SEQUENCE LISTING

<110> UCB Biopharma SPRL

<120> ANTIBODIES

<130> G0181-PCT

<150> GB1315487.7
<151> 2013-08-30

<160> 39

<170> PatentIn version 3.5

<210> 1
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CA019_969 Ab sequences CDR-L1

<400> 1

Leu Ala Ser Glu Asp Ile Tyr Asp Asn Leu Ala
1 5 10

<210> 2
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CA019_969 Ab sequences CDRL2

<400> 2

Tyr Ala Ser Ser Leu Gln Asp
1 5

<210> 3
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CA019_969 Ab sequences CDR-L3

<400> 3

Leu Gln Asp Ser Glu Tyr Pro Trp Thr
1 5

<210> 4
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CA019_969 Ab sequences CDR-H1

<400> 4

Gly Phe Ser Leu Thr Thr Tyr Gly Met Gly Val Gly

1 5 10

<210> 5
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CA019_969 Ab sequences CDR-H2

<400> 5

Asn Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Asn Pro Ser Leu Lys Asn
1 5 10 15

<210> 6
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CA019_969 Ab sequences CDR-H3

<400> 6

Ile Gly Pro Ile Lys Tyr Pro Thr Ala Pro Tyr Arg Tyr Phe Asp Phe
1 5 10 15

<210> 7
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Rat Ab 969 VL region

<400> 7

Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Glu Thr Val Ser Ile Glu Cys Leu Ala Ser Glu Asp Ile Tyr Asp Asn
20 25 30

Leu Ala Trp Tyr Gln Lys Lys Pro Gly Lys Ser Pro His Leu Leu Ile
35 40 45

Tyr Tyr Ala Ser Ser Leu Gln Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Glu Ser
65 70 75 80

Glu Asp Ala Ala Thr Tyr Phe Cys Leu Gln Asp Ser Glu Tyr Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 8
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Rat Ab 969 VL region

<400> 8
gacatccaga tgacacagtc tccagcttcc ctgtctgcat ctctgggaga aactgtctcc 60

atcgaatgtc tagcaagtga ggacatttac gataatttag cgtggtacca gaagaagcca 120

ggaaaatctc ctcacctcct catctattat gcaagtagct tgcaagatgg ggtcccatca 180

cggttcagtg gcagtggatc tggcacacag tattctctca aaatcaacag cctggaatct 240

gaagatgctg cgacttattt ctgtctacag gattctgagt atccgtggac gttcggtgga 300

ggcaccaagc tggaattgaa a 321

<210> 9
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> Rat Ab 969 VL region with signal sequence underlined and italicised

<400> 9

Met Gly Val Pro Thr Gln Leu Leu Val Leu Leu Leu Leu Trp Ile Thr
1 5 10 15

Asp Ala Ile Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
20 25 30

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

Ile Tyr Asp Asn Leu Ala Trp Tyr Gln Lys Lys Pro Gly Lys Ser Pro
50 55 60

His Leu Leu Ile Tyr Tyr Ala Ser Ser Leu Gln Asp Gly Val Pro Ser
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn
85 90 95

Ser Leu Glu Ser Glu Asp Ala Ala Thr Tyr Phe Cys Leu Gln Asp Ser
100 105 110

Glu Tyr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys
115 120 125

<210> 10
<211> 381

<212> DNA
<213> Artificial Sequence

<220>
<223> Rat Ab 969 VL region with signal sequence underlined and italicised

<400> 10
atgggtgtcc ccactcagct cttggtgttg ttgctgctgt ggattacaga tgccatatgt 60

gacatccaga tgacacagtc tccagcttcc ctgtctgcat ctctgggaga aactgtctcc 120

atcgaatgtc tagcaagtga ggacatttac gataatttag cgtggtacca gaagaagcca 180

ggaaaatctc ctcacctcct catctattat gcaagtagct tgcaagatgg ggtcccatca 240

cggttcagtg gcagtggatc tggcacacag tattctctca aaatcaacag cctggaatct 300

gaagatgctg cgacttattt ctgtctacag gattctgagt atccgtggac gttcggtgga 360

ggcaccaagc tggaattgaa a 381

<210> 11
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Rat Ab 969 VH region

<400> 11

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

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

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

Trp Leu Ala Asn Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Asn Arg Leu Thr Ile Ser Lys Asp Thr Ser Asn Asn Gln Ala
65 70 75 80

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

Cys Ala Arg Ile Gly Pro Ile Lys Tyr Pro Thr Ala Pro Tyr Arg Tyr
100 105 110

Phe Asp Phe Trp Gly Pro Gly Thr Met Val Thr Val Ser
115 120 125

<210> 12
<211> 375
<212> DNA

<213> Artificial Sequence

<220>
<223> Rat Ab 969 VH region

<400> 12
caggttactc tgaaagagtc tggccctggg atattgcagc cctcccagac cctcagtctg 60

acttgcactt tctctgggtt ttcactgacc acttatggta tgggtgtggg ctggattcgt 120

cagccttcag ggaagggtct ggagtggctg gcaaacattt ggtgggatga tgataagtat 180

tacaatccat ctctgaaaaa ccggctcaca atctccaagg acacctccaa caaccaagca 240

ttcctcaagc tcaccaatgt acacacttca gattctgcca catactactg tgctcggata 300

gggccgatta aatacccgac ggccccctac cggtactttg acttctgggg cccaggaacc 360

atggtcaccg tctcg 375

<210> 13
<211> 144
<212> PRT
<213> Artificial Sequence

<220>
<223> Rat Ab 969 VH region with signal sequence underlined and italicised

<400> 13

Met Asp Arg Leu Thr Ser Ser Phe Leu Leu Leu Ile Val Pro Ala Tyr
1 5 10 15

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

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

Thr Thr Tyr Gly Met Gly Val Gly Trp Ile Arg Gln Pro Ser Gly Lys
50 55 60

Gly Leu Glu Trp Leu Ala Asn Ile Trp Trp Asp Asp Asp Lys Tyr Tyr
65 70 75 80

Asn Pro Ser Leu Lys Asn Arg Leu Thr Ile Ser Lys Asp Thr Ser Asn
85 90 95

Asn Gln Ala Phe Leu Lys Leu Thr Asn Val His Thr Ser Asp Ser Ala
100 105 110

Thr Tyr Tyr Cys Ala Arg Ile Gly Pro Ile Lys Tyr Pro Thr Ala Pro
115 120 125

Tyr Arg Tyr Phe Asp Phe Trp Gly Pro Gly Thr Met Val Thr Val Ser
130 135 140

<210> 14
<211> 432
<212> DNA
<213> Artificial Sequence

<220>
<223> Rat Ab 969 VH region with signal sequence underlined and italicised

<400> 14
atggacaggc ttacttcctc attcctactg ctgattgtcc ctgcatatgt cctgtctcag 60

gttactctga aagagtctgg ccctgggata ttgcagccct cccagaccct cagtctgact 120

tgcactttct ctgggttttc actgaccact tatggtatgg gtgtgggctg gattcgtcag 180

ccttcaggga agggtctgga gtggctggca aacatttggt gggatgatga taagtattac 240

aatccatctc tgaaaaaccg gctcacaatc tccaaggaca cctccaacaa ccaagcattc 300

ctcaagctca ccaatgtaca cacttcagat tctgccacat actactgtgc tcggataggg 360

ccgattaaat acccgacggc cccctaccgg tactttgact tctggggccc aggaaccatg 420

gtcaccgtct cg 432

<210> 15
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> 969 gL7 V-region

<400> 15

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Leu Ala Ser Glu Asp Ile Tyr Asp Asn
20 25 30

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

Tyr Tyr Ala Ser Ser Leu Gln Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Ser Glu Tyr Pro Trp
85 90 95

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

<210> 16
<211> 321
<212> DNA

<213> Artificial Sequence

<220>
<223> 969 gL7 V-region

<400> 16
gacatacaga tgactcagtc accctcaagc ctgagtgcca gtgtgggaga cagggtgaca 60

atcacctgtc tggcctccga ggatatctac gataacctgg catggtatca gcagaaacct 120

ggaaaggctc ccaagctcct gatttattat gcctcctctc tccaagacgg cgttccatct 180

cggttcagcg gaagcggctc cgggacggat tacacactga caattagctc tctgcaaccg 240

gaggattttg ctacttacta ctgcctgcaa gactccgaat acccatggac cttcggtggt 300

ggcaccaaag tggaaatcaa g 321

<210> 17
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> 969 gL7 V-region with signal sequence underlined and italicized

<400> 17

Met Ser Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr
1 5 10 15

Asp Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

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

Ile Tyr Asp Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
50 55 60

Lys Leu Leu Ile Tyr Tyr Ala Ser Ser Leu Gln Asp Gly Val Pro Ser
65 70 75 80

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

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Ser
100 105 110

Glu Tyr Pro Trp Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
115 120 125

<210> 18
<211> 381
<212> DNA
<213> Artificial Sequence

<220>
<223> 969 gL7 V-region with signal sequence underlined and italicized

<400> 18
atgagcgtgc ctactcaagt cttggggctg ctcttgcttt ggcttaccga cgcaagatgc 60

gacatacaga tgactcagtc accctcaagc ctgagtgcca gtgtgggaga cagggtgaca 120

atcacctgtc tggcctccga ggatatctac gataacctgg catggtatca gcagaaacct 180

ggaaaggctc ccaagctcct gatttattat gcctcctctc tccaagacgg cgttccatct 240

cggttcagcg gaagcggctc cgggacggat tacacactga caattagctc tctgcaaccg 300

gaggattttg ctacttacta ctgcctgcaa gactccgaat acccatggac cttcggtggt 360

ggcaccaaag tggaaatcaa g 381

<210> 19
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> 969 gL7 light chain (V + constant)

<400> 19

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Leu Ala Ser Glu Asp Ile Tyr Asp Asn
20 25 30

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

Tyr Tyr Ala Ser Ser Leu Gln Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Ser Glu Tyr Pro Trp
85 90 95

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

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

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

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser

165 170 175

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

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

Phe Asn Arg Gly Glu Cys
210

<210> 20
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> 969 gL7 light chain (V + constant)

<400> 20
gacatacaga tgactcagtc accctcaagc ctgagtgcca gtgtgggaga cagggtgaca 60

atcacctgtc tggcctccga ggatatctac gataacctgg catggtatca gcagaaacct 120

ggaaaggctc ccaagctcct gatttattat gcctcctctc tccaagacgg cgttccatct 180

cggttcagcg gaagcggctc cgggacggat tacacactga caattagctc tctgcaaccg 240

gaggattttg ctacttacta ctgcctgcaa gactccgaat acccatggac cttcggtggt 300

ggcaccaaag tggaaatcaa gcgtacggta gcggccccat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

<210> 21
<211> 234
<212> PRT
<213> Artificial Sequence

<220>
<223> 969 gL7 light chain (V + constant) with signal sequence
underlined and italicized

<400> 21

Met Ser Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr
1 5 10 15

Asp Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

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

```
Ile Tyr Asp Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
    50                  55                  60

Lys Leu Leu Ile Tyr Tyr Ala Ser Ser Leu Gln Asp Gly Val Pro Ser
65                  70                  75                  80

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

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Ser
            100                 105                 110

Glu Tyr Pro Trp Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
        115                 120                 125

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

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

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

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

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

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

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


<210>  22
<211>  702
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  969 gL7 light chain (V + constant) with signal sequence
       underlined and italicized

<400>  22
atgagcgtgc ctactcaagt cttggggctg ctcttgcttt ggcttaccga cgcaagatgc       60

gacatacaga tgactcagtc accctcaagc ctgagtgcca gtgtgggaga cagggtgaca      120

atcacctgtc tggcctccga ggatatctac gataacctgg catggtatca gcagaaacct      180

ggaaaggctc ccaagctcct gatttattat gcctcctctc tccaagacgg cgttccatct      240
```

cggttcagcg gaagcggctc cgggacggat tacacactga caattagctc tctgcaaccg 300

gaggattttg ctacttacta ctgcctgcaa gactccgaat acccatggac cttcggtggt 360

ggcaccaaag tggaaatcaa gcgtacggta gcggccccat ctgtcttcat cttcccgcca 420

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 480

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 540

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 600

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 660

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 702

<210> 23
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> 969 gH2 V-region

<400> 23

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

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

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

Trp Leu Ala Asn Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Asn Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Gly Pro Ile Lys Tyr Pro Thr Ala Pro Tyr Arg Tyr
100 105 110

Phe Asp Phe Trp Gly Gln Gly Thr Met Val Thr Val Ser
115 120 125

<210> 24
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> 969 gH2 V-region

<400> 24

gaagtgacac tcaaggagtc tggacccgct ctggtgaaac caacccaaac actcactttg 60

acatgtactt ttagtggctt ctcattgact acctatggaa tgggcgtggg atggatcaga 120

cagccacctg gcaaggctct ggaatggctg gccaacatct ggtgggatga cgacaagtac 180

tataacccgt ccctgaaaaa ccggctgacc attagcaagg atacttctaa aaatcaagtg 240

gtgctgacca tgacaaatat ggatcccgtt gacaccgcaa cctactactg cgcccgcatt 300

ggtcccataa agtaccctac ggcaccttac cgatatttcg acttttgggg ccaagggaca 360

atggttactg tctcg 375

<210> 25
<211> 144
<212> PRT
<213> Artificial Sequence

<220>
<223> 969 gH2 V-region with signal sequence underlined and italicized

<400> 25

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

Val His Ser Glu Val Thr Leu Lys Glu Ser Gly Pro Ala Leu Val Lys
20 25 30

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

Thr Thr Tyr Gly Met Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys
50 55 60

Ala Leu Glu Trp Leu Ala Asn Ile Trp Trp Asp Asp Asp Lys Tyr Tyr
65 70 75 80

Asn Pro Ser Leu Lys Asn Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys
85 90 95

Asn Gln Val Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala
100 105 110

Thr Tyr Tyr Cys Ala Arg Ile Gly Pro Ile Lys Tyr Pro Thr Ala Pro
115 120 125

Tyr Arg Tyr Phe Asp Phe Trp Gly Gln Gly Thr Met Val Thr Val Ser
130 135 140

<210> 26
<211> 432
<212> DNA
<213> Artificial Sequence

<220>
<223> 969 gH2 V-region with signal sequence underlined and italicized

<400> 26
atggagtggt cctgggtgtt tctgttcttc ctgagtgtga ccaccggggt ccactccgaa 60

gtgacactca aggagtctgg acccgctctg gtgaaaccaa cccaaacact cactttgaca 120

tgtactttta gtggcttctc attgactacc tatggaatgg gcgtgggatg gatcagacag 180

ccacctggca aggctctgga atggctggcc aacatctggt gggatgacga caagtactat 240

aacccgtccc tgaaaaaccg gctgaccatt agcaaggata cttctaaaaa tcaagtggtg 300

ctgaccatga caaatatgga tcccgttgac accgcaacct actactgcgc ccgcattggt 360

cccataaagt accctacggc accttaccga tatttcgact tttggggcca agggacaatg 420

gttactgtct cg 432

<210> 27
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> 969 gH2 heavy chain (V + constant - hu IgG4P)

<400> 27

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

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

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

Trp Leu Ala Asn Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Asn Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Gly Pro Ile Lys Tyr Pro Thr Ala Pro Tyr Arg Tyr
100 105 110

Phe Asp Phe Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser
115 120 125

Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr
130 135 140

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

```
Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
                165                 170                 175

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
            180                 185                 190

Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr
        195                 200                 205

Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val
    210                 215                 220

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
225                 230                 235                 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

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

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

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
                325                 330                 335

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

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

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

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

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
            420                 425                 430
```

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

Leu Ser Leu Gly Lys
450

<210> 28
<211> 1966
<212> DNA
<213> Artificial Sequence

<220>
<223> 969 gH2 heavy chain (V + constant - hu IgG4P, exons underlined)

<400> 28
gaagtgacac tcaaggagtc tggacccgct ctggtgaaac caacccaaac actcactttg 60

acatgtactt ttagtggctt ctcattgact acctatggaa tgggcgtggg atggatcaga 120

cagccacctg gcaaggctct ggaatggctg gccaacatct ggtgggatga cgacaagtac 180

tataacccgt ccctgaaaaa ccggctgacc attagcaagg atacttctaa aaatcaagtg 240

gtgctgacca tgacaaatat ggatcccgtt gacaccgcaa cctactactg cgcccgcatt 300

ggtcccataa agtaccctac ggcaccttac cgatatttcg acttttgggg ccaagggaca 360

atggttactg tctcgagcgc ttctacaaag ggcccatccg tcttcccccc ggcgccctgc 420

tccaggagca cctccgagag cacagccgcc ctgggctgcc tggtcaagga ctacttcccc 480

gaaccggtga cggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccg 540

gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtgaccgt gccctccagc 600

agcttgggca cgaagaccta cacctgcaac gtagatcaca agcccagcaa caccaaggtg 660

gacaagagag ttggtgagag gccagcacag ggagggaggg tgtctgctgg aagccaggct 720

cagccctcct gcctggacgc accccggctg tgcagcccca gcccagggca gcaaggcatg 780

ccccatctgt ctcctcaccc ggaggcctct gaccacccca ctcatgccca gggagagggt 840

cttctggatt tttccaccag gctccgggca gccacaggct ggatgcccct accccaggcc 900

ctgcgcatac aggggcaggt gctgcgctca gacctgccaa gagccatatc cgggaggacc 960

ctgcccctga cctaagccca ccccaaaggc caaactctcc actccctcag ctcagacacc 1020

ttctctcctc ccagatctga gtaactccca atcttctctc tgcagagtcc aaatatggtc 1080

ccccatgccc accatgccca ggtaagccaa cccaggcctc gccctccagc tcaaggcggg 1140

acaggtgccc tagagtagcc tgcatccagg gacaggcccc agccgggtgc tgacgcatcc 1200

acctccatct cttcctcagc acctgagttc ctgggggggac catcagtctt cctgttcccc 1260

ccaaaaccca aggacactct catgatctcc cggacccctg aggtcacgtg cgtggtggtg 1320

gacgtgagcc aggaagaccc cgaggtccag ttcaactggt acgtggatgg cgtggaggtg 1380

cataatgcca agacaaagcc gcgggaggag cagttcaaca gcacgtaccg tgtggtcagc 1440

gtcctcaccg tcctgcacca ggactggctg aacggcaagg agtacaagtg caaggtctcc 1500

aacaaaggcc tcccgtcctc catcgagaaa accatctcca aagccaaagg tgggacccac 1560

ggggtgcgag ggccacatgg acagaggtca gctcggccca ccctctgccc tgggagtgac 1620

cgctgtgcca acctctgtcc ctacagggca gccccgagag ccacaggtgt acaccctgcc 1680

cccatcccag gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt 1740

ctaccccagc gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa 1800

gaccacgcct cccgtgctgg actccgacgg ctccttcttc ctctacagca ggctaaccgt 1860

ggacaagagc aggtggcagg aggggaatgt cttctcatgc tccgtgatgc atgaggctct 1920

gcacaaccac tacacacaga agagcctctc cctgtctctg ggtaaa 1966

<210> 29
<211> 472
<212> PRT
<213> Artificial Sequence

<220>
<223> 969 gH2 heavy chain (V + constant - hu IgG4P) with signal sequence underlined and italicised

<400> 29

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

Val His Ser Glu Val Thr Leu Lys Glu Ser Gly Pro Ala Leu Val Lys
20 25 30

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

Thr Thr Tyr Gly Met Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys
50 55 60

Ala Leu Glu Trp Leu Ala Asn Ile Trp Trp Asp Asp Asp Lys Tyr Tyr
65 70 75 80

Asn Pro Ser Leu Lys Asn Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys
85 90 95

Asn Gln Val Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala
100 105 110

Thr Tyr Tyr Cys Ala Arg Ile Gly Pro Ile Lys Tyr Pro Thr Ala Pro
115 120 125

Tyr Arg Tyr Phe Asp Phe Trp Gly Gln Gly Thr Met Val Thr Val Ser
130 135 140

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

```
Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
                165                 170                 175

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
            180                 185                 190

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

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys
    210                 215                 220

Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp
225                 230                 235                 240

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Leu Ser Leu Ser Leu Gly Lys
465 470

<210> 30
<211> 2023
<212> DNA
<213> Artificial Sequence

<220>
<223> 969 gH2 heavy chain (V + constant - hu IgG4P, exons underlined) with signal sequence underlined and italicized

<400> 30
atggagtggt cctgggtgtt tctgttcttc ctgagtgtga ccaccggggt ccactccgaa 60

gtgacactca aggagtctgg acccgctctg gtgaaaccaa cccaaacact cactttgaca 120

tgtacttta gtggcttctc attgactacc tatggaatgg gcgtgggatg gatcagacag 180

ccacctggca aggctctgga atggctggcc aacatctggt gggatgacga caagtactat 240

aacccgtccc tgaaaaaccg gctgaccatt agcaaggata cttctaaaaa tcaagtggtg 300

ctgaccatga caaatatgga tcccgttgac accgcaacct actactgcgc ccgcattggt 360

cccataaagt accctacggc accttaccga tatttcgact tttggggcca agggacaatg 420

gttactgtct cgagcgcttc tacaaagggc ccatccgtct tccccctggc gccctgctcc 480

aggagcacct ccgagagcac agccgccctg ggctgcctgg tcaaggacta cttccccgaa 540

ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct 600

gtcctacagt cctcaggact ctactccctc agcagcgtgg tgaccgtgcc ctccagcagc 660

ttgggcacga agacctacac ctgcaacgta gatcacaagc ccagcaacac caaggtggac 720

aagagagttg gtgagaggcc agcacaggga gggagggtgt ctgctggaag ccaggctcag 780

ccctcctgcc tggacgcacc ccggctgtgc agccccagcc cagggcagca aggcatgccc 840

catctgtctc ctcacccgga ggcctctgac caccccactc atgcccaggg agagggtctt 900

ctggattttt ccaccaggct ccgggcagcc acaggctgga tgcccctacc ccaggccctg 960

cgcatacagg ggcaggtgct gcgctcagac ctgccaagag ccatatccgg gaggaccctg 1020

cccctgacct aagcccaccc caaaggccaa actctccact ccctcagctc agacaccttc 1080

tctcctccca gatctgagta actcccaatc ttctctctgc agagtccaaa tatggtcccc 1140

catgcccacc atgcccaggt aagccaaccc aggcctcgcc ctccagctca aggcgggaca 1200

ggtgccctag agtagcctgc atccagggac aggccccagc cgggtgctga cgcatccacc 1260

tccatctctt cctcagcacc tgagttcctg gggggaccat cagtcttcct gttcccccca 1320

aaacccaagg acactctcat gatctcccgg acccctgagg tcacgtgcgt ggtggtggac 1380

gtgagccagg aagaccccga ggtccagttc aactggtacg tggatggcgt ggaggtgcat 1440

aatgccaaga caaagccgcg ggaggagcag ttcaacagca cgtaccgtgt ggtcagcgtc 1500

ctcaccgtcc tgcaccagga ctggctgaac ggcaaggagt acaagtgcaa ggtctccaac 1560

aaaggcctcc cgtcctccat cgagaaaacc atctccaaag ccaaaggtgg gacccacggg 1620

gtgcgagggc cacatggaca gaggtcagct cggcccaccc tctgccctgg gagtgaccgc 1680

tgtgccaacc tctgtcccta cagggcagcc ccgagagcca caggtgtaca ccctgccccc 1740

atcccaggag gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta 1800

ccccagcgac atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac 1860

cacgcctccc gtgctggact ccgacggctc cttcttcctc tacagcaggc taaccgtgga 1920

caagagcagg tggcaggagg ggaatgtctt ctcatgctcc gtgatgcatg aggctctgca 1980

caaccactac acacagaaga gcctctccct gtctctgggt aaa 2023

<210> 31
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Human VK1 2-1-(1) O12 JK4 acceptor framework

<400> 31

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu
85 90 95

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

<210> 32
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Human VK1 2-1-(1) O12 JK4 acceptor framework

<400> 32
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagta ccctctcac tttcggcgga 300

gggaccaagg tggagatcaa a 321

<210> 33
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> Human VH2 3-1 2-70 JH3 acceptor framework

<400> 33

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

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

Trp Leu Ala Arg Ile Asp Trp Asp Asp Asp Lys Phe Tyr Ser Thr Ser
50 55 60

Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr
100 105 110

Val Ser

<210> 34
<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<223> Human VH2 3-1 2-70 JH3 acceptor framework

<400> 34
caggtcacct tgaaggagtc tggtcctgcg ctggtgaaac ccacacagac cctcacactg 60

acctgcacct tctctgggtt ctcactcagc actagtggaa tgcgtgtgag ctggatccgt 120

cagcccccag ggaaggccct ggagtggctt gcacgcattg attgggatga tgataaattc 180

tacagcacat ctctgaagac caggctcacc atctccaagg acacctccaa aaaccaggtg 240

gtccttacaa tgaccaacat ggaccctgtg gacacagcca cgtattactg tgcacggata 300

gcttttgata tctggggcca agggacaatg gtcaccgtct ct 342

<210> 35
<211> 972
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence for CSF-1R

<400> 35

Met Gly Pro Gly Val Leu Leu Leu Leu Val Ala Thr Ala Trp His
1 5 10 15

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

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

Glu Trp Asp Gly Pro Pro Ser Pro His Trp Thr Leu Tyr Ser Asp Gly
50 55 60

Ser Ser Ser Ile Leu Ser Thr Asn Asn Ala Thr Phe Gln Asn Thr Gly
65 70 75 80

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

Ile His Leu Tyr Val Lys Asp Pro Ala Arg Pro Trp Asn Val Leu Ala
100 105 110

Gln Glu Val Val Val Phe Glu Asp Gln Asp Ala Leu Leu Pro Cys Leu
115 120 125

Leu Thr Asp Pro Val Leu Glu Ala Gly Val Ser Leu Val Arg Val Arg
130 135 140

Gly Arg Pro Leu Met Arg His Thr Asn Tyr Ser Phe Ser Pro Trp His
145 150 155 160

Gly Phe Thr Ile His Arg Ala Lys Phe Ile Gln Ser Gln Asp Tyr Gln
165 170 175

Cys Ser Ala Leu Met Gly Gly Arg Lys Val Met Ser Ile Ser Ile Arg
180 185 190

```
Leu Lys Val Gln Lys Val Ile Pro Gly Pro Pro Ala Leu Thr Leu Val
        195                 200                 205

Pro Ala Glu Leu Val Arg Ile Arg Gly Glu Ala Ala Gln Ile Val Cys
    210                 215                 220

Ser Ala Ser Ser Val Asp Val Asn Phe Asp Val Phe Leu Gln His Asn
225                 230                 235                 240

Asn Thr Lys Leu Ala Ile Pro Gln Gln Ser Asp Phe His Asn Asn Arg
                245                 250                 255

Tyr Gln Lys Val Leu Thr Leu Asn Leu Asp Gln Val Asp Phe Gln His
            260                 265                 270

Ala Gly Asn Tyr Ser Cys Val Ala Ser Asn Val Gln Gly Lys His Ser
        275                 280                 285

Thr Ser Met Phe Phe Arg Val Val Glu Ser Ala Tyr Leu Asn Leu Ser
    290                 295                 300

Ser Glu Gln Asn Leu Ile Gln Glu Val Thr Val Gly Glu Gly Leu Asn
305                 310                 315                 320

Leu Lys Val Met Val Glu Ala Tyr Pro Gly Leu Gln Gly Phe Asn Trp
                325                 330                 335

Thr Tyr Leu Gly Pro Phe Ser Asp His Gln Pro Glu Pro Lys Leu Ala
            340                 345                 350

Asn Ala Thr Thr Lys Asp Thr Tyr Arg His Thr Phe Thr Leu Ser Leu
        355                 360                 365

Pro Arg Leu Lys Pro Ser Glu Ala Gly Arg Tyr Ser Phe Leu Ala Arg
    370                 375                 380

Asn Pro Gly Gly Trp Arg Ala Leu Thr Phe Glu Leu Thr Leu Arg Tyr
385                 390                 395                 400

Pro Pro Glu Val Ser Val Ile Trp Thr Phe Ile Asn Gly Ser Gly Thr
                405                 410                 415

Leu Leu Cys Ala Ala Ser Gly Tyr Pro Gln Pro Asn Val Thr Trp Leu
            420                 425                 430

Gln Cys Ser Gly His Thr Asp Arg Cys Asp Glu Ala Gln Val Leu Gln
        435                 440                 445

Val Trp Asp Asp Pro Tyr Pro Glu Val Leu Ser Gln Glu Pro Phe His
    450                 455                 460
```

```
Lys Val Thr Val Gln Ser Leu Leu Thr Val Glu Thr Leu Glu His Asn
465                 470                 475                 480

Gln Thr Tyr Glu Cys Arg Ala His Asn Ser Val Gly Ser Gly Ser Trp
                485                 490                 495

Ala Phe Ile Pro Ile Ser Ala Gly Ala His Thr His Pro Pro Asp Glu
            500                 505                 510

Phe Leu Phe Thr Pro Val Val Val Ala Cys Met Ser Ile Met Ala Leu
        515                 520                 525

Leu Leu Leu Leu Leu Leu Leu Leu Leu Tyr Lys Tyr Lys Gln Lys Pro
    530                 535                 540

Lys Tyr Gln Val Arg Trp Lys Ile Ile Glu Ser Tyr Glu Gly Asn Ser
545                 550                 555                 560

Tyr Thr Phe Ile Asp Pro Thr Gln Leu Pro Tyr Asn Glu Lys Trp Glu
                565                 570                 575

Phe Pro Arg Asn Asn Leu Gln Phe Gly Lys Thr Leu Gly Ala Gly Ala
            580                 585                 590

Phe Gly Lys Val Val Glu Ala Thr Ala Phe Gly Leu Gly Lys Glu Asp
        595                 600                 605

Ala Val Leu Lys Val Ala Val Lys Met Leu Lys Ser Thr Ala His Ala
    610                 615                 620

Asp Glu Lys Glu Ala Leu Met Ser Glu Leu Lys Ile Met Ser His Leu
625                 630                 635                 640

Gly Gln His Glu Asn Ile Val Asn Leu Leu Gly Ala Cys Thr His Gly
                645                 650                 655

Gly Pro Val Leu Val Ile Thr Glu Tyr Cys Cys Tyr Gly Asp Leu Leu
            660                 665                 670

Asn Phe Leu Arg Arg Lys Ala Glu Ala Met Leu Gly Pro Ser Leu Ser
        675                 680                 685

Pro Gly Gln Asp Pro Glu Gly Gly Val Asp Tyr Lys Asn Ile His Leu
    690                 695                 700

Glu Lys Lys Tyr Val Arg Arg Asp Ser Gly Phe Ser Ser Gln Gly Val
705                 710                 715                 720

Asp Thr Tyr Val Glu Met Arg Pro Val Ser Thr Ser Ser Asn Asp Ser
                725                 730                 735
```

```
Phe Ser Glu Gln Asp Leu Asp Lys Glu Asp Gly Arg Pro Leu Glu Leu
            740                 745                 750

Arg Asp Leu Leu His Phe Ser Ser Gln Val Ala Gln Gly Met Ala Phe
        755                 760                 765

Leu Ala Ser Lys Asn Cys Ile His Arg Asp Val Ala Ala Arg Asn Val
    770                 775                 780

Leu Leu Thr Asn Gly His Val Ala Lys Ile Gly Asp Phe Gly Leu Ala
785                 790                 795                 800

Arg Asp Ile Met Asn Asp Ser Asn Tyr Ile Val Lys Gly Asn Ala Arg
                805                 810                 815

Leu Pro Val Lys Trp Met Ala Pro Glu Ser Ile Phe Asp Cys Val Tyr
            820                 825                 830

Thr Val Gln Ser Asp Val Trp Ser Tyr Gly Ile Leu Leu Trp Glu Ile
        835                 840                 845

Phe Ser Leu Gly Leu Asn Pro Tyr Pro Gly Ile Leu Val Asn Ser Lys
    850                 855                 860

Phe Tyr Lys Leu Val Lys Asp Gly Tyr Gln Met Ala Gln Pro Ala Phe
865                 870                 875                 880

Ala Pro Lys Asn Ile Tyr Ser Ile Met Gln Ala Cys Trp Ala Leu Glu
                885                 890                 895

Pro Thr His Arg Pro Thr Phe Gln Gln Ile Cys Ser Phe Leu Gln Glu
            900                 905                 910

Gln Ala Gln Glu Asp Arg Arg Glu Arg Asp Tyr Thr Asn Leu Pro Ser
        915                 920                 925

Ser Ser Arg Ser Gly Gly Ser Gly Ser Ser Ser Ser Glu Leu Glu Glu
    930                 935                 940

Glu Ser Ser Ser Glu His Leu Thr Cys Cys Glu Gln Gly Asp Ile Ala
945                 950                 955                 960

Gln Pro Leu Leu Gln Pro Asn Asn Tyr Gln Phe Cys
                965                 970


<210>  36
<211>  277
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Amino acid sequence for CSF-1R
```

<400> 36

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

Ala Thr Val Thr Leu Arg Cys Val Gly Asn Gly Ser Val Glu Trp Asp
            20                  25                  30

Gly Pro Pro Ser Pro His Trp Thr Leu Tyr Ser Asp Gly Ser Ser Ser
        35                  40                  45

Ile Leu Ser Thr Asn Asn Ala Thr Phe Gln Asn Thr Gly Thr Tyr Arg
    50                  55                  60

Cys Thr Glu Pro Gly Asp Pro Leu Gly Gly Ser Ala Ala Ile His Leu
65                  70                  75                  80

Tyr Val Lys Asp Pro Ala Arg Pro Trp Asn Val Leu Ala Gln Glu Val
                85                  90                  95

Val Val Phe Glu Asp Gln Asp Ala Leu Leu Pro Cys Leu Leu Thr Asp
            100                 105                 110

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

Leu Met Arg His Thr Asn Tyr Ser Phe Ser Pro Trp His Gly Phe Thr
    130                 135                 140

Ile His Arg Ala Lys Phe Ile Gln Ser Gln Asp Tyr Gln Cys Ser Ala
145                 150                 155                 160

Leu Met Gly Gly Arg Lys Val Met Ser Ile Ser Ile Arg Leu Lys Val
                165                 170                 175

Gln Lys Val Ile Pro Gly Pro Pro Ala Leu Thr Leu Val Pro Ala Glu
            180                 185                 190

Leu Val Arg Ile Arg Gly Glu Ala Ala Gln Ile Val Cys Ser Ala Ser
        195                 200                 205

Ser Val Asp Val Asn Phe Asp Val Phe Leu Gln His Asn Asn Thr Lys
    210                 215                 220

Leu Ala Ile Pro Gln Gln Ser Asp Phe His Asn Asn Arg Tyr Gln Lys
225                 230                 235                 240

Val Leu Thr Leu Asn Leu Asp Gln Val Asp Phe Gln His Ala Gly Asn
                245                 250                 255

Tyr Ser Cys Val Ala Ser Asn Val Gln Gly Lys His Ser Thr Ser Met
```

260 265 270

Phe Phe Arg Val Val
275

<210> 37
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence for CSF-1R

<400> 37

Met Arg His Thr Asn Tyr Ser Phe Ser Pro Trp His Gly Phe Thr Ile
1 5 10 15

His Arg Ala Lys Phe Ile Gln Ser Gln Asp Tyr Gln Cys Ser Ala Leu
20 25 30

Met Gly Gly Arg Lys Val Met Ser Ile Ser Ile Arg Leu Lys Val Gln
35 40 45

Lys

<210> 38
<211> 493
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence for CSF-1R (SNP V32G, A245S, H247P, V279M, position underlined)

<400> 38

Ile Pro Val Ile Glu Pro Ser Val Pro Glu Leu Val Val Lys Pro Gly
1 5 10 15

Ala Thr Val Thr Leu Arg Cys Val Gly Asn Gly Ser Val Glu Trp Asp
20 25 30

Gly Pro Pro Ser Pro His Trp Thr Leu Tyr Ser Asp Gly Ser Ser Ser
35 40 45

Ile Leu Ser Thr Asn Asn Ala Thr Phe Gln Asn Thr Gly Thr Tyr Arg
50 55 60

Cys Thr Glu Pro Gly Asp Pro Leu Gly Gly Ser Ala Ala Ile His Leu
65 70 75 80

Tyr Val Lys Asp Pro Ala Arg Pro Trp Asn Val Leu Ala Gln Glu Val
85 90 95

```
Val Val Phe Glu Asp Gln Asp Ala Leu Leu Pro Cys Leu Leu Thr Asp
            100                 105                 110

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

Leu Met Arg His Thr Asn Tyr Ser Phe Ser Pro Trp His Gly Phe Thr
    130                 135                 140

Ile His Arg Ala Lys Phe Ile Gln Ser Gln Asp Tyr Gln Cys Ser Ala
145                 150                 155                 160

Leu Met Gly Gly Arg Lys Val Met Ser Ile Ser Ile Arg Leu Lys Val
                165                 170                 175

Gln Lys Val Ile Pro Gly Pro Pro Ala Leu Thr Leu Val Pro Ala Glu
            180                 185                 190

Leu Val Arg Ile Arg Gly Glu Ala Ala Gln Ile Val Cys Ser Ala Ser
        195                 200                 205

Ser Val Asp Val Asn Phe Asp Val Phe Leu Gln His Asn Asn Thr Lys
    210                 215                 220

Leu Ala Ile His Gln Gln Ser Asp Phe His Asn Asn Arg Tyr Gln Lys
225                 230                 235                 240

Val Leu Thr Leu Asn Leu Asp Gln Val Asp Phe Gln His Ala Gly Asn
                245                 250                 255

Tyr Ser Cys Val Ala Ser Asn Val Gln Gly Lys His Ser Thr Ser Met
            260                 265                 270

Phe Phe Arg Val Val Glu Ser Ala Tyr Leu Asn Leu Ser Ser Glu Gln
        275                 280                 285

Asn Leu Ile Gln Glu Val Thr Val Gly Glu Gly Leu Asn Leu Lys Val
    290                 295                 300

Met Val Glu Ala Tyr Pro Gly Leu Gln Gly Phe Asn Trp Thr Tyr Leu
305                 310                 315                 320

Gly Pro Phe Ser Asp His Gln Pro Glu Pro Lys Leu Ala Asn Ala Thr
                325                 330                 335

Thr Lys Asp Thr Tyr Arg His Thr Phe Thr Leu Ser Leu Pro Arg Leu
            340                 345                 350

Lys Pro Ser Glu Ala Gly Arg Tyr Ser Phe Leu Ala Arg Asn Pro Gly
        355                 360                 365
```

```
Gly Trp Arg Ala Leu Thr Phe Glu Leu Thr Leu Arg Tyr Pro Pro Glu
    370                 375                 380

Val Ser Val Ile Trp Thr Phe Ile Asn Gly Ser Gly Thr Leu Leu Cys
385                 390                 395                 400

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

Gly His Thr Asp Arg Cys Asp Glu Ala Gln Val Leu Gln Val Trp Asp
            420                 425                 430

Asp Pro Tyr Pro Glu Val Leu Ser Gln Glu Pro Phe His Lys Val Thr
        435                 440                 445

Val Gln Ser Leu Leu Thr Val Glu Thr Leu Glu His Asn Gln Thr Tyr
    450                 455                 460

Glu Cys Arg Ala His Asn Ser Val Gly Ser Gly Ser Trp Ala Phe Ile
465                 470                 475                 480

Pro Ile Ser Ala Gly Ala His Thr His Pro Pro Asp Glu
                485                 490


<210>  39
<211>  512
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  sequence of human CSF-1R extracellular domain

<400>  39

Met Gly Pro Gly Val Leu Leu Leu Leu Leu Val Ala Thr Ala Trp His
1               5                   10                  15

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

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

Glu Trp Asp Gly Pro Pro Ser Pro His Trp Thr Leu Tyr Ser Asp Gly
    50                  55                  60

Ser Ser Ser Ile Leu Ser Thr Asn Asn Ala Thr Phe Gln Asn Thr Gly
65                  70                  75                  80

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

Ile His Leu Tyr Val Lys Asp Pro Ala Arg Pro Trp Asn Val Leu Ala
            100                 105                 110
```

```
Gln Glu Val Val Val Phe Glu Asp Gln Asp Ala Leu Leu Pro Cys Leu
        115                 120                 125

Leu Thr Asp Pro Val Leu Glu Ala Gly Val Ser Leu Val Arg Val Arg
    130                 135                 140

Gly Arg Pro Leu Met Arg His Thr Asn Tyr Ser Phe Ser Pro Trp His
145                 150                 155                 160

Gly Phe Thr Ile His Arg Ala Lys Phe Ile Gln Ser Gln Asp Tyr Gln
                165                 170                 175

Cys Ser Ala Leu Met Gly Gly Arg Lys Val Met Ser Ile Ser Ile Arg
            180                 185                 190

Leu Lys Val Gln Lys Val Ile Pro Gly Pro Pro Ala Leu Thr Leu Val
        195                 200                 205

Pro Ala Glu Leu Val Arg Ile Arg Gly Glu Ala Ala Gln Ile Val Cys
    210                 215                 220

Ser Ala Ser Ser Val Asp Val Asn Phe Asp Val Phe Leu Gln His Asn
225                 230                 235                 240

Asn Thr Lys Leu Ala Ile Pro Gln Gln Ser Asp Phe His Asn Asn Arg
                245                 250                 255

Tyr Gln Lys Val Leu Thr Leu Asn Leu Asp Gln Val Asp Phe Gln His
            260                 265                 270

Ala Gly Asn Tyr Ser Cys Val Ala Ser Asn Val Gln Gly Lys His Ser
        275                 280                 285

Thr Ser Met Phe Phe Arg Val Val Glu Ser Ala Tyr Leu Asn Leu Ser
    290                 295                 300

Ser Glu Gln Asn Leu Ile Gln Glu Val Thr Val Gly Glu Gly Leu Asn
305                 310                 315                 320

Leu Lys Val Met Val Glu Ala Tyr Pro Gly Leu Gln Gly Phe Asn Trp
                325                 330                 335

Thr Tyr Leu Gly Pro Phe Ser Asp His Gln Pro Glu Pro Lys Leu Ala
            340                 345                 350

Asn Ala Thr Thr Lys Asp Thr Tyr Arg His Thr Phe Thr Leu Ser Leu
        355                 360                 365

Pro Arg Leu Lys Pro Ser Glu Ala Gly Arg Tyr Ser Phe Leu Ala Arg
    370                 375                 380
```

```
Asn Pro Gly Gly Trp Arg Ala Leu Thr Phe Glu Leu Thr Leu Arg Tyr
385                 390                 395                 400

Pro Pro Glu Val Ser Val Ile Trp Thr Phe Ile Asn Gly Ser Gly Thr
                405                 410                 415

Leu Leu Cys Ala Ala Ser Gly Tyr Pro Gln Pro Asn Val Thr Trp Leu
            420                 425                 430

Gln Cys Ser Gly His Thr Asp Arg Cys Asp Glu Ala Gln Val Leu Gln
        435                 440                 445

Val Trp Asp Asp Pro Tyr Pro Glu Val Leu Ser Gln Glu Pro Phe His
    450                 455                 460

Lys Val Thr Val Gln Ser Leu Leu Thr Val Glu Thr Leu Glu His Asn
465                 470                 475                 480

Gln Thr Tyr Glu Cys Arg Ala His Asn Ser Val Gly Ser Gly Ser Trp
                485                 490                 495

Ala Phe Ile Pro Ile Ser Ala Gly Ala His Thr His Pro Pro Asp Glu
            500                 505                 510
```