SEQUENCE LISTING

<110> Allgenesis Biotherapeutics Inc.
AP Biosciences, Inc.

<120> Multi-targeting fusion proteins and uses thereof

<130> 688947.3WO

<160> 50

<170> PatentIn version 3.5

<210> 1
<211> 897
<212> DNA
<213> Homo sapiens

<400> 1
cagggcctgg tcgtcacacc cccggggcca gagcttgtcc tcaatgtctc cagcaccttc 60

gttctgacct gctcgggttc agctccggtg gtgtgggaac ggatgtccca ggagccccca 120

caggaaatgg ccaaggccca ggatggcacc ttctccagcg tgctcacact gaccaacctc 180

actgggctag acacgggaga atacttttgc acccacaatg actcccgtgg actggagacc 240

gatgagcgga aacggctcta catctttgtg ccagatccca ccgtgggctt cctccctaat 300

gatgccgagg aactattcat ctttctcacg gaaataactg agatcaccat tccatgccga 360

gtaacagacc cacagctggt ggtgacactg cacgagaaga aaggggacgt tgcactgcct 420

gtcccctatg atcaccaacg tggctttttt ggtatctttg aggacagaag ctacatctgc 480

aaaaccacca ttggggacag ggaggtggat tctgatgcct actatgtcta cagactccag 540

gtgtcatcca tcaacgtctc tgtgaacgca gtgcagactg tggtccgcca gggtgagaac 600

atcaccctca tgtgcattgt gatcgggaat gaggtggtca acttcgagtg gacatacccc 660

cgcaaagaaa gtgggcggct ggtggagccg gtgactgact tcctcttgga tatgccttac 720

cacatccgct ccatcctgca catccccagt gccgagttag aagactcggg gacctacacc 780

tgcaatgtga cggagagtgt gaatgaccat caggatgaaa aggccatcaa catcaccgtg 840

gttgagagcg gctacgtgcg gctcctggga gaggtgggca cactacaatt tgctgag 897

<210> 2
<211> 299
<212> PRT
<213> Homo sapiens

<400> 2

Gln Gly Leu Val Val Thr Pro Pro Gly Pro Glu Leu Val Leu Asn Val
1 5 10 15

Ser Ser Thr Phe Val Leu Thr Cys Ser Gly Ser Ala Pro Val Val Trp
20 25 30

Glu Arg Met Ser Gln Glu Pro Pro Gln Glu Met Ala Lys Ala Gln Asp
35 40 45

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Gly Thr Phe Ser Ser Val Leu Thr Leu Thr Asn Leu Thr Gly Leu Asp
    50                  55                  60

Thr Gly Glu Tyr Phe Cys Thr His Asn Asp Ser Arg Gly Leu Glu Thr
65                  70                  75                  80

Asp Glu Arg Lys Arg Leu Tyr Ile Phe Val Pro Asp Pro Thr Val Gly
                85                  90                  95

Phe Leu Pro Asn Asp Ala Glu Glu Leu Phe Ile Phe Leu Thr Glu Ile
            100                 105                 110

Thr Glu Ile Thr Ile Pro Cys Arg Val Thr Asp Pro Gln Leu Val Val
        115                 120                 125

Thr Leu His Glu Lys Lys Gly Asp Val Ala Leu Pro Val Pro Tyr Asp
    130                 135                 140

His Gln Arg Gly Phe Phe Gly Ile Phe Glu Asp Arg Ser Tyr Ile Cys
145                 150                 155                 160

Lys Thr Thr Ile Gly Asp Arg Glu Val Asp Ser Asp Ala Tyr Tyr Val
                165                 170                 175

Tyr Arg Leu Gln Val Ser Ser Ile Asn Val Ser Val Asn Ala Val Gln
            180                 185                 190

Thr Val Val Arg Gln Gly Glu Asn Ile Thr Leu Met Cys Ile Val Ile
        195                 200                 205

Gly Asn Glu Val Val Asn Phe Glu Trp Thr Tyr Pro Arg Lys Glu Ser
    210                 215                 220

Gly Arg Leu Val Glu Pro Val Thr Asp Phe Leu Leu Asp Met Pro Tyr
225                 230                 235                 240

His Ile Arg Ser Ile Leu His Ile Pro Ser Ala Glu Leu Glu Asp Ser
                245                 250                 255

Gly Thr Tyr Thr Cys Asn Val Thr Glu Ser Val Asn Asp His Gln Asp
            260                 265                 270

Glu Lys Ala Ile Asn Ile Thr Val Val Glu Ser Gly Tyr Val Arg Leu
        275                 280                 285

Leu Gly Glu Val Gly Thr Leu Gln Phe Ala Glu
    290                 295
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<210> 3
<211> 891
<212> DNA

<213> Artificial Sequence

<220>
<223> Coding sequence for modified PID

<400> 3
ctggtcgtga cacctcccgg acccgagctg gtgctcaacg tctcctccac ctttgtgctg 60

acatgcagcg gcagcgctcc tgtggtctgg gaacggatgt cccaggagcc tccccaggaa 120

atggccaagg cccaggacgg caccttttcc agcgtcctca cactcaccaa cctgacaggc 180

ctggacaccg gcgagtactt ttgcacccac aatgactcca ggggactgga aaccgatgag 240

cggaagcggc tctacatttt cgtccccgac cccaccgtcg gatttctgcc taatgacgct 300

gaagagctgt ttatcttcct gacagagatc accgaaatca ccatcccctg tcgggtcacc 360

gatccccagc tggtggtcac actgcacgag aagaagggag atgtcgccct gcctgtgcct 420

tatgaccatc agaggggctt ttccggcatt ttcgaggaca ggagctacat ctgcaaaacc 480

accatcggag accgggaggt cgacagcgat gcctattacg tctaccggct ccaggtctcc 540

tccatcaatg tgagcgtgaa tgctgtccag acagtggtcc ggcagggcga gaatatcaca 600

ctgatgtgca ttgtcattgg caacgaggtg gtcaacttcg agtggaccta tcctaggaag 660

gagagcggcc ggctcgtcga acctgtgacc gacttcctcc tggacatgcc ttaccacatt 720

cggtccatcc tgcacattcc tagcgccgag ctggaggaca gcggaaccta cacctgcaac 780

gtgaccgagt ccgtgaatga ccaccaggat gagaaggcca tcaacatcac agtcgtggag 840

agcggatacg tcaggctgct cggagaagtc ggcacactgc agttcgccga g 891

<210> 4
<211> 891
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence for modified PID

<400> 4
ctggtcgtca cacccccggg gccagagctt gtcctcaatg tctccagcac cttcgttctg 60

acctgctcgg gttcagctcc ggtggtgtgg gaacggatgt cccaggagcc cccacaggaa 120

atggccaagg cccaggatgg caccttctcc agcgtgctca cactgaccaa cctcactggg 180

ctagacacgg gagaatactt ttgcacccac aatgactccc gtggactgga gaccgatgag 240

cggaaacggc tctacatctt tgtgccagat cccaccgtgg gcttcctccc taatgatgcc 300

gaggaactat tcatctttct cacggaaata actgagatca ccattccatg ccgagtaaca 360

gacccacagc tggtggtgac actgcacgag aagaaagggg acgttgcact gcctgtcccc 420

tatgatcacc aacgtggctt ttccggtatc tttgaggaca gaagctacat ctgcaaaacc 480

accattgggg acagggaggt ggattctgat gcctactatg tctacagact ccaggtgtca 540

tccatcaacg tctctgtgaa cgcagtgcag actgtggtcc gccagggtga gaacatcacc 600

ctcatgtgca ttgtgatcgg gaatgaggtg gtcaacttcg agtggacata cccccgcaaa 660

gaaagtgggc ggctggtgga gccggtgact gacttcctct tggatatgcc ttaccacatc 720

cgctccatcc tgcacatccc cagtgccgag ttagaagact cggggaccta cacctgcaat 780

gtgacggaga gtgtgaatga ccatcaggat gaaaaggcca tcaacatcac cgtggttgag 840

agcggctacg tgcggctcct gggagaggtg ggcacactac aatttgctga g 891

<210> 5
<211> 297
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified PID sequence

<400> 5

Leu Val Val Thr Pro Pro Gly Pro Glu Leu Val Leu Asn Val Ser Ser
1 5 10 15

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

Met Ser Gln Glu Pro Pro Gln Glu Met Ala Lys Ala Gln Asp Gly Thr
35 40 45

Phe Ser Ser Val Leu Thr Leu Thr Asn Leu Thr Gly Leu Asp Thr Gly
50 55 60

Glu Tyr Phe Cys Thr His Asn Asp Ser Arg Gly Leu Glu Thr Asp Glu
65 70 75 80

Arg Lys Arg Leu Tyr Ile Phe Val Pro Asp Pro Thr Val Gly Phe Leu
85 90 95

Pro Asn Asp Ala Glu Glu Leu Phe Ile Phe Leu Thr Glu Ile Thr Glu
100 105 110

Ile Thr Ile Pro Cys Arg Val Thr Asp Pro Gln Leu Val Val Thr Leu
115 120 125

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

Arg Gly Phe Ser Gly Ile Phe Glu Asp Arg Ser Tyr Ile Cys Lys Thr
145 150 155 160

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

Leu Gln Val Ser Ser Ile Asn Val Ser Val Asn Ala Val Gln Thr Val
180 185 190

Val Arg Gln Gly Glu Asn Ile Thr Leu Met Cys Ile Val Ile Gly Asn

195 200 205

Glu Val Val Asn Phe Glu Trp Thr Tyr Pro Arg Lys Glu Ser Gly Arg
210 215 220

Leu Val Glu Pro Val Thr Asp Phe Leu Leu Asp Met Pro Tyr His Ile
225 230 235 240

Arg Ser Ile Leu His Ile Pro Ser Ala Glu Leu Glu Asp Ser Gly Thr
245 250 255

Tyr Thr Cys Asn Val Thr Glu Ser Val Asn Asp His Gln Asp Glu Lys
260 265 270

Ala Ile Asn Ile Thr Val Val Glu Ser Gly Tyr Val Arg Leu Leu Gly
275 280 285

Glu Val Gly Thr Leu Gln Phe Ala Glu
290 295

<210> 6
<211> 612
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence for VID

<400> 6
gacactggta gacctttgt tgaaatgtat tctgaaattc ctgaaattat tcatatgact 60

gaaggaagag aacttgttat tccttgtaga gttacttctc ctaatattac tgttactctt 120

aagaagtttc ctcttgatac tcttattcct gatggaaaga gaattatttg ggattctaga 180

aagggattta ttatttctaa tgctacttat aaggaaattg gacttcttac ttgtgaagct 240

actgttaatg gacatcttta taagactaat tatcttactc atagacaaac taataccatc 300

atcgacgtgg ttctgagtcc gtctcatgga attgaactat ctgttggaga aaagcttgtc 360

ttaaattgta cagcaagaac tgaactaaat gtggggattg acttcaactg ggaataccct 420

tcttcgaagc atcagcataa gaaacttgta aaccgagacc taaaaaccca gtctgggagt 480

gagatgaaga aattcttgag caccctgact atagatggtg taacccggag tgaccaagga 540

ttgtacacct gtgcagcatc cagtgggctg atgaccaaga agaacagcac atttgtcagg 600

gtccatgaaa aa 612

<210> 7
<211> 204
<212> PRT
<213> Artificial Sequence

<220>
<223> VID sequence

<400> 7

Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu Ile
1 5 10 15

Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val Thr
20 25 30

Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu
35 40 45

Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile
50 55 60

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

Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln
85 90 95

Thr Asn Thr Ile Ile Asp Val Val Leu Ser Pro Ser His Gly Ile Glu
100 105 110

Leu Ser Val Gly Glu Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu
115 120 125

Leu Asn Val Gly Ile Asp Phe Asn Trp Glu Tyr Pro Ser Ser Lys His
130 135 140

Gln His Lys Lys Leu Val Asn Arg Asp Leu Lys Thr Gln Ser Gly Ser
145 150 155 160

Glu Met Lys Lys Phe Leu Ser Thr Leu Thr Ile Asp Gly Val Thr Arg
165 170 175

Ser Asp Gln Gly Leu Tyr Thr Cys Ala Ala Ser Ser Gly Leu Met Thr
180 185 190

Lys Lys Asn Ser Thr Phe Val Arg Val His Glu Lys
195 200

<210> 8
<211> 609
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence for modified VID

<400> 8
ggaaggccct tcgtggagat gtacagcgag attcctgaga ttatccacat gaccgaggga 60

cgggaactgg tgattccctg ccgggtcacc agccccaaca tcaccgtgac cctcaagaag 120

ttccccctgg acaccctgat ccctgacggc aaaaggatta tctgggacag ccggaagggc 180

tttatcatca gcaatgccac atacaaggag attggactcc tgacctgcga ggctacagtc 240

aacggacacc tgtacaagac caactacctg acccaccggc agaccaatac catcatcgac 300

gtggtgctga gccccagcca cggaattgag ctgagcgtgg gagaaaaact cgtgctcaac 360

tgcacagccc ggaccgaact caatgtcgga atcgacttca actgggaata ccccagctcc 420

aagcaccagc acaagaagct ggtcaaccgg gatctcaaga cccagtccgg cagcgaaatg 480

aagaagttcc tcagcaccct gaccatcgat ggcgtcacaa ggagcgatca gggactctac 540

acctgcgccg ctagctccgg actcatgacc aagaagaact ccacatttgt ccgggtgcac 600

gaaaagtga 609

<210> 9
<211> 606
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence for modified VID

<400> 9
ggtagacctt ttgttgaaat gtattctgaa attcctgaaa ttattcatat gactgaagga 60

agagaacttg ttattccttg tagagttact tctcctaata ttactgttac tcttaagaag 120

tttcctcttg atactcttat tcctgatgga aagagaatta tttgggattc tagaaaggga 180

tttattattt ctaatgctac ttataaggaa attggacttc ttacttgtga agctactgtt 240

aatggacatc tttataagac taattatctt actcatagac aaactaatac catcatcgac 300

gtggttctga gtccgtctca tggaattgaa ctatctgttg gagaaaagct tgtcttaaat 360

tgtacagcaa gaactgaact aaatgtgggg attgacttca actgggaata cccttcttcg 420

aagcatcagc ataagaaact tgtaaaccga gacctaaaaa cccagtctgg gagtgagatg 480

aagaaattct tgagcaccct gactatagat ggtgtaaccc ggagtgacca aggattgtac 540

acctgtgcag catccagtgg gctgatgacc aagaagaaca gcacatttgt cagggtccat 600

gaaaaa 606

<210> 10
<211> 202
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified VID sequence

<400> 10

Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu Ile Ile His
1 5 10 15

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

Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro

35 40 45

Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser
50 55 60

Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val
65 70 75 80

Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln Thr Asn
85 90 95

Thr Ile Ile Asp Val Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser
100 105 110

Val Gly Glu Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn
115 120 125

Val Gly Ile Asp Phe Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His
130 135 140

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

Lys Lys Phe Leu Ser Thr Leu Thr Ile Asp Gly Val Thr Arg Ser Asp
165 170 175

Gln Gly Leu Tyr Thr Cys Ala Ala Ser Ser Gly Leu Met Thr Lys Lys
180 185 190

Asn Ser Thr Phe Val Arg Val His Glu Lys
195 200

<210> 11
<211> 681
<212> DNA
<213> Homo sapiens

<400> 11
gacaaaactc acacatgtcc accgtgtcca gcacctgaac tcctgggtgg accgtcagtc 60

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 120

tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 180

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 240

cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 300

tgcaaggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa 360

gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag 420

aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 480

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 540

gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 600

aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 660

ctctccctgt ctccgggtaa a 681

<210> 12
<211> 227
<212> PRT
<213> Homo sapiens

<400> 12

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

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

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

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

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

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

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

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

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

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

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

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

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

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220
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Pro Gly Lys
225

<210> 13
<211> 678
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence for Fc sequence of Fusion Protein 6

<400> 13
gataagaccc acacctgtcc tccttgtcct gctcctgagc tcctcggcgg acctagcgtg 60

ttcctgtttc cccctaagcc taaagacacc ctcatgatca gccggacccc cgaggtcaca 120

tgcgtggtgg tcgacgtctc ccatgaggat cccgaggtga agttcaattg gtacgtcgac 180

ggcgtcgagg tccacaatgc caaaaccaaa ccccgggagg agcagtacaa cagcacctat 240

agggtggtca gcgtcctgac cgtgctgcac caagactggc tgaacggcaa ggagtacaaa 300

tgcaaagtca gcaataaggc cctccccgcc cccattgaga agaccatctc caaggctaag 360

ggccaaccta gggagcccca ggtgtacacc ctgcctccca gccgggatga gctgacaaag 420

aaccaggtga gcctcacctg tctggtgaag ggcttttacc cctccgatat tgccgtggag 480

tgggaaagca acggacagcc tgagaacaac tacaagacaa ccccccctgt cctggacagc 540

gatggctcct tcttcctgta cagcaagctg acagtggata agagccggtg gcagcaggga 600

aacgtcttta gctgcagcgt gatgcatgag gccctgcaca atcactacac ccagaagtcc 660

ctgtccctga gccctggc 678

<210> 14
<211> 678
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence for Fc sequence of Fusion Protein 4

<400> 14
gacaaaactc acacatgtcc accgtgtcca gcacctgaac tcctgggtgg accgtcagtc 60

ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 120

tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac 180

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 240

cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 300

tgcaaggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa 360

gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag 420

aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 480

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 540

gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 600

aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 660

ctctccctgt ctccgggt 678

<210> 15
<211> 226
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified Fc sequence of fusion proteins

<400> 15

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

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

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

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

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

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

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

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

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

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

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

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

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

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

210 215 220

Pro Gly
225

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

<220>
<223> Coding sequence of a linker sequence

<400> 16
gccagc 6

<210> 17
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence of a linker sequence

<400> 17
gctagc 6

<210> 18
<211> 2
<212> PRT
<213> Artificial Sequence

<220>
<223> linker sequence

<400> 18

Ala Ser
1

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

<220>
<223> Coding sequence of a linker sequence

<400> 19
ggaggaggcg gtggatct 18

<210> 20
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> linker sequence

<400> 20

Gly Gly Gly Gly Gly Ser

1 5

<210> 21
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence of a linker sequence

<400> 21
ggaggc 6

<210> 22
<211> 2
<212> PRT
<213> Artificial Sequence

<220>
<223> linker sequence

<400> 22

Gly Gly
1

<210> 23
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence of a linker sequence

<400> 23
ggcggcggcg gcagcggcgg aggcggatcc ggcggaggcg gctcc 45

<210> 24
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> linker sequence

<400> 24

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

<210> 25
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence of a linker sequence

<400> 25
ggagacacc 9

<210> 26

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

<220>
<223> linker sequence

<400> 26

Gly Asp Thr
1

<210> 27
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence of a linker sequence

<400> 27
ggtgga 6

<210> 28
<211> 2
<212> PRT
<213> Artificial Sequence

<220>
<223> linker sequence

<400> 28

Gly Gly
1

<210> 29
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence of a linker sequence

<400> 29
ggaggcggtg gatctggtgg cggtggaagc ggaggtggag gttcc 45

<210> 30
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> linker sequence

<400> 30

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

<210> 31
<211> 9
<212> DNA

<213> Artificial Sequence

<220>
<223> Coding sequence of a linker sequence

<400> 31
ggagacact 9

<210> 32
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> linker sequence

<400> 32

Gly Asp Thr
1

<210> 33
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence of a signal peptide sequence

<400> 33
atggagacag acacactcct gctatgggta ctgcttcttt gggttcccgg atccactggc 60

<210> 34
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Signal peptide sequence

<400> 34

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly
20

<210> 35
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence of a signal peptide sequence

<400> 35
atggagtttg gcctgtcctg gctcttcctc gtggctatcc tgaagggcgt gcagtgt 57

<210> 36
<211> 19
<212> PRT

<213> Artificial Sequence

<220>
<223> Signal peptide sequence

<400> 36

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

Val Gln Cys

<210> 37
<211> 2217
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence of Fusion Protein 1 sequence

<400> 37
gacactggaa gacctttgt tgaaatgtat tctgaaattc ctgaaattat tcatatgact 60

gaaggaagag aacttgttat tccttgtaga gttacttctc ctaatattac tgttactctt 120

aagaagtttc ctcttgatac tcttattcct gatggaaaga gaattatttg ggattctaga 180

aagggattta ttatttctaa tgctacttat aaggaaattg gacttcttac ttgtgaagct 240

actgttaatg gacatcttta taagactaat tatcttactc atagacaaac taataccatc 300

atcgacgtgg ttctgagtcc gtctcatgga attgaactat ctgttggaga aaagcttgtc 360

ttaaattgta cagcaagaac tgaactaaat gtggggattg acttcaactg ggaataccct 420

tcttcgaagc atcagcataa gaaacttgta aaccgagacc taaaaaccca gtctgggagt 480

gagatgaaga aattcttgag caccctgact atagatggtg taacccggag tgaccaagga 540

ttgtacacct gtgcagcatc cagtgggctg atgaccaaga agaacagcac atttgtcagg 600

gtccatgaaa aagacaaaac tcacacatgt ccaccgtgtc cagcacctga actcctgggt 660

ggaccgtcag tcttcctctt ccccccaaaa cccaaggaca ccctcatgat ctcccggacc 720

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 780

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 840

aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 900

aaggagtaca agtgcaaggt ctccaacaaa gccctcccag cccccatcga gaaaaccatc 960

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggat 1020

gagctgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1080

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1140

gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1200

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1260

acgcagaaga gcctctccct gtctccgggt aaaggtggag gaggcggtgg atccggatct 1320

cagggcctgg tcgtcacacc cccggggcca gagcttgtcc tcaatgtctc cagcaccttc 1380

gttctgacct gctcgggttc agctccggtg gtgtgggaac ggatgtccca ggagccccca 1440

caggaaatgg ccaaggccca ggatggcacc ttctccagcg tgctcacact gaccaacctc 1500

actgggctag acacgggaga atacttttgc acccacaatg actcccgtgg actggagacc 1560

gatgagcgga aacggctcta catctttgtg ccagatccca ccgtgggctt cctccctaat 1620

gatgccgagg aactattcat ctttctcacg gaaataactg agatcaccat tccatgccga 1680

gtaacagacc cacagctggt ggtgacactg cacgagaaga aaggggacgt tgcactgcct 1740

gtcccctatg atcaccaacg tggctttttt ggtatctttg aggacagaag ctacatctgc 1800

aaaaccacca ttggggacag ggaggtggat tctgatgcct actatgtcta cagactccag 1860

gtgtcatcca tcaacgtctc tgtgaacgca gtgcagactg tggtccgcca gggtgagaac 1920

atcaccctca tgtgcattgt gatcgggaat gaggtggtca acttcgagtg gacatacccc 1980

cgcaaagaaa gtgggcggct ggtggagccg gtgactgact tcctcttgga tatgccttac 2040

cacatccgct ccatcctgca catccccagt gccgagttag aagactcggg gacctacacc 2100

tgcaatgtga cggagagtgt gaatgaccat caggatgaaa aggccatcaa catcaccgtg 2160

gttgagagcg gctacgtgcg gctcctggga gaggtgggca cactacaatt tgctgag 2217

<210> 38
<211> 739
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Protein 1 sequence

<400> 38

Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu Ile
1 5 10 15

Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val Thr
20 25 30

Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu
35 40 45

Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile
50 55 60

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

Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln
85 90 95

Thr Asn Thr Ile Ile Asp Val Val Leu Ser Pro Ser His Gly Ile Glu
100 105 110

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Leu Ser Val Gly Glu Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu
        115                 120                 125

Leu Asn Val Gly Ile Asp Phe Asn Trp Glu Tyr Pro Ser Ser Lys His
    130                 135                 140

Gln His Lys Lys Leu Val Asn Arg Asp Leu Lys Thr Gln Ser Gly Ser
145                 150                 155                 160

Glu Met Lys Lys Phe Leu Ser Thr Leu Thr Ile Asp Gly Val Thr Arg
                165                 170                 175

Ser Asp Gln Gly Leu Tyr Thr Cys Ala Ala Ser Ser Gly Leu Met Thr
            180                 185                 190

Lys Lys Asn Ser Thr Phe Val Arg Val His Glu Lys Asp Lys Thr His
        195                 200                 205

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
    210                 215                 220

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
225                 230                 235                 240

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

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
            260                 265                 270

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
        275                 280                 285

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
    290                 295                 300

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
305                 310                 315                 320

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
                325                 330                 335

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
            340                 345                 350

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

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
    370                 375                 380
```

```
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
385                 390                 395                 400

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
                405                 410                 415

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly
            420                 425                 430

Gly Gly Gly Gly Gly Ser Gly Ser Gln Gly Leu Val Val Thr Pro Pro
        435                 440                 445

Gly Pro Glu Leu Val Leu Asn Val Ser Ser Thr Phe Val Leu Thr Cys
    450                 455                 460

Ser Gly Ser Ala Pro Val Val Trp Glu Arg Met Ser Gln Glu Pro Pro
465                 470                 475                 480

Gln Glu Met Ala Lys Ala Gln Asp Gly Thr Phe Ser Ser Val Leu Thr
                485                 490                 495

Leu Thr Asn Leu Thr Gly Leu Asp Thr Gly Glu Tyr Phe Cys Thr His
            500                 505                 510

Asn Asp Ser Arg Gly Leu Glu Thr Asp Glu Arg Lys Arg Leu Tyr Ile
        515                 520                 525

Phe Val Pro Asp Pro Thr Val Gly Phe Leu Pro Asn Asp Ala Glu Glu
    530                 535                 540

Leu Phe Ile Phe Leu Thr Glu Ile Thr Glu Ile Thr Ile Pro Cys Arg
545                 550                 555                 560

Val Thr Asp Pro Gln Leu Val Val Thr Leu His Glu Lys Lys Gly Asp
                565                 570                 575

Val Ala Leu Pro Val Pro Tyr Asp His Gln Arg Gly Phe Phe Gly Ile
            580                 585                 590

Phe Glu Asp Arg Ser Tyr Ile Cys Lys Thr Thr Ile Gly Asp Arg Glu
        595                 600                 605

Val Asp Ser Asp Ala Tyr Tyr Val Tyr Arg Leu Gln Val Ser Ser Ile
    610                 615                 620

Asn Val Ser Val Asn Ala Val Gln Thr Val Val Arg Gln Gly Glu Asn
625                 630                 635                 640

Ile Thr Leu Met Cys Ile Val Ile Gly Asn Glu Val Val Asn Phe Glu
                645                 650                 655
```

Trp Thr Tyr Pro Arg Lys Glu Ser Gly Arg Leu Val Glu Pro Val Thr
660 665 670

Asp Phe Leu Leu Asp Met Pro Tyr His Ile Arg Ser Ile Leu His Ile
675 680 685

Pro Ser Ala Glu Leu Glu Asp Ser Gly Thr Tyr Thr Cys Asn Val Thr
690 695 700

Glu Ser Val Asn Asp His Gln Asp Glu Lys Ala Ile Asn Ile Thr Val
705 710 715 720

Val Glu Ser Gly Tyr Val Arg Leu Leu Gly Glu Val Gly Thr Leu Gln
725 730 735

Phe Ala Glu

<210> 39
<211> 2250
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence of Fusion Protein 2 sequence

<400> 39
cagggcctgg tcgtcacacc cccggggcca gagcttgtcc tcaatgtctc cagcaccttc 60

gttctgacct gctcgggttc agctccggtg gtgtgggaac ggatgtccca ggagccccca 120

caggaaatgg ccaaggccca ggatggcacc ttctccagcg tgctcacact gaccaacctc 180

actgggctag acacgggaga atacttttgc acccacaatg actcccgtgg actggagacc 240

gatgagcgga aacggctcta catctttgtg ccagatccca ccgtgggctt cctccctaat 300

gatgccgagg aactattcat ctttctcacg gaaataactg agatcaccat tccatgccga 360

gtaacagacc cacagctggt ggtgacactg cacgagaaga aaggggacgt tgcactgcct 420

gtcccctatg atcaccaacg tggctttttt ggtatctttg aggacagaag ctacatctgc 480

aaaaccacca ttggggacag ggaggtggat tctgatgcct actatgtcta cagactccag 540

gtgtcatcca tcaacgtctc tgtgaacgca gtgcagactg tggtccgcca gggtgagaac 600

atcaccctca tgtgcattgt gatcgggaat gaggtggtca acttcgagtg gacatacccc 660

cgcaaagaaa gtgggcggct ggtggagccg gtgactgact tcctcttgga tatgccttac 720

cacatccgct ccatcctgca catccccagt gccgagttag aagactcggg gacctacacc 780

tgcaatgtga cggagagtgt gaatgaccat caggatgaaa aggccatcaa catcaccgtg 840

gttgagagcg gctacgtgcg gctcctggga gaggtgggca cactacaatt tgctgaggct 900

agcgacaaaa ctcacacatg tccaccgtgt ccagcacctg aactcctggg tggaccgtca 960

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 1020

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 1080

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 1140

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 1200

aagtgcaagg tctccaacaa agccctccca gcccccatcg agaaaaccat ctccaaagcc 1260

aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1320

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1380

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1440

tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 1500

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1560

agcctctccc tgtctccggg taaaggtgga ggaggcggtg gatctggtgg cggtggaagc 1620

ggaggtggag gttccggaga cactggtaga ccttttgttg aaatgtattc tgaaattcct 1680

gaaattattc atatgactga aggaagagaa cttgttattc cttgtagagt tacttctcct 1740

aatattactg ttactcttaa gaagtttcct cttgatactc ttattcctga tggaaagaga 1800

attatttggg attctagaaa gggatttatt atttctaatg ctacttataa ggaaattgga 1860

cttcttactt gtgaagctac tgttaatgga catctttata agactaatta tcttactcat 1920

agacaaacta ataccatcat cgacgtggtt ctgagtccgt ctcatggaat tgaactatct 1980

gttggagaaa agcttgtctt aaattgtaca gcaagaactg aactaaatgt ggggattgac 2040

ttcaactggg aataccttc ttcgaagcat cagcataaga aacttgtaaa ccgagaccta 2100

aaaacccagt ctgggagtga gatgaagaaa ttcttgagca ccctgactat agatggtgta 2160

acccggagtg accaaggatt gtacacctgt gcagcatcca gtgggctgat gaccaagaag 2220

aacagcacat ttgtcagggt ccatgaaaaa 2250

<210> 40
<211> 750
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Protein 2 sequence

<400> 40

Gln Gly Leu Val Val Thr Pro Pro Gly Pro Glu Leu Val Leu Asn Val
1 5 10 15

Ser Ser Thr Phe Val Leu Thr Cys Ser Gly Ser Ala Pro Val Val Trp
20 25 30

Glu Arg Met Ser Gln Glu Pro Pro Gln Glu Met Ala Lys Ala Gln Asp
35 40 45

Gly Thr Phe Ser Ser Val Leu Thr Leu Thr Asn Leu Thr Gly Leu Asp
50 55 60

```
Thr Gly Glu Tyr Phe Cys Thr His Asn Asp Ser Arg Gly Leu Glu Thr
65                  70                  75                  80

Asp Glu Arg Lys Arg Leu Tyr Ile Phe Val Pro Asp Pro Thr Val Gly
                85                  90                  95

Phe Leu Pro Asn Asp Ala Glu Glu Leu Phe Ile Phe Leu Thr Glu Ile
            100                 105                 110

Thr Glu Ile Thr Ile Pro Cys Arg Val Thr Asp Pro Gln Leu Val Val
        115                 120                 125

Thr Leu His Glu Lys Lys Gly Asp Val Ala Leu Pro Val Pro Tyr Asp
    130                 135                 140

His Gln Arg Gly Phe Phe Gly Ile Phe Glu Asp Arg Ser Tyr Ile Cys
145                 150                 155                 160

Lys Thr Thr Ile Gly Asp Arg Glu Val Asp Ser Asp Ala Tyr Tyr Val
                165                 170                 175

Tyr Arg Leu Gln Val Ser Ser Ile Asn Val Ser Val Asn Ala Val Gln
            180                 185                 190

Thr Val Val Arg Gln Gly Glu Asn Ile Thr Leu Met Cys Ile Val Ile
        195                 200                 205

Gly Asn Glu Val Val Asn Phe Glu Trp Thr Tyr Pro Arg Lys Glu Ser
    210                 215                 220

Gly Arg Leu Val Glu Pro Val Thr Asp Phe Leu Leu Asp Met Pro Tyr
225                 230                 235                 240

His Ile Arg Ser Ile Leu His Ile Pro Ser Ala Glu Leu Glu Asp Ser
                245                 250                 255

Gly Thr Tyr Thr Cys Asn Val Thr Glu Ser Val Asn Asp His Gln Asp
            260                 265                 270

Glu Lys Ala Ile Asn Ile Thr Val Val Glu Ser Gly Tyr Val Arg Leu
        275                 280                 285

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

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
305                 310                 315                 320

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                325                 330                 335
```

```
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            340                 345                 350

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        355                 360                 365

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

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
385                 390                 395                 400

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
                405                 410                 415

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

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
        435                 440                 445

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    450                 455                 460

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
465                 470                 475                 480

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                485                 490                 495

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            500                 505                 510

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        515                 520                 525

Gly Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    530                 535                 540

Ser Gly Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro
545                 550                 555                 560

Glu Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg
                565                 570                 575

Val Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp
            580                 585                 590

Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly
        595                 600                 605
```

Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys
610 615 620

Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His
625 630 635 640

Arg Gln Thr Asn Thr Ile Ile Asp Val Val Leu Ser Pro Ser His Gly
645 650 655

Ile Glu Leu Ser Val Gly Glu Lys Leu Val Leu Asn Cys Thr Ala Arg
660 665 670

Thr Glu Leu Asn Val Gly Ile Asp Phe Asn Trp Glu Tyr Pro Ser Ser
675 680 685

Lys His Gln His Lys Lys Leu Val Asn Arg Asp Leu Lys Thr Gln Ser
690 695 700

Gly Ser Glu Met Lys Lys Phe Leu Ser Thr Leu Thr Ile Asp Gly Val
705 710 715 720

Thr Arg Ser Asp Gln Gly Leu Tyr Thr Cys Ala Ala Ser Ser Gly Leu
725 730 735

Met Thr Lys Lys Asn Ser Thr Phe Val Arg Val His Glu Lys
740 745 750

<210> 41
<211> 2301
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence of Fusion Protein 6 sequence

<400> 41
atggagtttg gcctgtcctg gctcttcctc gtggctatcc tgaagggcgt gcagtgtctg 60

gtcgtgacac ctcccggacc cgagctggtg ctcaacgtct cctccacctt tgtgctgaca 120

tgcagcggca gcgctcctgt ggtctgggaa cggatgtccc aggagcctcc ccaggaaatg 180

gccaaggccc aggacggcac cttttccagc gtcctcacac tcaccaacct gacaggcctg 240

gacaccggcg agtacttttg cacccacaat gactccaggg gactggaaac cgatgagcgg 300

aagcggctct acattttcgt ccccgacccc accgtcggat ttctgcctaa tgacgctgaa 360

gagctgttta tcttcctgac agagatcacc gaaatcacca tcccctgtcg ggtcaccgat 420

ccccagctgg tggtcacact gcacgagaag aagggagatg tcgccctgcc tgtgccttat 480

gaccatcaga ggggcttttc cggcattttc gaggacagga gctacatctg caaaaccacc 540

atcggagacc gggaggtcga cagcgatgcc tattacgtct accggctcca ggtctcctcc 600

atcaatgtga gcgtgaatgc tgtccagaca gtggtccggc agggcgagaa tatcacactg 660

atgtgcattg tcattggcaa cgaggtggtc aacttcgagt ggacctatcc taggaaggag 720

agcggccggc tcgtcgaacc tgtgaccgac ttcctcctgg acatgcctta ccacattcgg 780

tccatcctgc acattcctag cgccgagctg gaggacagcg gaacctacac ctgcaacgtg 840

accgagtccg tgaatgacca ccaggatgag aaggccatca acatcacagt cgtggagagc 900

ggatacgtca ggctgctcgg agaagtcggc acactgcagt tcgccgaggc cagcgataag 960

acccacacct gtcctccttg tcctgctcct gagctcctcg gcggacctag cgtgttcctg 1020

tttcccccta agcctaaaga caccctcatg atcagccgga cccccgaggt cacatgcgtg 1080

gtggtcgacg tctcccatga ggatcccgag gtgaagttca attggtacgt cgacggcgtc 1140

gaggtccaca atgccaaaac caaaccccgg gaggagcagt acaacagcac ctatagggtg 1200

gtcagcgtcc tgaccgtgct gcaccaagac tggctgaacg gcaaggagta caaatgcaaa 1260

gtcagcaata aggccctccc cgcccccatt gagaagacca tctccaaggc taagggccaa 1320

cctagggagc cccaggtgta caccctgcct cccagccggg atgagctgac aaagaaccag 1380

gtgagcctca cctgtctggt gaagggcttt tacccctccg atattgccgt ggagtgggaa 1440

agcaacggac agcctgagaa caactacaag acaacccccc ctgtcctgga cagcgatggc 1500

tccttcttcc tgtacagcaa gctgacagtg gataagagcc ggtggcagca gggaaacgtc 1560

tttagctgca gcgtgatgca tgaggccctg cacaatcact acacccagaa gtccctgtcc 1620

ctgagccctg gcggaggcgg cggcggcggc agcggcggag gcggatccgg cggaggcggc 1680

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accctcaaga agttcccccc ggacaccctg atccctgacg gcaaaaggat tatctgggac 1860

agccggaagg gctttatcat cagcaatgcc acatacaagg agattggact cctgacctgc 1920

gaggctacag tcaacggaca cctgtacaag accaactacc tgacccaccg gcagaccaat 1980

accatcatcg acgtggtgct gagccccagc cacggaattg agctgagcgt gggagaaaaa 2040

ctcgtgctca actgcacagc ccggaccgaa ctcaatgtcg gaatcgactt caactgggaa 2100

taccccagct ccaagcacca gcacaagaag ctggtcaacc gggatctcaa gacccagtcc 2160

ggcagcgaaa tgaagaagtt cctcagcacc ctgaccatcg atggcgtcac aaggagcgat 2220

cagggactct acacctgcgc cgctagctcc ggactcatga ccaagaagaa ctccacattt 2280

gtccgggtgc acgaaaagtg a 2301

<210> 42
<211> 766
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Protein 6 sequence

<400> 42

Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly

```
1               5                  10                  15

Val Gln Cys Leu Val Val Thr Pro Pro Gly Pro Glu Leu Val Leu Asn
            20                  25                  30

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

Trp Glu Arg Met Ser Gln Glu Pro Pro Gln Glu Met Ala Lys Ala Gln
    50                  55                  60

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

Asp Thr Gly Glu Tyr Phe Cys Thr His Asn Asp Ser Arg Gly Leu Glu
                85                  90                  95

Thr Asp Glu Arg Lys Arg Leu Tyr Ile Phe Val Pro Asp Pro Thr Val
            100                 105                 110

Gly Phe Leu Pro Asn Asp Ala Glu Glu Leu Phe Ile Phe Leu Thr Glu
        115                 120                 125

Ile Thr Glu Ile Thr Ile Pro Cys Arg Val Thr Asp Pro Gln Leu Val
    130                 135                 140

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

Asp His Gln Arg Gly Phe Ser Gly Ile Phe Glu Asp Arg Ser Tyr Ile
                165                 170                 175

Cys Lys Thr Thr Ile Gly Asp Arg Glu Val Asp Ser Asp Ala Tyr Tyr
            180                 185                 190

Val Tyr Arg Leu Gln Val Ser Ser Ile Asn Val Ser Val Asn Ala Val
        195                 200                 205

Gln Thr Val Val Arg Gln Gly Glu Asn Ile Thr Leu Met Cys Ile Val
    210                 215                 220

Ile Gly Asn Glu Val Val Asn Phe Glu Trp Thr Tyr Pro Arg Lys Glu
225                 230                 235                 240

Ser Gly Arg Leu Val Glu Pro Val Thr Asp Phe Leu Leu Asp Met Pro
                245                 250                 255

Tyr His Ile Arg Ser Ile Leu His Ile Pro Ser Ala Glu Leu Glu Asp
            260                 265                 270

Ser Gly Thr Tyr Thr Cys Asn Val Thr Glu Ser Val Asn Asp His Gln
```

275 280 285

Asp Glu Lys Ala Ile Asn Ile Thr Val Val Glu Ser Gly Tyr Val Arg
290 295 300

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

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
325 330 335

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
340 345 350

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
355 360 365

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
370 375 380

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
385 390 395 400

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
405 410 415

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
420 425 430

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
435 440 445

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
450 455 460

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
465 470 475 480

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
485 490 495

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
500 505 510

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
515 520 525

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
530 535 540

Gly Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

545 550 555 560

Ser Gly Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro
565 570 575

Glu Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg
580 585 590

Val Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp
595 600 605

Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly
610 615 620

Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys
625 630 635 640

Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His
645 650 655

Arg Gln Thr Asn Thr Ile Ile Asp Val Val Leu Ser Pro Ser His Gly
660 665 670

Ile Glu Leu Ser Val Gly Glu Lys Leu Val Leu Asn Cys Thr Ala Arg
675 680 685

Thr Glu Leu Asn Val Gly Ile Asp Phe Asn Trp Glu Tyr Pro Ser Ser
690 695 700

Lys His Gln His Lys Lys Leu Val Asn Arg Asp Leu Lys Thr Gln Ser
705 710 715 720

Gly Ser Glu Met Lys Lys Phe Leu Ser Thr Leu Thr Ile Asp Gly Val
725 730 735

Thr Arg Ser Asp Gln Gly Leu Tyr Thr Cys Ala Ala Ser Ser Gly Leu
740 745 750

Met Thr Lys Lys Asn Ser Thr Phe Val Arg Val His Glu Lys
755 760 765

<210> 43
<211> 2307
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence of Fusion Proteins 3 and 4 sequence

<400> 43
atggagacag acacactcct gctatgggta ctgcttcttt gggttcccgg atccactggc 60

cagggcctgg tcgtcacacc cccggggcca gagcttgtcc tcaatgtctc cagcaccttc 120

gttctgacct gctcgggttc agctccggtg gtgtgggaac ggatgtccca ggagccccca 180

caggaaatgg ccaaggccca ggatggcacc ttctccagcg tgctcacact gaccaacctc 240

actgggctag acacgggaga atacttttgc acccacaatg actcccgtgg actggagacc 300

gatgagcgga aacggctcta catctttgtg ccagatccca ccgtgggctt cctccctaat 360

gatgccgagg aactattcat ctttctcacg gaaataactg agatcaccat tccatgccga 420

gtaacagacc cacagctggt ggtgacactg cacgagaaga aaggggacgt tgcactgcct 480

gtcccctatg atcaccaacg tggcttttcc ggtatctttg aggacagaag ctacatctgc 540

aaaaccacca ttggggacag ggaggtggat tctgatgcct actatgtcta cagactccag 600

gtgtcatcca tcaacgtctc tgtgaacgca gtgcagactg tggtccgcca gggtgagaac 660

atcaccctca tgtgcattgt gatcgggaat gaggtggtca acttcgagtg gacatacccc 720

cgcaaagaaa gtgggcggct ggtggagccg gtgactgact tcctcttgga tatgccttac 780

cacatccgct ccatcctgca catccccagt gccgagttag aagactcggg gacctacacc 840

tgcaatgtga cggagagtgt gaatgaccat caggatgaaa aggccatcaa catcaccgtg 900

gttgagagcg gctacgtgcg gctcctggga gaggtgggca cactacaatt tgctgaggct 960

agcgacaaaa ctcacacatg tccaccgtgt ccagcacctg aactcctggg tggaccgtca 1020

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 1080

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 1140

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 1200

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 1260

aagtgcaagg tctccaacaa agccctccca gcccccatcg agaaaaccat ctccaaagcc 1320

aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1380

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1440

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1500

tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 1560

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1620

agcctctccc tgtctccggg tggtggagga ggcggtggat ctggtggcgg tggaagcgga 1680

ggtggaggtt ccggagacac tggtagacct tttgttgaaa tgtattctga aattcctgaa 1740

attattcata tgactgaagg aagagaactt gttattcctt gtagagttac ttctcctaat 1800

attactgtta ctcttaagaa gtttcctctt gatactctta ttcctgatgg aaagagaatt 1860

atttgggatt ctagaaaggg atttattatt tctaatgcta cttataagga aattggactt 1920

cttacttgtg aagctactgt taatggacat ctttataaga ctaattatct tactcataga 1980

caaactaata ccatcatcga cgtggttctg agtccgtctc atggaattga actatctgtt 2040

ggagaaaagc ttgtcttaaa ttgtacagca agaactgaac taaatgtggg gattgacttc 2100

aactgggaat acccttcttc gaagcatcag cataagaaac ttgtaaaccg agacctaaaa 2160

acccagtctg ggagtgagat gaagaaattc ttgagcaccc tgactataga tggtgtaacc 2220

cggagtgacc aaggattgta cacctgtgca gcatccagtg ggctgatgac caagaagaac 2280

agcacatttg tcagggtcca tgaaaaa 2307

<210> 44
<211> 769
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion Protein 3 or 4 plus a signal peptide sequence

<400> 44

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

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

Val Leu Asn Val Ser Ser Thr Phe Val Leu Thr Cys Ser Gly Ser Ala
35 40 45

Pro Val Val Trp Glu Arg Met Ser Gln Glu Pro Pro Gln Glu Met Ala
50 55 60

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

Thr Gly Leu Asp Thr Gly Glu Tyr Phe Cys Thr His Asn Asp Ser Arg
85 90 95

Gly Leu Glu Thr Asp Glu Arg Lys Arg Leu Tyr Ile Phe Val Pro Asp
100 105 110

Pro Thr Val Gly Phe Leu Pro Asn Asp Ala Glu Glu Leu Phe Ile Phe
115 120 125

Leu Thr Glu Ile Thr Glu Ile Thr Ile Pro Cys Arg Val Thr Asp Pro
130 135 140

Gln Leu Val Val Thr Leu His Glu Lys Lys Gly Asp Val Ala Leu Pro
145 150 155 160

Val Pro Tyr Asp His Gln Arg Gly Phe Ser Gly Ile Phe Glu Asp Arg
165 170 175

Ser Tyr Ile Cys Lys Thr Thr Ile Gly Asp Arg Glu Val Asp Ser Asp
180 185 190

Ala Tyr Tyr Val Tyr Arg Leu Gln Val Ser Ser Ile Asn Val Ser Val
195 200 205

```
Asn Ala Val Gln Thr Val Val Arg Gln Gly Glu Asn Ile Thr Leu Met
    210                 215                 220

Cys Ile Val Ile Gly Asn Glu Val Val Asn Phe Glu Trp Thr Tyr Pro
225                 230                 235                 240

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

Asp Met Pro Tyr His Ile Arg Ser Ile Leu His Ile Pro Ser Ala Glu
            260                 265                 270

Leu Glu Asp Ser Gly Thr Tyr Thr Cys Asn Val Thr Glu Ser Val Asn
        275                 280                 285

Asp His Gln Asp Glu Lys Ala Ile Asn Ile Thr Val Val Glu Ser Gly
    290                 295                 300

Tyr Val Arg Leu Leu Gly Glu Val Gly Thr Leu Gln Phe Ala Glu Ala
305                 310                 315                 320

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
                325                 330                 335

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            340                 345                 350

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        355                 360                 365

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    370                 375                 380

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
385                 390                 395                 400

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                405                 410                 415

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            420                 425                 430

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        435                 440                 445

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    450                 455                 460

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
465                 470                 475                 480
```

```
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                485                 490                 495

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            500                 505                 510

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        515                 520                 525

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    530                 535                 540

Ser Pro Gly Gly Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
545                 550                 555                 560

Gly Gly Gly Ser Gly Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser
                565                 570                 575

Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile
            580                 585                 590

Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe
        595                 600                 605

Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser
    610                 615                 620

Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu
625                 630                 635                 640

Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr
                645                 650                 655

Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Val Leu Ser Pro
            660                 665                 670

Ser His Gly Ile Glu Leu Ser Val Gly Glu Lys Leu Val Leu Asn Cys
        675                 680                 685

Thr Ala Arg Thr Glu Leu Asn Val Gly Ile Asp Phe Asn Trp Glu Tyr
    690                 695                 700

Pro Ser Ser Lys His Gln His Lys Lys Leu Val Asn Arg Asp Leu Lys
705                 710                 715                 720

Thr Gln Ser Gly Ser Glu Met Lys Lys Phe Leu Ser Thr Leu Thr Ile
                725                 730                 735

Asp Gly Val Thr Arg Ser Asp Gln Gly Leu Tyr Thr Cys Ala Ala Ser
            740                 745                 750
```

Ser Gly Leu Met Thr Lys Lys Asn Ser Thr Phe Val Arg Val His Glu
755 760 765

Lys

<210> 45
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence of VEGF Trap sequence

<400> 45
atggagacag acacactcct gctatgggta ctgctgctct gggttccagg gtcgactggc 60

gacactggaa gacctttgt tgaaatgtat tctgaaattc ctgaaattat tcatatgact 120

gaaggaagag aacttgttat tccttgtaga gttacttctc ctaatattac tgttactctt 180

aagaagtttc ctcttgatac tcttattcct gatggaaaga gaattatttg ggattctaga 240

aagggattta ttatttctaa tgctacttat aaggaaattg gacttcttac ttgtgaagct 300

actgttaatg gacatcttta taagactaat tatcttactc atagacaaac taataccatc 360

atcgacgtgg ttctgagtcc gtctcatgga attgaactat ctgttggaga aaagcttgtc 420

ttaaattgta cagcaagaac tgaactaaat gtggggattg acttcaactg ggaataccct 480

tcttcgaagc atcagcataa gaaacttgta aaccgagacc taaaaaccca gtctgggagt 540

gagatgaaga aattcttgag caccctgact atagatggtg taacccggag tgaccaagga 600

ttgtacacct gtgcagcatc cagtgggctg atgaccaaga agaacagcac atttgtcagg 660

gtccatgaaa aagacaaaac tcacacatgt ccaccgtgtc cagcacctga actcctgggt 720

ggaccgtcag tcttcctctt ccccccaaaa cccaaggaca ccctcatgat ctcccggacc 780

cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac 840

tggtacgtgg acggcgtgga ggtgcataat gccaagacaa agccgcggga ggagcagtac 900

aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc 960

aaggagtaca agtgcaaggt ctccaacaaa gccctcccag cccccatcga gaaaaccatc 1020

tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgccccc atcccgggat 1080

gagctgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1140

atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cacgcctccc 1200

gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg 1260

tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac 1320

acgcagaaga gcctctccct gtctccgggt aaa 1353

<210> 46
<211> 451
<212> PRT

<213> Artificial Sequence

<220>
<223> VEGF Trap sequence Plus a signal sequence

<400> 46

```
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1               5                  10                  15

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

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

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

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

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

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

Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Val Leu Ser Pro Ser
        115                 120                 125

His Gly Ile Glu Leu Ser Val Gly Glu Lys Leu Val Leu Asn Cys Thr
    130                 135                 140

Ala Arg Thr Glu Leu Asn Val Gly Ile Asp Phe Asn Trp Glu Tyr Pro
145                 150                 155                 160

Ser Ser Lys His Gln His Lys Lys Leu Val Asn Arg Asp Leu Lys Thr
                165                 170                 175

Gln Ser Gly Ser Glu Met Lys Lys Phe Leu Ser Thr Leu Thr Ile Asp
            180                 185                 190

Gly Val Thr Arg Ser Asp Gln Gly Leu Tyr Thr Cys Ala Ala Ser Ser
        195                 200                 205

Gly Leu Met Thr Lys Lys Asn Ser Thr Phe Val Arg Val His Glu Lys
    210                 215                 220

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

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
```

245 250 255

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

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

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

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

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

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

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

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

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

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

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

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

Pro Gly Lys
450

<210> 47
<211> 1644
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence of PDGF Trap sequence

<400> 47
atggagacag acacactcct gctatgggta ctgcttcttt gggttcccgg atccactggc 60

cagggcctgg tcgtcacacc cccggggcca gagcttgtcc tcaatgtctc cagcaccttc 120

gttctgacct gctcgggttc agctccggtg gtgtgggaac ggatgtccca ggagccccca 180

caggaaatgg ccaaggccca ggatggcacc ttctccagcg tgctcacact gaccaacctc 240

actgggctag acacgggaga atacttttgc acccacaatg actcccgtgg actggagacc 300

gatgagcgga aacggctcta catctttgtg ccagatccca ccgtgggctt cctccctaat 360

gatgccgagg aactattcat ctttctcacg gaaataactg agatcaccat tccatgccga 420

gtaacagacc cacagctggt ggtgacactg cacgagaaga aaggggacgt tgcactgcct 480

gtcccctatg atcaccaacg tggctttttt ggtatctttg aggacagaag ctacatctgc 540

aaaaccacca ttggggacag ggaggtggat tctgatgcct actatgtcta cagactccag 600

gtgtcatcca tcaacgtctc tgtgaacgca gtgcagactg tggtccgcca gggtgagaac 660

atcaccctca tgtgcattgt gatcgggaat gaggtggtca acttcgagtg gacatacccc 720

cgcaaagaaa gtgggcggct ggtggagccg gtgactgact tcctcttgga tatgccttac 780

cacatccgct ccatcctgca catccccagt gccgagttag aagactcggg gacctacacc 840

tgcaatgtga cggagagtgt gaatgaccat caggatgaaa aggccatcaa catcaccgtg 900

gttgagagcg gctacgtgcg gctcctggga gaggtgggca cactacaatt tgctgaggct 960

agcgacaaaa ctcacacatg tccaccgtgt ccagcacctg aactcctggg tggaccgtca 1020

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 1080

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 1140

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 1200

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 1260

aagtgcaagg tctccaacaa agccctccca gcccccatcg agaaaaccat ctccaaagcc 1320

aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1380

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1440

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1500

tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 1560

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1620

agcctctccc tgtctccggg taaa 1644

<210> 48
<211> 548
<212> PRT
<213> Artificial Sequence

<220>
<223> PDGF Trap sequence plus a signal sequence

<400> 48

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Gln Gly Leu Val Val Thr Pro Pro Gly Pro Glu Leu

```
            20                  25                  30

Val Leu Asn Val Ser Ser Thr Phe Val Leu Thr Cys Ser Gly Ser Ala
        35                  40                  45

Pro Val Val Trp Glu Arg Met Ser Gln Glu Pro Pro Gln Glu Met Ala
    50                  55                  60

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

Thr Gly Leu Asp Thr Gly Glu Tyr Phe Cys Thr His Asn Asp Ser Arg
                85                  90                  95

Gly Leu Glu Thr Asp Glu Arg Lys Arg Leu Tyr Ile Phe Val Pro Asp
            100                 105                 110

Pro Thr Val Gly Phe Leu Pro Asn Asp Ala Glu Glu Leu Phe Ile Phe
        115                 120                 125

Leu Thr Glu Ile Thr Glu Ile Thr Ile Pro Cys Arg Val Thr Asp Pro
    130                 135                 140

Gln Leu Val Val Thr Leu His Glu Lys Lys Gly Asp Val Ala Leu Pro
145                 150                 155                 160

Val Pro Tyr Asp His Gln Arg Gly Phe Phe Gly Ile Phe Glu Asp Arg
                165                 170                 175

Ser Tyr Ile Cys Lys Thr Thr Ile Gly Asp Arg Glu Val Asp Ser Asp
            180                 185                 190

Ala Tyr Tyr Val Tyr Arg Leu Gln Val Ser Ser Ile Asn Val Ser Val
        195                 200                 205

Asn Ala Val Gln Thr Val Val Arg Gln Gly Glu Asn Ile Thr Leu Met
    210                 215                 220

Cys Ile Val Ile Gly Asn Glu Val Val Asn Phe Glu Trp Thr Tyr Pro
225                 230                 235                 240

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

Asp Met Pro Tyr His Ile Arg Ser Ile Leu His Ile Pro Ser Ala Glu
            260                 265                 270

Leu Glu Asp Ser Gly Thr Tyr Thr Cys Asn Val Thr Glu Ser Val Asn
        275                 280                 285

Asp His Gln Asp Glu Lys Ala Ile Asn Ile Thr Val Val Glu Ser Gly
```

290 295 300

Tyr Val Arg Leu Leu Gly Glu Val Gly Thr Leu Gln Phe Ala Glu Ala
305 310 315 320

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
325 330 335

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
340 345 350

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
355 360 365

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
370 375 380

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
385 390 395 400

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
405 410 415

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
420 425 430

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
435 440 445

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
450 455 460

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
465 470 475 480

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
485 490 495

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
500 505 510

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
515 520 525

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
530 535 540

Ser Pro Gly Lys
545

<210> 49

<211> 2250
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence of Fusion Protein 5 sequence

<400> 49
cagggcctgg tcgtgacacc tcccggaccc gagctggtgc tcaacgtctc ctccaccttt 60

gtgctgacat gcagcggcag cgctcctgtg gtctgggaac ggatgtccca ggagcctccc 120

caggaaatgg ccaaggccca ggacggcacc ttttccagcg tcctcacact caccaacctg 180

acaggcctgg acaccggcga gtacttttgc acccacaatg actccagggg actggaaacc 240

gatgagcgga agcggctcta cattttcgtc cccgacccca ccgtcggatt tctgcctaat 300

gacgctgaag agctgtttat cttcctgaca gagatcaccg aaatcaccat cccctgtcgg 360

gtcaccgatc cccagctggt ggtcacactg cacgagaaga agggagatgt cgccctgcct 420

gtgccttatg accatcagag gggcttttcc ggcattttcg aggacaggag ctacatctgc 480

aaaaccacca tcggagaccg ggaggtcgac agcgatgcct attacgtcta ccggctccag 540

gtctcctcca tcaatgtgag cgtgaatgct gtccagacag tggtccggca gggcgagaat 600

atcacactga tgtgcattgt cattggcaac gaggtggtca acttcgagtg gacctatcct 660

aggaaggaga gcggccggct cgtcgaacct gtgaccgact tcctcctgga catgccttac 720

cacattcggt ccatcctgca cattcctagc gccgagctgg aggacagcgg aacctacacc 780

tgcaacgtga ccgagtccgt gaatgaccac caggatgaga aggccatcaa catcacagtc 840

gtggagagcg gatacgtcag gctgctcgga gaagtcggca cactgcagtt cgccgaggcc 900

agcgataaga cccacacctg tcctccttgt cctgctcctg agctcctcgg cggacctagc 960

gtgttcctgt ttcccccctaa gcctaaagac accctcatga tcagccggac ccccgaggtc 1020

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gacggcgtcg aggtccacaa tgccaaaacc aaaccccggg aggagcagta caacagcacc 1140

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

Val Val Trp Glu Arg Met Ser Gln Glu Pro Pro Gln Glu Met Ala Lys
50 55 60

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

Gly Leu Asp Thr Gly Glu Tyr Phe Cys Thr His Asn Asp Ser Arg Gly
85 90 95

Leu Glu Thr Asp Glu Arg Lys Arg Leu Tyr Ile Phe Val Pro Asp Pro
100 105 110

Thr Val Gly Phe Leu Pro Asn Asp Ala Glu Glu Leu Phe Ile Phe Leu
115 120 125

Thr Glu Ile Thr Glu Ile Thr Ile Pro Cys Arg Val Thr Asp Pro Gln
130 135 140

Leu Val Val Thr Leu His Glu Lys Lys Gly Asp Val Ala Leu Pro Val
145 150 155 160

Pro Tyr Asp His Gln Arg Gly Phe Ser Gly Ile Phe Glu Asp Arg Ser

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                165                 170                 175

Tyr Ile Cys Lys Thr Thr Ile Gly Asp Arg Glu Val Asp Ser Asp Ala
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Tyr Tyr Val Tyr Arg Leu Gln Val Ser Ser Ile Asn Val Ser Val Asn
        195                 200                 205

Ala Val Gln Thr Val Val Arg Gln Gly Glu Asn Ile Thr Leu Met Cys
    210                 215                 220

Ile Val Ile Gly Asn Glu Val Val Asn Phe Glu Trp Thr Tyr Pro Arg
225                 230                 235                 240

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

Met Pro Tyr His Ile Arg Ser Ile Leu His Ile Pro Ser Ala Glu Leu
            260                 265                 270

Glu Asp Ser Gly Thr Tyr Thr Cys Asn Val Thr Glu Ser Val Asn Asp
        275                 280                 285

His Gln Asp Glu Lys Ala Ile Asn Ile Thr Val Val Glu Ser Gly Tyr
    290                 295                 300

Val Arg Leu Leu Gly Glu Val Gly Thr Leu Gln Phe Ala Glu Ala Ser
305                 310                 315                 320

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
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Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            340                 345                 350

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
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Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    370                 375                 380

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
385                 390                 395                 400

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
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Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            420                 425                 430

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
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Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
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Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
465                 470                 475                 480

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                485                 490                 495

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            500                 505                 510

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        515                 520                 525

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
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Pro Gly Gly Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
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Gly Gly Ser Gly Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu
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Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro
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Cys Arg Val Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro
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Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg
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Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu
625                 630                 635                 640

Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu
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Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Val Leu Ser Pro Ser
            660                 665                 670

His Gly Ile Glu Leu Ser Val Gly Glu Lys Leu Val Leu Asn Cys Thr
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Ala Arg Thr Glu Leu Asn Val Gly Ile Asp Phe Asn Trp Glu Tyr Pro
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Ser Ser Lys His Gln His Lys Lys Leu Val Asn Arg Asp Leu Lys Thr
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Gln Ser Gly Ser Glu Met Lys Lys Phe Leu Ser Thr Leu Thr Ile Asp
725 730 735

Gly Val Thr Arg Ser Asp Gln Gly Leu Tyr Thr Cys Ala Ala Ser Ser
740 745 750

Gly Leu Met Thr Lys Lys Asn Ser Thr Phe Val Arg Val His Glu Lys
755 760 765