SEQUENCE LISTING

<110> GENZYME CORPORATION
SCARIA, Abraham

<120> COMPOSITIONS AND METHODS FOR TREATING AND PREVENTING MACULAR DEGENERATION

<130> 0800-0066.40

<150> US 61/936,797
<151> 2014-02-06

<160> 23

<170> PatentIn version 3.5

<210> 1
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 1

Gly Gly Gly Gly Gly Gly Gly Gly Gly
1 5

<210> 2
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 2

Glu Glu Glu Glu Glu Glu Glu Glu Glu
1 5

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

<220>
<223> Synthetic

<400> 3

Ser Ser Ser Ser Ser Ser Ser Ser Ser
1 5

<210> 4
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 4

Gly Gly Gly Gly Gly Cys Pro Pro Cys
1 5

<210> 5
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 5

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

<210> 6
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 6

Ser Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn
1 5 10

<210> 7
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 7

Pro Ser Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn
1 5 10

<210> 8
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 8

Gly Asp Leu Ile Tyr Arg Asn Gln Lys

1 5

<210> 9
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 9

Gly Gly Gly Gly Gly Gly Gly Gly Gly Pro Ser Cys Val Pro Leu Met
1 5 10 15

Arg Cys Gly Gly Cys Cys Asn
20

<210> 10
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> sFLT01 protein: DNA sequence for a fusion protein including Flt-1

<400> 10
atggtcagct actgggacac cggggtcctg ctgtgcgcgc tgctcagctg tctgcttctc 60

acaggatctg gtagaccttt cgtagagatg tacagtgaaa tccccgaaat tatacacatg 120

actgaaggaa gggagctcgt cattccctgc cgggttacgt cacctaacat cactgttact 180

ttaaaaaagt ttccacttga cactttgatc cctgatggaa aacgcataat ctgggacagt 240

agaaagggct tcatcatatc aaatgcaacg tacaaagaaa tagggcttct gacctgtgaa 300

gcaacagtca atgggcattt gtataagaca aactatctca cacatcgaca aaccggtgga 360

ggtggaggtg gaggtggagg tcctaaatct tgtgacaaaa ctcacacatg cccaccgtgc 420

ccagcacctg aactcctggg gggaccgtca gtcttcctct tcccccccaaa acccaaggac 480

accctcatga tctcccggac ccctgaggtc acatgcgtgg tggtggacgt gagccacgaa 540

gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca 600

aagccgcggg aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg 660

caccaggact ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca 720

gcccccatcg agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac 780

accctgcccc catcccggga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc 840

aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac 900

aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag 960

ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat 1020

gaggctctgc acaaccacta cacgcagaag agcctctccc tgtctccggg taaatag 1077

<210> 11
<211> 358
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid sequence for the sFLT01 protein

<400> 11

Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
1 5 10 15

Cys Leu Leu Leu Thr Gly Ser Gly Arg Pro Phe Val Glu Met Tyr Ser
20 25 30

Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile
35 40 45

Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe
50 55 60

Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser
65 70 75 80

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

Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr
100 105 110

Leu Thr His Arg Gln Thr Gly Gly Gly Gly Gly Gly Gly Gly Gly Pro
115 120 125

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
130 135 140

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
145 150 155 160

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
165 170 175

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
180 185 190

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn

195 200 205

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
210 215 220

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
225 230 235 240

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
245 250 255

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
260 265 270

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
275 280 285

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
290 295 300

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
305 310 315 320

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
325 330 335

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
340 345 350

Ser Leu Ser Pro Gly Lys
355

<210> 12
<211> 1188
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> DNA sequence encoding VEGF

<400> 12
ctgacggaca gacagacaga caccgccccc agccccagct accacctcct ccccggccgg 60

cggcggacag tggacgcggc ggcgagccgc gggcaggggc cggagcccgc gcccggaggc 120

ggggtggagg gggtcggggc tcgcggcgtc gcactgaaac ttttcgtcca acttctgggc 180

tgttctcgct tcggaggagc cgtggtccgc gcgggggaag ccgagccgag cggagccgcg 240

agaagtgcta gctcgggccg ggaggagccg cagccggagg agggggagga ggaagaagag 300

aaggaagagg agaggggcc gcagtggcga ctcggcgctc ggaagccggg ctcatggacg 360

ggtgaggcgg cggtgtgcgc agacagtgct ccagccgcgc gcgctcccca ggccctggcc 420

cgggcctcgg gccggggagg aagagtagct cgccgaggcg ccgaggagag cgggccgccc 480

cacagcccga gccggagagg gagcgcgagc cgcgccggcc ccggtcgggc ctccgaaacc 540

atgaactttc tgctgtcttg ggtgcattgg agccttgcct tgctgctcta cctccaccat 600

gccaagtggt cccaggctgc acccatggca gaaggaggag ggcagaatca tcacgaagtg 660

gtgaagttca tggatgtcta tcagcgcagc tactgccatc caatcgagac cctggtggac 720

atcttccagg agtaccctga tgagatcgag tacatcttca agccatcctg tgtgcccctg 780

atgcgatgcg ggggctgctg caatgacgag ggcctggagt gtgtgcccac tgaggagtcc 840

aacatcacca tgcagattat gcggatcaaa cctcaccaag gccagcacat aggagagatg 900

agcttcctac agcacaacaa atgtgaatgc agaccaaaga aagatagagc aagacaagaa 960

aaaaaatcag ttcgaggaaa gggaaagggg caaaaacgaa agcgcaagaa atcccggtat 1020

aagtcctgga gcgttccctg tgggccttgc tcagagcgga gaaagcattt gtttgtacaa 1080

gatccgcaga cgtgtaaatg ttcctgcaaa aacacagact cgcgttgcaa ggcgaggcag 1140

cttgagttaa acgaacgtac ttgcagatgt gacaagccga ggcggtga 1188

<210> 13
<211> 395
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> amino acid sequence for VEGF

<400> 13

Met Thr Asp Arg Gln Thr Asp Thr Ala Pro Ser Pro Ser Tyr His Leu
1 5 10 15

Leu Pro Gly Arg Arg Arg Thr Val Asp Ala Ala Ala Ser Arg Gly Gln
20 25 30

Gly Pro Glu Pro Ala Pro Gly Gly Gly Val Glu Gly Val Gly Ala Arg
35 40 45

Gly Val Ala Leu Lys Leu Phe Val Gln Leu Leu Gly Cys Ser Arg Phe
50 55 60

Gly Gly Ala Val Val Arg Ala Gly Glu Ala Glu Pro Ser Gly Ala Ala
65 70 75 80

```
Arg Ser Ala Ser Ser Gly Arg Glu Glu Pro Gln Pro Glu Glu Gly Glu
                85                  90                  95

Glu Glu Glu Glu Lys Glu Glu Glu Arg Gly Pro Gln Trp Arg Leu Gly
            100                 105                 110

Ala Arg Lys Pro Gly Ser Trp Thr Gly Glu Ala Ala Val Cys Ala Asp
        115                 120                 125

Ser Ala Pro Ala Ala Arg Ala Pro Gln Ala Leu Ala Arg Ala Ser Gly
    130                 135                 140

Arg Gly Gly Arg Val Ala Arg Arg Gly Ala Glu Glu Ser Gly Pro Pro
145                 150                 155                 160

His Ser Pro Ser Arg Arg Gly Ser Ala Ser Arg Ala Gly Pro Gly Arg
                165                 170                 175

Ala Ser Glu Thr Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu
            180                 185                 190

Ala Leu Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro
        195                 200                 205

Met Ala Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys Phe Met
    210                 215                 220

Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp
225                 230                 235                 240

Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser
                245                 250                 255

Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu
            260                 265                 270

Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg
        275                 280                 285

Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln
    290                 295                 300

His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu
305                 310                 315                 320

Lys Lys Ser Val Arg Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys
                325                 330                 335
```

Lys Ser Arg Tyr Lys Ser Trp Ser Val Pro Cys Gly Pro Cys Ser Glu
340 345 350

Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr Cys Lys Cys Ser
355 360 365

Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln Leu Glu Leu Asn
370 375 380

Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg
385 390 395

<210> 14
<211> 426
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA sequence for an additional fusion protein including a soluble Flt-1 linked by a Gly9 linker to the VEGF multimerization domain, Ex3

<400> 14
atggtcagct actgggacac cggggtcctg ctgtgcgcgc tgctcagctg tctgcttctc 60

acaggatctg gtagaccttt cgtagagatg tacagtgaaa tccccgaaat tatacacatg 120

actgaaggaa gggagctcgt cattccctgc cgggttacgt cacctaacat cactgttact 180

ttaaaaaagt ttccacttga cactttgatc cctgatggaa aacgcataat ctgggacagt 240

agaaagggct tcatcatatc aaatgcaacg tacaaagaaa tagggcttct gacctgtgaa 300

gcaacagtca atgggcattt gtataagaca aactatctca cacatcgaca aaccggtgga 360

ggtggaggtg gaggtggagg tccttcctgt gtgcccctga tgcgatgcgg gggctgctgc 420

aattag 426

<210> 15
<211> 141
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic amino acid sequence encoded by the DNA sequence of Figure 5

<400> 15

Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
1 5 10 15

Cys Leu Leu Leu Thr Gly Ser Gly Arg Pro Phe Val Glu Met Tyr Ser
20 25 30

```
Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile
        35                  40                  45

Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe
    50                  55                  60

Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser
65                  70                  75                  80

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

Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr
            100                 105                 110

Leu Thr His Arg Gln Thr Gly Gly Gly Gly Gly Gly Gly Gly Gly Pro
        115                 120                 125

Ser Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn
    130                 135                 140
```

<210> 16
<211> 744
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA sequence for an additional fusion protein including a soluble Flt-1 linked by Gly9 to the VEGF multimerization domain, Ex3 and a sequence from the IgG1 CH3 region

<400> 16

```
atggtcagct actgggacac cggggtcctg ctgtgcgcgc tgctcagctg tctgcttctc       60

acaggatctg gtagaccttt cgtagagatg tacagtgaaa tccccgaaat tatacacatg      120

actgaaggaa gggagctcgt cattccctgc cgggttacgt cacctaacat cactgttact      180

ttaaaaaagt ttccacttga cactttgatc cctgatggaa aacgcataat ctgggacagt      240

agaaagggct tcatcatatc aaatgcaacg tacaaagaaa tagggcttct gacctgtgaa      300

gcaacagtca atgggcattt gtataagaca aactatctca cacatcgaca aaccggtgga      360

ggtggaggtg gaggtggagg tccttcctgt gtgcccctga tgcgatgcgg gggctgctgc      420

aatcagcccc gagaaccaca ggtgtacacc ctgccccccat cccgggatga gctgaccaag      480

aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag      540

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc      600

gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg      660
```

aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 720

ctctccctgt ctccgggtaa atag 744

<210> 17
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic amino acid sequence encoded by the DNA sequence of Figure 7

<400> 17

```
Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
1               5                  10                  15

Cys Leu Leu Leu Thr Gly Ser Gly Arg Pro Phe Val Glu Met Tyr Ser
            20                  25                  30

Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile
        35                  40                  45

Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe
    50                  55                  60

Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser
65                  70                  75                  80

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

Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr
            100                 105                 110

Leu Thr His Arg Gln Thr Gly Gly Gly Gly Gly Gly Gly Gly Gly Pro
        115                 120                 125

Ser Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Gln Pro Arg
    130                 135                 140

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
145                 150                 155                 160

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
                165                 170                 175

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
            180                 185                 190
```

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
195 200 205

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
210 215 220

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
225 230 235 240

Leu Ser Leu Ser Pro Gly Lys
245

<210> 18
<211> 7120
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<223> DNA sequence encoding for a representative Flt-1 receptor protein

<400> 18
atcgaggtcc gcgggaggct cggagcgcgc caggcggaca ctcctctcgg ctcctccccg 60

gcagcggcgg cggctcggag cgggctccgg ggctcgggtg cagcggccag cgggcgcctg 120

gcggcgagga ttacccgggg aagtggttgt ctcctggctg gagccgcgag acgggcgctc 180

agggcgcggg gccggcggcg gcgaacgaga ggacggactc tggcggccgg gtcgttggcc 240

gcggggagcg cgggcaccgg gcgagcaggc cgcgtcgcgc tcaccatggt cagctactgg 300

gacaccgggg tcctgctgtg cgcgctgctc agctgtctgc ttctcacagg atctagttca 360

ggttcaaaat taaaagatcc tgaactgagt ttaaaaggca cccagcacat catgcaagca 420

ggccagacac tgcatctcca atgcaggggg gaagcagccc ataaatggtc tttgcctgaa 480

atggtgagta aggaaagcga aaggctgagc ataactaaat ctgcctgtgg aagaaatggc 540

aaacaattct gcagtacttt aaccttgaac acagctcaag caaaccacac tggcttctac 600

agctgcaaat atctagctgt acctacttca aagaagaagg aaacagaatc tgcaatctat 660

atatttatta gtgatacagg tagacctttc gtagagatgt acagtgaaat ccccgaaatt 720

atacacatga ctgaaggaag ggagctcgtc attccctgcc gggttacgtc acctaacatc 780

actgttactt taaaaaagtt tccacttgac actttgatcc ctgatggaaa acgcataatc 840

tgggacagta gaaagggctt catcatatca aatgcaacgt acaaagaaat agggcttctg 900

acctgtgaag caacagtcaa tgggcatttg tataagacaa actatctcac acatcgacaa 960

accaatacaa tcatagatgt ccaaataagc acaccacgcc cagtcaaatt acttagaggc 1020

catactcttg tcctcaattg tactgctacc actcccttga acacgagagt tcaaatgacc 1080

tggagttacc ctgatgaaaa aaataagaga gcttccgtaa ggcgacgaat tgaccaaagc 1140

aattcccatg ccaacatatt ctacagtgtt cttactattg acaaaatgca gaacaaagac 1200

aaaggacttt atacttgtcg tgtaaggagt ggaccatcat tcaaatctgt taacacctca 1260

gtgcatatat atgataaagc attcatcact gtgaaacatc gaaaacagca ggtgcttgaa 1320

accgtagctg gcaagcggtc ttaccggctc tctatgaaag tgaaggcatt tccctcgccg 1380

gaagttgtat ggttaaaaga tgggttacct gcgactgaga aatctgctcg ctatttgact 1440

cgtggctact cgttaattat caaggacgta actgaagagg atgcagggaa ttatacaatc 1500

ttgctgagca taaaacagtc aaatgtgttt aaaaacctca ctgccactct aattgtcaat 1560

gtgaaacccc agatttacga aaaggccgtg tcatcgtttc cagacccggc tctctaccca 1620

ctgggcagca gacaaatcct gacttgtacc gcatatggta tccctcaacc tacaatcaag 1680

tggttctggc acccctgtaa ccataatcat tccgaagcaa ggtgtgactt ttgttccaat 1740

aatgaagagt cctttatcct ggatgctgac agcaacatgg gaaacagaat tgagagcatc 1800

actcagcgca tggcaataat agaaggaaag aataagatgg ctagcacctt ggttgtggct 1860

gactctagaa tttctggaat ctacatttgc atagcttcca ataaagttgg gactgtggga 1920

agaaacataa gcttttatat cacagatgtg ccaaatgggt ttcatgttaa cttggaaaaa 1980

atgccgacgg aaggagagga cctgaaactg tcttgcacag ttaacaagtt cttatacaga 2040

gacgttactt ggattttact gcggacagtt aataacagaa caatgcacta cagtattagc 2100

aagcaaaaaa tggccatcac taaggagcac tccatcactc ttaatcttac catcatgaat 2160

gtttccctgc aagattcagg cacctatgcc tgcagagcca ggaatgtata cacaggggaa 2220

gaaatcctcc agaagaaaga aattacaatc agagatcagg aagcaccata cctcctgcga 2280

aacctcagtg atcacacagt ggccatcagc agttccacca ctttagactg tcatgctaat 2340

ggtgtccccg agcctcagat cacttggttt aaaaacaacc acaaaataca acaagagcct 2400

ggaattattt taggaccagg aagcagcacg ctgtttattg aaagagtcac agaagaggat 2460

gaaggtgtct atcactgcaa agccaccaac cagaagggct ctgtggaaag ttcagcatac 2520

ctcactgttc aaggaacctc ggacaagtct aatctggagc tgatcactct aacatgcacc 2580

tgtgtggctg cgactctctt ctggctccta ttaaccctct ttatccgaaa aatgaaaagg 2640

tcttcttctg aaataaagac tgactaccta tcaattataa tggacccaga tgaagttcct 2700

ttggatgagc agtgtgagcg gctcccttat gatgccagca agtgggagtt tgcccgggag 2760

agacttaaac tgggcaaatc acttggaaga ggggcttttg gaaaagtggt tcaagcatca 2820

gcatttggca ttaagaaatc acctacgtgc cggactgtgg ctgtgaaaat gctgaaagag 2880

ggggccacgg ccagcgagta caaagctctg atgactgagc taaaaatctt gacccacatt 2940

ggccaccatc tgaacgtggt taacctgctg ggagcctgca ccaagcaagg agggcctctg 3000

atggtgattg ttgaatactg caaatatgga aatctctcca actacctcaa gagcaaacgt 3060

gacttatttt ttctcaacaa ggatgcagca ctacacatgg agcctaagaa agaaaaaatg 3120

gagccaggcc tggaacaagg caagaaacca agactagata gcgtcaccag cagcgaaagc 3180

tttgcgagct ccggctttca ggaagataaa agtctgagtg atgttgagga agaggaggat 3240

tctgacggtt tctacaagga gcccatcact atggaagatc tgatttctta cagttttcaa 3300

gtggccagag gcatggagtt cctgtcttcc agaaagtgca ttcatcggga cctggcagcg 3360

agaaacattc ttttatctga gaacaacgtg gtgaagattt gtgattttgg ccttgcccgg 3420

gatatttata agaaccccga ttatgtgaga aaaggagata ctcgacttcc tctgaaatgg 3480

atggctcctg aatctatctt tgacaaaatc tacagcacca agagcgacgt gtggtcttac 3540

ggagtattgc tgtgggaaat cttctcctta ggtgggtctc catacccagg agtacaaatg 3600

gatgaggact tttgcagtcg cctgagggaa ggcatgagga tgagagctcc tgagtactct 3660

actcctgaaa tctatcagat catgctggac tgctggcaca gagacccaaa agaaaggcca 3720

agatttgcag aacttgtgga aaaactaggt gatttgcttc aagcaaatgt acaacaggat 3780

ggtaaagact acatcccaat caatgccata ctgacaggaa atagtgggtt tacatactca 3840

actcctgcct tctctgagga cttcttcaag gaaagtattt cagctccgaa gtttaattca 3900

ggaagctctg atgatgtcag atacgtaaat gctttcaagt tcatgagcct ggaaagaatc 3960

aaaacctttg aagaactttt accgaatgcc acctccatgt ttgatgacta ccagggcgac 4020

agcagcactc tgttggcctc tcccatgctg aagcgcttca cctggactga cagcaaaccc 4080

aaggcctcgc tcaagattga cttgagagta accagtaaaa gtaaggagtc ggggctgtct 4140

gatgtcagca ggcccagttt ctgccattcc agctgtgggc acgtcagcga aggcaagcgc 4200

aggttcacct acgaccacgc tgagctggaa aggaaaatcg cgtgctgctc cccgccccca 4260

gactacaact cggtggtcct gtactccacc ccacccatct agagtttgac acgaagcctt 4320

atttctagaa gcacatgtgt atttataccc ccaggaaact agcttttgcc agtattatgc 4380

atatataagt ttacaccttt atctttccat gggagccagc tgctttttgt gatttttta 4440

atagtgcttt ttttttttg actaacaaga atgtaactcc agatagagaa atagtgacaa 4500

gtgaagaaca ctactgctaa atcctcatgt tactcagtgt tagagaaatc cttcctaaac 4560

ccaatgactt ccctgctcca acccccgcca cctcagggca cgcaggacca gtttgattga 4620

ggagctgcac tgatcaccca atgcatcacg taccccactg ggccagccct gcagcccaaa 4680

acccagggca acaagcccgt tagccccagg gatcactggc tggcctgagc aacatctcgg 4740

gagtcctcta gcaggcctaa gacatgtgag gaggaaaagg aaaaaaagca aaaagcaagg 4800

gagaaaagag aaaccgggag aaggcatgag aaagaatttg agacgcacca tgtgggcacg 4860

gaggggggacg gggctcagca atgccatttc agtggcttcc cagctctgac ccttctacat 4920
ttgagggccc agccaggagc agatggacag cgatgagggg acattttctg gattctggga 4980
ggcaagaaaa ggacaaatat ctttttgga actaaagcaa attttagaac tttacctatg 5040
gaagtggttc tatgtccatt ctcattcgtg gcatgttttg atttgtagca ctgagggtgg 5100
cactcaactc tgagcccata cttttggctc ctctagtaag atgcactgaa aacttagcca 5160
gagttaggtt gtctccaggc catgatggcc ttacactgaa aatgtcacat tctattttgg 5220
gtattaatat atagtccaga cacttaactc aatttcttgg tattattctg ttttgcacag 5280
ttagttgtga aagaaagctg agaagaatga aaatgcagtc ctgaggagag gagttttctc 5340
catatcaaaa cgagggctga tggaggaaaa aggtcaataa ggtcaaggga aaaccccgtc 5400
tctataccaa ccaaaccaat tcaccaacac agttgggacc caaaacacag gaagtcagtc 5460
acgtttcctt ttcatttaat ggggattcca ctatctcaca ctaatctgaa aggatgtgga 5520
agagcattag ctggcgcata ttaagcactt taagctcctt gagtaaaaag gtggtatgta 5580
atttatgcaa ggtatttctc cagttgggac tcaggatatt agttaatgag ccatcactag 5640
aagaaaagcc cattttcaac tgctttgaaa cttgcctggg gtctgagcat gatgggaata 5700
gggagacagg gtaggaaagg gcgcctactc ttcagggtct aaagatcaag tgggccttgg 5760
atcgctaagc tggctctgtt tgatgctatt tatgcaagtt agggtctatg tatttatgat 5820
gtctgcacct tctgcagcca gtcagaagct ggagaggcaa cagtggattg ctgcttcttg 5880
gggagaagag tatgcttcct tttatccatg taatttaact gtagaacctg agctctaagt 5940
aaccgaagaa tgtatgcctc tgttcttatg tgccacatcc ttgtttaaag gctctctgta 6000
tgaagagatg ggaccgtcat cagcacattc cctagtgagc ctactggctc ctggcagcgg 6060
cttttgtgga agactcacta gccagaagag aggagtggga cagtcctcta ccaagatcta 6120
aatccaaaca aaagcaggct agagccagaa gagaggacaa atctttgttc ttcctcttct 6180
ttacatacgc aaaccacctg tgacagctgg caattttata aatcaggtaa ctggaaggag 6240
gttaaacaca gaaaaaagaa gacctcagtc aattctctac ttttttttttt ttttccaaat 6300
cagataatag cccagcaaat agtgataaca aataaaacct tagctattca tgtcttgatt 6360
tcaataatta attcttaatc attaagagac cataataaat actccttttc aagagaaaag 6420
caaaaccatt agaattgtta ctcagctcct tcaaactcag gtttgtagca tacatgagtc 6480
catccatcag tcaaagaatg gttccatctg gagtcttaat gtagaaagaa aaatggagac 6540
ttgtaataat gagctagtta caaagtgctt gttcattaaa atagcactga aaattgaaac 6600
atgaattaac tgataatatt ccaatcattt gccatttatg acaaaaatgg ttggcactaa 6660
caaagaacga gcacttcctt tcagagtttc tgagataatg tacgtggaac agtctgggtg 6720

gaatggggct gaaaccatgt gcaagtctgt gtcttgtcag tccaagaagt gacaccgaga 6780

tgttaatttt agggacccgt gccttgtttc ctagcccaca agaatgcaaa catcaaacag 6840

atactcgcta gcctcattta aattgattaa aggaggagtg catctttggc cgacagtggt 6900

gtaactgtat gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt gtgtgggtgt atgtgtgttt 6960

tgtgcataac tatttaagga aactggaatt ttaaagttac ttttatacaa accaagaata 7020

tatgctacag atataagaca gacatggttt ggtcctatat ttctagtcat gatgaatgta 7080

ttttgtatac catcttcata taataaactt ccaaaacaca 7120

<210> 19
<211> 1338
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> amino acid sequence of a representative Flt-1 receptor protein

<400> 19

Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
1 5 10 15

Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys Asp Pro
20 25 30

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

Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro
50 55 60

Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala
65 70 75 80

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

Ala Gln Ala Asn His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val
100 105 110

Pro Thr Ser Lys Lys Lys Glu Thr Glu Ser Ala Ile Tyr Ile Phe Ile
115 120 125

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

```
Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val
145                 150                 155                 160

Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr
                165                 170                 175

Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe
            180                 185                 190

Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu
        195                 200                 205

Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg
    210                 215                 220

Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val
225                 230                 235                 240

Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr
                245                 250                 255

Pro Leu Asn Thr Arg Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Lys
            260                 265                 270

Asn Lys Arg Ala Ser Val Arg Arg Arg Ile Asp Gln Ser Asn Ser His
        275                 280                 285

Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys
    290                 295                 300

Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys
305                 310                 315                 320

Ser Val Asn Thr Ser Val His Ile Tyr Asp Lys Ala Phe Ile Thr Val
                325                 330                 335

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

Tyr Arg Leu Ser Met Lys Val Lys Ala Phe Pro Ser Pro Glu Val Val
        355                 360                 365

Trp Leu Lys Asp Gly Leu Pro Ala Thr Glu Lys Ser Ala Arg Tyr Leu
    370                 375                 380

Thr Arg Gly Tyr Ser Leu Ile Ile Lys Asp Val Thr Glu Glu Asp Ala
385                 390                 395                 400
```

```
Gly Asn Tyr Thr Ile Leu Leu Ser Ile Lys Gln Ser Asn Val Phe Lys
                405                 410                 415

Asn Leu Thr Ala Thr Leu Ile Val Asn Val Lys Pro Gln Ile Tyr Glu
            420                 425                 430

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

Arg Gln Ile Leu Thr Cys Thr Ala Tyr Gly Ile Pro Gln Pro Thr Ile
    450                 455                 460

Lys Trp Phe Trp His Pro Cys Asn His Asn His Ser Glu Ala Arg Cys
465                 470                 475                 480

Asp Phe Cys Ser Asn Asn Glu Glu Ser Phe Ile Leu Asp Ala Asp Ser
                485                 490                 495

Asn Met Gly Asn Arg Ile Glu Ser Ile Thr Gln Arg Met Ala Ile Ile
            500                 505                 510

Glu Gly Lys Asn Lys Met Ala Ser Thr Leu Val Val Ala Asp Ser Arg
        515                 520                 525

Ile Ser Gly Ile Tyr Ile Cys Ile Ala Ser Asn Lys Val Gly Thr Val
    530                 535                 540

Gly Arg Asn Ile Ser Phe Tyr Ile Thr Asp Val Pro Asn Gly Phe His
545                 550                 555                 560

Val Asn Leu Glu Lys Met Pro Thr Glu Gly Glu Asp Leu Lys Leu Ser
                565                 570                 575

Cys Thr Val Asn Lys Phe Leu Tyr Arg Asp Val Thr Trp Ile Leu Leu
            580                 585                 590

Arg Thr Val Asn Asn Arg Thr Met His Tyr Ser Ile Ser Lys Gln Lys
        595                 600                 605

Met Ala Ile Thr Lys Glu His Ser Ile Thr Leu Asn Leu Thr Ile Met
    610                 615                 620

Asn Val Ser Leu Gln Asp Ser Gly Thr Tyr Ala Cys Arg Ala Arg Asn
625                 630                 635                 640

Val Tyr Thr Gly Glu Glu Ile Leu Gln Lys Lys Glu Ile Thr Ile Arg
                645                 650                 655
```

```
Asp Gln Glu Ala Pro Tyr Leu Leu Arg Asn Leu Ser Asp His Thr Val
            660                 665                 670

Ala Ile Ser Ser Ser Thr Thr Leu Asp Cys His Ala Asn Gly Val Pro
        675                 680                 685

Glu Pro Gln Ile Thr Trp Phe Lys Asn Asn His Lys Ile Gln Gln Glu
    690                 695                 700

Pro Gly Ile Ile Leu Gly Pro Gly Ser Ser Thr Leu Phe Ile Glu Arg
705                 710                 715                 720

Val Thr Glu Glu Asp Glu Gly Val Tyr His Cys Lys Ala Thr Asn Gln
                725                 730                 735

Lys Gly Ser Val Glu Ser Ser Ala Tyr Leu Thr Val Gln Gly Thr Ser
            740                 745                 750

Asp Lys Ser Asn Leu Glu Leu Ile Thr Leu Thr Cys Thr Cys Val Ala
        755                 760                 765

Ala Thr Leu Phe Trp Leu Leu Leu Thr Leu Leu Ile Arg Lys Met Lys
    770                 775                 780

Arg Ser Ser Ser Glu Ile Lys Thr Asp Tyr Leu Ser Ile Ile Met Asp
785                 790                 795                 800

Pro Asp Glu Val Pro Leu Asp Glu Gln Cys Glu Arg Leu Pro Tyr Asp
                805                 810                 815

Ala Ser Lys Trp Glu Phe Ala Arg Glu Arg Leu Lys Leu Gly Lys Ser
            820                 825                 830

Leu Gly Arg Gly Ala Phe Gly Lys Val Val Gln Ala Ser Ala Phe Gly
        835                 840                 845

Ile Lys Lys Ser Pro Thr Cys Arg Thr Val Ala Val Lys Met Leu Lys
    850                 855                 860

Glu Gly Ala Thr Ala Ser Glu Tyr Lys Ala Leu Met Thr Glu Leu Lys
865                 870                 875                 880

Ile Leu Thr His Ile Gly His His Leu Asn Val Val Asn Leu Leu Gly
                885                 890                 895

Ala Cys Thr Lys Gln Gly Gly Pro Leu Met Val Ile Val Glu Tyr Cys
```

```
            900                 905                 910

Lys Tyr Gly Asn Leu Ser Asn Tyr Leu Lys Ser Lys Arg Asp Leu Phe
        915                 920                 925

Phe Leu Asn Lys Asp Ala Ala Leu His Met Glu Pro Lys Lys Glu Lys
    930                 935                 940

Met Glu Pro Gly Leu Glu Gln Gly Lys Lys Pro Arg Leu Asp Ser Val
945                 950                 955                 960

Thr Ser Ser Glu Ser Phe Ala Ser Ser Gly Phe Gln Glu Asp Lys Ser
                965                 970                 975

Leu Ser Asp Val Glu Glu Glu Glu Asp Ser Asp Gly Phe Tyr Lys Glu
            980                 985                 990

Pro Ile Thr Met Glu Asp Leu Ile  Ser Tyr Ser Phe Gln  Val Ala Arg
        995                 1000                1005

Gly Met  Glu Phe Leu Ser Ser  Arg Lys Cys Ile His  Arg Asp Leu
    1010                1015                1020

Ala Ala  Arg Asn Ile Leu Leu  Ser Glu Asn Asn Val  Val Lys Ile
    1025                1030                1035

Cys Asp  Phe Gly Leu Ala Arg  Asp Ile Tyr Lys Asn  Pro Asp Tyr
    1040                1045                1050

Val Arg  Lys Gly Asp Thr Arg  Leu Pro Leu Lys Trp  Met Ala Pro
    1055                1060                1065

Glu Ser  Ile Phe Asp Lys Ile  Tyr Ser Thr Lys Ser  Asp Val Trp
    1070                1075                1080

Ser Tyr  Gly Val Leu Leu Trp  Glu Ile Phe Ser Leu  Gly Gly Ser
    1085                1090                1095

Pro Tyr  Pro Gly Val Gln Met  Asp Glu Asp Phe Cys  Ser Arg Leu
    1100                1105                1110

Arg Glu  Gly Met Arg Met Arg  Ala Pro Glu Tyr Ser  Thr Pro Glu
    1115                1120                1125

Ile Tyr  Gln Ile Met Leu Asp  Cys Trp His Arg Asp  Pro Lys Glu
    1130                1135                1140
```

```
Arg Pro  Arg Phe Ala Glu Leu  Val Glu Lys Leu Gly  Asp Leu Leu
    1145                 1150                 1155

Gln Ala  Asn Val Gln Gln Asp  Gly Lys Asp Tyr Ile  Pro Ile Asn
    1160                 1165                 1170

Ala Ile  Leu Thr Gly Asn Ser  Gly Phe Thr Tyr Ser  Thr Pro Ala
    1175                 1180                 1185

Phe Ser  Glu Asp Phe Phe Lys  Glu Ser Ile Ser Ala  Pro Lys Phe
    1190                 1195                 1200

Asn Ser  Gly Ser Ser Asp Asp  Val Arg Tyr Val Asn  Ala Phe Lys
    1205                 1210                 1215

Phe Met  Ser Leu Glu Arg Ile  Lys Thr Phe Glu Glu  Leu Leu Pro
    1220                 1225                 1230

Asn Ala  Thr Ser Met Phe Asp  Asp Tyr Gln Gly Asp  Ser Ser Thr
    1235                 1240                 1245

Leu Leu  Ala Ser Pro Met Leu  Lys Arg Phe Thr Trp  Thr Asp Ser
    1250                 1255                 1260

Lys Pro  Lys Ala Ser Leu Lys  Ile Asp Leu Arg Val  Thr Ser Lys
    1265                 1270                 1275

Ser Lys  Glu Ser Gly Leu Ser  Asp Val Ser Arg Pro  Ser Phe Cys
    1280                 1285                 1290

His Ser  Ser Cys Gly His Val  Ser Glu Gly Lys Arg  Arg Phe Thr
    1295                 1300                 1305

Tyr Asp  His Ala Glu Leu Glu  Arg Lys Ile Ala Cys  Cys Ser Pro
    1310                 1315                 1320

Pro Pro  Asp Tyr Asn Ser Val  Val Leu Tyr Ser Thr  Pro Pro Ile
    1325                 1330                 1335
```

<210> 20
<211> 702
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA sequence for a fusion protein including Flt-1, termed "sFLT02 protein" herein which includes a soluble Flt-1 linked by Gly9 to the a sequence from the IgG1 CH3 region

<400> 20

atggtcagct actgggacac cggggtcctg ctgtgcgcgc tgctcagctg tctgcttctc 60

acaggatctg gtagaccttt cgtagagatg tacagtgaaa tccccgaaat tatacacatg 120

actgaaggaa gggagctcgt cattccctgc cgggttacgt cacctaacat cactgttact 180

ttaaaaaagt ttccacttga cactttgatc cctgatggaa aacgcataat ctgggacagt 240

agaaagggct tcatcatatc aaatgcaacg tacaaagaaa tagggcttct gacctgtgaa 300

gcaacagtca atgggcattt gtataagaca aactatctca cacatcgaca aaccggtgga 360

ggtggaggtg gaggtggagg tcagccccga gaaccacagg tgtacaccct gcccccatcc 420

cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatccc 480

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 540

cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 600

agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac 660

cactacacgc agaagagcct ctccctgtct ccgggtaaat ag 702

<210> 21
<211> 233
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid sequence for the sFLT02 protein

<400> 21

Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
1 5 10 15

Cys Leu Leu Leu Thr Gly Ser Gly Arg Pro Phe Val Glu Met Tyr Ser
20 25 30

Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile
35 40 45

Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe
50 55 60

Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser
65 70 75 80

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

Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr
100 105 110

Leu Thr His Arg Gln Thr Gly Gly Gly Gly Gly Gly Gly Gly Gln
115 120 125

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

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
165 170 175

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

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
195 200 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
210 215 220

Lys Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 22
<211> 1434
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> nucleotide sequence of the IgG1 lambda heavy chain

<400> 22
atggagtttg ggctgagctg ggttttcctc gttgctcttt taagaggtgt ccagtgtcag 60

gtgcagctgg tggagtctgg gggaggcgtg gtccagcctg ggaggtccct gagactctcc 120

tgtgcagcgt ctggattcac cttcagtaat atggcatgc actgggtccg ccaggctcca 180

ggcaaggggc tggagtgggt ggcagctata tggtatgatg gaagtaataa atactatgca 240

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gttgtatatg 300

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt attgtgcgag agagggtcgg 360

tgggtacgat atactacggt gactactatc ggatactact ttgactactg gggccaggga 420

accctggtca ccgtctcctc agcctccacc aagggcccat cggtcttccc cctggcaccc 480

tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctggtcaa ggactacttc 540

cccgaaccgg tgacggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc 600

ccggctgtcc tacagtcctc aggactctac tccctcagca gcgtggtgac cgtgccctcc 660

agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag 720

gtggacaaga gagttgagcc caaatcttgt gacaaaactc acacatgccc accgtgccca 780

gcacctgaac tcctgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc 840

ctcatgatct cccggacccc tgaggtcaca tgcgtggtgg tggacgtgag ccacgaagac 900

cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 960

ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 1020

caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 1080

cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc 1140

ctgcccccat cccgggagga gatgaccaag aaccaggtca gcctgacctg cctggtcaaa 1200

ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 1260

tacaagacca cgcctcccgt gctggactcc gacggctcct tcttcctcta tagcaagctc 1320

accgtggaca agagcaggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag 1380

gctctgcaca accactacac gcagaagagc ctctccctgt ccccgggtaa atga 1434

<210> 23
<211> 477
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> amino acid sequence of the IgG1 lambda heavy chain

<400> 23

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

Val Gln Cys Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
20 25 30

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

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

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

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

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

Tyr Tyr Cys Ala Arg Glu Gly Arg Trp Val Arg Tyr Thr Thr Val Thr
        115                 120                 125

Thr Ile Gly Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
    130                 135                 140

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

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
                165                 170                 175

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

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

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

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

Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
                245                 250                 255

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

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

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
    290                 295                 300

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
305                 310                 315                 320

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
                325                 330                 335

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
```

340 345 350

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
355 360 365

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

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
385 390 395 400

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

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

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

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

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475