SEQUENCE LISTING

<110> Daiichi Sankyo Company, Limited

<120> Anti B7-H3 antibody

<130> DSPCT-FP1214

<150> JP 2011-097645
<151> 2011-04-25

<150> US 61/478878
<151> 2011-04-25

<160> 97

<170> PatentIn version 3.4

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<223> PCR primer

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<212> DNA
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ccctactcga agcccagcat gaccctggag cccaacaagg acctgcggcc aggggacacg 480

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<211> 534
<212> PRT
<213> Homo sapiens

<400> 6

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Val Pro Glu Asp Pro Val Val Ala Leu Val Gly Thr Asp Ala Thr Leu
35 40 45

Cys Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn
50 55 60

Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe Ala
65 70 75 80

Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe
85 90 95

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

Arg Val Ala Asp Glu Gly Ser Phe Thr Cys Phe Val Ser Ile Arg Asp
115 120 125

Phe Gly Ser Ala Ala Val Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys
130 135 140

Pro Ser Met Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr
145 150 155 160

Val Thr Ile Thr Cys Ser Ser Tyr Gln Gly Tyr Pro Glu Ala Glu Val
165 170 175

Phe Trp Gln Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr
180 185 190

Ser Gln Met Ala Asn Glu Gln Gly Leu Phe Asp Val His Ser Ile Leu
195 200 205

Arg Val Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn
210 215 220

Pro Val Leu Gln Gln Asp Ala His Ser Ser Val Thr Ile Thr Pro Gln
225 230 235 240

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245                 250                 255

Val Ala Leu Val Gly Thr Asp Ala Thr Leu Arg Cys Ser Phe Ser Pro
            260                 265                 270

Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr
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Asp Thr Lys Gln Leu Val His Ser Phe Thr Glu Gly Arg Asp Gln Gly
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Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln
305                 310                 315                 320

Gly Asn Ala Ser Leu Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly
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Ser Phe Thr Cys Phe Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val
            340                 345                 350

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

Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr Val Thr Ile Thr Cys Ser
    370                 375                 380

Ser Tyr Arg Gly Tyr Pro Glu Ala Glu Val Phe Trp Gln Asp Gly Gln
385                 390                 395                 400

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

Gln Gly Leu Phe Asp Val His Ser Val Leu Arg Val Val Leu Gly Ala
            420                 425                 430

Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn Pro Val Leu Gln Gln Asp
        435                 440                 445

Ala His Gly Ser Val Thr Ile Thr Gly Gln Pro Met Thr Phe Pro Pro
    450                 455                 460

Glu Ala Leu Trp Val Thr Val Gly Leu Ser Val Cys Leu Ile Ala Leu
465                 470                 475                 480

Leu Val Ala Leu Ala Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys
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Glu Glu Glu Asn Ala Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly
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<223> PCR primer

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<210> 9
<211> 948
<212> DNA
<213> Homo sapiens

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gcacagctca acctcatctg gcagctgaca gataccaaac agctggtgca cagctttgct 240

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ccctactcga agcccagcat gaccctggag cccaacaagg acctgcggcc aggggacacg 480

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cctctgaaac actctgacag caaagaagat gatggacaag aaatagcc 948

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<213> Homo sapiens

<400> 10

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20 25 30

Val Pro Glu Asp Pro Val Val Ala Leu Val Gly Thr Asp Ala Thr Leu
35 40 45

Cys Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn
50 55 60

Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe Ala
65 70 75 80

Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe
85 90 95

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

Arg Val Ala Asp Glu Gly Ser Phe Thr Cys Phe Val Ser Ile Arg Asp
115 120 125

Phe Gly Ser Ala Ala Val Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys
130 135 140

Pro Ser Met Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr
145 150 155 160

Val Thr Ile Thr Cys Ser Ser Tyr Arg Gly Tyr Pro Glu Ala Glu Val
165 170 175

Phe Trp Gln Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr
180 185 190

Ser Gln Met Ala Asn Glu Gln Gly Leu Phe Asp Val His Ser Val Leu
195 200 205

Arg Val Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn
210 215 220

Pro Val Leu Gln Gln Asp Ala His Gly Ser Val Thr Ile Thr Gly Gln
225 230 235 240

Pro Met Thr Phe Pro Pro Glu Ala Leu Trp Val Thr Val Gly Leu Ser
245 250 255

Val Cys Leu Ile Ala Leu Leu Val Ala Leu Ala Phe Val Cys Trp Arg
260 265 270

Lys Ile Lys Gln Ser Cys Glu Glu Glu Asn Ala Gly Ala Glu Asp Gln
275 280 285

Asp Gly Glu Gly Glu Gly Ser Lys Thr Ala Leu Gln Pro Leu Lys His
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Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile Ala
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<210> 12
<211> 55
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<223> PCR primer

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<211> 52
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<400> 13
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<211> 55
<212> DNA
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<220>
<223> PCR primer

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<210> 16
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<210> 17
<211> 42
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<210> 18
<211> 43
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<223> PCR primer

<400> 18
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<210> 19
<211> 27
<212> DNA
<213> Artificial Sequence

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<400> 19
gggcagccta tgacattccc cccagag 27

<210> 20
<211> 576
<212> DNA
<213> Homo sapiens

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tggcagctga cagataccaa acagctggtg cacagctttg ctgagggcca ggaccagggc 180

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cgggatttcg gcagcgctgc cgtcagcctg caggtggccg ggcagcctat gacattcccc 360

ccagaggccc tgtgggtgac cgtggggctg tctgtctgtc tcattgcact gctggtggcc 420

ctggctttcg tgtgctggag aaagatcaaa cagagctgtg aggaggagaa tgcaggagct 480

gaggaccagg atggggaggg agaaggctcc aagacagccc tgcagcctct gaaacactct 540

gacagcaaag aagatgatgg acaagaaata gcctga 576

<210> 21
<211> 191
<212> PRT
<213> Homo sapiens

<400> 21

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Gly Thr Asp Ala Thr Leu Cys Cys Ser Phe Ser Pro Glu Pro Gly Phe
20 25 30

Ser Leu Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln
35 40 45

Leu Val His Ser Phe Ala Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala
50 55 60

Asn Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser
65 70 75 80

Leu Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly Ser Phe Thr Cys
85 90 95

Phe Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val Ser Leu Gln Val
100 105 110

Ala Gly Gln Pro Met Thr Phe Pro Pro Glu Ala Leu Trp Val Thr Val
115 120 125

Gly Leu Ser Val Cys Leu Ile Ala Leu Leu Val Ala Leu Ala Phe Val
130 135 140

Cys Trp Arg Lys Ile Lys Gln Ser Cys Glu Glu Glu Asn Ala Gly Ala
145 150 155 160

Glu Asp Gln Asp Gly Glu Gly Glu Gly Ser Lys Thr Ala Leu Gln Pro
165 170 175

Leu Lys His Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile Ala
180 185 190

<210> 22
<211> 552
<212> DNA
<213> Homo sapiens

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<210> 23
<211> 183
<212> PRT
<213> Homo sapiens

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Pro Glu Ala Glu Val Phe Trp Gln Asp Gly Gln Gly Val Pro Leu Thr
35 40 45

Gly Asn Val Thr Thr Ser Gln Met Ala Asn Glu Gln Gly Leu Phe Asp
50 55 60

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

Cys Leu Val Arg Asn Pro Val Leu Gln Gln Asp Ala His Ser Ser Val
85 90 95

Thr Ile Thr Pro Gln Arg Ser Pro Thr Gly Gln Pro Met Thr Phe Pro
100 105 110

Pro Glu Ala Leu Trp Val Thr Val Gly Leu Ser Val Cys Leu Ile Ala
115 120 125

Leu Leu Val Ala Leu Ala Phe Val Cys Trp Arg Lys Ile Lys Gln Ser
130 135 140

Cys Glu Glu Glu Asn Ala Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu
145 150 155 160

Gly Ser Lys Thr Ala Leu Gln Pro Leu Lys His Ser Asp Ser Lys Glu
165 170 175

Asp Asp Gly Gln Glu Ile Ala
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<210> 24
<211> 576
<212> DNA
<213> Homo sapiens

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tggcagctga cagacaccaa acagctggtg cacagtttca ccgaaggccg ggaccagggc 180

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gacagcaaag aagatgatgg acaagaaata gcctga 576

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<212> PRT
<213> Homo sapiens

<400> 25

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Gly Thr Asp Ala Thr Leu Arg Cys Ser Phe Ser Pro Glu Pro Gly Phe
20 25 30

Ser Leu Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln
35 40 45

Leu Val His Ser Phe Thr Glu Gly Arg Asp Gln Gly Ser Ala Tyr Ala
50 55 60

Asn Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser
65 70 75 80

Leu Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly Ser Phe Thr Cys
85 90 95

Phe Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val Ser Leu Gln Val
100 105 110

Ala Gly Gln Pro Met Thr Phe Pro Pro Glu Ala Leu Trp Val Thr Val
115 120 125

Gly Leu Ser Val Cys Leu Ile Ala Leu Leu Val Ala Leu Ala Phe Val
130 135 140

Cys Trp Arg Lys Ile Lys Gln Ser Cys Glu Glu Glu Asn Ala Gly Ala
145 150 155 160

Glu Asp Gln Asp Gly Glu Gly Glu Gly Ser Lys Thr Ala Leu Gln Pro
165 170 175

Leu Lys His Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile Ala
180 185 190

<210> 26
<211> 534
<212> DNA
<213> Homo sapiens

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gaggagaatg caggagctga ggaccaggat ggggagggag aaggctccaa gacagccctg 480

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<210> 27
<211> 177
<212> PRT
<213> Homo sapiens

<400> 27

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            20                  25                  30

Pro Glu Ala Glu Val Phe Trp Gln Asp Gly Gln Gly Val Pro Leu Thr
        35                  40                  45

Gly Asn Val Thr Thr Ser Gln Met Ala Asn Glu Gln Gly Leu Phe Asp
    50                  55                  60

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

Cys Leu Val Arg Asn Pro Val Leu Gln Gln Asp Ala His Gly Ser Val
                85                  90                  95

Thr Ile Thr Gly Gln Pro Met Thr Phe Pro Pro Glu Ala Leu Trp Val
            100                 105                 110

Thr Val Gly Leu Ser Val Cys Leu Ile Ala Leu Leu Val Ala Leu Ala
        115                 120                 125

Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys Glu Glu Glu Asn Ala
    130                 135                 140

Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly Ser Lys Thr Ala Leu
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Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile
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Ala
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<210> 28
<211> 1188
<212> DNA
<213> Homo sapiens

<400> 28

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ggcttgtttg atgtgcacag catcctgcgg gtggtgctgg gtgcaaatgg cacctacagc    240

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cagagaagcc ccacaggagc cgtggaggtc caggtccctg aggacccggt ggtggcccta    360

gtgggcaccg atgccaccct gcgctgctcc ttctcccccg agcctggctt cagcctggca    420
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tgcttcgtga gcatccggga tttcggcagc gctgccgtca gcctgcaggt ggccgctccc 660

tactcgaagc ccagcatgac cctggagccc aacaaggacc tgcggccagg ggacacggtg 720

accatcacgt gctccagcta ccggggctac cctgaggctg aggtgttctg gcaggatggg 780

cagggtgtgc ccctgactgg caacgtgacc acgtcgcaga tggccaacga gcagggcttg 840

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atgacattcc ccccagaggc cctgtgggtg accgtggggc tgtctgtctg tctcattgca 1020

ctgctggtgg ccctggcttt cgtgtgctgg agaaagatca aacagagctg tgaggaggag 1080

aatgcaggag ctgaggacca ggatggggag ggagaaggct ccaagacagc cctgcagcct 1140

ctgaaacact ctgacagcaa agaagatgat ggacaagaaa tagcctga 1188

<210> 29
<211> 395
<212> PRT
<213> Homo sapiens

<400> 29

Ala Pro Tyr Ser Lys Pro Ser Met Thr Leu Glu Pro Asn Lys Asp Leu
1 5 10 15

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

Pro Glu Ala Glu Val Phe Trp Gln Asp Gly Gln Gly Val Pro Leu Thr
35 40 45

Gly Asn Val Thr Thr Ser Gln Met Ala Asn Glu Gln Gly Leu Phe Asp
50 55 60

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

Cys Leu Val Arg Asn Pro Val Leu Gln Gln Asp Ala His Ser Ser Val
85 90 95

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

Pro Glu Asp Pro Val Val Ala Leu Val Gly Thr Asp Ala Thr Leu Arg
115 120 125

Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn Leu
130 135 140

```
Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe Thr Glu
145                 150                 155                 160

Gly Arg Asp Gln Gly Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe Pro
                165                 170                 175

Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu Arg Leu Gln Arg Val Arg
            180                 185                 190

Val Ala Asp Glu Gly Ser Phe Thr Cys Phe Val Ser Ile Arg Asp Phe
        195                 200                 205

Gly Ser Ala Ala Val Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys Pro
    210                 215                 220

Ser Met Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr Val
225                 230                 235                 240

Thr Ile Thr Cys Ser Ser Tyr Arg Gly Tyr Pro Glu Ala Glu Val Phe
                245                 250                 255

Trp Gln Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr Ser
            260                 265                 270

Gln Met Ala Asn Glu Gln Gly Leu Phe Asp Val His Ser Val Leu Arg
        275                 280                 285

Val Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn Pro
    290                 295                 300

Val Leu Gln Gln Asp Ala His Gly Ser Val Thr Ile Thr Gly Gln Pro
305                 310                 315                 320

Met Thr Phe Pro Pro Glu Ala Leu Trp Val Thr Val Gly Leu Ser Val
                325                 330                 335

Cys Leu Ile Ala Leu Leu Val Ala Leu Ala Phe Val Cys Trp Arg Lys
            340                 345                 350

Ile Lys Gln Ser Cys Glu Glu Glu Asn Ala Gly Ala Glu Asp Gln Asp
        355                 360                 365

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

Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile Ala
385                 390                 395

<210>  30
<211>  873
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<212> DNA
<213> Homo sapiens

<400> 30
ggagccgtgg aggtccaggt ccctgaggac ccggtggtgg ccctagtggg caccgatgcc 60

accctgcgct gctccttctc ccccgagcct ggcttcagcc tggcacagct caacctcatc 120

tggcagctga cagacaccaa acagctggtg cacagtttca ccgaaggccg ggaccagggc 180

agcgcctatg ccaaccgcac ggccctcttc ccggacctgc tggcacaagg caatgcatcc 240

ctgaggctgc agcgcgtgcg tgtggcggac gagggcagct tcacctgctt cgtgagcatc 300

cgggatttcg gcagcgctgc cgtcagcctg caggtggccg ctccctactc gaagcccagc 360

atgaccctgg agcccaacaa ggacctgcgg ccaggggaca cggtgaccat cacgtgctcc 420

agctaccggg gctaccctga ggctgaggtg ttctggcagg atgggcaggg tgtgcccctg 480

actggcaacg tgaccacgtc gcagatggcc aacgagcagg gcttgtttga tgtgcacagc 540

gtcctgcggg tggtgctggg tgcgaatggc acctacagct gcctggtgcg caaccccgtg 600

ctgcagcagg atgcgcacgg ctctgtcacc atcacagggc agcctatgac attcccccca 660

gaggccctgt gggtgaccgt ggggctgtct gtctgtctca ttgcactgct ggtggccctg 720

gctttcgtgt gctggagaaa gatcaaacag agctgtgagg aggagaatgc aggagctgag 780

gaccaggatg gggagggaga aggctccaag acagccctgc agcctctgaa acactctgac 840

agcaaagaag atgatggaca agaaatagcc tga 873

<210> 31
<211> 290
<212> PRT
<213> Homo sapiens

<400> 31

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

Gly Thr Asp Ala Thr Leu Arg Cys Ser Phe Ser Pro Glu Pro Gly Phe
20 25 30

Ser Leu Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln
35 40 45

Leu Val His Ser Phe Thr Glu Gly Arg Asp Gln Gly Ser Ala Tyr Ala
50 55 60

Asn Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser
65 70 75 80

Leu Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly Ser Phe Thr Cys
85 90 95

Phe Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val Ser Leu Gln Val
100 105 110

```
Ala Ala Pro Tyr Ser Lys Pro Ser Met Thr Leu Glu Pro Asn Lys Asp
        115                 120                 125

Leu Arg Pro Gly Asp Thr Val Thr Ile Thr Cys Ser Ser Tyr Arg Gly
    130                 135                 140

Tyr Pro Glu Ala Glu Val Phe Trp Gln Asp Gly Gln Gly Val Pro Leu
145                 150                 155                 160

Thr Gly Asn Val Thr Thr Ser Gln Met Ala Asn Glu Gln Gly Leu Phe
                165                 170                 175

Asp Val His Ser Val Leu Arg Val Val Leu Gly Ala Asn Gly Thr Tyr
            180                 185                 190

Ser Cys Leu Val Arg Asn Pro Val Leu Gln Gln Asp Ala His Gly Ser
        195                 200                 205

Val Thr Ile Thr Gly Gln Pro Met Thr Phe Pro Pro Glu Ala Leu Trp
    210                 215                 220

Val Thr Val Gly Leu Ser Val Cys Leu Ile Ala Leu Leu Val Ala Leu
225                 230                 235                 240

Ala Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys Glu Glu Glu Asn
                245                 250                 255

Ala Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly Ser Lys Thr Ala
            260                 265                 270

Leu Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu
        275                 280                 285

Ile Ala
    290
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<210> 32
<211> 909
<212> DNA
<213> Homo sapiens

<400> 32
atgcggctgg gcagtcctgg actgctcttc ctgctcttca gcagccttcg agctgatact 60

caggagaagg aagtcagagc gatggtaggc agcgacgtgg agctcagctg cgcttgccct 120

gaaggaagcc gttttgattt aaatgatgtt tacgtatatt ggcaaaccag tgagtcgaaa 180

accgtggtga cctaccacat cccacagaac agctccttgg aaaacgtgga cagccgctac 240

cggaaccgag ccctgatgtc accggccggc atgctgcggg gcgacttctc cctgcgcttg 300

ttcaacgtca ccccccagga cgagcagaag tttcactgcc tggtgttgag ccaatccctg 360

ggattccagg aggttttgag cgttgaggtt acactgcatg tggcagcaaa cttcagcgtg 420

cccgtcgtca gcgcccccca cagcccctcc caggatgagc tcaccttcac gtgtacatcc 480

ataaacggct accccaggcc caacgtgtac tggatcaata agacggacaa cagcctgctg 540

gaccaggctc tgcagaatga caccgtcttc ttgaacatgc ggggcttgta tgacgtggtc 600

agcgtgctga ggatcgcacg gacccccagc gtgaacattg gctgctgcat agagaacgtg 660

cttctgcagc agaacctgac tgtcggcagc cagacaggaa atgacatcgg agagagagac 720

aagatcacag agaatccagt cagtaccggc gagaaaaacg cggccacgtg gagcatcctg 780

gctgtcctgt gcctgcttgt ggtcgtggcg gtggccatag gctgggtgtg cagggaccga 840

tgcctccaac acagctatgc aggtgcctgg gctgtgagtc cggagacaga gctcactggc 900

cacgtttga 909

<210> 33
<211> 302
<212> PRT
<213> Homo sapiens

<400> 33

Met Arg Leu Gly Ser Pro Gly Leu Leu Phe Leu Leu Phe Ser Ser Leu
1 5 10 15

Arg Ala Asp Thr Gln Glu Lys Glu Val Arg Ala Met Val Gly Ser Asp
20 25 30

Val Glu Leu Ser Cys Ala Cys Pro Glu Gly Ser Arg Phe Asp Leu Asn
35 40 45

Asp Val Tyr Val Tyr Trp Gln Thr Ser Glu Ser Lys Thr Val Val Thr
50 55 60

Tyr His Ile Pro Gln Asn Ser Ser Leu Glu Asn Val Asp Ser Arg Tyr
65 70 75 80

Arg Asn Arg Ala Leu Met Ser Pro Ala Gly Met Leu Arg Gly Asp Phe
85 90 95

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

Cys Leu Val Leu Ser Gln Ser Leu Gly Phe Gln Glu Val Leu Ser Val
115 120 125

Glu Val Thr Leu His Val Ala Ala Asn Phe Ser Val Pro Val Val Ser
130 135 140

Ala Pro His Ser Pro Ser Gln Asp Glu Leu Thr Phe Thr Cys Thr Ser
145 150 155 160

```
Ile Asn Gly Tyr Pro Arg Pro Asn Val Tyr Trp Ile Asn Lys Thr Asp
                165                 170                 175

Asn Ser Leu Leu Asp Gln Ala Leu Gln Asn Asp Thr Val Phe Leu Asn
            180                 185                 190

Met Arg Gly Leu Tyr Asp Val Val Ser Val Leu Arg Ile Ala Arg Thr
        195                 200                 205

Pro Ser Val Asn Ile Gly Cys Cys Ile Glu Asn Val Leu Leu Gln Gln
    210                 215                 220

Asn Leu Thr Val Gly Ser Gln Thr Gly Asn Asp Ile Gly Glu Arg Asp
225                 230                 235                 240

Lys Ile Thr Glu Asn Pro Val Ser Thr Gly Glu Lys Asn Ala Ala Thr
                245                 250                 255

Trp Ser Ile Leu Ala Val Leu Cys Leu Leu Val Val Val Ala Val Ala
            260                 265                 270

Ile Gly Trp Val Cys Arg Asp Arg Cys Leu Gln His Ser Tyr Ala Gly
        275                 280                 285

Ala Trp Ala Val Ser Pro Glu Thr Glu Leu Thr Gly His Val
    290                 295                 300
```

<210> 34
<211> 873
<212> DNA
<213> Homo sapiens

<400> 34

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atgaggatat ttgctgtctt tatattcatg acctactggc atttgctgaa cgcatttact     60
gtcacggttc ccaaggacct atatgtggta gagtatggta gcaatatgac aattgaatgc     120
aaattcccag tagaaaaaca attagacctg gctgcactaa ttgtctattg ggaaatggag     180
gataagaaca ttattcaatt tgtgcatgga gaggaagacc tgaaggttca gcatagtagc     240
tacagacaga gggcccggct gttgaaggac cagctctccc tgggaaatgc tgcacttcag     300
atcacagatg tgaaattgca ggatgcaggg gtgtaccgct gcatgatcag ctatggtggt     360
gccgactaca agcgaattac tgtgaaagtc aatgccccat acaacaaaat caaccaaaga     420
attttggttg tggatccagt cacctctgaa catgaactga catgtcaggc tgagggctac     480
cccaaggccg aagtcatctg gacaagcagt gaccatcaag tcctgagtgg taagaccacc     540
accaccaatt ccaagagaga ggagaagctt ttcaatgtga ccagcacact gagaatcaac     600
acaacaacta atgagatttt ctactgcact tttaggagat tagatcctga ggaaaaccat     660
acagctgaat tggtcatccc agaactacct ctggcacatc ctccaaatga aaggactcac     720
ttggtaattc tgggagccat cttattatgc cttggtgtag cactgacatt catcttccgt     780
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ttaagaaaag ggagaatgat ggatgtgaaa aaatgtggca tccaagatac aaactcaaag 840

aagcaaagtg atacacattt ggaggagacg taa 873

<210> 35
<211> 290
<212> PRT
<213> Homo sapiens

<400> 35

Met Arg Ile Phe Ala Val Phe Ile Phe Met Thr Tyr Trp His Leu Leu
1 5 10 15

Asn Ala Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr
20 25 30

Gly Ser Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu
35 40 45

Asp Leu Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile
50 55 60

Ile Gln Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser
65 70 75 80

Tyr Arg Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn
85 90 95

Ala Ala Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr
100 105 110

Arg Cys Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val
115 120 125

Lys Val Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val
130 135 140

Asp Pro Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr
145 150 155 160

Pro Lys Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser
165 170 175

Gly Lys Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn
180 185 190

Val Thr Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr
195 200 205

Cys Thr Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu
210 215 220

Val Ile Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr His
225 230 235 240

Leu Val Ile Leu Gly Ala Ile Leu Leu Cys Leu Gly Val Ala Leu Thr
245 250 255

Phe Ile Phe Arg Leu Arg Lys Gly Arg Met Met Asp Val Lys Lys Cys
260 265 270

Gly Ile Gln Asp Thr Asn Ser Lys Lys Gln Ser Asp Thr His Leu Glu
275 280 285

Glu Thr
290

<210> 36
<211> 909
<212> DNA
<213> Homo sapiens

<400> 36
atgcggctgg gcagtcctgg actgctcttc ctgctcttca gcagccttcg agctgatact 60

caggagaagg aagtcagagc gatggtaggc agcgacgtgg agctcagctg cgcttgccct 120

gaaggaagcc gttttgattt aaatgatgtt tacgtatatt ggcaaaccag tgagtcgaaa 180

accgtggtga cctaccacat cccacagaac agctccttgg aaaacgtgga cagccgctac 240

cggaaccgag ccctgatgtc accggccggc atgctgcggg gcgacttctc cctgcgcttg 300

ttcaacgtca ccccccagga cgagcagaag tttcactgcc tggtgttgag ccaatccctg 360

ggattccagg aggttttgag cgttgaggtt acactgcatg tggcagcaaa cttcagcgtg 420

cccgtcgtca gcgcccccca cagcccctcc caggatgagc tcaccttcac gtgtacatcc 480

ataaacggct accccaggcc caacgtgtac tggatcaata agacggacaa cagcctgctg 540

gaccaggctc tgcagaatga caccgtcttc ttgaacatgc ggggcttgta tgacgtggtc 600

agcgtgctga ggatcgcacg gacccccagc gtgaacattg gctgctgcat agagaacgtg 660

cttctgcagc agaacctgac tgtcggcagc cagacaggaa atgacatcgg agagagagac 720

aagatcacag agaatccagt cagtaccggc gagaaaaacg cggccacgtg gagcatcctg 780

gctgtcctgt gcctgcttgt ggtcgtggcg gtggccatag gctgggtgtg cagggaccga 840

tgcctccaac acagctatgc aggtgcctgg gctgtgagtc cggagacaga gctcactggc 900

cacgtttga 909

<210> 37
<211> 302
<212> PRT
<213> Homo sapiens

<400> 37

Met Arg Leu Gly Ser Pro Gly Leu Leu Phe Leu Leu Phe Ser Ser Leu
1 5 10 15

```
Arg Ala Asp Thr Gln Glu Lys Glu Val Arg Ala Met Val Gly Ser Asp
            20                  25                  30

Val Glu Leu Ser Cys Ala Cys Pro Glu Gly Ser Arg Phe Asp Leu Asn
        35                  40                  45

Asp Val Tyr Val Tyr Trp Gln Thr Ser Glu Ser Lys Thr Val Val Thr
    50                  55                  60

Tyr His Ile Pro Gln Asn Ser Ser Leu Glu Asn Val Asp Ser Arg Tyr
65                  70                  75                  80

Arg Asn Arg Ala Leu Met Ser Pro Ala Gly Met Leu Arg Gly Asp Phe
                85                  90                  95

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

Cys Leu Val Leu Ser Gln Ser Leu Gly Phe Gln Glu Val Leu Ser Val
        115                 120                 125

Glu Val Thr Leu His Val Ala Ala Asn Phe Ser Val Pro Val Val Ser
    130                 135                 140

Ala Pro His Ser Pro Ser Gln Asp Glu Leu Thr Phe Thr Cys Thr Ser
145                 150                 155                 160

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

Asn Ser Leu Leu Asp Gln Ala Leu Gln Asn Asp Thr Val Phe Leu Asn
            180                 185                 190

Met Arg Gly Leu Tyr Asp Val Val Ser Val Leu Arg Ile Ala Arg Thr
        195                 200                 205

Pro Ser Val Asn Ile Gly Cys Cys Ile Glu Asn Val Leu Leu Gln Gln
    210                 215                 220

Asn Leu Thr Val Gly Ser Gln Thr Gly Asn Asp Ile Gly Glu Arg Asp
225                 230                 235                 240

Lys Ile Thr Glu Asn Pro Val Ser Thr Gly Glu Lys Asn Ala Ala Thr
                245                 250                 255

Trp Ser Ile Leu Ala Val Leu Cys Leu Leu Val Val Val Ala Val Ala
            260                 265                 270

Ile Gly Trp Val Cys Arg Asp Arg Cys Leu Gln His Ser Tyr Ala Gly
        275                 280                 285
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Ala Trp Ala Val Ser Pro Glu Thr Glu Leu Thr Gly His Val
290 295 300

<210> 38
<211> 867
<212> DNA
<213> Homo sapiens

<400> 38
atgggccaca cacggaggca gggaacatca ccatccaagt gtccatacct caatttcttt 60

cagctcttgg tgctggctgg tctttctcac ttctgttcag gtgttatcca cgtgaccaag 120

gaagtgaaag aagtggcaac gctgtcctgt ggtcacaatg tttctgttga agagctggca 180

caaactcgca tctactggca aaaggagaag aaaatggtgc tgactatgat gtctggggac 240

atgaatatat ggcccgagta caagaaccgg accatctttg atatcactaa taacctctcc 300

attgtgatcc tggctctgcg cccatctgac gagggcacat acgagtgtgt tgttctgaag 360

tatgaaaaag acgctttcaa gcgggaacac ctggctgaag tgacgttatc agtcaaagct 420

gacttcccta cacctagtat atctgacttt gaaattccaa cttctaatat tagaaggata 480

atttgctcaa cctctggagg ttttccagag cctcacctct cctggttgga aaatggagaa 540

gaattaaatg ccatcaacac aacagtttcc caagatcctg aaactgagct ctatgctgtt 600

agcagcaaac tggatttcaa tatgacaacc aaccacagct tcatgtgtct catcaagtat 660

ggacatttaa gagtgaatca gaccttcaac tggaatacaa ccaagcaaga gcattttcct 720

gataacctgc tcccatcctg ggccattacc ttaatctcag taaatggaat ttttgtgata 780

tgctgcctga cctactgctt tgccccaaga tgcagagaga gaaggaggaa tgagagattg 840

agaagggaaa gtgtacgccc tgtatag 867

<210> 39
<211> 288
<212> PRT
<213> Homo sapiens

<400> 39

Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr
1 5 10 15

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

Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu
35 40 45

Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile
50 55 60

Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp
65 70 75 80

Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr
85 90 95

Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly
100 105 110

Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg
115 120 125

Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr
130 135 140

Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile
145 150 155 160

Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu
165 170 175

Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp
180 185 190

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

Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg
210 215 220

Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro
225 230 235 240

Asp Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly
245 250 255

Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg
260 265 270

Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val
275 280 285

<210> 40
<211> 990
<212> DNA
<213> Homo sapiens

<400> 40
atggatcccc agtgcactat gggactgagt aacattctct ttgtgatggc cttcctgctc 60

tctggtgctg ctcctctgaa gattcaagct tatttcaatg agactgcaga cctgccatgc 120

caatttgcaa actctcaaaa ccaaagcctg agtgagctag tagtattttg gcaggaccag 180

gaaaacttgg ttctgaatga ggtatactta ggcaaagaga aatttgacag tgttcattcc 240

aagtatatgg gccgcacaag ttttgattcg gacagttgga ccctgagact tcacaatctt 300

cagatcaagg acaagggctt gtatcaatgt atcatccatc acaaaaagcc cacaggaatg 360

attcgcatcc accagatgaa ttctgaactg tcagtgcttg ctaacttcag tcaacctgaa 420

atagtaccaa tttctaatat aacagaaaat gtgtacataa atttgacctg ctcatctata 480

cacggttacc cagaacctaa gaagatgagt gttttgctaa gaaccaagaa ttcaactatc 540

gagtatgatg gtattatgca gaaatctcaa gataatgtca cagaactgta cgacgtttcc 600

atcagcttgt ctgtttcatt ccctgatgtt acgagcaata tgaccatctt ctgtattctg 660

gaaactgaca agacgcggct tttatcttca cctttctcta tagagcttga ggaccctcag 720

cctcccccag accacattcc ttggattaca gctgtacttc caacagttat tatatgtgtg 780

atggttttct gtctaattct atggaaatgg aagaagaaga agcggcctcg caactcttat 840

aaatgtggaa ccaacacaat ggagagggaa gagagtgaac agaccaagaa aagagaaaaa 900

atccatatac ctgaaagatc tgatgaagcc cagcgtgttt ttaaaagttc gaagacatct 960

tcatgcgaca aaagtgatac atgtttttag 990

<210> 41
<211> 329
<212> PRT
<213> Homo sapiens

<400> 41

Met Asp Pro Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met
1 5 10 15

Ala Phe Leu Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe
20 25 30

Asn Glu Thr Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln
35 40 45

Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val
50 55 60

Leu Asn Glu Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser
65 70 75 80

Lys Tyr Met Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg
85 90 95

Leu His Asn Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile
100 105 110

His His Lys Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser
115 120 125

Glu Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile
130 135 140

Ser Asn Ile Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile
145 150 155 160

His Gly Tyr Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys
165 170 175

Asn Ser Thr Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser Gln Asp Asn
180 185 190

Val Thr Glu Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro
195 200 205

Asp Val Thr Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys
210 215 220

Thr Arg Leu Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln
225 230 235 240

Pro Pro Pro Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val
245 250 255

Ile Ile Cys Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys
260 265 270

Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu
275 280 285

Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro
290 295 300

Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser
305 310 315 320

Ser Cys Asp Lys Ser Asp Thr Cys Phe
325

<210> 42
<211> 849
<212> DNA
<213> Homo sapiens

<400> 42
atggcttccc tggggcagat cctcttctgg agcataatta gcatcatcat tattctggct 60

ggagcaattg cactcatcat tggctttggt atttcaggga gacactccat cacagtcact 120

actgtcgcct cagctgggaa cattggggag gatggaatcc tgagctgcac ttttgaacct 180

gacatcaaac tttctgatat cgtgatacaa tggctgaagg aaggtgtttt aggcttggtc 240

catgagttca aagaaggcaa agatgagctg tcggagcagg atgaaatgtt cagaggccgg 300

acagcagtgt ttgctgatca agtgatagtt ggcaatgcct ctttgcggct gaaaaacgtg 360

caactcacag atgctggcac ctacaaatgt tatatcatca cttctaaagg caaggggaat 420

gctaaccttg agtataaaac tggagccttc agcatgccgg aagtgaatgt ggactataat 480

gccagctcag agaccttgcg gtgtgaggct ccccgatggt tcccccagcc cacagtggtc 540

tgggcatccc aagttgacca gggagccaac ttctcggaag tctccaatac cagctttgag 600

ctgaactctg agaatgtgac catgaaggtt gtgtctgtgc tctacaatgt tacgatcaac 660

aacacatact cctgtatgat tgaaaatgac attgccaaag caacagggga tatcaaagtg 720

acagaatcgg agatcaaaag gcggagtcac ctacagctgc taaactcaaa ggcttctctg 780

tgtgtctctt ctttctttgc catcagctgg gcacttctgc ctctcagccc ttacctgatg 840

ctaaaatag 849

<210> 43
<211> 282
<212> PRT
<213> Homo sapiens

<400> 43

Met Ala Ser Leu Gly Gln Ile Leu Phe Trp Ser Ile Ile Ser Ile Ile
1 5 10 15

Ile Ile Leu Ala Gly Ala Ile Ala Leu Ile Ile Gly Phe Gly Ile Ser
20 25 30

Gly Arg His Ser Ile Thr Val Thr Thr Val Ala Ser Ala Gly Asn Ile
35 40 45

Gly Glu Asp Gly Ile Leu Ser Cys Thr Phe Glu Pro Asp Ile Lys Leu
50 55 60

Ser Asp Ile Val Ile Gln Trp Leu Lys Glu Gly Val Leu Gly Leu Val
65 70 75 80

His Glu Phe Lys Glu Gly Lys Asp Glu Leu Ser Glu Gln Asp Glu Met
85 90 95

Phe Arg Gly Arg Thr Ala Val Phe Ala Asp Gln Val Ile Val Gly Asn
100 105 110

Ala Ser Leu Arg Leu Lys Asn Val Gln Leu Thr Asp Ala Gly Thr Tyr
115 120 125

Lys Cys Tyr Ile Ile Thr Ser Lys Gly Lys Gly Asn Ala Asn Leu Glu
130 135 140

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

Ala Ser Ser Glu Thr Leu Arg Cys Glu Ala Pro Arg Trp Phe Pro Gln
165 170 175

```
Pro Thr Val Val Trp Ala Ser Gln Val Asp Gln Gly Ala Asn Phe Ser
            180                 185                 190

Glu Val Ser Asn Thr Ser Phe Glu Leu Asn Ser Glu Asn Val Thr Met
        195                 200                 205

Lys Val Val Ser Val Leu Tyr Asn Val Thr Ile Asn Asn Thr Tyr Ser
    210                 215                 220

Cys Met Ile Glu Asn Asp Ile Ala Lys Ala Thr Gly Asp Ile Lys Val
225                 230                 235                 240

Thr Glu Ser Glu Ile Lys Arg Arg Ser His Leu Gln Leu Leu Asn Ser
                245                 250                 255

Lys Ala Ser Leu Cys Val Ser Ser Phe Phe Ala Ile Ser Trp Ala Leu
            260                 265                 270

Leu Pro Leu Ser Pro Tyr Leu Met Leu Lys
        275                 280
```

<210> 44
<211> 10
<212> PRT
<213> Mus musculus

<400> 44

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

<210> 45
<211> 14
<212> PRT
<213> Mus musculus

<400> 45

```
Ile Val Leu Ser Gln Ser Pro Thr Ile Leu Ser Ala Ser Pro
1               5                   10
```

<210> 46
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 46
aagaattcat ggaatggagt tggata 26

<210> 47
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 47
aagatatctc atttacccgg agtccgggag aa 32

<210> 48
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 48
aagaattcat ggattttctg gtgcag 26

<210> 49
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 49
aagatatctt aacactcatt cctgttgaag ct 32

<210> 50
<211> 1413
<212> DNA
<213> Mus musculus

<400> 50
atggaatgga gttggatatt tctctttctc ctgtcaggaa ctgcaggtgt ccactctgag 60

gtccagctgc agcagtctgg acctgagctg gtaaagcctg gggcttcagt gaagatgtcc 120

tgcaaggctt ctggatacac attcactaac tatgttatgc actgggtgaa gcagaagcct 180

gggcagggcc ttgagtggat tggatatatt aatccttaca atgatgatgt taagtacaat 240

gagaagttca aaggcaaggc cacacagact tcagacaaat cctccagcac agcctacatg 300

gagctcagca gcctgacctc tgaggactct gcggtctatt actgtgcaag atgggggtac 360

tacggtagtc ccttatacta ctttgactac tggggccaag gcaccactct cacagtctcc 420

tcagccaaaa caacagcccc atcggtctat ccactggccc ctgtgtgtgg agatacaact 480

ggctcctcgg tgactctagg atgcctggtc aagggttatt tccctgagcc agtgaccttg 540

acctggaact ctggatccct gtccagtggt gtgcacacct tcccagctgt cctgcagtct 600

gacctctaca ccctcagcag ctcagtgact gtaacctcga gcacctggcc cagccagtcc 660

atcacctgca atgtggccca cccggcaagc agcaccaagg tggacaagaa aattgagccc 720

agagggccca caatcaagcc ctgtcctcca tgcaaatgcc cagcacctaa cctcttgggt 780

ggaccatccg tcttcatctt ccctccaaag atcaaggatg tactcatgat ctccctgagc 840

cccatagtca catgtgtggt ggtggatgtg agcgaggatg acccagatgt ccagatcagc 900

tggtttgtga acaacgtgga agtacacaca gctcagacac aaacccatag agaggattac 960

aacagtactc tccgggtggt cagtgccctc cccatccagc accaggactg gatgagtggc 1020

aaggagttca aatgcaaggt caacaacaaa gacctcccag cgcccatcga gagaaccatc 1080

tcaaaaccca aagggtcagt aagagctcca caggtatatg tcttgcctcc accagaagaa 1140

gagatgacta agaaacaggt cactctgacc tgcatggtca cagacttcat gcctgaagac 1200

atttacgtgg agtggaccaa caacgggaaa acagagctaa actacaagaa cactgaacca 1260

gtcctggact ctgatggttc ttacttcatg tacagcaagc tgagagtgga aaagaagaac 1320

tgggtggaaa gaaatagcta ctcctgttca gtggtccacg agggtctgca caatcaccac 1380

acgactaaga gcttctcccg gactccgggt aaa 1413

<210> 51
<211> 471
<212> PRT
<213> Mus musculus

<400> 51

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

Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
20 25 30

Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Thr Asn Tyr Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
50 55 60

Glu Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Asp Val Lys Tyr Asn
65 70 75 80

Glu Lys Phe Lys Gly Lys Ala Thr Gln Thr Ser Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Trp Gly Tyr Tyr Gly Ser Pro Leu Tyr Tyr Phe
115 120 125

Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Lys Thr
130 135 140

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

Gly Ser Ser Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu
165 170 175

```
Pro Val Thr Leu Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His
            180                 185                 190

Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser
        195                 200                 205

Val Thr Val Thr Ser Ser Thr Trp Pro Ser Gln Ser Ile Thr Cys Asn
    210                 215                 220

Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Glu Pro
225                 230                 235                 240

Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro
                245                 250                 255

Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys
            260                 265                 270

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

Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn
    290                 295                 300

Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr
305                 310                 315                 320

Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp
                325                 330                 335

Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu
            340                 345                 350

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

Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys
    370                 375                 380

Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp
385                 390                 395                 400

Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys
                405                 410                 415

Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser
            420                 425                 430

Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser
        435                 440                 445
```

```
Cys Ser Val Val His Glu Gly Leu His Asn His His Thr Thr Lys Ser
    450                 455                 460

Phe Ser Arg Thr Pro Gly Lys
465                 470
```

<210> 52
<211> 705
<212> DNA
<213> Mus musculus

<400> 52

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atggattttc tggtgcagat tttcagcttc ctgctaatca gtgcttcagt cataatgtcc     60

agaggacaaa ttgttctctc ccagtctcca acaatcctgt ctgcatctcc aggggagaag    120

gtcacaatga cttgcagggc cagctcaaga ctaatttaca tgcattggta tcagcagaag    180

ccaggatcct cccccaaacc ctggatttat gccacatcca acctggcttc tggagtccct    240

gctcgcttca gtggcagtgg gtctgggacc tcttactctc tcacaatcag cagagtggag    300

gctgaagatg ctgccactta ttactgccag cagtggaata gtaacccacc cacgttcggt    360

actgggacca agctggagct gaaacgggct gatgctgcac caactgtatc catcttccca    420

ccatccagtg agcagttaac atctggaggt gcctcagtcg tgtgcttctt gaacaacttc    480

taccccaaag acatcaatgt caagtggaag attgatggca gtgaacgaca aaatggcgtc    540

ctgaacagtt ggactgatca ggacagcaaa gacagcacct acagcatgag cagcaccctc    600

acgttgacca aggacgagta tgaacgacat aacagctata cctgtgaggc cactcacaag    660

acatcaactt cacccattgt caagagcttc aacaggaatg agtgt                    705
```

<210> 53
<211> 235
<212> PRT
<213> Mus musculus

<400> 53

```
Met Asp Phe Leu Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1               5                   10                  15

Val Ile Met Ser Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Thr Ile
            20                  25                  30

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

Ser Arg Leu Ile Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
    50                  55                  60

Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro
65                  70                  75                  80
```

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95

Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110

Asn Ser Asn Pro Pro Thr Phe Gly Thr Gly Thr Lys Leu Glu Leu Lys
115 120 125

Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu
130 135 140

Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe
145 150 155 160

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

Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser
180 185 190

Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu
195 200 205

Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser
210 215 220

Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
225 230 235

<210> 54
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 54
ccacgcgccc tgtagcggcg cattaagc 28

<210> 55
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 55
aaacccggga gctttttgca aaagcctagg 30

<210> 56
<211> 1704
<212> DNA
<213> Artificial Sequence

<220>
<223> human kappa chain secretion signal, human kappa chain constant region and human poly A additional signal

<400> 56
ggtaccaccc aagctggcta ggtaagcttg ctagcgccac catggtgctg cagacccagg 60

tgttcatctc cctgctgctg tggatctccg gcgcatatgg cgatatcgtg atgattaaac 120

gtacggtggc cgccccctcc gtgttcatct tccccccctc cgacgagcag ctgaagtccg 180

gcaccgcctc cgtggtgtgc ctgctgaata acttctaccc cagagaggcc aaggtgcagt 240

ggaaggtgga caacgccctg cagtccggga actcccagga gagcgtgacc gagcaggaca 300

gcaaggacag cacctacagc ctgagcagca ccctgaccct gagcaaagcc gactacgaga 360

agcacaaggt gtacgcctgc gaggtgaccc accagggcct gagctccccc gtcaccaaga 420

gcttcaacag gggggagtgt taggggcccg tttaaacggg tggcatccct gtgacccctc 480

cccagtgcct ctcctggccc tggaagttgc cactccagtg cccaccagcc ttgtcctaat 540

aaaattaagt tgcatcattt tgtctgacta ggtgtccttc tataatatta tggggtggag 600

gggggtggta tggagcaagg ggcaagttgg gaagacaacc tgtagggcct gcggggtcta 660

ttgggaacca agctggagtg cagtggcaca atcttggctc actgcaatct ccgcctcctg 720

ggttcaagcg attctcctgc ctcagcctcc cgagttgttg ggattccagg catgcatgac 780

caggctcacc taatttttgt ttttttggta gagacggggt ttcaccatat tggccaggct 840

ggtctccaac tcctaatctc aggtgatcta cccaccttgg cctcccaaat tgctgggatt 900

acaggcgtga accactgctc cacgcgccct gtagcggcgc attaagcgcg gcgggtgtgg 960

tggttacgcg cagcgtgacc gctacacttg ccagcgccct agcgcccgct cctttcgctt 1020

tcttcccttc ctttctcgcc acgttcgccg gctttccccg tcaagctcta aatcgggggc 1080

tccctttagg gttccgattt agtgctttac ggcacctcga ccccaaaaaa cttgattagg 1140

gtgatggttc acgtagtggg ccatcgccct gatagacggt ttttcgccct ttgacgttgg 1200

agtccacgtt ctttaatagt ggactcttgt tccaaactgg aacaacactc aaccctatct 1260

cggtctattc ttttgattta taagggattt tgccgatttc ggcctattgg ttaaaaaatg 1320

agctgattta acaaaaattt aacgcgaatt aattctgtgg aatgtgtgtc agttagggtg 1380

tggaaagtcc ccaggctccc cagcaggcag aagtatgcaa agcatgcatc tcaattagtc 1440

agcaaccagg tgtggaaagt ccccaggctc cccagcaggc agaagtatgc aaagcatgca 1500

tctcaattag tcagcaacca tagtcccgcc cctaactccg cccatcccgc ccctaactcc 1560

gcccagttcc gcccattctc cgccccatgg ctgactaatt ttttttattt atgcagaggc 1620

cgaggccgcc tctgcctctg agctattcca gaagtagtga ggaggctttt ttggaggcct 1680

aggcttttgc aaaaagctcc cggg 1704

<210> 57
<211> 1120
<212> DNA

<213> Artificial Sequence

<220>
<223> human IgG1 signal sequence and constant region

<400> 57
tgctagcgcc accatgaaac acctgtggtt cttcctcctg ctggtggcag ctcccagatg 60

ggtgctgagc caggtgcaat tgtgcaggcg gttagctcag cctccaccaa gggcccaagc 120

gtcttccccc tggcaccctc ctccaagagc acctctggcg gcacagccgc cctgggctgc 180

ctggtcaagg actacttccc cgaacccgtg accgtgagct ggaactcagg cgccctgacc 240

agcggcgtgc acaccttccc cgctgtcctg cagtcctcag gactctactc cctcagcagc 300

gtggtgaccg tgccctccag cagcttgggc acccagacct acatctgcaa cgtgaatcac 360

aagcccagca acaccaaggt ggacaagaga gttgagccca aatcttgtga caaaactcac 420

acatgcccac cctgcccagc acctgaactc ctgggggggac cctcagtctt cctcttcccc 480

ccaaaaccca aggacaccct catgatctcc cggaccccctg aggtcacatg cgtggtggtg 540

gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 600

cataatgcca agacaaagcc ccgggaggag cagtacaaca gcacgtaccg ggtggtcagc 660

gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 720

aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg ccagccccgg 780

gaaccacagg tgtacaccct gcccccatcc cgggaggaga tgaccaagaa ccaggtcagc 840

ctgacctgcc tggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 900

ggccagcccg agaacaacta caagaccacc cctcccgtgc tggactccga cggctccttc 960

ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcagggcaa cgtcttctca 1020

tgctccgtga tgcatgaggc tctgcacaac cactacaccc agaagagcct ctccctgtct 1080

cccggcaaat gagatatcgg gcccgtttaa acgggtggca 1120

<210> 58
<211> 699
<212> DNA
<213> Artificial Sequence

<220>
<223> Light chain of chimeric M30

<400> 58
atggtgctgc agacccaggt gttcatctcc ctgctgctgt ggatctccgg cgcatatggc 60

caaattgttc tctcccagtc tccaacaatc ctgtctgcat ctccagggga gaaggtcaca 120

atgacttgca gggccagctc aagactaatt tacatgcatt ggtatcagca gaagccagga 180

tcctcccccа aaccctggat ttatgccaca tccaacctgg cttctggagt ccctgctcgc 240

ttcagtggca gtgggtctgg gacctcttac tctctcacaa tcagcagagt ggaggctgaa 300

gatgctgcca cttattactg ccagcagtgg aatagtaacc cacccacgtt cggtactggg 360

accaagctgg agctgaaacg tacggtggcc gccccctccg tgttcatctt cccccctcc 420

gacgagcagc tgaagtccgg caccgcctcc gtggtgtgcc tgctgaataa cttctacccc 480

agagaggcca aggtgcagtg gaaggtggac aacgccctgc agtccgggaa ctcccaggag 540

agcgtgaccg agcaggacag caaggacagc acctacagcc tgagcagcac cctgaccctg 600

agcaaagccg actacgagaa gcacaaggtg tacgcctgcg aggtgaccca ccagggcctg 660

agctcccccg tcaccaagag cttcaacagg ggggagtgt 699

<210> 59
<211> 233
<212> PRT
<213> Artificial Sequence

<220>
<223> Light chain of chimeric M30

<400> 59

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

Gly Ala Tyr Gly Gln Ile Val Leu Ser Gln Ser Pro Thr Ile Leu Ser
20 25 30

Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Arg
35 40 45

Leu Ile Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys
50 55 60

Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg
65 70 75 80

Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg
85 90 95

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

Asn Pro Pro Thr Phe Gly Thr Gly Thr Lys Leu Glu Leu Lys Arg Thr
115 120 125

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
130 135 140

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

Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
165 170 175

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
180 185 190

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
195 200 205

Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
210 215 220

Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 60
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 60
aaacatatgg ccaaattgtt ctctcccagt ctccaacaat cc 42

<210> 61
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 61
aaacgtacgt ttcagctcca gcttggtccc agtaccg 37

<210> 62
<211> 1413
<212> DNA
<213> Artificial Sequence

<220>
<223> Heavy chain of chimeric M30

<400> 62
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgag 60

gtccagctgc agcagtctgg acctgagctg gtaaagcctg gggcttcagt gaagatgtcc 120

tgcaaggctt ctggatacac attcactaac tatgttatgc actgggtgaa gcagaagcct 180

gggcagggcc ttgagtggat tggatatatt aatccttaca atgatgatgt taagtacaat 240

gagaagttca aaggcaaggc cacacagact tcagacaaat cctccagcac agcctacatg 300

gaactcagca gcctgacctc tgaggactct gcggtctatt actgtgcaag atgggggtac 360

tacggtagtc ccttatacta ctttgactac tggggccaag gcaccactct cacagtcagc 420

tcagcctcca ccaagggccc aagcgtcttc cccctggcac cctcctccaa gagcacctct 480

ggcggcacag ccgccctggg ctgcctggtc aaggactact tccccgaacc cgtgaccgtg 540

agctggaact caggcgccct gaccagcggc gtgcacacct tccccgctgt cctgcagtcc 600

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 660

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gagagttgag 720

cccaaatctt gtgacaaaac tcacacatgc ccaccctgcc cagcacctga actcctgggg 780

ggaccctcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 840

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 900

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccccggga ggagcagtac 960

aacagcacgt accgggtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 1020

aaggagtaca agtgcaaggt ctccaacaaa gccctcccag cccccatcga gaaaaccatc 1080

tccaaagcca aaggccagcc ccgggaacca caggtgtaca ccctgccccc atcccgggag 1140

gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1200

atcgccgtgg agtgggagag caatggccag cccgagaaca actacaagac cacccctccc 1260

gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1320

tggcagcagg gcaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1380

acccagaaga gcctctccct gtctcccggc aaa 1413

<210> 63
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy chain of chimeric M30

<400> 63

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
20 25 30

Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Thr Asn Tyr Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
50 55 60

Glu Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Asp Val Lys Tyr Asn
65 70 75 80

Glu Lys Phe Lys Gly Lys Ala Thr Gln Thr Ser Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Trp Gly Tyr Tyr Gly Ser Pro Leu Tyr Tyr Phe
115 120 125

```
Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr
    130                 135                 140

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145                 150                 155                 160

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
                165                 170                 175

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            180                 185                 190

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
        195                 200                 205

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    210                 215                 220

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
225                 230                 235                 240

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

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

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

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

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

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

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

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

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
    370                 375                 380

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

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

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

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

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

Leu Ser Leu Ser Pro Gly Lys
465 470

<210> 64
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 64
aaagctgagc gaggtccagc tgcagcagtc tggacctgag 40

<210> 65
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 65
gaggtcaggc tgctgagttc catgtaggct gtgctg 36

<210> 66
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 66
cagcacagcc tacatggaac tcagcagcct gacctc 36

<210> 67
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 67
aaagctgagc tgactgtgag agtggtgcct tggccccag 39

<210> 68
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 68
aaagctgagc gaggtccagc tgcagcagtc tggacctgag 40

<210> 69
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 69
aaagctgagc tgactgtgag agtggtgcct tggccccag 39

<210> 70
<211> 699
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized light chain of M30

<400> 70
atggtgctgc agacccaggt gttcatctcc ctgctgctgt ggatctccgg cgcatatggc 60

gagatcgtgc tgacccagag ccccgccacc ctgtctctga gccctggcga gagagccacc 120

ctgagctgca gagccagcag ccgcctgatc tacatgcact ggtatcagca gaagcccggc 180

caggccccca gactgctgat ctacgccacc agcaacctgg ccagcggcat ccccgccaga 240

ttttctggca gcggcagcgg caccgacttc accctgacca tctctcggct ggaacccgag 300

gacttcgccg tgtactactg ccagcagtgg aacagcaacc cccccacctt cggccagggc 360

accaaggtcg aaatcaagcg tacggtggcc gccccctccg tgttcatctt cccccccctcc 420

gacgagcagc tgaagtccgg caccgcctcc gtggtgtgcc tgctgaataa cttctacccc 480

agagaggcca aggtgcagtg gaaggtggac aacgccctgc agtccgggaa ctcccaggag 540

agcgtgaccg agcaggacag caaggacagc acctacagcc tgagcagcac cctgaccctg 600

agcaaagccg actacgagaa gcacaaggtg tacgcctgcg aggtgaccca ccagggcctg 660

agctcccccg tcaccaagag cttcaacagg ggggagtgt 699

<210> 71
<211> 233
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized light chain of M30

<400> 71

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Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1               5                  10                  15

Gly Ala Tyr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
            20                  25                  30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Arg
        35                  40                  45

Leu Ile Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg
    50                  55                  60

Leu Leu Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg
65                  70                  75                  80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg
                85                  90                  95

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Asn Ser
            100                 105                 110

Asn Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
        115                 120                 125

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
    130                 135                 140

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

Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
                165                 170                 175

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
            180                 185                 190

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
        195                 200                 205

Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
    210                 215                 220

Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230
```

<210> 72
<211> 699
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized light chain of M30

<400> 72
atggtgctgc agacccaggt gttcatctcc ctgctgctgt ggatctccgg cgcatatggc 60

gagatcgtgc tgacccagag ccccgccacc ctgtctctga gccctggcga gagagccacc 120

ctgagctgca gagccagcag caggctgatc tacatgcact ggtatcagca gaagcccggc 180

caggccccca gactgtggat ctacgccacc agcaacctgg ccagcggcat ccccgccaga 240

ttttctggca gcggcagcgg caccgactac accctgacca tcagccgcct ggaacccgag 300

gacttcgccg tgtactactg ccagcagtgg aacagcaacc cccccacctt cggccagggc 360

accaaggtcg aaatcaagcg tacggtggcc gccccctccg tgttcatctt cccccccctcc 420

gacgagcagc tgaagtccgg caccgcctcc gtggtgtgcc tgctgaataa cttctacccc 480

agagaggcca aggtgcagtg gaaggtggac aacgccctgc agtccgggaa ctcccaggag 540

agcgtgaccg agcaggacag caaggacagc acctacagcc tgagcagcac cctgaccctg 600

agcaaagccg actacgagaa gcacaaggtg tacgcctgcg aggtgaccca ccagggcctg 660

agctcccccg tcaccaagag cttcaacagg ggggagtgt 699

<210> 73
<211> 233
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized light chain of M30

<400> 73

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

Gly Ala Tyr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Arg
35 40 45

Leu Ile Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg
50 55 60

Leu Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg
65 70 75 80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Arg
85 90 95

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Asn Ser
100 105 110

Asn Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
115 120 125

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
130 135 140

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

Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
165 170 175

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
180 185 190

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
195 200 205

Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
210 215 220

Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 74
<211> 699
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized light chain of M30

<400> 74
atggtgctgc agacccaggt gttcatctcc ctgctgctgt ggatctccgg cgcatatggc 60

cagatcgtgc tgtcccagag ccccgccacc ctgtctctga gccctggcga gagagccacc 120

ctgacctgca gagccagcag caggctgatc tacatgcact ggtatcagca gaagcccggc 180

agcgccccca agctgtggat ctacgccacc agcaacctgg ccagcggcat ccccgccaga 240

ttttctggca gcggcagcgg caccagctac accctgacca tctcccgcct ggaacccgag 300

gacttcgccg tgtactactg ccagcagtgg aacagcaacc cccccacctt cggccagggc 360

accaaggtcg aaatcaagcg tacggtggcc gccccctccg tgttcatctt cccccccctcc 420

gacgagcagc tgaagtccgg caccgcctcc gtggtgtgcc tgctgaataa cttctacccc 480

agagaggcca aggtgcagtg gaaggtggac aacgccctgc agtccgggaa ctcccaggag 540

agcgtgaccg agcaggacag caaggacagc acctacagcc tgagcagcac cctgaccctg 600

agcaaagccg actacgagaa gcacaaggtg tacgcctgcg aggtgaccca ccagggcctg 660

agctcccccg tcaccaagag cttcaacagg ggggagtgt 699

<210> 75
<211> 233
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized light chain of M30

<400> 75

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Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1               5                  10                  15

Gly Ala Tyr Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Thr Leu Ser
            20                  25                  30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys Arg Ala Ser Ser Arg
        35                  40                  45

Leu Ile Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ala Pro Lys
    50                  55                  60

Leu Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg
65                  70                  75                  80

Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Thr Leu Thr Ile Ser Arg
                85                  90                  95

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Asn Ser
            100                 105                 110

Asn Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
        115                 120                 125

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
    130                 135                 140

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

Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
                165                 170                 175

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
            180                 185                 190

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
        195                 200                 205

Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
    210                 215                 220

Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230
```

<210> 76
<211> 699
<212> DNA

<213> Artificial Sequence

<220>
<223> Humanized light chain of M30

<400> 76
atggtgctgc agacccaggt gttcatctcc ctgctgctgt ggatctccgg cgcatatggc 60

gagatcgtgc tgacccagag ccccgccacc ctgtctctga gccctggcga gagagccacc 120

ctgagctgca gagccagcag ccgcctgatc tacatgcact ggtatcagca gaagcccggc 180

caggccccca gacctctgat ctacgccacc agcaacctgg ccagcggcat ccccgccaga 240

ttttctggca gcggcagcgg caccgacttc accctgacca tcagcagcct ggaacccgag 300

gacttcgccg tgtactactg ccagcagtgg aacagcaacc cccccacctt cggccagggc 360

accaaggtcg aaatcaagcg tacggtggcc gcccccctccg tgttcatctt cccccccctcc 420

gacgagcagc tgaagtccgg caccgcctcc gtggtgtgcc tgctgaataa cttctacccc 480

agagaggcca aggtgcagtg gaaggtggac aacgccctgc agtccgggaa ctcccaggag 540

agcgtgaccg agcaggacag caaggacagc acctacagcc tgagcagcac cctgaccctg 600

agcaaagccg actacgagaa gcacaaggtg tacgcctgcg aggtgaccca ccagggcctg 660

agctcccccg tcaccaagag cttcaacagg ggggagtgt 699

<210> 77
<211> 233
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized light chain of M30

<400> 77

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

Gly Ala Tyr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Arg
35 40 45

Leu Ile Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg
50 55 60

Pro Leu Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg
65 70 75 80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
85 90 95

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Asn Ser
100 105 110

Asn Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
115 120 125

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
130 135 140

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

Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
165 170 175

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
180 185 190

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
195 200 205

Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
210 215 220

Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 78
<211> 699
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized light chain of M30

<400> 78
atggtgctgc agacccaggt gttcatctcc ctgctgctgt ggatctccgg cgcatatggc 60

cagatcgtgc tgtcccagag ccccgccacc ctgtctctga gccctggcga gagagccacc 120

ctgacctgca gagccagcag caggctgatc tacatgcact ggtatcagca gaagcccggc 180

agcgccccca agccttggat ctacgccacc agcaacctgg ccagcggcat ccccgccaga 240

ttttctggca gcggcagcgg caccagctac accctgacca tctcccgcct ggaacccgag 300

gacttcgccg tgtactactg ccagcagtgg aacagcaacc cccccacctt cggccagggc 360

accaaggtcg aaatcaagcg tacggtggcc gccccctccg tgttcatctt cccccccctcc 420

gacgagcagc tgaagtccgg caccgcctcc gtggtgtgcc tgctgaataa cttctacccc 480

agagaggcca aggtgcagtg gaaggtggac aacgccctgc agtccgggaa ctcccaggag 540

agcgtgaccg agcaggacag caaggacagc acctacagcc tgagcagcac cctgaccctg 600

agcaaagccg actacgagaa gcacaaggtg tacgcctgcg aggtgaccca ccagggcctg 660

agctcccccg tcaccaagag cttcaacagg ggggagtgt 699

<210> 79

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

<220>
<223> Humanized light chain of M30

<400> 79

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Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1               5                  10                  15

Gly Ala Tyr Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Thr Leu Ser
            20                  25                  30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Thr Cys Arg Ala Ser Ser Arg
        35                  40                  45

Leu Ile Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ala Pro Lys
    50                  55                  60

Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg
65                  70                  75                  80

Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Thr Leu Thr Ile Ser Arg
                85                  90                  95

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Asn Ser
            100                 105                 110

Asn Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
        115                 120                 125

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
    130                 135                 140

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

Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
                165                 170                 175

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
            180                 185                 190

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
        195                 200                 205

Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
    210                 215                 220

Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230
```

<210> 80
<211> 699
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized light chain of M30

<400> 80
atggtgctgc agacccaggt gttcatctcc ctgctgctgt ggatctccgg cgcatatggc 60

gagatcgtgc tgacccagag ccccgccacc ctgtctctga gccctggcga gagagccacc 120

ctgagctgca gagccagcag ccgcctgatc tacatgcact ggtatcagca gaagcccggc 180

caggccccca gacctctgat ctacgccacc agcaacctgg ccagcggcat ccccgccaga 240

ttttctggca gcggcagcgg caccgacttc accctgacca tcagccgcct ggaacccgag 300

gacttcgccg tgtactactg ccagcagtgg aacagcaacc cccccacctt cggccagggc 360

accaaggtcg aaatcaagcg tacggtggcc gcccccctccg tgttcatctt cccccccctcc 420

gacgagcagc tgaagtccgg caccgcctcc gtggtgtgcc tgctgaataa cttctacccc 480

agagaggcca aggtgcagtg gaaggtggac aacgccctgc agtccgggaa ctcccaggag 540

agcgtgaccg agcaggacag caaggacagc acctacagcc tgagcagcac cctgaccctg 600

agcaaagccg actacgagaa gcacaaggtg tacgcctgcg aggtgaccca ccagggcctg 660

agctcccccg tcaccaagag cttcaacagg ggggagtgt 699

<210> 81
<211> 233
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized light chain of M30

<400> 81

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

Gly Ala Tyr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Arg
35 40 45

Leu Ile Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg
50 55 60

Pro Leu Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg
65 70 75 80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg
85 90 95

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Asn Ser
100 105 110

Asn Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
115 120 125

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
130 135 140

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

Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
165 170 175

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
180 185 190

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
195 200 205

Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
210 215 220

Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 82
<211> 699
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized light chain of M30

<400> 82
atggtgctgc agacccaggt gttcatctcc ctgctgctgt ggatctccgg cgcatatggc 60

gagatcgtgc tgacccagag ccccgccacc ctgtctctga gccctggcga gagagccacc 120

ctgagctgca gagccagcag ccgcctgatc tacatgcact ggtatcagca gaagcccggc 180

caggccccca gacctctgat ctacgccacc agcaacctgg ccagcggcat ccccgccaga 240

ttttctggca gcggcagcgg caccgactac accctgacca tcagccgcct ggaacccgag 300

gacttcgccg tgtactactg ccagcagtgg aacagcaacc cccccacctt cggccagggc 360

accaaggtcg aaatcaagcg tacggtggcc gccccctccg tgttcatctt cccccccctcc 420

gacgagcagc tgaagtccgg caccgcctcc gtggtgtgcc tgctgaataa cttctacccc 480

agagaggcca aggtgcagtg gaaggtggac aacgccctgc agtccgggaa ctcccaggag 540

agcgtgaccg agcaggacag caaggacagc acctacagcc tgagcagcac cctgaccctg 600

agcaaagccg actacgagaa gcacaaggtg tacgcctgcg aggtgaccca ccagggcctg 660

agctcccccg tcaccaagag cttcaacagg ggggagtgt 699

<210> 83
<211> 233
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized light chain of M30

<400> 83

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

Gly Ala Tyr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Arg
35 40 45

Leu Ile Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg
50 55 60

Pro Leu Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg
65 70 75 80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Arg
85 90 95

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Asn Ser
100 105 110

Asn Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
115 120 125

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
130 135 140

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

Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
165 170 175

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
180 185 190

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
195 200 205

Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
210 215 220

Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 84
<211> 1413
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized heavy chain of M30

<400> 84
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagccag 60

gtgcagctgg tgcagtctgg cgccgaagtg aagaaacccg gcagcagcgt gaaggtgtcc 120

tgcaaggcca gcggctacac cttcaccaac tacgtgatgc actgggtgcg ccaggcccct 180

gggcagggac tggaatggat gggctacatc aacccctaca acgacgacgt gaagtacaac 240

gagaagttca agggcagagt gaccatcacc gccgacgaga gcaccagcac cgcctacatg 300

gaactgagca gcctgcggag cgaggacacc gccgtgtact actgcgccag atggggctac 360

tacggcagcc ccctgtacta cttcgactac tggggccagg gcaccctggt gacagtcagc 420

tcagcctcca ccaagggccc aagcgtcttc cccctggcac cctcctccaa gagcacctct 480

ggcggcacag ccgccctggg ctgcctggtc aaggactact tccccgaacc cgtgaccgtg 540

agctggaact caggcgccct gaccagcggc gtgcacacct tccccgctgt cctgcagtcc 600

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 660

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gagagttgag 720

cccaaatctt gtgacaaaac tcacacatgc ccaccctgcc cagcacctga actcctgggg 780

ggaccctcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 840

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 900

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccccggga ggagcagtac 960

aacagcacgt accgggtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 1020

aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc 1080

tccaaagcca aaggccagcc ccgggaacca caggtgtaca ccctgccccc atcccgggag 1140

gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1200

atcgccgtgg agtgggagag caatggccag cccgagaaca actacaagac cacccctccc 1260

gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1320

tggcagcagg gcaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1380

acccagaaga gcctctccct gtctcccggc aaa 1413

<210> 85
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized heavy chain of M30

<400> 85

```
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45

Thr Asn Tyr Val Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
    50                  55                  60

Glu Trp Met Gly Tyr Ile Asn Pro Tyr Asn Asp Asp Val Lys Tyr Asn
65                  70                  75                  80

Glu Lys Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser
                85                  90                  95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Arg Trp Gly Tyr Tyr Gly Ser Pro Leu Tyr Tyr Phe
        115                 120                 125

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
    130                 135                 140

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145                 150                 155                 160

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
                165                 170                 175

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            180                 185                 190

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
        195                 200                 205

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    210                 215                 220

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
225                 230                 235                 240

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255
```

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

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

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

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

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

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

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

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
370 375 380

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

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

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

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

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

Leu Ser Leu Ser Pro Gly Lys
465 470

<210> 86
<211> 1413
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized heavy chain of M30

<400> 86
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagccag 60

gtgcagctgg tgcagtctgg cgccgaagtg aagaaacccg gcagcagcgt gaaggtgtcc 120

tgcaaggcca gcggctacac cttcaccaac tacgtgatgc actgggtgcg ccaggcccct 180

gggcagggac tggaatggat cggctacatc aacccctaca acgacgacgt gaagtacaac 240

gagaagttca agggcagagt gaccatcacc gccgacgaga gcaccagcac cgcctacatg 300

gaactgagca gcctgcggag cgaggacacc gccgtgtact actgcgccag atggggctac 360

tacggcagcc ccctgtacta cttcgactac tggggccagg gcaccctggt gacagtcagc 420

tcagcctcca ccaagggccc aagcgtcttc cccctggcac cctcctccaa gagcacctct 480

ggcggcacag ccgccctggg ctgcctggtc aaggactact tccccgaacc cgtgaccgtg 540

agctggaact caggcgccct gaccagcggc gtgcacacct tccccgctgt cctgcagtcc 600

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 660

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gagagttgag 720

cccaaatctt gtgacaaaac tcacacatgc ccaccctgcc cagcacctga actcctgggg 780

ggaccctcag tcttcctctt cccccccaaaa cccaaggaca ccctcatgat ctcccggacc 840

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 900

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccccggga ggagcagtac 960

aacagcacgt accgggtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 1020

aaggagtaca agtgcaaggt ctccaacaaa gccctcccag cccccatcga gaaaaccatc 1080

tccaaagcca aaggccagcc ccgggaacca caggtgtaca ccctgccccc atcccgggag 1140

gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1200

atcgccgtgg agtgggagag caatggccag cccgagaaca actacaagac cacccctccc 1260

gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1320

tggcagcagg gcaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1380

acccagaaga gcctctccct gtctcccggc aaa 1413

<210> 87
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized heavy chain of M30

<400> 87

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

```
Thr Asn Tyr Val Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
    50                  55                  60

Glu Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Asp Val Lys Tyr Asn
65                  70                  75                  80

Glu Lys Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser
                85                  90                  95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Arg Trp Gly Tyr Tyr Gly Ser Pro Leu Tyr Tyr Phe
        115                 120                 125

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
    130                 135                 140

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145                 150                 155                 160

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
                165                 170                 175

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            180                 185                 190

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
        195                 200                 205

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    210                 215                 220

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
225                 230                 235                 240

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

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

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

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

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305                 310                 315                 320
```

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

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

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

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
370 375 380

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

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

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

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

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

Leu Ser Leu Ser Pro Gly Lys
465 470

<210> 88
<211> 1413
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized heavy chain of M30

<400> 88
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgag 60

gtgcagctgg tgcagtctgg cgccgaagtg aagaaacccg gcagcagcgt gaaggtgtcc 120

tgcaaggcca gcggctacac cttcaccaac tacgtgatgc actgggtgaa acaggcccct 180

gggcagggcc tggaatggat cggctacatc aacccctaca acgacgacgt gaagtacaac 240

gagaagttca agggcaaggc caccatcacc gccgacgaga gcaccagcac cgcctacatg 300

gaactgagca gcctgcggag cgaggacacc gccgtgtact actgcgccag atggggctac 360

tacggcagcc ccctgtacta cttcgactac tggggccagg gcaccctggt gacagtcagc 420

tcagcctcca ccaagggccc aagcgtcttc cccctggcac cctcctccaa gagcacctct 480

ggcggcacag ccgccctggg ctgcctggtc aaggactact tccccgaacc cgtgaccgtg 540

agctggaact caggcgccct gaccagcggc gtgcacacct tccccgctgt cctgcagtcc 600

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 660

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gagagttgag 720

cccaaatctt gtgacaaaac tcacacatgc ccaccctgcc cagcacctga actcctgggg 780

ggaccctcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 840

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 900

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccccggga ggagcagtac 960

aacagcacgt accgggtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 1020

aaggagtaca agtgcaaggt ctccaacaaa gccctcccag cccccatcga gaaaaccatc 1080

tccaaagcca aaggccagcc ccgggaacca caggtgtaca ccctgccccc atcccgggag 1140

gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1200

atcgccgtgg agtgggagag caatggccag cccgagaaca actacaagac cacccctccc 1260

gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1320

tggcagcagg gcaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1380

acccagaaga gcctctccct gtctcccggc aaa 1413

<210> 89
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized heavy chain of M30

<400> 89

Met Lys His Leu Trp Phe Phe Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Thr Asn Tyr Val Met His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu
50 55 60

Glu Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Asp Val Lys Tyr Asn
65 70 75 80

Glu Lys Phe Lys Gly Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Ser
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Trp Gly Tyr Tyr Gly Ser Pro Leu Tyr Tyr Phe
115 120 125

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
130 135 140

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145 150 155 160

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
165 170 175

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
180 185 190

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
195 200 205

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
210 215 220

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
225 230 235 240

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
245 250 255

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

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

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

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

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

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

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

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
370 375 380

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

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

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

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

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

Leu Ser Leu Ser Pro Gly Lys
465 470

<210> 90
<211> 1413
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized heavy chain of M30

<400> 90
atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgag 60

gtgcagctgg tgcagtctgg cgccgaagtg aagaaacccg gcagcagcgt gaaggtgtcc 120

tgcaaggcca gcggctacac cttcaccaac tacgtgatgc actgggtcaa gcaggccct 180

gggcagggcc tggaatggat cggctacatc aacccctaca acgacgacgt gaagtacaac 240

gagaagttca agggcaaggc cacccagacc agcgacaaga gcaccagcac cgcctacatg 300

gaactgagca gcctgcggag cgaggacacc gccgtgtact actgcgccag atggggctac 360

tacggcagcc ccctgtacta cttcgactac tggggccagg gcaccctggt caccgtcagc 420

tcagcctcca ccaagggccc aagcgtcttc cccctggcac cctcctccaa gagcacctct 480

ggcggcacag ccgccctggg ctgcctggtc aaggactact tccccgaacc cgtgaccgtg 540

agctggaact caggcgccct gaccagcggc gtgcacacct tccccgctgt cctgcagtcc 600

tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcacccag 660

acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gagagttgag 720

cccaaatctt gtgacaaaac tcacacatgc ccaccctgcc cagcacctga actcctgggg 780

ggaccctcag tcttcctctt cccccaaaa cccaaggaca ccctcatgat ctcccggacc 840

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 900

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccccggga ggagcagtac 960

aacagcacgt accgggtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 1020

aaggagtaca agtgcaaggt ctccaacaaa gccctcccag cccccatcga gaaaaccatc 1080

tccaaagcca aaggccagcc ccgggaacca caggtgtaca ccctgccccc atcccgggag 1140

gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1200

atcgccgtgg agtgggagag caatggccag cccgagaaca actacaagac cacccctccc 1260

gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1320

tggcagcagg gcaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1380

acccagaaga gcctctccct gtctcccggc aaa 1413

<210> 91
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized heavy chain of M30

<400> 91

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Thr Asn Tyr Val Met His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu
50 55 60

Glu Trp Ile Gly Tyr Ile Asn Pro Tyr Asn Asp Asp Val Lys Tyr Asn
65 70 75 80

Glu Lys Phe Lys Gly Lys Ala Thr Gln Thr Ser Asp Lys Ser Thr Ser
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Trp Gly Tyr Tyr Gly Ser Pro Leu Tyr Tyr Phe
115 120 125

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
130 135 140

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145 150 155 160

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
165 170 175

```
Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            180                 185                 190

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
        195                 200                 205

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    210                 215                 220

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
225                 230                 235                 240

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

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

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

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

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

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

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

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

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
    370                 375                 380

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

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

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

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

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

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

<210> 92
<211> 5
<212> PRT
<213> Mus musculus

<400> 92

```
Asn Tyr Val Met His
1               5
```

<210> 93
<211> 17
<212> PRT
<213> Mus musculus

<400> 93

```
Tyr Ile Asn Pro Tyr Asn Asp Asp Val Lys Tyr Asn Glu Lys Phe Lys
1               5                   10                  15

Gly
```

<210> 94
<211> 13
<212> PRT
<213> Mus musculus

<400> 94

```
Trp Gly Tyr Tyr Gly Ser Pro Leu Tyr Tyr Phe Asp Tyr
1               5                   10
```

<210> 95
<211> 10
<212> PRT
<213> Mus musculus

<400> 95

```
Arg Ala Ser Ser Arg Leu Ile Tyr Met His
1               5                   10
```

<210> 96
<211> 7
<212> PRT
<213> Mus musculus

<400> 96

```
Ala Thr Ser Asn Leu Ala Ser
1               5
```

<210> 97
<211> 9
<212> PRT
<213> Mus musculus

<400> 97

Gln Gln Trp Asn Ser Asn Pro Pro Thr
1 5