SEQUENCE LISTING

<110> Chi, Andrew S

<120> Improved Methods for the Treatment of Vascularizing Cancers

<130> 1301.0113PCT

<150> US 61/939,804
<151> 2014-02-14

<160> 110

<170> PatentIn version 3.5

<210> 1
<211> 316
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(316)
<223> "2Ig" form of human B7-H3

<400> 1

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Ala Leu Gly Ala Leu Trp Phe Cys Leu Thr Gly Ala Leu Glu Val Gln
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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 Arg Gly Tyr Pro Glu Ala Glu Val
                165                 170                 175
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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
    290                 295                 300

Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile Ala
305                 310                 315
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<210> 2
<211> 948
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(948)
<223> Polynucleotide Sequence Encoding the "2Ig" Form of Human B7-H3

<400> 2

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ctgtggttct gcctcacagg agccctggag gtccaggtcc ctgaagaccc agtggtggca      120

ctggtgggca ccgatgccac cctgtgctgc tccttctccc ctgagcctgg cttcagcctg      180

gcacagctca acctcatctg gcagctgaca gataccaaac agctggtgca cagctttgct      240

gagggccagg accagggcag cgcctatgcc aaccgcacgg ccctcttccc ggacctgctg      300

gcacagggca acgcatccct gaggctgcag cgcgtgcgtg tggcggacga gggcagcttc      360

acctgcttcg tgagcatccg ggatttcggc agcgctgccg tcagcctgca ggtggccgct      420

ccctactcga agcccagcat gaccctggag cccaacaagg acctgcggcc aggggacacg      480

gtgaccatca cgtgctccag ctaccggggc taccctgagg ctgaggtgtt ctggcaggat      540

gggcagggtg tgcccctgac tggcaacgtg accacgtcgc agatggccaa cgagcagggc      600

ttgtttgatg tgcacagcgt cctgcgggtg gtgctgggtg cgaatggcac ctacagctgc      660

ctggtgcgca accccgtgct gcagcaggat gcgcacggct ctgtcaccat cacagggcag      720
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cctatgacat tccccccaga ggccctgtgg gtgaccgtgg ggctgtctgt ctgtctcatt 780

gcactgctgg tggccctggc tttcgtgtgc tggagaaaga tcaaacagag ctgtgaggag 840

gagaatgcag gagctgagga ccaggatggg gagggagaag gctccaagac agccctgcag 900

cctctgaaac actctgacag caaagaagat gatggacaag aaatagcc 948

<210> 3
<211> 534
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(534)
<223> "4Ig" form of human B7-H3

<400> 3

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Ala Leu Gly Ala Leu Trp Phe Cys Leu Thr Gly Ala Leu Glu Val Gln
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 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

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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

Arg Ser Pro Thr Gly Ala Val Glu Val Gln Val Pro Glu Asp Pro Val
                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
        275                 280                 285

Asp Thr Lys Gln Leu Val His Ser Phe Thr Glu Gly Arg Asp Gln Gly
    290                 295                 300

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
                325                 330                 335

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
                485                 490                 495

Glu Glu Glu Asn Ala Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly
            500                 505                 510

Ser Lys Thr Ala Leu Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp
        515                 520                 525
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Asp Gly Gln Glu Ile Ala
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<210> 4
<211> 1602
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(1602)
<223> Polynucleotide Sequence Encoding the "4Ig" Form of Human B7-H3

<400> 4
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ctggtgggca ccgatgccac cctgtgctgc tccttctccc ctgagcctgg cttcagcctg 180

gcacagctca acctcatctg gcagctgaca gataccaaac agctggtgca cagctttgct 240

gagggccagg accagggcag cgcctatgcc aaccgcacgg ccctcttccc ggacctgctg 300

gcacagggca acgcatccct gaggctgcag cgcgtgcgtg tggcggacga gggcagcttc 360

acctgcttcg tgagcatccg ggatttcggc agcgctgccg tcagcctgca ggtggccgct 420

ccctactcga agcccagcat gaccctggag cccaacaagg acctgcggcc aggggacacg 480

gtgaccatca cgtgctccag ctaccagggc taccctgagg ctgaggtgtt ctggcaggat 540

gggcagggtg tgcccctgac tggcaacgtg accacgtcgc agatggccaa cgagcagggc 600

ttgtttgatg tgcacagcat cctgcgggtg gtgctgggtg caaatggcac ctacagctgc 660

ctggtgcgca accccgtgct gcagcaggat gcgcacagct ctgtcaccat cacaccccag 720

agaagcccca caggagccgt ggaggtccag gtccctgagg acccggtggt ggccctagtg 780

ggcaccgatg ccaccctgcg ctgctccttc tcccccgagc ctggcttcag cctggcacag 840

ctcaacctca tctggcagct gacagacacc aaacagctgg tgcacagttt caccgaaggc 900

cgggaccagg gcagcgccta tgccaaccgc acggccctct tcccggacct gctggcacaa 960

ggcaatgcat ccctgaggct gcagcgcgtg cgtgtggcgg acgagggcag cttcacctgc 1020

ttcgtgagca tccgggattt cggcagcgct gccgtcagcc tgcaggtggc cgctccctac 1080

tcgaagccca gcatgaccct ggagcccaac aaggacctgc ggccagggga cacggtgacc 1140

atcacgtgct ccagctaccg gggctaccct gaggctgagg tgttctggca ggatgggcag 1200

ggtgtgcccc tgactggcaa cgtgaccacg tcgcagatgg ccaacgagca gggcttgttt 1260

gatgtgcaca gcgtcctgcg ggtggtgctg ggtgcgaatg gcacctacag ctgcctggtg 1320

cgcaaccccg tgctgcagca ggatgcgcac ggctctgtca ccatcacagg gcagcctatg 1380

acattccccc cagaggccct gtgggtgacc gtggggctgt ctgtctgtct cattgcactg 1440

ctggtggccc tggctttcgt gtgctggaga aagatcaaac agagctgtga ggaggagaat 1500

gcaggagctg aggaccagga tggggaggga gaaggctcca agacagccct gcagcctctg 1560

aaacactctg acagcaaaga agatgatgga caagaaatag cc 1602

<210> 5
<211> 107
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(107)
<223> Amino Acid Sequence of BRCA69D Variable Light Chain

<400> 5

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Pro
85 90 95

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

<210> 6
<211> 321
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(321)
<223> Polynucleotide Sequence Encoding BRCA69D Variable Light Chain

<400> 6
gatatccaga tgacacagac tacatcctcc ctgtctgcct ctctgggaga cagagtcacc 60

atcagttgca gggcaagtca ggacattagt aattatttaa actggtatca gcagaaacca 120

gatggaactg ttaaactcct gatctactac acatcacgat tacactcagg agtcccatca 180

aggttcagtg gcagtgggtc tggaacagat tattctctca ccattgacaa cctggagcaa 240

gaagatattg ccacttactt ttgccaacag ggtaatacgc ttcctccgac gttcggtgga 300

ggcaccaaac tggaaatcaa a 321

<210> 7
<211> 11
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(11)
<223> BRCA69D Variable Light Chain CDR1

<400> 7

Arg Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
1 5 10

<210> 8
<211> 33
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(33)
<223> Polynucleotide Sequence Encoding BRCA69D Variable Light Chain CDR1

<400> 8
agggcaagtc aggacattag taattattta aac 33

<210> 9
<211> 7
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(7)
<223> BRCA69D Variable Light Chain CDR2

<400> 9

Tyr Thr Ser Arg Leu His Ser
1 5

<210> 10
<211> 21
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(21)
<223> Polynucleotide Sequence Encoding BRCA69D Variable Light Chain CDR2

<400> 10
tacacatcac gattacactc a 21

<210> 11
<211> 9
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(9)
<223> BRCA69D Variable Light Chain CDR3

<400> 11

Gln Gln Gly Asn Thr Leu Pro Pro Thr
1 5

<210> 12
<211> 27
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(27)
<223> Polynucleotide Sequence Encoding BRCA69D Variable Light Chain CDR3

<400> 12
caacagggta atacgcttcc tccgacg 27

<210> 13
<211> 120
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(120)
<223> Amino Acid Sequence of BRCA69D Variable Heavy Chain

<400> 13

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

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

Gly Thr Ile Tyr Pro Gly Asp Gly Asp Thr Arg Tyr Thr Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Arg Gly Ile Pro Arg Leu Trp Tyr Phe Asp Val Trp Gly Ala
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 14
<211> 360
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(360)
<223> Polynucleotide Sequence Encoding BRCA69D Variable Heavy Chain

<400> 14
caggttcagc tccagcagtc tggggctgag ctggcaagac ctggggcttc agtgaagttg 60

tcctgcaagg cttctggcta cacctttact agctactgga tgcagtgggt aaaacagagg 120

cctggacagg gtctggaatg gattgggact atttatcctg gagatggtga tactaggtac 180

actcagaagt tcaagggcaa ggccacattg actgcagata aatcctccag cacagcctac 240

atgcaactca gcagcttggc atctgaggac tctgcggtct attactgtgc aagaagaggg 300

attccacggc tttggtactt cgatgtctgg ggcgcaggga ccacggtcac cgtctcctca 360

<210> 15
<211> 5
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> BRCA69D Variable Heavy Chain CDR1

<400> 15

Ser Tyr Trp Met Gln
1 5

<210> 16
<211> 15
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(15)
<223> Polynucleotide Sequence Encoding BRCA69D Variable Heavy Chain CDR1

<400> 16
agctactgga tgcag 15

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

<220>

<221> MISC_FEATURE
<222> (1)..(17)
<223> BRCA69D Variable Heavy Chain CDR2

<400> 17

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

Gly

<210> 18
<211> 51
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(51)
<223> Polynucleotide Sequence Encoding BRCA69D Variable Heavy Chain CDR2

<400> 18
actatttatc ctggagatgg tgatactagg tacactcaga agttcaaggg c 51

<210> 19
<211> 11
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(11)
<223> BRCA69D Variable Heavy Chain CDR3

<400> 19

Arg Gly Ile Pro Arg Leu Trp Tyr Phe Asp Val
1 5 10

<210> 20
<211> 33
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(33)
<223> Polynucleotide Sequence Encoding BRCA69D Variable Heavy Chain CDR3

<400> 20
agagggattc cacggctttg gtacttcgat gtc 33

<210> 21
<211> 108
<212> PRT
<213> Mus musculus

<220>

<221> MISC_FEATURE
<222> (1)..(108)
<223> Amino Acid Sequence of PRCA157 Variable Light Chain

<400> 21

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

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

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

Tyr Asn Thr Lys Thr Leu Pro Glu Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Gly Arg Tyr Tyr Cys Gln His His Tyr Gly Thr Pro Pro
85 90 95

Trp Thr Phe Gly Gly Gly Thr Asn Leu Glu Ile Lys
100 105

<210> 22
<211> 324
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(324)
<223> Polynucleotide Sequence Encoding PRCA157 Variable Light Chain

<400> 22
gacatccaga tgactcagtc tccagcctcc ctatctgtat ctgtgggaga aactgtcacc 60

attacatgtc gagcaagtga gagtatttac agttatttag catggtatca gcagaaacag 120

ggaaaatctc ctcagctcct ggtctataat acaaaaacct taccagaggg tgtgccatca 180

aggttcagtg gcagtggatc aggcacacag ttttctctga agatcaacag cctgcagcct 240

gaagattttg ggagatatta ctgtcaacat cattatggta ctcctccgtg gacgttcggt 300

ggaggcacca acctggaaat caaa 324

<210> 23
<211> 11
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(11)
<223> PRCA157 Variable Light Chain CDR1

<400> 23

Arg Ala Ser Glu Ser Ile Tyr Ser Tyr Leu Ala
1 5 10

<210> 24
<211> 33
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(33)
<223> Polynucleotide Sequence Encoding PRCA157 Variable Light Chain CDR1

<400> 24
cgagcaagtg agagtattta cagttattta gca 33

<210> 25
<211> 7
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(7)
<223> PRCA157 Variable Light Chain CDR2

<400> 25

Asn Thr Lys Thr Leu Pro Glu
1 5

<210> 26
<211> 21
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(21)
<223> Polynucleotide Sequence Encoding PRCA157 Variable Light Chain CDR2

<400> 26
aatacaaaaa ccttaccaga g 21

<210> 27
<211> 9
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(9)
<223> PRCA157 Variable Light Chain CDR3

<400> 27

Gln His His Tyr Gly Thr Pro Pro Trp
1 5

<210> 28
<211> 27
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(27)
<223> Polynucleotide Sequence Encoding PRCA157 Variable Light Chain CDR3

<400> 28
caacatcatt atggtactcc tccgtgg 27

<210> 29
<211> 117
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(117)
<223> Amino Acid Sequence of PRCA157 Variable Heavy Chain

<400> 29

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

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

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

Ala Thr Ile Asn Ser Gly Gly Ser Asn Thr Tyr Tyr Pro Asp Ser Leu
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Arg Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg His Asp Gly Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
100 105 110

Val Thr Val Ser Ser
115

<210> 30
<211> 351
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(351)
<223> Polynucleotide Sequence Encoding PRCA157 Variable Heavy Chain

<400> 30
gaggtgcagc aggtggagtc ggggggagac ttagtgaagc ctggagggtc cctgaaactc 60

tcctgtgcag cctctggatt cactttcagt tcctatggca tgtcttgggt tcgccagact 120

ccagacaaga ggctggagtg ggtcgcaacc attaatagtg gtggaagtaa cacctactat 180

ccagacagtt tgaaggggcg attcaccatc tccagagaca atgccaagaa cacccttttac 240

ctgcaaatgc gcagtctgaa gtctgaggac acagccatgt attactgtgc aagacatgac 300

gggggagcta tggactactg gggtcaagga acctcagtca ccgtctcctc a 351

<210> 31
<211> 5
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> PRCA157 Variable Heavy Chain CDR1

<400> 31

Ser Tyr Gly Met Ser
1 5

<210> 32
<211> 15
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(15)
<223> Polynucleotide Sequence Encoding PRCA157 Variable Heavy Chain CDR1

<400> 32
tcctatggca tgtct 15

<210> 33
<211> 19
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(19)
<223> PRCA157 Variable Heavy Chain CDR2

<400> 33

Val Ala Thr Ile Asn Ser Gly Gly Ser Asn Thr Tyr Tyr Pro Asp Ser
1 5 10 15

Leu Lys Gly

<210> 34
<211> 57
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(57)
<223> Polynucleotide Sequence Encoding PRCA157 Variable Heavy Chain CDR2

<400> 34
gtcgcaacca ttaatagtgg tggaagtaac acctactatc cagacagttt gaagggg 57

<210> 35
<211> 8
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(8)
<223> PRCA157 Variable Heavy Chain CDR3

<400> 35

His Asp Gly Gly Ala Met Asp Tyr
1 5

<210> 36
<211> 24
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(24)
<223> Polynucleotide Sequence Encoding PRCA157 Variable Heavy Chain CDR3

<400> 36
catgacgggg gagctatgga ctac 24

<210> 37
<211> 107
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(107)
<223> Amino Acid Sequence of BRCA84D Variable Light Chain

<400> 37

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

Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Asp Thr Asn
20 25 30

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

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

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

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

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
            100                 105
```

<210> 38
<211> 321
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(321)
<223> Polynucleotide Sequence Encoding BRCA84D Variable Light Chain

<400> 38
gacattgcga tgacccagtc tcaaaaattc atgtccacat cagtaggaga cagggtcagc 60

gtcacctgca aggccagtca gaatgtggat actaatgtag cctggtatca acagaaacca 120

gggcaatctc ctaaagcact gatttactcg gcatcctacc ggtacagtgg agtccctgat 180

cgcttcacag gcagtggatc tgggacagat ttcactctca ccatcaacaa tgtgcagtct 240

gaagacttgg cagagtattt ctgtcagcaa tataacaact atccattcac gttcggctcg 300

gggacaaagt tggaaataaa a 321

<210> 39
<211> 11
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(11)
<223> BRCA84D Variable Light Chain CDR1

<400> 39

```
Lys Ala Ser Gln Asn Val Asp Thr Asn Val Ala
1               5                   10
```

<210> 40
<211> 33
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(33)

<223> Polynucleotide Sequence Encoding BRCA84D Variable Light Chain CDR1

<400> 40
aaggccagtc agaatgtgga tactaatgta gcc 33

<210> 41
<211> 7
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(7)
<223> BRCA84D Variable Light Chain CDR2

<400> 41

Ser Ala Ser Tyr Arg Tyr Ser
1 5

<210> 42
<211> 21
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(21)
<223> Polynucleotide Sequence Encoding BRCA84D Variable Light Chain CDR2

<400> 42

Thr Cys Gly Gly Cys Ala Thr Cys Cys Thr Ala Cys Cys Gly Gly Thr
1 5 10 15

Ala Cys Ala Gly Thr
20

<210> 43
<211> 9
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(9)
<223> BRCA84D Variable Light Chain CDR3

<400> 43

Gln Gln Tyr Asn Asn Tyr Pro Phe Thr
1 5

<210> 44
<211> 27
<212> DNA
<213> Mus musculus

<220>

<221> misc_feature
<222> (1)..(27)
<223> Polynucleotide Sequence Encoding BRCA84D Variable Light Chain CDR3

<400> 44
cagcaatata acaactatcc attcacg 27

<210> 45
<211> 122
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(122)
<223> Amino Acid Sequence of BRCA84D Variable Heavy Chain

<400> 45

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

Ser Arg Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe
20 25 30

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

Ala Tyr Ile Ser Ser Asp Ser Ser Ala Ile Tyr Tyr Ala Asp Thr Val
50 55 60

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

Leu Gln Met Thr Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Gly Arg Gly Arg Glu Asn Ile Tyr Tyr Gly Ser Arg Leu Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
115 120

<210> 46
<211> 366
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(366)
<223> Polynucleotide Sequence Encoding BRCA84D Variable Heavy Chain

<400> 46
gatgtgcagc tggtggagtc tgggggaggc ttagtgcagc ctggagggtc ccggaaactc 60

tcctgtgcag cctctggatt cactttcagt agctttggaa tgcactgggt tcgtcaggct 120

ccagagaagg ggctggagtg ggtcgcatac attagtagtg acagtagtgc catctactat 180

gcagacacag tgaagggccg attcaccatc tccagagaca atcccaagaa caccctgttc 240

ctgcaaatga ccagtctaag gtctgaggac acggccatgt attactgtgg aagagggagg 300

gaaaacattt actacggtag taggcttgac tactggggcc aaggcaccac tctcacagtc 360

tcctca 366

<210> 47
<211> 4
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(4)
<223> BRCA84D Variable Heavy Chain CDR1

<400> 47

Phe Gly Met His
1

<210> 48
<211> 12
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(12)
<223> Polynucleotide Sequence Encoding BRCA84D Variable Heavy Chain CDR1

<400> 48
tttggaatgc ac 12

<210> 49
<211> 16
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(16)
<223> BRCA84D Variable Heavy Chain CDR2

<400> 49

Tyr Ile Ser Ser Asp Ser Ser Ala Ile Tyr Tyr Ala Asp Thr Val Lys
1 5 10 15

<210> 50
<211> 48
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(48)

<223> Polynucleotide Sequence Encoding BRCA84D Variable Heavy Chain CDR2

<400> 50
tacattagta gtgacagtag tgccatctac tatgcagaca cagtgaag 48

<210> 51
<211> 13
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(13)
<223> BRCA84D Variable Heavy Chain CDR3

<400> 51

Gly Arg Glu Asn Ile Tyr Tyr Gly Ser Arg Leu Asp Tyr
1 5 10

<210> 52
<211> 39
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(39)
<223> Polynucleotide Sequence Encoding BRCA84D Variable Heavy Chain CDR3

<400> 52
gggagggaaa acatttacta cggtagtagg cttgactac 39

<210> 53
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized BRCA84D-1 Variable Light Chain

<400> 53

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

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

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

Tyr Ser Ala Ser Tyr Arg Tyr 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 Tyr Asn Asn Tyr Pro Phe
85 90 95

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

<210> 54
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide Sequence Encoding Humanized BRCA84D-1 Variable Light Chain

<400> 54
gacatccagc tgacccagtc cccctccttc ctgtctgcct ccgtgggcga cagagtgacc 60

atcacatgca aggcctccca gaacgtggac accaacgtgg cctggtatca gcagaagcct 120

ggcaaggccc ctaagctgct gatctactcc gcctcctacc ggtactccgg cgtgccttcc 180

aggttctccg gctccggctc tggcaccgac ttcaccctga ccatctccag cctgcagcct 240

gaggacttcg ccacctacta ctgccagcag tacaacaact acccctttcac cttcggccag 300

ggcaccaagc tggaaatcaa g 321

<210> 55
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized BRCA84D-1 Variable Light Chain CDR1

<400> 55

Lys Ala Ser Gln Asn Val Asp Thr Asn Val Ala
1 5 10

<210> 56
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide Sequence Encoding Humanized BRCA84D-1 Variable Light Chain CDR1

<400> 56
aaggccagtc agaatgtgga tactaatgta gcc 33

<210> 57
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized BRCA84D-1 Variable Light Chain CDR2

<400> 57

Ser Ala Ser Tyr Arg Tyr Ser
1 5

<210> 58
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide Sequence Encoding Humanized BRCA84D-1 Variable Light Chain CDR2

<400> 58
tcggcatcct accggtacag t 21

<210> 59
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized BRCA84D-1 Variable Light Chain CDR3

<400> 59

Gln Gln Tyr Asn Asn Tyr Pro Phe Thr
1 5

<210> 60
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide Sequence Encoding Humanized BRCA84D-1 Variable Light Chain CDR3

<400> 60
cagcaatata acaactatcc attcacg 27

<210> 61
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence of Humanized BRCA84D-1 Variable Heavy Chain

<400> 61

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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

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

```
Ala Tyr Ile Ser Ser Asp Ser Ser Ala Ile Tyr Tyr Ala Asp Thr Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Arg Glu Asn Ile Tyr Tyr Gly Ser Arg Leu Asp Tyr Trp
            100                 105                 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 62
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide Sequence Encoding Humanized BRCA84D-1 Variable Heavy Chain

<400> 62

```
gaggtgcagc tggtcgagtc tggcggagga ctggtgcagc ctggcggctc cctgagactg       60

tcttgcgccg cctccggctt caccttctcc agcttcggca tgcactgggt ccgccaggct      120

ccaggcaagg gactggaatg ggtggcctac atctcctccg actcctccgc catctactac      180

gccgacaccg tgaagggcag gttcaccatc tcccgggaca acgccaagaa ctccctgtac      240

ctgcagatga actccctgcg ggacgaggac accgccgtgt actactgcgc cagaggccgg      300

gagaatatct actacggctc ccggctggat tattggggcc agggcaccac cgtgaccgtg      360

tcctct                                                                 366
```

<210> 63
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized BRCA84D-1 Variable Heavy Chain CDR1

<400> 63

```
Phe Gly Met His
1
```

<210> 64
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide Sequence Encoding Humanized BRCA84D-1 Variable Heavy Chain CDR1

<400> 64
tttggaatgc ac 12

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

<220>
<223> Humanized BRCA84D Variable Heavy Chain CDR2

<400> 65

Tyr Ile Ser Ser Asp Ser Ser Ala Ile Tyr Tyr Ala Asp Thr Val Lys
1 5 10 15

<210> 66
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide Sequence Encoding Humanized BRCA84D-1 Variable Heavy Chain CDR2

<400> 66
tacattagta gtgacagtag tgccatctac tatgcagaca cagtgaag 48

<210> 67
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized BRCA84D-1 Variable Heavy Chain CDR3

<400> 67

Gly Arg Glu Asn Ile Tyr Tyr Gly Ser Arg Leu Asp Tyr
1 5 10

<210> 68
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide Sequence Encoding Humanized BRCA84D-1 Variable Heavy Chain CDR3

<400> 68
gggagggaaa acatttacta cggtagtagg cttgactac 39

<210> 69
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence of hBRCA84D-2VL

<400> 69

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

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

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

Tyr Ser Ala Ser Tyr Arg Tyr 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 Tyr Asn Asn Tyr Pro Phe
85 90 95

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

<210> 70
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide Encoding hBRCA84D-2VL

<400> 70
gacatccagc tgacccagtc cccctccttc ctgtctgcct ccgtgggcga cagagtgacc 60

atcacatgca aggcctccca gaacgtggac accaacgtgg cctggtatca gcagaagcct 120

ggcaaggccc ctaaggcgct gatctactcc gcctcctacc ggtactccgg cgtgccttcc 180

aggttctccg gctccggctc tggcaccgac ttcaccctga ccatctccag cctgcagcct 240

gaggacttcg ccacctacta ctgccagcag tacaacaact acccctttcac cttcggccag 300

ggcaccaagc tggaaatcaa g 321

<210> 71
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence of hBRCA84D-3VL

<400> 71

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

Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Asp Thr Asn
20 25 30

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

Tyr Ser Ala Ser Tyr Arg Tyr 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 Tyr Asn Asn Tyr Pro Phe
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105
```

<210> 72
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide Encoding hBRCA84D-3VL

<400> 72

```
gacatccagc tgacccagtc cccctccttc ctgtctgcct ccgtgggcga cagagtgtcc       60

gtcacatgca aggcctccca gaacgtggac accaacgtgg cctggtatca gcagaagcct      120

ggcaaggccc ctaagctgct gatctactcc gcctcctacc ggtactccgg cgtgccttcc      180

aggttctccg gctccggctc tggcaccgac ttcaccctga ccatctccag cctgcagcct      240

gaggacttcg ccacctacta ctgccagcag tacaacaact acccctttcac cttcggccag      300

ggcaccaagc tggaaatcaa g                                                321
```

<210> 73
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence of hBRCA84D-4VL

<400> 73

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

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

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

Tyr Ser Ala Ser Tyr Arg Tyr 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 Tyr Asn Asn Tyr Pro Phe
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105
```

<210> 74
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide Encoding hBRCA84D-4VL

<400> 74

```
gacatccagc tgacccagtc cccctccttc ctgtctgcct ccgtgggcga cagagtgacc       60

atcacatgca aggcctccca gaacgtggac accaacgtgg cctggtatca gcagaagcct      120

ggccaggccc ctaagctgct gatctactcc gcctcctacc ggtactccgg cgtgccttcc      180

aggttctccg gctccggctc tggcaccgac ttcaccctga ccatctccag cctgcagcct      240

gaggacttcg ccacctacta ctgccagcag tacaacaact acccctttcac cttcggccag      300

ggcaccaagc tggaaatcaa g                                                321
```

<210> 75
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence of hBRCA84D-5VL

<400> 75

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

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

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

Tyr Ser Ala Ser Tyr Arg Tyr 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 Tyr Asn Asn Tyr Pro Phe
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105
```

<210> 76
<211> 321
<212> DNA

<213> Artificial Sequence

<220>
<223> Polynucleotide Encoding hBRCA84D-5VL

<400> 76
gacatccagc tgacccagtc cccctccttc ctgtctgcct ccgtgggcga cagagtgacc 60

atcacatgca aggcctccca gaacgtggac accaacgtgg cctggtatca gcagaagcct 120

ggccaggccc ctaaggcgct gatctactcc gcctcctacc ggtactccgg cgtgccttcc 180

aggttctccg gctccggctc tggcaccgac ttcaccctga ccatctccag cctgcagcct 240

gaggacttcg ccacctacta ctgccagcag tacaacaact acccctttcac cttcggccag 300

ggcaccaagc tggaaatcaa g 321

<210> 77
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence of hBRCA84D-6VL

<400> 77

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

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

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

Tyr Ser Ala Ser Tyr Arg Tyr 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 Glu Tyr Tyr Cys Gln Gln Tyr Asn Asn Tyr Pro Phe
85 90 95

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

<210> 78
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide Encoding hBRCA84D-6VL

<400> 78
gacatccagc tgacccagtc cccctccttc ctgtctgcct ccgtgggcga cagagtgacc 60

atcacatgca aggcctccca gaacgtggac accaacgtgg cctggtatca gcagaagcct 120

ggcaaggccc ctaagctgct gatctactcc gcctcctacc ggtactccgg cgtgccttcc 180

aggttctccg gctccggctc tggcaccgac ttcaccctga ccatctccag cctgcagcct 240

gaggacttcg ccgagtacta ctgccagcag tacaacaact acccttttcac cttcggccag 300

ggcaccaagc tggaaatcaa g 321

<210> 79
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence of hBRCA84D-2VH

<400> 79

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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

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

Ala Tyr Ile Ser Ser Asp Ser Ser Ala Ile Tyr Tyr Ala Asp Thr Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Gly Arg Gly Arg Glu Asn Ile Tyr Tyr Gly Ser Arg Leu Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 80
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide Encoding hBRCA84D-2VH

<400> 80
gaggtgcagc tggtcgagtc tggcggagga ctggtgcagc ctggcggctc cctgagactg 60

tcttgcgccg cctccggctt caccttctcc agcttcggca tgcactgggt ccgccaggct 120

ccaggcaagg gactggaatg ggtggcctac atctcctccg actcctccgc catctactac 180

gccgacaccg tgaagggcag gttcaccatc tcccgggaca acgccaagaa ctccctgtac 240

ctgcagatga actccctgcg ggacgaggac accgccgtgt actactgcgg cagaggccgg 300

gagaatatct actacggctc ccggctggat tattggggcc agggcaccac cgtgaccgtg 360

tcctct 366

<210> 81
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence of hBRCA84D-3VH

<400> 81

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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

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

Ala Tyr Ile Ser Ser Asp Ser Ser Ala Ile Tyr Tyr Ala Asp Thr Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

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

Gly Arg Gly Arg Glu Asn Ile Tyr Tyr Gly Ser Arg Leu Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 82
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide Encoding hBRCA84D-3VH

<400> 82
gaggtgcagc tggtcgagtc tggcggagga ctggtgcagc ctggcggctc cctgagactg 60

tcttgcgccg cctccggctt caccttctcc agcttcggca tgcactgggt ccgccaggct 120

ccaggcaagg gactggaatg ggtggcctac atctcctccg actcctccgc catctactac 180

gccgacaccg tgaagggcag gttcaccatc tcccgggaca acgccaagaa ctccctgtac 240

ctgcagatga actccctgcg ggacgaggac accgccatgt actactgcgg cagaggccgg 300

gagaatatct actacggctc ccggctggat tattggggcc agggcaccac cgtgaccgtg 360

tcctct 366

<210> 83
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence of hBRCA84D-4VH

<400> 83

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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

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

Ala Tyr Ile Ser Ser Asp Ser Ser Ala Ile Tyr Tyr Ala Asp Thr Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Glu Asn Ile Tyr Tyr Gly Ser Arg Leu Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 84
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide Encoding hBRCA84D-4VH

<400> 84
gaggtgcagc tggtcgagtc tggcggagga ctggtgcagc ctggcggctc cctgagactg 60

tcttgcgccg cctccggctt caccttctcc agcttcggca tgcactgggt ccgccaggct 120

ccaggcaagg gactggaatg ggtggcctac atctcctccg actcctccgc catctactac 180

gccgacaccg tgaagggcag gttcaccatc tcccgggaca acgccaagaa ctccctgtac 240

ctgcagatga actccctgcg gagcgaggac accgccgtgt actactgcgc cagaggccgg 300

gagaatatct actacggctc ccggctggat tattggggcc agggcaccac cgtgaccgtg 360

tcctct 366

<210> 85
<211> 214
<212> PRT

<213> Artificial Sequence

<220>
<223> Amino Acid Sequence of chBRCA84D Light Chain

<400> 85

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

Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Asp Thr Asn
20 25 30

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

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

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

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

Thr Phe Gly Ser Gly Thr Lys Leu 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> 86
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide Encoding chBRCA84D Light Chain

<400> 86
gacattgcga tgacccagtc tcaaaaattc atgtccacat cagtaggaga cagggtcagc 60

gtcacctgca aggccagtca gaatgtggat actaatgtag cctggtatca acagaaacca 120

gggcaatctc ctaaagcact gatttactcg gcatcctacc ggtacagtgg agtccctgat 180

cgcttcacag gcagtggatc tgggacagat ttcactctca ccatcaacaa tgtgcagtct 240

gaagacttgg cagagtattt ctgtcagcaa tataacaact atccattcac gttcggctcg 300

gggacaaagt tggaaataaa acgtacggtg gctgcaccat 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 gttag 645

<210> 87
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence of chBRCA84D Heavy Chain

<400> 87

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

Ser Arg Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe
20 25 30

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

Ala Tyr Ile Ser Ser Asp Ser Ser Ala Ile Tyr Tyr Ala Asp Thr Val
50 55 60

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

Leu Gln Met Thr Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Gly Arg Gly Arg Glu Asn Ile Tyr Tyr Gly Ser Arg Leu Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125

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

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

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
165 170 175

```
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
            180                 185                 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
        195                 200                 205

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

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
225                 230                 235                 240

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

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

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        275                 280                 285

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

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

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

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

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

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

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

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                405                 410                 415

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

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

Ser Pro Gly Lys
    450
```

<210> 88
<211> 1359
<212> DNA
<213> Artificial Sequence

<220>

<223> Polynucleotide Encoding chBRCA84D Heavy Chain

<400> 88
gatgtgcagc tggtggagtc tgggggaggc ttagtgcagc ctggagggtc ccggaaactc 60

tcctgtgcag cctctggatt cactttcagt agctttggaa tgcactgggt tcgtcaggct 120

ccagagaagg ggctggagtg ggtcgcatac attagtagtg acagtagtgc catctactat 180

gcagacacag tgaagggccg attcaccatc tccagagaca atcccaagaa caccctgttc 240

ctgcaaatga ccagtctaag gtctgaggac acggccatgt attactgtgg aagagggagg 300

gaaaacattt actacggtag taggcttgac tactggggcc aaggcaccac tctcacagtc 360

tcctcagcct ccaccaaggg cccatcggtc ttcccctgg caccctcctc caagagcacc 420

tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 480

gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 540

tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 600

cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagagagtt 660

gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 720

gggggaccgt cagtcttcct cttccccca aaacccaagg acaccctcat gatctcccgg 780

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 840

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 900

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 960

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccca cgagaaaacc 1020

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 1080

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 1140

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 1200

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 1260

aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 1320

tacacgcaga agagcctctc cctgtctccg ggtaaatga 1359

<210> 89
<211> 191
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(191)
<223> Amino Acid Sequence of VEGF Isoform 162

<400> 89

```
Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
1               5                  10                  15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
            20                  25                  30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
        35                  40                  45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
    50                  55                  60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
65                  70                  75                  80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
                85                  90                  95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
            100                 105                 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
        115                 120                 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly
    130                 135                 140

Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr
145                 150                 155                 160

Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln
                165                 170                 175

Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg
            180                 185                 190
```

<210> 90
<211> 990
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(990)
<223> Polynucleotide Encoding the Amino Acid Sequence of VEGF Isoform 162

<400> 90

```
cagtgtgctg gcggcccggc gcgagccggc ccggccccgg tcgggcctcc gaaaccatga       60

actttctgct gtcttgggtg cattggagcc tcgccttgct gctctacctc caccatgcca      120

agtggtccca ggctgcaccc atggcagaag gaggagggca gaatcatcac gaagtggtga      180

agttcatgga tgtctatcag cgcagctact gccatccaat cgagaccctg gtggacatct      240

tccaggagta ccctgatgag atcgagtaca tcttcaagcc atcctgtgtg cccctgatgc      300

gatgcggggg ctgctgcaat gacgagggcc tggagtgtgt gcccactgag gagtccaaca      360

tcaccatgca gattatgcgg atcaaacctc accaaggcca gcacatagga gagatgagct      420
```

tcctacagca caacaaatgt gaatgcagac caaagaaaga tagagcaaga caagaaaatc 480

cctgtgggcc ttgctcagag cggagaaagc atttgtttgt acaagatccg cagacgtgta 540

aatgttcctg caaaaacaca gactcgcgtt gcaaggcgag gcagcttgag ttaaacgaac 600

gtacttgcag atgtgacaag ccgaggcggt gagccgggca ggaggaagga gcctccctca 660

gggtttcggg aaccagatct ctcaccagga aagactgata cagaacgatc gatacagaaa 720

ccacgctgcc gccaccacac catcaccatc gacagaacag tccttaatcc agaaacctga 780

aatgaaggaa gaggagactc tgcgcagagc actttgggtc cggagggcga gactccggcg 840

gaagcattcc cgggcgggtg acccagcacg gtccctcttg gaattggatt cgccatttta 900

tttttcttgc tgctaaatca ccgagcccgg aagattagag agttttattt ctgggattcc 960

tgtagacaca ccgcggccgc cagcacactg 990

<210> 91
<211> 232
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(232)
<223> Amino Acid Sequence of VEGF Isoform 206

<400> 91

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Lys Ser Val
130 135 140

```
Arg Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys Lys Ser Arg Tyr
145                 150                 155                 160

Lys Ser Trp Ser Val Tyr Val Gly Ala Arg Cys Cys Leu Met Pro Trp
                165                 170                 175

Ser Leu Pro Gly Pro His Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys
            180                 185                 190

His Leu Phe Val Gln Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn
        195                 200                 205

Thr Asp Ser Arg Cys Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr
    210                 215                 220

Cys Arg Cys Asp Lys Pro Arg Arg
225                 230
```

<210> 92
<211> 1338
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(1338)
<223> Amino Acid Sequence of VEGF Receptor VEGFR-1

<400> 92

```
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 Phe 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>  93
<211>  1356
<212>  PRT
<213>  Homo sapiens

<220>
<221>  MISC_FEATURE
<222>  (1)..(1356)
<223>  Amino Acid Sequence of VEGF Receptor VEGFR-2

<400>  93

Met Gln Ser Lys Val Leu Leu Ala Val Ala Leu Trp Leu Cys Val Glu
1               5                  10                  15
```

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

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

Leu Gln Ile Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro
    50                  55                  60

Asn Asn Gln Ser Gly Ser Glu Gln Arg Val Glu Val Thr Glu Cys Ser
65                  70                  75                  80

Asp Gly Leu Phe Cys Lys Thr Leu Thr Ile Pro Lys Val Ile Gly Asn
                85                  90                  95

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

Val Ile Tyr Val Tyr Val Gln Asp Tyr Arg Ser Pro Phe Ile Ala Ser
        115                 120                 125

Val Ser Asp Gln His Gly Val Val Tyr Ile Thr Glu Asn Lys Asn Lys
    130                 135                 140

Thr Val Val Ile Pro Cys Leu Gly Ser Ile Ser Asn Leu Asn Val Ser
145                 150                 155                 160

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

Ile Ser Trp Asp Ser Lys Lys Gly Phe Thr Ile Pro Ser Tyr Met Ile
            180                 185                 190

Ser Tyr Ala Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp Glu Ser
        195                 200                 205

Tyr Gln Ser Ile Met Tyr Ile Val Val Val Val Gly Tyr Arg Ile Tyr
    210                 215                 220

Asp Val Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly Glu
225                 230                 235                 240

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

Asp Phe Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys Lys Leu
            260                 265                 270

Val Asn Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe
        275                 280                 285

Leu Ser Thr Leu Thr Ile Asp Gly Val Thr Arg Ser Asp Gln Gly Leu
    290                 295                 300

Tyr Thr Cys Ala Ala Ser Ser Gly Leu Met Thr Lys Lys Asn Ser Thr
305                 310                 315                 320

Phe Val Arg Val His Glu Lys Pro Phe Val Ala Phe Gly Ser Gly Met
                325                 330                 335
```

```
Glu Ser Leu Val Glu Ala Thr Val Gly Glu Arg Val Arg Ile Pro Ala
            340                 345                 350

Lys Tyr Leu Gly Tyr Pro Pro Pro Glu Ile Lys Trp Tyr Lys Asn Gly
        355                 360                 365

Ile Pro Leu Glu Ser Asn His Thr Ile Lys Ala Gly His Val Leu Thr
    370                 375                 380

Ile Met Glu Val Ser Glu Arg Asp Thr Gly Asn Tyr Thr Val Ile Leu
385                 390                 395                 400

Thr Asn Pro Ile Ser Lys Glu Lys Gln Ser His Val Val Ser Leu Val
                405                 410                 415

Val Tyr Val Pro Pro Gln Ile Gly Glu Lys Ser Leu Ile Ser Pro Val
            420                 425                 430

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

Ala Ile Pro Pro Pro His His Ile His Trp Tyr Trp Gln Leu Glu Glu
    450                 455                 460

Glu Cys Ala Asn Glu Pro Ser Gln Ala Val Ser Val Thr Asn Pro Tyr
465                 470                 475                 480

Pro Cys Glu Glu Trp Arg Ser Val Glu Asp Phe Gln Gly Gly Asn Lys
                485                 490                 495

Ile Glu Val Asn Lys Asn Gln Phe Ala Leu Ile Glu Gly Lys Asn Lys
            500                 505                 510

Thr Val Ser Thr Leu Val Ile Gln Ala Ala Asn Val Ser Ala Leu Tyr
        515                 520                 525

Lys Cys Glu Ala Val Asn Lys Val Gly Arg Gly Glu Arg Val Ile Ser
    530                 535                 540

Phe His Val Thr Arg Gly Pro Glu Ile Thr Leu Gln Pro Asp Met Gln
545                 550                 555                 560

Pro Thr Glu Gln Glu Ser Val Ser Leu Trp Cys Thr Ala Asp Arg Ser
                565                 570                 575

Thr Phe Glu Asn Leu Thr Trp Tyr Lys Leu Gly Pro Gln Pro Leu Pro
            580                 585                 590

Ile His Val Gly Glu Leu Pro Thr Pro Val Cys Lys Asn Leu Asp Thr
        595                 600                 605

Leu Trp Lys Leu Asn Ala Thr Met Phe Ser Asn Ser Thr Asn Asp Ile
    610                 615                 620

Leu Ile Met Glu Leu Lys Asn Ala Ser Leu Gln Asp Gln Gly Asp Tyr
625                 630                 635                 640

Val Cys Leu Ala Gln Asp Arg Lys Thr Lys Lys Arg His Cys Val Val
                645                 650                 655
```

```
Arg Gln Leu Thr Val Leu Glu Arg Val Ala Pro Thr Ile Thr Gly Asn
            660                 665                 670

Leu Glu Asn Gln Thr Thr Ser Ile Gly Glu Ser Ile Glu Val Ser Cys
        675                 680                 685

Thr Ala Ser Gly Asn Pro Pro Pro Gln Ile Met Trp Phe Lys Asp Asn
    690                 695                 700

Glu Thr Leu Val Glu Asp Ser Gly Ile Val Leu Lys Asp Gly Asn Arg
705                 710                 715                 720

Asn Leu Thr Ile Arg Arg Val Arg Lys Glu Asp Glu Gly Leu Tyr Thr
                725                 730                 735

Cys Gln Ala Cys Ser Val Leu Gly Cys Ala Lys Val Glu Ala Phe Phe
            740                 745                 750

Ile Ile Glu Gly Ala Gln Glu Lys Thr Asn Leu Glu Ile Ile Ile Leu
        755                 760                 765

Val Gly Thr Ala Val Ile Ala Met Phe Phe Trp Leu Leu Leu Val Ile
    770                 775                 780

Ile Leu Arg Thr Val Lys Arg Ala Asn Gly Gly Glu Leu Lys Thr Gly
785                 790                 795                 800

Tyr Leu Ser Ile Val Met Asp Pro Asp Glu Leu Pro Leu Asp Glu His
                805                 810                 815

Cys Glu Arg Leu Pro Tyr Asp Ala Ser Lys Trp Glu Phe Pro Arg Asp
            820                 825                 830

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

Ile Glu Ala Asp Ala Phe Gly Ile Asp Lys Thr Ala Thr Cys Arg Thr
    850                 855                 860

Val Ala Val Lys Met Leu Lys Glu Gly Ala Thr His Ser Glu His Arg
865                 870                 875                 880

Ala Leu Met Ser Glu Leu Lys Ile Leu Ile His Ile Gly His His Leu
                885                 890                 895

Asn Val Val Asn Leu Leu Gly Ala Cys Thr Lys Pro Gly Gly Pro Leu
            900                 905                 910

Met Val Ile Val Glu Phe Cys Lys Phe Gly Asn Leu Ser Thr Tyr Leu
        915                 920                 925

Arg Ser Lys Arg Asn Glu Phe Val Pro Tyr Lys Thr Lys Gly Ala Arg
    930                 935                 940

Phe Arg Gln Gly Lys Asp Tyr Val Gly Ala Ile Pro Val Asp Leu Lys
945                 950                 955                 960

Arg Arg Leu Asp Ser Ile Thr Ser Ser Gln Ser Ser Ala Ser Ser Gly
                965                 970                 975
```

```
Phe Val Glu Glu Lys Ser Leu Ser Asp Val Glu Glu Glu Glu Ala Pro
            980                 985                 990

Glu Asp Leu Tyr Lys Asp Phe Leu  Thr Leu Glu His Leu  Ile Cys Tyr
        995                 1000                1005

Ser Phe  Gln Val Ala Lys Gly  Met Glu Phe Leu Ala  Ser Arg Lys
    1010                1015                1020

Cys Ile  His Arg Asp Leu Ala  Ala Arg Asn Ile Leu  Leu Ser Glu
    1025                1030                1035

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

Tyr Lys  Asp Pro Asp Tyr Val  Arg Lys Gly Asp Ala  Arg Leu Pro
    1055                1060                1065

Leu Lys  Trp Met Ala Pro Glu  Thr Ile Phe Asp Arg  Val Tyr Thr
    1070                1075                1080

Ile Gln  Ser Asp Val Trp Ser  Phe Gly Val Leu Leu  Trp Glu Ile
    1085                1090                1095

Phe Ser  Leu Gly Ala Ser Pro  Tyr Pro Gly Val Lys  Ile Asp Glu
    1100                1105                1110

Glu Phe  Cys Arg Arg Leu Lys  Glu Gly Thr Arg Met  Arg Ala Pro
    1115                1120                1125

Asp Tyr  Thr Thr Pro Glu Met  Tyr Gln Thr Met Leu  Asp Cys Trp
    1130                1135                1140

His Gly  Glu Pro Ser Gln Arg  Pro Thr Phe Ser Glu  Leu Val Glu
    1145                1150                1155

His Leu  Gly Asn Leu Leu Gln  Ala Asn Ala Gln Gln  Asp Gly Lys
    1160                1165                1170

Asp Tyr  Ile Val Leu Pro Ile  Ser Glu Thr Leu Ser  Met Glu Glu
    1175                1180                1185

Asp Ser  Gly Leu Ser Leu Pro  Thr Ser Pro Val Ser  Cys Met Glu
    1190                1195                1200

Glu Glu  Glu Val Cys Asp Pro  Lys Phe His Tyr Asp  Asn Thr Ala
    1205                1210                1215

Gly Ile  Ser Gln Tyr Leu Gln  Asn Ser Lys Arg Lys  Ser Arg Pro
    1220                1225                1230

Val Ser  Val Lys Thr Phe Glu  Asp Ile Pro Leu Glu  Glu Pro Glu
    1235                1240                1245

Val Lys  Val Ile Pro Asp Asp  Asn Gln Thr Asp Ser  Gly Met Val
    1250                1255                1260

Leu Ala  Ser Glu Glu Leu Lys  Thr Leu Glu Asp Arg  Thr Lys Leu
    1265                1270                1275
```

```
Ser Pro  Ser Phe Gly Gly Met  Val Pro Ser Lys Ser  Arg Glu Ser
    1280                 1285                 1290

Val Ala  Ser Glu Gly Ser Asn  Gln Thr Ser Gly Tyr  Gln Ser Gly
    1295                 1300                 1305

Tyr His  Ser Asp Asp Thr Asp  Thr Thr Val Tyr Ser  Ser Glu Glu
    1310                 1315                 1320

Ala Glu  Leu Leu Lys Leu Ile  Glu Ile Gly Val Gln  Thr Gly Ser
    1325                 1330                 1335

Thr Ala  Gln Ile Leu Gln Pro  Asp Ser Gly Thr Thr  Leu Ser Ser
    1340                 1345                 1350

Pro Pro  Val
    1355
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<210> 94
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence of the Light Chain of Bevacizumab

<400> 94

```
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 Ser Ala Ser Gln Asp Ile Ser Asn Tyr
            20                  25                  30

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

Tyr Phe Thr Ser Ser Leu His 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 Tyr Ser Thr Val Pro Trp
                85                  90                  95

Thr Phe Gly Gln 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 Glu 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> 95
<211> 453
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence of the Heavy Chain of Bevacizumab

<400> 95

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
            20                  25                  30

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

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Ala Asp Phe
    50                  55                  60

Lys Arg Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Lys Tyr Pro His Tyr Tyr Gly Ser Ser His Trp Tyr Phe Asp Val
            100                 105                 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

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

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

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
    210                 215                 220
```

```
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
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 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala
                325                 330                 335

Pro 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 Arg 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 Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln 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 Pro Gly Lys
    450
```

<210> 96
<211> 218
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(218)
<223> Amino Acid Sequence of the IgG1 Fc Region

<400> 96

```
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
1               5                   10                  15
```

```
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
            20                  25                  30

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
        35                  40                  45

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
    50                  55                  60

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
65                  70                  75                  80

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
                85                  90                  95

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
            100                 105                 110

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
        115                 120                 125

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
    130                 135                 140

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
145                 150                 155                 160

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

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

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
        195                 200                 205

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
    210                 215
```

<210> 97
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Preferred Linker of VL and VH Diabody Domains

<400> 97

```
Gly Gly Gly Ser Gly Gly Gly Gly
1               5
```

<210> 98
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide Encoding Preferred Linker of VL and VH Diabody Domains

<400> 98
ggaggcggat ccggaggcgg aggc 24

<210> 99
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Cysteine-Containing Linker

<400> 99

Leu Gly Gly Cys
1

<210> 100
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence of Hinge Domain Linker

<400> 100

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

<210> 101
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence of Hinge Domain Linker

<400> 101

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser
1 5 10

<210> 102
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Cysteine-Containing, Heterodimer-Promoting Linker Derived from IgG Hinge Domain

<400> 102

Val Glu Pro Lys Ser Cys
1 5

<210> 103
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide Encoding Cysteine-Containing,
Heterodimer-Promoting Linker Derived from IgG Hinge Domain

<400> 103
gttgagccca aatcttgt 18

<210> 104
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Cysteine-Containing, Heterodimer-Promoting Linker Derived from
Human Kappa Light Chain Domain

<400> 104

Leu Gly Gly Cys Phe Asn Arg Gly Glu Cys
1 5 10

<210> 105
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide Encoding Cysteine-Containing,
Heterodimer-Promoting Linker Derived from Human Kappa Light Chain
Domain

<400> 105
ctgggaggct gcttcaacag gggagagtgt 30

<210> 106
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Cysteine-Containing, Heterodimer-Promoting Linker Derived from
Human Kappa Light Chain Domain

<400> 106

Phe Asn Arg Gly Glu Cys
1 5

<210> 107
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide Encoding Cysteine-Containing,
Heterodimer-Promoting Linker Derived from Human Kappa Light Chain
Domain

<400> 107
ttcaacaggg gagagtgt 18

<210> 108
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence of E-coil Heterodimer-Promoting Domain

<400> 108

Glu Val Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys Glu Val
1 5 10 15

Ala Ala Leu Glu Lys Glu Val Ala Ala Leu Glu Lys
20 25

<210> 109
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence of K-coil Heterodimer-Promoting Domain

<400> 109

Lys Val Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu Lys Val
1 5 10 15

Ala Ala Leu Lys Glu Lys Val Ala Ala Leu Lys Glu
20 25

<210> 110
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino Acid Sequence of Linker

<400> 110

Gly Gly Gly Asn Ser
1 5