cga gga cca gct cgc ttc ctg cca cta cca ggc ctg ccc        432
Pro Gln Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro
    130                 135                 140

ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc ccc gat        480
Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145                 150                 155                 160

gtg ggc tcc tcg gac cct ctg agc atg gtg gga cct tcc cag ggc cga        528
Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
                165                 170                 175

agc ccc agc tac gct tcc taa                                           549
Ser Pro Ser Tyr Ala Ser
            180


<210>  117
<211>  182
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  117

Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1               5                   10                  15


Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
            20                  25                  30


His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
        35                  40                  45


Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
    50                  55                  60
```

Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp
65 70 75 80

Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe
85 90 95

Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
100 105 110

His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
115 120 125

Pro Gln Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro
130 135 140

Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145 150 155 160

Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
165 170 175

Ser Pro Ser Tyr Ala Ser
180

<210> 118
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> FGF21 A134K

<220>
<221> CDS
<222> (1)..(549)

<400> 118
atg cat cca att cca gat tct tct cca tta tta caa ttc ggg ggc caa 48
Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1 5 10 15

gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca gaa gcc 96
Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
20 25 30

cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct gac cag 144
His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
35 40 45

agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga gtt att 192
Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
50 55 60

caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg cca gat 240
Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp
65 70 75 80

ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc agc ttc 288

```
Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe
                85                  90                  95

cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc gaa gcc        336
Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
            100                 105                 110

cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac cgg gac        384
His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
        115                 120                 125

cct gca ccc cga gga cca aaa cgc ttc ctg cca cta cca ggc ctg ccc        432
Pro Ala Pro Arg Gly Pro Lys Arg Phe Leu Pro Leu Pro Gly Leu Pro
    130                 135                 140

ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc ccc gat        480
Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145                 150                 155                 160

gtg ggc tcc tcg gac cct ctg agc atg gtg gga cct tcc cag ggc cga        528
Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
                165                 170                 175

agc ccc agc tac gct tcc taa                                           549
Ser Pro Ser Tyr Ala Ser
            180
```

<210> 119
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 119

```
Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1               5                   10                  15

Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
            20                  25                  30

His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
        35                  40                  45

Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
    50                  55                  60

Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp
65                  70                  75                  80

Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe
                85                  90                  95

Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
            100                 105                 110

His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
        115                 120                 125
```

```
Pro Ala Pro Arg Gly Pro Lys Arg Phe Leu Pro Leu Pro Gly Leu Pro
    130                 135                 140

Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145                 150                 155                 160

Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
                165                 170                 175

Ser Pro Ser Tyr Ala Ser
            180


<210>  120
<211>  549
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  FGF21 A134Y


<220>
<221>  CDS
<222>  (1)..(549)

<400>  120
atg cat cca att cca gat tct tct cca tta tta caa ttc ggg ggc caa         48
Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1               5                   10                  15

gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca gaa gcc         96
Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
            20                  25                  30

cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct gac cag        144
His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
        35                  40                  45

agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga gtt att        192
Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
    50                  55                  60

caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg cca gat        240
Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp
65                  70                  75                  80

ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc agc ttc        288
Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe
                85                  90                  95

cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc gaa gcc        336
Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
            100                 105                 110

cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac cgg gac        384
His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
        115                 120                 125

cct gca ccc cga gga cca tat cgc ttc ctg cca cta cca ggc ctg ccc        432
Pro Ala Pro Arg Gly Pro Tyr Arg Phe Leu Pro Leu Pro Gly Leu Pro
    130                 135                 140
```

```
ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc ccc gat        480
Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145                 150                 155                 160

gtg ggc tcc tcg gac cct ctg agc atg gtg gga cct tcc cag ggc cga        528
Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
                165                 170                 175

agc ccc agc tac gct tcc taa                                        549
Ser Pro Ser Tyr Ala Ser
            180


<210>  121
<211>  182
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  121

Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1               5                   10                  15


Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
            20                  25                  30


His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
        35                  40                  45


Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
    50                  55                  60


Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp
65                  70                  75                  80


Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe
                85                  90                  95


Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
            100                 105                 110


His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
        115                 120                 125


Pro Ala Pro Arg Gly Pro Tyr Arg Phe Leu Pro Leu Pro Gly Leu Pro
    130                 135                 140


Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145                 150                 155                 160


Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
                165                 170                 175


Ser Pro Ser Tyr Ala Ser
```

180

<210> 122
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> FGF21 A134E

<220>
<221> CDS
<222> (1)..(549)

<400> 122

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atg cat cca att cca gat tct tct cca tta tta caa ttc ggg ggc caa          48
Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1               5                   10                  15

gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca gaa gcc          96
Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
            20                  25                  30

cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct gac cag         144
His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
        35                  40                  45

agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga gtt att         192
Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
    50                  55                  60

caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg cca gat         240
Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp
65                  70                  75                  80

ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc agc ttc         288
Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe
                85                  90                  95

cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc gaa gcc         336
Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
            100                 105                 110

cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac cgg gac         384
His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
        115                 120                 125

cct gca ccc cga gga cca gaa cgc ttc ctg cca cta cca ggc ctg ccc         432
Pro Ala Pro Arg Gly Pro Glu Arg Phe Leu Pro Leu Pro Gly Leu Pro
    130                 135                 140

ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc ccc gat         480
Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145                 150                 155                 160

gtg ggc tcc tcg gac cct ctg agc atg gtg gga cct tcc cag ggc cga         528
Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
                165                 170                 175

agc ccc agc tac gct tcc taa                                             549
Ser Pro Ser Tyr Ala Ser
            180
```

<210> 123
<211> 182

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 123

Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1 5 10 15

Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
20 25 30

His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
35 40 45

Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
50 55 60

Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp
65 70 75 80

Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe
85 90 95

Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
100 105 110

His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
115 120 125

Pro Ala Pro Arg Gly Pro Glu Arg Phe Leu Pro Leu Pro Gly Leu Pro
130 135 140

Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145 150 155 160

Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
165 170 175

Ser Pro Ser Tyr Ala Ser
180

<210> 124
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> FGF21 A129K

<220>
<221> CDS
<222> (1)..(549)

<400> 124
atg cat cca att cca gat tct tct cca tta tta caa ttc ggg ggc caa 48
Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1 5 10 15

gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca gaa gcc 96
Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
20 25 30

cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct gac cag 144
His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
35 40 45

agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga gtt att 192
Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
50 55 60

caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg cca gat 240
Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp
65 70 75 80

ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc agc ttc 288
Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe
85 90 95

cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc gaa gcc 336
Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
100 105 110

cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac cgg gac 384
His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
115 120 125

cct aaa ccc cga gga cca gct cgc ttc ctg cca cta cca ggc ctg ccc 432
Pro Lys Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro
130 135 140

ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc ccc gat 480
Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145 150 155 160

gtg ggc tcc tcg gac cct ctg agc atg gtg gga cct tcc cag ggc cga 528
Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
165 170 175

agc ccc agc tac gct tcc taa 549
Ser Pro Ser Tyr Ala Ser
180

<210> 125
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 125

Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1 5 10 15

Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
20 25 30

```
His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
        35                  40                  45

Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
    50                  55                  60

Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp
65                  70                  75                  80

Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe
                85                  90                  95

Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
            100                 105                 110

His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
        115                 120                 125

Pro Lys Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro
    130                 135                 140

Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145                 150                 155                 160

Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
                165                 170                 175

Ser Pro Ser Tyr Ala Ser
            180
```

<210> 126
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> FGF21 P78C

<220>
<221> CDS
<222> (1)..(549)

<400> 126

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atg cat cca att cca gat tct tct cca tta tta caa ttc ggg ggc caa          48
Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1               5                   10                  15

gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca gaa gcc          96
Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
            20                  25                  30

cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct gac cag         144
His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
        35                  40                  45

agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga gtt att         192
```

```
Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
    50                  55                  60

caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg tgc gat        240
Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Cys Asp
65                  70                  75                  80

ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc agc ttc        288
Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe
                85                  90                  95

cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc gaa gcc        336
Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
            100                 105                 110

cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac cgg gac        384
His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
        115                 120                 125

cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc ctg ccc        432
Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro
    130                 135                 140

ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc ccc gat        480
Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145                 150                 155                 160

gtg ggc tcc tcg gac cct ctg agc atg gtg gga cct tcc cag ggc cga        528
Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
                165                 170                 175

agc ccc agc tac gct tcc taa                                           549
Ser Pro Ser Tyr Ala Ser
            180
```

<210> 127
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 127

```
Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1               5                   10                  15

Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
            20                  25                  30

His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
        35                  40                  45

Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
    50                  55                  60

Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Cys Asp
65                  70                  75                  80

Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe
                85                  90                  95
```

```
Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
            100                 105                 110

His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
        115                 120                 125

Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro
    130                 135                 140

Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145                 150                 155                 160

Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
                165                 170                 175

Ser Pro Ser Tyr Ala Ser
            180


<210>  128
<211>  549
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  FGF21 P78R


<220>
<221>  CDS
<222>  (1)..(549)

<400>  128
atg cat cca att cca gat tct tct cca tta tta caa ttc ggg ggc caa         48
Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1               5                   10                  15

gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca gaa gcc         96
Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
            20                  25                  30

cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct gac cag        144
His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
        35                  40                  45

agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga gtt att        192
Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
    50                  55                  60

caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg cgt gat        240
Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Arg Asp
65                  70                  75                  80

ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc agc ttc        288
Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe
                85                  90                  95

cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc gaa gcc        336
Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
            100                 105                 110
```

```
cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac cgg gac        384
His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
        115                 120                 125

cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc ctg ccc        432
Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro
    130                 135                 140

ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc ccc gat        480
Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145                 150                 155                 160

gtg ggc tcc tcg gac cct ctg agc atg gtg gga cct tcc cag ggc cga        528
Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
                165                 170                 175

agc ccc agc tac gct tcc taa                                           549
Ser Pro Ser Tyr Ala Ser
            180
```

<210> 129
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 129

```
Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1               5                   10                  15

Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
            20                  25                  30

His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
        35                  40                  45

Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
    50                  55                  60

Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Arg Asp
65                  70                  75                  80

Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe
                85                  90                  95

Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
            100                 105                 110

His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
        115                 120                 125

Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro
    130                 135                 140

Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
```

145 150 155 160

Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
165 170 175

Ser Pro Ser Tyr Ala Ser
180

<210> 130
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> FGF21 L86T

<220>
<221> CDS
<222> (1)..(549)

<400> 130
atg cat cca att cca gat tct tct cca tta tta caa ttc ggg ggc caa 48
Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1 5 10 15

gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca gaa gcc 96
Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
20 25 30

cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct gac cag 144
His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
35 40 45

agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga gtt att 192
Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
50 55 60

caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg cca gat 240
Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp
65 70 75 80

ggg gcc ctg tat gga tcg acc cac ttt gac cct gag gcc tgc agc ttc 288
Gly Ala Leu Tyr Gly Ser Thr His Phe Asp Pro Glu Ala Cys Ser Phe
85 90 95

cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc gaa gcc 336
Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
100 105 110

cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac cgg gac 384
His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
115 120 125

cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc ctg ccc 432
Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro
130 135 140

ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc ccc gat 480
Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145 150 155 160

gtg ggc tcc tcg gac cct ctg agc atg gtg gga cct tcc cag ggc cga 528
Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
165 170 175

agc ccc agc tac gct tcc taa 549
Ser Pro Ser Tyr Ala Ser
180

<210> 131
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 131

Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1 5 10 15

Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
20 25 30

His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
35 40 45

Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
50 55 60

Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp
65 70 75 80

Gly Ala Leu Tyr Gly Ser Thr His Phe Asp Pro Glu Ala Cys Ser Phe
85 90 95

Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
100 105 110

His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
115 120 125

Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro
130 135 140

Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145 150 155 160

Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
165 170 175

Ser Pro Ser Tyr Ala Ser
180

<210> 132
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> FGF21 L86C

<220>
<221> CDS
<222> (1)..(549)

<400> 132
atg cat cca att cca gat tct tct cca tta tta caa ttc ggg ggc caa 48
Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1 5 10 15

gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca gaa gcc 96
Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
20 25 30

cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct gac cag 144
His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
35 40 45

agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga gtt att 192
Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
50 55 60

caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg cca gat 240
Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp
65 70 75 80

ggg gcc ctg tat gga tcg tgc cac ttt gac cct gag gcc tgc agc ttc 288
Gly Ala Leu Tyr Gly Ser Cys His Phe Asp Pro Glu Ala Cys Ser Phe
85 90 95

cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc gaa gcc 336
Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
100 105 110

cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac cgg gac 384
His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
115 120 125

cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc ctg ccc 432
Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro
130 135 140

ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc ccc gat 480
Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145 150 155 160

gtg ggc tcc tcg gac cct ctg agc atg gtg gga cct tcc cag ggc cga 528
Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
165 170 175

agc ccc agc tac gct tcc taa 549
Ser Pro Ser Tyr Ala Ser
180

<210> 133
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 133

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Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1               5                   10                  15

Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
            20                  25                  30

His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
        35                  40                  45

Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
    50                  55                  60

Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp
65                  70                  75                  80

Gly Ala Leu Tyr Gly Ser Cys His Phe Asp Pro Glu Ala Cys Ser Phe
                85                  90                  95

Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
            100                 105                 110

His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
        115                 120                 125

Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro
    130                 135                 140

Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145                 150                 155                 160

Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
                165                 170                 175

Ser Pro Ser Tyr Ala Ser
            180
```

<210> 134
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> FGF21 L98C

<220>
<221> CDS
<222> (1)..(549)

<400> 134

```
atg cat cca att cca gat tct tct cca tta tta caa ttc ggg ggc caa          48
Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1               5                   10                  15

gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca gaa gcc          96
```

```
Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
            20                  25                  30

cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct gac cag        144
His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
        35                  40                  45

agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga gtt att        192
Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
    50                  55                  60

caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg cca gat        240
Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp
65                  70                  75                  80

ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc agc ttc        288
Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe
                85                  90                  95

cgg gag tgc ctt ctt gag gac gga tac aat gtt tac cag tcc gaa gcc        336
Arg Glu Cys Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
            100                 105                 110

cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac cgg gac        384
His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
        115                 120                 125

cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc ctg ccc        432
Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro
    130                 135                 140

ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc ccc gat        480
Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145                 150                 155                 160

gtg ggc tcc tcg gac cct ctg agc atg gtg gga cct tcc cag ggc cga        528
Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
                165                 170                 175

agc ccc agc tac gct tcc taa                                           549
Ser Pro Ser Tyr Ala Ser
            180


<210>  135
<211>  182
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  135

Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1               5                   10                  15


Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
            20                  25                  30


His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
        35                  40                  45


Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
    50                  55                  60
```

```
Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp
65                  70                  75                  80

Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe
                85                  90                  95

Arg Glu Cys Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
            100                 105                 110

His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
        115                 120                 125

Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro
    130                 135                 140

Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145                 150                 155                 160

Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
                165                 170                 175

Ser Pro Ser Tyr Ala Ser
            180
```

<210> 136
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> FGF21 L98R

<220>
<221> CDS
<222> (1)..(549)

<400> 136

```
atg cat cca att cca gat tct tct cca tta tta caa ttc ggg ggc caa         48
Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1               5                   10                  15

gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca gaa gcc         96
Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
            20                  25                  30

cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct gac cag        144
His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
        35                  40                  45

agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga gtt att        192
Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
    50                  55                  60

caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg cca gat        240
Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp
65                  70                  75                  80
```

```
ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc agc ttc        288
Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe
                85                  90                  95

cgg gag cgt ctt ctt gag gac gga tac aat gtt tac cag tcc gaa gcc        336
Arg Glu Arg Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
            100                 105                 110

cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac cgg gac        384
His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
        115                 120                 125

cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc ctg ccc        432
Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro
    130                 135                 140

ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc ccc gat        480
Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145                 150                 155                 160

gtg ggc tcc tcg gac cct ctg agc atg gtg gga cct tcc cag ggc cga        528
Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
                165                 170                 175

agc ccc agc tac gct tcc taa                                           549
Ser Pro Ser Tyr Ala Ser
            180
```

<210> 137
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 137

```
Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1               5                   10                  15

Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
            20                  25                  30

His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
        35                  40                  45

Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
    50                  55                  60

Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp
65                  70                  75                  80

Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe
                85                  90                  95

Arg Glu Arg Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
            100                 105                 110

His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
```

115 120 125

Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro
130 135 140

Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145 150 155 160

Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
165 170 175

Ser Pro Ser Tyr Ala Ser
180

<210> 138
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> FGF21 L52T

<220>
<221> CDS
<222> (1)..(549)

<400> 138
atg cat cca att cca gat tct tct cca tta tta caa ttc ggg ggc caa 48
Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1 5 10 15

gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca gaa gcc 96
Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
20 25 30

cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct gac cag 144
His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
35 40 45

agc ccc gaa agt acc ctg cag ctg aaa gcc ttg aag ccg gga gtt att 192
Ser Pro Glu Ser Thr Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
50 55 60

caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg cca gat 240
Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp
65 70 75 80

ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc agc ttc 288
Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe
85 90 95

cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc gaa gcc 336
Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
100 105 110

cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac cgg gac 384
His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
115 120 125

cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc ctg ccc 432
Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro
130 135 140

```
ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc ccc gat        480
Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145                 150                 155                 160

gtg ggc tcc tcg gac cct ctg agc atg gtg gga cct tcc cag ggc cga        528
Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
                165                 170                 175

agc ccc agc tac gct tcc taa                                        549
Ser Pro Ser Tyr Ala Ser
            180
```

<210> 139
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 139

```
Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1               5                   10                  15

Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
            20                  25                  30

His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
        35                  40                  45

Ser Pro Glu Ser Thr Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile
    50                  55                  60

Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp
65                  70                  75                  80

Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe
                85                  90                  95

Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
            100                 105                 110

His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
        115                 120                 125

Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro
    130                 135                 140

Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145                 150                 155                 160

Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
                165                 170                 175
```

Ser Pro Ser Tyr Ala Ser
180

<210> 140
<211> 549
<212> DNA
<213> Artificial Sequence

<220>
<223> FGF21 L58E

<220>
<221> CDS
<222> (1)..(549)

<400> 140
atg cat cca att cca gat tct tct cca tta tta caa ttc ggg ggc caa 48
Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1 5 10 15

gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca gaa gcc 96
Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
20 25 30

cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct gac cag 144
His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
35 40 45

agc ccc gaa agt ctc ctg cag ctg aaa gcc gaa aag ccg gga gtt att 192
Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Glu Lys Pro Gly Val Ile
50 55 60

caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg cca gat 240
Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp
65 70 75 80

ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc agc ttc 288
Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe
85 90 95

cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc gaa gcc 336
Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
100 105 110

cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac cgg gac 384
His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
115 120 125

cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc ctg ccc 432
Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro
130 135 140

ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc ccc gat 480
Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145 150 155 160

gtg ggc tcc tcg gac cct ctg agc atg gtg gga cct tcc cag ggc cga 528
Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
165 170 175

agc ccc agc tac gct tcc taa 549
Ser Pro Ser Tyr Ala Ser
180

<210> 141

<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 141

Met His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
1 5 10 15

Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala
20 25 30

His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln
35 40 45

Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Glu Lys Pro Gly Val Ile
50 55 60

Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp
65 70 75 80

Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe
85 90 95

Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala
100 105 110

His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp
115 120 125

Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro
130 135 140

Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp
145 150 155 160

Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg
165 170 175

Ser Pro Ser Tyr Ala Ser
180

<210> 142
<211> 1278
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc-L15-L98R P171G 182P

<220>
<221> CDS

<222> (1)..(1278)

<400> 142

```
atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg          48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                  10                  15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc          96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc         144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag         192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg         240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat         288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc         336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag         384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc         432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg         480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct         528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc         576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg         624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg         672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

tct ccg ggt aaa ggt gga ggt ggt ggt tct ggt ggt ggt agc ggt ggt         720
Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

ggt gga tcc cat cca att cca gat tct tct cca tta tta caa ttc ggg         768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggc caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca         816
```

```
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

gaa gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct        864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga        912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg        960
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc       1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

agc ttc cgg gag cgt ctt ctt gag gac gga tac aat gtt tac cag tcc       1056
Ser Phe Arg Glu Arg Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac       1104
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

cgg gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc       1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

ctg ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc       1200
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg gga ggt tcc cag       1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Gly Ser Gln
                405                 410                 415

ggc cga agc ccc agc tac gct tcc ccg taa                              1278
Gly Arg Ser Pro Ser Tyr Ala Ser Pro
            420                 425
```

<210> 143
<211> 425
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 143

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335
```

```
Ser Phe Arg Glu Arg Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Gly Ser Gln
                405                 410                 415

Gly Arg Ser Pro Ser Tyr Ala Ser Pro
            420                 425
```

<210> 144
<211> 1278
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc-L15-L98R P171G 182G

<220>
<221> CDS
<222> (1)..(1278)

<400> 144

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atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg          48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                   10                  15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc          96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc         144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag         192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg         240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat         288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc         336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110
```

```
atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag        384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc        432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg        480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct        528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc        576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg        624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg        672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

tct ccg ggt aaa ggt gga ggt ggt ggt tct ggt ggt ggt agc ggt ggt        720
Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

ggt gga tcc cat cca att cca gat tct tct cca tta tta caa ttc ggg        768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggc caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca        816
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

gaa gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct        864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga        912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg        960
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc       1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

agc ttc cgg gag cgt ctt ctt gag gac gga tac aat gtt tac cag tcc       1056
Ser Phe Arg Glu Arg Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac       1104
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

cgg gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc       1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380
```

```
ctg ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc       1200
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg gga ggt tcc cag       1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Gly Ser Gln
                405                 410                 415

ggc cga agc ccc agc tac gct tcc ggc taa                               1278
Gly Arg Ser Pro Ser Tyr Ala Ser Gly
            420                 425
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<210> 145
<211> 425
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 145

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

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

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

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

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

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

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

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

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

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

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

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
```

180 185 190

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225 230 235 240

Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
245 250 255

Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
260 265 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
275 280 285

Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
290 295 300

Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305 310 315 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
325 330 335

Ser Phe Arg Glu Arg Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
340 345 350

Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
355 360 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
370 375 380

Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385 390 395 400

Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Gly Ser Gln
405 410 415

Gly Arg Ser Pro Ser Tyr Ala Ser Gly
420 425

<210> 146
<211> 1281
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc-L15-L98R P171G 182G 183G

<220>
<221> CDS
<222> (1)..(1281)

<400> 146

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atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg          48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                  10                  15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc          96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc         144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag         192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg         240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat         288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc         336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag         384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc         432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg         480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct         528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc         576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg         624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg         672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

tct ccg ggt aaa ggt gga ggt ggt ggt tct ggt ggt ggt agc ggt ggt         720
Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240
```

```
ggt gga tcc cat cca att cca gat tct tct cca tta tta caa ttc ggg        768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggc caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca        816
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

gaa gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct        864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga        912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg        960
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc       1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

agc ttc cgg gag cgt ctt ctt gag gac gga tac aat gtt tac cag tcc       1056
Ser Phe Arg Glu Arg Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac       1104
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

cgg gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc       1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

ctg ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc       1200
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg gga ggt tcc cag       1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Gly Ser Gln
                405                 410                 415

ggc cga agc ccc agc tac gct tcc ggt ggc taa                          1281
Gly Arg Ser Pro Ser Tyr Ala Ser Gly Gly
            420                 425
```

<210> 147
<211> 426
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 147

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300
```

```
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

Ser Phe Arg Glu Arg Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Gly Ser Gln
                405                 410                 415

Gly Arg Ser Pro Ser Tyr Ala Ser Gly Gly
            420                 425
```

<210> 148
<211> 1275
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc-L15-L98R P171G Y179S

<220>
<221> CDS
<222> (1)..(1275)

<400> 148

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atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg          48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                   10                  15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc          96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc         144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag         192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg         240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat         288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
```

```
                  85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc        336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag        384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc        432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg        480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct        528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc        576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg        624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg        672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

tct ccg ggt aaa ggt gga ggt ggt ggt tct ggt ggt ggt agc ggt ggt        720
Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

ggt gga tcc cat cca att cca gat tct tct cca tta tta caa ttc ggg        768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggc caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca        816
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

gaa gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct        864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga        912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg        960
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc       1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

agc ttc cgg gag cgt ctt ctt gag gac gga tac aat gtt tac cag tcc       1056
Ser Phe Arg Glu Arg Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac       1104
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
```

```
        355                 360                 365

cgg gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc       1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

ctg ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc       1200
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg gga ggt tcc cag       1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Gly Ser Gln
                405                 410                 415

ggc cga agc ccc agc tcc gct tcc taa                                  1275
Gly Arg Ser Pro Ser Ser Ala Ser
            420


<210>  149
<211>  424
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  149

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

Ser Phe Arg Glu Arg Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Gly Ser Gln
                405                 410                 415

Gly Arg Ser Pro Ser Ser Ala Ser
            420
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<210> 150
<211> 1275
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc-L15-L98R P171G Y179F

<220>
<221> CDS
<222> (1)..(1275)

<400> 150

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atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg          48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                  10                  15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc          96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc         144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag         192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg         240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat         288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc         336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag         384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc         432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg         480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct         528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc         576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg         624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg         672
```

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

tct ccg ggt aaa ggt gga ggt ggt ggt tct ggt ggt ggt agc ggt ggt        720
Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

ggt gga tcc cat cca att cca gat tct tct cca tta tta caa ttc ggg        768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggc caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca        816
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

gaa gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct        864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga        912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg        960
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc       1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

agc ttc cgg gag cgt ctt ctt gag gac gga tac aat gtt tac cag tcc       1056
Ser Phe Arg Glu Arg Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac       1104
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

cgg gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc       1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

ctg ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc       1200
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg gga ggt tcc cag       1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Gly Ser Gln
                405                 410                 415

ggc cga agc ccc agc ttc gct tcc taa                                  1275
Gly Arg Ser Pro Ser Phe Ala Ser
            420
```

<210> 151
<211> 424
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 151

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285
```

```
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

Ser Phe Arg Glu Arg Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Gly Ser Gln
                405                 410                 415

Gly Arg Ser Pro Ser Phe Ala Ser
            420
```

<210> 152
<211> 1275
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc-L15-L98R P171G Y179A

<220>
<221> CDS
<222> (1)..(1275)

<400> 152

```
atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg         48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                   10                  15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc         96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc        144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag        192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60
```

```
gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg        240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat        288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc        336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag        384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc        432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg        480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct        528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc        576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg        624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg        672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

tct ccg ggt aaa ggt gga ggt ggt ggt tct ggt ggt ggt agc ggt ggt        720
Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

ggt gga tcc cat cca att cca gat tct tct cca tta tta caa ttc ggg        768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggc caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca        816
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

gaa gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct        864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga        912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg        960
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc       1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335
```

```
agc ttc cgg gag cgt ctt ctt gag gac gga tac aat gtt tac cag tcc       1056
Ser Phe Arg Glu Arg Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac       1104
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

cgg gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc       1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

ctg ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc       1200
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg gga ggt tcc cag       1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Gly Ser Gln
                405                 410                 415

ggc cga agc ccc agc gct gct tcc taa                                  1275
Gly Arg Ser Pro Ser Ala Ala Ser
            420
```

<210> 153
<211> 424
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 153

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

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

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

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

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

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

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

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

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
```

130 135 140

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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225 230 235 240

Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
245 250 255

Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
260 265 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
275 280 285

Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
290 295 300

Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305 310 315 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
325 330 335

Ser Phe Arg Glu Arg Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
340 345 350

Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
355 360 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
370 375 380

Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385 390 395 400

Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Gly Ser Gln

405 410 415

Gly Arg Ser Pro Ser Ala Ala Ser
420

<210> 154
<211> 1275
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc-L15-L98R P171G A180S

<220>
<221> CDS
<222> (1)..(1275)

<400> 154

```
atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg          48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                  10                  15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc          96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc         144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag         192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg         240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat         288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc         336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag         384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc         432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg         480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct         528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc         576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190
```

```
gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg        624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg        672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

tct ccg ggt aaa ggt gga ggt ggt ggt tct ggt ggt ggt agc ggt ggt        720
Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

ggt gga tcc cat cca att cca gat tct tct cca tta tta caa ttc ggg        768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggc caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca        816
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

gaa gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct        864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga        912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg        960
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc       1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

agc ttc cgg gag cgt ctt ctt gag gac gga tac aat gtt tac cag tcc       1056
Ser Phe Arg Glu Arg Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac       1104
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

cgg gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc       1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

ctg ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc       1200
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg gga ggt tcc cag       1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Gly Ser Gln
                405                 410                 415

ggc cga agc ccc agc tac tcc tcc taa                                  1275
Gly Arg Ser Pro Ser Tyr Ser Ser
            420
```

<210> 155
<211> 424
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 155

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255
```

```
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

Ser Phe Arg Glu Arg Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Gly Ser Gln
                405                 410                 415

Gly Arg Ser Pro Ser Tyr Ser Ser
            420
```

<210> 156
<211> 1275
<212> DNA
<213> Artificial Sequence

<220>
<223> Fc-L15-L98R P171G A180G

<220>
<221> CDS
<222> (1)..(1275)

<400> 156

```
atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg          48
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                   10                  15

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc          96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

atg atc tcc cgt acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc         144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
```

```
        35                  40                  45

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag        192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

gtg cat aat gcc aag aca aag ccg cgt gag gag cag tac aac agc acg        240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat        288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc        336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag        384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

gtg tac acc ctg ccc cca tcc cgt gat gag ctg acc aag aac cag gtc        432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg        480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct        528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc        576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

gtg gac aag agc cgt tgg cag cag ggg aac gtc ttc tca tgc tcc gtg        624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg        672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

tct ccg ggt aaa ggt gga ggt ggt ggt tct ggt ggt ggt agc ggt ggt        720
Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

ggt gga tcc cat cca att cca gat tct tct cca tta tta caa ttc ggg        768
Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

ggc caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca        816
Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

gaa gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct        864
Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga        912
Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

gtt att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg        960
Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
```

```
305                 310                 315                 320

cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc       1008
Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

agc ttc cgg gag cgt ctt ctt gag gac gga tac aat gtt tac cag tcc       1056
Ser Phe Arg Glu Arg Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc cca cac       1104
Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

cgg gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc       1152
Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380

ctg ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc       1200
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg gga ggt tcc cag       1248
Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Gly Ser Gln
                405                 410                 415

ggc cga agc ccc agc tac ggt tcc taa                                  1275
Gly Arg Ser Pro Ser Tyr Gly Ser
            420
```

<210> 157
<211> 424
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 157

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
225                 230                 235                 240

Gly Gly Ser His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly
                245                 250                 255

Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr
            260                 265                 270

Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala
        275                 280                 285

Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly
    290                 295                 300

Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg
305                 310                 315                 320

Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys
                325                 330                 335

Ser Phe Arg Glu Arg Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser
            340                 345                 350

Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His
        355                 360                 365

Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly
    370                 375                 380
```

```
Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro
385                 390                 395                 400

Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Gly Ser Gln
                405                 410                 415

Gly Arg Ser Pro Ser Tyr Gly Ser
            420
```

<210> 158
<211> 1287
<212> DNA
<213> Artificial Sequence

<220>
<223> MKEDD-FGF21-(L15)-Fc

<220>
<221> CDS
<222> (1)..(1287)

<400> 158

```
atg aaa gaa gat gat cac cca att cca gat tct tct cca tta tta caa          48
Met Lys Glu Asp Asp His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln
1               5                   10                  15

ttc ggg ggc caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag          96
Phe Gly Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln
            20                  25                  30

cag aca gaa gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc         144
Gln Thr Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly
        35                  40                  45

gct gct gac cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag         192
Ala Ala Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys
    50                  55                  60

ccg gga gtt att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc         240
Pro Gly Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys
65                  70                  75                  80

cag cgg cca gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag         288
Gln Arg Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu
                85                  90                  95

gcc tgc agc ttc cgg gag ctg ctt ctt gag gac gga tac aat gtt tac         336
Ala Cys Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr
            100                 105                 110

cag tcc gaa gcc cac ggc ctc ccg ctg cac ctg cca ggg aac aag tcc         384
Gln Ser Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser
        115                 120                 125

cca cac cgg gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta         432
Pro His Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu
    130                 135                 140

cca ggc ctg cca ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc         480
Pro Gly Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro
145                 150                 155                 160

cag ccc ccc gat gtg ggc tcc tcg gac cct ctg agc atg gtg gga cct         528
```

```
Gln Pro Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro
                165                 170                 175

tcc cag ggc cga agc ccc agc tac gct tcc ggt gga ggt ggt ggt tct        576
Ser Gln Gly Arg Ser Pro Ser Tyr Ala Ser Gly Gly Gly Gly Gly Ser
            180                 185                 190

ggt ggt ggt agc ggt ggt ggt gga tcc gac aaa act cac aca tgc cca        624
Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro
        195                 200                 205

ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc        672
Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
    210                 215                 220

ccc cca aaa ccc aag gac acc ctc atg atc tcc cgt acc cct gag gtc        720
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
225                 230                 235                 240

aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc        768
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
                245                 250                 255

aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg        816
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
            260                 265                 270

cgt gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc        864
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
        275                 280                 285

gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc        912
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
    290                 295                 300

tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc        960
Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
305                 310                 315                 320

aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg       1008
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
                325                 330                 335

gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc       1056
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
            340                 345                 350

ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg       1104
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
        355                 360                 365

gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc       1152
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
    370                 375                 380

ttc ttc ctc tat agc aag ctc acc gtg gac aag agc agg tgg cag cag       1200
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
385                 390                 395                 400

ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac       1248
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
                405                 410                 415

tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa taa                  1287
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
            420                 425
```

<210> 159
<211> 428
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 159

```
Met Lys Glu Asp Asp His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln
1               5                  10                  15

Phe Gly Gly Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln
            20                  25                  30

Gln Thr Glu Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly
        35                  40                  45

Ala Ala Asp Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys
    50                  55                  60

Pro Gly Val Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys
65                  70                  75                  80

Gln Arg Pro Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu
                85                  90                  95

Ala Cys Ser Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr
            100                 105                 110

Gln Ser Glu Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser
        115                 120                 125

Pro His Arg Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu
    130                 135                 140

Pro Gly Leu Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro
145                 150                 155                 160

Gln Pro Pro Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro
                165                 170                 175

Ser Gln Gly Arg Ser Pro Ser Tyr Ala Ser Gly Gly Gly Gly Gly Ser
            180                 185                 190

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Lys Thr His Thr Cys Pro
        195                 200                 205

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
    210                 215                 220

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
225                 230                 235                 240
```

```
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
                245                 250                 255

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
            260                 265                 270

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

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
    290                 295                 300

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
305                 310                 315                 320

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
                325                 330                 335

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

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
        355                 360                 365

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
    370                 375                 380

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
385                 390                 395                 400

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
                405                 410                 415

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
            420                 425
```

<210> 160
<211> 630
<212> DNA
<213> Artificial Sequence

<220>
<223> FGF21 Y179N S181T, 28AA signal sequence removed during processing

<220>
<221> CDS
<222> (1)..(630)

<400> 160

```
atg gac tcg gac gag acc ggg ttc gag cac tca gga ctg tgg gtt tct        48
Met Asp Ser Asp Glu Thr Gly Phe Glu His Ser Gly Leu Trp Val Ser
1               5                   10                  15
```

```
gtg ctg gct ggt ctt ctg ctg gga gcc tgc cag gca cac ccc atc cct          96
Val Leu Ala Gly Leu Leu Leu Gly Ala Cys Gln Ala His Pro Ile Pro
            20                  25                  30

gac tcc agt cct ctc ctg caa ttc ggg ggc caa gtc cgg cag cgg tac         144
Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln Arg Tyr
        35                  40                  45

ctc tac aca gat gat gcc cag cag aca gaa gcc cac ctg gag atc agg         192
Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His Leu Glu Ile Arg
    50                  55                  60

gag gat ggg acg gtg ggg ggc gct gct gac cag agc ccc gaa agt ctc         240
Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser Pro Glu Ser Leu
65                  70                  75                  80

ctg cag ctg aaa gcc ttg aag ccg gga gtt att caa atc ttg gga gtc         288
Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu Gly Val
                85                  90                  95

aag aca tcc agg ttc ctg tgc cag cgg cca gat ggg gcc ctg tat gga         336
Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly Ala Leu Tyr Gly
            100                 105                 110

tcg ctc cac ttt gac cct gag gcc tgc agc ttc cgg gag ctg ctt ctt         384
Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu Leu Leu
        115                 120                 125

gag gac gga tac aat gtt tac cag tcc gaa gcc cac ggc ctc ccg ctg         432
Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu Pro Leu
    130                 135                 140

cac ctg cca ggg aac aag tcc cca cac cgg gac cct gca ccc cga gga         480
His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro Ala Pro Arg Gly
145                 150                 155                 160

cca gct cgc ttc ctg cca cta cca ggc ctg cca ccc gca ccc ccg gag         528
Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro Ala Pro Pro Glu
                165                 170                 175

cca ccc gga atc ctg gcc ccc cag ccc ccc gat gtg ggc tcc tcg gac         576
Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp Val Gly Ser Ser Asp
            180                 185                 190

cct ctg agc atg gtg gga cct tcc cag ggc cga agc ccc agc aac gct         624
Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg Ser Pro Ser Asn Ala
        195                 200                 205

acc tga                                                                 630
Thr
```

<210> 161
<211> 209
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 161

```
Met Asp Ser Asp Glu Thr Gly Phe Glu His Ser Gly Leu Trp Val Ser
1               5                   10                  15

Val Leu Ala Gly Leu Leu Leu Gly Ala Cys Gln Ala His Pro Ile Pro
```

20 25 30

Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln Arg Tyr
35 40 45

Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His Leu Glu Ile Arg
50 55 60

Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser Pro Glu Ser Leu
65 70 75 80

Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu Gly Val
85 90 95

Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly Ala Leu Tyr Gly
100 105 110

Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu Leu Leu
115 120 125

Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu Pro Leu
130 135 140

His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro Ala Pro Arg Gly
145 150 155 160

Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro Ala Pro Pro Glu
165 170 175

Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp Val Gly Ser Ser Asp
180 185 190

Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg Ser Pro Ser Asn Ala
195 200 205

Thr

<210> 162
<211> 630
<212> DNA
<213> Artificial Sequence

<220>
<223> FGF21 Y179N, 28 AA signal sequence removed during processing

<220>
<221> CDS
<222> (1)..(630)

<400> 162
atg gac tcg gac gag acc ggg ttc gag cac tca gga ctg tgg gtt tct 48
Met Asp Ser Asp Glu Thr Gly Phe Glu His Ser Gly Leu Trp Val Ser
1 5 10 15

```
gtg ctg gct ggt ctt ctg ctg gga gcc tgc cag gca cac ccc atc cct          96
Val Leu Ala Gly Leu Leu Leu Gly Ala Cys Gln Ala His Pro Ile Pro
            20                  25                  30

gac tcc agt cct ctc ctg caa ttc ggg ggc caa gtc cgg cag cgg tac         144
Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln Arg Tyr
        35                  40                  45

ctc tac aca gat gat gcc cag cag aca gaa gcc cac ctg gag atc agg         192
Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His Leu Glu Ile Arg
    50                  55                  60

gag gat ggg acg gtg ggg ggc gct gct gac cag agc ccc gaa agt ctc         240
Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser Pro Glu Ser Leu
65                  70                  75                  80

ctg cag ctg aaa gcc ttg aag ccg gga gtt att caa atc ttg gga gtc         288
Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu Gly Val
                85                  90                  95

aag aca tcc agg ttc ctg tgc cag cgg cca gat ggg gcc ctg tat gga         336
Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly Ala Leu Tyr Gly
            100                 105                 110

tcg ctc cac ttt gac cct gag gcc tgc agc ttc cgg gag ctg ctt ctt         384
Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu Leu Leu
        115                 120                 125

gag gac gga tac aat gtt tac cag tcc gaa gcc cac ggc ctc ccg ctg         432
Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu Pro Leu
    130                 135                 140

cac ctg cca ggg aac aag tcc cca cac cgg gac cct gca ccc cga gga         480
His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro Ala Pro Arg Gly
145                 150                 155                 160

cca gct cgc ttc ctg cca cta cca ggc ctg cca ccc gca ccc ccg gag         528
Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro Ala Pro Pro Glu
                165                 170                 175

cca ccc gga atc ctg gcc ccc cag ccc ccc gat gtg ggc tcc tcg gac         576
Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp Val Gly Ser Ser Asp
            180                 185                 190

cct ctg agc atg gtg gga cct tcc cag ggc cga agc ccc agc aac gct         624
Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg Ser Pro Ser Asn Ala
        195                 200                 205

tcc tga                                                                 630
Ser
```

<210> 163
<211> 209
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 163

```
Met Asp Ser Asp Glu Thr Gly Phe Glu His Ser Gly Leu Trp Val Ser
1               5                   10                  15
```

Val Leu Ala Gly Leu Leu Leu Gly Ala Cys Gln Ala His Pro Ile Pro
20 25 30

Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln Arg Tyr
35 40 45

Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His Leu Glu Ile Arg
50 55 60

Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser Pro Glu Ser Leu
65 70 75 80

Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu Gly Val
85 90 95

Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly Ala Leu Tyr Gly
100 105 110

Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu Leu Leu
115 120 125

Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu Pro Leu
130 135 140

His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro Ala Pro Arg Gly
145 150 155 160

Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro Ala Pro Pro Glu
165 170 175

Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp Val Gly Ser Ser Asp
180 185 190

Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg Ser Pro Ser Asn Ala
195 200 205

Ser

<210> 164
<211> 630
<212> DNA
<213> Artificial Sequence

<220>
<223> FGF21 P124S, 28 AA signal sequence removed during processing

<220>
<221> CDS
<222> (1)..(630)

<400> 164
atg gac tcg gac gag acc ggg ttc gag cac tca gga ctg tgg gtt tct 48
Met Asp Ser Asp Glu Thr Gly Phe Glu His Ser Gly Leu Trp Val Ser

```
1               5                   10                  15

gtg ctg gct ggt ctt ctg ctg gga gcc tgc cag gca cac ccc atc cct          96
Val Leu Ala Gly Leu Leu Leu Gly Ala Cys Gln Ala His Pro Ile Pro
            20                  25                  30

gac tcc agt cct ctc ctg caa ttc ggg ggc caa gtc cgg cag cgg tac         144
Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln Arg Tyr
        35                  40                  45

ctc tac aca gat gat gcc cag cag aca gaa gcc cac ctg gag atc agg         192
Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His Leu Glu Ile Arg
    50                  55                  60

gag gat ggg acg gtg ggg ggc gct gct gac cag agc ccc gaa agt ctc         240
Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser Pro Glu Ser Leu
65                  70                  75                  80

ctg cag ctg aaa gcc ttg aag ccg gga gtt att caa atc ttg gga gtc         288
Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu Gly Val
                85                  90                  95

aag aca tcc agg ttc ctg tgc cag cgg cca gat ggg gcc ctg tat gga         336
Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly Ala Leu Tyr Gly
            100                 105                 110

tcg ctc cac ttt gac cct gag gcc tgc agc ttc cgg gag ctg ctt ctt         384
Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu Leu Leu
        115                 120                 125

gag gac gga tac aat gtt tac cag tcc gaa gcc cac ggc ctc ccg ctg         432
Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu Pro Leu
    130                 135                 140

cac ctg cca ggg aac aag tcc tca cac cgg gac cct gca ccc cga gga         480
His Leu Pro Gly Asn Lys Ser Ser His Arg Asp Pro Ala Pro Arg Gly
145                 150                 155                 160

cca gct cgc ttc ctg cca cta cca ggc ctg cca ccc gca ccc ccg gag         528
Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro Ala Pro Pro Glu
                165                 170                 175

cca ccc gga atc ctg gcc ccc cag ccc ccc gat gtg ggc tcc tcg gac         576
Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp Val Gly Ser Ser Asp
            180                 185                 190

cct ctg agc atg gtg gga cct tcc cag ggc cga agc ccc agc tac gct         624
Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg Ser Pro Ser Tyr Ala
        195                 200                 205

tcc tga                                                                 630
Ser
```

<210> 165
<211> 209
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 165

```
Met Asp Ser Asp Glu Thr Gly Phe Glu His Ser Gly Leu Trp Val Ser
1               5                   10                  15
```

Val Leu Ala Gly Leu Leu Leu Gly Ala Cys Gln Ala His Pro Ile Pro
20 25 30

Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln Arg Tyr
35 40 45

Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His Leu Glu Ile Arg
50 55 60

Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser Pro Glu Ser Leu
65 70 75 80

Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu Gly Val
85 90 95

Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly Ala Leu Tyr Gly
100 105 110

Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu Leu Leu
115 120 125

Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu Pro Leu
130 135 140

His Leu Pro Gly Asn Lys Ser Ser His Arg Asp Pro Ala Pro Arg Gly
145 150 155 160

Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro Ala Pro Pro Glu
165 170 175

Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp Val Gly Ser Ser Asp
180 185 190

Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg Ser Pro Ser Tyr Ala
195 200 205

Ser